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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To obtain feedback and seek future directions for an ISDS initiative to establish and update research questions in Informatics, Analytics, Communications, and Systems Research with the greatest perceived impact for improving surveillance practice. Introduction Over the past fifteen years, syndromic surveillance (SyS) has evolved from a set of ad hoc methods used mostly in post-disaster settings, then expanded with broad support and development because of bioterrorism concerns, and subsequently evolved to a mature technology that runs continuously to detect and monitor a widerange of health issues. Continued enhancements needed to meet the challenges of novel health threats with increasingly complex information sources will require technical advances focused on day-to-day public health needs. Since its formation in 2005, the International Society for Disease Surveillance (ISDS) has sought to clarify and coordinate global priorities in surveillance research. As part of a practitioner-driven initiative to identify current research priorities in SyS, ISDS polled its members about capabilities needed by SyS practitioners that could be improved as a result of research efforts. A task force of the ISDS Research Committee, consisting of national and global subject matter experts (SMEs) in SyS and ISDS professional staff, carried out the project. This panel will discuss the results and the preferred means to determine and communicate priorities in the future.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
This roundtable will address how multiple data sources, including administrative and syndromic surveillance data, can enhance public health surveillance activities at the local, state, regional, and national levels. Provisional findings from three studies will be presented to promote discussion about the complementary uses, strengths and limitations, and value of these data sources to address public health priorities and surveillance strategies.

Introduction
Healthcare data, including emergency department (ED) and outpatient health visit data, are potentially useful to the public health community for multiple purposes, including programmatic and surveillance activities. These data are collected through several mechanisms, including administrative data sources [e.g., MarketScan claims data1; American Hospital Association (AHA) data2] and public health surveillance programs [e.g., the National Syndromic Surveillance Program (NSSP)3]. Administrative data typically become available months to years after healthcare encounters; however, data collected through NSSP provide near real time information not otherwise available to public health. To date, 46 state and 16 local health departments participate in NSSP, and the estimated national percentage of ED visits covered by the NSSP BioSense platform is 54%. NSSP’s new data visualization tool, ESSENCE, also includes additional types of healthcare visit (e.g., urgent care) data. Although NSSP is designed to support situational awareness and emergency response, potential expanded use of data collected through NSSP (i.e., by additional public health programs) would promote the utility, value, and long-term sustainability of NSSP and enhance surveillance at the local, state, regional, and national levels. On the other hand, studies using administrative data may help public health programs better understand how NSSP data could enhance their surveillance activities. Such studies could also inform the collection and utilization of data reported to NSSP.

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Abstract

Objective: The Department of Defense data is available to National Syndromic Surveillance Program (NSSP) users to conduct syndromic surveillance. This report summarizes the demographic characteristics of DoD health encounter visits. Introduction: The DoD provides daily outpatient and emergency room data feeds to the BioSense Platform within NSSP, maintained by the Centers for Disease Control and Prevention. This data includes demographic characteristics and diagnosis codes for health encounter visits of Military Health System beneficiaries, including active duty, activated family members, retirees, and retiree family members. NSSP functions through collaboration with local, state, and federal public health partners utilizing the BioSense Platform, an electronic health information system. Methods: DoD data was pulled from the BioSense Platform through an RStudio server on October 11, 2016, querying data from November 1, 2015 to September 30, 2016. Appointment type and beneficiary category data was not available in BioSense until November 1, 2015. Appointment type was categorized into clinic visits and telephone consults. Demographic characteristics (age group, gender, beneficiary category) are stratified by appointment type. Results: During the time period of November 1, 2015 to September 30, 2016, data were received from 452 clinics. There is a military treatment facility located in 45 states and a military treatment facility may have one to 12 clinics. There were a total of 86,840,632 healthcare encounter records. The age group, 25-44 years, accounted for 39.4% of the medical encounters; the mean age was 33.9 (SD=19.1). Males accounted for 55.6% of the medical encounters. For the time period from November 1, 2015 to September 30, 2016, 78.9% of medical encounters were clinic visits. The remaining medical encounters were telephone consults. Of the clinic visits, 53.7% of the medical encounters were for active duty personnel. Conclusions: This report highlights the DoD data available to NSSP users for collaborative syndromic surveillance efforts, promoting a community of practice. It is important to understand the population demographics and limitations to the DoD data when conducting syndromic surveillance.

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Abstract

ObjectiveTo describe how syndromic surveillance was enhanced to detect health events during the 9th Indian Ocean Island Games (IOIG) in Reunion Island.

IntroductionThe 9th IOIG took place in Reunion Island from July 31 to August 9, 2015. This sport event gathered approximately 1,640 athletes, 2,000 volunteers and several thousand spectators from seven islands: Comoros, Madagascar, Maldives, Mauritius, Mayotte, Seychelles and Reunion. In response to the import risk of infectious diseases from these countries where some of them are endemics, the syndromic surveillance system, which captures 100% of all Emergency Department visits, was enhanced in order to detect any health event.

MethodsIn Reunion Island, syndromic surveillance system is based on OSCOUR® network (Organisation de la surveillance coordonnées urgences) that collects data from all emergency departments of the island. Data are daily transmitted to the French national public health agency then are available to the regional office. At the regional level, data are integrated into an application that allows the build of predefined syndromic groups according to the health risks related to mass gatherings (Table 1, parts 1 to 3) and complemented by specific syndromic groups (table 1, part 4). Daily analyses with temporal [1] and spatial-temporal [2] algorithms were performed during the surveillance period of July 27 to August 13, 2015. In addition to this monitoring, ED physicians were requested to proactively tag Y33 (ICD-10) as secondary diagnosis, each ED visit related to IOIG. Line lists were reviewed daily. Each day, an epidemiological report was sent to public health authorities.

ResultsFrom July 31 to August 9, 2015, the activity of EDs was in accordance with that expected. No health events were detected by the syndromic surveillance system except for the syndrome “alcohol intoxication” for which consecutive signals were observed from August 6 to 9, 2015. This increase occurs commonly at the beginning of each month (due to the social benefits payday) [3] nevertheless this event has probably been increased by IOIG (finals for team sports and games closing ceremony). In total, 8 ED visits were tagged Y33 as secondary diagnosis. In over half the cases, visits were related to trauma.

ConclusionsThe syndromic surveillance system proved to be useful for the surveillance of mass gathering events due to its capacity to detect health events but also to provide reassurance to public health authorities [4]. As described in literature [5], few ED visits were tagged in relation to IOIG. Indeed, the tag of ED visits was implemented two weeks before the games, and given the shifts of ED physicians, some of them may have not been informed. In the future, preparation meetings with physicians will have to be planned several months before in order to improve the response rate for mass gathering events.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective 1. To assess the knowledge, perception, and practices of mothers/caregivers on vaccine preventable diseases in children aged 12-23 months in Kaduna State, Nigeria. 2. To determine the immunization coverages in Kaduna State, Nigeria. 3. To determine the sources of information on routine immunization among mothers/caregivers of children aged 12-23 months in the study area. Introduction Immunization is one of the safest and most effective interventions to prevent disease and early child death. Although, about three-quarters of the world’s child population is reached with the required vaccines, only half of the children in Sub-Saharan Africa get access to basic immunization. A substantial number of children worldwide do not complete immunization schedules because neither health services nor conventional communication mechanisms regularly reach their communities. Separate studies in Australia and Papua New Guinea have shown that knowledge gaps underlie low compliance with vaccination schedules. Mothers are less likely to complete immunization schedules if they are poorly informed about the need for immunization, logistics (which includes time, date, and place of vaccination), and the appropriate series of vaccines to be followed. Although knowledge in itself is insufficient to create demand, poor knowledge about the need for vaccination and when the next vaccination is due is a good indicator of poor compliance. Up-to-date, complete, and scientifically valid information about vaccines can help parents to make informed decisions. Immunity gap created by this low immunization coverage in Northern Nigeria favors the emergence and transmission of some vaccine preventable diseases (VPDs) especially measles and polio. Methods A cross-sectional descriptive study was conducted using multistage sampling technique; 379 mothers/caregivers with children aged 12-23 months were recruited. Data collection was done using semistructured interviewer-administered questionnaire and analyzed using Epi info TM version 7. Descriptive statistics using absolute numbers and proportions and Odds ratio/Chi2 were determined between variables and p≤0.05 was considered statistically significant. Multivariate analysis was conducted using logistic regression. Results Mean age of respondents was 28.6 (SD=±6.6), 245 (64.7%) practiced Islam, 128 (33.8%) completed Secondary school, 246 (64.9%) unemployed, 361 (92.3%) were married and 186 (49.1%) were from rural settlements. Among the children whose mothers/caregivers were interviewed, 163 (43.01%) were between aged 16-19 months old while most 238 (62.80%) fell within the birth order of 2nd -5th child. Only 59 (15.6%) of these children were found to be fully immunized, evidenced by vaccination card history. Majority of respondents 244 (64.4%) had unsatisfactory knowledge while 197 (55.4%) and 204 (54.0%) exhibited poor perception and bad practices respectively, regarding routine immunization. Commonest source of information was radio 69 (61.61%). Educational status [OR=1.9 (95% CI:1.1-3.3)] and good perception [OR=2.6 (95% CI:1.5-4.5)] of mothers were found to be associated with getting information on routine immunization within 12 months prior to this study while Polygamous family setting [OR=0.6 (95% CI:0.2-0.6)], unsatisfactory knowledge [OR=0.3 (95% CI:0.2-0.7)] and bad practices [OR=0.5 (95% CI:0.3-0.9)] of mothers were independently associated with lack of information on routine immunization. Conclusions There is low immunization coverage in this community. Mother’s educational status, family setting, knowledge, perception and practices about immunization are important factors that influence access to information on routine immunization.

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Abstract

Objective To analyse population coverage of syndromic surveillance (SS) based on emergency care data by studying i) the attractiveness of respectively SOS Médecins (Emergency care general practitioners) and Hospital emergency departments in the Centre-Val de Loire region and ii) the contribution of ecological deprivation factors in emergency access to healthcare. Introduction SOS Médecins France (SOS Med) is the first private and permanent network of general practitioners providing emergency care in France. Besides Hospital emergency departments (HED), SOS Med is therefore a major source of data for detecting and measuring near-real-time health phenomena. The emergency services provided by the SOS Med have been subject to important changes in the recent years. Their services are enriched by a medical consultation center together with extended working hours. Besides, the south of the region is markedly affected by a declining number of medical practitioners. This study was conducted to analyze the regional population coverage of emergency healthcare data provided by HED and SOS Med to the French syndromic surveillance system (SurSaUD®) taking into account distance, health care offer, demographic factors and ecological deprivation factors. Methods An analysis of the activities and geographic attraction was carried out based on the data respectively provided by the three regional SOS Med and three HED (Bourges, Orléans and Tours). Quasi-Poisson regression modelling was used to identify the factors influencing the attractiveness of each organization. Next, the findings were refined through spatial analysis of the attractiveness of HED and SOS Med and analysis of the contribution of deprivation based on socio-economic and healthcare facilities ecological indexes. Results In terms of age group, children under 2 years required the largest service consultations as well as seniors over 75 who sought more emergency visits at home. The SOS Med were almost always active in urban areas and at least once in two due to continuity of care. So they are an efficient source of general medical care given present workhours. Distance as an influential factor may explain the differences in attraction to the support type. The extent of the attraction appears in 36% SOS Med Bourges and 14% for SOS Med Orleans. Add the extent of attraction for SOS, remote consultation for SOS Med associations are a good use of care in general practice in present workhours scheme. In terms of monitoring of epidemics, we note that the SOS Médecins associations are most active in winter, particularly during the seasonal epidemics of influenza. This can be explained by the factor of patient referrals during calls. The most serious cases are redirected to the ED and cases of general medicine to the SOS Médecins. It is also important to note that the attraction of ED of CHR Orléans covers more or less important a large part of the regional territory, which is not visible to the ED of Bourges. It should nevertheless be noted that the CHR Orléans has a larger bed capacity than the CH Bourges. Conclusions This research has analysed the changes taking place in the SOS Médecins associations in the Centre-Val de Loire region. Findings show that these associations help ensure access to general medical care in a context of strongly reduced medical demography although with an uneven, primarily urban, geographical coverage. With better knowledge of the geographic span and sources and types of emergency care provision, further research can be undertaken to further refine and interpret the data.

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Abstract

Objective The study aimed at: i) analyses the regional characteristics and risk factors of severe influenza, taking into account dominant circulating virus(es) ii) estimate the regional completeness of the surveillance system. Introduction Every year, circulating influenza viruses generate a significant number of deaths. During the 2009 pandemic influenza A(H1N1), a national non mandatory surveillance system of severe influenza cases admitted to intensive care units (ICU) was set up in France. This surveillance is regionally driven by the regional offices (CIRE) of Santé publique France, the French Public Health Agency. This report provides epidemiologic analysis of the recorded data since the implementation of surveillance in the Centre-Val de Loire region over seasons 2009-10 to 2015-16 in regard of influenza epidemics dynamics. Methods Surveillance was carried out each year from October to April. Descriptive and analytic analyses were conducted to compare population characteristics, pre-existing risk factors and the clinical data according to influenza season and dominant circulating influenza virus(es). Logistic regressions were performed to identify factors associated with an increased risk of acute respiratory distress syndrome (ARDS) or death. Two capture-recapture analyses were performed to establish the completeness of the surveillance system in the region. The first one was realized on all cases, using two data sources (hospital records/surveillance data) and the second one, only on deaths, using three data sources (additional source: medical death certificates). Results From 2009-10 to 2015-16, the outbreak of influenza epidemics started more and more late. The number of severe influenza cases reported in the Loire Valley varied from 19 in 2010-11 to 75 in 2014-15. Overall, the most affected population was adults, from 41% in 2011-12 to 83% in 2009-10. However seniors (more than 65 years old) represented an important part of patients during three epidemics: 50% in 2011-12 and around 45% during the two last seasons; during these epidemics, men (60%-68%), were more affected than women. Patients' pre-existing risk factors were mainly: being older than 65 years old and suffering of cardiac or pulmonary diseases. The comparison by dominant viruses over the seasons revealed that when A(H1N1) virus prevailed, severe influenza occurred mainly in adults patients with any type of pre-existing risk factors whereas when A(H3N2) virus prevailed, seniors with pre-existing pulmonary disease were the most affected. More than a third of patients declared an ARDS. The overall observed lethality was close to 16%. ARDS occurred more frequently in patients who were middle-aged (45-64 years), immunocompromised or infected with A(H1N1). Pre-existing pulmonary disease was a protective factor. Risk factors associated with death were being older than 65 years, male and having declared an ARDS. The completeness of this surveillance system was estimated by capture-recapture methods at 59% for severe influenza cases and 40% for death cases. Conclusions The epidemiology of severe influenza and epidemics dynamics in the Centre-Val de Loire follow the national trends. Every season is characterized by the same dominant virus at national and regional levels in intensive care units. Influenza epidemics 2009-10 and 2014-15 were particularly long and severe, the first dominated by the A(H1N1)pdm09 virus and the second by the A(H3N2). Our study has demonstrated that the populations at risk of severe influenza differ according to the circulating virus(es). According to the obtained estimations, the completeness of the surveillance system, based on voluntary report by physicians, can be considered satisfactory. Regarding influenza deaths relatively low percentage of completeness may be explained by the fact that two sources are hospital based whereas the third one, medical death certificates, includes all influenza deaths with no information on the death place. Many patients were not vaccinated or their status was unknown. Most cases admitted to ICU presented pre-existing risk factors included in eligibility criteria in influenza vaccination policies. This study outlines the importance of vaccination as the first prevention measure.


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Abstract

Objective To describe the surveillance indicators implemented for the health impact assessment of a potential health event occurring before, during or after the UEFA Euro 2016 football matches in order to timely implement control and prevention measures. Introduction France hosted 2016 UEFA European Football Championship between June 10 and July 10. In the particular context of several terrorist attacks occurring in France in 2015 [1], the French national public health agency « Santé publique France » (formerly French Institute for Public Health Surveillance-InVS) was mandated by the Ministry of Health to reinforce health population surveillances systems during the UEFA 2016 period. Six French regions and 10 main stadiums hosted 51 matches and several official and non-official dedicated Fan Zones were implemented in many cities across national territory. Three types of hazard have been identified in this context: outbreak of contagious infectious disease, environmental exposure and terrorist attack. The objectives of health surveillance of this major sporting event were the same as for an exceptional event including massgathering: 1/ timely detection of a health event (infec- tious cluster, environmental pollution, collective foodborne disease...) to investigate and timely implement counter measures (control and prevention), 2/ health impact assessment of an unexpected event. The French national syndromic surveillance system SurSaUD® was one of the main tools for timely health impact assessment in the context of this event. Methods French national syndromic SurSaUD® system has been setup in 2004 and supervised by Santé publique France for 12 years. It allows the daily automatic collation of individual data from over 650 emergency departments (ED) involved in the OSCOUR® network and 61 emergency general practitioners’ (GPs) associations (SOS Médecins) [3]. About 60,000 attendances in ED (88% of total national attendances) and 8,000 visits in SOS Médecins associations (95% of the national visits) are daily recorded all over the territory and transmitted to Santé publique France. Medical information such as provisional medical diagnoses coded according to the International Classification of Diseases, 10th Revision (ICD-10) for EDs and specific thesaurus for SOS Médecins is routinely monitored through different syndromic indicators (SI). SI are defined by medically relevant clusters of one or several diagnoses, serving as proxies for conditions of public health interest. From June 10 to July 10, 19 SI were daily analyzed through automatic national and regional dashboards. SI were divided into 3 groups of public health surveillance interest: 1/ description of population health: injuries, faintness, myocar- dial infarction, alcohol, asthma, heat-related symptoms, anxious troubles; 2/ infectious diseases/symptoms with epidemic potential or diseases/symptoms linked with an environmental exposure: fever, fevers associated with cutaneous rash, meningitis, pneumonia, gastroenteritis, collective foodborne disease; 3/ symptoms potentially linked with a CBRN-E exposure: influenza-like illness, burns, conjunctivitis, dyspnea/difficulty breathing, neurological troubles, acute respiratory failure. Daily analysis were integrated into specific UEFA 2016 surveillance bulletins and daily sent to the Ministry of Health including week-ends. Results SI followed during the UEFA Euro 2016 period were nonspecific and potentially affected or influenced by several events apart from the championship. Between June 10 and July 10, two moderate-heat-wave periods occurred on a large part of mainland France: the first one from June 22 to 25 (beginning in the West-South of France) and then moving North and East of the country) and the second one from July 8 to 11 in the East-South. An increase in heat-related indicators (hyperthermia/heat stroke, dehydration, hyponatremia and burns) has been observed during both periods in five French regions including four hosting regions. Only minor increases in the other SIfollowed during the Euro 2016 period were observed. Conclusions Health surveillance implemented during 2016 UEFA European Football Championship through a daily analysis of non-specific SI from the French syndromic surveillance system SurSaUD® did not show any major variation associated with the sporting event. The observed variations were related with specific environmental conditions (heat-waves). Together with the health surveillancesystem, preventive plans were set up during the event essentially by offering flyers with information and useful tips on the main preventive attitudes and measures to adopt in a summer festive context (riskss associated with alcohol and drug intake, injuries, heat and sun exposure, dehydration, unprotected sexual behaviour...).


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Abstract

The International Society for Disease Surveillance (ISDS) held its fifteenth annual conference in Atlanta, GA, from December 6-8, 2016. Since 2001, individuals interested in sharing and learning emerging trends in surveillance research and practice have found the ISDS Annual Conference a unique forum to advance their knowledge in the discipline of disease surveillance. The 15th ISDS conference received a total of 233 abstracts from 23 countries. From the submissions, 189 (81%) were accepted for presentation at the conference as an oral presentation (N=96) or poster (N=93). The theme for the 15th annual conference was New Frontiers in Surveillance: Data Science and Health Security. The theme united two dominant trends in public health surveillance: 1) a growing desire to extract knowledge from increasing volumes of structured and unstructured data available from health information systems; and 2) increased pressure on nations to strengthen their capacity for disease surveillance and response to outbreaks when and where they occur across the globe. In addition to the major themes of the conference, abstracts were accepted in additional tracks that remain important to the practice of public health around the world: One Health unifying animal and human health; Methodological advances in applied epidemiology; Public health informatics; Public health policy; and Biosurveillance practice. As usual, accepted abstracts for the 2016 ISDS Conference span the breadth of surveillance practice around the globe. There are timely abstracts on the detection and response to vector-borne diseases such as Zika virus and chikungunya across the Americas, as well as abstracts on the surveillance of opioid abuse observed in many parts of the U.S. Other abstracts cover the surveillance of non-communicable diseases that are now the leading causes of death globally. Additionally, some abstracts focus on capacity building within low resource settings on multiple continents to enhance global health security. While other abstracts describe the impact of health information technology (or eHealth) policies on surveillance practice at local, national, or regional levels. And still other abstracts contain emerging, novel methods that advance our understanding of how to analyze “Big” data or reduce the messiness associated with realworld surveillance data. Together these abstracts represent the broad, diverse and interesting nature of surveillance practice. Furthermore, the abstracts represent important work being done in high income countries such as the U.S., Canada and the U.K. as well as critical work being done in low- and middle-income nations such as Nigeria, Pakistan, and Sierra Leone. I wish to thank the dedicated members of the Scientific Programming Committee (SPC) and ISDS staff who helped to manage the process of selecting this year’s abstracts for presentation. These individuals are domain experts across the spectrum of tracks and themes represented in the program, and their service is much appreciated. The SPC helped to recruit dozens of public health researchers and practitioners who also spent time reviewing abstracts. I also thank these volunteers for contributing to the richness and diversity of this year’s program. Finally, I wish to thank the Track Chairs who reviewed abstracts and recruited peers to perform reviews, and whom helped me organize presentations into meaningful sessions for the final conference program. Their names are listed in the proceedings to recognize their selfless service to ISDS and the field of public health surveillance. I hope that these proceedings help to advance scientific understanding and the practice of surveillance in public health. Please use the knowledge herein to improve how you practice or evaluate surveillance in your jurisdiction. Or you may find ways to apply the knowledge elsewhere in population health. However you use it, I ask that you document your lessons or findings and submit to ISDS in the future to share the outcomes with others. Together we can reduce the burden of disease and improve health outcomes for populations globally.

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Abstract

ObjectiveTo describe characteristics of Veterans Health Administration (VHA) patients with ICD 9/10 CM inpatient discharge and/or emergency department (ED)/urgent care outpatient encounter codes for carbon monoxide (CO) poisoning. IntroductionIt is estimated that in the United States (US), unintentional non-fire-related CO poisoning causes an average of 439 deaths annually, and in 2007 confirmed CO poisoning cases resulted in 21,304 ED visits and 2,302 hospitalizations (71 per million and 8 per million population, respectively). Despite the significant risk of morbidity and mortality associated with CO poisoning, existing surveillance systems in the United States are limited. This study is the first to focus specifically on CO poisoning trends within the VHA population.

Methods Queries were performed in VA PraedicompTM Public Health Surveillance System for inpatient discharges and emergency room and urgent care outpatient visits with ICD 9/10 CM codes for CO poisoning from 1/1/2010 – 6/30/2016. A dataset of unique patient encounters with CO poisoning was compiled and further classified as accidental, self-harm or unspecified. Patients with carboxyhemoglobin (COHb) blood level measurements ≥10% for the same timeframe were extracted and merged with the CO poisoning dataset. We analyzed for demographic, geographic and seasonal variables. Rates were calculated using total unique users of VHA care formatting time frame and geographic area as denominators.

Results There were a total of 671 unique VHA patients identified with CO poisoning. Of these, 298 (44%) were classified as accidental, 104 (15%) self-harm, and 269 (40%) unspecified. A total of 6 patients died within 30 days of their coded diagnosis, however only 1 of these was directly attributable to CO poisoning. The overall rate of CO poisoning over the study time frame was 18 per million unique users of VHA care. CO poisoning diagnoses were obtained from 396 (59%) outpatients, 216 (32%) inpatients, and 59 (9%) patients with both outpatient visit and inpatient admission. Patients with self-harm classification were less likely to be seen in the ED (only 24 (6%) unique patients compared to 190 (48%) accidental and 182 (46%) unspecified classifications). Of patients seen in the ED and subsequently admitted, patients with the classification of accidental poisoning made up the largest percentage with 36 unique patients (61%). There were 71 (11%) females compared to 600 (89%) males. The highest represented age group was 45-64 with 342 unique patients (51%). Rates by U.S. Census Region were highest in the Midwest and Northeast (27 and 23 per million unique users, respectively) compared to the West and South (15 and 13 per million unique users, respectively) (Figure 1). Accidental CO poisonings showed a seasonal pattern with peaks occurring in late fall, winter, and early spring months (Figure 2). CO poisonings classified as unspecified had a similar but less pronounced pattern, while those classified as self-harm were too few to observe any pattern over time. COHb blood levels ≥10% were present in 111 (17%) of patients with CO poisoning codes. Of patients with COHb measures ≥10%, those with self-harm classification were least represented with only 7 unique patients (6%). Accidental and unspecified classifications were equally represented with 53 (48%) and 51 (46%) unique patients, respectively. Conclusions The impact of CO poisoning on the VHA patient population has not been well studied. The geographic distribution of the majority of cases in the Midwest and Northeast, and the seasonal distribution of accidental cases in colder months seems to be appropriate with respect to what is known of unintentional CO poisoning as often associated with heat-generating sources. Opportunities for further investigation include how potential CO poisoning cases are evaluated in VHA given the low percentage of cases with COHb blood level measurements.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To characterize fentanyl-associated mortality in Florida using freetext queries of the literal causes of death listed on death certificates. Introduction In October 2015, the Centers for Disease Control and Prevention (CDC) released health advisory #384 to inform people about increases in fentanyl fatalities. Florida’s statewide syndromic surveillance system, Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE-FL), captures electronic death record data in near real time which allows for the monitoring of mortality trends across the state. One limitation of using death record data for fentanyl surveillance is the lack of a fentanyl-specific overdose ICD-10 code; however, the literal cause of death fields (“literals”) provide a level of detail that is rich enough to capture mentions of fentanyl use. The “literals” are a free text field on the death certificate, recorded by a physician at the time of death and detail the factors that led to the death. ESSENCE-FL has the benefit of not only receiving death record data in near real-time, but also receiving the literal cause of death fields. This work analyzes trends in fentanyl-associated mortality in Florida over time by using the literal cause of death fields within death records data obtained from ESSENCE-FL. Methods The “literals” elements of Florida Vital Statistics mortality data from 2010 through 2015 accessed via ESSENCE-FL were queried for the term “fent”. No necessary negations or extra term inclusions were deemed necessary after looking at the records pulled with “fent” alone. Deaths were analyzed by various demographic and geographic variables to characterize this population in order to assess which groups are most heavily burdened by fentanyl-associated mortality. Population estimates by county for 2015 were obtained from the U.S. Census Bureau to calculate mortality rates. Language processing in RStudio was used to determine which other substances were commonly reported when fentanyl was listed on the death certificate, in order to assess polydrug use and its impact on increased mortality. Results Compared to the number of fentanyl-associated mortalities in 2010 (82), fentanyl-associated mortality in 2015 (599) was 6.5 times higher after controlling for the natural increase in total mortality between 2010 and 2015. Almost three-fourths of the deaths in 2015 were male (73%), which is higher than the proportion of male deaths in 2010 (55%). The age group with the largest burden of fentanyl-associated mortality was the 30–39 age group, with almost one-third of the deaths in 2015 coming from this age group (31%) compared to only 10% in 2010, a roughly 200% increase. Fentanyl-associated mortality was almost exclusive to people that are Caucasian, with 94% of the fentanyl-associated mortalities in 2015 occurring among Caucasians. Multi-drug use was also identified for those with fentanyl-associated mortality. Mentions of other drugs were present in at least 10% of the deaths. Some of the other drugs mentioned in the “literals” included heroin, cocaine, and alprazolam. There was county variation in the number of fentanyl mortality deaths ranging from 21.19 deaths per 100,000 to 0.29 deaths per 100,000 residents. Two counties with the highest rates were located adjacent to one another. Conclusions Having death record data readily available within the state’s syndromic surveillance system is beneficial for rapid analysis of mortality trends and the analytic methods used for syndromic surveillance can be applied to mortality data. Free text querying of the “literals” in the vital statistics death records data allowed for surveillance of fentanyl-associated mortality, similar to methods used for querying emergency department chief complaint data. Although underlying ICD-10 codes can lack detail about certain causes of death, the “literals” provide a clearer picture as to what caused the death. The “literals” also make it possible to look at potential drug combinations that may have increased risk of mortality, which will be explored more thoroughly. Further work will explore other data sources for fentanyl usage and mortality trends, as well as examine potential risk factors and confounders.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo evaluate syndrome definitions capturing storm- and extremeweather-related emergency department visits in Kansas hospitals participating in the National Syndromic Surveillance Program (NSSP). Introduction Kansas storms can occur without warning and have potential to cause a multitude of health issues. Extreme weather preparedness and event monitoring for public health effects is being developed as a function of syndromic surveillance at the Kansas Department of Health and Environment (KDHE). The Syndromic Surveillance Program at KDHE utilized emergency department (ED) data to detect direct health effects of the weather events in the first 9 months of 2016. Current results show injuries directly related to the storms and also some unexpected health effects that warrant further exploration. Methods A basic syndrome definition was defined based on extreme spring and summer weather events experienced in Kansas. This broad definition pulled records from Kansas EDs that included the following in the Chief Complaint or Triage Notes fields: ● Storm ● Rain ● Tornados ● Wind ● Flood This broad syndrome definition was performed on data submitted to the Kansas’s production server through NSSP between January 1st and August 30th, 2016. After the initial pull, duplicate records for the same patient and visit were removed. The remaining set was then searched by hand to identify terms caught by the syndrome definition that were not related to storm activity or extreme weather. Record chief complaints were thenscanned by hand to identify common words containing the search criteria and then removed. Keywords not of interest to the syndromedefinition that were caught were: migraine, window, drain, restrain, train, and many other proper nouns that contained one of the keywords. These remaining visits were then sorted by nature of visit and unexpected records were recorded for future direction of syndromedefinition development. Results The initial data pull under these conditions yielded 17,691 unique emergency department visits from January 1st to August 30th during the 2016 year. From this, records were classified based on key words resulting in the pull. The table below shows the initial pull results, the remaining records after errant results were expunged, the percentage of visits that were removed, and the most common reason for removal. Of these records remaining after cleaning, 20 were related to storms, 62 were related to rain, 7 were related to tornado activity, 66 were related to wind, and 14 were related to flooding along with the mixed variable instances shown in the table. A majority of the wind-related ED visits were injuries and the majority of the tornado activity events were related to injuries sustained while taking shelter. Many of the injuries mentioning storms were sustained in preparation for the storm, and a handful were due to mental stresses regarding storm activity. Conclusions Syndrome definition development is an iterative process that will vary by region. By manually looking at line-level data details, future searches can better accommodate these errant results and false positives. These studies will facilitate more rapid extreme weather response in Kansas and allow better situational awareness. Along with general storm-related injuries, knowledge of the unusual recordscought by a syndrome definition can also help direct public education in preparation of future storms. With injuries sustained while taking shelter and injuries sustained in preparation for the storm, we can takethese unique ED visits and work on interventions to prevent future occurrences.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

We pilot a RTI surveillance system using data from FRSC, Policemotor division and Health facilities in Kaduna metropolis, Nigeria to ascertain its feasibility and generate data needed for actiontoward achieving sustainable development goals 3.6 target.

Introduction

Road Traffic Injury is common cause of unintentional injuryglobally and Low and middle income countries account for 90% of 1.3 million Road Traffic Injury (RTI) deaths. In Africa region, Nigeria accounts for 25% of RTI mortality but has no comprehensive and reliable RTI surveillance system. Data from Federal Road Safety Commissions (FRSC) shows gaps in RTI reporting with largedisparity with estimated value from World Health Organization.

Methods

Kaduna metropolis is the capital of Kaduna State with estimated population of 1.96 million. It is a major route between Abuja, the National capital and 15 northern Nigeria states with high vehicular movement. We adapted WHO Injury surveillance guideline and Centers for Disease Control and Prevention surveillance training manual for this study. A case of RTI is any person injured or died within 30 days as a result of injuries incurred from vehicular collision on a public road in Kaduna Metropolis. Data collected using a pretested questionnaire for RTI cases at health facilities, Police and FRSC. Data were linked by deterministic method, cleaned and analysed. Frequency and proportion were calculated to characterize the RTI. The study was supported by a mini-grant from Center for Disease Control and Prevention.

Results

Data was collected from February to April 2016. Of the 324 crashes reported, 566 people injured and 66 deaths with case fatality rate of 11.7%. Male gender accounts for 81.8% and age 20 – 39 years were 64.6%. Commercial drivers were 20.7%, pedestrian 21% and passengers were 53.7%. Sixty percent of the crash occurred between cars or buses while 21% were without collision with any vehicle or stationary objects. Of the 66 deaths reported 61 (92.4%) died at crashsite. FRSC evacuated 21%, 38.6% were evacuated by other road users. No use of seat belt and crash helmets reported and only 5.1% received first aid care before reaching reporting facility. RTI Incidence peaked between 6:00 PM to 8:59 PM with 26 persons per hour.

Conclusions

Essential to sustainable development goal 3, a multisector RTI surveillance system that generate data for action in Kadunametropolis, Nigeria is feasible and data generated was used for action at different levels to mitigate against the burden of RTI.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To discuss the implementation of confidentiality practices at the Kumasi Cancer Registry.

Introduction: Cancer registration involves collecting information on patients with cancer. Population-based cancer registries in particular are useful in estimating the disease burden and to inform the institution of prevention and control measures. Collecting personal information on patients with cancer requires strict adherence to principles of confidentiality to ensure the safety of the collected data. Failure may have legal and medical implications. The Kumasi Cancer Registry was established as a population-based cancer Registry in 2012. The registry collects data on cases of cancer occurring among residents of the Kumasi Metropolitan area of Ghana. Issues bordering on confidentiality were an integral part of the establishment of the registry. We discuss the implementation of confidentiality plans during the four years of existence of the Kumasi Cancer Registry.

Methods: The registry has a designed abstraction form which is used to collect data. Data sources for the Registry are all major hospitals in Kumasi providing cancer treatment services. Data sources also include private pathology laboratories and the Births and Deaths Registry. Trained research assistants collect data from the folders of patients. This is followed by coding and then entering into the Canreg 5 software. Coded and entered into the Canreg5 software for management and analysis. After data entry, the forms are filed in order of registry numbers as generated by the canreg5 software for easy reference.

Results: Confidentiality of KsCR data is ensured through the following measures. The signing of a confidentiality agreement by all registry staff. The confidentiality agreement spells out terms for the release of data to third parties in particular but even staff of the various facilities. The agreement also spells out the consequences of a breach of any of the clauses. No direct contact is made with patients during the process of abstraction of data by registrars. The data abstraction forms are kept in a secured safe in the registry office. The computers that house the registry data are password enabled and are changed on a regular basis to ensure security. The Canreg5 software used for electronic data management also has individual profiles with usernames for all registrars and supervisors. The scope of access to Canreg data is limited by the profile status of the respective staff members. Supervisors have full access to all data including summarized reports. Registrars have limited access mostly restricted to data entry. Access to the registry office is restricted to registry staff and other personnel authorized by the Registry Manager or Director. An established Registry Advisory Board is responsible for assessing requests and approval of data from the registry. Where files have to be sent electronically, they are password protected and sent in separate emails.

Conclusions: Despite the potential challenges to maintaining confidentiality of data in developing countries, evidence from four years of cancer data management in Kumasi suggests stringent measures can ensure confidentiality. The use of multiple measures to ensure confidentiality is essential in surveillance data management.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To demonstrate a method for estimating neighborhood food selection with secondary use of digital marketing data; grocery transaction records and retail business registry.

Introduction Unhealthy diet is becoming the most important preventable cause of chronic disease burden (1). Dietary patterns vary across neighborhoods as a function of policy, marketing, social support, economy, and the commercial food environment (2). Assessment of community-specific response to these socio-ecological factors is critical for the development and evaluation policy interventions and identification of nutrition inequality. Mass administration of dietary surveys is impractical and prohibitory expensive, and survey typically fail to address variation of food selection at high geographic resolution. Marketing companies such as the Nielsen cooperation continuously collect and centralize scanned grocery transaction records from a geographically representative sample of retail food outlets to guide product promotions. These data can be harnessed to develop a model for the demand of specific foods using store and neighborhood attributes, providing a rich and detailed picture of the “foodscape” in an urban environment. In this study, we generated a spatial profile of food selection from estimated sales in food outlets in the Census Metropolitan Area (CMA) of Montreal, Canada, using regular carbonated soft drinks (i.e. non-diet soda) as an initial example.

Methods From the Nielsen cooperation, we obtained weekly grocery transaction data generated by a sample of 86 grocery stores and 42 pharmacies in the Montreal CMA in 2012. Extracted store-specific soda sales were standardized to a single serving size (240ml) and averaged across 52 weeks, resulting in 128 data points. Using linear regression, natural log-transformed soda sales were modelled as a function of store type (grocery vs. pharmacies), chain identification code and socio-demographic attributes of store neighborhood, which are median family income, proportion of individuals who received post-secondary diplomas, and population density as measured by the 2011 Canadian Household Survey. Selection of the predictors and first-order interaction terms was guided by the minimization of the mean squared error using 10-fold cross-validation. The final model was applied to all operating chain grocery stores and pharmacies in 2012 (n=980) recorded in a comprehensive and commonly available business establishment database. The resulting predicted store-specific weekly average soda sales was spatially interpolated to provide a graphical representation of the soda sales (representing an unhealthy foodscape) across the Montreal CMA.

Results Figure 2 demonstrates the spatial distribution of the predicted soda sales in the Montreal CMA.

Conclusions The current lack of neighborhood-level dietary surveillance impedes effective public health actions aimed at encouraging healthy food selection and subsequent reduction of chronic illness. Our method leverages existing grocery transaction data and store location information to address the gap in population monitoring of nutrition status and urban foodscape. Future applications of our methodology to other store types (e.g. convenience stores) and food products across multiple time points (e.g. months and years) will permit a comprehensive, timely and automated assessment of dietary trends, identification of neighborhoods in special dietary needs, development of tailored community health promotions, and the measurement of neighborhood-specific response to nutrition policies and unhealthy food advertising.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Introduction
Firearm violence is an issue of public health concern leading to more than 30,000 deaths and 80,000 nonfatal injuries in the United States annually. To date, firearm-related studies among Veterans have focused primarily on suicide and attempted suicide. Herein, we examine firearm violence among VHA enrollees for all manners/intents, including assault, unintentional, self-inflicted, undetermined, and other firearm-related injury encounters in both the inpatient and outpatient settings. Methods
Inpatient and Outpatient encounters with one or more ICD-9-CM firearm external-cause-of-injury codes (E-codes) from 1/1/2010-9/30/2015 were extracted from the VHA’s Praedico™ Public Health Surveillance System, including demographics, era of service/eligibility, encounter type, and deaths. Firearm E-codes were classified for manner/intent based on the CDC’s Web-based Injury Statistics Query and Reporting System (WISQARS™) matrix. Outpatient/emergency department (ED) data were exclusively from VHA facilities (a single pediatric patient seen as a humanitarian emergency was excluded from the dataset). Inpatient data included VHA facilities and some records received from non-VHA facilities. VHA rate of hospitalization for firearm-related admissions was calculated using the total VHA acute-care admissions for the same time period as the denominator.

Results
During the time frame examined, 5,205 unique individuals were seen with a firearm E-code. Of these, 4,221 were seen in the outpatient/ED setting only, 597 in the inpatient setting only, and the remaining 387 had encounters in both the outpatient/ED and inpatient settings. VHA firearm admission rate was 1.63 per 10,000 VHA admissions, compared to a national rate of 1.96 per 10,000 in 2010. Table 1 shows the breakdown of encounters by manner/intent. Unintentional was the most common firearm injury manner/intent. Overall, the median age at initial encounter was 54 (range 19-100 years), and 96% were male. The highest percentage served in the Persian Gulf War Era (2,136, 41%), followed by Vietnam Era (1,816, 35%) and Post-Vietnam Era (716, 14%). The greatest number of patients with a firearm-coded encounter resided in Texas (453), California (349), Florida (326), Arizona (214) and Ohio (212). Conclusions
Unintentional injuries were the most common form of firearm injury among VHA enrollees, representing over half of all outpatient/ED firearm encounters and more than twice the number of firearm hospitalizations compared with any other manner/intent. Limitations include that not all U.S. Veterans are VHA enrollees; miscoding and misclassification of firearm-related injuries may have occurred; and data from non-VHA outpatient/ED encounters and some non-VHA hospitalizations are not available to our surveillancesystem for analysis. Additional study is needed to further understand the epidemiology of firearm-related injuries among Veterans and inform VHA leadership and providers.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The objective of this presentation is to describe the new word alert capability in ESSENCE and how it has been used by the Florida Department of Health (FDOH). Specifically, this presentation will describe how the word alert feature works to find individual chief complaint terms that are occurring at an abnormal rate. It will then provide usage statistics and first-person accounts of how the alerts have impacted public health practice for the users. Finally, the presentation will offer future enhancement possibilities and a summary of the benefits and shortcomings of this new feature.

Introduction Syndromic surveillance systems have historically focused on aggregating data into syndromes for analysis and visualization. These syndromes provide users a way to quickly filter large amounts of data into a manageable number of streams to analyze. Additionally, ESSENCE users have the ability to build their own case definitions to look for records matching particular sets of criteria. Those user-defined queries can be stored and analyzed automatically, along with the pre-defined syndromes. Aside from these predefined and user-defined syndromic categories, ESSENCE did not previously provide alerts based on individual words in the chief complaint text that had not been specified a priori. Thus, an interesting cluster of records linked only by non-syndromic keywords would likely not be brought to a user's attention.

Methods In the FDOH ESSENCE system a new detection feature was developed to trigger alerts based on anomalous occurrence of terms in chief complaints. This feature used Fisher's Exact Test to test frequencies of individual chief complaint terms relative to all terms in a 1-month baseline. The feature used a 7-day guard-band, and automatically switched to an efficient chi-square test for sufficiently large term counts. A term triggered an alert if its p-value ≤ 10E-4.

This algorithm was then run on chief complaint sets both by hospital and by region, with region assignment according to patient zip code. Results were then displayed in new visualizations showing alerts in word cloud and line listing form. Additionally, users were given the option to ignore stop words, syndromic terms, and a user-created list of ignorable words in order to focus on words of greater interest.

Results The result of using the tool since June 2016 has seen three major benefits. First, the original intent for the system to notify users of abnormal word clusters has proven useful. Users have been able to see terms such as Disaster, Shelter and Fireworks which were not part of any prior syndromes and use these notifications to investigate possible issues. The second benefit found by users was the ability to find new misspellings or abbreviations commonly used by hospitals. The terms ZYkka and GLF (Ground Level Fall) are examples of these. Finally, the system has helped discover new trends in hospital processes. For example, the tool has helped discover first person and non-English phrases in the chief complaint. This observation led to the discovery that some hospitals are using kiosks or mobile phone apps to allow patients to enter their own chief complaints.

Conclusions The word alert feature has provided value to the users of FDOH ESSENCE. While accomplishing its initial goal of triggering abnormal non-syndromic term usage, the additional ability to find new misspellings and abbreviations may have even larger impact by keeping syndrome and subsyndrome definitions up-to-date over time for traditional syndromic alerting. Beyond these current benefits, additional visualization enhancements are under consideration. Additionally, the resources required to perform the detection are substantial, and implementation improvements are under development to improve the performance and enable more advanced free-text anomaly detection.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To streamline production of a daily epidemiology report including syndromic surveillance, notifiable disease, and outbreak data during mass gathering

Introduction
The 2016 U.S. Olympic Track and Field Team Trials were held July 1-10 in Eugene, OR. This mass gathering included over 1,000 athletes, 1,500 volunteers, and 175,000 spectators. The Oregon Public Health Division (PHD) and Lane County Public Health (LCPH) participated in pre-event planning and collaborated to produce a daily epidemiology report for the Incident Management Team (IMT) during the event. The state and county public health agencies had collaborated on surveillance for prior mass gatherings, including the 2012 Trials. However, 2016 was the first opportunity to use complete state and county syndromic surveillance data.

Methods
PHD staff developed an ESSENCE report, highlighting seven priority health outcomes: total emergency department visits; injury, gastrointestinal, respiratory, and fever syndromes; and asthma-like and heat-related illness queries. The report included side-by-side comparisons of county and state time series graphs, a table summarizing reportable diseases, and space to narratively describe outbreaks. PHD staff did a virtual demonstration and in-person tutorial for LCPH staff on how to run the report. ESSENCE access permissions had to be modified so that county users could see and produce state time-series graphs but not data details for non-Lane County visits. Emphasis was placed on interpretation of likely scenarios, i.e., one or two days with a warning that was not indicative of an incident of public health importance.

Results
During the event, LCPH staff were able to run the report successfully, i.e., there were no technical glitches. For the first few days, LCPH staff consulted with PHD staff about epidemiological interpretation. State data were of specific interest since data details were suppressed. Additionally, increases were seen in the injury syndrome in the days preceding the July 4 holiday. Stratification by key demographic factors and looking at subsyndrome breakdown on warning and alert days provided the needed information without requiring the use of the detail details.

Conclusions
After the event, there were three main recommendations for improving the process. LCPH suggested that the side-by-side visualization of county and state time series graphs was useful to see trends but the relative scale of the number of visits was unclear due to size and placement (see figure 1). Solutions for future reports include additional explanatory text, limiting the report to only county data, and alternative visualizations that highlight the differences in visit magnitude. As part of the IMT process, the LCPH lead felt that her efforts to physically go to the Emergency Operations Center to run the report helped facilitate communication with partners. However, it is not clear if this effort directly translated into IMT use of the report, which was posted to the online event management system and not included in the daily situation status reports. While LCPH leadership and staff reported anecdotally that they found the report to be very useful, no formal evaluation of use was done with either public health or IMT staff. In advance of the next event, state and county staff should prepare evaluation metrics. The report feature in ESSENCE is a bit cumbersome to set up, but it allows for easy production of appealing and customizable reports. This template can be modified for future mass gatherings, including athletic competitions and county fairs. PHD staff will continue to collaborate with LCPH to repurpose and improve the report for use in Lane and other counties. Fostering local user comfort with interpreting ESSENCE data and generating summaries for local use is a priority of the OR ESSENCE team.


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Abstract

Objective
To assess the use of syndromic surveillance to assess trends in mental health-related emergency department (ED) visits among school-aged children and adolescents in New York City (NYC).

Introduction
From 2001-2011, mental health-related hospitalizations and ED visits increased among United States children nationwide [1]. During this period, mental health-related hospitalizations among NYC children increased nearly 23% [2]. To estimate mental health-related ED visits in NYC and assess the use of syndromic surveillance chief complaint data to monitor these visits, we compared trends from an early real-time syndromic system with those from a less timely, coded ED visit database.

Methods
The NYC ED syndromic surveillance system receives anonymized patient chief complaint and basic demographic data for nearly every ED visit citywide to provide timely surveillance information to health authorities. Using NYC ED syndromic surveillance data from 2003-2015, we applied previously developed definitions for general psychiatric syndromes. We aggregated ED visits by age group (5-12 years, 13-17 years, and 18-20 years), geography, and temporality. Syndromic data were compared with Statewide Planning and Research Collaborative System (SPARCS) data from 2006-2014 which reported mental health diagnosis (ICD-9), treatment, service, and basic demographics for patients visiting facilities in NYC. Using these two data sources, we compared daily visit patterns and annual trends overall as well as stratified by age group, area-based poverty (ZIP code), and time of visit.

Results
Both syndromic surveillance and SPARCS data for NYC showed an increasing trend during the period. While both showed relative increases with similar slopes, mental health-related chief complaint data captured fewer overall visits than the ICD-9 coded SPARCS data. Trends in syndromic data during 2003-2015 differed by age group and area-based poverty, e.g., among children ages 5-12 years the annual proportion of mental health-related ED visits increased roughly 3-fold from 1.2% to 3.8% in the poorest areas, which was greater than the increase in the richest areas (1.7% to 2.6%). Seasonal, day-of-week, and school holiday patterns found far fewer visits during the periods of NYC public school breaks (Figure).

Conclusions
We conclude that syndromic surveillance data can provide a reliable indicator of mental health-related ED visit trends. These findings suggest potential benefit of syndromic surveillance data as they may help capture temporal and spatial clustering of events in a much more timely manner than the >1 year delay in availability of ED discharge data. Next steps include a qualitative study exploring the causes of these patterns and the role of various factors driving them, as well as the use of patient disposition and matched data to better characterize ED visit patient outcomes.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo detect increases in health complaints resulting from the July 2016 Sand Fire near Santa Clarita, CA using syndromic surveillance and complementary systems.

Introduction

On July 22, 2016, the Sand Fire began burning in the Santa Clarita Valley of Los Angeles County (LAC), CA. This urban-adjacent wildfire breached the city limits of Santa Clarita (population 180,000). Fueled by record heat and an ongoing exceptional drought, the Sand Fire burned over 40,000 acres in 13 days and caused a large increase in the air concentration of fine particulate matter. The syndromicsurveillance team was tasked with reporting on possible health effects from the fire. Fire, asthma, and heat related data were monitored until the fire was reported as 98% contained. The team prepared and distributed a daily special summary report to key stakeholders in the LAC Department of Public Health.

Methods

Emergency department (ED) data were queried for cases related to fire, asthma, cardiac events, eye irritation, heat, and total volume. These queries consisted of key word searches within chief complaint (CC), diagnosis and triage note data fields. Queries were conducted on all participating syndromic EDs in LAC, and also restricted to nine EDs closest to the fire. The resulting line lists were reviewed daily to rule out visits that were unrelated to the Sand Fire. The fire query was refined periodically with additional exclusion terms. Complaints related to asthma were tallied in a second query. In order to assess heat-related ED visits and temperature trends, existing queries and report templates were modified to focus on the nine fire-area EDs. Local temperatures were taken from the Weather Underground website. Complementary systems were also monitored, including over-the-counter medication sales and nurse hotline call data. Trend graphs for hospital admissions and ED visits were produced daily to assess volume from 19 Reddinet participating hospitals. In addition to internal data sources, the South Coast Air Quality Management District website was checked daily to monitor air quality in the Santa Clarita Valley.

Results

There were 48 syndromic ED patient records with direct mention of the fire in LAC’s syndromic hospitals in 13 days. Of these, 26 did not include asthma, and 32 came from the nine hospitals in the Sand Fire region; 32 were identified from the CC, six by diagnosis and ten by triage note. Despite an increase in fire-related visits, overall trends in ED data were not affected; no increase was found for cardiac events, eye irritation, heat-related illness or total volume. Asthma visits increased at the time of the fire, which correlates with a sharp increase in the concentration of fine particulate matter in the Santa Clarita Valley following the start of the fire. However, these increases were no higher than other peaks observed in previous months. No increases in calls to a nurse hotline or over-the-counter medication sales were observed. Among Reddinet hospitals, admissions increased slightly but ED visits remained unchanged.

Conclusions

For the Sand Fire, ED volume alone was not enough to estimate the subsequent health effects on residents of LAC; instead a specific fire query was needed. Several factors could explain why overall trends were not affected. In a region where air quality is already compromised, it is challenging to distinguish between asthma increases from air pollution from those exacerbated by wildfires smoke. It is also likely that residents heeded warnings about air quality during active fires, thus reducing their outdoor exposure. Although the majority of cases were identified using the CC field, additional data fields such as triage notes available from some hospitals improved the ability to elicit fire related visits. Regardless of the challenges presented in measuring health effects related to wildfires, syndromicsurveillance and complementary systems continue to be the primary tools for near real-time assessments in LAC.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To describe Carolinas Poison Control Center (CPC) calls data collected in the NC DETECT syndromic surveillance system.

Introduction
CPC provides the 24/7/365 poison hotline for the entire state of North Carolina and currently handles approximately 80,000 calls per year. CPC consultation services that assist callers with poison exposure, diagnosis, optimal patient management, therapy, and patient disposition guidance remain indispensable to the public and health care providers. Poison control center data have been used for years in syndromic surveillance practice as a reliable data source for early event detection. This information has been useful for a variety of public health issues, including environmental exposures, foodborne diseases, overdoses, medication errors, drug identification, drug abuse trends and other information needs. The North Carolina Department of Health and Human Services started formal integration of CPC information into surveillance activities in 2004. CPC call data are uploaded in real-time (hourly), 24/7/365, to the NC DETECT state database.

Methods
CPC calls collected by NC DETECT from 2009-2015 were analyzed in this descriptive study. Counts of CPC calls were examined by year to assess total volume and changes over time, by month to assess seasonality, by geographic location, and call site/facility and call originator. CPC calls were also categorized by type of call – exposure calls versus information calls – in order to determine why people call CPC and to assess if any trends exist amongst these categories.

Results
The majority of CPC calls originate from the caller’s own residence (53.40%). The age groups most represented are 0-1 years old, 2-4 years old, and 25-44 years old. Calls to CPC were for male and female patients in approximately equal numbers. The region of NC that has the highest number of calls, by a fairly wide margin, is the Charlotte Metro region. In 2009, the total number of CPC calls was over 120,000. This number decreased monotonically every year following, with the total in 2015 being 80,000. This is a 1/3 reduction in the total number of calls over 7 years. When the calls were analyzed by type of call, an interesting trend emerged. The total number of exposure calls remained relatively constant over the time period, ranging from 64,000 to 68,000 per year. However, the total number of information calls decreased each year going from just over 40,000 to about 5,000. When examined by month to assess seasonality, the data show an increase in the number of calls beginning in February and peaking in May, and then a steady and slow decline throughout the rest of the year.

Conclusions
Our study shows that CPC consultations from callers with exposures have remained stable over time. However, in the absence of exposure, fewer people call CPC for information on various substances. Drug identification calls saw a decrease each year during the study time period. In 2009 there were 34,495 drug identification calls and in 2015 there were 5,722. This dramatic decrease in information calls is most likely due to the increased use of the internet and search engines. Because people have more access to the internet, especially via mobile devices, they may not feel the need to call CPC to obtain information.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
In this paper we used hospital charges to assess costs incurred due to prescription drug/opioid hospitalizations.

Introduction
There is a resurgence in the need to evaluate the economic burden of prescription drug hospitalizations in the United States. We used the Wisconsin 2014 Hospital Discharge data to examine opioid related hospitalization incidence and costs. Fentanyl, a powerful synthetic opioid, is frequently being used for as an intraoperative agent in anesthesia, and post-operative recovery in hospitals. According to a 2013 study, synthetic Fentanyl is 40 times more potent than heroin and other prescription opioids; the strength of Fentanyl leads to substantial hospitalizations risks. Since, 1990 it has been available with a prescription in various forms such as transdermal patches or lollipops for treatment of serious chronic pain, most often prescribed for late stage cancer patients. There have been reported fatal overdoses associated with misuse of prescription fentanyl. In Wisconsin number of total opioid related deaths increased by 51% from 2010 to 2014 with the number of deaths involving prescription opioids specifically increased by 23% and number of deaths involving heroin increased by 192%. We hypothesized that opioids prescription drugs, as a proxy of Fentanyl use, result in excessive health care costs.

Methods
Opioid hospitalizations was defined as any mention of the ICD9 codes (304,305) in any diagnostic field or the mention of (E935.09) on the first listed E-code. Our analysis used the Heckman 2-stage model, a method often used by Economists in absence of randomized control trials. In presence of unobserved choice, for example opioid related hospitalizations, there usually is a correlation between error in an underlying function (fentanyl prescription) and an estimated function (hospital charges) that introduces a selection bias. Heckman treats this correlation between errors as an omitted variable bias. Therefore, we estimate a Heckman two step model using hospitalization: where the selection function is the probability of being hospitalized for synthetic opioid via logistic regression. Finally, we estimate the hospital charges realized if the patient was given opioids. Results
Male patients are significantly more likely to be hospitalized for opioids than are female patients; while white patients are significantly more likely to be admitted for opioid usage than other racial groups. We also find that comorbid factors, such as mental health, significantly impact hospital charges associated with opioid use. We find that persons with private health insurance are associated with higher rates of opioid use. Conclusions
Using a Heckman two step approach we show that comorbid conditions such as mental health, Hepatitis C, injuries, etc significantly affect hospital charges associated with hospitalization. We use these findings to explore the impact of the 2013 rule mandating doctors share opioid prescription information on the incidence of opioid related death and hospital charges associated with opioid prescriptions. This work is policy relevant because alternatives to opioid prescription such as meditation, pain management therapies may be relevant.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

We will describe a real-time mobile surveillance and casemanagement system designed to organize data collected by multiple officers about cases and their contacts. We will discuss this surveillance system and its application for Ebola and other infectious diseases in the Democratic Republic of the Congo (DRC) and othersimilar settings. We will review the technology, results, challenges, lessons-learned, and applicability to other contexts.

Introduction

Improving surveillance and response is a critical component of the Global Health Security Agenda. While it is impossible to predict where the next Ebola outbreak will occur, it is very likely that another outbreak will occur in the DRC. Of the 20 known outbreaks, 7 have occurred in the DRC, one as recently as 2014. To rapidly detect and respond to an Ebola outbreak, we sought to develop a real-time surveillance and response system for use in DRC and similar settings.

RTI International developed Coconut Surveillance mobile software, which is currently used for real-time malaria surveillance and response in Zanzibar, Africa, where malaria elimination efforts are underway. We took this system and adapted it for Ebola as a possible tool for surveillance and response to Ebola and other (re)emerging diseases. Plans include pilot testing functionality at clinical sites in DRC, where surveillance infrastructure is limited at the local level. Coconut Surveillance is a mobile disease surveillance and rapid response system currently used for malaria elimination activities. It receives suspected positive case alerts from the field via mobile phones and uses mobile software to guide surveillance officersthrough a follow-up process. Coconut Surveillance runs on Android mobile devices that are used to coordinate work in the field as well as provide decision support during data collection and case management.

In addition to standard case information, the GPS coordinates of the case’s household are captured as well as malaria status of all household members. Data are collected and accessed off-line, and resynchronized with a shared database when Internet connectivity is available. This tool has been used successfully in Zanzibar for more than three years and has been recognized as one of the most advanced applications of its kind.

Methods

We adapted the Coconut Surveillance system for Ebola surveillance and response, and expanded the system for use with other communicable diseases. With a near real-time outbreak detectionsystem for Ebola, we may reduce the response time and contain an outbreak faster. Using a cloud-based data repository, the modified Coconut System, known as Coconut Plus, also has the added value of case and case-contacts specific information sharing in real-time with the national, provincial, and district level public health authorities, who would have convenient and secure access to case and contact information via the Internet. The software modifications to the Coconut System have been informed by testing and stakeholder feedback.

Results

We have developed Coconut Plus around the Coconut software architecture, which allows the team to quickly develop specific workflows and applications, such as contact tracing, on top of a solid and well-supported base. Additionally, the adaptation was structured to accommodate the build-out of multiple diseases, and is uniquely helpful for diseases that require tracking many contacts. We were granted access in DRC to test interoperability with DHIS 2, the most widely used health information system software in Ebola affected countries. Coconut Plus is now using the DHIS 2 organizational hierarchy definition, which means that organizational hierarchy (including information on administrative units and health care facilities) can be exported directly from DHIS 2 to Coconut Plus. Stakeholder feedback on the usability and feasibility of the adapted system has been enthusiastic, and stressed the need for additional resources to make a pilot successful, including mobile phones and improved mobility of surveillance staff in the field.

The following screen cast provides an overview of the application:

https://www.youtube.com/watch?v=jjLT3pLLW-U

Conclusions

Coconut Surveillance Plus solves an absence of a real-time mobile decision support disease surveillance and response system that can be used for Ebola and other infectious diseases in countries with limited surveillance infrastructure. More broadly, this system could also be used for many communicable diseases that require contact tracing and an urgent outbreak response in environments that require rapid scale up of a distributed surveillance, rapid response, and case management system.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To assess the impact on human health observed in association with periods of poor air quality which extended across international borders, affecting both London (UK) and Paris (France). In particular to quantify increased levels of emergency department (ED) attendances for asthma and wheeze/difficulty breathing, and how different age groups were affected. Here, using ED syndromic surveillance from England and France, we aimed to identify and describe the acute impact of periods of particularly poor air quality during 2014 on human health in both London and Paris.

Introduction The impact of poor air quality (AQ) on human health is a global issue, with periods of poor AQ known to occur in multiple locations, across different countries at, or around the same time. The Public Health England (PHE) Emergency Department Syndromic Surveillance System (EDSSS) is a public health legacy of the London 2012 Olympic and Paralympic Games, monitoring anonymised daily attendance data in near real-time from a sentinel network of up to 38 EDs across England and Northern Ireland during 2014. The Organisation de la Surveillance Coordonnée des URgences (OSCOUR®) is a similar ED system coordinated by Santé publique France and has been running in France since 2004, established following a major heatwave in 2003 to improve real-time public health surveillance capabilities. This truly national network included around 540 EDs in 2014.

Methods Periods of poor AQ during 2014 in both London and Paris, which were likely to have an acute impact on human health were identified from the daily particulate monitoring data made available by the monitoring authorities in each location. 1,2 Daily ED syndromic surveillance data for selected health indicators (asthma, difficulty breathing type attendances and myocardial ischaemia (MI)) were gathered from EDSSS and OSCOUR® for London and Paris respectively. The standard method used for the daily statistical analysis of EDSSS (RAMMIE method), 3 was also applied to OSCOUR® and used to identify days where the numbers of attendances reported in both the EDSSS and OSCOUR® systems were statistically significantly different to the historical data, based on the previous 2 years.

Results Distinct differences were identified between the impact observed on different age groups, with increased asthma ED attendances in children during and following some AQ events, though a greater impact was observed in adults around other AQ events. Increases in ED attendances for asthma were identified at several points where no AQ events were reported, both short lived spikes during the summer period in particular and a more sustained increase towards the start of autumn.

Conclusions Despite EDSSS and OSCOUR® having been developed in different countries, at different times and resulting from different drivers, both systems use very similar syndromic indicators to identify asthma, difficulty breathing and MI attendances. Using these systems, short term impacts of multiple AQ events which crossed international boundaries were successfully identified and investigated by English and French public health authorities. Periods of poor AQ are not the only events that can affect asthma type attendances as identified here, thunderstorm activity and the beginning of a new academic year also coincided with increased attendances in both London and Paris. Harmonisation of surveillance methods across different international jurisdictions is possible and there is the potential for future cross border surveillance and harmonisation of methods between countries to improve international health surveillance and early warning of potential public health threats affecting multiple countries.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the process, benefits, and challenges of implementing a distributed model for chronic disease surveillance across thirteen Canadian jurisdictions.

Introduction The Public Health Agency of Canada (PHAC) established the Canadian Chronic Disease Surveillance System (CCDSS) in 2009 to facilitate national estimates of chronic disease prevalence, incidence, and health outcomes. The CCDSS uses population-based linked health administrative databases from all provinces/territories (P/Ts) and a distributed analytic protocol to produce standardized disease estimates.

Methods The CCDSS is founded on deterministic linkage of three administrative health databases in each Canadian P/T: health insurance registration files, physician billing claims, and hospital discharge abstracts. Data on all residents who are eligible for provincial or territorial health insurance (about 97% of the Canadian population) are captured in the health insurance registration files. Thus, the CCDSS coverage is near-universal. Disease case definitions are developed by expert Working Groups after literature reviews are completed and validation studies are undertaken. Feasibility studies are initiated in selected P/Ts to identify challenges when implementing the disease case definitions. Analytic code developed by PHAC is then distributed to all P/Ts. Data quality surveys are routinely conducted to identify database characteristics that may bias disease estimates over time or across P/Ts or affect implementation of the analytic code. The summary data produced in each P/T are approved by Scientific Committee and Technical Committee members and then submitted to PHAC for further analysis and reporting.

Results National surveillance or feasibility studies are currently ongoing for diabetes, hypertension, selected mental illnesses, chronic respiratory diseases, heart disease, neurological conditions, musculoskeletal conditions, and stroke. The advantages of the distributed analytic protocol are (Figure 1): (a) changes in methodology can be easily made, and (b) technical expertise to implement the methodology is not required in each P/T. Challenges in the use of the distributed analytic protocol are: (a) heterogeneity in healthcare databases across P/Ts and over time, (b) the requirement that each P/T use the minimum set of data elements common to all jurisdictions when producing disease estimates, and (c) balancing disclosure guidelines to ensure data confidentiality with comprehensive reporting. Additional challenges, which include incomplete data capture for some databases and poor measurement validity of disease diagnosis codes for some chronic conditions, must be continually addressed to ensure the scientific rigor of the CCDSS methodology.

Conclusions The CCDSS distributed analytic protocol offers one model for national chronic disease surveillance that has been successfully implemented and sustained by PHAC and its P/T partners. Many lessons have been learned about national chronic disease surveillance involving jurisdictions that are heterogeneous with respect to healthcare databases, expertise, and population characteristics.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To build capacity to conduct syndromic surveillance at the local level by leveraging a health surveillance need.

Introduction
Wildfires occur annually in Oregon, and the health risks of wildfiresmoke are well documented. Before implementing syndromic surveillance through Oregon ESSENCE, assessing the health effects of wildfires in real time was very challenging. Summer 2015 marked the first wildfire season with 60 of 60 eligible Oregon emergency departments (EDs) reporting to ESSENCE. The Oregon ESSENCE team developed a wildfire surveillance pilot project with two local public health authorities (LPHAs) to determine their surveillance needs and practices and developed a training program to increase capacity to conduct surveillance at the local level. Following the training, one of the LPHAs integrated syndromic surveillance into its routine surveillance practices. Oregon ESSENCE also integrated the evaluation findings into the summer 2016 statewide wildfiresurveillance plan.

Methods
Oregon ESSENCE staff recruited two LPHA preparedness coordinators whose jurisdictions are regularly affected by wildfiresmoke to participate in the pilot project. A state public health emergency preparedness liaison served as facilitator in order to increase syndromic surveillance capacity among state preparedness staff. A pre-season interview assessed data and surveillance needs, risk communication practices, and typical response activities during wildfires. Initial project calls focused on determining specific queries that would meet local needs. Participants wanted total ED visit numbers and health outcomes including asthma, chest pain or heart problems. Both LPHAs were interested in using the data to assess health effects on vulnerable populations, including elderly, children, and migrant workers. Oregon ESSENCE staff also recommended queries that would be used if large numbers of people were displaced (e.g., medication refills, dialysis). Before the onset of wildfire season, Oregon ESSENCE epidemiologists created queries and a MyESSENCE page for each participant. LPHA staff practiced running the queries, modifying them, and discussed interpretation and data-sharing best practices. During wildfire season, brief weekly webinars enabled participants to ask questions and learn additional techniques including playing time series as proportions and adjusting geographic parameters to focus on areas with poor air quality. Results
2015 was a severe wildfire season in Oregon, with over 685,000 acres burned. For the first time, local and state public health were able to monitor and share near real-time health information on interagency smoke calls. In the post project evaluation, participants reported increased knowledge of syndromic surveillance, interpretation, and risk communications. There were no marked increases in total emergency department visits, or visits for asthma, heart palpitations, or other heart complaints. The public may have adhered to warnings and effectively protected themselves against exposure to wildfiresmoke, or health effects may have been less severe and not reflected in emergency department data. Over the next several years, Oregon ESSENCE will integrate select urgent care data, which may better capture morbidity due to wildfire smoke. Conclusions
Framing syndromic surveillance training around a health surveillance need was effective because participants were engaged around a high-priority health hazard. In summer 2016, Oregon ESSENCE integrated wildfire health surveillance into a biweekly ESSENCE seasonal hazard surveillance report and invited wildfireresponse partners to subscribe. Local ESSENCE users can use or modify the queries. In 2017, Oregon ESSENCE will incorporate air quality data from the Environmental Protection Agency so partners can monitor air quality and health effects simultaneously.

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Abstract

Objective
The objective of this pilot study was to develop and evaluate syndromic definitions for the monitoring of alcohol-related emergency department (ED) visits in near-real-time syndromic surveillance (SyS) data. This study also evaluates the utility of SyS ED data for the monitoring of underage drinking. ED data could help underage drinking prevention efforts by providing timelier actionable public health information.

Introduction
Underage drinking is a significant public health problem in the United States as well as in Nebraska. Alcohol consumption among underage youth accounts for approximately 5,000 deaths each year in the United States, including motor vehicle crash related deaths, homicides and suicides. In Nebraska, 23% of 12-20 year olds have reported alcohol use during the past 30 days. In 2010, the estimated total costs of underage drinking in Nebraska were $423 million. These costs included medical care, work loss along with pain and suffering. The health consequences of underage drinking include alcohol-related motor vehicle crashes and other unintentional injuries, physical and sexual assault, suicide, self-inflicted injury, death from alcohol poisoning, and abuse of other drugs. The monitoring of near-real-time ED data could help underage drinking prevention efforts by providing timelier actionable public health information.

Methods
Nebraska SyS data from 32 ED facilities was analyzed for visits of 12 to 20 year olds during October 1, 2015 to August 31, 2016. Three syndromic definitions were developed and tested for the monitoring of alcohol-related ED visits in near-real-time SyS data by using ESSENCE. The first and second definitions were based on querying the chief complaint (CC) field for search terms associated with alcohol use and alcohol abuse or intoxication respectively. The third definition consisted of ICD-9-CM and ICD-10-CM diagnostic codes associated to alcohol abuse or intoxication. The three definitions were evaluated for internal consistency: reported diagnostic codes were used to evaluate the first and second definition, while text in the CC field was used to evaluate the third definition. Records with missing CC or diagnostic codes were excluded from the consistency analysis. In addition, the CC field of records detected by the third definition was evaluated for possible alcohol-related health consequences.

Results
A total of 126 cases were detected by using the first definition (CC search terms for alcohol use); 61% (50/82) of these identified alcohol abuse-related diagnostic codes. On the other hand, a total of 64 cases were detected by using the second definition (CC search terms specific for alcohol abuse or intoxication); 89% (33/37) of these identified alcohol abuse-related diagnostic codes. The third definition (diagnostic codes only) detected 111 cases; 49% (51/105) of these identified alcohol-related search terms in records with reported CC. However, keywords associated to alcohol-related health consequences, such as injury, assault, and use of other drugs were found in records with no alcohol-related search terms in the CC field. Diagnostic codes associated to alcohol-related health consequences were observed in 93% (50/54) of these records. These results indicate that alcohol use is underreported in the CC field.

Conclusions
A higher internal consistency was observed for the syndromic definition based on CC search terms associated with alcohol abuse or intoxication. However, a syndromic definition based on diagnostic codes is preferred due to the underreporting of alcohol use in the CC field. The detection of underage alcohol use-related cases could be improved by adding alcohol abuse or intoxication CC search terms to a syndromic definition based on diagnostic codes. Overall, results of this pilot study suggest that a syndromic definition based on diagnostic codes can potentially enhance the surveillance of underage drinking and alcohol-related health consequences.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo describe the potential impact of using toxicology data to support drug overdose mortality surveillance.

Introduction Although Marin County ranks as the healthiest county in California, it ranks poorly in substance abuse indicators, including drug overdose mortality. Death certificates do not always include specific detail on the substances involved in a drug overdose. This lack of specificity makes it difficult to identify public health issues related to specific prescription drugs in our community. We analyzed 2013 drug overdose death toxicology reports to determine if they could improve the description of drug overdose deaths in our community and to describe associated data characteristics.

Methods Toxicology reports were requested from the Office of the Sheriff-Coroner for 37 drug overdose deaths among Marin County residents, comprising 95% of the 39 total drug overdose deaths in 2013. The remaining two deaths were excluded as they were associated with inhalation of therapeutic gases. Select information from toxicology reports was entered into a database for aggregate analyses. Drug overdose deaths were considered “fully detailed” if they included the specific types of drugs involved in the death and did not use any broad language to describe the death (i.e., narcotic, multiple drugs). Student’s t-tests (α=0.05) were used to identify significant differences between groups of interest.

Results Of the 37 drug poisoning deaths analyzed, 34 (92%) had available toxicology information. The remaining three (8%) deaths occurred outside of Marin County and were thus investigated by another jurisdiction. A basic toxicology panel was ordered on 17 (50%) of the 34 drug overdose deaths, while an expanded toxicology panel was ordered on the remaining 17 (50%). Alcohol was identified in the toxicology screen of 15 (44%); Amphetamines were identified in 8 (24%); and opiates were identified in 25 (74%) drug overdose deaths. Among the 25 deaths with at least one opiate identified on the toxicology screen, the majority (52%, n=13) also had alcohol present. The majority of drug overdose deaths, 18 (53%), did not have full information about the type of drug involved. The average number of drugs identified on the toxicology screen of all 34 drug overdose deaths was 6 (SD: 3). The average number of drugs identified in the toxicology screen significantly differed (p<0.0001) between causes of death that were fully detailed (Mean: 4; 95% CI: 3-5) and those that were not fully detailed (Mean: 8; 95% CI: 7-10).

Conclusions Data from the Sheriff-Coroner’s office provided detail on the types of drugs involved in overdose deaths; however, it is difficult for local public health practitioners to make decisions about causality or contributions of these drugs to the death. These data may be useful in understanding the difference between fully detailed and non-detailed drug overdose deaths, and a broader context of drug combinations associated with these deaths. Less drugs were identified in the toxicology screen of deaths that were fully detailed, suggesting that overdose deaths that are not fully detailed may be exceedingly complex, making it difficult for medical examiners and coroners to assess causality. Approximately three-quarters of 2013 drug overdose deaths contained opiates on the toxicology screen, indicating that opiates may be a significant contributor to overdose deaths in our community. Our results are descriptive in nature; therefore, even though alcohol or opiates were identified on the toxicology screen, they may not be responsible for the overdose death. Given that over half of our 2013 overdose deaths were not fully detailed with drug type, local jurisdictions should work closely with their coroner and/or medical examiner to fully detail death certificates with drugs involved in overdose deaths.

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Abstract

Objective To explore the use of emergency department syndromicc surveillance data to identify adverse health events related to electronic cigarettes in order to enhance existing surveillance.

Introduction The North Dakota Department of Health (NDDoH) investigated the feasibility of using syndromic surveillance (SyS) data to identify health care visits due to electronic cigarette (e-cigarette) use. E-cigarettes have been associated with injuries and fatalities in all age groups, including young children attracted to the colorful liquidnicotine carriage packaging [1]. Previously, poison control data was the only resource available to the NDDoH for e-cigarette adverse outcomes surveillance.

Methods Data for all visits from June 28, 2014 to June 28, 2015 were downloaded using the BioSense 2.0 SyS analytic tool. Excel was used to identify visits containing key words related to e-cigarettes in line-level data. We initially searched for visits using variations of the term “e-cigarette.” After meeting with NDDoH subject matter experts, we expanded our search to include other related terms: nicotine, clouding, vaping and variations of “electronic nicotine delivery system (ENDS)”. No diagnosis codes were used as none refer specifically to e-cigarettes. Visits were identified solely through searching free text chief complaint and triage notes fields. Not all facilities participating in the NDDoH SyS program during this time period submitted free text data. Results Out of 650,069 unique visits, four e-cigarette-related visits were identified in rich-text data fields searching for “E-cig” and “E cig.” An additional visit was identified using the search term “nicotine,” although this search primarily identified visits including references to nicotine patches. Of the five visits identified, two were poisonings resulting from small children sucking on liquid nicotine cartridges, one referred to eye irritation as a result of accidentally using liquid nicotine as eye drops, and two referred to cardiac issues (chest pain, heart palpitations) after e-cigarette use. Searches including terms “clouding” and “vaping,” street terms related to e-cigarettes, did not result in the identification of any additional visits related to e-cigarettes; nor did searches related to ENDS. Poison control data from the same time period yielded two calls related to e-cigarette adverse events.

Conclusions It is possible to identify emergency department visits associated with e-cigarette use utilizing SyS data. More visits were identified using SyS data than poison control data, although neither source identified many occurrences of adverse outcomes related to e-cigarettes; nor did searches related to ENDS. Poison control data from the same time period yielded two calls related to e-cigarette adverse events. Visits were identified using SyS data than poison control data, although neither source identified many occurrences of adverse outcomes related to e-cigarettes. E-cig, e cig and nicotine were the most useful search terms, although a search for “nicotine” must exclude the word “patch” to avoid false identifications. The NDDoH receives free-text data from majority of the visits in our system, but not all facilities submit free-text fields, and the number that did varied over the study period. Because no drop-down chief complaints or diagnosis codes related to e-cigarettes exist, data from facilities that did not provide free text data were not helpful in identifying e-cigarette-related visits. This investigation emphasizes the need for free text fields when using SyS to investigate emerging issues.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Demonstrate that use of the Washington State health information exchange (HIE) to facilitate access to prescription monitoring program (PMP) data enhances the effectiveness of a PMP. The increased accessibility will lead to improved patient care by giving providers more complete and recent data on patients’ controlled substance prescriptions. 

Introduction Washington State experienced a five-fold increase in deaths from unintentional drug overdoses between 1998 and 2014. The PMP collects data on controlled substances prescribed to patients and makes the data available to healthcare providers, giving providers another tool for patient care and safety. Optimal impact for the program depends on providers regularly accessing the information to review patients’ dispensing history. We have found through providers’ surveys and work with stakeholders that the best way to increase use is to make data seamlessly accessible through electronic health record systems (EHRs). This approach does not require a separate login to the PMP portal. This linkage works through the Health Information Exchange (HIE) to make PMP data available to providers via EHRs. The HIE facilitates electronic communication of patient information among organizations including hospitals and providers. In addition to the PMP, another resource to address the prescription drug abuse problem is the Emergency Department Information Exchange (EDIE), a web-based technology that specifically connects emergency departments statewide to track patients who visit multiple EDs. We also developed a connection between EDIE and PMP data through the HIE.

Methods Increased provider utilization of the PMP will be achieved by using the HIE to create more seamless access to PMP data through providers’ EHRs and through the EDIE system. This will be done by completing the build out of a transaction using NCPCP 10.6, piloting the connection with healthcare systems and EHR vendors, and by continuing to promote and encourage the PMP to remain an MU option through recent rule changes being proposed by CMS/ONC. The pilot with Epic was conducted in 2015 from April to October. Epic has released an update, available to Washington customers, that includes the connection between EHR and PMP. PMP data is also connected to EDIE. That connection is now live in 80 of 93 acute care hospital emergency departments. Results To date the transaction is in production with 80 emergency departments and achieving positive results. In 2015 the PMP received more than 2 million queries from the EDIE system via the HIE, compared to 900,000 queries via the online PMP portal in the year before the link through the HIE was available. We have also finished a pilot with a major EHR vendor and are working to on-board their customers. We are also working directly with healthcare systems, and as of September 2016 there are 3 healthcare facilities testing that are expected to go live by the end of the year. Over 90 registrations for meaningful use of the PMP have been received, representing more than 1000 clinics. Improved access to PMP data benefits providers by allowing them to check the history of transactions linked to their DEAnumbers, which can alert them to fraudulent prescriptions.

Conclusions Integration of PMP data with other information systems will greatly enhance the accessibility and impact of the data. Making a connection to EDIE alone more than doubled the number of queries we received from providers in 2015. We anticipate even more inquiries once additional care settings are connected. We hope from this to see continued decline in unintentional poisonings due to prescription drugs.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
The purpose of this study was to investigate the use of large-scale medical claims data for local surveillance of under-immunization for childhood infections in the United States, to develop a statistical framework for integrating disparate data sources on surveillance of vaccination behavior, and to identify the determinants of vaccine hesitancy behavior.

Introduction
In the United States, surveillance of vaccine uptake for childhood infections is limited in scope and spatial resolution. The National Immunization Survey (NIS) - the gold standard tool for monitoring vaccine uptake among children aged 19-35 months - is typically constrained to producing coarse state-level estimates. In recent years, vaccine hesitancy (i.e., a desire to delay or refuse vaccination, despite availability of vaccination services) has resurfaced in the United States, challenging the maintenance of herd immunity. In December 2014, foreign importation of the measles virus to Disney theme parks in Orange County, California resulted in an outbreak of 111 measles cases, 45% of which were among unvaccinated individuals. Digital health data offer new opportunities to study the social determinants of vaccine hesitancy in the United States and identify finer spatial resolution clusters of under-immunization using data with greater clinical accuracy and rationale for hesitancy.

Methods
Our U.S. medical claims data comprised monthly reports of diagnosis codes for under-immunization and vaccine refusal (Figure 1). These claims were aggregated to five-digit zip-codes by patient age-group from 2012 to 2015. Spatial generalized linear mixed models were used to generate county-level maps for surveillance of under-immunization and to identify the determinants of vaccine hesitancy, such as income, education, household size, religious group representation, and healthcare access. We developed a Bayesian modeling framework that separates the observation of vaccine hesitancy in our data from true underlying rates of vaccine hesitancy in the community. Our model structure also enabled us to borrow information from neighboring counties, which improves predictions of vaccine hesitancy in areas with missing or minimal data. Estimates of the posterior distributions of model parameters were generated via Markov chain Monte Carlo (MCMC) methods.

Results
Our modeling framework enabled the production of county-level maps of under-immunization and vaccine refusal in the United States between 2012-2015, the identification of geographic clusters of under-immunization, and the quantification of the association between various epidemiological factors and vaccination status. In addition, we found that our model structure enabled us to account for spatial variation in reporting vaccine hesitancy, which improved our estimation.

Conclusions
Our work demonstrates the utility of using large-scale medical claims data to improve surveillance systems for vaccine uptake and to assess the social and ecological determinants of vaccine hesitancy. We describe a flexible, hierarchical modeling framework for integrating disparate data sources, particularly for data collected through different measurement processes or at different spatial scales. Our findings will enhance our understanding of the causes of under-immunization, inform the design of vaccination policy, and aid in the development of targeted public health strategies for optimizing vaccine uptake. Figure 1. Instances of vaccine refusal (per 100,000 population) for U.S. counties in 2014 as observed in medical claims data.

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Abstract

Objective This study aims to show the application of longitudinal statistical and epidemiological methods for building a proactive prescription drug surveillance system for public health. Introduction Prescription Drug Monitoring Programs (PDMPs) are operating in 49 states and several U.S. territories. Current methods for surveillance of prescription drug related behaviors, include the mean daily dosage of morphine milligram equivalent (MME) per patient, annual percentage of days with overlapping prescriptions per patient, and annual multiple provider episodes for multiple controlled substance prescription drugs per patient that are described elsewhere.1,2 This work builds on these efforts by extending longitudinal method to prescription drug behavior surveillance in order to predict risks associated with prescription drug use.

Methods Schedule II prescription opioids from January 1, 2014 to February 29, 2016 from the Kansas Tracking and Reporting of Controlled Substances (KTRACS) was used for this analysis. Prescription opioids were linked to the 2016 version of the morphine milligram equivalent conversion table from the National Center for Injury Prevention and Control.3 Population estimates were based on the 2015 County Vintage single-year of age bridged-race estimates from the National Center for Health Statistics and used to calculate age-adjusted rates. A daily high dose opioid prescription was defined as having greater than or equal to 90 morphine milligram equivalent. Since this is a unit-day measure with patients experiencing multiple daily high dose opioid days, the Prentice, William, and Peterson (PWP) recurrent event model was used to estimate the number of high-dose opioid days for Kansas patients by gender and age groups.4,5 Start time was the first prescription date with a high-dose opioid and stop time was the next high-dose opioid date during a study period from January 1, 2014 to Feb 29, 2016. The PWP model is a statistical model that allows for the estimation of covariates on an event history (i.e. total time with prescription opioids, specifically high-dose opioids). Analysis was completed with a stratified Cox-proportional hazard model, sandwich covariance for dependent observations, and statistical significance was assessed with a Wald Chi-square.

PROC PHREG in SAS/STAT(R) 14.1 was used since it has a new FAST option for fitting large proportional counting process hazard model. Results The age-adjusted rate of daily high-dose opioid patients was 3.2 patients per 100 Kansas population-year (95% CI: 3.1 – 3.2). Kansas patients aged 85 and older had the highest age-specific rate of 11.7 (95% CI: 11.5 – 11.9). Preliminary recurrent event analysis shows on average nearly a quarter of approximately 50 million Schedule II opioid patient days were high-dose opioid patient days among 785,514 Kansas patients with any prescribed opioid history. In an initial result stratified by the number of high-dose opioid days and adjusting only for age, males on average had approximately 7% higher hazard of recurrent Schedule II high-dose opioid prescription days than females (β: 0.07, S.E: 0.002, p<0.0001). Kansas patients aged 45 to 54 compared to Kansas patients 85 and older on average had approximately 14% higher hazard of recurrent Schedule II high-dose opioid prescription days (β: 0.14, S.E: 0.007, p<0.0001).

Conclusions This work demonstrates the application of survival analysis techniques to estimate the population at risk for high-dose opioids, which varies by the length of the total opioid prescription history. Early results from the recurrent event analysis showed that Kansas male and patients aged 45 to 54 years had the longest history of high-dose opioids. Annual cross-sectional population estimates may incorrectly estimate the estimated risk of high-dose prescription opioids since it assumes all patients have the same prescription history. PDMPs are longitudinal databases. Survival analysis methods like recurrent event models can leverage the longitudinal structure to more precisely estimate risk statistics. Future work includes incorporation of health outcomes data and further prescription covariates to assess the timing and intensity of opioid potency escalation.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Influenza is a contagious disease that causes epidemics in many parts of the world. The World Health Organization estimates that influenza causes three to five million severe illnesses each year and 250,000-500,000 deaths [1]. Predicting and characterizing outbreaks of influenza is an important public health problem and significant progress has been made in predicting single outbreaks. However, multiple temporally overlapping outbreaks are also common. These may be caused by different subtypes or outbreaks in multipledemographic groups. We describe our Multiple Outbreak Detection System (MODS) and its performance on two actual outbreaks. This work extends previous work by our group [2,3,4] by using model-averaging and a new method to estimate non-influenza influenza-like illness (NI-ILI). We also apply MODS to a real dataset with a double outbreak.

Methods

MODS is part of a framework for disease surveillance developed by our group. In this framework, a natural language processing system extracts symptoms from emergency department patient-care reports. These features are combined with laboratory results and passed to a case detection system that infers a probability distribution over the diseases each patient may have. These diseases include influenza, NI-ILI, and other (appendicitis, trauma, etc.). This distribution is expressed in terms of the likelihoods of the patients’ data. These are given to MODS which searches a space of multiple outbreak models, computes the likelihood of each model, and calculates the expected number of influenza cases day-by-day. This work differs from pastwork in three important ways. First, we address the problem of detecting and characterizing multiple, overlapping outbreaks. Second, we do not rely on simple counts, but use likelihoods given evidence in the free-text portion of patient-care reports as well as laboratory findings. Third, we explicitly account for non-influenza influenza-like illnesses. This is important because some forms of influenza-like illness (such as respiratory syncytial virus) are contagious and exhibit outbreak activity.

This research was approved by the University of Pittsburgh and Intermountain Healthcare IRBs. Results

We conducted a set of experiments with simulated outbreaks. MODS is able to detect a single outbreak six to eight weeks before the peak. It is also able to recognize a second outbreak approximately halfway between peaks for simulated double outbreaks. We conducted experiments using real outbreaks and compared our results to thermometer sales [5]. Using data from Allegheny County Pennsylvania for the 2009-2010 influenza season, on September 1, MODS predicted an outbreak with a peak on October 5. The thermometer peak was October 21. The figure “Prediction on October 1 for Allegheny County” compares MODS’ prediction on October 1 to thermometer sales.

Using data from Salt Lake City Utah for the 2010-2011 influenza season, on November 1 MODS predicted an outbreak with a peak on December 7. The first thermometer peak was December 29. On January 20 MODS predicted a second outbreak with peak on February 9. The second thermometer peak was March 5. The figure “Prediction on January 20 for Salt Lake City” compares MODS’ prediction on January 20 to thermometer sales.

Conclusions

We have built a Multiple Outbreak Detection System that can detect and characterize overlapping outbreaks of influenza. Although the system currently predicts outbreaks of influenza, it is built on a general Bayesian framework that can be extended to other diseases. Future work includes incorporating multiple forms of evidence, modeling other known contagious diseases, and detecting outbreaks of new previously unknown diseases.

Prediction on October 1 for Allegheny County 2009-2010

Prediction on January 20 for Salt Lake City 2010-2011

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

To develop and evaluate syndrome definitions for the identification of acute unintentional drug overdose events including opioid, heroin, and unspecified substances among emergency department (ED) visits in Virginia.

Introduction

Nationally, deaths due to opioid overdose have continually increased for the past 15 years. Deaths specifically related to heroin increased more than four-fold between 2002 and 2014. Hospital inpatient discharge data provide information on non-fatal overdoses, but include a significant lag in reporting time. Syndromic ED visit data provide near real-time identification of public health issues and can be leveraged to inform public health actions on the emerging threat of drug overdose.

Methods

Virginia Department of Health (VDH) developed two syndromedefinitions in 2014 to capture acute unintentional drug overdose events among syndromic ED visit data. Syndrome 1 captured visits for overdose, whether or not a specific substance was mentioned. Syndrome 2 captured only visits for heroin overdose. Definitions were based on free-text terms found within the chief complaint and standardized text or International Classification of Diseases (ICD) codes within the diagnosis field. In 2016, both definitions were revised to identify additional inclusion and exclusion criteria according to CDC guidance documentation and syndrome definitions used by other state jurisdictions. Microsoft SQL was used to modify both definitions based on the newly identified chief complaint and diagnosis criteria. Record level data were analyzed for their adherence to established criteria using an iterative evaluation process. The scope of Syndrome 1 (2016) was narrowed from the 2014 version by excluding visits for non-opioid substances, heroin, and non-acute indicators. It included chief complaint and diagnosis terms related to opioids, unspecified substance overdose, narcotics, and Narcan or naloxone, and excluded terms related to suicide, alcohol overdose alone, withdrawal, detoxification, rehab, addiction, constipation, chronic pain, and any specified non-opioid drug medication. Syndrome 2 (2016) included chief complaint or diagnosis terms mentioning heroin overdose and excluded suicide, withdrawal, detoxification, rehab, and addiction. Visits with mention of suicide, rehab, or addiction were identified during the evaluation process, resulting in the exclusion of these terms in the revised query.

From January 1, 2015 to July 31, 2016, the number of visits captured by the revised syndrome definitions was compared to the number captured by the 2014 definitions. Correlation coefficients were calculated using SAS 9.3. Results

The revised Syndrome 1 found 4296 fewer ED visits (29% decrease) for acute unintentional drug overdose between January 1, 2015 and July 31, 2016 compared to the 2014 definition. Despite the drop in volume, the monthly trends were similar for the 2014 and 2016 definitions (correlation coefficient = 0.95, p < 0.001). For the same time period, the revised Syndrome 2 definition returned 108 fewer visits (6% decrease) for acute unintentional heroin overdose. The monthly trends were also similar for the 2014 and 2016 definitions (correlation coefficient = 0.98, p < 0.001).

Conclusions

Both revised syndrome definitions improved specificity in capturing overdose visits as Syndrome 1 (2016) identified 29% fewer visits and Syndrome 2 (2016) identified 6% fewer visits found to be unrelated to the desired overdose criteria. When developing the revised syndrome definitions, VDH decided to exclude non-acute drug-related visits. Terms such as addiction, detoxification, rehab, withdrawal, chronic pain, and constipation were indicative of habitual drug use or abuse instead of acute overdose and were thus excluded. In narrowing the scope of Syndrome 1, VDH also identified and excluded visits for specified drug and medication overdose. Together, these expanded exclusion criteria resulted in greater specificity with both updated syndromes. These revised syndrome definitions enable VDH to better track opioid and heroin overdose trends in near real-time and overextended time periods which can be used to inform public health actions. Limitations include the inconsistency of diagnosis coding among syndromic data submitters, which may lead to geographic underrepresentation of unintentional drug overdose visits based on the location of health care systems. VDH will continue to evaluate and redefine these overdose syndrome definitions as this emerging health issue evolves.

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Abstract

Objective
The transition from ICD-9-CM to ICD-10-CM requires evaluation of syndrome mappings to obtain a baseline for syndromic surveillance purposes. Two syndrome mappings are evaluated in this report.

Introduction
The Department of Defense conducts syndromic surveillance of health encounter visits of Military Health System (MHS) beneficiaries. Providers within the MHS assign up to 10 diagnostic codes to each health encounter visit. The diagnosis codes are grouped into syndrome and sub-syndrome categories. On October 1, 2015, the Health and Human Services-mandated transition from ICD-9-CM to ICD-10-CM required evaluation of the syndrome mappings to establish a baseline of syndrome rates within the DoD. The DoD data within the BioSense system currently utilizes DoD ESSENCE syndrome mappings. The Master Mapping Reference Table (MMRT) was developed by the CDC to translate diagnostic codes across the ICD-9-CM and ICD-10-CM encoding systems to prepare for the transition. The DoD ESSENCE and MMRT syndrome definitions are presented in this analysis for comparison.

Methods
DoD data was pulled from the BioSense Platform through a RStudio server on October 11, 2016, querying data from October 1, 2014 to September 30, 2016. This time period provides twelve months of ICD-9-CM data and twelve months of ICD-10-CM data. The ICD codes were binned to both DoD ESSENCE syndromes and MMRT macro syndromes for comparison. Although a patient visit may contain up to 10 ICD codes, only the first four were included for this analysis. Providers are trained to prioritize diagnosis codes by position. Only 2.2% of visits had greater than 4 diagnostic codes. Each ICD code in a visit is binned to an applicable syndrome. The total number of visits includes visits that binned and did not bin to a syndrome. Multiple syndromes may be assigned to one patient’s health encounter visit if multiple ICD codes are binned. Additionally, more than one code per visit may be assigned to the same syndrome; however, only unique syndromes are counted in the total syndrome rate. The total syndrome rate was calculated by total unique syndrome visits as the numerator and total number of visits during the ICD-9-CM or ICD-10-CM time period as the denominator. The rates per 1000 total visits were calculated.

Results
Among the DoD ESSENCE syndromes, the ICD-9-CM rate for ILI was 36.3 per 1,000 compared to the ICD-10-CM rate of 38.6 per 1,000. The ICD-9-CM rate for neurological was 18.1 per 1,000 compared to the ICD-10-CM rate of 0.2 per 1,000. Among the MMRT syndromes, the ICD-9-CM rate for ILI was 16.7 per 1,000 compared to the ICD-10-CM rate of 38.4 per 1,000. The ICD-9-CM rate for mental disorders was 73.8 per 1,000 compared to the ICD-10-CM rate of 73.2 per 1,000.

Conclusions
This analysis provides baseline rates of MMRT syndromes and sub-syndromes for syndromic surveillance during the ICD-9-CM to ICD-10-CM transition. These data will serve for future comparison and tracking of syndrome-specific trends for military-relevant health threats.


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Abstract

Objective

Our objective was to determine if the detection performance of current surveillance algorithms to detect call clusters is improved by stratifying by exposure category.

Introduction

The Centers for Disease Control and Prevention (CDC) uses the National Poison Data System (NPDS) to conduct surveillance of calls to United States poison centers (PCs) to identify clusters of reports of hazardous exposures and illnesses. NPDS stores basic information from PC calls including call type (information request only or call reporting a possible chemical exposure), exposure agent, demographics, clinical, and other variables. CDC looks for anomalies in PC data by using automated algorithms to analyze call and clinical effect volume, and by identifying calls reporting exposures to pre-specified high priority agents. Algorithms analyzing call and clinical effect volume identify anomalies when the number of calls exceeds a threshold using the historical limits method (HLM). Clinical toxicologists and epidemiologists at the American Association of Poison Control Centers and CDC apply standardized criteria to determine if the anomaly is a potential incident of public health significance (IPHS) and then notify the respective health departments and PCs as needed. Discussions with surveillance system users and analysis of past IPHS determined that call volume-based surveillance results in a high proportion of false positive anomalies. A study assessing the positive predictive value (PPV) of this approach determined that fewer than four percent of anomalies over five-year period were IPHS. A low PPV can cause an unnecessary waste of staff time and resources. We hypothesized that first stratifying call volume by exposure category would reduce the number of false positives. With the help of medical toxicologists, we created 20 toxicologically-relevant exposure categories to test this hypothesis.

Methods

To compare cluster detection performance between the two approaches, we used a historical testbed of hourly exposure call counts with and without initial stratification by exposure category from 10 selected PCs from Jan 1, 2006 - Jul 31, 2015. We ran the HLM for both non-stratified and stratified testbeds to estimate the monthly number of anomalies triggered (i.e., alert burden). Our target signals to assess detection performance consisted of call samples from three large public health events: the 2009 Salmonella food poisoning event from contaminated peanut butter, the 2012 Hurricane Sandy-associated carbon monoxide poisonings in New Jersey, and the 2014 Elk River contaminated water spill in West Virginia (WV). For each event, we chose 30 random calls one thousand times to obtain 1000 random sets of inject clusters. Each inject cluster was iteratively added into the testbed with and without initial stratification by exposure category. We then applied the HLM for each iteration to see if the algorithm identified the inject cluster. The sensitivity for each approach for each PC was calculated as the proportion of iterations where the algorithm identified the inject cluster. We reported mediansensitivities from the ten PCs for each of the time windows of 1, 2, 4, 8, and 24 hours.

Results

Figure 1 summarizes results for the WV event with markers showing anomaly burden (x-axis) and sensitivity (y-axis) using the stratified (Δ) and the non-stratified (○) approach by different timewindows (hrs). The results from the other two events are not shown but established similar patterns. Anomaly burden is shown as the estimated monthly anomaly count for each approach. For example, markers linked by the arrow show that with a 4-hour time window, the stratified approach achieves nearly perfect sensitivity with ~10 anomalies as the monthly anomaly burden while sensitivity of the non-stratified approach is below 20% with ~40 monthly anomalies. The stratified approach gave improved overall sensitivity across all time windows, and reduced anomaly burden for 1-, 2-, and 4-hour time windows.

Conclusions

We found a consistent detection advantage (higher sensitivity and lower anomaly burden) for the stratified vs traditional non-stratified approach for 1-, 2-, and 4-hour time windows. Further research should focus on refining the stratified approach and the specific surveillance parameters (such as time windows) that increase algorithm performance. Figure 1: Detection performance comparison: stratified vs non-stratified approach; 2014 Elk River contaminated water spill in West Virginia scenario

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Abstract

Objective
Our objective was to compare the effectiveness of applying the historical limits method (HLM) to poison center (PC) call volumes with vs without stratifying by exposure type.

Introduction
The Centers for Disease Control and Prevention (CDC) uses the National Poison Data System (NPDS) to conduct surveillance of calls to United States PCs. PCs provide triage and treatment advice for hazardous exposures through a free national hotline. Information on demographics, health effects, implicated substance(s), medical outcome of the patient, and other variables are collected. CDC uses automated algorithms to identify anomalies in both pure call volume and specific clinical effect volume, and to identify calls reporting exposure to high priority agents. Pure and clinical effect volume anomalies are identified when an hourly call count exceeds a threshold based on historical data using HLM. Clinical toxicologists and epidemiologists at the American Association of Poison Control Centers and CDC apply standardized criteria to determine if an anomaly identifies a potential incident of public health significance (IPHS) and to notify the respective health departments and local PCs as needed. Discussions with NPDS users and analysis of IPHS showed that alerting based on pure call volume yielded excessive false positives. A study using a 5-year NPDS call dataset assessed the positive predictive value (PPV) of the call volume-based approach. This study showed that less than 4% of anomalies were IPHS. A low PPV can cause unnecessary waste of staff time and resources analyzing false positive anomalies. As an alternative to pure call volume-based detection where all calls to each PC are aggregated for anomaly detection, we considered separating calls by toxicologically-relevant exposure categories for more targeted anomaly detection. We hypothesized that this stratified approach would reduce the number of false positives.

Methods
We derived our exposure categories based on the criteria that the categories must: 1) relate to hazardous exposures of public health importance, 2) reflect categories based on clinical effects and treatment modalities, 3) avoid high priority exposures that may be triggered by single calls, 4) be compatible with exposure substance identification codes currently used by PCs and NPDS, and 5) include enough calls for meaningful tracking. We queried all calls reporting exposures to the proposed categories between January 1, 2009 and July 31, 2015 for ten PCs. We applied the HLM method after stratifying by exposure category and tabulated the number of alerts triggered for each category during the study period. We then applied the HLM method for the ten PCs on all combined exposure calls to represent the traditional non-stratified approach. We compared the combined alert burden generated by stratifying by exposure category with the alert burden for the non-stratified approach for varying timewindows (1-, 2-, 4-, 8- and 24-hours). We conducted analysis in R.

Results
We derived a total of 20 exposure categories, including chemicals (n=4), drugs of abuse (n=6), pesticides (n=3), gas/fume/vapors (n=2), contaminated food/water (n=1), and others (n=4). Call counts during 2015 for these categories ranged from approximately 5,000 to 90,000. Table 1 shows the total number of alerts triggered for each method by time windows. There was a marked reduction of alert burden when first stratifying by exposure category for time windows shorter than eight hours compared to the alert burden for the non-stratified approach. Conclusions: Stratification of call volume by exposure category and timewindow suggests potential improvement over traditional non-stratified approach by having a lower alert burden. Further work should focus on refining the exposure categories, refining the timewindow for surveillance, and assessing other detection performance metrics, such as sensitivity.

Table 1: Alert burden comparison for the non-stratified vs stratified approach

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Abstract

Objective
To improve understanding of the relative burden of different causative respiratory pathogens on respiratory syndromic indicators monitored using syndromic surveillance systems in England. Introduction
Public Health England (PHE) uses syndromic surveillance systems to monitor for seasonal increases in respiratory illness. Respiratory illnesses create a considerable burden on health care services and therefore identifying the timing and intensity of peaks of activity is important for public health decision-making. Furthermore, identifying the incidence of specific respiratory pathogens circulating in the community is essential for targeting public health interventions, e.g. vaccination. Syndromic surveillance can provide early warnings of increases, but cannot explicitly identify the pathogens responsible for such increases. PHE uses a range of general and specific respiratory syndromic indicators in their syndromic surveillance systems, e.g. “all respiratory disease”, “influenza-like illness”, “bronchitis” and “cough”. Previous research has shown that “influenza-like illness” is associated with influenza circulating in the community, whilst “cough” and “bronchitis” syndromic indicators in children under 5 are associated with respiratory syncytial virus (RSV). However, the relative burden of other pathogens, e.g. rhinovirus and parainfluenza, is less well understood. We have sought to further understand the relationship between specific pathogens and syndromic indicators and to improve estimates of disease burden. Therefore, we modelled the association between pathogen incidence, using laboratory reports and health care presentations, using syndromic data. Methods
We used positive laboratory reports for the following pathogens as a proxy for community incidence in England: human metapneumovirus (HMPV), RSV, coronavirus, influenza strains, invasive haemophilus influenzae, invasive streptococcus pneumoniae, mycoplasma pneumoniae, parainfluenza and rhinovirus. Organisms were chosen that were found to be important in previous work and were available from routine laboratory testing. Syndromic data included consultations with family doctors (called General Practitioners or GPs), calls to anational telephone helpline “NHS 111” and attendances at emergency departments (EDs). Associations between laboratory reports and syndromic data were examined over four winter seasons (weeks 40 to 20), between 2011 and 2015. Multiple linear regression was used to model correlations and to estimate the proportion of syndromic consultations associated with specific pathogens. Finally, burden estimates were used to infer the proportion of patients affected by specific pathogens that would be diagnosed with different symptoms. Results
Influenza and RSV exhibited the greatest seasonal variation and were responsible for the strongest associated burden on general respiratory infections. However, associations were found with the other pathogens and the burden of streptococcus pneumoniae was important in adult age groups (25 years and over). The model estimates suggested that only a small proportion of patients with influenza receive a specific diagnosis that is coded to an “influenza-like illness” syndromic indicator, (6% for both GP in-hours consultations and for emergency department attendances), compared to a more general respiratory diagnosis. Also, patients with influenza calling NHS 111 were more likely to receive a diagnosis of fever or cough than cold/flu. Despite these findings, the specific syndromic indicators remained more sensitive to changes in influenza incidence than the general indicators. Conclusions
The majority of patients affected by a seasonal respiratory pathogen are likely to receive a non-specific respiratory diagnosis. Therefore, estimates of community burden using more specific syndromic indicators such as “influenza-like illness” are likely to be a severe underestimate. However, these specific indicators remain important for detecting changes in incidence and providing added intelligence on likely causative pathogens. Specific syndromic indicators were associated with multiple pathogens and we were unable to identify indicators that were good markers for pathogens other than influenza or RSV. However, future work focusing on differences between ages and the relative levels of overall burden of pathogens may be able to provide estimates for the mix of pathogens present in the community in real-time.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
We present the multidimensional tensor scan (MDTS), a new method for identifying emerging patterns in multidimensional spatio-temporal data, and demonstrate the utility of this approach for discovering emerging geographic, demographic, and behavioral trends in fatal drug overdoses.

Introduction
Drug overdoses are an increasingly serious problem in the United States and worldwide. The CDC estimates that 47,055 drug overdose deaths occurred in the United States in 2014, 61% of which involved opioids (including heroin, pain relievers such as oxycodone, and synthetics). Overdose deaths involving opioids increased 3-fold from 2000 to 2014. These statistics motivate public health to identify emerging trends in overdoses, including geographic, demographic, and behavioral patterns (e.g., which combinations of drugs are involved). Early detection can inform prevention and response efforts, as well as quantifying the effects of drug legislation and other policy changes. The fast subset scan detects significant spatial patterns of disease by efficiently maximizing a log-likelihood ratio statistic over subsets of data points, and has recently been extended to multidimensional data (MD-Scan). While MD-Scan is a potentially useful tool for overdose surveillance, the high dimensionality and sparsity of the data requires a new approach to estimate and represent baselines (expected counts), maintaining both accuracy and efficient computation when searching over subsets.

Methods
The multidimensional tensor scan (MDTS) is a new approach to subset scanning in multidimensional data. In addition to detecting the spatial area (subset of locations) and time window affected by an emerging outbreak, MDTS can also identify the affected subset of values for each observed attribute. For example, given the overdose surveillance data described below, MDTS can identify the affected genders, races, age ranges, and which drugs were involved. MDTS finds subsets of the attribute space with higher than expected case counts, first using a novel tensor decomposition approach to estimate the expected counts. MDTS then iteratively applies a conditional optimization step, optimizing over all subsets of values for each attribute conditional on the current subsets of values for all other attributes, and using the linear-time subset scanning property to make each conditional optimization step computationally efficient. The resulting approach has high power to detect and characterize emerging trends which may only affect a subset of the monitored population (e.g., specific ages, genders, neighborhoods, or users of particular combinations of drugs).

Results
We used MDTS to analyze publicly available data from the Allegheny County, PA medical examiner’s office and to detect emerging overdose patterns and trends. The dataset consists of ~2000 fatal accidental drug overdoses between 2008 and 2015. For each overdose victim, we have date, location (zip code), age, gender, race, and the presence/absence of 27 commonly abused drugs in their system. The highest-scoring clusters discovered by MDTS were shared with Allegheny County’s Dept. of Human Services and their feedback obtained. One set of potentially relevant findings from our analysis involves fentanyl, a dangerous and potent opioid which has been a serious problem in western PA. In addition to identifying two well-known, large clusters of overdoses—14 deaths in January 2014 and 26 deaths in March-April 2015—MDTS was able to provide additional information about each cluster. For example, the first cluster was likely due to fentanyl-laced heroin, while the second was more likely due to fentanyl disguised as heroin (only 11 victims had heroin in their system). Moreover, the second cluster was initially confined to the Pittsburgh suburb of McKeesport and a typical demographic of white males ages 20-49, before spreading across the county. Our analysis demonstrated that prospective surveillance using MDTS would have identified the cluster as early as March 29th, enabling targeted prevention efforts. MDTS also discovered a previously unidentified, highly localized cluster of fentanyl-related overdoses affecting an unusual and underserved demographic (elderly black males near downtown Pittsburgh). This cluster occurred in January-February 2015, and may have been related to the larger cluster of fentanyl-related overdoses that occurred two months later. Finally, we identified multiple overdose clusters involving combinations of methadone and Xanax between 2008 and 2012, and observed dramatic reductions in these clusters corresponding to the passage of the Methadone Death and Incident Review Act (October 2012), which increased state oversight of methadone clinics and prescribing physicians. Conclusions
Retrospective analysis of Allegheny County overdose data suggests high potential utility for a prospective overdose surveillance system, which would enable public health users to identify emerging patterns of overdoses in their early stages and facilitate targeted and effective health interventions. The MDTS approach can also be used for other multidimensional public health surveillance tasks, such as STI surveillance, where the patterns or outbreaks of interest may have demographic, geographic, and behavioral components.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective We present the support vector subset scan (SVSS), a new method for detecting localized and irregularly shaped patterns in spatial data. SVSS integrates the penalized fast subset scan with a kernel support vector machine classifier to accurately detect disease clusters that are compact and irregular in shape.

Introduction Neill’s fast subset scan detects significant spatial patterns of disease by efficiently maximizing a log-likelihood ratio statistic over subsets of locations, but may result in patterns that are not spatially compact. The penalized fast subset scan (PFSS) provides a flexible framework for adding soft constraints to the fast subset scan, rewarding or penalizing inclusion of individual points into a cluster with additive point-specific penalty terms. We propose the support vector subset scan (SVSS), a novel method that iteratively assigns penalties according to distance from the separating hyperplane learned by a kernel support vector machine (SVM). SVSS efficiently detects disease clusters that are geometrically compact and irregular.

Methods Speakman observes that for a fixed value of relative risk, the log-likelihood ratio for the exponential family of expectation-based scan statistics can be written as an additive set function over all data elements. This property enables addition of element-specific penalty terms to the log-likelihood ratio, interpreted as the prior log-odds of including a data point in the cluster. We propose an iterative method for setting the penalty terms which leads to spatially compact clusters, alternately running PFSS to obtain an optimal subset and training a kernel SVM to maximize the margin between points within and outside of the subset. On each iteration of PFSS, penalties are assigned based on distance to the SVM decision boundary. We apply random restarts across the penalty space to approach a global optimum in the non-convex SVSS objective function.

Results We demonstrate detection of disease clusters in mosquito pool tested for West Nile Virus (WNV), using data made publicly available by the Chicago Department of Public Health through the City of Chicago Data Portal. In comparison to the circular scan, which detects circular patterns with elevated WNV, SVSS has improved power to detect disease clusters that are elongated or irregular in shape. For example, the top WNV cluster detected by SVSS roughly conforms to sections of two major rivers in North Chicago, overlapping significant portions of the forest preserves adjacent to these rivers. The unconstrained fast subset scan has high detection power for subtle and irregular disease clusters, but finds patterns that are spatially sparse and intermingled with non-anomalous points. SVSS rewards patterns with spatial coherence, detecting clusters that are compact and separated from non-anomalous points. SVSS introduces soft spatial constraints to the fast subset scan in the form of penalties to the log-likelihood ratio statistic, learned iteratively based on distance to a high-dimensional SVM decision boundary. These constraints give SVSS greater power to detect spatially compact and irregular patterns of disease. Clusters of West Nile Virus detected by three scanning algorithms.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To improve the ability of syndromic surveillance systems to detect unusual events. Introduction Syndromic surveillance systems are used by Public Health England (PHE) to detect changes in health care activity that are indicative of potential threats to public health. By providing early warning and situational awareness, these systems play a key role in supporting infectious disease surveillance programmes, decision making and supporting public health interventions. In order to improve the identification of unusual activity, we created new baselines to model seasonally expected activity in the absence of outbreaks or other incidents. Although historical data could be used to model seasonality, changes due to public health interventions or working practices affected comparability. Specific examples of these changes included a major change in the way telehealth services were provided in England and the rotavirus vaccination programme introduced in July 2013 that changed the seasonality of gastrointestinal consultations. Therefore, we needed to incorporate these temporal changes in our baselines. Methods We used negative binomial regression to model daily syndromic surveillance, allowing for day of week and public holiday effects. To account for step changes in data caused by changes in healthcare system working practices or public health interventions we introduced specific independent variables into the models. Finally, we smoothed the regression models to provide short term forecasts of expected trends. The new baselines were applied to PHE’s four syndromic surveillance systems for daily surveillance and public-facing weekly bulletins. Results We replaced traditional surveillance baselines (based on simple averages of historical data) with the regression models for daily surveillance of 53 syndromes across four syndromic surveillance systems. The improved models captured current seasonal trends and more closely reflected actual data outside of outbreaks. Conclusions Syndromic surveillance baselines provide context for epidemiologists to make decisions about seasonal disease activity and emerging public health threats. The improved baselines developed here showed whether current activity was consistent with expected activity, given all available information, and improved interpretation when trends diverged from expectations.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
This study assesses the utilization of triage notes from emergency departments (EDs) and urgent care centers (UCCs) for active case finding in ESSENCE-FL during the Zika response.

Introduction
The Florida Department of Health (DOH) utilizes the Electronic Surveillance System for the Early Notification of Community Based Epidemics (ESSENCE-FL) as its statewide syndromic surveillance system. ESSENCE-FL comprises of chief complaint data from 231 of 240 EDs, representing 96 percent of the total number of EDs in Florida. Historically, syndromic surveillance has categorized patient chief complaint data into syndromes for the purpose of disease surveillance or outbreak detection. Triage notes are much longer free-text, pre-diagnostic data that capture the presenting symptoms and complaints of a patient.

Methods
Triage notes are being collected from 24 EDs, representing ten percent of total reporting EDs, and seven UCCs, representing 17 percent of total reporting UCCs. Triage notes were made a searchable field in ESSENCE-FL during Zika enhanced surveillance efforts, which facilitated additional case finding of Zika. During the period of February 3, 2016 – July 25, 2016, a free-text query was created to run against the concatenated chief complaint-discharge diagnosis (CCDD) and triage note fields: ^ Zika ^, or ^ ziki ^, or ^ zica ^, or ^ zeka ^, or ^ zeca ^, or ^ microcep ^, or ^ zyka ^.

Additional queries were created to detect foreign travel visits of interest within the CCDD and triage note fields. Results of these queries were analyzed and communicated to county and regional epidemiologists daily for investigation.

Results
The triage note specific queries identified 18 Zika triage note and 11 foreign travel triage note visits of interest. All of these visits were reviewed and investigated by county epidemiologists. These triage note queries identified one case of Zika that had not been previously reported to public health. Of note, seven additional cases of Zika infection were identified using the CCDD field in ESSENCE-FL (five of the seven flagged in both the CCDD and triage note field).

Conclusions
Results from this analysis provide evidence that triage notes within syndromic surveillance systems play a role in active case finding when emerging diseases arise. However, only 31 out of 272 total reporting facilities are submitting triage note to ESSENCE-FL, representing only 11 percent of reporting facilities. Relying on chief complaint and discharge diagnosis data only would have resulted in an undetected case of Zika that would not have been captured by our free-text Zika query. The increased detection of Zika cases allows for public health intervention, including mosquito control response, which in turn reduces the chance of Zika spreading locally in Florida. Triage notes often provide pertinent information for determining when a flagged CCDD needs to be investigated further. Making triage notes a required data element for Meaningful Use compliance would benefit case finding conducted through syndromic surveillance.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To investigate whether aberration detection methods for syndromic surveillance would be more useful if data were stratified by age band.

Introduction When monitoring public health incidents using syndromic surveillance systems, Public Health England (PHE) uses the age of the presenting patient as a key indicator to further assess the severity, impact of the incident, and to provide intelligence on the likely cause. However the age distribution of cases is usually not considered until after unusual activity has been identified in the all-ages population data. We assessed whether monitoring specific age groups contemporaneously could improve the timeliness, specificity and sensitivity of public health surveillance.

Methods First, we examined a wide range of health indicators from the PHE syndromic surveillance systems to identify for further study those with the greatest seasonal variation in the age distribution of cases. Secondly, we examined the identified indicators to ascertain whether any age bands consistently lagged behind other age bands. Finally, we applied outbreak detection methods retrospectively to age-specific data, identifying periods of increased activity that were only detected or detected earlier when age-specific surveillance was used.

Results Seasonal increases in respiratory indicators occurred first in younger age groups, with increases in children under 5 providing early warning of subsequent increases occurring in older age groups. Also, we found age specific indicators improved the specificity of surveillance using indicators relating to respiratory and eye problems; identifying unusual activity that was less apparent in the all-ages population.

Conclusions Routine surveillance of respiratory indicators in young children would have provided early warning of increases in older age groups, where the burden on health care usage, e.g. hospital admissions, is greatest. Furthermore this cross-correlation between ages occurred consistently even though the age distribution of the burden of respiratory cases varied between seasons. Age specific surveillance can improve sensitivity of outbreak detection although all-ages surveillance remains more powerful when case numbers are low.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective We aimed to describe the theoretical basis and the potential applications of the test-negative design for estimating influenza vaccination effectiveness in sentinel influenza surveillance.

Introduction

The test-negative design is a variation of the case-control study in which patients are enrolled in outpatient clinics (and/or hospitals) based on a clinical case definition such as influenza-like illness (ILI). Patients are then tested for influenza virus, and VE is estimated from the odds ratio comparing the odds of vaccination among patients testing positive for influenza versus those testing negative, adjusting for potential confounding factors. The design leverages existing disease surveillance networks and as a result, studies using it are increasingly being reported.

Methods

We sought to examine the theoretical basis for this design using causal analysis including directed acyclic graphs. We reviewed studies that used this design and examined the study populations and settings, the methodologic choices including analytic approaches, and the estimates of influenza VE provided. We conducted simulation studies to examine specific potential biases.

Results

We show how studies using this design can avoid or minimize biases, and where bias may be introduced with particular study design variations. A purported advantage of the test-negative design is to minimize selection bias by health-care seeking behaviour and we demonstrate why residual bias may occur. Another purported advantage of the test-negative design is minimization of misclassification of the exposure; however we show how this source of bias may persist and how exposure misclassification may be a greater cause for concern not dealt with by the study design. In our review, we found great variation in estimates, but consistency between interim and final VE estimates from the same locations, and consistency between VE estimates from inpatient and outpatient studies in the same locations, age groups and years. One outstanding issue is the potential bias due to non-collapsibility.

Conclusions

Our work provides a starting point for further consideration of the validity of the test-negative design, which is an efficient approach for routine monitoring of influenza VE that can be implemented in existing surveillance systems without substantial additional resources. Harmonization of analytic approaches may improve the potential for pooling VE estimates.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To comparatively analyze Google, Twitter, and Wikipedia by evaluating how well change points detected in each web-based source correspond to change points detected in CDC ILI data.

Introduction Traditional influenza surveillance relies on reports of influenza-like illness (ILI) by healthcare providers, capturing individuals who seek medical care and missing those who may search, post, and tweet about their illnesses instead. Existing research has shown some promise of using data from Google, Twitter, and Wikipedia for influenza surveillance, but with conflicting findings, studies have only evaluated these web-based sources individually or dually without comparing all three of them. A comparative analysis of all three web-based sources is needed to know which of the web-based sources performs best in order to be considered to complement traditional methods.

Methods We collected publicly available, de-identified data from the CDC ILINet system, Google Flu Trends, HealthTweets.org, and Wikipedia for the 2012-2015 influenza seasons. Bayesian change point analysis was the method used to detect change points, or seasonal changes, in each of the web-data sources for comparison to change points in CDC ILI data. All analyses were conducted using the R package 'bcp' v4.0.0 in RStudio v0.99.484. Sensitivity and positive predictive values (PPV) were then calculated.

Results During the 2012-2015 influenza seasons, a high sensitivity of 92% was found for Google, while the PPV for Google was 85%. A low sensitivity of 50% was found for Twitter; a low PPV of 43% was found for Twitter also. Wikipedia had the lowest sensitivity of 33% and lowest PPV of 40%.

Conclusions Google had the best combination of sensitivity and PPV in detecting change points that corresponded with change points found in CDC data. Overall, change points in Google, Twitter, and Wikipedia data occasionally aligned well with change points found in CDC data, yet these sources did not detect all changes in CDC data, which could indicate limitations of the web-based data or signify that the Bayesian method is not adequately sensitive. These three web-based sources need to be further studied and compared using other statistical methods before being incorporated as surveillance data to complement traditional systems.

Figure 1. Detection of change points, 2012-2013 influenza season
Figure 2. Detection of change points, 2013-2014 influenza season
Figure 3. Detection of change points, 2014-2015 influenza season

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo explain the utility of using an automated syndromic surveillance program with advanced natural language processing (NLP) to improvecinical quality measures reporting for influenza immunization.IntroductionClinical quality measures (CQMs) are tools that help measure and track the quality of health care services. Measuring and reporting CQMs helps to ensure that our health care system is delivering effective, safe, efficient, patient-centered, equitable, and timely care. The CQM for influenza immunization measures the percentage of patients aged 6 months and older seen for a visit between October 1 and March 31 who received (or reports previous receipt of) an influenza immunization. Centers for Disease Control and Prevention recommends that everyone 6 months of age and older receive an influenza immunization every season, which can reduce influenza-related morbidity and mortality and hospitalizations.MethodsPatients at a large academic medical center who had a visit to an affiliated outpatient clinic during June 1 - 8, 2016 were initially identified using their electronic medical record (EMR). The 2,543 patients who were selected did not have documentation of influenza immunization in a discrete field of the EMR. All free text notes for these patients between August 1, 2015 and March 31, 2016 were retrieved and analyzed using the sophisticated NLP built within Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) – a syndromic surveillance program – to identify any mention of influenza immunization. The goal was to identify additional cases that met the CQM measure for influenza immunization and to distinguish documented exceptions. The patients with influenza immunization mentioned were further categorized by GUARDIAN NLP into: Received, Recommended, Refused, Allergic, and Unavailable. If more than one category was applicable for a patient, they were independently counted in their respective categories. A descriptive analysis was conducted, along with manual review of a sample of cases per each category. ResultsFor the 2,543 patients who did not have influenza immunization documentation in a discrete field of the EMR, a total of 78,642 free text notes were processed using GUARDIAN. Four hundred fifty-three (17.8%) patients had some mention of influenza immunization within the notes, which could potentially be utilized to meet the CQM influenza immunization requirement. Twenty two percent (n=101) of patients mentioned already having received the immunization while 34.7% (n=157) patients refused it during the study time frame. There were 27 patients with the mention of influenza immunization who could not be differentiated into a specific category. The number of patients placed into a single category of influenza immunization was 351 (77.5%), while 75 (16.6%) were classified into more than one category. See Table 1. Conclusions Using GUARDIAN’s NLP can identify additional patients whom may meet the CQM measure for influenza immunization or whom may be exempt. This tool can be used to improve CQM reporting and improve overall influenza immunization coverage by using it to alert providers. Next steps involve further refinement of influenza immunization categories, automating the process of using the NLPtr identify and report additional cases, as well as using the NLP for other CQMs. Table 1. Categorization of influenza immunization documentation within free text notes of 453 patients using NLP

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective We apply an empirical Bayesian framework to perform changepoint analysis on multiple cattle mortality data streams, accounting for delayed reporting of syndromes. Introduction Taking into account reporting delays in surveillance systems is not methodologically trivial. Consequently, most use the date of the reception of data, rather than the (often unknown) date of the health event itself. The main drawback of this approach is the resulting reduction in sensitivity and specificity. Combining syndromic data from multiple data streams (most health events may leave a “signature” in multiple data sources) may be performed in a Bayesian framework where the result is presented in the form of a posterior probability for a disease. Methods We used a historical national database on Swiss cattle mortality to model daily baseline counts of two syndromic time series. Reporting delay was defined as the number of days between reported occurrence and reporting date. The cumulative probability distribution of the estimated reporting delays was used to calculate for each day the proportion of cases that were reported either on the same day or with a delay of 1 to 14 days. We evaluated outbreak detection performance under three scenarios: (A) delayed data reporting occurs but is not accounted for; (B) delayed data reporting occurs and is accounted for; and (C) absence of delayed data reporting (i.e., an ideal system). Outputs are presented as the value of evidence (V) in favour of an ongoing outbreak accumulated over time (30 days in this case). At each time point, V is defined as the ratio between the posterior and prior odds for H1 versus H0: [insert equation 1 here] Using sensitivity, time to detection and in-control run length, performance of the (V-based) system on large and small non-specific outbreaks was measured. Results The evolution of V based on the information available on the 1st, 5th and 10th day after the onset of an outbreak can be visualised in Fig. 1. After 5 days, V shows evidence in favour of an outbreak for both syndromes combined, as well as for on-farm deaths alone, only in the “Delay aware” and “No delay” scenarios. The development of V for the perinatal deaths alone highlights the importance of considering multiple syndromic data streams for outbreak detection, as it speaks in favour of an outbreak at a later stage than on-farm deaths alone or both syndromes combined. Conclusions Our empirical Bayes approach is an attractive alternative to multivariate CUSUM algorithms offering a logical approach to weighting variables and incorporating additional information such as delayed reporting, and a performance on a comparable level to an ideal (no delay) system. Outbreaks are detected earlier and with only a marginal loss of specificity compared to a system where reporting delay is present but unaccounted for. We also found that the accumulation of evidence from several days resulted in a significantly better outbreak detection timeliness, for a given specificity; or a similar timeliness, but higher specificity, compared to an algorithm that only looks for days with unusual high number of counts. Fig. 1: Evolution of V over three time points (t) for the three scenarios. Outbreak starts at t=651. Number of observed perinatal (circle) and on-farm deaths (cross), V for both (solid grey) and individual syndromes (dotted grey and black respectively), prior probability that an outbreak is ongoing (grey dashed) and posterior probability that an outbreak is ongoing given the evidence (black dashed). Horizontal grey solid line shows V=1.


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Abstract

Introduction

Technology that combines traditional manipulations with databases and complete visualization of geographic (spatial) analysis employing maps has been developed in order to explore the possibilities for Geographical Information Systems (GIS) to be used in sanitary and epidemiological surveillance system based on the analysis of morbidity and identification of influence of hazardous chemical environmental factors on human health.

Methods

Graphical analytic method of information processing allowed visual establishing of mathematically determined cause-and-effect relationships between levels of air chemical pollution and morbidity levels for purulent bacterial meningitis.

Results

Calculated average annual contaminations of atmosphere of 20 administrative rayons and seven cities of Lviv oblast with carbon oxide, lead, sulfur dioxide, and dust during the period 2006-2014 were the objects of the study. During a year, 1,920 air samples were collected per each ingredient for each rayon and city according to the laboratorial data of facilities of the State Sanitary and Epidemiological Service in Lviv oblast. Average annual levels of the chemical substances were determined within the M.A.C. in all rayons and cities. However, 4-6% of individual samples in the rayons and 8-10% of individual samples in the cities exceeded the allowed concentrations, which imposed a real ecological danger.

Fig. 1. Levels of carbon oxide air contamination within rayons of Lviv oblast. Morbidity intensity rates for purulent bacterial meningitis were determined for the same period according to statistical reports on infectious disease morbidity in Lviv oblast. In different years, human morbidity fluctuated from 0.7 to 2.3 per 100 thousand of population in the oblast.

The study found the correlation between the concentrations of carbon monoxide, lead, sulfur dioxide, and dust in the air and levels of incidence of bacterial meningitis in people in the cities of Lviv oblast with 1,092 thousand inhabitants, which compose 42.3% of all oblast population. Correlation coefficients are \( r = 0.78 \) (p<0.001), \( r = 0.70 \) (p<0.001), \( r = 0.51 \) (p<0.005), and \( r = 0.68 \) (p<0.02), respectively.

Fig. 2. Correlation dependencies between air contamination and population morbidity rates for purulent bacterial meningitis within rayons of Lviv oblast. The search for a correlation between chemical contamination of atmosphere and the morbidity level the rayon population of the oblast for purulent bacterial meningitis testified the existence of a statistically significant dependence between the level of morbidity for all population layers and atmosphere contamination with sulfur dioxide, lead, carbon monoxide, and dust. The correlation coefficients are \( r = 0.62 \) (p<0.002), \( r = 0.52 \) (p<0.005), \( r = 0.63 \) (p<0.005), \( r = 0.56 \) (p<0.05), correspondingly.

The study found the correlation between the concentrations of sulfur dioxide and lead in the air of Lviv oblast and levels of incidence of purulent bacterial meningitis in children. Correlation coefficients are \( r = 0.55 \) (p<0.05) and \( r = 0.57 \) (p<0.001), respectively.

Conclusions

Using GIS approach, the study resulted in the development of medical-geographical maps of administrative rayons of Lviv oblast. The maps include peculiarities for each year of surveillance. Cause-and-effect relationships between the levels of the anthropogenic pollution of the air basin of Lviv oblast and morbidity levels for purulent bacterial meningitis for the oblast population have been spatially and temporally visualized as a study result.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective HFMD incidence varies between geographic regions at the township in Beijing. The objective of this study was to examine spatial heterogeneity for the association between HFMD incidence and demographic and socioeconomic factors.

Introduction Hand-foot-mouth disease (HFMD) is a common childhood illness and the drivers of HFMD incidence are still not clear [1]. In mainland China, continuing and increasing HFMD epidemics have been recorded since 2008, causing millions of infections and hundreds of deaths annually. In Beijing, 28,667 cases were reported in 2015 and the incidence was 133.28/100,000. The variations in Beijing HFMD epidemics over population, space, and time that have been revealed [2] emphasize the need for further research about risk factors of HFMD occurrence. This study aims to explore local effects on HFMD incidence led by potential factors.

Methods HFMD Data. Beijing HFMD data during 2008–2012 period were provided by the Beijing Center for Disease Prevention and Control. HFMD incidence adopted in this study was the annual average value during the five years. Predictor variables. Potential risk factors obtained from the caserecords (demographic, occupation, health-seeking behavior and spatial POIs (points of interest) consisted of 22 variables involving residence, restaurant, education, medical facilities, business facilities, infrastructure. The scale of different kinds of POIs (1/100,000) was noted by calculating the ratio of the number of POIs to the population at certain township or street committee.

Model Specification. Some initial associations between HFMD incidence and 8 predictor variables (population density, shopping mall, supermarket, pharmacy, kindergarten, middle school, parking lot, health-seeking behavior) were revealed using Pearson correlation analysis and the exploratory regression. An ordinary least squares (OLS) model was fitted to diagnose the residual normality and dependence. Geographically weighted regression (GWR) was chosen to model the relationship, compare the difference from OLS regression and measure how much improvement the local model gained.

Results GWR model with residual independence (Moran’s I = 0.0214, p = 0.3405) and lower AICc, performing much better than OLS model with residual dependence (Moran’s I = 0.1271, p = 0.0000) and higher AICc. Prediction accuracy by GWR (local R² ranging from 0.42 to 0.90, R² = 0.88) was higher than that by OLS (R² = 0.57). The higher local R² values clustered in the east of Fangshan and Urban-Rural Transition Area. Higher coefficient for intercept mainly occurred in north-western and south-eastern portion of Beijing. The coefficients for predictors showed shifting patterns from positive to negative at different township. The local effects led by supermarket and shopping mall showed similar spatial pattern, as well as those by kindergarten and middle school. The scale of pharmacy was positively related to HFMD incidence in the west of Daxing and the junction part of Chaoyang and Tongzhou.

Conclusions This study quantitatively assessed local risk factors of Beijing HFMD occurred in China using GWR model which outperformed OLS regression. The findings could provide valuable information for adequate disease intervention measures and regional policy.

Abstract

Objective Our objective is to describe the environmental conditions associated with confirmed Coccidioides immitis growth and accumulation sites in south central Washington in an effort to understand the ecology and identify additional potential sites across this emerging endemic zone. Introduction Coccidioidomycosis, commonly referred to as Valley Fever, is caused by the soil-borne saprophytic fungus C. immitis and posadasii. These species have historically been found in the desert southwest and Mexico; however, in 2010 there were three coccidioidomycosis cases identified in central Washington. Colonization of soils by C. immitis has been confirmed at exposure sites associated with these cases. Multiple studies have identified a relationship between environmental conditions and C. immitis growth areas, but these relationships have not been evaluated in Washington. The Washington State Department of Health has been conducting environmental surveillance in an effort to understand the geographic distribution of C. immitis in central Washington and the associated risk to humans and animals. Here we describe our environmental surveillance efforts and present preliminary findings related to environmental conditions of C. immitis growth areas in central Washington. Methods We collected soil samples at potential human exposure sites in central Washington, as identified through clinical surveillance and patient interviews. Soil samples were also collected from areas not associated with human cases by looking for similar soils in areas of interest. Soil samples are analyzed by the U.S. Centers for Disease Control and Prevention using real-time PCR that detects Coccidioides-specific targets. We employed data from the USDA Soil Survey Geographic (SSURGO) database to describe environmental conditions associated with positive samples. We used our findings to identify un-sampled regions of central Washington that could potentially support C. immitis growth. Results We detected Coccidioides in 13 soil sampling sites at five locations within the region. These detections included locations not previously described in central Washington. We identified a band stretching across central Yakima and Benton counties with similar soil characteristics to our positive sample sites, which suggests these regions could potentially support the growth of C. immitis. Conclusions Coccidioidomycosis is emerging in south central Washington, and the ecology and geographic distribution of the pathogen are poorly understood. We found that C. immitis presents a risk to humans and animals across a larger region of central Washington than previously described and highlights a need for continued environmental surveillance. The potential growth sites we identified also provide a valuable tool for human and veterinary health care providers and public health practitioners to understand and mitigate disease risk.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To assess the use of medical claims records for surveillance and epidemiological inference through a case study that examines how ecological and social determinants and measurement error contribute to spatial heterogeneity in reports of influenza-like illness across the United States. Introduction Traditional infectious disease epidemiology is built on the foundation of high quality and high accuracy data on disease and behavior. Digital infectious disease epidemiology, on the other hand, uses existing digital traces, re-purposing them to identify patterns in health-related processes. Medical claims are an emerging digital datasource in surveillance; they capture patient-level data across an entire population of healthcare seekers, and have the benefits of medical accuracy through physician diagnoses, and fine spatial and temporal resolution in near real-time. Our work harnesses the large volume and high specificity of diagnosis codes in medical claims to improve our understanding of the mechanisms driving spatial variation in reported influenza activity each year. The mechanisms hypothesized to drive these patterns vary as: environmental factors affecting transmission or virus survival, travel flows between different populations, population age structure, and socioeconomic factors linked to healthcare access and quality of life. Beyond process mechanisms, the nature of surveillance data collection may affect our interpretation of spatial epidemiological patterns [1], particularly since influenza is a non-reportable disease with non-specific symptoms ranging from asymptomatic to severe. Considering the ways in which medical claims are generated, biases may arise from healthcare-seeking behavior, insurance coverage, and medical claims database coverage in study populations. Methods Using aggregated U.S. medical claims for influenza-like illness (ILI) from the 2001-2002 through 2008-2009 flu seasons [2], we developed a Bayesian hierarchical modeling framework to estimate the importance of both ecological and social determinants and measurement-related factors on observed county-level variation of influenza disease burden across the United States. Integrated Nested Laplace Approximation (INLA) techniques for Bayesian inference were used to render our questions computationally tractable due to the high spatial resolution of our data (Figure 1) and the multiplicity of models in our analysis [3]. Linking data from a variety of publicly available sources, we determined the strength, directionality, and consistency of these factors over multiple flu seasons. Results We found that measurement-related factors – healthcare-seeking behavior, insurance coverage, and medical claims database coverage – were strong predictors of greater ILI intensity across seasons. Secondarily, poverty and specific humidity were negatively associated with ILI intensity for several seasons. Finally, by incorporating mechanistic and measurement factors into our model, our model predictions present an improved map of influenza-like illness in the United States for the flu seasons in our study period. Conclusions We present a flexible modeling approach that applies to different medical claims diagnosis codes and disease surveillance data and demonstrates the utility of Bayesian hierarchical models for large-scale ecological analyses. Our results increase our knowledge of the spatial distribution of influenza and the underlying processes that drive these patterns, promote finer spatial targeting for different types of interventions, and enable the interpolation of burden in areas difficult to surveil through traditional public health. Moreover, they highlight the relative contributions of surveillance data collection and ecological processes to spatial variation in disease, and highlight the importance of considering measurement biases when using surveillance data for epidemiological inference.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To develop a mosquito surveillance module to collect mosquito information testing for West Nile, East Equine Encephalitis (EEE) and Zika viruses using national standards. To provide a common set of data for local health departments (LHDs) and state users to report share information. To monitor the type of mosquito species that carry diseases. Introduction There were several stand-alone vector surveillance applications being used by the New York State Department of Health (NYSDOH) to support the reporting of mosquito, bird, and mammal surveillance and infection information implemented in early 2000s in response to West Nile virus. In subsequent years, the Electronic Clinical Laboratory Reporting System (ECLRS) and the Communicable Disease Electronic Surveillance System (CDESS) were developed and integrated to be used for surveillance and investigations of human infectious diseases and management of outbreaks. An integrated vector surveillance system project was proposed to address the migration of the stand-alone vector surveillance applications into a streamlined, consolidated solution to support operational, management, and technical needs by using the national standards with the existing resources and technical environment. Methods A mosquito surveillance module was designed to link with CDESS, an electronic disease case reporting and investigation system, to allow LHDs to enter mosquito trap sites and mosquito pool information obtained from those traps. The mosquito test results are automatically transmitted to ECLRS through public health lab Clinical Laboratory Information Management System (CLIMS) using ELR standards. By utilizing these standards, the ECLRS was enhanced to add a new non-human specimen table and existing processes were used to obtain mosquito laboratory results and automatically transfer them to the surveillance system the same way that human results are transferred. The new mosquito surveillance module also utilizes the existing CDESS reporting module, thereby allowing users the flexibility to query and extract data of their choosing. The minimum infection rate (MIR) report calculates the number of infected pools with arbovirus divided by the total number of specimens tested*1000; a trap report shows number of mosquitoes trapped by species type, location and trap type; and a lab test result report shows the number of pools that tested positive and the percentage of positive pools by disease. Results The mosquito surveillance module was rolled out in May 2016 to all 57 LHDs. A non-human species lookup table was created to allow public health lab to report the test results using Health Level Seven (HL7) v 2.5.1 standards. As of August 31, 2016 there were 4,545 pools tested. A total of 201 (4.4%) pools were positive for West Nile and the MIR was 1.2. There were no pools positive for EEE or Zika virus. Various reports have been created for monitoring the surveillance of mosquitoes trapped and tested for mosquito-borne diseases. Conclusions The integration of mosquito surveillance module within CDESS allows LHDs and the State to monitor mosquito-borne disease activity more efficiently. The module also increases NYDOH’s ability to provide timely, accurate and consistent information to the local health departments and healthcare practitioners regarding mosquito-borne diseases.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
A framework and toolbox for creating point-and-click dashboard applications (at no cost) for monitoring several facets of syndromic surveillance data was created. These tools (and associated documentation) are being made available freely online for others to adopt.

Introduction
Public health surveillance largely relies on the use of surveillance systems to facilitate the identification and investigation of epidemiologic concerns reflected in data. In order to support public health response, these systems must present relevant information, and be user-friendly, dynamic, and easily-implementable. The abundance of R tools freely-available online for data analysis and visualization presents not only opportunities, but also challenges for adoption that these tools must be integrated so as to allow a structured workflow. Many public health surveillance practitioners do not have the time available to 1) scavenge for tools, 2) align their functions so as to create a relevant set of visuals, and 3) integrate these visuals into a dashboard that allows a streamlined surveillance workflow. An openly-available, structured framework that allows simple integration of analytic capabilities packaged into readily-implementable modules would simplify the creation of relevant dashboard visuals by surveillance practitioners.

Methods
R is a statistical computing application, known for its versatility and ability to create powerful visualizations. Shiny is an R package that allows the creation of interactive, easy-to-use point-and-click applications. We looked to R and its Shiny package extension as a candidate solution. However, creating a Shiny application from scratch requires knowing enough of the R programming language so as to be able to appropriately design and link several chunks of code that interact with one another to generate the desired output. To address this barrier, we sought to create a structured process by which one can easily browse a library of defined code snippets (each of which enables an analytic tool relevant to syndromic data analysis and visualization) and then integrate snippets of interest into a dashboard application in a way that requires experience with R is minimized.

Results
We first collected several analytic tools that support syndromic data analysis and have been developed for R; examples include heatmaps, change-point detection, outlier detection, tables, maps, etc. We then packaged them into snippets of code (one for each analytic tool) in a way that facilitates integration of the analytic tool into a dashboard application. A fake syndromic dataset was created as well for inclusion in a demo dashboard application that is available for sharing.

Conclusions
The online community of R users makes new tools for data analysis and visualization available every day. The abundance of options can be overwhelming and the process of integrating pieces of code can be time-consuming. This places a constraint on adoption of these tools by epidemiologists working at all levels of government. The present project alleviates this problem considerably by reducing the tool searching process through the introduction of a library of relevant tools for syndromic data analysis and visualization that can be easily integrated into a dashboard application that allows for streamlined syndromic surveillance activities. Our next step is to partner with interested jurisdictions to help them adopt this framework and associated tools. Given sufficient interest, we would set up a process for others to add their own modules to this library, perhaps through the online platform for collaborative code development and sharing, GitHub.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo describe how flexible surveillance systems can be rapidly adapted and deployed, and increase the efficiency and accuracy of surveillance, during responses to outbreaks and all hazard emergent events. Introduction Georgia Department of Public Health (DPH) epidemiologists have responded to multiple emergent outbreaks with diverse surveillance needs. During the 2009 H1N1 influenza response, it was necessary to electronically integrate multiple reporting sources and view population-level data, while during the 2014–2015 West African Ebola epidemic, it was necessary to easily collect and view individual level data from travelers to facilitate early detection of potential imported Ebola disease. DPH in-house information technology (IT) staff work closely with epidemiologists to understand and accommodate surveillance needs. Through this collaboration, IT created a robust electronic surveillance and outbreak management system (OMS) to accommodate routine reporting of notifiable diseases and outbreak investigations, and surveillance during emergent events. Methods OMS was created within the State Electronic Notifiable Disease Surveillance System (SendSS); a secure, HIPAA-compliant, Oracle and web-based platform which collects data on all notifiable diseases in Georgia. This flexible platform has multi-functionality including dynamic web-based surveys that link to case records or outbreaks, online case reporting, electronic laboratory reporting, contact tracing, visual dashboards summarizing outbreak data, electronic alerts, and individual accounts for users with varying privileges to limit access to specific modules. These features can be customized for any emergent event. Results SendSS and OMS are widely used by state and district epidemiologists. Individual case and outbreak management activities include but are not limited to: notifiable disease and condition cases; all disease clusters; animal bites surveillance including bite investigation and laboratory results; and syndromic surveillance data automatically collected from 90 emergency facilities. OMS has been rapidly modified to facilitate efficient epidemiologic responses to emergent events such as: integrating multiple reporting sources during the H1N1 outbreak; shelter surveillance during hurricanes Katrina and Rita in 2005; active monitoring of >2,500 travelers in Georgia during the Ebola response; tracking cases investigations during the Zika response, and future monitoring of poultry workers if highly-pathogenic avian influenza occurs in Georgia. Conclusions The flexible and customizable features of SendSS and OMS accommodate the changing needs of epidemiologists to monitor a variety of diseases. Rapid implementation has enabled DPH epidemiologists to respond efficiently to emergent events using limited human resources, achieving immediate situational awareness by incorporating multiple data sources into user friendly dashboards and notifications, and easily sharing information among state and federal stakeholders to facilitate rapid risk assessment and response as needed. The success of these systems illustrates the return on DPH’s preparedness investment in retaining technical staff to work with epidemiologists to meet urgent surveillance needs.

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Abstract

Objective The objective of this study was to evaluate several aspects of the electronic disease reporting system and its abilities used in Georgia. Also, the study assessed if the system abilities are tailored to the national surveillance requirements. User attitudes (system strength weaknesses) toward the system was also surveyed. Introduction The Ministry of Health of Georgia accepted the Electronic Integrated Disease Surveillance System (EIDSS) as the official disease reporting system in 2012. The Georgian government adopted electronic reporting for both veterinary and human diseases in 2015. We conducted a comparative assessment of progress in the implementation of electronic reporting. Methods A face-to-face initial survey was conducted in 2012, a follow-up survey (through telephone interviews) was performed in 2016. The initial survey was conducted in regions that had EIDSS installed and the follow-up survey was conducted in all regions. Standardized questionnaires were used and data was analyzed in Epi Info. Results Out of 450 trained EIDSS users, 32% were interviewed in the initial survey and 25% (of 550) EIDSS trained users were interviewed in the follow-up survey. Of 147 respondents in the initial survey and 138 in the follow-up survey, 44% and 79%, believed that they were using EIDSS effectively, respectively. The follow-up survey showed a 23% increase in respondents who acknowledge an improvement of the electronic reporting; acceptance of EIDSS increased from 80.3% to 97.8%. Of those interviewed in the follow-up survey, 19.7% mentioned that the main success in development of the system is due to improved collaboration between institutes. However, 17.36% of the respondents in the follow-up survey reported non-sufficient quality data. Conclusions Our study suggests that the acceptance and use of EIDSS has noticeably improved, indicating the successful implementation of electronic reporting. Recommendations have been made to further improve the data quality by conducting regular data cleaning and additional user training. We recommend the continuation of EIDSS training.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

This session will provide an overview of the current systems for influenza surveillance; review the role of schools in influenza transmission; discuss relationships between school closures, school absenteeism, and influenza transmission; and explore the usefulness of school absenteeism and unplanned school closure monitoring for early detection of influenza in schools and broader communities.

Introduction

Influenza surveillance is conducted through a complex network of laboratory and epidemiologic systems essential for estimating population burden of disease, selecting influenza vaccine viruses, and detecting novel influenza viruses with pandemic potential (1). Influenza surveillance faces numerous challenges, such as constantly changing influenza viruses, substantial variability in the number of affected people and the severity of disease, nonspecific symptoms, and need for laboratory testing to confirm diagnosis. Exploring additional components that provide morbidity information may enhance current influenza surveillance.

School-aged children have the highest influenza incidence rates among all age groups. Due to the close interaction of children in schools and subsequent introduction of influenza into households, it is recognized that schools can serve as amplification points of influenza transmission in communities. For this reason, pandemic preparedness recommendations include possible pre-emptive school closures, before transmission is widespread within a school system or broader community, to slow influenza transmission until appropriate vaccines become available. During seasonal influenza epidemics, school closures are usually reactive, implemented in response to high absenteeism of students and staff after the disease is already widespread in the community. Reactive closures are often too late to reduce influenza transmission and are ineffective.

To enhance timely influenza detection, a variety of nontraditional data sources have been explored. School absenteeism was suggested by several research groups to improve school-based influenza surveillance. A study conducted in Japan demonstrated that influenza-associated absenteeism can predict influenza outbreaks with high sensitivity and specificity (2). Another study found the use of all-causes absenteeism to be too nonspecific for utility in influenza surveillance (3). Creation of school-based early warning systems for pandemic influenza remains an interest, and further studies are needed. The panel will discuss how school-based surveillance can complement existing influenza surveillance systems.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To create a forum and database for FDA and CDC epidemiologists, laboratorians, and outbreak scientists for tracking recent food and environmental surveillance sampling isolates identified through Reportable Food Registries reports and regulatory inspectional findings, and analyzing them for matches to clinical isolates for early outbreak detection.

Introduction
Identifying, solving, and stopping foodborne outbreaks in the U.S. requires the collaboration and coordination of multiple federal agencies and centers as well as state and local authorities. FDA’s Coordinated Outbreak Response and Evaluation (CORE) network is responsible for outbreak surveillance, response, and post-response activities related to incidents involving multiple illnesses linked to FDA-regulated food. CORE collaborates with CDC to obtain data on foodborne illnesses and illness clusters and with FDA Centers and field staff to obtain laboratory and inspectional information related to contaminated foods and foodborne illness outbreaks. CORE’s Signals and Surveillance team coordinates isolate tracking activities among several organizations within FDA and CDC, and the isolate database was developed for timely information sharing and early signal detection.

Methods
The isolate tracking database combines information from established laboratory, inspectional, and regulatory programs; investigators across FDA and CDC evaluate the information for early outbreak signals. PulseNet is a national laboratory network that compares the Pulsed-field Gel Electrophoresis (PFGE) patterns of clinical and non-clinical bacterial isolates and identifies increases in numbers of isolates with matching PFGE patterns as outbreak clusters. Foodborne outbreak investigational partners, including the CDC and FDA, utilize the CDC/Palantir Technologies-developed platform, the System for Enteric Disease Response, Investigation, and Coordination (SEDRIC), to evaluate clinical, food, and environmental isolates. CORE provides additional firm-identifying metadata for new food and environmental isolates from FDA, contract lab, and Reportable Food Registry (RFR)-reported samples and analyzes them for PFGE patterns matching those of recent clinical isolates. FDA laboratorians provide early information about food and environmental isolates that are in queue for PFGE and whole genome sequence analyses, trend analysis for recently completed isolates, and genetic clustering with clinical and other isolates. The RFR is a FDA-hosted platform for industries and public health officials to report when there is a reasonable probability that a human or animal food that is regulated by FDA will cause serious adverse health consequences.

Results
The isolate tracking activities have provided investigators with information for hypothesis development, identified trends in laboratory and inspectional findings, aided in the identification of causal food sources in illness clusters, and provided early laboratory and inspectional information to outbreak investigations. Within the past year, isolate tracking activities identified early indicators of the presence of Listeria monocytogenes in frozen foods before a multistate outbreak of listeriosis was linked to frozen vegetables; identified early indicators of the presence of Salmonella pistachios before reidentification of a multistate outbreak of Salmonella Montevideo and Salmonella Senftenberg; further characterized the microbial hazards of cucumber and pepper contamination through FDA’s enhanced surveillance sampling program; and expanded the forum’s scope to include animal foods and their link to human and animal illnesses.

Conclusions
The database and forum provide a platform for information sharing, and collaboration between agencies, offices, and centers by informing the participating groups about early signals of contamination and emerging food risk trends.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective This roundtable will provide a forum for national, state, and local managers of syndromic surveillance systems to discuss how they identify, monitor, and respond to changes in the nature of their data. Additionally, this session will focus on the strengths and weaknesses of the syndromic surveillance systems for supporting program evaluation and trend analysis. This session will also provide a forum where subject matter experts can discuss the ways in which this deep understanding of their data can be leveraged to forge and improve partnerships with academic partners.

Introduction As syndromic surveillance systems continue to grow, new opportunities have arisen to utilize the data in new or alternative ways for which the system was not initially designed. For example, in many jurisdictions syndromic surveillance has recently become population-based, with 100% coverage of targeted emergency department encounters. This makes the data more valuable for real-time evaluation of public health and prevention programs. There has also been increasing pressure to make more data publicly available—to the media, academic partners, and the general public.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective


Introduction

Community influenza infection rates are highest among children. In children, influenza can cause severe illness and complications including, respiratory failure and death. Annual influenza vaccinations are recommended for all persons aged ≥6 months. In 2004, influenza-associated deaths in children became a notifiable condition.

Methods

Deaths that occurred in children aged <18 years with laboratory-confirmed influenza virus infection were reported from states and territories to the Centers for Disease Control and Prevention on a standard case report form. We used population estimates from the U.S. Census Bureau, 2011 to 2015, to calculate age group-adjusted incidence. We used Wilcoxon rank-sum test to compare medians and chi-square and Mantel-Haenszel chi-square to compare differences between proportions of two groups.

Results

From October 2010 through September 2015, 590 influenza-associated pediatric deaths were reported. The median age at time of death was 6 years (interquartile range, 1–12 years). Half of the children (285/572) had at least one underlying medical condition. Neurologic conditions (26%) and development delay (21%) were most commonly reported. The average annual incidence rate was 0.16 per 100,000 children (95% confidence interval [CI]: 0.15–0.17) and was highest among children aged ≤6 months (0.75, 95% CI: 0.60–0.94 per 100,000 children), followed by children aged 6–23 months (0.34, 95% CI: 0.28–0.41 per 100,000 children).

Only 21% (87/409) of pediatric deaths in children ≥6 months had evidence of full influenza vaccination. Vaccination coverage was lower in children aged 6–23 months (15%) and 5–8 years (17%) than with those aged 2–4 years and 9–17 years (25%, p<0.01). The majority of children aged ≤2 years who died had no underlying medical conditions (63%, 105/167); this proportion was significantly higher than that in children aged 2 years (45%, 182/405, p<0.01). Overall 65% (383) of pediatric deaths had influenza A virus detected, and 33% had influenza B virus detected. Children infected with influenza B virus had a higher frequency of sepsis/shock (41%, 72/174), acute respiratory distress syndrome (ARDS, 33%, 58/174), and hemorrhagic pneumonia/pneumonitis (8%, 14/174) than children infected with either influenza A (H1N1) pdm09 or influenza A (H3N2) virus (p<0.01, 0.03, 0.03, respectively). Overall 81% (421/521) of children had an influenza-associated complication; the most commonly reported were pneumonia (40%), sepsis/shock (31%) and ARDS (29%). Among those with testing reported, invasive bacteria coinfections were identified in 43% (139/322); β-hemolytic Streptococcus (20%) and Staphylococcus aureus (17%) were reported most frequently. Most children (39%, 212/548) died within 3 days of symptom onset, 28% died 4–7 days after onset, and 34% died ≥8 days after onset. The median days from illness onset to death for children with underlying condition was significantly longer than the time for previously healthy children (7 versus 4 days, p<0.01).

Conclusions

Each year, a substantial number of influenza-associated deaths occur among U.S. children, with rates highest among those aged ≥2 years. While half of the deaths were among children with underlying conditions, the majority of children aged ≤2 years who died were previously healthy. Vaccination coverage was very low. Influenza vaccination among pregnant women, young children and children with high-risk underlying conditions should be encouraged to reduce influenza-associated mortality among children.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To enable coordination of Swaziland Ministry of Health units for public health surveillance (PHS).

Introduction
In the Kingdom of Swaziland, a baseline assessment found that multiple functional units within the Ministry of Health (MoH) perform PHS activities. There is limited data sharing and coordination between units; roles and responsibilities are unclear. The Epidemiology and Disease Control Unit (EDCU) is mandated to coordinate efforts and strengthen PHS through implementing Integrated Disease Surveillance and Response (IDSR) to fulfill requirements of International Health Regulations (2005) (IHR[2005]), and the Global Health Security Agenda (GHSA).

Methods
A baseline assessment that included key informant interviews of unit representatives was conducted. Data flows were developed. Results were disseminated at a facilitated stakeholder workshop with unit representatives. A database was then built containing all distinct activities found within the IDS Technical Guidelines (2010), IHR[2005], GHSA Action Packages, the baseline assessment, a previous CDC IDSR assessment, and suggestions from the stakeholder workshop. Activities were categorized by IDSR function (identify, report, analyze, investigate, prepare, respond, provide feedback, and evaluate) and designated as an ongoing “role” or a one-time implementation activity. A document containing all PHS roles was presented at a facilitated consensus workshop; unit representatives discussed and designated a lead unit/agency for each role. One-time implementation activities were assigned a lead actor, target completion date, and compiled into a 3-year IDSR Roadmap to guide implementation.

Results
A Roles and Responsibilities Framework was developed that presents a consensus on lead units for all roles within an IDSR-based PHS system that fulfills requirements of IHR [2005] and GHSA. This document enables coordination by EDCU. The IDSR Roadmap provides time-bound activities with assigned actors to implement IDSR. EDCU is using these documents to guide coordination of multiple MOH units already performing PHS activities.

Conclusions
Coordinating well-established programs that already collect epidemiological data increases efficiency and enables more complete epidemiologic analysis. Stakeholder engagement and clarity of roles critical for EDCU to coordinate PHS. Consolidating activities for IDSR, IHR [2005], and GHSA in guiding documents enables an streamlined approach for public health surveillance strengthening. Future work aims to achieve data sharing through an electronic platform and introduce data standards for interoperability among datasets.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
Describe and explain the transition of the syndromic surveillance program at the Houston Health Department (HHD) from being a locally managed and aging system to an ESSENCE system governed by a regional Consortium of public health agencies and stakeholders in the 13-county area of the southeast Texas. Introduction
Syndromic surveillance systems are large and complex technology projects that increasingly require large investments of financial and political capital to be sustainable. What was once a minor surveillance tool in the mid-2000s has evolved into a program that is regarded as valuable to public health yet is increasingly difficult to maintain and operate for local health departments. The Houston Health Department installed a syndromic surveillance system (SyS) six years before Meaning Use became known to healthcare communities. The system chosen at the time was the Real-time Outbreak Disease Surveillance System (RODS) which, at the time and for its purpose, was a suitable platform for syndromic surveillance. During the past 13 years however, maintaining, operating, and growing a SyS by alocal health department has become increasingly difficult. Inclusion in Meaningful Use elevated the importance and profile of syndromic surveillance such that network growth, transparency of operations, ease of data sharing, and cooperation with other state systems in Texas became program imperatives.

Methods
With support from the informatics group at Tarrant County Public Health (TCPH) in the form of mentoring, HHD devised a two-prong strategy to re-invigorate the syndromic program. The first was to replace RODS with ESSENCE from Johns Hopkins Applied Physics Laboratory (JH/APL). The second was to strengthen the regional network by creating a governance structure that included outside agencies and stakeholders. The product of this second effort was the Syndromic Surveillance Consortium of Southeast Texas (SSCSeT) on the Communities of Practice model using parliamentary procedure.

Results
Acquiring ESSENCE and forming SSCSeT were necessary steps for the continuing operation of the SyS. The Consortium includes members from local health jurisdictions, health care providers, health policy advocates, academicians, and data aggregators. Created as a democratic society, SSCSeT wrote its constitution and by-laws, voted in officers, formed working groups and has begun developing policies. The Consortium is cooperating with the Texas Department of State Health Services (DSHS) as well as TCPH. Having ESSENCE will ensure the HHD-SyS will conform to standards being developed in the state and provide a robust syndromic platform for the partners of the Consortium.

Conclusions
Syndromic systems operated by local health departments can adapt to regulatory changes by growing their networks and engaging regional stakeholders using the Communities of Practice model.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The objective of this project is to advance the science of biosurveillance by providing a user curated cataloging system, to be used across health department and other users, that advances daily surveillance operations by better characterizing three key issues in available surveillance systems: duplication in biosurveillance activities; differing perspectives and analyses of the same data; and inadequate information sharing.

Introduction A variety of government reports have cited challenges in coordinating national biosurveillance efforts at strategic and tactical levels. The General Accountability Office (GAO), an independent nonpartisan agency that investigates how the federal government funding and performs analysis at the request of congressional committees or by public mandate, has published 64 reports on biosurveillance since 2005. The aim of this project is to better characterize these issues by collecting and analyzing a sample of publicly documented biosurveillance systems, and making our data and results available for the public health community to review and evaluate. This study openly publishes the data files of information collected (i.e. CSV, XLS), the Python NLP scripts, and a freely available web-based application developed in R Shiny that filters against the 227 biosurveillance systems and activities to promote a more transparent understanding of how public health practitioners conduct surveillance activities.

Methods Collected and reviewed data on 424 systems, of which 227 systems and activities met our criteria; Implemented a new approach to develop a standard framework for data collection using natural language processing (NLP); Openly published all data files publicly on Github and developed an online analytics application; and Convened a workshop of experts from across federal, state, not-for-profit, academic and commercial entities in November 2015 in Washington, D.C., to review the methodology and results of this study.

Results The results of this project include a fully functional web application and code (available through Github) for the continued expansion, categorization and analysis of surveillance systems. Unique findings currently rendered through the 227 surveillance systems include: Out of 227 systems, 20 were established in the year 2006, alone, with an increase in systems established following 1990; 68% of all systems cataloged are focused solely on human surveillance; 45% of all cataloged systems used statistical analysis and only 4% are using Natural Language Processing; and 43% of all biosurveillance systems in our inventory reported using “health department” data as a data source.

Conclusions We believe this project is the first step for public health practitioners and researchers to contribute to a transparent inventory of systems and activities. Results provide meaningful metadata on an over focus on human surveillance, over-reliance on a single data source (health departments) and a lack of advanced data science practices being applied to systems in the field. The value of this project 1) provides a starting point for the development of a standard framework of categories to use for cataloging biosurveillance systems, 2) offers openly available data and code on Github [3] for others to integrate into their research, and 3) introduces a set of methodological issues to consider in a biosurveillance inventorying exercise.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective 1. To develop a comprehensive model characterization framework to describe epidemiological models in an operational context. 2. To apply the framework to characterize “operational” models for specific infectious diseases and provide a web-based directory, the biosurveillance analytics resource directory (BARD) to the global infectious disease surveillance community. Introduction Epidemiological modeling for infectious disease is useful for disease management and routine implementation needs to be facilitated through better description of models in an operational context. A standardized model characterization process that allows selection or making manual comparisons of available models and their results is currently lacking. Los Alamos National Laboratory (LANL) has developed a comprehensive framework that can be used to characterize an infectious disease model in an operational context. We offer this framework and an associated database to stakeholders of the infectious disease modeling field as a tool for standardizing model description and facilitating the use of epidemiological models. Such a framework could help the understanding of diverse models by various stakeholders with different preconceptions, backgrounds, expertise, and needs, and can foster greater use of epidemiological models as tools in infectious disease surveillance. Methods We define, “operational” as the application of an epidemiological model to a real-world event for decision support and can be used by experts and non-experts alike. The term “model” covers three major types, risk mapping, disease dynamics and anomaly detection. To develop a framework for characterizing epidemiological models we collected information via a three-step process: a literature search of model characteristics, a review of current operational infectious disease epidemiological models, and subject matter expert (SME) panel consultation. We limited selection of operational models to five infectious diseases: influenza, malaria, dengue, cholera and foot-and-mouth disease (FMD). These diseases capture a variety of transmission modes, represent high or potentially high epidemic or endemic burden, and are well represented in the literature. We also developed working criteria for what attributes can be used to comprehensively describe an operational model including a model’s documentation, accessibility, and sustainability. To apply the model characterization framework, we built the BARD, which is publicly available (http://brd.bsvgateway.org). A document was also developed to describe the usability requirements for the BARD; potential users (and non-users) and use cases are formally described to explain the scope of use. Results 1. Framework for model characterization The framework is divided into six major components (Figure 1): Model Purpose, Model Objective, Model Scope, Biosurveillance (BSV) goals, Conceptual Model and Model Utility; each of which has several sub-categories for characterizing each aspect of a model. 2. Application to model characterization Models for five infectious diseases—cholera, malaria, influenza, FMD and dengue were characterized using the framework and are included in the BARD database. Our framework characterized disparate models in a streamlined fashion. Model information could be binned into the same categories, allowing easy manual comparison and understanding of the models. 3. Development of the BARD Our model characterization framework was implemented into an actionable tool which provides specific information about a model that has been systematically categorized. It allows manual category-to-category comparison of multiple models for a single disease and while the tool does not rank models it provides model information in a format that allows a user to make a ranking or an assessment of the utility of the model. Conclusions With the model characterization framework we hope to encourage model developers to start describing the many features of their models using a common format. We illustrate the application of the framework through the development of the BARD which is a scientific and non-biased tool for selecting an appropriate epidemiological model for infectious disease surveillance. Epidemiological models are not necessarily being developed with decision makers in mind. This gap between model developers and decision makers needs to be narrowed before modeling becomes routinely implemented in decision making. The characterization framework and the tool developed (BARD) are a first step towards addressing this gap. Keywords epidemiological models; database; decision support


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Here we use novel methods of phylogenetic transmission graph analysis to reconstruct the geographic spread of MERS-CoV. We compare these results to those derived from text mining and visualization of the World Health Organization’s (WHO) Disease Outbreak News. Introduction MERS-CoV was discovered in 2012 in the Middle East and human cases around the world have been carefully reported by the WHO. MERS-CoV virus is a novel betacoronavirus closely related to a virus (NeoCov) hosted by a bat, Neoromicia capensis. MERS-CoV infects humans and camels. In 2015, MERS-CoV spread from the Middle East to South Korea which sustained an outbreak. Thus, it is clear that the virus can spread among humans in areas in which camels are not husbanded. Methods Phylogenetic analyses We calculated a phylogenetic tree from 100 genomic sequences of MERS-CoV hosted by humans and camels using NeoCov as the outgroup. In order to evaluate the relative order and significance of geographic places in spread of the virus, we generated a transmission graph based on methods described in 1. The graph indicates places as nodes and transmission events as edges. Transmission direction and frequency are depicted with directed and weighted edges. Betweenness centrality, represented by node size, measures the number of shortest paths from all nodes to others that pass through the corresponding node. Places with high betweenness represent key hubs for the spread of the disease. In contrast, smaller nodes at the periphery of the network are less important for the spread of the disease. Web scraping and mapping Due to the journalistic style of the WHO data, it had to be structured such that mapping software can ingest the data. We used Import.io to build the API. We provided the software a sample page, selected the data that is pertinent, then provided a list of all URLs for the software. We used Tableau to map the information both geographically and temporally. Results Geographic spread of Mers-CoV based on transmissions identified in phylogenetic data Most important among the places in the MERS-CoV epidemic is Saudi Arabia as measured by the betweenness metric applied to a changes in place mapped to a phylogenetic tree. In figure 1, the circle representing Saudi Arabia is slightly larger compared to other location indicating its high importance in the epidemic. Saudi Arabia is the source of virus for Jordan, England, Qatar, South Korea, UAE, Indiana, and Egypt. The United Arab Emirates has a bidirectional connection with Saudi Arabia indicating the virus has spread between the two countries. The United Arab Emirates also has high betweenness. The United Arab Emirates is between Saudi Arabia and Oman and Between Saudi Arabia and France. South Korea, and Qatar have mild betweenness. South Korea is between Saudi Arabia and China. Qatar is between Saudi Arabia and Florida. Other locations (Jordan, England, Indiana, and Egypt) have low betweenness as they have no outbound connections. Visualization of geographical transmissions in WHO Data Certain articles include the infected individuals’ countries of origin. In constrast, many reports are in a lean format that includes a single paragraph that only summarizes the total number of cases for that country. If we build the API in a manner that recognizes features in the detailed reports, we can generate a map that draws lines from origin to reporting country and create visualizations. However, since only some of the articles contain this extra information, mapping in this manner will miss many of the cases that are reported in the lean format. Conclusions Our goal is to develop methods for understanding syndromic and pathogen genetic data on the spread of diseases. Drawing parallels between the transmissions events in the WHO data and the genetic data has shown to be challenging. Analyses of the genetic information can be used to imply a transmission pathway but it is hard to find epidemiological data in the public domain to corroborate the transmission pathway. There are rare cases in the WHO data that include travel history (e.g. “The patient is from Riyadh and flew to the UK”). We conclude that epidemiological data combined with genetic data and metadata have strong potential to understand the geographic progression of an infectious disease. However, reporting standards need to be improved where travel history does not impinge on privacy. A transmission graph for MERS-CoV based on viral genomes and place of isolation metadata. The direction of transmission is represented by the arrow. The frequency of transmission is indicated by the number. The size of the nodes indicates betweenness.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To introduce Soda Pop, an R/Shiny application designed to be a disease agnostic time-series clustering, alarming, and forecasting tool to assist in disease surveillance “triage, analysis and reporting” workflows within the Biosurveillance Ecosystem (BSVE) [1]. In this poster, we highlight the new capabilities that are brought to the BSVE by Soda Pop with an emphasis on the impact of methodological decisions. Introduction The Biosurveillance Ecosystem (BSVE) is a biological and chemical threat surveillance system sponsored by the Defense Threat Reduction Agency (DTRA). BSVE is intended to be user-friendly, multi-agency, cooperative, modular and threat agnostic platform for biosurveillance [2]. In BSVE, a web-based workbench presents the analyst with applications (apps) developed by various DTRA-funded researchers, which are deployed on-demand in the cloud (e.g., Amazon Web Services). These apps aim to address emerging needs and refine capabilities to enable early warning of chemical and biological threats for multiple users across local, state, and federal agencies. Soda Pop is an app developed by Pacific Northwest National Laboratory (PNNL) to meet the current needs of the BSVE for early warning and detection of disease outbreaks. Aimed for use by a diverse set of analysts, the application is agnostic to data source and spatial scale enabling it to be generalizable across many diseases and locations. To achieve this, we placed a particular emphasis on clustering and alerting of disease signals within Soda Pop without strong prior assumptions on the nature of observed disease counts. Methods Although designed to be agnostic to the data source, Soda Pop was initially developed and tested on data summarizing Influenza-Like Illness in military hospitals from collaboration with the Armed Forces Health Surveillance Branch. Currently, the data incorporated also includes the CDC’s National Notifiable Diseases Surveillance System (NNDSS) tables [3] and the WHO’s Influenza A/B Influenza Data (Flunet) [4]. These data sources are now present in BSVE’s Postgres database for direct access. Soda Pop is designed to automate time-series tasks of data summarization, exploration, clustering, alarming and forecasting. Built as an R/Shiny application, Soda Pop is founded on the powerful statistical tool R [5]. Where applicable, Soda Pop facilitates nonparametric seasonal decomposition of time-series; hierarchical agglomerative clustering across reporting areas and between diseases within reporting areas; and a variety of alarming techniques including Exponential Weighted Moving Average alarms and Early Aberration Detection [6]. Soda Pop embeds these techniques within a user-interface designed to enhance an analyst’s understanding of emerging trends in their data and enables the inclusion of its graphical elements into their dossier for further tracking and reporting. The ultimate goal of this software is to facilitate the discovery of unknown disease signals along with increasing the speed of detection of unusual patterns within these signals. Conclusions Soda Pop organizes common statistical disease surveillance tasks in a manner integrated with BSVE data source inputs and outputs. The app analyzes time-series disease data and supports a robust set of clustering and alarming routines that avoid strong assumptions on the nature of observed disease counts. This attribute allows for flexibility in the data source, spatial scale, and disease types making it useful to a wide range of analysts. Soda Pop within the BSVE. Keywords BSVE; Biosurveillance; R/Shiny; Clustering; Alarming


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To identify gaps in current U.S. animal data collection and surveillance systems, describe how surveillance of animal populations can provide important early warnings of emerging threats to human populations from infectious disease epidemics, and explain the benefits of integrating human and animal surveillance data into a common linked system.

Introduction: Since the majority of emerging infectious diseases over the past several decades have been zoonotic, animal health surveillance is now recognized as a key element in predicting public health risks. Surveillance of animal populations can provide important early warnings of emerging threats to human populations from bioterrorism or naturally occurring infectious disease epidemics. This study investigated current animal data collection and surveillance systems, isolated major gaps in state and national surveillance capabilities, and provided recommendations to fill those gaps.

Methods: Initially, an extensive literary review was performed to better understand what is currently available for Animal Health Disease Surveillance in the United States and recognize the gaps. After this review meetings were arranged with numerous animal health, public health surveillance experts to isolate their surveillance priorities: Department of Homeland Security (DHS), USDA Animal and Plant Health Inspection Service (APHIS), U.S. Army Veterinary Corps, University Laboratories/Veterinary Teaching Hospitals, The National Capital Region (NCR) ESSENCE Public Health Steering Committee, Maryland Arbovirus, Zoonotic, and Vector Disease Group, and the Maryland State Veterinarian. A key animal disease surveillance stakeholder group that has been underrepresented in prior requirements assessments is private practitioners. Preliminary discussions with key practitioners revealed clearly that there are monumental gaps in animal health surveillance and it frequently limits their ability to rapidly respond to potential disease risks within their animal population of concern. To better understand these gaps and potential ways to improve surveillance in this area, a voluntary survey was developed and sent out to members of the Maryland Veterinary Medical Association, Virginia Veterinary Medical Association, and the District of Columbia Academy of Veterinary Medicine.

Results: Through this comprehensive study three current U.S. animal health disease surveillance gaps were isolated: integrated human and animal health surveillance, real-time animal health data collection, and companion animal surveillance. The survey was also well received and had almost 160 participants. Key issues addressed in the survey included: Animal Medical Records—availability, capabilities, and concerns, Zoonotic disease exposure and reporting, and support for development of integrated human-animal disease surveillance tools.

Key Findings: - Almost 90% of responding practitioners reported having encountered a zoonotic disease in practice. - Although less than 50% have reported a zoonotic disease to the state or federal government. - Almost 70% of veterinarians in the National Capital Region (NCR) who participated in the survey also reported that they do not have access to a surveillance system. - Veterinarian’s responses to the question: “What is your opinion of the current status of local, regional, or national zoonotic diseases surveillance and the use of animal data for surveillance?”: “I think it is difficult to find up to date local and regional data. Email alerts etc. would be nice, rather than having to search for information that frequently isn’t current.” “I feel that many zoonotic diseases go unreported due to the lack of ease of reporting them and there is no communication between the human and veterinary medical communities as far as reportable diseases affecting both people and animals.” “With the proliferation of tick borne disease, closer surveillance of animal cases would benefit human medicine. We knew exactly when Lyme hit our area. It was three years later before VA Dept. of Health sent out a letter outlining the prevalence of disease in southwest VA human cases.”

Conclusions: Linking the systems that report human and animal diseases would enable health professionals to swiftly identify and respond to zoonotic disease outbreaks. Since funding for animal health surveillance is limited, integrating animal data into existing, well-established human health surveillance systems would reduce the resources needed while still providing the advanced capabilities that are available for human health surveillance. The need for integrated surveillance has been recognized by regulatory officials, but concerns regarding funding, data acquisition, data confidentiality, and identification of desired stakeholders must still be addressed. The sometimes disparate interests of large industry, private practitioners, and state governments make gaining access to large centralized pools of animal health data a challenge. By using existing human health surveillance systems as a platform to develop integrated human-animal surveillance systems, and by working with experts in the human surveillance field, these concerns can be ameliorated. This would lead to more advanced, integrated health surveillance capabilities and heighten the nation’s ability to quickly detect and respond to emerging zoonotic diseases.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

A preliminary serological survey was carried out to assess the likelihood of Influenza A (IA) infection in wild boars and begin to characterize the role of wild boars in the epidemiology of the IA virus. Introduction

Domestic swine have been viewed as important for the adaptation and spillover of IA from birds into human populations as they are sensitive to both avian and mammalian (including human) influenza viruses [1]. However, in much of Eurasia and North America wildswine are geographically widespread, abundant and often come in close contact with humans in rural and agricultural settings. Until recently, little attention has been paid to this as an alternate route for IA transmission to human and domestic populations and its significance is not clear. Therefore, the monitoring of the exposure of wild mammals to IA was viewed as essential as potential vectors impacting domestic animals and public health.

Methods

From September to December 2014, wild boar sera were collected by professional hunters in 4 Oblasts of Ukraine: Volyn, Rivne, Zhytomyr, and Chernihiv. Blood was collected from jugular veins. Sera were collected in Eppendorf type tubes, separated from whole blood without centrifugation and stored at -20C until serologically tested. To detect antibodies to IA, a blocking ELISA was used. Serum samples were tested using commercial test kits “Influenza A Ab Test” (IDEXX, USA). Specific antibodies in wild boar serum samples were detected based on manufacturer’s instructions. Briefly, sera were diluted 1:10, and incubated in test wells for 60 minutes at room temperature, followed by three washes. Anti-IA Horseradish Peroxidase HRP conjugate was then added and incubated for 30 minutes at room temperature. Following three washes, 3′,5′-tetramethylbenzidine (TMB), as a substrate, was added and incubated for 15 minutes. Absorbencies were measured at 650A using a iMark Microplate Absorbance Reader and data were analyzed using Microsoft Excel. Based on the manufacturer’s instructions, a serum sample was considered positive if the sample/negative control ratio (S/N) did not exceed a threshold of 0.60. Statistical analyses were performed with the program “StatisticsCalculator”. Results

Sera from 120 wild boars that were shot in 2014 were tested. Thirty boars from each of 4 Oblasts were collected in the north central and northwestern regions of Ukraine. Antibodies against IAV were detected in 27 samples (22.5%), (Table 1). Antibodies to IA virus were detected in at least some of the wild boars from all of the 4 Oblasts. The highest percentages of seropositive samples were detected in wild boar from Volyn and Zhytomyr Oblasts (Fig. 1). The prevalence differences were statistically significant only between samples from Volyn and Chernihiv Oblasts (P&lt;0.05). The average S/N value of all positive serum samples was 0.36±0.03.

Conclusions

This preliminary survey of IA antibodies in wild boar populations of northern Ukraine indicates a substantial presence of exposure to IAV throughout the region. Infection of wild boar populations provides an alternative or additional route for spillover from wild populations to domestic animals and humans. This potential has received relatively little attention until recently, likely in part because feral swine populations have not been viewed as a serious challenge in most regions of the world where the natural history of IA has received serious study. Table 1 Seroprevalence of IA virus in wild boars in Ukraine

Figure 1 Serological surveillance of wild boars for IA virus in northern Ukraine

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Objective The performance of comparative analysis of sensitivity and results of detection of avian influenza virus by real time polymerase chain reaction (PCR-RT) and loop-mediated isothermal amplification of the nucleic acids (LAMP) was the main goal of the study. 

Introduction As part of this surveillance study for Avian Influenza both active and passive surveillance samples were tested using PCR and also utilized to validate the LAMP method. Active surveillance samples include pathological material and tracheal and cloacal swabs from poultry, which were subsequently assessed for avian influenza during diagnosis, and birds collected by hunters. Passive surveillance included environmental samples such as sand and bird faeces. Active surveillance samples were taken mostly from poultry farms across Ukraine, where infected birds are required to be diagnosed by State Scientific Research Institute of Laboratory Diagnostics and Veterinary Sanitary Expertise (SSRILDVSE) by Ukraine Law. Passive surveillance samples were taken primarily during the annual bird migration season. Development of simple, sensitive, and cheap methods for diagnostics of avian influenza is a very important task for practical veterinary medicine. LAMP is one of such methods. The technique is based on isothermal amplification of nucleic acids. It does not require special conditions and equipment (PCR cyclers), therefore it is cheaper in comparison with PCR. Accurate diagnosis is necessary for determining the risk associated with avian influenza in Ukraine and along the Dnipro River during the migratory season. 

Methods For the research, we used PCR-RT commercial kit Bird-Flu-PCR (Ukrzooventprompostach, Ukraine), LAMP (the protocol has been optimized and patented by SSRILDVSE), QIAamp® Viral RNA MiniKit. For the study, we used pathological and biological materials from birds, which were sent to the SSRILDVSE from all regions of Ukraine according to the 2013–2014 State monitoring plan. 

Set up of the real time PCR reactions and parameters of amplifications are indicated in the instruction to the kit. The following protocol was used to set up the RT-LAMP: 2.5 μL 10X Thermopol buffer, 1 mmol/L betaine, 5 mmol/L MgSO4, 4,1.4 mmol/L - BNTP, 12.5 μmol/L SYBR GREEN, 0.5 mmol/L LMMCL2, up to 25 μL Nuclease-free water, 8 U Bsm DNA polymerase, 0.1 μM/1 of F3, 0.1 μM/1 of B3, 0.8 μM/1 of FIP, 0.8 μM/1 of BIP, 0.4 μM/1 of LF, 0.4 of LB, 2 μL cDNA. During our work, we used the following optimal temperature and time for the amplification – 59°C and 60 minutes. 

The sensitivity of diagnostic kit Bird-Flu-PCR and RT-LAMP was determined by testing cDNA of the reference strain of AIV H5N1, which was provided to us by NSC Institute for Experimental and Clinical Veterinary Medicine (Kharkiv, Ukraine). For the standard, we employed concentration in the range of 10.0–0.01 ng/sample. Results Table 1. This table shows the reproducibility results obtained by both methods. However, taken into account absence of highly pathogenic avian influenza virus circulating in Ukraine during the studied period, it was not possible to confirm these results with protocols of positivesamples. Table 2. It has been established that the sensitivity of PCR-RT kit Bird-Flu-PCR is 0.01 ng/sample for gene M and 0.1 ng/sample for subtype H5N1. Fig. 1. Visual detection of LAMP products with different concentrations of cDNA of avian influenza virus (ng per sample): 1 – 10; 2 – 5; 3 – 1.0; 4 – 0.1; 5 – 0.7 – 0.01; 8 – 9 – 0.1; 10 – negative. We have examined the LAMP results using electrophoresis for the confirmation of visual detection and correct interpretation of the results (Fig. 2). Fig. 2. Electrophoresis results for LAMP products. M – molecular weight marker; 1 – 10.0; 2 – 5.0; 3 – 1.0; 4 – 0.1; 5 – 0.7 – 0.01; 8 - negative control. It has been established that the sensitivity of LAMP is 0.1 ng/sample. Slightly lower sensitivity of LAMP in comparison to PCR-RT can be explained by visual detection of the products of the LAMP reaction. Conclusions 1. Sensitivity of both methods is high. 2. LAMP is a perspective screening method for the diagnosis of viral infectious diseases supported by confirmation of positive results by PCR-RT. 

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To evaluate the occurrence of Cryptosporidium species in edible frogs (Rana spp) sold at the Hanwa frog market Zaria, Kaduna State, Nigeria.

Introduction: Since Cryptosporidium can be transmitted by ingestion of infected food animals and poorly treated water and by direct contact, it is possible for infection to occur through ingestion of undercooked frogs and through handling and processing of infected frogs. In Burkina Faso, frogs caught are sold to market-women who treat the frogs by emptying their bowels and frying in oil before selling them. This is not always the case for the Nigerian frog markets where frogs are sometimes smoked or dried without necessarily being fried before consumption. This may pose a health risk for transmission of cryptosporidiosis from infected frogs.

Presence of Cryptosporidium oocysts in frogs may by implication reveal the Cryptosporidium status of water bodies from various sources where the frogs were caught. Water management programmes for treatment of Cryptosporidium is difficult as the oocyst is resistant to several disinfectants including chlorine. The consumption of such treated water in urban areas and untreated water in most rural communities may expose a great proportion of Nigerians to cryptosporidiosis. Owing to the number of HIV/AIDS patients who commonly suffer from cryptosporidial enteritis and cough, the control of cryptosporidiosis in animals and man is of public health significance.

Methods: A cross-sectional study was conducted between February and April, 2016 using intestinal contents from wild captured Rana species of frogs (n=117), sourced from 8 different locations, from the frog central collection, sales and processing point at Hanwa in Zaria. The intestinal contents from the frogs were examined by staining flotation and sedimentation smears with modified Ziehl-Neelsen stains followed by microscopy and micrometry of the oocysts.

Results: Overall, 35.9% of frogs sampled from the Hanwa frog market were positive for Cryptosporidium oocysts. There were more Cryptosporidium oocysts detected by sedimentation test (28.2%) than flotation test (23.9%). Although there was no significant statistical association between sex of frogs and oocyst detection ($\chi^2=0.5349, p>0.05$); sex wise, female frogs (40%) and frogs within the weight range 170-219g were more infected with Cryptosporidium (66.7%). Oocysts size ranging between 6.10 $\mu$m - 7.00 $\mu$m had the highest frequency of 10 (23.8%). By size 28.2% of the oocysts detected suggest infection with C. parvum and C. maleagridis.

Conclusions: We present the first report of Cryptosporidium oocysts in wild edible frogs (Rana spp) sold at the Hanwa frog market Zaria, Kaduna State, Nigeria. Frog consumption is on the increase in Nigeria, but baseline information on associated zoonoses is rare. A cross-sectional study conducted between February and April, 2016 using intestinal contents from wild captured frogs (n=117), sourced from 8 different locations using the modified Ziehl-Neelsen stains and micrometry revealed 35.9% were positive for Cryptosporidium oocysts. Of the oocysts detected 28.2% suggest infection with C. parvum and C. maleagridis; this may constitute a health risk for humans.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Introduction: Anthrax is an acute especially dangerous infectious disease of animals and humans. Bacillus anthracis is a potential bioterrorism tool. In Ukraine, there are favorable natural conditions for the spread of anthrax. There are 13.5 thousand of constantly anthrax-troubled points. Anthrax epidemic situation in Ukraine could be characterized as unstable. Because of the continuing reform of Ukrainian human health entities, the State Sanitary Epidemiological Service (SSES) has lost its control functions and is remaining in an uncertain state, which increases possible risks.

Methods: Epidemiological analysis of official data has been performed using information from the following sources: State Sanitary Epidemiological Service of Ukraine (SSES), State Veterinary and Phytosanitary Service of Ukraine, and analytical materials from SI UCDCM. Collected papers Distribution and Epidemiological Characteristics of Major Human Infectious Diseases in Ukraine (Kyiv Research Institute of Epidemiology, Microbiology and Parasitology, 1976) were also used during the study. Materials were compiled for the period from 1945 to 2015.

Results: In the early XX century, more than 10,000 cases of anthrax in humans were annually registered in tsarist Russia. In 1913, 1,473 cases of anthrax in animals were recorded only in Kherson province (currently, Kherson oblast of Ukraine). The morbidity among humans increased again during the WWII. In the late 40s, massive epizootic anthrax among animals was eliminated and morbidity among people significantly reduced because of planned government measures, strengthened veterinary, sanitary, and epidemiological surveillance. Since 1950, significant reduction of incidence of human anthrax has been being recorded in Ukraine. Since 1964, certification and mapping of persistent anthrax-troubled points in Ukraine have been being performed. Compulsory vaccination of people against anthrax was cancelled and compulsory vaccination of all livestock was introduced in 1990. The period from 1976 to 1993 is characterized as epidemiologically safe. Single cases of the disease in human were registered with an intensity rate of 0.01 – 0.002 per 100,000 population (excluding 1985). No human cases were registered during the certain years: 1978, 1982, 1987, 1988. The epidemic situation complicated during the period 1994-2001. The following outbreaks were registered: Table 1. Total number of disease cases/ including the number of cases during outbreaks within regions. The main reason for the complication of the epidemiological situation was weakening of epidemiological and veterinary surveillance during the economic crisis characterizing this period. Epizootiological outbreaks arose from incomplete anti-anthrax vaccination of agricultural animals and from violation of veterinary-sanitary rules for their keeping as well. More than 80% of human infection cases happened resulting compelled cattle slaughtering, while the rest 20% resulted from meat product distribution and consumption without corresponding sanitary-veterinary expertise. Six human cases of anthrax were registered during 2002-2015. Fig. 1. Dynamics of anthrax cases in humans in Ukraine during 1945 – 2015 (absolute numbers) Table 2. Chronology of anthrax epidemiological surveillance milestones in Ukraine. Conclusions: Relative wellbeing regarding anthrax in Ukraine persists owing to the implementation of ruled veterinary-sanitary activities and statesanitary epidemiological surveillance in meat- and leather-processing industries as well as because of active food control. The main risks, which could trigger complication in the current epidemiological situation with anthrax, are the following: 1) Uncertainty in the system of sanitary-epidemiological and veterinary surveillance, which resulted from the reformation of the State Sanitary-Epidemiological and State Veterinary services. 2) Existence of favorable conditions for anthrax agent circulation (considerable number of persistent anthrax-troubled points in all regions). 3) Economic instability in the country. 4) Uncontrolled epidemic situation in the zone of the Anti-terrorist operation (Donetsk and Luhansk oblasts).

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The purpose of this study was to describe the epidemiology of visceral leishmaniasis in Georgia and to define new control measures. Introduction Visceral leishmaniasis (VL) is a zoonotic, protozoal infection that is endemic in Georgia, which commonly affects young children. In recent years, the incidence of VL has increased sharply and the geographic distribution has increased. Recently, VL moved to highly populated areas as new foci appeared from 2010-2015, during which, 610 laboratory confirmed cases of VL were registered in Georgia. The majority of cases were found in East Georgia (94.2%) and 5.8% of cases in West Georgia (representing new foci of VL in Georgia). Methods Blood samples from 2,100 individuals suspected to have VL were tested using the rk39 based VL rapid diagnostic test, an enzyme-linked immunosorbent assay (ELISA). Also, 1,575 randomly selected dogs (stray and pet) and 77 wild canids were tested for VL using the same ELISA. Confirmed human cases were followed up for 9-12 months. Results The most affected age group was 0-5 years (72.2%). Of the patients, 13.9% were HIV positive and lethal outcomes were observed in 2.1% of patients. Mortality was associated with delayed diagnosis and HIV co-infection. Relapse developed in 6.4% of cases. Among HIV positive patients, secondary prophylaxis was conducted with liposomal amphotericin B, which decreased the number of relapses by 76% in 12-24 month follow-ups. A high incidence of VL in humans was associated with a high prevalence of leishmaniasis in stray and domestic dogs. Leishmania antibodies were found in 23.7% of stray and domestic dogs and 2.6% of wild animals screened in Tbilisi. Conclusions Overall, the VL situation in Georgia is concerning and new control measures are needed. Our study revealed a high prevalence of VL in humans and dogs in East Georgia. Early and accurate diagnosis/treatment and effective control measures should be conducted regularly to prevent the spread of VL in Georgia. In addition, secondary prophylaxis in HIV infected patients is also recommended.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To implement a systematic and uniform approach to evaluating data sources for syndromic surveillance within the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Services (APHIS) Veterinary Services (VS) group. Introduction USDA-APHIS-VS utilizes several continuous data streams to increase our knowledge of animal health and provide situational awareness of emerging animal health issues. In addition, USDA-APHIS-VS often conducts pilot projects to see if regular data access and analysis are feasible, and if so, if the information generated is useful. Syndromic surveillance was developed for three goals: a syndromic monitoring system to identify new diseases, as an emerging disease early warning system, and to provide situational awareness of animal health status. Current efforts focus on monitoring diverse data, such as laboratory accessions or poison center calls, grouped into syndromic or other health indicator categories, and are not intended to identify specific pre-determined diseases or pathogens. It is essential to regularly evaluate and re-evaluate the effectiveness of our surveillance program. However, there are difficulties when using traditional surveillance evaluation methods, since the objectives and outcomes of monitoring novel data streams from pilot projects are not easily measurable. An additional challenge in the evaluation of these data streams is the identification of a method that can adapt to various contexts and inputs to make objective decisions. Until recently, assessment efforts have looked at the feasibility of regular analysis and reporting, but not at the utility of the information generated, nor the plausibility and sustainability of longer term or expanded efforts. Methods Methods for surveillance evaluation, syndromic surveillance evaluation, and specifically for animal health syndromic surveillance evaluation were researched via a literature review, exploration of methods used in-house on traditional surveillance systems, and through development over time of criteria that were seen as key to the development of functioning, sustainable systems focusing on animal health syndromic surveillance. Several methods were adapted to create an approach that could organize information in a logical manner, clarify objectives, and make qualitative value assessments in situations where the quantitative aspects of costs and benefits were not always straightforward. More than 25 articles were reviewed to determine the best method of evaluation. Results The RISKSUR Evaluation Support Tool (EVA) provided the majority of the methodology for the evaluations of our data sources. The EVA tool allows for an integrated approach for evaluation, and flexible methods to measure effectiveness and benefits of various data streams. The most useful and common factors found to evaluate pilot data sources of interest were how well the information generated by the data streams could provide early detection of animal health events, and how well and how often situational awareness information on animal health was generated. The EVA tool also helps identify and organize criteria that are used to assess the objectives, and assign value. Conclusions The regular evaluation of syndromic surveillance data streams in animal health is necessary to make best use of resources and maximize benefits of data stream use. It is also useful to conduct regular interim assessments on data streams in pilot phase to be certain key information for a final evaluation will be generated during the project. The RISKSUR EVA tool was found to be very flexible and useful for allowing estimates of value to be made, even when evaluating systems that do not have very specific, quantitatively measurable objectives. This tool provides flexibility in the selection of attributes for evaluation, making it particularly useful when examining pilot project data streams. In combination with additional review methodologies from the literature review, a systematic and uniform approach to data stream evaluation was identified for future use.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

The purpose of this study was to detect the presence of circulating Salmonella spp. on backyard production systems (BPS) with poultry or swine breeding in central Chile.

Introduction

Characteristics and conditions of backyard production systems (BPS) transform them into potential maintainers of priority zoonotic agents, like Salmonella spp., highly important agent because of its impact in animal and public health (1). Methods

A stratified and proportional random sampling approach was performed (2), based on 15 provinces from the study area (regions of Valparaiso, Metropolitana and LGB O’Higgins). 329 BPS sampled (equivalent to 1,744 samples). Stool content inoculated in test tubes with peptone water (APT, Difco®) supplemented with Novobiocin (Sigma®), incubated for 18 to 24 hours at 37°C. Subcultured on modify semisolid Rappaport Vassiliadis (MSRV, Oxoid®) agar supplemented with Novobiocin, incubated for 24 to 48 hours at 41.5°C. Samples compatible with growth and/or diffusion were sub-cultured by exhaustion on Xylose Lysine Deoxychocolate (XLD, Difco®) agar and then incubated for 24 hours at 37°C (3). Confirmation made by conventional PCR for invA genes (4). Serotypes were predicted using a combination of PCR and sequencing, aimed directly at genes coding for O, H1 and H2 antigens (5). Results

1,744 samples were collected belonging to the 329 BPS. 15 positive BPS (4.6%) detected. Serotypes detected correspond to Salmonella Typhimurium (21.7%), followed by Salmonella Enteritidis (13.0%), Salmonella Infantis (13.0%), Salmonella Hadar or Istanbul (8.7%), Salmonella [z42] or Tennessee (4.4%), Salmonella Kentucky (4.4) and unknown (34.8%) (Table 1). Conclusions

This is the first evidence of serotypes of Salmonella spp. circulating at a regional level in BPS from central Chile. A relevant pathogen for public health.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The purpose of this study was to identify zoonotic influenza viruses in swine and poultry populations in Georgia and to define their pandemic potential. Introduction Aquatic birds are the main reservoirs of influenza viruses, however pigs represent an essential host in virus ecology as they are susceptible to both avian and human influenza viruses. Circulating zoonotic influenza (A/H7N9, A/H5N1, and A/H3N2v) viruses could mutate into forms easily transmissible from human-to-human and become a public health concern. Georgia is located along routes used by migrating birds where different species of aquatic birds are found. In 2006, highly pathogenic influenza virus A/H5N1 was detected in two wild swans in Adjara (western Georgia). Moreover, in the frame of wild bird surveillance, various subtypes of influenza A viruses were detected in mallard and gulls in Georgia (Lewis, 2013). Thus, domestic animals in Georgia have a potential chance to contract influenza viruses from wild birds. Methods The Kakheti region, the leading region in cattle breeding and poultry production in Georgia, was selected for study. Villages were selected for door-to-door visits to search for ill backyard animals showing influenza-like symptoms. In case of identification of a sick animal, samples were obtained for laboratory investigations; sample collection forms were filled out to generate epidemiological data. Cloacal and tracheal swabs were taken from poultry; and pharyngeal and nasal swabs were collected from pigs. Each specimen was screened for influenza A matrix gene by real-time RT-PCR using a protocol from the Centers for Disease Control Prevention. Results Eighty-four villages in the Kakheti region were surveyed for domestic animals with influenza-like illness symptoms. In total, 164 specimens were collected from 112 backyard animals in 55 households (107 samples were from 55 poultry and 57 samples were from 57 pigs). All samples tested negative for Influenza A virus by real-time RT-PCR. The questionnaire data revealed that the age range of both pigs and poultry varied from one month to two years; median and mode were both 1 year. Chickens and ducks primarily freely ranged in backyards (67%), while half the number of pigs were kept in closed premises. Equally, 61% of pigs and poultry had contact with other pigs or poultry within the premises. Conclusions In spite of the negative findings, we cannot exclude the circulation of influenza viruses in domestic animals in Georgia. Especially, considering the fact that a domestic duck with influenza A/H10virus was identified during veterinary training in 2010 in Grigoleti (Black sea cost of Georgia) manifesting no clinical symptoms. Therefore, larger scale studies, including swabbing more backyard animals without any clinical symptoms are necessary to identify inter-species virus transmission in the country.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
Analysis of brucellosis monitoring in agricultural animals in Ukraine to control epizootic situation and prevent possible brucellosis in humans.

Introduction
Brucellosis is one of the most widespread zoonosis in the world. Only 17 countries informed WHO that their territory is free from brucellosis. About 500 thousand cases of brucellosis in humans are registered in the world each year. The problem of brucellosis remains actual to agriculture and health care for many years. Almost all agricultural animals are highly susceptible to brucellosis. Socio-economic significance of brucellosis problem is determined by peculiarities of the course of the disease and the main contingent that can be infected, namely the working population that is connected with both professional factors and social reasons. Brucellosis is a chronic infectious disease. The disease in animals has the following signs: abortions and retention of secundines, orchitis, unviable litter and sterility. Brucellosis is included to the list of quarantine diseases due to its social threat.

Methods
Studies of blood sera of cattle, small ruminants, horses and pigs from different Ukrainian regions that were selected during the annual spring clinical examination in 2013-2015. The following serological methods were used for the studies: complement-fixation test (CFT), agglutination reaction (AR), Rose Bengal test (RBT), prolonged complement fixation test (PCFT).

Results
Currently, Ukraine is free from brucellosis of animals. The last case of brucellosis in pigs was registered in 2008 in Odesa Oblast. The last case of brucellosis in cattle in Ukraine was registered in 1992. According to the Ministry of Health, a case of brucellosis in humans is registered in Ukraine almost every year. Annual serological studies of service bulls, cows, heifers older than one year, horses, rams, ewes, boars and sows are held once a year in Ukraine. During 2013-2015, the monitoring serological brucellosis studies of blood sera from cattle, small ruminants, horses and pigs were held once a year in Ukraine. During 2013-2015, the monitoring serological brucellosis studies of blood sera from cattle, small ruminants, horses and pigs from different farms in 25 oblasts of Ukraine were conducted at State Laboratories of Veterinary Medicine and State Scientific and Research Institute of Laboratory Diagnostics and Veterinary and Sanitary Expertise. Table 1. Serological research results

In 2013, seropositive results were obtained in AR Crimea – six cases in cattle, Dnipropetrovsk oblast - 12, Kyiv oblast – 31, Sumy oblast – 118, and Luhansk oblast – 25 using AR and RBT techniques. In small ruminants, seropositive results were determined in Luhansk oblast – 26 animals (AR). Testing pigs by RBT showed the following positive results: 82 animals in Dnipropetrovsk oblast, 16 in Luhansk, and 1 in Sumy oblast. Twenty seven horses were detected positive by RBT in Luhansk oblast. Fig. 1. Brucellosis monitoring results, 2013

In 2014, seropositive results in cattle were received in Kyiv (20), Dnipropetrovsk (28), Sumy (66), Chernihiv (37) and Zhytomyr (2) oblasts using AR, RBT, and CFT. AR tests were positive for one small ruminant in Dnipropetrovsk and for three in Sumy oblasts. Five seropositive pigs were found in Sumy oblast using RBT. Fig. 2. Brucellosis monitoring results, 2014

In 2015, seropositive results (AR, RBT, and CFT) in cattle were obtained in Sumy (8 animals), Dnipropetrovsk (34), and Chernihiv (10) oblasts. For small ruminants, one seropositive animal was found in Dnipropetrovsk and in three in Sumy oblasts using AR. Employing RBT, one pig was diagnosed in Dnipropetrovsk oblast. Two horses were found positive using RBT in Sumy oblast. Fig. 3. Brucellosis monitoring results, 2015. The seropositive animals were destroyed. Bacteriological studies were not conducted.

Conclusions
During the studies of blood sera of agricultural animals from different Ukrainian regions, positive results were obtained in 7 oblasts of Ukraine indicating a possible circulation of the causative agent of brucellosis. Studies need the in-depth analysis that must include bacteriological testing of seropositive animals.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To determine the vaccination status of owned dogs, assess therabies antibody titre of vaccinated dogs and risk factors associated with vaccination of dogs in Abuja, Nigeria. Introduction Rabies is a zoonotic disease of high public health importance. There have been documented reports of rabies in vaccinated dogs. Rabies is enzootic in domestic dogs in Nigeria. Hence, annual vaccination campaigns of dogs are advocated with the aim of rabies elimination. Vaccination status, type of vaccination and the immunogenicity of the various rabies vaccines used in Abuja Nigeria has not been studied. To date, no effective medical therapy has been established for rabies. Most human rabies deaths occur in the developing countries and though effective and economical control measures are available their application in developing countries is hampered by a range of economic, social and political factors. It is widely recognized that the number of deaths officially reported in most developing countries greatly underestimates the true incidence of disease, with several factors contributing to widespread underreporting. Preventive vaccination against rabies virus is an highly effective method for preventing rabies in humans and animals but do people vaccinate and how long does the immunity confer from the vaccine remain protective in the dogs in Abuja? Rabies has high financial expenditure burden on any country where it is endemic mainly associated with costs incurred on post-exposure prophylaxis (determined by the type of vaccine, vaccine regimen and route of administration as well as the type of immunoglobulin used).

Methods Dog serum samples (n=276) were collected from Abuja the Federal Capital Territory (FCT) Nigeria, from 5 locations (Phase 1, 2, 3, Gwagwalada and Kubwa) based on availability and owners consent. Rabies antibody serum titer was determined using an indirect enzyme-linked immuno-sorbent assay. Face to face structured questionnaires were used to obtain demographic and zoographic information from the dog owners. Associations between the demographic variables, vaccination status and rabies antibody titer of each dog were assessed using $\chi^2$ analysis. Results Of the dogs sampled, 229 (83%) had certified antirabies vaccination record. The dogs sampled, which were vaccinated from Phase I, II, III and the satellite towns were; 109/118 (92.37%), 32/33 (96.97%), 48/49 (97.96%) and 40/76 (52.63%), respectively. A total of 276 serum samples were collected, processed and analyzed during this study. Out of the 276 dogs sampled, 239 (86.6%) had rabies antibody titre $\geq 0.6$EU/ml whilst 37 (13.4%) had less than 0.6EU/ml. There was a marked decline in rabies antibody titre with increase in time. Out of the 228 exotic breeds of dogs sampled, 218 (95.6%) were vaccinated whilst 11 (22.9%) of the 48 indigenous breed of dogs sampled were vaccinated. All the exotic breed of dogs had rabies antibody titre $\geq 0.6$EU/ml whilst 37 (77.1%) of the indigenous breed of dogs had less than 0.6 EU/ml levels of rabies antibody titre. All dogs within 6 months to 1 year and greater than 10 years of age had $\geq 0.6$EU/ml rabies antibody titre whilst dogs within 1-5 years had 1 (0.5%) and 36 (92.2%) dogs of age 6-10 years had rabies antibody titre < 0.6EU/ml. Twelve (7.6%) of the males and 25 (21.2%) of the females had less than 0.6EU/ml rabies antibody titre. All the dogs acquired by importation and from breeders had rabies antibody titre $\geq 0.6$EU/ml whilst 37 (27.2%) of the dogs acquired from friends had less than 0.6EU/ml rabies antibody titre. Significant associations were observed between breed ($\chi^2=203.6$, df = 1, P-value < 0.05), age ($\chi^2=172$, df = 3, P-value < 0.05), sex ($\chi^2=10.75$, df = 1, P-value < 0.05), source ($\chi^2=43.99$, df = 2, P-value < 0.05), rabies vaccination status ($\chi^2=276.00$, df = 2, P-value < 0.05) and the rabies antibody prevalence of sampled dogs.

Conclusions This cross-sectional study shows that not all dog owners vaccinatetheir dogs and that the vaccines conferred protection beyond 12 months. The Preventive vaccination against rabies virus is an highly effective method for preventing rabies in humans and animals. Policies to enhance mass mandatory annual vaccination to achieve 70% coverage should be implemented in order to eradicate rabies.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The purpose of this study was to describe anthrax foci along the Georgia-Azerbaijan border and to describe control measures in unidentified areas.

Introduction Anthrax is endemic in the South Caucasus region. There is a lack of understanding of the regional epidemiology of the causative pathogen, Bacillus anthracis, and the trans-boundary factors related to its persistence.

Methods To increase the local and regional understanding of anthrax ecology, ecological risk factors, and the genetic relationships and distribution among Georgian and Azerbaijani B. anthracis strains, a regional study of the ecology of anthrax foci was conducted in Georgia and Azerbaijan. Six regions in Georgia (that border Azerbaijan) were selected for environmental sampling based on historical data. Soil samples were collected in Lagodekhi and Sagarejo and tested at the Laboratory of the Ministry of Agriculture using standard bacteriological and molecular biology methods.

Results A total of 185 soil samples were collected. Bacteriological tests revealed four positive samples from Kakheti (two from Lagodekhi, Gelati; two from Dedoplistskaro), from which, cultures were isolated and confirmed by PCR. Georgian scientists continue collecting and testing soil samples. After sample collection and bacteriological testing is completed, the molecular characteristics of the pathogen will be examined.

Conclusions This study will assist in the formulation of targeted public health interventions aimed at increasing knowledge of the disease within specific demographics. Public health interventions can focus on livestock surveillance and control in identified areas.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
The purpose of this research was to study the seroprevalence of zoonotic diseases among farm animals in the Kvemo Kartli region of Georgia.

Introduction
Zoonotic diseases are an important cause of human morbidity and mortality; around 75% of recently emerging human infectious diseases are zoonoses. Herein we report the first seroprevalence study to include a range of emerging or re-emerging zoonotic pathogens of economic concern (including: Bacillus anthracis, Coxiella burnetii, Francisella tularensis, Brucella spp., and Crimean-Congo hemorrhagic fever virus (CCHFV)) affecting domestic animals (e.g., cattle, sheep, goat, and dog) in Georgia.

Methods
Cattle (n=177) from Gardabani, Marneuli, and Tsalka (Kvemo Kartli region) were sampled for the study as were small ruminants and dogs (n=30). Bacillus anthracis, Brucella spp., CCHFV, and C. burnetii (Phase I) were detected using ELISA methods. Francisella tularensis was detected using a microscopic agglutination test (MAT).

Results
Of the cattle sampled, 11 were positive for F. tularensis, 39 were positive for Brucella spp., and seven were positive for C. burnetii. All samples were negative for CCHFV. Three goat samples were positive for C. burnetii, one goat sample and one dog sample were positive for F. tularensis.

Conclusions
Domestic animals serve as a source of disease that can spread to humans through vectors or direct contact. In Georgia, domestic animals were not previously studied for exposure to zoonotic diseases, with the exception of cattle, which were surveyed for brucellosis. In particular, the finding of F. tularensis-positive animals is novel in Georgia, as this region was considered free of the pathogen. Screening studies of domestic/farm animals for zoonotic pathogens such as this can serve as a source of baseline data for regional risk assessments and to better inform One Health measures.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The main focus of this study was to study the spread of botulism in Georgia and the biological characteristics of the strains of *Clostridium botulinum* isolated from territories in the country.

Introduction Accumulation of *C. botulinum* in soil occurs through excretion of bacterial spores from the intestines of humans, animals, birds and fish. In Georgia, during the winter season, the population consumes homemade vegetable preserves, which are made of locally produced (as well as imported) vegetables. Historical surveys confirmed that the presence of *C. botulinum* in the soil is widespread. Some researchers consider *C. botulinum* a characteristic component of soil flora.

Methods Soil samples were collected from areas, where from 2001-2002 cases of botulism caused by homemade vegetable preserves (produced from vegetables cultivated in those areas) were registered. Soil samples were collected from Kakheti, Shida Kartli, Kvemo Kartli, Samtkhe-Javakheti, and Samegrelo regions. Standard bacteriology and PCR were used to confirm the presence of *C. botulinum* from soil samples. Separation of strains and their examination was conducted in accordance with the scheme provided by the CDC Atlanta Reference Laboratory (USA), which was later tested by NCDC. Toxigenicity and toxin production of strains were tested using a biotest on white mice.

Results In total, 258 soil samples were tested, from which, 40 (15.5%) cultures of *C. botulinum* type B were obtained. Toxigenicity and toxin production were confirmed through biotests. These results confirm the presence of *C. botulinum* in agricultural lands, which causes contamination of vegetables cultivated on those lands, which are used for the preparation of homemade preserves, causing botulism in humans.

Conclusions For the purpose of finding solutions to botulism, it is essential to verify the ecology of the pathogen through establishing the prevalence of bacteria in different soil types. It was shown that some areas of Georgia, where vegetable growing is greatly developed, and which are the main sources of crops, are highly contaminated with *C. botulinum*. In Georgia, land used for agriculture is contaminated with *C. botulinum*. *C. botulinum* type B was isolated from 40 cultures obtained from 258 soil samples, which represents contamination in 15.5% of sampled areas. These results suggest that vegetables and melons may be highly contaminated as well. All cases of *C. botulinum* humans that were researched were connected to homemade canned vegetables.


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Abstract

Introduction

Ukraine’s ability to respond to the spread of viruses that cause pandemics and reduce economic losses from influenza, can be strengthened only in the presence of a developed surveillance network including the monitoring of virus circulation in humans. Specialists of Dnipropetrovsk Oblast have great experience in virological surveillance on the circulation of influenza virus A/California/H1N1 and timely determination of the etiology of outbreaks caused by the virus.

Methods

Laboratory diagnostics of influenza was performed using serological methods, PCR, and virological studies in the cell culture. During the last seven epidemic seasons, including the flu pandemic of 2009-2010, most of samples came from four health-care facilities of Dnipropetrovsk, which were determined as basic hospitals for the sentinel center. Patients with severe acute respiratory infections (SARI) were examined. Nasopharyngeal washouts and swabs were collected into cryo-tubes with a transport medium. The samples were stored at hospitals in Dewar flasks. The delivery of the samples to the laboratory was performed according to cold-chain rules. After sample preparation stage, the samples were tested for the presence of influenza A/B virus RNA by PCR using Bio-Rad CFX-96 cycler and the following commercial test-kits AmpliSens® Influenza virus A/B-FL, AmpliSens® Influenzavirus A/H1-swine, and AmpliSens® Influenza virus A-type-FL. All positive samples with detected RNA of influenza virus A/H1-swine were tested using MDSK cell cultures (Canine Kidney Epithelial Cells). Flu viruses caused cytopathic changes in the cell cultures in the form of poppy-sand-like degeneracy not earlier than 72 hours after the infection of the cells followed by cell monolayer fragmentation.

Results

During the seven epidemic seasons, 5,467 people were examined for flu and acute respiratory viral infections. During the swine flu pandemic in 2009-2010, 1,217 severely ill patients were tested. Positive results were found in 50% of cases (607 persons). From those, pandemic influenza virus (RNA of influenza A/H1-swine virus) was detected in 100% of positive cases. Frequency of pandemic influenza virus detection declined to zero in the following epidemic seasons (2010-2011 and 2011-2012). However, incidence of the virus variant (influenza A/H1-swine) began to grow slowly during the last four epidemic flu seasons from separate cases (6 in 2012-2013, 1 in 2012-2013) to 26 cases in 2014-2015. During the last epidemic season (2015-2016), the number of pandemic influenza cases increased dramatically to 166, accounting 29% of all examined persons.

Conclusions

1. Circulation of the pandemic type of influenza virus A/California/(H1N1)/07/2009 among the population of Dnipropetrovsk Oblast is of sporadic character.
2. The return of the virus strain A/California/(H1N1)/07/2009 after the 2009-2010 pandemic occurred during the last 2015-2016 epidemic season.
3. Application of PCR can significantly shorten the examination of patients with severe course of influenza, but cannot help with virus isolation.
4. The use of express immunoassay tests accelerates the identification of viruses isolates.
5. The employment MDSK cell culture for influenza virus isolation allows obtaining of a spectrum of influenza strains circulating during an epidemic period including the strain A/California/(H1N1)/07/2009.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objectiveto show the instability of an epizootic situation on rabies cases of animals in the Republic of Azerbaijan, on the example of the cases analysis in Electronic Integrated Disease Surveillance System (EIDSS) electronic reporting system

Introduction

Rabies is an infectious disease which was and remains to be one of the most serious diseases of all species of hematothermal animals and humans, in many regions of the world. The epizootic situation on rabies in the Republic of Azerbaijan has been unfavorable for many years, which is confirmed by scientific data and the veterinary cases reporting in the EIDSS system. This system was introduced in the country in 2009 and is the electronic System of disease control. The program allows to provide monitoring and prevention of diseases within the concept “One World - One Health System” by integration of systems of observation of animal diseases, human diseases, and disease carriers.

Methods

On the basis of the data on rabies cases entered in special forms and also aggregative data collected on anti-rabies vaccination, the analysis of information on quantity of cases and their prevalence on administrative and territorial units (rayons) of the country is carried out. The graphical analysis (charts and the map) on the basis of necessary criteria are constituted in the analyses module, visualization of the AVR reporting and in the Microsoft Excel program.

Results

The analysis of the rabies cases confirmed at the Virology department of the Republican Veterinary Laboratory shows that rabies has been identified in 36 cases in 2015, 25 cases in January-June, 2016, in total 61 cases has been registered for the period of “January 2015 – June 2016”. An epizootologically unfavorable situation is revealed in 27 regions. The most unfavorable situation is the northwest regions of the country, the most part of which is covered with mountain-forest area with domination of wild fauna. Specific structure of animals: dogs – 31 cases in 19 areas (51%), cattle – 21 cases in 12 areas (34%), a small cattle – 1 case (2%), wild animals (specify types) - 8 cases in 8 areas (13%) that is visually shown on charts 1 and 2. The cattle were bitten by wolves and jackals.

Conclusions

Thus, prevalence of rabies cases of different species of animals in the country, once again proves natural and focal character of the disease: the reservoir of rabies is in the wild nature and geographical conditions impact the spread of rabies. Cases of rabies in animals are registered annually. In 2015, vaccination captured about 250000 dogs, and 244400 dogs were vaccinated in the first 6 months of 2016. Despite a huge group of vaccinations, restriction of rabies spread isn’t observed and the tendency is trending to the increase of rabies case indicators amongst the dogs. It is necessary to pay close attention to preventive vaccination of domestic (including non-productive) animals. If material resources are available, it is possible to carry out the vaccination of the cattle in the territories adjacent to the forests. In the threatened territories with woodlands, there is no alternative to oral vaccinations, which is confirmed by positive experience of many countries. There is an extreme need of carrying out of oral vaccination of wild carnivorous animals with obligatory control of the immune status.

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Abstract

Objective
This study aims to analyze the evolution of the epidemiological behavior of rabies in Chile during the period 2003 to 2013, through the epidemiological characterization of a number of variables and description of spatial and temporal patterns of animal cases.

Introduction
Rabies is a zoonotic disease caused by an RNA virus from the family Rhabdoviridae, genus Lyssavirus. Worldwide distributed, control of rabies has been considered to be particularly amenable to a “One Health” strategy (1). In Chile, rabies was considered endemic in domestic dog population until the late 1960s, when a surveillance program was established, decreasing the number of human cases related to canine variants until the year 1972 (2). Rabies is recognized as an endemic infection in chiropterans of Chile and prompted the surveillance of the agent in this and other species (3).

Methods
An epidemiological characterization of the registered cases from the National Program for Prevention and Control of Rabies was carried out. During the period 2003–2013, 927 cases were reported. Descriptive statistics and descriptive mapping, recording origin of the sample, number of cases per region, animal reservoir implicated, and viral variant were performed. A spatial autocorrelation analysis was carried out using Moran’s I indicator for the detection of spatial clusters (4), using the Local Indicators of Spatial Association (LISA) statistics (5), at national and regional level of categorization (north, central, and south zone). Temporal descriptive analysis was carried out.

Results
927 positive cases were recorded. 920 (99.2%) cases came from passive surveillance, while 7 (0.8%) cases by active surveillance, total positivity was 77.02% and 1.37% respectively. Positivity was reported mainly in the central zone (88.1%), mainly in Valparaiso (19.1%), Metropolitana (40.6%) (Figure 1), Maule (11.8%) regions concentrated in urban centers. Main positive reservoirs were bats (99.8%), specifically Tadarida brasiliensis and viral variant 4 was the most commonly diagnosed. LISA test gives a Moran’s I indicator of 0.1537 (p-value = 0.02) for the central zone (Table 1). Rabies tend to decrease in the fall and winter season (2.9 cases vs 13 cases during summer).

Conclusions
Wildlife rabies in bats remains endemic in Chile, concentrated in urban areas. The main reservoirs are insectivorous bats. There is a significant spatial autocorrelation of animal rabies cases in the central zone of Chile. Results are relevant to the design of preventive and control measures.

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Abstract

ISDS Annual Conference Proceedings 2017. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.38(page number not for citation purposes)ISDS 2016 Conference AbstractsIdentification of Sufferers of Rare Diseases Using Medical Claims DataJieshi Chen* and Artur DubrawskiAuton Lab, Carnegie Mellon University, Pittsburgh, PA, USAObjectiveTo identify sufferers of a rare and hard to diagnose diseases by detecting sequential patterns in historical medical claims.IntroductionPatients who suffer from rare diseases can be hard to diagnose for prolonged periods of time. In the process, they are often subjected to tentative treatments for ailments they do not have, risking anescalation of their actual condition and side effects from therapies they do not need. An early and accurate detection of these cases would enable follow-ups for precise diagnoses, mitigating the costs of unnecessary care and improving patients’ outcomes.MethodsA sequential rule learning algorithm was applied to a medical claim dataset of about 1.700 patients, who are pre-selected to have medical histories indicative of Gaucher Disease (GD) but only 25 of these patients were confirmed positives. About 168,000 medical claims and 142,000 pharmaceutical claims were featureized into sequences of asynchronous events and regularly sampled time series as inputs for the model, such that an occurrence of a certain diagnosis code in a medical claim was counted as one event along the timeline of the patient’s medical history. Similar method was applied to other key attributes of claims data including procedure codes, National Drug Codes, Diagnosis Related Groupers, etc. These types of events as well as their temporal statistics, e.g. moving frequencies, peaks, change points, etc., formed the input feature space for the algorithm which was trained to adjudicate each test case and estimate their likelihood of having GD. A random forest algorithm was also applied to the same feature set to comparatively evaluate the utility of sequential aspects of data. The models were evaluated with 10-fold cross-validation. ResultsFigure 1 shows the Receiver Operating Characteristic (ROC) curves of the temporal rule model with Area Under the Curve score exceeding 81% and significantly outperforming the random forest default models. Considering the practical costs to perform follow-up genetic tests, we prefer a model achieving high positive recall at low risk of false detection. Our model correctly identifies more than 25% of known positive cases well within 0.1% of the false positive rate, while the performance of a more popular alternative is indistinguishable from random. This demonstrates the utility of sequential structure of medical claims in identifying patients who suffer from rare diseases. Our algorithm infers from data highly interpretable rules it uses in case adjudication. Figure 2 illustrates one of them. The root node of the case adjudication tree (Event.7969) reflects the ICD-9 diagnosis code of “Other nonspecific abnormal findings”. Among the 14 patients that have this particular ICD-9 code present in their claim history, 36% are confirmed GD sufferers. Compared to default prevalence in our pre-selected data set of 1.47%, this rule lifts the estimated likelihood of GD 25 times. The rule further develops into two children nodes. The left child node adds the condition of having any outpatient claim observed within 43 claims recorded nearby the occurrence of the root node event. It isolates 5 patients all of whom are GD-positive. The right child shows that 3 patients without Event.7969 in their claim history but prescribed NDC62756-0137-02 (Gabapentin by Sun Pharmaceutical Industries Ltd.) are all GD-positive. This is just one example of a simple and easy to implement business rule that is capable of identifying previously undiagnosed sufferers of rare diseases. Conclusions Our model successfully utilizes sequential relationships among events recorded in medical claims data and reveals interpretable patterns that can identify sufferers of rare diseases with high confidence. The algorithm scales well to large volumes of medical claims data and it remains sensitive in despite of a very low prevalence of target cases in data. ROC diagrams of models trained to identify GD patients shown with decimal logarithmic scale of the false positive rate axis.


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Abstract

Objective To report the results of the application of New Jersey’s Severe Weather Classifier in New Jersey’s syndromic surveillance system during two extreme weather events. Introduction Hurricane ‘Superstorm’ Sandy struck New Jersey on October 29, 2012, causing harm to the health of New Jersey residents and billions of dollars of damage to businesses, transportation, and infrastructure. Monitoring health outcomes for increased illness and injury due to a severe weather event is important in measuring the severity of conditions and the efficacy of state response, as well as in emergency response preparations for future severe weather events. Following the experience with Hurricane Sandy, NJDOH initiated a project to develop a suite of 19 indicators, known as the Severe Weather Classifier (SWC) in EpiCenter, an online system which collects emergency department chief complaint data in real-time, to perform syndromic surveillance of extreme weather-related conditions. NJDOH has since used these classifiers in more recent events to monitor for weather-related visits to storm-affected area emergency departments (ED’s). In June, 2015, a squall line of damaging thunderstorms, known as “bow echo,” caused downed wires and multi-day power outages in Camden and Gloucester counties in southern New Jersey. Almost exactly seven months later, in January, 2016, Winter Storm Jonas dropped more than a foot of snow over New Jersey. These events provided an opportunity to assess the indicators within SWC. Methods The impact of these storms on ED visits was assessed in EpiCenter by using the SWC sub-classifications for disrupted outpatient medical care (dialysis and oxygen needs, and medication refills). Rates per 1,000 ED visits were calculated on two weeks of ED visits by classification for each storm. For the June 2015 bow echo storm, this assessment focused on Gloucester and Camden counties, the two hardest hit by the storm. For Winter Storm Jonas, rates per 1,000 ED visits were calculated statewide since all counties were impacted. Results After the June, 2015 bow echo storm, both Camden and Gloucester county ED’s experienced increases in disrupted medical care, the most notable being for oxygen needs (Figures 1 and 2). During and after Winter Storm Jonas, ED visits for oxygen assistance and medication refills were the most impacted (Figure 3). It is speculated that ED visits for dialysis were not noticeably higher since the storm occurred over a weekend when, generally, treatments take place during weekdays. Conclusions While not every classification in the suite that makes up the SWC would be relevant in every extreme weather event, having the 19 various elements available provides tools for state and local users to monitor storm impacts both locally and at the state level.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To create an informatics framework and provide guidance to help Minnesota’s public health surveillance systems achieve interoperability and transition to standards-based electronic information exchange with external health care providers using the state’s birth defects registry as an initial pilot program.

Introduction The Minnesota Department of Health (MDH) needs to be able to collect, use, and share clinical, individual-level health data electronically in secure and standardized ways in order to optimize surveillance capabilities, support public health goals, and ensure proper follow-up and action to public health threats. MDH programs, public health departments, and health care providers across the state are facing increasing demands to receive and submit electronic health data through approaches that are secure, coordinated, and efficient; use appropriate data standards; meet state and federal privacy laws; and align with best practices. This framework builds upon existing informatics models and two past studies assessing health information exchange (HIE) conducted by the MDH Office of Health Information Technology (OHIT) to provide MDH surveillance systems with an outline of the key elements and considerations for transitioning to more secure, standards-based, electronic data exchange.

Methods Development of the informatics framework incorporates information gathered in several phases. The first phase involves additional analysis of data collected from the MDH Informatics Assessment of Interoperability and HIE that was conducted in 2015 to evaluate the current state of interoperability and HIE readiness across the agency. The second phase involves a comprehensive environmental scan and literature review of existing standards, practices, models, toolkits, and other resources related to electronic HIE and interoperability. The third phase involves gathering additional information on programmatic needs, workflows, and capabilities through key informant interviews. Key informants include program managers, staff, and content-area experts from select MDH programs, the state’s central information technology organization (MN.IT), and external health care provider organizations including hospitals. Minnesota’s birth defects registry, the Birth Defects Information System (BDIS), was selected as the pilot program because it was identified in the 2015 MDH Informatics Assessment as having a high level of interest in implementing an interoperable and standards-driven approach to electronic health data exchange. The BDIS is also exploring options for being designated as an eligible public health registry for Meaningful Use.

As a pilot program for this project, the BDIS assists in the development and implementation of the informatics framework.

Results The 2015 MDH Informatics Assessment identified and evaluated 21 MDH programs with information systems that accept and manage clinical, individual-level health information. Among these 21 MDH programs, wide variations exist regarding information system size (range, 400 to 10,000,000 individuals), staffing numbers (range, 0.2 to 21 FTEs), budgets (range, $20,000 to $1,876,000), and other key characteristics. Despite these variations, programs identified similar barriers and needs related to achieving interoperability and electronic HIE. Areas of need include management and information technology support to make interoperability a priority; policies and governance; additional application functionality to support HIE; and additional skills for the workforce. Results from the environmental scan and key informant interviews will be incorporated with additional analyses of the 2015 MDH Informatics Assessment to inform the development of an agency-wide informatics framework to support MDH programs in achieving interoperability.

Conclusions MDH surveillance systems are calling for practical guidance to help implement and maintain a more efficient and effective way to electronically collect, use, and share health data with external and internal stakeholders. This informatics framework provides an outline of the key elements and considerations for achieving greater interoperability across MDH surveillance systems. Additional research is required to assess how system interoperability and HIE can improve data quality and advance population health goals.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To improve data quality and sustain a good quality data collected by Laboratory Automated Reporting System (LARS), we use a Three-stage Data Quality Correction (3DQC) strategy to ensure data accuracy. Introduction To immediately monitor disease outbreaks, the application of laboratory-based surveillance is more popular in recent years. Taiwan Centers for Disease Control (TCDC) has developed LARS to collect the laboratory-confirmed cases caused by any of 20 pathogens daily via automated submitting of reports from hospital laboratory information system (LIS) to LARS since 2014 [1]. LOINC is used as standardized format for messaging inspection data [1, 2]. There are 37 hospitals have joined LARS, coverage rate about 59% of all hospitals in Taiwan. Recently, more than 10,000 of data are collected weekly and used in monitoring pathogen activity [3]. Therefore, it is important to ensure data quality that the data will lead to valuable information for public health surveillance. Methods A 3DQC strategy was designed to improve data accuracy and carried out by teamwork among TCDC, Taiwan Association for Medical Informatics (TAMI) and IT Company (Figure 1). In the first stage of 3DQC, IT Company checked data format. In the second stage, TCDC verified information between hospital inspection reports and data receiving in LARS. In the third stage, TAMI evaluated LOINC mapping and TCDC monitored stability of data transmission. After correcting the data, hospitals were approved to join LARS. Results During the first stage of 3DQC, we observed that some problems with syntax error in data (e.g., incorrect patient identification number, or lack of residence codes). Because some data were stored in Hospital Information System (HIS) but not in LIS, an error may occur while hospital accessed records from HIS. In the second stage, 50-70% of inspection reports provided by each hospital had problems with semantic information error. For example, a positive result of influenza A on a screening flu test recorded in LIS but hospital transferred the wrong result with influenza B positive into LARS. In the third stage, we found that 20-30% of terms mismatched to LOINC code. This study categorized these terms into two groups (1) the Exception codes, which were considered reasonable and (2) the Error codes, and also reviewed Error codes and made a modified advice for hospital staff to improve LOINC mapping. Through 3DQC strategy, the LOINC mapping rate raised from 40 to 80%, Exception codes mapping was 20%, and the total mapping rate was near 95-99% (Figure 2). So far, most hospitals have maintained a good quality data even they formally participate in LARS. Conclusions This study suggested that 3DQC can effectively detect problems and reduce errors of data collected from LARS, and indicated that the effect of 3DQC can be maintained even hospital formally participates in LARS. Future research will focus on development of automatic programming of 3DQC to ensure high-quality data. Figure 1. A Three-stage Data Quality Correction strategy

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Abstract

Objective To determine whether mass casualty shooting events are captured via syndromic surveillance data. Introduction Shootings with multiple victims are a concern for public safety and public health. The precise impact of such events and the trends associated with them is dependent on which events are counted. Somereports only consider events with multiple deaths, typically four or more, while other reports also include events with multiple victims and at least one death. Underreporting is also a concern. Some commonly cited databases for these events are based on media reports of shootings which may or may not capture the complete set of events that meet whatever criteria are being considered. Many gunshot wounds are treated in the emergency department setting. Emergency department registrations routinely collected for syndromic surveillance will capture all of those visits. Analysis of that data may be useful as a supplement to mass shooting databases by identifying unreported events. In addition, clusters of gunshot wound incidents which are not the result of a single shooting event but still represent significant public safety and public health concerns may also be identified. Methods Emergency department registration data was collected from hospitals via the EpiCenter syndromic surveillance system. Gunshot-related visits were identified based on chief complaint contents using EpiCenter’s regular expression-based classification system. The gunshot wound classifier attempts to exclude patients with pre-existing wounds and shooting incidents involving weapon classes that are lesser concerns for public safety, such as nail guns and toy guns. Gunshot-related visits were clustered by day of registration and separately by facility, by patient home zip code, and by patient home county. The largest clusters of each type were compared via manual search against media reports of shootings and against the Gun Violence Archive mass shooting database. Results A total of 23,132 gunshot-related visits were identified from 635 healthcare facilities from 2013 to 2015. From these, the five largest clusters by facility, by zip code, and by county were identified. The clusters included 112 gunshot wounds in total, ranging in size from 4 to 12 with a median of 7. Of the 5 facility clusters, 5 had a corresponding media story and 2 were located in the shooting database. Of the 5 zip code clusters, 1 had a corresponding media story and none were located in the shooting database. Of the 5 county clusters, 4 had a corresponding media story and 1 was located in the shooting database. Conclusions Multiple gunshot wound patients being treated on the same day were not necessarily all shot during the same incident or by the same shooter. The information available in a syndromic surveillance feed does not allow for direct identification of the shooter or shooters. Given that limitation, a complete correspondence between clusters identified in syndromic surveillance data and mass shootings was not expected. The strong correlation between clusters and media coverage indicates that the news is a reasonable source for shooting data. The smaller overlap with the mass shooting database is likely due to the more stringent criteria required for an incident to qualify as a mass shooting. It is still notable that the majority of gunshot clusters were not associated with any particular mass shooting incident. This serves as a reminder that mass shootings represent only a small portion of the total gun violence in the United States. Healthcare data represents a significant additional data source for understanding the complete impact of gun violence on public health and safety. Weekly time series of gunshot-related emergency department visits

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To explore the difference between the reported date of admission and discharge date using discharge messages (A03), from hospital emergency departments participating in the Louisiana Early Event Detection System (LEEDS). Introduction The Infectious Disease Epidemiology Section (IDEpi) within the Office of Public Health (LaOPH) conducts syndromic surveillance of emergency departments by means of the Louisiana Early Event Detection System (LEEDS). LEEDS accepts ADT (admit-discharge-transfer) messages from participating hospitals, predominately A04 (registration) and A03 (discharge), to obtain symptom or syndrome information on patients reporting to hospital emergency departments. Capturing the data using discharge messages (A03) only could result in a delay in receipt of data by LaOPH, considering the variability in the length of stay of a patient in the ED. Methods Emergency department data from participating hospitals is imported daily to LEEDS and processed for syndrome classification. IDEpi syndromic surveillance messages received for the period of CDC week 1632 and 1636 (8/8/16-9/8/16) using MS Access and Excel to calculate the difference (in days) between the reported admit date and discharge date in A03 messages. Results 88.1% of the A03 messages submitted in the 4 week analysis period exhibited no delay (delay = 0 days) between the admit date and the reported discharge date, compared to only 10.7% showing a delay of one day (delay = 1 day) and 1.06% showing a delay of 2 days or more (delay ≥ 2 days). Less than 0.2% of the messages had missing information regarding discharge date (Table 1). Conclusions Syndromic surveillance systems operate under a constant need for improvement and enhancement. The quality of the data, independent of the quality of the system, should always strive to be of the highest pedigree in order to inform disease-specific programs and detect public health aberrations. In order to identify these potential concerns, it is imperative that the data be submitted to public health agencies in a timely manner. Based on this analysis, the lapse in time between admit and discharge results in little to no patient syndromic data delay for those hospital ED’s that exclusively send A03 messages. This statement is supported by the finding that close to 99% of messages demonstrated a delay between admit date and discharge date of one day or less. Table 1. Delay between reported Admit and Discharge date in A03 messages submitted to LEEDS


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Abstract

ObjectiveTo develop a detailed data validation strategy for facilities sending emergency department data to the Massachusetts Syndromic Surveillance program and to evaluate the validation strategy by comparing data quality metrics before and after implementation of the strategy.

IntroductionAs a participant in the National Syndromic Surveillance Program (NSSP), the Massachusetts Department of Public Health (MDPH) has worked closely with our statewide Health Information Exchange (HIE) and National Syndromic Surveillance Program (NSSP) technical staff to collect and transmit emergency department (ED) data from eligible hospitals (EHs) to the NSSP. Our goal is to ensure complete and accurate data using a multi-step process beginning with pre-production data and continuing after EHs are sending live data to production.

MethodsWe used an iterative process to establish a framework for monitoring data quality during onboarding of EHs into our syndromic surveillance system and kept notes of the process. To evaluate the framework, we compared data received during the month of January 2016 to the most recent full month of data (June 2016) to describe the following primary data quality metrics and their change over time: total and daily average of message and visit volume; percent of visits with a chief complaint or diagnosis code received in the NSSP dataset; and percentage of visits with a chief complaint/diagnosis code received within a specified time of admission to the ED.

ResultsThe strategies for validation we found effective included examination of pre-production test HL7 messages and the execution of R scripts for validation of live data in the staging and production environments. Both the staging and production validations are performed at the individual message level as well as the aggregated visit level, and included measures of completeness for required fields (Chief Complaint, Diagnosis Codes, Discharge Dispositions), timeliness, examples of text fields (Chief Complaint and Triage Notes), and demographic information. We required EHs to pass validation in the staging environment before granting access to send data to the production environment.

From January to June 2016, the number of EHs sending data to the production environment increased from 44 to 48, and the number of messages and visits captured in the production environment increased substantially (see Table 1). The percentage of visits with a chief complaint remained consistently high (>99%); however, the percentage of visits with a chief complaint within three hours of admission decreased during the study period. Both the overall percentage of visits with a diagnosis code and the percentage of visits with a diagnosis code within 24 hours of admission increased.

ConclusionsFrom January to June 2016, Massachusetts syndromic surveillance data improved in the percentage of visits with diagnosis codes and the time from admission to first diagnosis code. This was achieved while the volume of data coming into the system increased. The timeliness of chief complaints decreased slightly during the study period, which may be due to the inclusion of several new facilities that are unable to send real-time data. Even with the improvements in the timeliness of the diagnosis code field, and the subsequent decrease in the timeliness of the chief complaint field, chief complaints remained a more timely option for syndromic surveillance. Pre-production and ongoing data quality assurance activities are crucial to ensure meaningful data are acquired for secondary analyses. We found that reviewing test HL7 messages and staging data, daily monitoring of production data for key factors such as message volume and percent of visits with a diagnosis code, and monthly full validation in the production environment were and will continue to be essential to ensure ongoing data integrity.

Table 1: ED Data in the Production Environment

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Abstract

Objective

We reviewed CCDs (a type of consolidated clinical data architecture (C-CDA) document) shared by our clinical partner, Planned Parenthood of the Great Northwest and Hawaiian Islands (PPGNHI) since October, 2015. Analyses focuses on:

- Completeness
- Degree to which the CCD matches program area information needs
- Differences in EHR generation methods
- Presence and location of triggers (based on the Reportable Conditions Trigger Codes) that would initiate CCD generation.

Introduction

Under the CDC STD Surveillance Network (SSuN) Part B grant, WA DOH is testing electronic case reporting (eCR) of sexually transmitted infections (STI) from a clinical partner.

Methods

Two methods of CCD generation, based on existing EHR capabilities, were used to create CCDs that were delivered to WADOH using secure file transport protocol (SFTP). PPGNHI uses the NextGen EHR system. The first batch received was extracted using the Medical Summary Utility. Random selection of cases (25) from lab positive Chlamydia (CT), Gonorrhea (GC) or Syphilis encounters with a follow-up plan in the EHR (1/1/2015-3/31/2015). Each CCD contained manually selected encounters (related to STI case). Cases are now extracted directly from a patient chart (File --> Generate CCD). Two types of CCDs can be created: single encounter CCDs and longitudinal encounter CCDs. The CCDs were analyzed for completeness, crossover with the existing paper case report, and with relevant CDA and C-CDA Implementation Guide (IG) standards.

Results

This analysis includes four reportable events across 6 CCDs. One event is represented by both a longitudinal CCD and 2 single encounter CCDs. The CCDs contained most of the basic demographic information requested in the paper case report with the exception of “middle initial”. Information on the important paper case report components “gender of sex partner” and “partner management plan” are not found in the CCD. The CCD Results section contained lab tests and results that include site of infection and could confirm diagnosis. The ordered test (panel) is not coded, though the individual tests performed are LOINC coded. The CCD Medications section meets STI program needs for information about treatment in a case report. Information is represented using RxNorm codes as specified by the C-CDA IG. The CCD Problems section was not present in documents generated using the MSU but was present in documents created using File --> Generate CCD from the patient chart. The Problems section and coded entries (ICD-9-CM and ICD-10) are required for CCDs. The Problems do not include effective dates, which are not required by the IG. Pregnancy status, and information about HIV testing (including previous positive), are present in the CCD Problems section only if the encounter during which testing occurred is included in the CCD submitted. Using the CCD in place of the paper case report requires understanding of the clinical workflow and use of EHR. Two instances that require specific attention are the “exposure” status of the case (known/possibly exposed vs. not shared/not known), and the “presentation” of the diagnosis (symptomatic vs asymptomatic). For example, the ICD-10 code Z11.3 (encounter for screening for infections with a predominantly sexual mode of transmission), cannot be interpreted as a true “screening”, as this diagnosis is recorded for all visits that include STI testing. Similarly, a code for exposure to STIs is sometimes used, but not consistently enough to allow reliable identification of cases in which the patient was tested due to exposure or possible exposure. Work with our clinical partner to understand what inferences can and should be made is an important part of evaluating the CCD as a replacement to the paper case report.

Conclusions

The CCDs submitted to DOH show that most information requested in an STI case report can be found in a CCD with some exceptions, notably “gender of sex partners” and “partner management plan”. Some information is only inconsistently present, for example, exposure status and presentation. Understanding how the CCD could replace the paper case report requires working with the reporter to ensure that the information is interpreted in the same way that it is interpreted in the clinical workflow and entered in the EHR.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: LANL has built a software program that automatically collects global notifiable disease data—particularly data stored in files—and makes it available and shareable within the Biosurveillance Ecosystem (BSVE) as a new data source. This will improve the prediction and early warning of disease events and other applications.

Introduction: Most countries do not report national notifiable disease data in a machine-readable format. Data are often in the form of a file that contains text, tables, and graphs summarizing weekly or monthly disease counts. This presents a problem when information is needed for more data-intensive approaches to epidemiology, biosurveillance, and public health as exemplified by the Biosurveillance Ecosystem (BSVE). While most nations do likely store their data in a machine-readable format, the governments are often hesitant to share data openly for a variety of reasons that include technical, political, economic, and motivational issues [1]. For example, an attempt by LANL to obtain weekly version of openly available monthly data, reported by the Australian government, resulted in an onerous bureaucratic reply. The obstacles to obtaining data included: paperwork to request data from each of the Australian states and territories, a long delay to obtain data (up to 3 months) and extensive limitations on the data’s use that prohibit collaboration and sharing. This type of experience when attempting to contact public health departments or ministries of health for data is not uncommon. A survey conducted by LANL of national notifiable disease reporting systems identifying how the data is reported in two important dimensions: date standards and case definitions. The development of software to regularly ingest notifiable disease data from each country/website as well as what varies across the reporting mechanisms. We then designed and wrote code to automate the downloading of report pdf files, for each country. We stored report pdfs along with appropriate metadata for extracting and parsing. For extracting: we developed software that can extract notifiable disease data presented in tabular form from a pdf file. We combined the methodology of figure placement detection with the in-house developed table extraction and annotation heuristics. For parsing: we determined what to extract from each pdf dataset from the survey conducted. We then parsed the extracted data into uniform data structures correctly accommodating the dimensions surveyed and the various human languages. This task involved ingesting notifiable disease data in many disparate formats extracted from pdf files and coalescing the data into a standardized format. For persisting: we then store the data in the Epi Archive PostgreSQL database and make it available through the BSVE.

Results: The EpiArchive tool currently contains subnational notifiable disease data from 10 nations. When a user accesses the Epi Archive site, they are prompted with four fields: country, region, disease, and date duration. These fields allow the user to specify the location (down to the state level), the disease of interest, and the duration of interest. Upon form submission, a time series is generated from the users’ specifications. The generated time series can then be downloaded into a csv file if a user is interested in performing personal analysis. Additionally, the data from Epi Archive can be retrieved through an API. Conclusions: LANL as part of a currently funded DTRA effort so that it will automatically and continuously collect global notifiable disease data—particularly data stored in pdf files—and make it available and shareable within the Biosurveillance Ecosystem (BSVE) as a new data source. This will provide data to analytics and users that will improve the prediction and early warning of disease events and other applications.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To describe the evaluation process to assess data quality during development of an electronic case report application, and to describe the evaluation results. Introduction: Electronic case reporting (eCR) is defined as the fully or semi-automated generation and electronic transmission of reportable disease cases from an electronic health record (EHR) system to public health authorities, replacing the historically paper-based process. ECR has been reported to increase the number, accuracy, completeness, and timeliness of surveillance case reports. Chicago Department of Public Health (CDPH) collaborated with Alliance of Chicago (AOC) to develop an application to generate electronic provider reports (ePR) for chlamydia (CT) and gonorrhea (GC) cases from the EHR system managed by AOC and send ePR records to the Illinois National Electronic Disease Surveillance System (I-NEDSS). This application was tested in the EHR database of Health Center A in AOC’s network. It is essential to ensure ePR data are accurate, so that public health receives correct information to take actions if needed. Therefore, evaluation is needed to assess ePR records data quality. Methods: CDPH developed a five-step evaluation plan to validate ePR record data quality. Step 1 was to validate the ePR file format to ensure all I-NEDSS required fields are present, required value sets were used, and file format did not vary across files generated. Step 2 was to validate the algorithm accuracy. Chart review was conducted to ensure the ePR records do not include non-reportable cases. Step 3 was to review ePR records loaded in I-NEDSS to make sure all values in ePR raw files appeared correctly on the I-NEDSS front end. After the application passed steps 1 to 3, it moved to step 4, parallel validation. The first phase of parallel validation was to review historic cases. Test ePR records for CT and GC cases diagnosed by HealthCenter A in 2015 (n=510) were compared to the same 510 cases’ closed surveillance case reports in I-NEDSS. The completeness of treatment, race, and ethnicity was examined. The application then moved into testing daily data feed. Daily ePR records were compared with EHR charts and paper provider reports received by CDPH to assess completeness and timeliness. Step 5 was to re-evaluate algorithms. EPR records were validated against the electronic laboratory reports (ELR) records, which were used as gold standards of all reportable CT and GC cases, to find missing cases. Results: The first three steps of evaluation occurred from January to April 2016. Test ePR files containing historic cases from Health Center A were vetted weekly. A total of 14 test ePR files were reviewed. This process identified required fields not present (patient address, treatment date, treatment, and race), race value sets not returned correctly, and additional logic statements needed to return correct pregnancy status at the time of diagnosis. These issues were discussed with the project team, and the application was modified accordingly. The historic case review found ePR data were more complete than closed surveillance reports. Compared to closed surveillance reports in I-NEDSS, 18% (94/510) of the cases had incomplete treatment information in the ePR records compared to 78% (400/510), 0.2% (1/510) of the cases did not have race information in the ePR records compared to 47% (240/510), and 0.7% (4/510) of the cases had no ethnicity information in the ePR records compared to 50% (253/510). These preliminary evaluation results suggest that eCR improves surveillance case reports data quality. The daily data feed data quality evaluation is still ongoing, and ePR data quality will be monitored continuously. Conclusions: Evaluation plays an integral role in developing and implementing the eCR process in Chicago. The stepwise evaluation process ensures PR data quality meeting public health requirements, so that public health will be able to act on more complete information to improve population health.

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Abstract

ObjectiveTo identify heroin- and opioid-related emergency department visits using pre-diagnostic data. To demonstrate the value of clinical notesto public health surveillance and situational awareness.

Introduction

Overdoses of heroin and prescription opioids are a growing cause of mortality in the United States. Deaths from opioids have contributed to a rise in the overall mortality rate of middle-aged white males during an era when other demographics are experiencing life expectancy gains. A successful public health intervention to reverse this mortality trend requires a detailed understanding of which populations are most affected and where those populations live. While mortality is the most relevant metric for this emerging challenge, increased burden on laboratory facilities can create significant delays in obtaining confirmation of which patients died from opioid overdoses. Emergency department visits for opioid overdoses can provide amore timely proxy measure of overall opioid use. Unfortunately, chief complaints do not always contain an indication of opioid involvement. Overdose patients are not always conscious at registration which limits the amount of information they can provide. Menu-driven registration systems can lump all overdoses together regardless of substance. A more complete record of the emergency department interaction, such as that provided by triage notes, could provide the information necessary to differentiate opioid-related visits from other overdoses.

Methods

Emergency department registration data was collected from hospitals via the EpiCenter syndromic surveillance system. This data included chief complaints, triage notes, discharge disposition, and preliminary diagnosis codes. Data elements were linked across a given visit using patient identifiers and visit numbers as appropriate. Heroin- and opioid-related indicators were identified in chief complaints and triage notes using regular expressions. These were separated into three categories: visits with an indication of overdose, visits for withdrawal symptoms, and visits where opioids were mentioned in some other context such as history of use. These categories were designed to be mutually exclusive. Regular expression classification results were compared to classifications based on opioid-related diagnosis codes.

Results

A total of 2,934,610 ED registrations with triage notes and diagnosis codes were collected from 82 hospitals between January 1, 2015 and August 21, 2016. Of these encounters, 24,012 referenced opioid use in some way; 16,718 mentioned heroin specifically; 3,663 mentioned fentanyl specifically; and 5,350 mentioned opioids generically.

Table 1 shows the distribution of heroin-related ED visits across categories and source of the indicator. Column totals are not the sum of individual row amounts; they have been adjusted so that a given registration is only counted once. Table 2 shows the overlap of heroin-related ED visits betweensources of indicators. Triage notes showed the least overlap with the other two sources, while chief complaints showed the most. Conclusions

While it is possible to find indicators of opioid use or overdose in chief complaint data, that field alone does not provide total information about which ED visits are related to opioids. Triage notes in particular indicate opioid involvement in a large number of visits not identified by other data sources. While many of these are simply mentions of opioids, possibly indicating past history of use or even in some cases just that questions about opioid use were asked, a substantial number of visits with overdose indicators were also detected solely from triage note data. These results suggest that triage notes can be a valuable additional data source for more complex health concerns such as opioid drug use.

Table 1: Heroin-Related ED Visits By Indicator

<table>
<thead>
<tr>
<th>Source and Category</th>
<th>ED Visits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overdose</td>
<td>24,012</td>
</tr>
<tr>
<td>Withdraw</td>
<td>16,718</td>
</tr>
<tr>
<td>Other</td>
<td>5,350</td>
</tr>
<tr>
<td>Total</td>
<td>46,080</td>
</tr>
</tbody>
</table>

Table 2: Overlap of Heroin-Related ED Visits between Indicators


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: Evaluate the usage of triage note data from EpiCenter, a syndromic surveillance system utilized by New Jersey Department of Health (NJDOH), to enhance Healthcare-Associated Infections (HAIs) surveillance for infections following a surgical procedure. Introduction: In New Jersey, Health Monitoring Systems Inc.'s (HMS) EpiCenter collects chief complaint data for syndromic surveillance from 79 of 80 emergency departments (ED). Using keyword algorithms, these visits are classified into syndrome categories for monitoring unusual health events. HAIs are infections that patients acquire while they are receiving treatment for a health condition in a health care setting. Following the 2014 Ebola outbreak in West Africa, the New Jersey Department of Health (NJDOH) Communicable Disease Service (CDS) started recruiting EDs to include triage note data in addition to chief complaint data to enhance surveillance capability for Ebola and other HAIs. Research by the University of North Carolina suggests triage note data improve the ability to detect illness of interest by fivefold. Currently, there are three NJ EDs with triage note data in EpiCenter along with ICD 10 codes which can be used for comparison. This pilot study will assess whether infections following a surgical procedure can be captured in triage note data along with ICD codes. Also, this evaluation will determine if triage note data can be used to create HAI custom classifications for syndromic surveillance. These classifications can potentially be used by surveillance and/or preparedness personnel and local health departments, as well as hospitals, to better prepare for detecting and preventing HAIs that are a significant cause of morbidity and mortality in the U.S. Methods: Three NJ facilities with triage note data information sending to EpiCenter were included in this study. ED visits occurred from 10/23/2015 to 10/29/2015 and from 2/2/2016 to 2/10/2016 in these facilities with available ICD 10 codes information in EpiCenter were evaluated. This analysis focused on sepsis and post-surgery infections related ICD 10 codes: A400, A401, A402, A403, A408, A409, A410, A411, A412, A414, A4150, A4151, A4152, A4158, A418, A419, R571, R578, R579, T811, T81.43. The keywords tested in triage notes are abdominal pain, redness, fev, fver, pyrexia, temp, elev temp, elevated temp, temp elev, hi temp, high temp, temp hi, temp10, feeling hot, feel hot, fevers, fe, fver, cloudy fluid, cfluid, drainage, abscess, wound, tenderness, swelling, erythema, red, pain, post surgery, fever. The sensitivity, specificity and positive predictive value (PPV) of selected keywords applied in the triage notes were evaluated by comparing to patient's ICD 10 codes. Results: There were 2757 ED visits with triage notes and ICD 10 codes from 10/23/2015 to 10/29/2015 and from 2/2/2016 to 2/10/2016. During these time frames, one ED visit matched with both selected keywords and ICD codes, five matched with ICD 10 codes only, 59 matched with keywords only, and 2692 did not match with either keywords or ICD 10 codes. In Table 1, it indicates that selected keywords have a high specificity (97.9%) but with a relatively low sensitivity (16.7%) and PPV (1.7%). Conclusions: Selected keywords and ICD 10 codes from facilities sending triage notes were used to evaluate the surveillance system on identifying infections following a surgical procedure through analysis of ED triage note field. We also reviewed all NJ ED data during the same study period for other facilities not sending triage notes. It indicated that several key ICD codes, e.g. ICD code T81.4, infections following a surgical procedure, have been included in many facilities. This analysis will be repeated as more EDs participate in EpiCenter with triage notes and other data fields to refine the keywords and improve the sensitivity and PPV. Table 1: Sensitivity, specificity and PPV calculations of selected keywords applied in triage notes based on the ICD 10 codes related to infections following a surgical procedure.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To explore the quality of data submitted once a facility is moved into an ongoing submission status and address the importance of continuing data quality assessments. Introduction Once a facility meets data quality standards and is approved for production, an assumption is made that the quality of data received remains at the same level. When looking at production data quality reports from various states generated using a SAS data quality program, a need for production data quality assessment was identified. By implementing a periodic data quality update on all production facilities, data quality has improved for production data as a whole and/or individual facility data. Through this activity several root causes of data quality degradation have been identified, allowing processes to be implemented in order to mitigate impact on data quality. Methods Many jurisdictions work with facilities during the onboarding process to improve data quality. Once a certain level of data quality is achieved, the facility is moved into production. At this point the jurisdiction generally assumes that the quality of the data being submitted will remain fairly constant. To check this assumption in Kansas, a SAS Production Report program was developed specifically to look at production data quality. A legacy data set is downloaded from BioSense production servers by Earliest Date in order to capture all records for visits which occurred within a specified time frame. This data set is then run through a SAS data quality program which checks specific fields for completeness and validity and prints a report on counts and percentages of null and invalid values, outdated records, and timeliness of record submission, as well as examples of records from visits containing these errors. A report is created for the state as a whole, each facility, EHR vendor, and HIE sending data to the production servers, with examples provided only by facility. The facility, vendor, and HIE reports include state percentages of errors for comparison. The Production Report was initially run on Kansas data for the first quarter of 2016 followed by consultations with facilities on the findings. Monthly checks were made of data quality before and after facilities implemented changes. An examination of Kansas’ results showed a marked decrease in data quality for many facilities. Every facility had at least one area in need of improvement. The data quality reports and examples were sent to every facility sending production data during the first quarter attached to an email requesting a 30-60 minute call with each to go over the report. This call was deemed crucial to the process since it had been over a year, and in a few cases over two years, since some of the facilities had looked at data quality and would need a review of the findings and all requirements, new and old. Ultimately, over half of all production facilities scheduled a follow-up call. While some facilities expressed some degree of trepidation, most facilities were open to revisiting data quality and to making requested improvements. Reasons for data quality degradation included updates to EHR products, change of EHR product, workflow issues, engine updates, new requirements, and personnel turnover. A request was made of other jurisdictions (including Arizona, Nevada, and Illinois) to look at their production data using the same program and compare quality. Data was pulled for at least one week of July 2016 by Earliest Date. Results Monthly reports have been run on Kansas Production data both before and after the consultation meetings which indicate a marked improvement in both completeness of required fields and validity of values in those fields. Data for these monthly reports was again selected by Earliest Date. Conclusions In order to ensure production data continues to be of value for syndromic surveillance purposes, periodic data quality assessment should continue after a facility reaches ongoing submission status. Alterations in process include a review of production data at least twice per year with a follow up data review one month later to confirm adjustments have been correctly implemented.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To enhance Oregon ESSENCE’s surveillance capabilities by incorporating data from the Oregon Poison Center using limited resources.

Introduction
Oregon Public Health Division (OPHD), in collaboration with the Johns Hopkins University Applied Physics Laboratory, implemented Oregon ESSENCE in 2012. Oregon ESSENCE is an automated, electronic surveillance system that captures emergency department data. To strengthen the capabilities of Oregon ESSENCE, OPHD sought other sources of health-outcome information, including Oregon Poison Center (OPC). In the past, Oregon’s surveillance staff manually monitored OPC data on the National Poison Data Service (NPDS) website. Although functional, it was not integrated into Oregon’s syndromic surveillance system and required epidemiologiststo assess alerts on individual calls. To achieve data integration, OPHD pursued an automated solution to deliver OPC data into Oregon ESSENCE. OPHD’s growing interoperability infrastructure fostered development of a low-cost, reliable solution to automate the integration of these data sources.

Methods
OPC facilitated OPHD’s access to the free-of-charge NPDS web service with an approval request and a data use agreement. OPHD uses the Rhapsody Integration Engine 6.2.1 (Orion Health, Auckland, NZ) as its primary data transfer and translation mechanism. OPHD leveraged its existing Rhapsody installation to automatically request data from the NPDS web service daily. Each request contains custom search parameters that query calls from the previous day (24 hours). The service returns an XML file containing poison center call data with multiple nodes of related data. Rhapsody uses a JavaScript ‘filter’ to parse each call and its related data. The Oregon ESSENCE backend SQL database contains a parent table for the call and child tables for the related data (Clinical Effects, Routes, Scenarios, Therapies, and Generic Codes). Rhapsody inserts data into each of these backend SQL tables.

Results
Oregon ESSENCE displays OPC data through its web interface for interpretation by OPHD’s syndromic surveillance epidemiologists. Integrating NPDS data into Oregon ESSENCE allows OPHD staff to timely monitor data in an automated, routine manner. Syndromic surveillance staff first assess alerts generated by Oregon ESSENCE. Alerts that require follow-up trigger a call between OPHD epidemiologists and OPC. Oregon is the first state to use the NPDS web service to upload poison center data into Oregon ESSENCE. Conclusions
Oregon’s successful integration of the NPDS web service data into Oregon ESSENCE is the first known of its kind. It leverages OPHD’s growing infrastructure of interoperability software applications and staff expertise to create a cost-effective and sustainable solution that can be easily adapted by other public health agencies.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To visualize the incidence of notifiable infectious diseases spatially and interactively, we aimed to provide a friendly interface to access local epidemic information based on open data for health professionals and the public. Introduction Transparency of information on infectious disease epidemics is crucial for not only public health workers but also the residents in the communities. Traditionally, disease control departments created official websites for displaying disease maps or epi-curves with the confirmed case counts. The websites were usually very formal and static, without interaction, animation, or even the aid of spatial statistics. Therefore, we tried to take advantage of open data and use a lightweight programming language, JavaScript, to create an interactive website, named “Taiwan Infectious Disease Map (http://ide.geohealth.tw/)”. With the website, we expect to provide real-time incidence information and related epidemiological features using interactive maps and charts. Methods This study used infectious-disease-related open data from Taiwan’s open data platform (http://data.gov.tw) maintained by the Taiwan CDC. It covers 70 types of infectious diseases starting from 2004, and the latest status is updated every day. We then automatically bridge this data into our database and calculate the age-adjusted incidence rate by annual census data and 2000 WHO standard population. The spatial resolution is mostly at the township level, except that the resolution for sexually-transmitted infectious diseases is at the city level. The temporal resolution is month and year, except for dengue fever, which is by week. We used R software to automatically compute incidence everyday, and also used its package named “spdep” to compute the spatial clusters of the selected infectious diseases online. In addition, we used JavaScript language, PHP, OpenLayers 3 and Highcharts to implement interactive maps and charts. All the data and graphical figures from the charts viewed in this website can be downloaded freely. The temporal animation slider can be played and paused at any time point. The health education button can directly link to an introduction to the selected infectious disease maintained by the Taiwan CDC. Results The website of the Taiwan Infectious Disease Map is displayed in Figure 1. The users can select the temporal precision, types of infectious diseases, spatial precision and the gender at the beginning. In this case, the left map is the spatial distribution of the cumulative incidence of tuberculosis (TB) in 2016. The darker red color represents higher incidence. The right top panel is the ranking of TB incidence among 368 townships. The right middle panel is the ranking of TB incidence among 22 cities or counties. The right bottom panel is the annual TB incidence from 2004 to the current date. The highest TB incidence was 67.47 per 100,000 in 2004, and this declined sharply to 15.92 per 100,000 in 2015. Conclusions With this user-friendly web application, the public and local public health workers can easily understand the current risk for their townships. The application can provide relevant health education for the public to understand diseases and how to protect themselves. Thespatial clusters, gender distribution, age distribution, epi-curve and top ten infectious diseases are all practical and important information provided from this website to assist in preventing and mitigating next epidemic.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To streamline carbapenem-resistant enterobacteriaceae (CRE) surveillance by integrating electronic laboratory reporting (ELR) data and electronic case reports (eCR) automatically into Illinois' extensively drug-resistant organism (XDRO) registry.

Introduction CRE are drug-resistant bacteria that have a mortality rate of up to 50% in those infected. Several clusters of CRE have been detected in Illinois, often in long-term acute care hospitals. In response, Illinois created the XDRO registry, a mandatory reporting system designed to aid inter-facility communication concerning CRE. Despite being a high priority for control in the US, the case definition for CRE has been the subject of debate. There are over 70 Enterobacteriaceae which can have different mechanisms of carbapenem resistance. Criteria for carbapenem resistance include susceptibility results, and phenotypic or genotypic detection. The case definition for the XDRO registry is intentionally more exclusive (specific) than that used by CSTE (Table 1). CSTE utilizes a definition designed to maximize sensitivity. Illinois' XDRO registry's definition is more specific, meant to reduce unnecessary adoption of contact precautions and the negative consequences some patients may experience. Currently, case reporting to the XDRO registry is a manual data entry process, which has important advantages. However, transitioning to automatic ELR integration will streamline the reporting process and minimize data entry effort. Unfortunately, the clinical information needed to investigate XDROs is often not captured by ELR. The eCR is a new message type being piloted in Illinois that contains many clinical data elements. We examined the feasibility of combining ELR and eCR into reports for the XDRO registry. In the construction of these reports, we examined the impact of using CRE definitions from CSTE and the XDRO registry.

Methods We obtained sample HL7 CRE messages from Illinois' ELR database. Using these messages and the HL7 Implementation Guide for Electronic Laboratory Reporting, we mapped ELR fields to those in the XDRO registry. Specific codes corresponding to the registry fields were found through a systematic keyword search of LOINC, SNOMED, and sample messages. When there was no match for an XDRO field in ELR, we referred to the HL7 CDA Implementation Guide for the Electronic Initial Case Report and sample eCR messages. A collection of fields and codes was created to correspond to both the CSTE and Illinois CRE case definition. Results The XDRO registry has 37 unique fields. Twenty-six can be populated from ELR, four can be found in the eCR, and seven are generated within the system. In sample ELR and eCR messages all of the necessary fields were populated with appropriate text and codes. The mapping process was straightforward for demographic and facility information, but more complicated for culture and organism information. Some XDRO tests do not have corresponding LOINC or SNOMED codes, so we will develop a logic statement to fill these based on free-text. Addition of the eCR adds important information to the registry report, notably encounter type and encounter/admission date. We were able to create separate mapping schemas for the CSTE and XDRO registry definitions for CRE. Using each of these definitions, we will quantify how many ELR messages would be committed to the XDRO registry. Conclusions By combining the data captured in ELR and eCR, it is possible to populate the fields of the Illinois XDRO registry. When this merge is completed, it should result in more complete and better quality data on CRE in Illinois. As intended, the definition of CRE used by the registry is less inclusive than that used by CSTE. Future work will show the number of CRE lab results captured by each definition. Table 1: CRE Definition

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**Table 1: CRE Definition**

<table>
<thead>
<tr>
<th>Criteria</th>
<th>CSTE Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall</td>
<td>Maximize sensitivity</td>
</tr>
<tr>
<td>Illinois XDRO</td>
<td>More specific, reduce unnecessary adoption of contact precautions</td>
</tr>
</tbody>
</table>

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

To extend an open source platform for measuring the quality of electronic health data by adding functions useful for syndromic surveillance.

Introduction

Nearly all of the myriad activities (or use cases) in clinical and public health (e.g., patient care, surveillance, community health assessment, policy) involve generating, collecting, storing, analyzing, or sharing data about individual patients or populations. Effective clinical and public health practice in the twenty-first century requires access to data from an increasing array of information systems, including but not limited to electronic health records. However, the quality of data in electronic health record systems can be poor or “unfit for use.” Therefore measuring and monitoring data quality is an essential activity for clinical and public health professionals as well as researchers.

Methods

Using the Health Data Stewardship Framework, we will extend Automated Characterization of Health Information at Large-scale Longitudinal Evidence Systems (ACHILLES), a software package published open-source by the Observational Health Data Sciences and Informatics collaborative (OHDSI; www.ohdsi.org) to measure the quality of data electronically reported from disparate information systems. Our extensions will focus on analysis of data reported electronically to public health agencies for disease surveillance. Next we will apply the ACHILLES extensions to explore the quality of data captured from multiple real-world health systems, hospitals, laboratories, and clinics. We will further demonstrate the extended software to public health professionals, gathering feedback on the ability of the methods and software tool to support public health agencies’ efforts to routinely monitor the quality of data received for surveillance of disease prevalence and burden.

Results

To date we have mapped key surveillance data fields into the OHDSI common data model, and we have transformed 111 million syndromic surveillance message segments pertaining to 16.4 million emergency department encounters representing 6 million patients for importation into ACHILLES. Using these data, we are exploring the existing 167 metrics across 16 categories available within ACHILLES, including a person (e.g., number of unique persons); and observation period (e.g., distribution of age at first observation period). Syndromic surveillance (SS), however, is driven largely by monitoring patient stated chief complaints (non-standard freetext clinical data) in addition to coded diagnoses. Consequently, ACHILLES must be extended to maximally support use in analyzing SS datasets.

Conclusions

This work remains a work-in-progress. Over the coming year, we will not only explore existing ACHILLES constructs using real-world public health data but also introduce new functionality to explore 1) patient demographics; 2) facility and location (e.g., emergency department where care was delivered); and 3) clinical observations (e.g., chief complaint). The design and methods for examining these aspects of surveillance data will be included on the poster, and they will be made freely available for distribution with a future instance of the ACHILLES software. We ultimately envision these tools being available for use on platforms such as the CDC’s Biosense – open to all local and state health agencies as a one-stop portal for surveilled data analysis – or research environments where they can be used to examine and improve the quality of data output from informatics systems.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveThe National Biosurveillance Integration Center (NBIC) and the Defense Threat Reduction Agency’s Chemical and Biological Technologies Department (DTRA J9 CB) have partnered to co-develop the Biosurveillance Ecosystem (BSVE), an emerging capability that aims to provide a virtual, customizable analyst workbench that integrates health and non-health data. This partnership promotes engagement between diverse health surveillance entities to increase awareness and improve decision-making capabilities. Integration of this information enables early warning and shared situational awareness to inform critical decision making, and direct response and recovery efforts. DTRA J9 CB leads DoD to anticipate, defend, and safeguard against chemical and biological threats for the warfighter and the nation. These agencies have partnered to meet the evolving needs of the biosurveillance community and address gaps in technology and data sharing capabilities. High-profile events such as the 2009 H1N1 pandemic, the West African Ebola outbreak, and the recent emergence of Zika virus disease have underscored the need for integration of disparate biosurveillance systems to provide a more functional infrastructure. This allows analysts and others in the community to collect, analyze, and share relevant data across organizations securely and efficiently. Leveraging existing biosurveillance efforts provides the federal public health community and its partners, with comprehensive interagency platform that enables engagement and data sharing.

MethodsNBIC and DTRA are leveraging existing biosurveillance projects to share data feeds, work processes, resources, and lessons learned. A multi-stakeholder Agile process was implemented to represent the interests of NBIC, DTRA, and their respective partners. System requirements generated by both agencies were combined to form a backlog of prioritized needs. Functional requirements from NBIC support the development of the prototype by refining system capabilities and providing an operational perspective. DTRA’s technical expertise and research and development (R&D) portfolio ensures robust analytic applications are embedded within a secure, scalable system architecture. Integration of data from the NBIC Biofeed system serves as a gold-standard to improve analytic development in machine learning and natural language processing. Additionally, working groups are formed using NBIC and DTRA extended partnerships with academia and private industry to expand R&D possibilities. These expansions include leveraging existing ontologies and integrating social media algorithms for improved topic analysis output.

ResultsThe combined efforts of these two agencies to develop the BSVE and improve overall biosurveillance processes across the federal government has enhanced understanding of the needs of the community in a variety of mission spaces. To date, co-creation of products, joint analysis, and sharing of data feeds has become a major priority for both partners to advance biosurveillance outcomes. Within the larger efforts of system development, possible coordination with other agencies such as the Department of Veterans Affairs (VA) and the US Geological Survey (USGS) could expand reach of the system to ensure fulfillment of health surveillance requirements as a whole.

ConclusionsThe NBIC and DTRA partnership has demonstrated value in improving biosurveillance capabilities for each agency and their partners. BSVE will provide NBIC analysts with a collaborative tool that can leverage use of applications that visualize near real-time global epidemic and outbreak data from a range of unique and trusted sources. The continued collaboration means ongoing access to new data streams and analytic processes for all analysts, as well as advanced machine learning algorithms that increase capabilities for joint analysis, rapid product creation, and continuous interagency communication.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
The NEDSS Base System (NBS), an integrated disease surveillance system, implemented extensible functionality to support electronic data exchange for multiple use cases and public health workflow management of incoming messages and documents.

Introduction
The NBS is an integrated disease surveillance system deployed in 22 public health jurisdictions to support receipt, investigation, analysis and reporting, and data exchange for state reportable conditions. The NBS is governed by the Centers for Disease Control and Prevention (CDC) and state, local, and territorial users that make up the NBS Community. In the early 2000’s, electronic laboratory results reporting (ELR) was implemented in an effort to improve timeliness and completeness of disease reporting. As standards-based electronic health records (EHRs) are adopted and more surveillance data become available, modern surveillance systems must consume information in an automated way and provide more functionality to automate key surveillance processes.

Methods
Many use cases exist for exchanging data with an integrated public health surveillance system. These can include exchange of electronic case and laboratory reports from healthcare, data sharing between public health entities, migration from legacy systems, and ongoing exchange with other public health systems (e.g. immunization registries). The NBS implemented an interface specification called the Public Health Document Container (PHDC). PHDC is based on HL7 version 3 Clinical Document Architecture (CDA). It allows import of patient (cases and contacts), investigation, treatment, interview, and laboratory information into NBS. CDA was chosen as the building block to facilitate data exchange with the healthcare community. Through use of data integration tools, incoming data can be mapped from any format to PHDC and imported into the system. Existing services, such as patient, provider, and organization deduplication are applied. To assist with management of incoming electronic documents, NBS implemented a functionality called Workflow Decision Support (WDS). WDS uses configurable algorithms to automatically process incoming documents (including case reports, laboratory reports, etc.) into the public health workflow. Users can choose to mark an incoming document as reviewed or automatically create an investigation and case notification message to CDC (for nationally notifiable conditions).

Results
Through PHDC, NBS is able to receive data from healthcare using national standards, such as the HL7 Electronic Initial Case Report (eICR). Three NBS partners are currently collaborating to pilot eICR functionality. PHDC was successfully used to migrate large volumes of data from a legacy surveillance system into the NBS. Two NBS states are using PHDC to implement ongoing data exchange between separate surveillance systems within their jurisdiction. In several NBS jurisdictions, WDS is used to automatically create investigations and case notifications for high-morbidity conditions such as gonorrhea and chlamydia. In other jurisdictions, WDS is used to assist with managing high volumes of Hepatitis B and C reports.

Conclusions
CDA-based PHDC does require that public health have knowledge of standards and data integration resources to transform incoming messages to the PHDC interface; however, the flexibility provided by this approach ensures the system is able to respond to new and changing standards without system development. Additional enhancements are needed to support data exchange with immunization registries. WDS functionality does reduce burden on public health staff, especially when dealing with high-volume diseases. Future functionalities include the ability to define more criteria (such as age or gender) to drive the actions taken on an incoming lab or case report.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The NIST Syndromic Surveillance Test Suite for 2015 Edition ONC certification testing was published in February 2016. Key information related to the purpose, development, and use of this conformance test tool is provided via snapshots on a poster. Details about the ONC 2015 Edition certification criteria for Syndromic Surveillance and the related NIST Test Suite were explained previously. We now provide an overview and key information regarding updates to the Test Suite and how it is designed to be used. Methods Snapshots are provided on a poster and are used by the presenters to explain the steps involved in developing the NIST Syndromic Surveillance Test Suite 2015 Edition, to show key features of and updates to the Test Suite, and to illustrate the relationship of the Test Suite to various releases of the PHIN Messaging Guide for Syndromic Surveillance.

Results The NIST Syndromic Surveillance Test Suite for 2015 Edition ONC certification testing was published in February 2016. As the target stakeholders began using it and providing feedback, this tool and associated documentation were updated. The Test Suite is being used by test labs for ONC certification testing of health information technologies, by developers in preparation for certification testing, and ultimately by public health jurisdictions for on-boarding of provider organizations that need to submit surveillance data.

Conclusions Automated conformance test tools enable validation of health information technologies’ ability to support the requirements published in the PHIN Messaging Guide for Syndromic Surveillance. Having this standard and the means to validate conformance helps drive the industry toward the level of interoperability needed to promote efficient reporting and utilization of syndrome-based public health surveillance information.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
Demonstrate the value of consolidated claims data from community healthcare providers in Zika Virus Disease surveillance at local level.

Introduction
Zika virus disease and Zika virus congenital infection are nationally notifiable conditions that became prominent recently as ag rowing number of travel-associated infections have been identified in the United States. The Centers for Disease Control and Prevention (CDC) have dedicated significant time and effort on determining and addressing the risks and impact of Zika on pregnant women and their babies who are most vulnerable to the disease. CDC relies on two sources of information, reported voluntarily by healthcare providers, to monitor Zika virus disease: ArboNET and the newly established U.S. Zika Pregnancy Registry. A study by IMS Health compared U.S. trends of the Zika virus disease in general and pregnant women with Zika virus disease in particular observed in an IMS healthcare claims database and the CDC ArboNET and the newly established U.S. Zika Pregnancy Registry.

Methods
IMS used for this analysis claims for reimbursement from office-based healthcare providers, which are widely accepted standard business practice records throughout the healthcare industry. IMS claims data is collected daily from office-based providers throughout the U.S. and processed, stored and analyzed in a centralized database. The information is available at the patient and visit level, with the ability to characterize deidentified patients by age, gender and ZIP3 location and to trace a patient’s history of visits, diagnoses, procedures, drugs prescribed and tests performed or ordered. The general IMS study sample captured all patients throughout the continental United States covered in claims between October 1, 2016 and May 24, 2016 with ICD 10 diagnosis code A92.8, Other Specified Mosquito-Borne Viral Fevers. This sample was compared to the sample of laboratory-confirmed Zika virus disease cases reported to ArboNET by state or territory from the CDC Arboviral Disease Branch from January 1, 2015 through May 18, 2016. In addition, IMS compared the subset of patients with both a Zika virus disease diagnosis and any ICD 10 pregnancy diagnosis to the CDC sample of patients captured by the U.S. Zika Pregnancy Registry with any laboratory evidence of possible Zika virus infection in the United States and territories. Results
Throughout the continental United States, the IMS claims-based sample captured 875 patients with a Zika virus disease diagnosis compared to 548 travel-associated cases reported by CDC. At the state level, especially in New York, New Jersey, Illinois and Texas, the IMS data captured a much larger number of cases than the CDC reported cases. Most of these possible Zika cases are concentrated in the large metropolitan areas around New York City, Chicago and Houston. Many of them are diagnosed and treated by the same healthcare providers. The IMS sample captured 577 pregnant women with a possible Zika virus infection compared to the 168 pregnant women with a possible Zika virus infection reported in the U.S. Zika Pregnancy Registry as of May 24, 2016. Many of the pregnant women in the IMS sample had multiple visits, often in consecutive months, associated with the Zika virus disease diagnosis. Pregnant women are more likely to be tested and diagnosed with a Zika virus infection due to the risk of fetal malformations from the disease. As many as 250 of the 577 pregnant women with a possible Zika virus infection also had diagnosis of suspected fetal damage due to a viral disease. Of all women with a possible Zika virus infection in the IMS sample, 120 were in New Jersey, 111 in New York, 93 in Illinois and 74 in Texas, and most were concentrated in the large metropolitan areas around New York City, Chicago and Houston.

Conclusions
These findings suggest that all-payer claims data can be used successfully to monitor Zika transmission trends at local and state level, especially with a focus on pregnant women. Healthcare claims data is fast, granular, relevant at local level and can be used to supplement CDC ArboNET data for local and state level surveillance and response to the evolving Zika virus infection outbreak. This study is an example of a novel approach to surveillance for Zika virus disease and potentially many other infectious diseases.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

The presentation describes the design and the main functionalities of two user-friendly applications developed using R-shiny to support the statistical analysis of morbidity and mortality data from the French syndromic surveillance system SurSaUD. Introduction

The French syndromic surveillance system SurSaUD® has been set up by Santé publique France, the national public health agency (formerly French institute for public health - InVS) in 2004. In 2016, the system is based on three main data sources: the attendances in about 650 emergency departments (ED), the consultations to 62 emergency general practitioners’ (GPs) associations SOS Médecins and the mortality data from 3,000 civil status offices [1].

Introduction

Daily, about 60,000 attendances in ED (88% of the national attendances), 8,000 visits in SOS Médecins associations (95% of the national visits) and 1,200 deaths (80% of the national mortality) are recorded all over the territory and transmitted to Santé publique France. About 100 syndromic groupings of interest are constructed from the reported diagnostic codes, and monitored daily or weekly, for different age groups and geographical scales, to characterize trends, detect expected or unexpected events (outbreaks) and assess potential impact of both environmental and infectious events. All-causes mortality is also monitored in similar objectives. Two user-friendly interactive web applications have been developed using the R shiny package [2] to provide a homogeneous framework for all the epidemiologists involved in the syndromic surveillance at the national and the regional levels.

Methods

The first application, named MASS-SurSaUD, is dedicated to the analysis of the morbidity data sources in SurSaUD, along with data provided by a network of Sentinel GPs [3]. Based on pre-aggregated data available daily at 10:30 am, R programs create daily, weekly and monthly time series of the proportion of each syndromic grouping among all visits/attendances with a valid code at the national and regional levels. Twelve syndromic groupings (mainly infectious and respiratory groups, like ILI, gastroenteritis, bronchiolitis, pulmonary diseases) and 13 age groups have been chosen for this application. For ILI, 3 statistical methods (periodic regression, robust periodic regression and Hidden Markov model) have been implemented to identify outbreaks. The results of the 3 methods applied to the 3 data sources are combined with a voting algorithm to compile the influenza alarm level for each region each week: non-epidemic, pre/post epidemic or epidemic.

The second application, named MASS-Euromomo, allows consulting results provided by the model developed by the European project EuroMomo for the common analysis of mortality in the European countries (www.euromomo.eu). The EuroMomo model, initially developed using Stata software, has been transcribed in R. The model has been adapted to run in France both at a national, regional and other geographical administrative levels, and for 7 age groups.

Results

The two applications, accessible on a web-portal, are similarly designed, with:

- a dropdown menu and radio buttons on the left hand side to select the data to display (e.g. filter by data source, age group, geographical levels, syndromic grouping and/or time period),
- several tab panels allowing to consult data and statistical results through tables, static and dynamic charts, statistical alarm matrix, geographical maps, ...

(Figure 1),

- a “help” tab panel, including documentations and guidelines, links, contact details.

The MASS-SurSaUD application has been deployed in December 2015 and used during the 2015-2016 influenza season. The MASS-Euromomo application has been deployed in July 2016 for the heat-wave surveillance period. Positive feedbacks from several users have been reported.

Conclusions

Business Intelligence tools are generally focused on data visualisation and are not generally tailored for providing advanced statistical analysis. Web applications built with the R-shiny package combining user-friendly visualisations and advanced statistics can be rapidly built to support timely epidemiological analyses and outbreak detection.

Figure 1: screen-shots of a page of the two applications


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To explore how outpatient and urgent care syndromic surveillance for influenza-like illness (ILI) compare with emergency departmentsyndromic ILI and other seasonal ILI surveillance indicators.

Introduction The North Dakota Department of Health (NDDoH) collects outpatient ILI data through North Dakota Influenza-like Illness Network (ND ILINet), providing situational awareness regarding the percent of visits for ILI at sentinel sites across the state. Because of increased clinic staff time devoted to electronic health initiatives and an expanding population, we have found sentinel sites have been harder to maintain in recent years, and the number of participating sentinel sites has decreased. Outpatient sentinel surveillance for influenza is an important component of influenza surveillance because hospital and death surveillance does not capture the full spectrum of influenza illness. Syndemic surveillance (SyS) is another possible source of information for outpatient ILI that can be used for situational awareness during the influenza season; one benefit of SyS is that it can provide more timely information than traditional outpatient ILI surveillance [1,2]. The NDDoH collects SyS data from hospitals (emergency department and inpatient visits) and outpatient clinics, including urgent and primary care locations. Visits include chief complaint and/or diagnosis code data. This data is sent to the BioSense 2.0 SyS platform. We compared our outpatient SyS ILI without ND ILINet and reported influenza cases, and included hospital and combined SyS ILI for comparison.

Methods Weekly rates from ND ILINet, SyS ILI, and counts of reported cases from the influenza season (annual weeks 40 through 20) for the 2014-2015 and 2015-2016 seasons were compiled. Syndromic categories for outpatient, hospital (emergency department and inpatient), and combined hospital and outpatient data were created, and the BioSense 2.0 definition for ILI was used. These included data from 127,050 outpatient and 323,318 hospital visits for 2014-15, and 124,597 outpatient and 424,097 hospital visits for 2015-16. Because influenza is a reportable condition in North Dakota, case data is routinely used to represent the seasonal influenza trend, and is useful when other respiratory viruses are circulating. A Pearson Correlation Coefficient was calculated on all variables using SAS 9.4. Alpha was set to 0.05. There was no overlap between the outpatient clinics providing syndemic surveillance data and clinics participating in ND ILINet. Results All outpatient, hospital, and combined outpatient and hospital ILI rates from SyS data were positively and significantly correlated with both ND ILINet rates and influenza case counts (Table 1). The correlation between outpatient SyS ILI rates and traditional influenza indicators was lower than for hospital SyS ILI rates for both years, with correlation coefficients ranging from 0.38-0.48 and 0.56-0.92, respectively. Generally SyS data was more highly correlated with case counts than ND ILINET rates. For the 2014-15 season, hospital SyS data was the most strongly correlated with traditional influenza indicators. For 2015-16, combined SyS data was the most strongly correlated. Visual inspection of the chief complaint data for ILI visits found a significant number of gastrointestinal visits that included the phrase “flu-like illness” in both outpatient and hospital SyS data. Conclusions Although correlation coefficients were lower for outpatient SyS ILI rates, they are significant enough to be included in our ongoing influenza surveillance. One possible confounding factor for the relationship between ED surveillance and reported cases is that people with more severe illness may be more likely to be tested for influenza, and may be more likely to seek medical attention at a hospital setting. This may explain why hospital SyS data provided the strongest correlation during the 2014-15 season, a season with higher rates of more severe illness than 2015-16. The combination of outpatient data and hospital data provided the strongest correlation for the 2015-16 influenza season, indicating the addition of outpatient data, which may increase representativeness of ILI data, may be beneficial to the SyS ILI surveillance. We used an existing ILI syndrome from the BioSense2.0 tool, and revising this syndrome may improve correlations between SyS ILI and ND ILINet and case count data. Negation terms to remove visits for GI illness incorrectly referred to as “flu-like” would be one useful change. The nature of visits for influenza outpatient clinic versus hospitals is different, and it is possible these may account for the difference in the strength of correlations between the two data sources. Use of a different ILI syndrome definition for outpatient SyS data should be investigated. Table 1. Pearson correlation coefficient values for influenza-like illness in three syndemic surveillance categories compared with ND ILINET and influenza case counts.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

To explore the interest of Wikipedia as a data source to monitor seasonal diseases trends in metropolitan France.

Introduction

Today, Internet, especially Wikipedia, is an important part of everyday life. People can notably use this popular free online encyclopedia to search health-related information. Recent studies showed that Wikipedia data can be used to monitor and to forecast influenza-like illnesses in near real time in the United States [1,2]. We carried out a study to explore whether French Wikipedia data allow to monitor the trends of five seasonal diseases in metropolitan France: influenza-like illness, gastroenteritis, bronchiolitis, chickenpox and asthma.

Methods

To collect Wikipedia data, we used two free web applications (https://stats.grok.se and https://tools.wmflabs.org/pageviews), which aggregate daily views for each French entry of the encyclopedia. As some articles have several entries (redirects), we collected view statistics for all the article entries and added them to make timeseries from January 1st, 2009 to June 30, 2016 (Figure 1). Then, we compared these data to those of OSCOUR® network, which is a robust national surveillance system based on the emergency departments. For each disease, we modeled daily variations in Wikipedia views according to daily visits in ED using Poisson regression models allowing for overdispersion. The following adjustment variables were included in the model: long-term trend, seasonality, day of the week. We tested several lags (day-7 to day+7) in order to explore whether one of the two indicators (Wikipedia view or ED visits) varied earlier than the other.

Results

The mean number of daily views was 764 [16-8271] for influenza-like illness, 202 [6-1660] for bronchiolitis, 1228 [59-10030] for gastroenteritis, 475 [21-2729] for asthma and 879 [25-4081] for chickenpox. Times series analyses showed a positive association between page views and ED visits for each seasonal disease (Figure 2). For each increase in 100 Wikipedia views, the number of ED visits the same day increased by 2.9% (95% CI=[2.5-3.3]) for influenza, 1.8 (95% CI=[1.4-2.2]) for bronchiolitis, 2.4% (95% CI=[2.2-2.7]) for gastroenteritis, 1.4% (95% CI=[1.0-1.7]) for asthma and 2.9% (95% CI=[1.7-4.1]) for chickenpox. Globally, the highest relative risks were observed for lag-1 (day-1) to lag 0.

Conclusions

This study allowed to show that French Wikipedia data can be useful to monitor the trends of seasonal diseases. Indeed, they were significantly associated with data from a robust surveillance system, with a maximum lag of one day. Wikipedia can therefore be considered as an interesting complementary data source, notably when traditional surveillance systems are not available in real time. Further works will be necessary to elaborate forecasting models for these seasonal diseases.

Figure 1. Daily number of page views and ED visits for seasonal diseases, January 1st, 2009 to June 30, 2016

Figure 2. Relative risk between Wikipedia page views and ED visits for seasonal diseases by several lags

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Wisconsin is leading the way in novel approaches monitoring health outcomes for opioid-related adverse events. This panel will share innovative public health informatics methods that harness various data sources (e.g., Prescription Drug Monitoring Data (PDMP), death, birth and hospitalization data) for population health surveillance. Discussion will include topics on detection of drug abuse and diversion, identifying potential neonatal abstinence syndrome cases, surveillance of substance-related hospitalizations and overdosed deaths, and modeling opioid-related mortality risk factors. Figure 1. Health Outcomes Opioids Surveillance System Diagram Figure 2. Ratios of MME and Length of Prescription for Select Groups (2013-2015) Map 1. Filled Opioids Over 90MME, Southeast Region Local Health Departments, Wisconsin, 2015.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
The research objective was to develop and validate an automated system to extract and classify patient alcohol use based on unstructured (i.e., free) text in primary care electronic medical records (EMRs).

Introduction
EMRs are a potentially valuable source of information about a patient’s history of health risk behaviors, such as excessive alcohol consumption or smoking. This information is often found in the unstructured (i.e., free) text of physician notes. It may be difficult to classify and analyze health risk behaviors because there are no standardized formats for this type of information. As well, the completeness of the data may vary across clinics and physicians. The application of automated classification tools for this type of information could be useful for describing patterns within the population and developing disease risk prediction models.

Natural Language Processing (NLP) tools are currently used to process EMR free text in an automated and systematic way. However, these tools have primarily been applied to classify information about the presence or absence of disease diagnoses. The application of NLP tools to health risk behaviors, particularly alcohol use information from primary care EMRs, has thus far received limited attention.

Methods
Study data were from the Manitoba regional network of the Canadian Primary Care Sentinel Surveillance Network (CPCSSN) for the period from 1998 to 2016. CPCSSN is a national primary care surveillance network for chronic diseases comprised of 11 regional networks with publicly funded healthcare systems. Currently, a total of 53 clinics and more than 260 physicians provide data to CPCSSN in Manitoba. We classified each record based on unstructured text from physician notes into the following mutually exclusive categories: current drinker, not a current drinker, and unknown. A standardized de-identification process was applied to each record prior to applying an NLP tool to the data.

Text classification used a support vector machine (SVM) applied to both unigrams (i.e., single words) and mixed grams (i.e., unigrams, and pairs of words known as bigrams) from a bag-of-words model in which each record is quantified by the relative frequency of occurrence of each word in the record. The training dataset for the SVM was comprised of 2000 records classified by two primary care physicians. These physicians were initially trained using an independent sample of 200 EMR text strings containing specific reference to alcohol use. Cohen’s kappa statistic, a chance-adjusted measure, was used to estimate agreement. Internal validation of the SVM was conducted using 10-fold cross-validation techniques.

Model performance was assessed using recall and precision statistics, as well as the F-measure statistic, which is a function of their average. All analyses were conducted using the R open-source software package.

Results
A total of 57,663 unique records were included in the study. The estimate of the kappa statistic for the physician training phase was 0.98, indicating excellent agreement. Subsequent classification of the training dataset by the physicians resulted in 1.7% of records assigned as not a current drinker, 16.8% as current drinker, and 81.5% as unknown. Average estimates of recall for the 10 validation folds using unigrams were 0.62 for not current drinkers, 0.86 for current drinkers, and 0.98 for the unknown category. Average estimates of recall using mixed grams were 0.48, 0.84, and 0.97, respectively. Estimates of precision were higher with mixed grams than unigrams for the not currently drinking category, but the opposite was true for the current drinker category. There was no difference in precision between the two methods for the unknown category. The F-measure statistic was higher for classification of current drinkers using unigrams (0.89) than mixed grams (0.83), although the differences for the unknown category were negligible (0.98 versus 0.97). Application of the SVM with unigrams to the entire dataset resulted in 15.3% of records classified as current drinkers, 2.0% classified as not current drinkers, and 82.7% as unknown.

Conclusions
This study developed an automated system to classify unstructured text about alcohol consumption into mutually exclusive alcohol use categories. However, we found that only a small percentage of primary care records contained documentation about alcohol consumption, which limits the utility of the automated tool and the data source for disease risk prediction or alcohol use prevalence estimation. While our automated approach is useful for processing existing EMR data, systematic documentation of alcohol consumption will benefit from standardized entry fields and terms to produce clinically meaningful information that will improve the understanding of health risk behaviors in primary care populations.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the effect of symptom negation in emergency department (ED) chief complaint data received by the New York City (NYC) Department of Health and Mental Hygiene (DOHMH), and to devise a solution to avoid syndrome and symptom misclassification for commonly used negations using SAS Perl Regular Expression (PRX) functions. Introduction In July 2016, 77% of ED data was transmitted daily via Health Level 7 (HL7) messages, compared to only 27% in July 2015 (Figure). During this same period, chief complaint (CC) word counts increased from an average of 3.8 words to 6.0 words, with a twenty-fold increase in the appearance of the word “denies” in the chief complaint (Figure). While HL7 messages provide robust chief complaint data, this may also introduce errors that could lead to symptom and syndrome misclassification. Methods Using SAS 9.4 and Tableau 9.3, we examined data submissions from 14 EDs responsible for 97% of the occurrences of the word ‘denies’ in chief complaints in July 2016. To account for variation in chief complaint format among hospitals, we developed three PRX patterns to identify entire phrases in the chief complaint data field that began with conjugations of the word “deny” followed by various combinations of words, punctuation, spaces, and/or characters. Pattern 1: ‘’/DEN(Y|I(ES|ED|NG))(\s|\w|(|\(|\(|\($|\(\)$|\)|\)|\)|(-))’’; Pattern 2: ‘’/DEN(Y|I(ES|ED|NG))(\s|\w|(|\(|\(|\($|\(\)$|\)|\)|\)|(-)|(,))/’’; Pattern 3: ‘’/DENIES:(\s|\w|(|\(|\(|\($|\(\)$|\)|\)|\)|(-))’’; We separated the ‘denies’ statement from the chief complaint and identified commonly negated symptoms. We then defined symptoms using keyword searches of the chief complaint and the ‘denies’ statement. Results Of the 14 EDs analyzed, we applied pattern 1 to 8 of the ED’s, pattern 2 to 5 EDs, and patterns 2 and 3 to 1 ED. Approximately 98% of denies statements were extracted from chief complaints. Only 2% of symptom negation was not captured due to uncommon chief complaint format whose symptom negation didn’t meet one of the previously described PRX patterns. The most common words associated with a “denies” statement were: pain, chest, fever, loc, shortness, breath, vomiting, nausea, travel, headache, recent, trauma, history, abdominal, injury, diarrhea, SOB (shortness of breath), V (vomit), Head, N (nausea), PMH (past medical history), suicidal, dizziness, homicidal and D (diarrhea) (see Table). By not taking negation into consideration in symptom definitions, between 3.5% and 16.5% of symptom visits were misclassified. Symptom misclassification varied greatly by hospital, ranging from 0% to 55%. Conclusions As hospitals in NYC implement HL7 messaging, symptom negation is becoming increasingly common in chief complaint data. Current symptom definitions are based on keyword searches that don’t take into account symptom negations. This leads to symptom misclassification, and could potentially cause false signals or inflates syndrome baselines, causing true signals to go undetected. SAS PRX functions can be used to flexibly identify symptom negation patterns and exclude them from syndrome definitions. Future studies will quantify the effect symptom negation has had on signal frequency in NYC, and examine symptoms associated with other forms of negations such as “Personal Medical History”, “No” and “Negative.”


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To evaluate prediction of laboratory diagnosis of acute respiratory infection (ARI) from participatory data using machine learning models.

Introduction ARIs have epidemic and pandemic potential. Prediction of presence of ARIs from individual signs and symptoms in existing studies have been based on clinically-sourced data. Clinical data generally represents the most severe cases, and those from locations with access to healthcare institutions. Thus, the viral information that comes from clinical sampling is insufficient to either capture disease incidence in general populations or its predictability from symptoms. Participatory data — information that individuals today can produce on their own — enabled by the ubiquity of digital tools, can help fill this gap by providing self-reported data from the community. Internet-based participatory efforts such as Flu Near You have augmented existing ARI surveillance through early and widespread detection of outbreaks and public health trends.

Methods The GoViral platform was established to obtain self-reported symptoms and diagnostic specimens from the community (Table 1 summarises participation details). Participants from states with the most data, MA, NY, CT, NH, and CA were included. Age, gender, zip code, and vaccination status were requested from each participant. Participants submitted saliva and nasal swab specimens and reported symptoms from: fever, cough, sore throat, shortness of breath, chills, fatigue, body aches, headache, nausea, and diarrhea. Pathogens were confirmed via RT-PCR on a GenMark respiratory panel assay (full virus list reported previously). Observations with missing, invalid or equivocal lab tests were removed. Table 2 summarises the binary features. Age categories were: ≤20, >20 and <40, and ≥40 to represent young, middle-aged, and old. Missing age and gender values were imputed based on overall distributions.

Three machine learning algorithms — Support Vector Machines (SVMs), Random Forests (RFs), and Logistic Regression (LR) — were considered. Both individual features and their combinations were assessed. Outcome was the presence (1) or absence (0) of laboratory diagnosis of ARI. Results Ten-fold cross validation was repeated ten times. Evaluations metrics used were: positive predictive value (PPV), negative predictive value (NPV), sensitivity, and specificity. LR and SVMs yielded the best PPV of 0.64 (standard deviation: ±0.08) with cough and fever as predictors. The best sensitivity of 0.59 (±0.14) was from LR using cough, fever, and sore throat. RFs had the best NPV and specificity of 0.62 (±0.15) and 0.83 (±0.10) respectively with the CDC ILI symptom profile of fever and (cough or sore throat). Adding demographics and vaccination status did not improve performance of the classifiers. Results are consistent with studies using clinically-sourced data: cough and fever together were found to be the best predictors of flu-like illness. Because our data include mildly infectious and asymptomatic cases, the classifier sensitivity and PPV are low compared to results from clinical data.

Conclusions Evidence of fever and cough together are good predictors of ARI in the community, but clinical data may overestimate this due to sampling bias. Integration of participatory data can not only improve population health by actively engaging the general public but also improve the scope of studies solely based on clinically-sourced surveillance data. Table 1. Details of included participants. Table 2. Coding of binary features

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
The objective of this analysis is to leverage recent advances in natural language processing (NLP) to develop new methods and system capabilities for processing social media (Twitter messages) for situational awareness (SA), syndromic surveillance (SS), and event-based surveillance (EBS). Specifically, we evaluated the use of human-in-the-loop semantic analysis to assist public health (PH) SA stakeholders in SS and EBS using massive amounts of publicly available social media data.

Introduction
Social media messages are often short, informal, and ungrammatical. They frequently involve text, images, audio, or video, which makes the identification of useful information difficult. This complexity reduces the efficacy of standard information extraction techniques. However, recent advances in NLP, especially methods tailored to social media, have shown promise in improving real-time PH surveillance and emergency response. Surveillance data derived from semantic analysis combined with traditional surveillance processes has the potential to improve event detection and characterization. The CDC Office of Public Health Preparedness and Response (OPHPR), Division of Emergency Operations (DEO) and the Georgia Tech Research Institute have collaborated on the advancement of PH SA through development of new approaches in using semantic analysis for social media.

Methods
To understand how computational methods may benefit SS and EBS, we studied an iterative refinement process, in which the data user actively cultivated text-based topics (“semantic culling”) in a semi-automated SS process. This ‘human-in-the-loop’ process was critical for creating accurate and efficient extraction functions in large, dynamic volumes of data. The general process involved identifying a set of expert-supplied keywords, which were used to collect an initial set of social media messages. For purposes of this analysis, researchers applied topic modeling to categorize related messages into clusters. Topic modeling uses statistical techniques to semantically cluster and automatically determine salient aggregations. A user then semantically culled messages according to their PH relevance. In June 2016, researchers collected 7,489 worldwide English-language Twitter messages (tweets) and compared three sampling methods: a baseline random sample (C1, n=2700), a keyword-based sample (C2, n=2689), and one gathered after semantically culling C2 topics of irrelevant messages (C3, n=2100).

Researchers utilized a software tool, Luminoso Compass, to sample and perform topic modeling using its real-time modeling and Twitter integration features. For C2 and C3, researchers sampled tweets that the Luminoso service matched to both clinical and layman definitions of Rash, Gastro-Intestinal syndromes, and Zika-like symptoms. Layman terms were derived from clinical definitions from plain language medical thesauri. ANOVA statistics were calculated using SPSS software, version. Post-hoc pairwise comparisons were conducted using ANOVA Turkey’s honest significant difference (HSD) test. Results: An ANOVA was conducted, finding the following mean relevance values: 3% (+/- 0.01%), 24% (+/- 6.6%) and 27% (+/- 9.4%) respectively for C1, C2, and C3. Post-hoc pairwise comparison tests showed the percentages of discovered messages related to the event tweets using C2 and C3 methods were significantly higher than for the C1 method (random sampling) (p<0.05). This indicates that the human-in-the-loop approach provides benefits in filtering social media data for SS and EBS; notably, this increase is on the basis of a single iteration of semantic culling; subsequent iterations could be expected to increase the benefits.

Conclusions
This work demonstrates the benefits of incorporating non-traditional data sources into SS and EBS. It was shown that an NLP-based extraction method in combination with human-in-the-loop semantic analysis may enhance the potential value of social media (Twitter) for SS and EBS. It also supports the claim that advanced analytical tools for processing non-traditional SA, SS, and EBS sources, including social media, have the potential to enhance disease detection, risk assessment, and decision support, by reducing the time it takes to identify public health events.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
We aim to develop an automated method to track opium related discussions that are made in the social media platform called Reddit. As a first step towards this goal, we use a keyword-based approach to track how often Reddit members discuss opium related issues.

Introduction
In recent years, the use of social media has increased at an unprecedented rate. For example, the popular social media platform Reddit (http://www.reddit.com) had 83 billion page views from over 88,000 active sub-communities (subreddits) in 2015. Members of Reddit made over 73 million individual posts and over 725 million associated comments in the same year [1]. We use Reddit to track opium related discussions, because Reddittallows for throwaway and unidentifiable accounts that are suitable for stigmatized discussions that may not be appropriate for identifiable accounts. Reddit members exchange conversation via a forum like platform, and members who have achieved a certain status within the community are able to create new topically focused group called subreddits.

Methods
First, we use a dataset archived by one of Reddit members who used Reddit’s official Application Programming Interface (API) to collect the data (https://www.reddit.com/r/datasets/comments/3bxlg7/i_have_every_publicly_available_reddit_comment/). The dataset is comprised of 239,772 (including both active and inactive) subreddits, 13,213,173 unique user IDs, 114,320,798 posts, and 1,659,361,605 associated comments that are made from Oct of 2007 to May of 2015. Second, we identify 10 terms that are associated with opium. The terms are ‘opium’, ‘opioid’, ‘morphine’, ‘opiate’, ‘hydrocodone’, ‘oxycodeone’, ‘fentanyl’, ‘oxy’, ‘heroin’, ‘methadone’. Third, we preprocess the entire dataset, which includes structuring the data into monthly time frame, converting text to lower cases, and stemming keywords and text. Fourth, we employed a dictionary approach to count and extract timestamps, user IDs, posts, and comments containing opium related terms. Fifth, we normalized the frequency count by dividing the frequency count by the overall number of respective variable for that period.

Results
According to our dataset, Reddit members discuss opium related topics in social media. The normalized frequency count of posters shows that less than one percent members, on average, talk about opium related topics (Figure 1). Although the community as a whole does not frequently talk about opium related issues, this still amounts to more than 10,000 members in 2015 (Figure 2). Moreover, members of Reddit created a number of subreddits, such as ‘oxycontin’, ‘opioid’, ‘heroin’, ‘oxycodeon’, that explicitly focus on opioids.

Conclusions
We present preliminary findings on developing an automated method to track opium related discussions in Reddit. Our initial results suggest that on the basis of our analysis of Reddit, members of the Reddit community discuss opium related issues in social media, although the discussions are contributed by a small fraction of themembers. We provide several interesting directions to future work to better track opium related discussions in Reddit. First, the automated method needs to be further developed to employ more sophisticated methods like knowledge-based and corpus-based approaches to better extract opium related discussions. Second, the automated method needs to be thoroughly evaluated and measure precision, recall, accuracy, and F1-score of the system. Third, given how many members use social media to discuss these issues, it will be helpful to investigate the specifics of their discussions.

Line Graphs of normalized frequency counts for posters, comments, and posts that contained opium related terms

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To examine community engagement as a means to strengthen tobacco-related policies and programs use in marginalized populations.

Introduction Although significant progress has been made in tobacco control in the United States (US) over the past 50 years, more than 15% of the population currently use tobacco products. Tobacco use continues to be the leading cause of preventable death, contributing to over 480,000 deaths and about $300 billion in economic costs each year. To achieve the Healthy People 2020 (HP2020) objective of 12% national adult smoking rate by 2020, it is important to focus our tobacco control efforts on surveillance and addressing disparities in tobacco use prevalence and tobacco-induced diseases across different subpopulations and geographic areas. Utah reported the lowest prevalence rate (9.7% in 2014), while rates as high as 28% were identified in central Appalachia. Modern epidemiology is limited in its ability to explain patterns of tobacco use and tobacco-related interventions and policies in these highly prevalent, marginalized environments. Therefore, a combination of quantitative and community-based participatory research (CBPR), as proposed in Public Health 3.0, will expand the scope and reach to address all factors of tobacco use, including cross-sector collaboration and multi-level actions. This study aimed to comprehensively investigate counties in the Northeast Tennessee region where tobacco use prevalence is disproportionately highest, and to identify regional and culturally specific evidence-based practices for tobacco control. Additionally, the study examined how these practices can be scaled up to address similar high tobacco use and disadvantaged populations elsewhere in the US and worldwide.

Methods Grounded by the CBPR framework, a mixed-methods approach triangulated multiple sources of data using a three-prong assemblage of Protection, Prevention, and Cessation, to develop tobacco control recommendations and goals as part of a Population Health Improvement Plan for Tennessee. Information gained from health council discussions, focus groups, interviews, and stakeholder meetings were combined with quantitative analyses of secondary data from Tennessee Department of Health, school-based surveys, and qualitative analyses conducted for descriptive and inferential statistics. All discussions and interviews involving 222 individuals from 91 organizations were recorded and organized using NVivo10, thematically coded using grounded theory, and analyzed using descriptive statistics. The results utilized aggregated themes generated from the data. Results Tobacco use in the Northeast Tennessee region comprises cigarettesmoking and smokeless tobacco, with increasing uptake of electronic cigarettes across all age groups. Among others, culture of tobacco use and cultivation was identified as the most salient factor for tobacco use. Reducing tobacco use requires a foundation built on informatics, community engagement, and a model for sustainable funding to support infrastructure and program interventions. While state and national policies and programs have received less attention in this region, several effective community-based policies and programs to prevent tobacco use were identified, including incentive programs such as Baby and Me, voluntary smoke-free campus policies by businesses and colleges, 100% screening programs by hospitals, and nicotine-free employee population. Overall, a total of 25 recommendations were identified, with 14 aimed at protection, four at prevention, and seven at cessation. These recommendations culminated into five overarching goals: Protect the population from tobacco and secondhand smoke exposure through policy enforcement and implementation and counter-marketing; Prevent initiation of tobacco use with comprehensive youth-focused programs that increase knowledge and awareness; Expand access to cessation resources and treatment, especially in high risk populations; Foster collaboration and partnership; and Monitor data for evaluation and validity.

Conclusions This is one of the few comprehensive attempts to address the social dynamics of tobacco use and identify population and geographic policies and programs in highly prevalent communities. Among the myriad issues identified, the expansion of surveillance data to inform tobacco policy and culturally-tailored tobacco policies and programs are essential to reduce tobacco use in population subgroups. Combining CBPR with actionable data can spur innovations in local efforts, highlight social determinants of health, and contribute evidence-based policy. While the results of this study primarily provide in-depth descriptions of central Appalachia’s tobacco-related risks and their perceptions of and reactions to tobacco prevention intervention, the policies and programs identified through the process may be more readily adopted and scaled-up to address the disparities in tobacco use and tobacco-induced diseases, particularly pertaining to low-income, disadvantaged, and hard-to-reach populations.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo develop a spatially accurate biosurveillance synthetic datagenerator for the testing, evaluation, and comparison of new outbreakdetection techniques.

IntroductionDevelopment of new methods for the rapid detection of emergingdisease outbreaks is a research priority in the field of biosurveillance. Because real-world data are often proprietary in nature, scientists mustutilize synthetic data generation methods to evaluate new detectionmethodologies. Colizza et. al. have shown that epidemic spread isdependent on the airline transportation network [1], yet current datagenerators do not operate over network structures. Here we present a new spatial data generator that models the spread of contagion across a network of cities connected by airlineroutes. The generator is developed in the R programming languageand produces data compatible with the popular ‘surveillance’ softwarepackage.

MethodsColizza et. al. demonstrate the power-law relationships between city population, air traffic, and degree distribution [1]. We generate a transportation network as a Chung-Lu random graph [2] that preserves these scale-free relationships (Figure 1). First, given a power-law exponent and a desired number of cities, a probability mass function (PMF) is generated that mirrors the expected degree distribution for the given power-law relationship. Values are then sampled from this PMF to generate an expected degree (number of connected cities) for each city in the network. Edges (airline connections) are added to the network probabilistically as described in [2]. Unconnected graph components are each joined to the largest component using linear preferential attachment. Finally, city sizes are calculated based on an observed three-quarter power-law scaling relationship with the sampled degree distribution. Each city is represented as a customizable stochastic compartmental SIR model. Transportation between cities is modeled similar to [2]. An infection is initialized in a single random city and infection counts are recorded in each city for a fixed period of time. A consistent fraction of the modeled infection cases are recorded as daily clinic visits. These counts are then added onto statically generated baselinedata for each city to produce a full synthetic data set. Alternatively, data sets can be generated using real-world networks, such as the onemaintained by the International Air Transport Association.

ResultsDynamics such as the number of cities, degree distribution power-law exponent, traffic flow, and disease kinetics can be customized. In the presented example (Figure 2) the outbreak spreads over a 20-city transportation network. Infection spreads rapidly once the morepopulated hub cities are infected. Cities that are multiple flights away from the initially infected city are infected late in the process. The generator is capable of creating data sets of arbitrary size, length, and connectivity to better mirror a diverse set of observed network types.

ConclusionsNew computational methods for outbreak detection and surveillance must be compared to established approaches. Outbreakmitigation strategies require a realistic model of human transportation behavior to best evaluate impact. These actions require test data that accurately reflect the complexity of the real-world data they wouldbe applied to. The outbreak data generated here represents the complexity of modern transportation networks and are made to be easily integrated with established software packages to allow for rapid testing and deployment. Randomly generated scale-free transportation network with a power-law degree exponent of $\lambda = 1.8$. City and link sizes are scaled to reflect their weight. An example of observed daily outbreak-related clinic visits across a randomly generated network of 20 cities. Each city is colored by the number of flights required to reach the city from the initial infection location. These generated counts are then added onto baseline data to create a synthetic data set for experimentation.

KeywordsSimulation; Network; Spatial; Synthetic; Data

Abstract

Introduction
Mitigating the spread of infectious disease is of great importance for policy makers. Taking the recent outbreak of Ebola as an example, it was difficult for policy makers to identify the best course of action based on the cost-effectiveness of what was available. In effort to address the needs of policy makers to mitigate the spread of infectious disease before an outbreak becomes uncontrollable, we have devised a cost-benefit disease control model to simulate the effect of various control methods on disease incidence and the cost associated with each of the scenarios. Here, we present a case study of Ebola used to quantify the cost effectiveness of vaccination and isolation methods to minimize the spread of the disease. We evaluate the impact of changing strategy levels on the incidence of the disease and address the benefits of choosing one strategy over the other with regards to cost of vaccine and isolation.

Methods
Disease. We use a general SEIRJ model for disease transmission. Here, S—Susceptible, E—Exposed (latent), IA—Infected (asymptomatic), IM—Infected (mild symptoms), IS—Infected (severe symptoms), JM—Isolated (mild symptoms at home), JS—Isolated (severe symptoms in hospital), and R—Recovered individuals. In this model, we consider the dynamics of the system and the effect of the relative transmissibility of isolated individuals (L) compared to other infected individuals.1 Cost. Ebola vaccination and treatment are very expensive and not widely available. Some preliminary data shows that it will take $73 million (M) to produce 27 M vaccines plus the cost for vaccine delivery and health care professionals (not included here). On the other hand, the treatment for Ebola in the U.S. would cost $25,000 dollars a day per person to ensure proper isolation and adequate care (treatment, health care professionals, facilities and special equipment). Although not included in this research, the proper isolation of Ebola patients would also lead to a loss in hospital revenue of $148,000 per day due to reduced patient capacity.3 Here, we use $27,000 per individual hospitalized per day and $2.70 per person vaccinated. Model. To evaluate the cost-effectiveness of control methods on disease transmission, we assessed the effect of different levels of vaccination coverage on the resulting number of infected individuals. Then, we calculated the overall estimated cost of vaccination and resulting hospitalization for each scenario to identify the lowest cost-benefit ratio.

Results
Using a base population of 10 M individuals, we ran scenarios for different levels of vaccination (μ= 0.01, 0.05, 0.1) while varying the relative transmissibility of isolated individuals (L = 0.5, 0.6, 0.65). For each combination, we calculated the incidence, vaccination and hospitalization cost per individual per day (Fig 1). We note that an increase in the relative transmissibility of isolated individuals leads to a higher number of infected people and, therefore, a reduced number of candidates for vaccination and an overall increase in cost. Since the cost of vaccination is 1 ten-thousandth of the cost of hospitalization, our results clearly show the cost-benefit of vaccinating over hospital treatment. In every scenario studied, we observed a measurable reduction in disease incidence when vaccinating a higher fraction of the population compared to isolating individuals post infection. Conclusions

Given these preliminary results, we plan to extend the framework of our model to a dynamic control system where we consider the cost of vaccination and isolation embedded in the system of differential equations. This approach will allow us see the best available control implementation while minimizing the cost of treatment and vaccination.

Keywords
Control; Epidemiological Modeling; Transmission Dynamics; Cost; EBOLA

References

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The purpose of this project is to demonstrate progress in developing a scientific and practical approach for public health (PH) emergency preparedness and response informatics (EPRI) that supports the National Health Security Strategy and Global Health Security Agenda (GHSA) objectives. PH emergency operations centers (EOC) contribute to health security objectives because they operationalize response, recovery and mitigation activities during national and international PH events. The primary focus of this presentation is to describe the results of an analysis of CDC’s EOC, and other EOCs, in building their EPRI capabilities.

Introduction Global travel and human migration patterns facilitate the spread of diseases such as influenza A/H1N1, Ebola, and Zika, increasing pressure to PH systems to protect their constituents against global health threats. Effective prevention, detection, and rapid response to threats rely heavily on adequate information sharing. This requires effective information management through PH EPRI applications such as information systems and tools, knowledge management, and a continuous cycle improvement to maintain system quality. Enhancement of PH EPRI capabilities contributes to improved decision making during emergencies.

It transforms public health practice and improves health outcomes through better surveillance, epidemiology, integrated delivery of services, and other emergency preparedness and response activities. EPRI activities depend on both technical systems and the people who use them. Without adequate training, these systems cannot be effective. CDC’s PH EOC information processes and data flows are notable use case, utilized by hundreds of emergency responders during large-scale PH events. By analyzing this use case, CDC’s informaticians have identified multiple opportunities for advancing PH EPRI and advance the objectives of the GHSA.

Methods PH EPRI is an interdisciplinary science, incorporating knowledge and techniques from a multiple fields of research and practice. These include epidemiology and surveillance, gathering and distributing information for situational awareness (SA), technology infrastructure development, incident management, and several other disciplines. CDC’s Situational Awareness Branch used three sources for this analysis: direct analysis of CDC’s EOC information systems and SA activities; WHO’s Framework for a Public Health Emergency Operations Centre, and HHS’ Public Health and Medical Situational Awareness Strategy. This assessment also included a comparison of the objectives of PH EPRI to the objectives of other emerging disciplines, such as PH informatics and emergency preparedness informatics. This helped in avoiding overlap with other disciplines and fixing gaps within PH EPRI.

Results The following information flows were identified as part of the CDC’s EOC operations: Managing and Commanding, Operations, Planning and Intelligence, Logistics, and Finance/Administration. These information flows are standard for PH EPRI's. Each information flow is supported by an information structure that consists of hierarchical categories. For example, the Operations information flow includes Task Tracking, Event Investigation, and Controlling. As of August, 2016, CDC’s EOC defined 41 hierarchical categories for PHEPRI data flows. CDC’s EOC harmonized different information flows by using a consistent vocabulary to describe the hierarchical components of each information flow. Two hundred thirty six data elements of this vocabulary were harmonized as of August 2016 to standardize its EPRI systems. The hierarchy of PH EOC data flows and harmonized data elements were published in the CDC Vocabulary and Access Distribution System, VADS. Some information flows were unique to PH EPRI, and were not covered by other emerging disciplines. Examples of these unique information flows include some incident management data, logistics for deployment of PH personnel and resources, and some event mitigation data. Conclusions CDC’s EOC has several harmonized information flows that benefit users and CDC emergency activations. Understanding these unique PH EPRI data flows helps improve preparedness of staff for working with information flows during emergency activations. Advances in harmonization and standardization helped improve PH EPRI and optimize staff training.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To develop agent-based model of sexually transmitted infection spreading by example of Syphilis and its analysis.

Introduction Every year nearly 12 million new cases of syphilis in the world are registered. Currently, in many countries of the world the stabilization or even reduction of the incidence of syphilis is marked, but this does not apply to Ukraine. The current stage of development of the syphilis problem in Ukraine is characterized by not only high morbidity, but also the fact that in the overwhelming number of cases, we are talking about the latent forms and atypical manifestations of the disease and resistance to therapy [1]. Preventive and prophylactic measures are important in maintaining the public health. Predicting the dynamics of disease spreading allows developing appropriate countermeasures and ensuring rational use of human and material resources.

Qualitative forecast of syphilis spreading is possible to implement by means of mathematical modeling. Methods Deterministic analytical models that are most common in epidemiological studies do not take into account the dynamic and stochastic nature of epidemics. Agent-based simulation approach to modeling allows fixing these shortcomings. It allows conveying the social structure of simulated system in the most natural and easy way. Each agent has individual state variables and rules of behavior that allows detailing the model very deeply. Therefore there is no need to describe the complex system of mathematical formulas and probability of the dynamics of the epidemic process is defined parametrically. The NetLogo software has been used for the program realization of the developed model.

Results The model of morbidity by syphilis spreading has been developed by the tradition SIR model expansion. Thus, agents can be in following states: S (Susceptible) for health people, IP (Infected Primary) for infected people who stay in primary stage and can transmit the infection by direct sexual contact with susceptible person, IS (Infected Secondary) for infected people who stay in secondary stage and have also infectious skin lesions, IL (Infected Latent) for infected people who stay in latent stage and change its contagious rate from early latent syphilis to late latent syphilis, IT (Infected Tertiary) for infected people who stay in tertiary stage and transmit the infection partially, and R (Recovered) for people who are recovered from the infection. Infecting of agents in the model depends on the number and state of agents and the stage of infected agent’s disease.

Also, in order to correctly determine the intensity of contacts with other agents different age groups of agents have been highlighted in the model. The transmission between agent’s states are defined by probabilistic way and depends on features of particular states as well as different factors, such as coupling tendency, condom use, commitment, test frequency etc. The analysis of experiments under developed model has shown that the most influencing factor in the reduction in the percentage of patients is frequency of checks on the disease and isolation of patients, the second most important factor is constancy of sexual partners, the third is the use of condoms, and finally, the fourth is the number of exchangeable partners. Conclusions The agent-based model of syphilis spreading has been developed. The model allows forecasting the morbidity by infection and analyzing the disease by changing the initial data. All data has been checked by the factual statistics on the syphilis incidence in Kharkiv region (Ukraine) from 1975 to 2015 years. The simulation results allow determining the direction of prevention of syphilis treatment and the main factors in reducing morbidity. As is evident from the simulation results, social factors take precedence over the healthcare that gives grounds for advocacy in health policy among the population, especially the youth. Developed model can be configured for other sexually transmitted infections by changing the disease transition rules.

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Abstract

Objective: Implement a mobile technology platform to capture and transmit syndromic cattle data collected at Texas market sales. An active syndromic surveillance system was designed to collect cattle health information from a sample of Texas cattle market sales. Texas Animal Health Commission livestock inspectors record the total number of animals observed along with the total number displaying clinical signs of interest grouped into body system categories (e.g., respiratory, neurologic, etc.). Inspection reports are submitted to the United States Department of Agriculture Veterinary Services (VS) Risk Identification Team for monitoring.

Methods: The pilot project started in 2012 with paper-based data collection forms to both 1) gain trust from the inspector supervisors and 2) evaluate the value of the system with minimal early investment. The data collected at each sale on paper-based forms were later entered into spreadsheets at the office. These sale inspection reports were then submitted to the inspector’s supervisor for review prior to forwarding by email to VS. VS staff aggregated data from each spreadsheet in a centralized database and conducted weekly monitoring. Recently, a new reporting system was developed at VS to enable collection and transmission of the data on mobile devices running an Android operating system capable of transmitting data to VS via Wi-Fi connection. The new system was deployed March 2016 following in-person training, release of a user guide document, and a month of user testing.

Results: Between March 2014 and June 2016 a total of 1,330 sale inspection reports from 16 markets were submitted by spreadsheet an average 11 days following the sale (range: 1 day through 141 days following the sale). These reports were tracked for data quality issues that required manual intervention. It was discovered that 64 (4.8%) of the reports required correction. The most common types of data quality issues were market sale date not provided, market alias ID not provided, report submitted more than once, and report not submitted as an Excel file but as an image, such as a pdf file. Between March and June 2016 a total of 160 sale inspection reports from 16 markets were submitted using mobile devices an average 7 days following the sale (range: same day through 47 days following the sale). All data submitted could be directly imported into the centralized database and processed as needed for monitoring without any data correction required. Some challenges encountered with deploying the mobile technology system included addressing the VS Information Technology security requirements for establishing user accounts and implementing direct data upload into VS systems. Additionally, Wi-Fi connectivity can be difficult in some remote areas. Some advantages to using the mobile technology included having the option to download and run the application on most mobile devices running the Android operating system. There was an improvement in data reporting timeliness of 4 days on average, and the range substantially narrowed. There was also time savings for inspectors who no longer needed to transfer hard copy data to a spreadsheet, and for VS personnel who no longer needed to aggregate data from individual spreadsheets. Improvements in data quality included the ability to directly report that sales were canceled or not attended; the ability to provide comments at various levels of detail related to the sale, the pen of animals observed, or specific signs observed; and the requirement to supply essential data elements such as sale date and market ID.

Conclusions: The conversion from a paper and spreadsheet-based sale inspection report to a mobile technology platform resulted in significant timesavings and data quality improvements that appeared to justify the system development and deployment costs and challenges. These benefits support potential expansion of the system.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To build an open source spatiotemporal system that integrates analysis and visualization for disease surveillance.

Introduction Most surveillance methods in the literature focus on temporal aberration detections with data aggregated to certain geographical boundaries. SaTScan has been widely used for spatiotemporal aberration detection due to its user-friendly software interface. However, the software is limited to spatial scan statistics and suffers from location imprecision and heterogeneity of population. RSurveillance has a collection of spatiotemporal methods that focus more on research instead of surveillance.

Methods Based in Ontario, Canada, we used postal codes for determining the location of cases of reportable infectious diseases. The variation in geographic sizes and shapes of the case and census geographies created challenges for developing a uniform temporal spatiotemporal surveillance system, including: Linking case and population data due to misclassification errors, Distance based correlations due to irregularly shaped areas (e.g., FSA’s), and Visualization bias due to variation in population density, e.g., large area with little population. To overcome these challenges, we developed the Ontario Hybrid Information Map (OHIM) boundary, which is a combination of Public Health Unit boundaries (rural areas), census subdivisions (rural-urban mixed) and regular grid cells (urban). The goal is to capture population details in urban areas without losing information in rural areas. OHIM has around 4600 geographies with more than half located in urban centers. Population distribution by gender and age group was calculated for each OHIM geography. A lookup file was also created to link all Ontario postal codes to OHIM geography.

To create baselines, historical data for influenza A were used to model the seasonality and calculate expected case count for each OHIM geography for each week. Standardized incidence ratios (SIR) were calculated as exploratory statistics, and a spatiotemporal Besag-York-Mollie (BYM) model was used to calculate the probability that the risk is higher than a pre-specified threshold. Integrated Nested Laplace Approximation (R-INLA) was used in R to explore different types of spatiotemporal interactions and for fast Bayesian inference. The ability to apply the models was verified by examining previous outbreaks and seeking the opinion of staff that routinely perform surveillance on influenza. To ensure the visualization integrates with the analysis, R package Shiny was used to build an interactive spatiotemporal visualization on OHIM boundary utilizing Open Street Map and html5. Shiny application not only allows users to pan and zoom in space and time to explore the results and locate high risk areas, it also gives users the flexibility to change algorithm parameters for instant feedback. Figure 1 demonstrates a zoomed-in OHIM boundary with pointers signaling “high risk” areas at user-specified statistics exceed a threshold (e.g., SIR > 2). Using the algorithms and visualization tools, surveillance experts pick the optimal time and place to be notified based on historical data and therefore the optimal threshold, which will be verified by prospectively running the algorithms.

Results The OHIM boundaries build the foundation for efficient spatial modeling and visualization for public health surveillance in Ontario. Together with the integrated modeling and visualization system, staff are able to interactively optimize the aberration thresholds and identify potential outbreaks in real time. Staff reported preference of SIR due to its faster computations and easier interpretation. One major challenge was scalability: the ability to handle high-resolution spatiotemporal data. When the system was applied on 4600 polygons by 200 weeks, significant delays were encountered in both analysis and visualization. Difficulties in computational time, memory requirement and visualization interactivity created delays and freezing, thereby limited user experience. This problem was partially addressed by optimizing parameters for fast computations.

Conclusions This work shows the “proof of concept” for an open source, customizable spatiotemporal surveillance system that overcomes existing data challenges in Ontario. However, more work is required to make this fully operational and efficient in production.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The National Biosurveillance Integration Center (NBIC) is developing a scalable, flexible open source data collection, analysis, and dissemination tool to support biosurveillance operations by the U.S. Department of Homeland Security (DHS) and its federal interagency partners. Introduction The NBIC integrates, analyzes, and distributes key information about health and disease events to help ensure the nation’s responses are well-informed, save lives, and minimize economic impact. NBIC serves as a bridge between Federal, State, Local, Territorial, and Tribal entities to conduct biosurveillance across human, animal, plant, and environmental domains. The integration of information enables early warning and shared situational awareness of biological events to inform critical decisions directing response and recovery efforts. To meet its mission objectives, NBIC utilizes a variety of data sets, including open source information, to provide comprehensive coverage of biological events occurring across the globe. NBIC Biofeeds is a digital tool designed to improve the efficiency of reviewing and analyzing large volumes of open source reporting by biosurveillance analysts on a daily basis; moreover, the system provides a mechanism to disseminate tailored feeds allowing NBIC to better meet the specific information needs of individual, interagency partners. The tool is currently under development by the Department of Energy (DOE), Pacific Northwest National Laboratory (PNNL) and it is in a testing and evaluation phase supported by NBIC biosurveillance subject matter experts. Integration with the Defense Threat Reduction Agency (DTRA), Biosurveillance Ecosystem (BSVE) is also underway. NBIC Biofeeds Version 1 is expected to be fully operational in Fiscal Year 2017. Methods The PNNL is applying agile methodology to streamline the build of NBIC Biofeeds to specifications required for operational use by NBIC and its federal interagency partners. Biosurveillance, analytics, and system engineering subject matter experts provide guidance on the implementation of features in the tool to ensure functionality aligns with operational workflows and production support. PNNL is leveraging software from a previous government effort to repurpose the technology to meet NBIC needs. NBIC Biofeeds incorporates the open source, document-orientated MongoDB database to capture user- and system-generated metadata on hundreds of thousands of records, in part, to establish baselines to aid prospective and retrospective analysis on emerging biological events. NBIC Biofeeds integrates a biosurveillance taxonomy (uniquely developed by NBIC), which includes input from interagency partners to recognize critical characteristics of a biological event. In NBIC Biofeeds Version 1, metadata capture of reported events is done manually by NBIC analysts; however, moving forward in Version 2, the tool will be further automated to flag significant reporting on biological events with a human remaining in the loop to confirm the validity of the system-generated tags. Results To serve as a one-stop tool for open source biosurveillance, NBIC Biofeeds automatically harvests information from thousands of websites, utilizing third party aggregators, paid subscriptions to data feeds, and scraping of high priority sources. Users can develop desired queries for automatic updating, leverage a unique review and curation mechanism, and further analyze data from topical, geographic, and temporal visualization features in the tool. To meet NBIC’s information sharing needs, the tool allows for design of tailored RSS feeds and electronic message-based delivery of analysis on biological events, intended for recipients in the government with unique missions around human, animal, plant, and environmental health. Conclusions Through current testing and evaluation – underway by biosurveillance subject matter experts – NBIC Biofeeds is demonstrating value in supporting open source biosurveillance by the Center for more rapid recognition and sharing of key event characteristics. Centralizing access and analysis of this dataset into a single system is increasing the efficiency of daily, global biosurveillance, while enhancing the value of information identified through use of the querying, curation, and production support features in the tool.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

The NEDSS Base System (NBS) is designed and developed using input from CDC programs, public health standards organizations, as well as its expansive user community. This community-based approach to development of an integrated surveillance system is described.

Introduction

The NEDSS Base System (NBS) is a web-based, standards-driven, integrated disease surveillance system launched in 2001 and is currently in use in twenty-two public health jurisdictions. Over the past fifteen years, the NBS has grown into a highly functional, modern application that supports: case management, electronic data exchange, metadata-driven data collection, workflow decision support, and a host of other functionalities, all of which are defined and designed through a community-based approach.

Methods

In order to encourage open communication and collaboration across and among the community, there is a well-publicized, long-standing communication plan in place. Further, tools such as an online collaboration and support forum, NBSCentral, are made available to anyone who requests access. Also, the NBS source code is provided in an open source package to anyone interested, along with each release, and a demonstration version of the application is accessible online by anyone to review the latest release of the application. All of these channels are in place to ensure there are ways for all who have an interest in collaborating to easily participate. The NBS community regularly meets to provide input into further development of the system, as well as discuss topics affecting public health. As a community, members:

- Share best practices, tools, and lessons learned across jurisdictions
- Share innovative local approaches to disease surveillance and reporting
- Access NBSCentral for support and collaboration
- Participate in the change control and planning process for each NBS release
- Work collaboratively with CDC to define high-level vision and priorities
- Provide input to create community-defined requirements for system development
- Participate in weekly subject matter expert (SME) calls to discuss development and best practices
- Have the opportunity to participate in beta testing for releases
- Attend a bi-weekly NBS User Group (NUG) call to discuss the system as well as reach out to colleagues to brainstorm creative solutions to common problems in public health surveillance

All meetings with stakeholders are recorded and shared with the larger public health community to ensure full transparency and for historical reference.

Results

Through this inclusive development approach, the NBS has evolved into a highly extensible, configurable system that can meet the needs of twenty-two very different public health jurisdictions; the system can be implemented without the need for custom development in a relatively short timeframe due to the fact that it was designed to meet the needs of many. Further, it has encouraged interoperability projects, such as: piloting electronic case reporting use cases between NBS implementation sites and building and sharing electronic case investigation forms for data collection using the NBS Page Builder module. All NBS sites use the same translation routes for electronic lab report, case report, and Nationally Notifiable Disease message processing – embracing the build once, use many concept. Most recently, having this collaboration network in place made it very easy for the NBS community to quickly adapt to the changing needs of Zika virus surveillance.

Conclusions

It does require clear definition of processes and communication channels, as well as regular update and transparency into the process for community-based development to work. However, when the proper tools and processes are in place, the benefits of collaboration with all key stakeholders are exponential when realized. Developing an application in this way has provided NBS users not only with amuch better, integrated surveillance system, but also a forum for understanding how other jurisdictions have solved similar issues; it provides a springboard for sharing and building upon novel ideas and new approaches in public health surveillance.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Pacific Northwest National Laboratory hosted an intern-based web application development contest in the summer of 2016 centered around developing novel chemical surveillance applications to aid in health situational awareness. Making up the three teams were three graduate students (n=9) from various US schools majoring in non-public health domains, such as computer science and user design. The interns successfully developed three applications that demonstrated a value-add to chemical surveillance—ChemAnalyzer (text analytics), RetroSpect (retrospective analysis of chemical events), and ToxicBusters (geo-based trend analytics). These applications will be the basis for the first chemical surveillance application to be incorporated into the DTRA Biosurveillance Ecosystem (BSVE).

Introduction Pacific Northwest National Laboratory (PNNL), on behalf of the Defense Threat Reduction Agency (DTRA; project number CB10190), hosts an annual intern-based web app development contest. Previous competitions have focused on mobile biosurveillance applications. The 2016 competition pivoted away from biosurveillance to focus on addressing challenges within the field of chemical surveillance and increasing public health chemical situational awareness. The result of the app will be integrated within the DTRA BSVE.

Methods PNNL hosted nine graduate interns for a 10-week period in the summer of 2016 as participants in a summer web application development contest. Students were drawn from such fields as software engineering and user experience and design and placed into three teams of three students. The challenge presented to the interns was to design and develop a fully-functional web application that would address a critical need within the chemical surveillance community. The interns developed their own ideas (vetted by PNNL and DTRA), discovered and integrated their own data sources, and produced their own visualizations and analytics, independent of any assistance outside of that provided in an advisory capacity. The competition ended with a judging event with a panel of subject matter experts and cash awards were distributed to the teams. Results Each team produced a unique application. Although there was mild overlap between some of the ideas, the applications were developed independently and each reflected the unique contributions of the teams. ChemAnalyzer is a text-analytics platform designed to facilitate more data-driven decision making, given a corpus of text data about a chemical event. Their platform provided the ability to automatically identify and highlight key words in documents related to chemical events. The keywords are drawn from an ontology installed with the system, as well as any user-identified keywords. The ChemAnalyzer team finished in third place. The RetroSpect team developed a visual analytic tool for performing retrospective analysis and monitoring of chemical events. Their app provided the ability to search and analyze past events, as well as visualization of state and county information for the recorded chemical events. The ToxicBusters team—the winners of the competition—created a geo-based situational awareness tool for tracking chemical events. Their app featured an updateable map overlay, search functionality for finding specific or related events, incident and city/state/national-level statistics and trends, as well as news and social media integration based on keywords related to chemical surveillance.

Conclusions Each of the apps developed by the teams provides value to an analyst tasked with monitoring chemical events. The apps integrated unique data sources to provide a full picture of a chemical event, and its effects upon the surrounding population. This integrated analytics provides a valuable benefit over existing workflows, where analysts must monitor news, social, and other information sources manually for real-time information. The apps developed by these interns were designed to enable identification and analysis of the incident as quickly as possible, allowing for more timely assessments of the incident and its impacts. The web app development contest provided a unique opportunity for students to learn about the emerging needs in chemical surveillance as it relates to health situational awareness. Students were drawn from a variety of fields and were tasked with developing novel web apps addressing some of the most pressing challenges in the field of chemical surveillance. The ideas generated by the students will help form the basis for future chemicals surveillance application development to be integrated with the DTRABSVE.
Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To assess the feasibility of tracking the prevalence of chronic conditions at the state and community level over time using MDPHnet, a distributed network for querying electronic health record systems.

Introduction Public health agencies and researchers have traditionally relied on the Behavioral Risk Factor Surveillance System (BRFSS) and similar tools for surveillance of non-reportable conditions. These tools are valuable but the data are delayed by more than a year, limited in scope, and based only on participant self-report. These characteristics limit the utility of traditional surveillance systems for program monitoring and impact assessments. Automated surveillance using electronic health record (EHR) data has the potential to increase the efficiency, breadth, accuracy, and timeliness of surveillance. We sought to assess the feasibility and utility of public health surveillance for chronic diseases using EHR data using MDPHnet. MDPHnet is a distributed data network that allows the Massachusetts Department of Public Health to query participating practices’ EHR data for the purposes of public health surveillance (www.esphealth.org). Practices retain the ability to approve queries on a case-by-case basis and the network is updated daily.

Methods We queried the quarterly prevalence of pediatric asthma, smoking, type 2 diabetes, obesity, overweight, and hypertension statewide and in 9 Massachusetts communities between January 1, 2012 and July 1, 2016. We selected these 9 communities because they were participating in a state-funded initiative to decrease the prevalence of one or more of these conditions. Conditions were defined using algorithms based upon vital signs, diagnosis codes, laboratory measures, prescriptions, and self-reported smoking status. Eligible patients were those with at least 1 encounter of any kind within the 2 years preceding the start of each quarter. Results were adjusted for age, sex, and race/ethnicity using the 2010 Massachusetts census data. Results

Surveillance data were available for 1.2 million people overall, approximately 20% of the state population. Coverage varied by community with ≥28% coverage for 7 of the communities and 11% coverage in the eighth. The ninth community had only 2% coverage and was dropped from further analyses. The race/ethnicity distribution in MDPHnet data was comparable to census data statewide and in most communities. Queries for all six conditions successfully executed across the network for all time periods of interest. The prevalence of asthma among children under 10 yrs rose from 12% in January 2012 to 13% in July 2016. Current smoking in adults age ≥20 rose from 14% in 2013 to 16% in 2016 (we excluded results from 2012 due to changes in documentation propelled by the introduction of meaningful use criteria). This is comparable to the 15% rate of smoking per BRFSS in 2014. Obesity among adults increased slightly from 22% to 24% during the study period, results nearly identical to the most recent BRFSS results for Massachusetts (23% in 2014 and 24% in 2015). The prevalence of each condition varied widely across the communities under study. For example, for the third quarter of 2016, the prevalence of asthma among children under 10 yrs ranged from 5% to 23% depending on the community. The prevalence of smoking among adults ranged from 11% to 35%, and the prevalence of type 2 diabetes among adults ranged from 7% to 14%. We also examined differences in disease estimates by race/ethnicity. Substantial racial/ethnic differences were evident for type 2 diabetes among adults, with whites having the lowest prevalence at 7% and blacks having the highest at 12% in the third quarter of 2016; this trend was consistent over the study period.

Conclusions Our study demonstrates that MDPHnet can provide the Massachusetts Department of Public Health with timely population-level estimates of chronic diseases for numerous conditions at both the state and community level. MDPHnet surveillance provides prevalence estimates that align well with BRFSS and other traditional surveillance sources but is able to make surveillance more timely and more efficient with more geographical specificity compared to traditional surveillance systems. Our ability to generate real-time time-series data supports the use of MDPHnet as a source for project/program evaluation.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To design a low budget process to enroll, track and approve syndromic submitters for ongoing submission of data to the Oregon Public Health Division

Introduction
In 2012, the Oregon Public Health Division (OPHD) took advantage of the opportunity created by Meaningful Use, a Centers for Medicare & Medicaid Services (CMS) Incentive Program, to implement statewide syndromic surveillance. The Oregon syndromic surveillance project, or Oregon ESSENCE, began accepting MU-compliant HL7 v2.5.1 data in late 2013. Early onboarding efforts were labor-intensive and led to the creation of a testing queue. As interest in submitting syndromic data increased, Oregon ESSENCE streamlined the onboarding process by creating guidance for HL7 message construction, message testing, and submitter business process details (collectively referred to as “onboarding documents”).

Oregon ESSENCE also built a project management database to track MU testing statuses and data quality variations. With this system, Oregon ESSENCE collected, tested, and approved all 32 eligible health systems (56 hospitals) for production-level submission by mid-2015. One health system (with four hospitals) continued to send non-MU compliant syndromic data for the duration of the project period. Methods

Initially, Oregon ESSENCE began onboarding syndromic submitters on a first-come-first-served basis. The lack of a clear process for onboarding, a single FTE devoted the endeavor and substantial interest in submitting, led to a testing queue. To streamline the onboarding process and accommodate the testing timelines of all submitters, Oregon ESSENCE created tools to allow for self-paced testing followed by short duration, intensive testing with the project.

Oregon ESSENCE-branded onboarding documents incorporated available resources such as the CDC’s Public Health Information Network Messaging Guide for Syndromic Surveillance: Emergency Department and Urgent Care Data, Release 1.1 (August 2012) and the NIST 2014 Edition ONC Health IT Certification HL7 v2 Syndromic Surveillance Reporting Validation Tool.

Submitters began self-paced testing by testing their own messages using the NIST tool and sending successful reports back to Oregon ESSENCE. They then filled out an Oregon ESSENCE Business Process Survey which asked for meta-data and project contact information. Oregon ESSENCE built a project management database in FileMaker v14 (FileMaker Inc., Santa Clara, CA, USA), used to support the statewide communicable disease database, to store information from the Business Process Survey. After completing self-paced testing, submitters selected a single week for intensive testing with Oregon ESSENCE. Each health system’s project staff (registration staff, technical project lead, HL7 translator and data exchange lead) met daily with Oregon ESSENCE to test messages. Oregon ESSENCE used Rhapsody Integration Engine v6.2.1 (Orion Health, Auckland, NZ), already in use at OPHD for electronic lab reporting, to parse test data into a test database and then generate a report for each testing session using SAS v9.4 (SAS Institute Inc., Cary, NC, USA). The report indicated whether or not the submitter had achieved production-level syndromic messaging by the end of this week of intensive testing. The project management database stored notes from each testing session along with MU testing dates.

Results
Oregon ESSENCE developed their onboarding documents between November, 2012 and March, 2013 and achieved 100% syndromic submission from eligible health systems in June, 2015. The average duration of onboarding (from initiation of the testing process to achieving production submission) of a single health system decreased from 23 months in 2012 to 4 months in 2014 (see Duration of Onboarding Syndromic Submitters: Oregon 2012-2015). As interest in the project grew (number of submitters contacting OPHD), the amount of time spent onboarding decreased. Oregon ESSENCE uses their project management database for ongoing syndromic data quality improvement and to communicate MU dates to submitters (by generating health system-specific emails directly from the database). FileMaker, Rhapsody and SAS are all currently used by OPHD and did not require any additional expense for their use in this testing process. Oregon ESSENCE plans to use this onboarding process to collect urgent care data for Stage 3 MU.

Conclusions
The onboarding process created by Oregon ESSENCE streamlined syndromic data submission without the purchase of additional programs or the hiring of additional project staff. Submitting facilities benefited from this process by testing syndromic messages without waiting in a testing queue. The project management database created for the testing process will continue to benefit submitters by storing MU testing dates and information for ongoing quality assurance evaluations. The success of this project took advantage of existing informatics capabilities at OPHD and speaks to the importance of these skills in public health practice. Oregon ESSENCE will use these methods again in 2017 to collect urgent care data for syndromic surveillance.

Duration of Onboarding Syndromic Submitters: Oregon 2012-2015

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

This presentation will share findings from more than three years of using mobile technology for reactive case detection (RACD) to help eliminate malaria in a well-defined geographic area. It will review the concepts of RACD, the application of mobile technology, lessons learned from more than three years of application, and considerations in applying this technology in other malaria elimination contexts.

Introduction

Zanzibar is comprised primarily of two large islands with a population of 1.3 million. Indoor Residual Spraying (IRS) campaigns, distribution of long-lasting insecticide treated bed nets (LLINs), and use of Rapid Diagnostic Tests (RDTs) have reduced malaria prevalence from 39% in 2005 to less than 1% in 2011-2012. As malaria burden decreases, there is an increasing need to track and follow up individual cases to contain transmission that could lead to resurgence. One method being used to achieve these aims is reactive case detection (RACD). RACD is generally understood to be triggered whenever a case is identified by passive case detection. The response involves visiting the household of the newly reported case and screening family members. Depending on program protocol, it may also involve screening neighbors within a defined radius. RACD has been used or tested in Cambodia, China, India, Peru, Senegal, Swaziland, Tanzania, and Zambia. RACD can be resource intensive. Several studies raise questions concerning whether and how RACD can be prioritized and targeted effectively as case numbers continue to decline.

Methods

Since September 2012 Zanzibar Malaria Elimination Programme (ZAMEP) has used RACD to limit onward transmission, reduce the local parasite reservoir, and gather data needed to improve program effectiveness. Zanzibar is one of very few malaria elimination contexts using a mobile technology system to support RACD. This system, called the Malaria Case Notification system (MCN) uses mobile software called Coconut Surveillance. Coconut Surveillance is free and open source software designed for malaria elimination. It includes an interactive SMS system for casenotification, a mobile software application designed to guide mobile case workers through RACD, and an analytics software application designed for surveillance and response program managers. Data were collected in the Coconut Surveillance database formore than three years, beginning in September 2012. Reports were monitored in real time and periodically to assess RACD responsetimes against protocol targets, case trends, case locations, and other data. Geographical Information System (GIS) software was used to produce detailed maps of case households. Three independent assessments were conducted of various aspects of the malaria surveillance system.

Results

From September 2012 to December 2015, Coconut Surveillance has helped malaria surveillance officers in Zanzibar respond to more than 8,617 (84%) reported cases of malaria, complete nearly 10,245 household visits, test more than 36,185 household members, and identify and treat 2,032 previously unknown cases. The average number of RACD activities occurring within 48 hours increased from 72% in 2013 to 89% in 2015. The number of household members screened during RACD also increased from 7,589 in 2013 to 14,987 in 2015. Challenges included incomplete registers at health care facilities, lack of transport, inadequate training for clinicians and surveillance officers, and insufficient communication to the affected communities.

Conclusions

In Zanzibar twenty malaria surveillance officers equipped with inexpensive Android tablets and motorbikes are keeping malaria prevalence at less than 1%. The effectiveness of the system might be enhanced by improving training for clinicians and surveillance officers, ensuring the availability of transportation for surveillance officers, and improving communications to the affected communities. These results suggest key considerations for applying this and similar systems in other malaria elimination contexts.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo describe the development of an evaluation framework that allows quantification of surveillance functions and subsequent aggregation towards an overall score for biosurveillance system performance.

IntroductionEvaluation and strengthening of biosurveillance systems is a complex process that involves sequential decision steps, numerous stakeholders, and requires accommodating multiple and conflicting objectives. Biosurveillance evaluation, the initiating step towards biosurveillance strengthening, is a multi-dimensional decision problem that can be properly addressed via multi-criteria decision models. Existing evaluation frameworks tend to focus on “hard” technical attributes (e.g. sensitivity) while ignoring other “soft” criteria (e.g. transparency) of difficult measurement and aggregation. As a result, biosurveillance value, a multi-dimensional entity, is not properly defined or assessed. Not addressing the entire range of criteria leads to partial evaluations that may fail to convene sufficient support across the stakeholders’ base for biosurveillance improvements. We seek to develop a generic and flexible evaluation framework capable of integrating the multiple and conflicting criteria and values of different stakeholders, and which is sufficiently tractable to allow quantification of the value of specific biosurveillance projects towards the overall performance of biosurveillance systems.

MethodsWe chose a Multi Attribute Value Theory model (MAVT) to support the development of the evaluation framework. Development of the model was done through online decision conferencing sessions with expert judgement, an indispensable part of MAVT modeling provided by surveillance experts recruited from the member pool of the International Society for Disease Surveillance. The surveillance functions or quality criteria that were considered for the framework were initially gathered from a review of the literature with specific attention to a subset of public health quality criteria (1). Group discussions with the experts led to a final list of functions, finally reviewed to comply with the properties for good criteria in decision models. The eleven functions were: sensitivity; timeliness; positive predictive value (PPV); transparency; versatility; multiple utility; representativeness; sustainability; advancing the field and innovation; risk reduction; and actionable information. In addition, 24 different scenarios were developed for sensitivity, PPV, and timeliness since their values may differ with the level of infectiousness of the condition/event of interest, its severity and the availability of treatment and/or prevention measures. Four or five levels of performance were also developed for each criterion. Macbeth (Measuring Attractiveness by a Category-Based Evaluation Technique) tables were used to elicit values of different levels of performance from the experts using qualitative pairwise comparisons and then convert them into numerical values.

ResultsTo date, two criteria, sensitivity and transparency, have been assessed by more than one expert working on the same scenario. Value functions were generated for each criterion and scenario by calculating the median of the different values produced by the experts. For both sensitivity and transparency, value functions were mostly linear, indicating similar preferences between levels of performance. However, for some scenarios, experts allocated greater value to increases at the higher end of the performance level distribution.

ConclusionsAt the time of writing new elicitation sessions are planned to conclude the model. Next, we will apply swing weights to support the trade-offs between the different criteria. We will present the baseline model elicited from the experts and demonstrate how to apply portfolio decision analysis to assess overall performance of biosurveillance systems according to the specific needs of stakeholders and in conjunction with macro-epidemiological models.


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Abstract

Objective Facing challenges to establish a new national syndromic surveillance system in the Netherlands for infectious diseases among asylum seekers.

Introduction Most European countries are facing a continuous increased influx of asylum seekers [1]. Poor living conditions in crowded shelters and refugee camps increase the risk for outbreaks of infectious diseases in this vulnerable population. In line with ECDC recommendations [2], we aim to improve information on infectious diseases among asylum seekers by establishing a new syndromic surveillance system in the Netherlands. This system will complement the notifiable disease system for infectious diseases. The aim of the syndromic surveillance system is to improve the detecting of outbreaks of infectious diseases in asylum seekers’ centres in an early stage of development to be able to take adequate and timely measures to prevent further spread, and to collect information on the burden of infection within this population.

Methods Primary health care for asylum seekers in the Netherlands is organized nationally by the Asylum Seekers Health Centre, with general practitioners providing care in each reception centre. General practitioners (GPs) act as gatekeepers for specialized, secondary health care and the GP is the first professional to consult for health problems. Therefore, electronic health records (EHR) kept by GPs provide a complete picture of this population. These EHRs contain data on diagnoses/symptoms and treatment of asylum seekers, using the International Classification of Primary Care (ICPC). This data is recorded routinely, as part of the health care process. During summer 2016, about 30,000 asylum seekers were housed in about 60 reception centres across the Netherlands.

Results The governance structure was laid down in a collaboration agreement between the Asylum Seekers Health Centre, the national institute of public health RIVM and NIVEL. To ensure privacy of the asylum seekers, a privacy protocol has been drawn, taking into account strict privacy regulations in the Netherlands. The information system provider of the health care centre developed an extraction tool that automatically generates weekly data extracts from the electronic health records system to a Trusted Third Party (TTP). Before transferring the data to NIVEL, the TTP removes directly identifying patient information, indirectly identifying information like date of birth is replaced by quarter and year, and the personal identification number is replaced by a pseudonym. At NIVEL, all data is stored in a relational database, from which weekly research extracts are generated for infectious disease surveillance at RIVM after applying a second pseudonymisation step (two-way pseudonymisation) [3]. First, data extracts are being expected mid-October 2016, after which data quality will be evaluated. Weekly, or daily, consultations rates will be calculated based on the number of cases meeting predefined definitions, stratified by immigration centre, age group, sex and nationality. Numerators will be based on the number of population housed in the immigration centres.

Conclusions With the cooperation of a national health care centre, providing primary care to asylum seekers housed at several locations, and the information system provider of the health care centre, EHRs can be used for syndromic surveillance, taking into account strict privacy regulations. The new surveillance system will be evaluated after one year, focusing on data quality, usefulness, and the added value above the notification of diseases.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective A mixed methods study is being conducted on the statewide Early Notification of Community Based Epidemics (ESSENCE) system in Missouri to identify factors that can improve the timeliness and identification of outbreaks. This research will provide stakeholders with guidance on how best to implement and improve ESSENCE usage statewide, and by sharing this research input can be solicited on the utility of the applied framework as well as future implications from this body of work.

Introduction In spite of the noted benefits of syndromic surveillance, and more than a decade after it started gaining support, the primary use for syndromic surveillance appears to be largely for seasonal and jurisdictional disease monitoring, event response and situational awareness as opposed to its intended purpose of early event detection. Research assessing the user characteristics and standards applied at local public health agencies (LPHA’s) for syndromic surveillance is scarce, and in national surveys epidemiologists frequently tend to utilize their own syndromic surveillance systems as opposed to a national system such as Biosense. While the National Syndromic Surveillance Program (NSSP) has addressed many operational concerns from stakeholders, and is in the process of providing access to the cloud-based Biosense platform along with ESSENCE as a key tool, there is still a paucity of research that exists as to what can be done to improve the utilization of syndromic surveillance systems for its primary purpose of early event detection.

Methods This research proposes to evaluate the use of ESSENCE within Missouri and the surrounding areas, to comprehensively identify its strengths and limitations, through an assessment of the user experience. This research will evaluate three key areas: 1) the quality of the data received by the syndromic surveillance system, 2) the characteristics of the individuals and organizations utilizing the system (end-users), 3) the influence and extent of syndromic surveillance data on public health actions. ESSENCE data will be evaluated directly with special attention to the top three data quality attributes across the literature, completeness, accuracy and timeliness. A survey will also be administered to ESSENCE system users and public health leadership at LPHA’s, to gain insight into perspectives, perceptions and general practices, as well as how they interact with data from ESSENCE.

Results The data for this research is primarily being collected throughout the fall of 2016, so the hope is to bring preliminary data to this conference as a means to validate some of the findings, solicit input on the proposed framework and share this research in a timely manner for the NSSP roll out of Biosense and ESSENCE.

Conclusions Through a thorough evaluation, the application and utility of ESSENCE for early event detection will be better understood, along with the identification of factors that can be targeted in the future (and across syndromic surveillance platforms) for improvement in the timely identification of outbreaks.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To use syndromic surveillance data to assess whether there has been an increase in GP fever consultations since the inclusion of the meningococcal B (MenB) vaccine in the UK vaccination schedule.

Introduction: From 1 September 2015, babies in the United Kingdom (UK) born on/after 1 July 2015 became eligible to receive the MenB vaccine, given at 2 and 4 months of age, with a booster at 12 months. Early trials found a high prevalence of fever (over 38°C) in babies given the vaccine with other routine vaccines at 2 and 4 months. We used syndromic surveillance data to assess whether there had been increased family doctor (general practitioner (GP)) consultations for fever in young infants following the introduction of the vaccine.

Methods: GP consultations for fever in infants aged under 1 year were extracted from The Phoenix Partnership (TPP) ResearchOne database (400 GP surgeries in England). Data were stratified by week of age over the period 1 September 2015 to 30 November 2015 and 1 December 2015 to 29 February 2016. Fever consultation rates (per 100,000 registered practice population in the database) were compared to the same 3 month periods of the previous 5 years (2010-14) using incident rate ratios (IRR). Pre- and post-vaccination consultation rates were applied to the England 0-26 week population to estimate excess fever consultations.

Results: Between 1 September and 30 November 2015 the average daily fever consultation rate for infants aged 0-26 weeks was 4.72/100,000; the incident rate ratio was 1.46 (95% CI, 1.09-1.92). In the 7-10 week age group the average daily fever consultation rate was 7.79/100,000. The incidence rate was 2.68 times higher than in previous years (95% CI, 1.42-4.94). Between 1 December 2015 and 29 February 2016 the averaged daily consultation rate for infants aged 0-26 weeks was 6.19/100,000. The incidence rate was 1.49 times higher than in the same 3 month period of previous years (95% CI, 1.16-1.90). In infants aged 7-10 weeks the average daily consultation rate was 8.44/100,000 and the incidence rate was 1.83 times higher than previous years (95% CI 1.03-3.16). Between 1 September 2015 and 29 February 2016 there were an estimated additional 959 fever consultations for infants aged 0-26 weeks to English family doctors.

Conclusions: We have demonstrated an innovative use of syndromic surveillance to quickly and easily assess the impact on healthcare seeking behaviour for infants with fever following the introduction of a new vaccination into the routine vaccination programme in England. Our study provides reassurance that in infants aged 0-26 weeks there was no marked increase in consultations following the introduction of the new MenB vaccination. However, in some age groups below 0-26 weeks there was an increase in healthcare seeking behaviour for fever, in particular, the 7-10 week age group which includes infants aged 8 weeks receiving their first vaccination. Other age groups also demonstrated increased fever consultations during these two periods, albeit at less significant levels. We will analyse data for the full year from 1 September 2015 to further explore these findings, investigate potential confounders and assess trends since vaccine introduction.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To provide surveillance tools to support policymakers and practitioners to identify epidemiological situations and inform the progressive implementation of rabies elimination programmes. Introduction Global targets for elimination of human rabies mediated by dogs have been set for 2030. In the Americas, countries are progressing towards interruption of transmission and declaration of rabies freedom. Guidance for managing elimination programmes to ensure continued progress during the endgame is critical, yet often limited and lacking in specific recommendations. Characteristics spatiotemporal incidence patterns are indicative of progress, and through their identification, tailored guidance can be provided. Methods Using SIRVERA, a surveillance database for rabies in the Americas, we developed a classification framework for identification of epidemiological situations at subnational level. Each situation exhibits a characteristic pattern identified via a set of objective criteria including trends in case detection, assessment of virus variants, case locations, and measures of incursion risk. We refined our framework through application to Mexico in consultation with stakeholders. To understand factors predicting incursions, we analysed state-level data on vaccination campaigns, populations, and socioeconomic indicators employing multivariate regression models. Results We were able to classify all states in Mexico and provide correspondingly tailored guidance. Control efforts have resulted in progress towards elimination; however, rabies still circulates endemically in one state Chiapas, putting its neighbours at risk of re-emergence. Epidemiological and socioeconomic factors associated with incursions were primarily geographic proximity to endemic and high-prevalence states, and inconsistent vaccination campaigns associated with a low human development index. Conclusions Our management tool can support rabies programme managers at subnational levels to identify their epidemiological situation, develop tailored plans to meet targets, and sustainably maintain rabies freedom, as demonstrated for Mexico. Effective surveillance is critical for disease elimination. Control options differ depending on whether disease circulates intermittently through reintroductions or persists focally, but with poor detection these situations might be indistinguishable. Our analysis enables identification of at-risk areas and methods to reduce risk. Investment in remaining endemic areas, through improved implementation and monitoring of mass dog vaccinations, is expected to provide the most cost-effective approach to elimination whilst preventing re-emergence elsewhere. Decision-tree framework. Rabies incursions in Mexico, 2005–2015. Blue circles indicate incursion locations, and resulting outbreak sizes, with darker shading for more recent incursions. Red shading indicates the duration of endemic circulation over the then-year period.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To describe the Caribbean Public Health Agency’s (CARPHA) Tourism and Health Information System (THiS), a web-based syndromic surveillance system to increase the capacity of Caribbean countries to monitor the health of visitors and staff in hotels, and detect potential infectious disease outbreaks for early and coordinated public health response. Introduction
The tourism industry is highly vulnerable to Health, Safety, and Environmental Sanitation (HSE) threats. The Caribbean is the most tourism-dependent region in the world, with over 54.2 million stay-over and cruise ship arrivals in 2015, generating revenues of SUS29.6 billion and contributing to 15% of the Gross Domestic Product (GDP) and 2,255,000 jobs [1]. Tourists and staff are at an increased risk of acquiring infectious diseases, given the mass-gathering of individuals with varying levels of susceptibility and often times in close quarters in hotels and cruise ships. To prevent the spread of infectious diseases in these settings, early warning and response to potential public health threats is essential. To increase the capacity of countries in the Caribbean to monitor and protect the health of tourists and staff in their hotel establishments, THiS was designed as an early warning system for infectious disease outbreaks.

Methods
CARPHA launched the Regional Tourism Health Information, Monitoring and Response System in 2016 with donor funding received from the Inter-American Development Bank (IDB). The overall objective of THMRS project from 2016-2018 is to improve participating country’s capacity to provide cost-effective and quality health, food safety and environmental solutions to HSE threats. As part of the THMRS project, the development of a hotel-based syndromic surveillance system for early warning and response to infectious diseases was developed. THiS was developed in collaboration with six participating IDB countries: Barbados, Bahamas, Belize, Guyana, Jamaica, Trinidad and Tobago. The implementation plan (2016-2018) with each country involved three stages: 1) Project Operations, Coordination, Management (including Advocacy, and Endorsement) 2) Development of the project outputs: gap analysis and best practices; development of surveillance guidelines and training modules, HSE Standards 3) Implementation in participating countries (i.e. technical visits, ongoing technical coordination): Preparation, Buy-in, Training and Launch

The web-based design of THiS enables the collection of real-time data which will inform health service delivery decisions/policies, strengthen national and regional health monitoring efforts, and trigger a rapid coordinated response to outbreaks, and prevent escalation of tourism HSE incidents. The system involves a web-based questionnaire with a series of 11 short questions that ask the user for basic non-identifiable demographic information as well as symptoms. The reported symptoms are used by the system to generate six syndromes: Gastroenteritis, Undifferentiated Fever, Hemorrhagic Fever, Fever with Respiratory symptoms, Fever with Neurologic symptoms, Fever with Rash. Data entry persons include hotel staff, physicians, and the case. Access to analytic dashboards of the aggregated data is limited to registered hotel staff (i.e. Managers), the Ministry of Health of the country where the hotel reporting is located, and CARPHA. The limited level of baseline data for syndromes in the Caribbean region means that statistical aberration detection mechanisms for most syndromes will not be available until THiS collects at least one year’s worth of data. However, for acute gastroenteritis, until a more accurate threshold can be generated, a cut-off of 3% ill (staff and guests) will be used for alerting potential outbreaks. This is scheduled to be live and functional beginning in hotel facilities in Trinidad and Tobago at the beginning of October 2016. By the end of 2016, THiS will be operating in facilities in all six participating countries, allowing for the collection of baseline data for syndromes occurring among tourists and staff in hotel settings, and providing a mechanism to detect and response to emerging public health threats early and efficiently.

Conclusions
Establishing this system is critical to improving countries’ capacities to support the overall health surveillance system of the tourism-dependent Caribbean economies, enabling countries to collect real-time data which will inform health service delivery decisions/policies, strengthen national and regional health monitoring efforts to trigger a rapid coordinated response to outbreaks and other crises and thus prevent tourism HSE incidents.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To describe the results of the new organization of influenza surveillance in France, based on a regional approach.

Introduction
In France, until winter 2014-2015, management and preventive actions for the control of the flu epidemic were implemented when the national incidence of influenza-like illness (ILI) consultations in general practice was over an epidemic threshold. The 2014-2015 influenza epidemic had a major public health impact, particularly in the elderly, and caused a severe overloading of the health care system, in particular emergency departments (ED) [1]. The epidemic alert emitted by the French National Public Health Agency at the national level was too late for the hospitals to prepare themselves in many regions. After a national feedback organized in April 2015 with all partners involved in influenza surveillance and management, it was recommended to improve influenza surveillance in France following 3 axes: 1) regionalize surveillance so that healthcare structures can adapt to the particular situation of their region; 2) use a pre-epidemic alert level for better anticipating the outbreak; 3) use multiple data sources and multiple outbreak detection methods to strengthen the determination of influenza alert level.

Methods
A user-friendly web application was developed to provide common data visualizations and statistical results of outbreak detection methods to all the epidemiologists involved in influenza surveillance at the national level or in the 15 regional units of our agency [2]. It relies on 3 data sources, aggregated on a weekly time step: 1) the proportion of ILI among all coded attendances in the ED participating to the OSCOUR Network [3]; 2) the proportion of ILI among all coded visits made by emergency general practitioners (GPs) working in the SOS Médecins associations [3]; 3) the incidence rate of ILI estimated from a sample of sentinel GPs [4]. For each region each week, 3 statistical outbreak detection methods were applied to the 3 data sources, generating 9 results that were combined to obtain a weekly regional influenza alarm level. Based on this alarm level and on other information (e.g. virological data), the epidemiologists then determined the epidemiological status of each region as either 1) epidemic-free, 2) in pre/post epidemic or 3) epidemic. The R software was used for programming algorithms and building the web interface (package shiny). Results: The epidemiological status of influenza at the regional level was communicated through maps published in the weekly influenza reports of the Agency throughout the surveillance season [5]. In week 2016-W03, Brittany was the first French region to declare the influenza epidemic, with nine other regions in pre-epidemic alert. The epidemic then spread over the whole mainland territory. The peak of the epidemic was declared in week 11, the end in week 16.

Conclusions
This regional multi-source approach has been made possible by the sharing of data visualizations and statistical results through a web application. This application helped detecting early the epidemic start and allowed a reactive communication with the regional health authorities in charge of the organization of health care, management and the setting up of the appropriate preventive measures.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To develop and validate a Zika virus disease syndrome definition within the GUARDIAN (Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification) surveillance system.

Introduction
In 2016, the World Health Organization declared Zika virus a global public health emergency. Zika infection during pregnancy can cause microcephaly and other fetal brain defects. To facilitate clinicians’ ability to detect Zika, various syndrome definitions have been developed.

Methods
To create and validate a detailed syndrome definition for Zika, we utilized the literature-based methodology developed and documented by GUARDIAN researchers. The syndrome definition utilized clinical signs and symptoms that were documented in historical Zika cases. A testing sample of 1,000 randomly selected emergency department cases (i.e., true negative cases) and 200 synthetically generated cases (i.e., true positive cases) was created. These 1,200 sample cases were evaluated by the GUARDIAN surveillance system to determine the probability of matching the Zika syndrome definition. A probability of ≥ 90% was utilized to designate positive Zika cases. We identified the main signs and symptoms contributing to the identification of Zika cases and conducted statistical performance metrics. Clinical review of the false positive and false negative cases along with a sample of true positive and true negative cases was conducted by a board-certified emergency physician.

Results
The Zika syndrome definition was developed with eleven articles (six used for developing the syndrome definition, and five used for testing the definition). The sample size for these articles was between 1 and 72 positive Zika cases, with a total of 139 cases across the 11 articles. The article with the most number of Zika cases was based on pregnant women with rash. The publication timeframe for the articles was from 1962 to 2016. Some of the main signs and symptoms from the historical cases that contribute to the Zika syndrome definition are presented in Table 1. The initial results for the sample testing data showed accuracy, sensitivity, and specificity were 94.7%, 93%, and 95% respectively. There were a total of 14 false negative and 50 false positive cases.

Conclusions
The initial Zika syndrome definition utilized by the GUARDIAN surveillance system contains similar signs and symptoms to the current CDC case definition, but also includes additional signs and symptoms such as pruritus/itching, malaise/fatigue/generalized weakness, headache, retro-orbital pain, myalgia/muscle pain, and lymphadenopathy. In addition, the GUARDIAN system provides the relative importance of identified signs and symptoms and allows for proactive surveillance of emergency department patients in real-time. Though we did not include epidemiologic risk factors, such as travel to an infected region or contact with an infected person in the syndrome definition, GUARDIAN has above 90% sensitivity and specificity. Thus, inclusion of epidemiologic risk factors would further enhance the early detection of Zika, when used with the appropriate high-risk population.

Table 1. Main signs and symptoms of Zika syndrome definition

<table>
<thead>
<tr>
<th>Signs and symptoms included in the Centers for Disease Control and Prevention (CDC)’s Zika clinical case definition</th>
</tr>
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<tbody>
<tr>
<td>Independence and freedom to make decisions about health care choices, abilities to know enough about health conditions to allow decision making, and understand health care instructions</td>
</tr>
<tr>
<td>Knowledge about health conditions, ability to follow health advice, and understanding of health care instructions</td>
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<td>Awareness of health care options, ability to make decisions about health care options, and understanding of health care instructions</td>
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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
Study the activity of natural foci of tularemia and identify the main types of reservoirs and vectors of Francisella tularensis.

Introduction
Annually sporadic cases of tularemia in humans are registered in Ukraine and new enzootic areas are found. Monitoring of tularemianatural foci is important given the potential significant financial losses in case of tularemia outbreaks and taken into account that this pathogen can be used as a bioterrorist agent.

Methods
1. Light microscopy of smears of organs and tissues of animals, bacterial suspension (Gram staining) - the study of morphological and tinctorial properties of the pathogen.
2. Immunofluorescence method for detection of antibody (IFA) - detection of tularemia bacterial cells using specific fluorescent immunoglobulin.
3. Biological method - subcutaneous infection of laboratory animals (white mice) with material from environmental samples and bacterial suspension (for accumulation of tularemia agent in organs and tissues of laboratory animals).
4. Bacteriological method - inoculation of samples of wild and laboratory animals in differential diagnostic nutrient media (for isolation of a pure culture of tularemia agent).
5. Serological method:
   - Indirect reaction of agglutination - detection of antibodies to tularemia agent in blood of humans, wild rodents (liquid tularemia antigen erythrocyte diagnostic agent).
   - Indirect reaction of agglutination - detection of tularemia agent and its antigen in suspensions of organs, swabs of substrate from nests of rodents, pellets of birds (liquid tularemia immunoglobulin erythrocyte diagnostic agent).
   - Reaction of agglutination - detection of tularemia agent and its antigen (dry tularemia diagnostic serum).

Results
Tularemia in Lviv oblast has been studied for more than 40 years, 69 enzootic localities in 14 administrative districts have been registered. More than 200 cultures of Francisella tularensis have been isolated, mostly from ticks (58.3%) and Myomorphic rodents (24.5%), the rest from water, straw, other rodents, and patients. In 2012-2015, 210 suspected patients were studied for tularemia, negative results were obtained. 22,320 ticks, 1,810 Myomorphic rodents, 282 water samples, 15 straw samples, and 3 bird nests were tested for tularemia. Tularemia cultures have not been isolated bacteriologically over the last few years. Pathogen circulation in natural foci was confirmed by immuno-serological studies of field material. Antibodies to the pathogen were detected in 6.5% out of 630 samples from Myomorphicrodents of seven species studied by Indirect Hemagglutination test. Most of the positive results were obtained from the samples of striped field mouse (46.3%), red-backed vole (17.0%), and common vole (14.6%). Francisella tularensis antigen was detected in 32 samples out of 14,600 ticks D. reticulatus collected in natural biotopes and in 8.9% out of 289 samples of pellets.

Conclusions
No incidence registered in Lviv oblast and difficulty of isolation of Francisella tularensis cultures over the last years in other oblasts (the last one happened in 2006) may indicate the decrease of foci activity under the influence of anthropogenic and environmental factors or changes in parasitic systems. But there are some evidence of agent circulation in the oblast, so some precautions should be taken, especially considering the fact that there have been no specific preventive measures taken over the last years.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
We evaluated the AFP surveillance system in Oyo State to assess its attributes and determine if it was meeting its set objectives.

Introduction
In September 2015, Nigeria was delisted from the list of polioendemic countries globally. To be certified polio free, the country must attain and maintain certification standard Acute Flaccid Paralysis (AFP) surveillance for additional two-years. In Oyo State, no case of Wild Polio Virus (WPV) has been reported since February 2009.

Methods
We used the Centre for Disease Control and Prevention updated guidelines for evaluating public health surveillance system. We conducted a retrospective review of AFP surveillance database between 1st January 2008 and 31st December 2014. We conducted in-depth interviews with identified stakeholders. Semi-structured questionnaires were administered to Disease Surveillance and Notification Officers (DSNOs) and AFP focal persons. Univariate analysis was performed by calculating frequencies, means and proportions using Microsoft Excel 2010.

Results
The case definition of AFP and the tools for reporting are simple. Of the 897 AFP cases detected during the period under review (2008-2014), 20 (2.2%) were laboratory confirmed WPV. The sensitivity of the system between 2008 and 2014 measured by the Annualized Non-Polio AFP (NPAFP) rate was consistently above the target of \( \geq \frac{2}{100,000} \) population (Mean=3.96, Standard deviation (SD): 0.48). The mean NPAFP rate for underperforming LGAs during the review period was 1.6, SD: 0.31. The mean Stool adequacy and Timeliness were 91.43% (SD: 18.3) and 91.3% (SD: 20.3) above the target of \( \geq 80\% \) respectively. The mean Data quality was 90% (target is \( \geq 90\% \); SD: 3.8). Positive Predictive Value (PVP) was 2% (2008-2009), and 0% in 2010-2014.

Conclusions
The Oyo State AFP surveillance system is simple, flexible, sensitive and meeting its set objectives. However, PVP was low and the system’s operating conditions are not stable. All the LGAs, at one point during the period under review did not meet the NPAFP and NPENT rates. We recommended that more logistic support should be provided for non-performing LGAs to improve case reporting, investigation, and response. DSNOs should be re-sensitized on reverse cold chain, so as to improve the NPENT rate.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: Enhanced daily surveillance is used to identify reportable diseases, outbreaks, and clusters and provides situational awareness. This project examines how health care visits requiring additional information are detected using enhanced syndromic surveillance and the resources required from detection through completion.

Introduction: The Florida Department of Health in Hillsborough County (FDOH-Hillsborough) conducts enhanced syndromic surveillance on a daily basis. The Electronic Surveillance System for the Early Notification of Community-based Epidemics in Florida (ESSENCE-FL) is the syndromic surveillance system used by epidemiologists within the Florida Department of Health (FDOH). During the time of this study, ESSENCE-FL receives data from 210 of emergency departments (ED) and 33 urgent care centers (UCC) throughout the state of Florida, including 12 EDs and 3 UCCs in Hillsborough County. In 2014, the ESSENCE-FL system added a feature that delivers an automated daily email to designated primary ESSENCE-FL users in each county containing all visits which have been detected by the state’s visits of interest (VOI) query. The email contains all visits which have been detected by the visits of interest (VOI) query for each ESSENCE-FL user’s designated county. The VOI query utilizes the combined chief complaint and discharge diagnosis (CCDD) field of a visit for keywords related to reportable diseases and exposures of public health interest. In addition to this VOI email, Hillsborough County analyzes time of arrival alerts, specialized emerging infectious disease queries, poison information center data, and volume levels of syndromes and sub-syndromes predetermined by ESSENCE-FL. A daily summary report of the enhanced daily surveillance analysis is then provided to area public health officials within FDOH-Hillsborough and the surrounding counties. This study examines how visits requiring additional investigation are detected and the resources required to complete the investigation.

Methods: During the study period from July 23 through September 30, 2015, visits identified were recorded along with the time and method of detection. Each day this surveillance began with the review of the visits of interest email, facility and syndrome volumes, the VOI query, emerging infectious disease queries (MERS-CoV, Ebola virus disease, chikungunya, etc.), time of arrival alerts, and the review of Florida Poison Information Center data. A daily summary report of the enhanced surveillance was manually created and provided by email to public health officials. After completion of the daily analysis, facilities were contacted about any visits identified as requiring additional investigation, such as a reportable disease or cluster of public health concern. The time of the information request, receipt of the requested information, and completion of the investigation was recorded. Results: An average of 1740 visits were made each day in Hillsborough County in the month prior to the start of this project. During this same time period the daily VOI email identified an average of 5.5 visits per day. During the study period, an average of 7.8 visits were detected each day during the enhanced syndromic surveillance protocol. The VOI email detected 6 visits per day. Overall 558 total visits were detected from the enhanced daily surveillance and 82 percent of these visits were found in the system generated VOI email. Of the visits identified 149 required additional investigation and 15 were determined to be associated with a reportable disease, most commonly carbon monoxide poisoning and varicella. An average of 1.3 days elapsed from the time a visit occurred to the time it was detected through surveillance. Follow-up was started within 1 day of detection and completed in an average of 1.1 days. Overall the daily enhanced syndromic surveillance data analysis required an average of 60 minutes of work time daily with a range of 18-144 minutes.

Conclusions: During the study period, 15 visits were found to be cases of reportable diseases, primarily carbon monoxide poisoning and varicella, which would have otherwise gone unreported to FDOH-Hillsborough. The enhanced surveillance process also allows for the quick detection and evaluation of diseases or conditions requiring immediate action that may not always be reported immediately such as meningitis or an emerging infectious disease. The enhanced daily syndromic surveillance in Hillsborough County has been useful in detecting reportable diseases, clusters, and providing situational awareness in a timely manner without an overwhelming burden on staff and resources.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the recent trends in the burden of disease and mortality associated with vaccine preventable diseases (VPDs).

Introduction Vaccination is one of the most successful public health interventions. Despite this, there are a variety of reasons that VPDs continue to be seen in developed countries such as Canada. This analysis describes the recent trends in the burden of disease and mortality associated with VPDs for which publicly funded vaccination programs for infants or children are implemented across the country and for which national surveillance data are available.

Methods Surveillance data on VPDs were obtained from the Canadian Notifiable Disease Surveillance System. Population and death data were obtained from Statistics Canada. Death data were only available to 2012. In total, 11 VPDs have been included in the analyses namely tetanus, diphtheria, pertussis, polio, haemophilus influenza (Hi), measles, mumps, rubella, congenital rubella syndrome (CRS), invasive meningococcal disease (IMD), invasive pneumococcal disease (IPD). Exclusion of non-vaccine preventable serotypes from either data source was not possible. Analyses included incidence rate, proportion, mortality rate and risk ratio.

Results Surveillance data indicate that from 2010 to 2014, an average of 6,020 cases of VPDs were reported annually, representing an average annual crude incidence rate of 17.3 cases per 100,000 population. VPDs accounting for the largest proportion of reported cases include IPD (54.4%) and pertussis (29.6%). Age groups most affected include children less than 1 year of age (92.6 cases per 100,000) and children between 1 and 4 years of age (36.0 cases per 100,000). Age groups least affected include adults between 20 and 24 years old (6.9 cases per 100,000 population) and between 25 and 29 years old (7.3 cases per 100,000 population). Age groups affected differed by VPD.

Death data indicate that from 2010 to 2012, VPDs accounting for the largest proportion of deaths across all ages include IPD (58.2%), Hi (16.3%) and IMD (15.3%). Youth aged 19 years and under accounted for 26.1% of VPD deaths (mortality rate of 0.17 per 100,000 population). Children less than one year old have the highest mortality rate due to VPDs (2.0 per 100,000 population) and were 26.9 times more likely to die from VPDs compared to children between 1 and 19 years of age. Adults aged 20 years and older accounted for 73.9% of VPD deaths (mortality rate of 0.14 per 100,000 population). A high mortality rate was also seen in adults 60 year old and over (0.3 per 100,000 population); adults 60 years old and over were more 2.6 times more likely to die from VPDs compared to adults between 20 and 59 years old.

Conclusions The results of routine Canadian surveillance data suggest that despite high vaccine coverage rates generally seen in developed countries such as Canada, a possible preventable burden of illness due to VPDs still occurs across all age groups. Consideration of VPDs as a whole allows a real appreciation of the burden and death associated with VPDs in general. The analysis has shown that while the incidence rates are highest among children 4 years old and younger, mortality due to VPDs continues to occur and primarily affects infants and elderly. Due to the asymptomatic nature of some VPDs and data limitations, reported cases are likely underestimates of the true burden.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To examine demographic as well as clinical characteristics of the Carbapenam Resistant Enterobacteriaceae (CRE) Organisms cases in Houston, Texas, 2015-2016

Introduction According to CDC, CRE is used to describe bacteria that are non-susceptible to one or more carbapenems; doripenem, meropenem or imipenem and resistant to third generation cephalosporins likeceftriaxone, cefotaxime and ceftazidime. These organisms cause infections that are associated with high mortality rates and they have the potential to spread widely. Antibiotic resistant bacteria cause more than 2 million illnesses and at least 23,000 deaths each year in the United States. CREs are found in many health care settings like acute care hospitals, long term care facilities, nursing homes, rehabilitation facilities and other health care settings. Although CREs includes a number of species, reporting in State of Texas is limited to CRE-Klebsiellaspecies and CRE-E. coli.

Methods Population-based surveillance data was generated from Houston’s electronic disease surveillance system reported to Houston Health Department (HHD) from October 2015 to July 2016. Descriptive analysis was performed to examine demographic and clinical characteristics across different age groups, gender and race/ethnicity. HHD has received a total of 463 CRE cases during the time period, out of which 72 were non-reportable and did not meet the case criteria, 187 were out of jurisdiction. The remaining 204 cases were included in this study.

Results Out of a total of 204 cases, males and females were represented equally (50% each). The mean age of the cases was 67 years (age ranges from 22-98). Majority of the cases were in the older age group, 70 years and above 53 (26%), followed by 48 (24%) in age group 80 and above years. Among the different race/ethnic groups, African-Americans comprised of 82 (40%), followed by Whites 67 (33%) and Hispanics 33 (16%). Out of 204 cases, 156 (76%) were hospitalized, which included acute care hospital, long-term acute care or nursing home. Out of 156 hospitalized cases, 71 (34%) were in Intensive Care Unit (ICU) and 136 (67%) had an invasive indwelling device. Of all the cases, 80% had CRE-Klebsiella pneumoniae, followed by 11% who had CRE-E. coli. The cases were distributed evenly across the city when plotted on ArcGIS with their residential addresses.

Conclusions CRE cases are found to be more common among older age groups, African American population and in hospitalized patients. CRE can be a ground for increasing infectious diseases in the community and one of the reason may be unnecessary use of antimicrobial agents. This study provides a glimpse into the number of CRE cases reported in Houston since CREs are classified a separate disease in Texas. Further studies are needed to explore the occurrence of anti-microbial drug resistance among the specific population groups and how the case investigation efforts can be targeted to enhance prevention.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the planning strategies and lessons learned by the Virginia Department of Health (VDH) when conducting enhanced surveillance during mass gathering events and coordinating with healthcare entities to distinguish event-related emergency department (ED) visits from community-related ED visits. Introduction Mass gatherings can result in morbidity and mortality from communicable and non-communicable diseases, injury, and bioterrorism. Therefore, it is important to identify event-related visits as opposed to community-related visits when conducting public health surveillance. Previous mass gatherings in Virginia have demonstrated the importance of implementing enhanced surveillance to facilitate early detection of public health issues to allow for timely response. Methods Between June 2015 and September 2015, VDH coordinated with two healthcare entities representing six acute care hospitals to conduct enhanced surveillance for the 2015 World Police and Fire Games and 2015 Union Cycliste Internationale (UCI) Road World Championships. VDH established initial communication with each healthcare entity between 1 week to 2 months before the event start date to discuss functional requirements with technical, informatics, and clinical staff. Requirements included: 1) healthcare entity identifying gathering attendees during the ED registration, 2) capturing a standardized mass gathering indicator within the patient’s electronic health record (EHR), and 3) transmitting the gathering indicator to VDH through existing electronic syndromic surveillance reporting processes. ED visit records with the gathering indicator were analyzed by VDH using the Virginia Electronic Surveillance System for the Notification Community-based Epidemics (ESSENCE) and findings were incorporated in daily VDH situational reports. This same methodology will be applied for the upcoming U.S. Vice Presidential Debate in October 2016. Results The duration of the two gatherings in 2015 ranged from 9 to 10 days and the locations were categorized as urban. The population density of the gathering location ranged from 1,950 to 2,889 population per square mile. The estimated number of attendees ranged from 45,000 to 400,000. Attendees were defined as having attended at least one day of the mass gathering event. The mass gathering indicator captured during the ED registration included the gathering acronym or a gathering specific field with a drop down menu containing true/false options. VDH utilized ESSENCE to identify 42 ED visits (0.5%) with the gathering acronym out of 8,768 total ED visits during the 2015 World Police and Fire Games and 60 ED visits (2.6%) with the gathering specific field out of 2,296 total visits during the 2015 UCI Road World Championships. The results of the U.S. Vice Presidential Debate in October 2016 are pending. Conclusions In 2015, VDH partnered with two healthcare entities to conduct enhanced surveillance during two mass gatherings. Although VDH routinely uses syndromic surveillance data to identify issues of public health concern, it has previously lacked the ability to identify ED visits specific to mass gatherings. Prior to collaboration with VDH, the healthcare entities did not capture gathering-specific ED visits using their EHR systems. The two healthcare entities successfully modified their business procedures and EHR system to capture and transmit a gathering indicator for ED visits despite some challenges. These challenges include constraints with customization of the EHR and syndromic surveillance systems, lack of standardized training among ED registration staff for interpreting and applying the gathering indicator, and limited functionality testing prior to the event. Lessons learned from this coordinated effort are to: 1) initiate the planning phase and identification of requirements as early as possible to ensure they are well defined and understandable, 2) implement frequent communications with the healthcare entity, and 3) customize requirements for the specific gathering as much as possible while balancing the burden and benefit to public health and the healthcare entity. The coordinated enhanced surveillance efforts provided both VDH and the healthcare entities with improved situational awareness and capacity building during mass gathering events. The strategies and lessons learned from these two events will be applied to improve enhanced surveillance of public health issues during future mass gatherings, including the U.S. Vice Presidential Debate in October 2016.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To assess the correlations between weekly rates of elementary school absenteeism due to illness (SAi) and percent positivity for influenza A from laboratory testing (PPFluA) when conducted at a city level from September to December over multiple years.

Introduction Rates of student absenteeism in schools have been mainly used to detect outbreaks in schools and prompt public health action to stop local transmission. A report by Mogto et al. stated that aggregated counts of school absenteeism (SAi) were correlated with PPFluA, but the sample may have been biased. The purpose of this study was to reassess the correlation between aggregated rates of SAi and PPFluA for two cities, Calgary and Edmonton, in Alberta. In such situations, SAi could potentially be used as a proxy for PPFluA when there are not enough samples for stable laboratory estimates.

Methods The Alberta Real-Time Syndromic Surveillance Net (ARTSSN) collects elementary SA data from the two major school boards in two cities in Alberta with populations >800,000. Since reasons for SA are stated, rates of SAi can be calculated. Data were obtained for three years, 2012 to 2014, for each city. Laboratory data on tests of respiratory agents using a standardized protocol were obtained from Alberta’s Provincial Laboratory for Public Health for the same time period and locations. The dates of the specimens being received by the laboratory were used in this analysis. For each data source, the relative proportions (SAi and PPFluA) were calculated. Data for the first week of school in September and for the last two weeks of December were removed for each year due to the SAi rates being unstable. Linear regression models were constructed, with rates of SAi predicted by PPFluA. Separate models were run for each city and for each year, resulting in a total of 6 models. Percent positivity for entero-rhinoviruses (PPERV) was added to see if it improved the model. The regression models were created using Excel and checked in the statistical programs, SAS and R. An analysis to assess the influence of a lag period was assessed using R. Results For each city, the provincial lab tested between 4,000 and 6,000 specimens each fall and SAi rates were based on denominators of between 20,000 and 36,000 children. The R2, betas, and p-values for all 6 regression models are shown in Table 1. The minimum correlation value was 0.693 and the maximum was 0.935. Due to the strong negative correlations between PPERV and PPFluA, PPERV was not retained in the models. Looking at the lag periods, the maximum correlations occurred at a zero week lag in two years (2012 and 2014) and at a -1 week lag in 2013. The two years with a zero lag were both dominated by a H3N2 strain while the year with mainly a H1N1 strain showed a lag of -1. Only one year of H1N1 data was available for analysis.

Conclusions We observed strong correlations between the weekly rates of elementary SAi and PPFluA at the city level over three years, from September to December. The reasons for the difference in lag times between the H1N1 and H3N2 seasons are being investigated.
Abstract

Objective

We describe surveillance for Dengue virus (DENV), Chikungunya virus (CHIKV) and Zika virus (ZIKV) in VA Caribbean Healthcare System (VACHS) from the start of ZIKV transmission in Puerto Rico. Introduction

DENV, CHIKV and ZIKV are all transmitted by mosquitoes and have occurred in outbreaks in the Caribbean. Common symptoms (which can be severe and disabling) are similar among the 3 viruses and include fever, joint pain/swelling, headache, muscle pain and rash. In December 2015, the first endemic case of ZIKV infection was reported by VACHS. Since that time, an increasing number of ZIKV infections have been reported in Puerto Rico. Due to the growing ZIKV outbreak, we performed ongoing testing and surveillance.

Methods

DENV, CHIKV and ZIKV infection surveillance from November 2015 - August 2016 at VACHS was performed from 2 primary data sources: (1) VA Praedico TMPublic Health Surveillance System for laboratory results documented within the electronic medical record (EMR) and (2) communications with facility clinicians for laboratory results not entered into the EMR. Laboratory tests were considered unique tests if they were performed &gt;30 days apart. A positive test was defined as a positive IgM or RT-PCR test result. Serial infection was defined as infection with CHIKV and ZIKV or CHIKV and DENV. Potential cross-reaction of assays was defined as positive DENV and ZIKV IgM results within 30 days. Demographic and clinical data was obtained on all positive ZIKV cases including cases with serial infection.

Results

For the time period evaluated, 2,218 unique tests were performed for DENV (744), CHIKV (741), and ZIKV (744). Five hundred thirty-three positive tests were identified for: DENV (34), CHIKV (55) and ZIKV (444) (Figure 1). Demographic and virus breakdown of testing is shown in Table 1. Percent positive range for DENV testing was 0-23%, for CHIKV was 0-14%, and for ZIKV 0-73%. Temporal timing of positive tests for each virus by percent positive is depicted in Figure 2. Serial infections were identified in 39 patients (1 CHIKV IgM/ZIKV IgM/PCR+, 7 CHIKV IgM/ZIKV IgM+, 26 CHIKV IgM/ZIKV PCR+, 2 CHIKV IgM/ZIKV PCR/DENV IgM+, 2 DENV IgM/CHIKV IgM+, 1 DENV IgM/CHIKV IgM/ZIKV IgM+). The average age of patients with serial infection was 63.5 years (range 33-85) and occurred in 4 females and 35 males. 21 patients were identified with positive DENV and ZIKV IgM tests, which could represent cross-reactivity between the assays or co-infection. Confirmatory testing of these specimens is pending. Conclusions

Laboratory surveillance demonstrated co-circulation of all 3 viruses, although ZIKV was the dominant infection identified during this time period. In addition, laboratory data suggests serial infection with CHIKV and ZIKV while also identifying patients with probable cross-reaction between DENV and ZIKV tests. Additional investigation is needed to determine whether patients with serial infection have increased severity of symptoms or different clinical outcomes. Since number of ZIKV infections continues to increase and all 3 viruses continue to circulate, continued public health messaging remains important. Figure 1 Table 1: VA Caribbean Healthcare System Dengue Virus (DENV), Chikungunya Virus (CHIKV) and Zika Virus (ZIKV) Demographics and Testing, Nov. 2015-Aug. 2016.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

A test kit for the detection of antibodies to Newcastle disease virus (NDV) based on haemagglutination inhibition (HI) assay has been developed and introduced into practice for the first time in Ukraine. Introduction

Newcastle disease (ND) is the most important infectious viral disease of poultry. The world-wide economic loss from it is 2-3 billion USD per year. ND is reportable to the World Organization for Animal Health (OIE). ND is caused by virulent strains of avian Paramyxoviruses belonging to type 1. Industrial poultry farming is rapidly developing in Ukraine. Ornithological fauna of Ukraine includes about four hundred species of birds, 207 of which nest within its borders. The territory of Ukraine transits 3 out of 14 transcontinental global migration flows. The wild birds are the main natural reservoir of ND agents. It is necessary to control the intensity of post-vaccination immunity in poultry and the timing of revaccinations. OIE recommends enzyme linked immunosorbent assays (ELISA) and HI test for these purposes [1]. However, it should be noted that HI test, possessing high specificity and sensitivity, is much cheaper. Therefore, it is the excellent means for ND timely surveillance.

Methods

During the development of a new diagnostic kit, we used the reference strain “La-Sota”, which was obtained from the National Center of Microorganism Strains of Ukraine. We have produced haemagglutinating antigen using embryonated SPF fowl eggs and 10-11 day incubation. A dilution of the virus was inoculated into 0.1 ml volumes into the allantoic cavity and incubated at 35-37°C for 80-96 hours. For the purpose of NDV inactivation, we used aminoethyleneimine at the final concentration of 0.1%. Positive serum was prepared by immunizing 60-day-old chickens with live virus once and inactivated virus twice with an interval of 2 weeks. Negative serum was obtained from healthy birds that did not contain antibodies to NDV. The investigated blood sera were inactivated by heating (56°C/30 minutes). Samples of 1% suspension of chicken erythrocytes in phosphate buffered saline (pH 7.0-7.1) were used in HI tests.

Results

The specific haemagglutination activity of the obtained antigen amounted to 10-11 log2. The test was performed using the 4 HA unit of the antigen. Positive control serum activity was in the range of 7-9 log2. Negative control serum did not give results of more than 2 log2. The estimation of the quality indexes of the components of the diagnostic test-kit was performed using harmonized methods. In order to examine specificity and sensitivity of HI test kits, antigens and sera from commercial diagnostic kits were used. Also, certified negative control serum and samples of International Standard sera were used, which were obtained from reference laboratories, namely against the following pathogens: Avian Influenza A (H5), Avian Influenza A (H7), Egg Drop Syndrome Virus, Paramyxoviruses of 2 and 3 serotypes, Reovirus, Avian Infectious Laryngotracheitis, Avian Infectious Bronchitis Virus, Mycoplasma gallisepticum, and NDV. In order to ensure a high degree of specificity for the antigen, special attention was given to the selection of a stabilizer for freeze-drying (the subject of a patent).

Comparison between the national diagnostic test kit for HI and commercial ELISA kit (IDEXX) in the evaluation of humoral immune response to ND in vaccinated chickens was investigated by examining of serum samples (n=152). Statistical analysis of data showed that the correlation coefficient for the results of both tests was 0.92. The relative sensitivity of HI test kit was 93.5% and the relative specificity - 91.5%. The developed test kit was successfully used for the examination of field samples. We developed regulatory documents, completed the procedure of validation and registration in Ukraine of the commercial HI test kit for the detection of antibodies to NDV.

Conclusions

The use of the national standardized diagnostic test kit based on HI for detection of antibodies to NDV allows assessing the post-vaccination antibodies level that helps to maintain the disease-free status of the Ukrainian poultry industry with regard to ND.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective This surveillance project aims to increase and broaden coverage of *Aedes* spp. ovitrap locations in Arizona’s U.S.-Mexico border region through interagency collaboration. Introduction As part of a statewide effort to enhance surveillance for *Aedes* spp. mosquitoes (1,2) the Office of Border Health (OBH) took the lead in improving technical assistance on surveillance in counties bordering Mexico. In 2016, OBH sought ways to enhance surveillance in a wider geographic area. Trap locations closer to the border were established a priority, given high amounts of traffic across the international line, high border *Aedes* mosquito activity, and native cases of dengue reported at the border in Mexico. Methods The Arizona Office of Border Health partnered with U.S. Customs and Border Protection to select possible locations for ovitrapning near the border. Border Patrol Health and Safety Tucson coordination accompanied OBH and preparedness staff on three occasions to scout areas around pre-selected border patrol facilities. County, and border patrol staff contributed to trap maintenance. BIDS provided technical assistance to identify positive traps, collected data for reporting to the state, and collaborated with experts at the University of Arizona entomology department to verify results and identify *Aedes* spp. Results Out of 15 border patrol stations within border lands in Santa Cruz County, and Cochise County, OBH epidemiologist considered 10 viable trapping sites. Two facilities were eventually eliminated because of logistical challenges. OBH visited eight facilities and selected five locations within five miles of the U.S.-Mexico border and two located less than 30 miles from the border. OBH epidemiologists inspected sites for potential mosquito habitat and set ovitraps low to the ground in areas protected from rain. Some facilities had areas of standing water discovered in unused tires, truck-washing stations, heavy-lifting equipment, and natural washes. Border Patrol staff complained of mosquito activity around some of the stations. After inspection OBH set an average of three traps at each site. One site had evidence of mosquito larvae activity. Conclusions Border patrol facilities offer ideal trap locations given their proximity to the international line. Secure facilities offer extraprotection for traps against tampering. The partnership across local, state, tribal, and federal lines allowed Arizona Office of Border Health to expand surveillance locations, allowing two jurisdictions to set first *Aedes*-specific traps since Arizona began the 2016 campaign, “Fight the Bite.”

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Abstract

Objective To determine avian influenza A(H5N6) virus infection in human and environment using extensive surveillances. To evaluate the prevalence of H5N6 infection among high risk population. Introduction Since the emergence of avian influenza A(H7N9) virus in 2013, extensive surveillances have been established to monitor the human infection and environmental contamination with avian influenza virus in southern China. At the end of 2015, human infection with influenza A(H5N6) virus was identified in Shenzhen for the first time through these surveillances. These surveillances include severe pneumonia screening, influenza like illness (ILI) surveillance, follow-up on close contact of the confirmed case, serological survey among poultry workers, environment surveillance in poultry market. Methods Severe pneumonia screening was carried out in all hospitals of Shenzhen. When a patient with severe pneumonia is suspected for infection with avian influenza virus, after consultation with at least two senior respiratory physicians from the designated expert panel receiving their approval, the patient will be reported to local CDC. Nasal and pharyngeal swabs will be collected and sent for detection of H5N6 virus by RT-PCR.ILI surveillance was conducted in 11 sentinel hospitals, 5-20 ILI cases were sampled for detection of seasonal influenza virus by RT-PCR test every week for one sentinel. If swab sample is tested positive for influenza type A and negative for subtypes of seasonal A(H3N2) and A(H1N1), it will be detected further for influenza A(H5N6) virus. Follow-up on close contacts was immediately carried out when human case of infection with H5N6 was identified. All of close contacts were requested to report any signs and symptoms of acute respiratory illness for 10 days, nasal and pharyngeal swabs were collected and tested for influenza A(H5N6) virus by RT-PCR test. The meantime, environmental samples were collected in the market which was epidemiologically associated with patient and tested for H5N6 virus by RT-PCR test. Serological survey among poultry workers was conducted in 11 districts of Shenzhen. Poultry workers were recruited in poultry markets and screened for any signs and symptoms of acute respiratory illness, blood samples were collected to detect haemagglutination-inhibition (HI) antibody for influenza A(H5N6) virus. Environment surveillance was conducted twice a month in 11 districts of Shenzhen. For each district, 10 swab samples were collected at a time. All environmental samples were tested for influenza A(H5N6) virus by RT-PCR test. Results From Nov 1, 2015 to May 31, 2016, 50 patients with severe pneumonia were reported and detected for H5N6 virus, three patients were confirmed to be infected with H5N6 virus. Case 1 was a 26 years old woman and identified on Dec 29, 2015. She purchased a duck at a poultry stall of nearby market, cooked and ate the duck 4 days before symptom onset. After admission to hospital on Dec 27, her condition deteriorated rapidly, on Dec 30 she died. The case 2 was an 82 years old man and confirmed on Jan 7, 2016. He visited a market everyday and had no close contact with poultry, except for passing by live poultry stalls. He recovered and was discharged from hospital on Jan 22. The case 3 was a 31 years old woman and reported on Jun 16, 2016, she had no contact with live poultry and died on Feb 8. For 60 close contacts of three cases, none of them reported signs or symptoms of acute respiratory illness, all of nasal and pharyngeal swabs were tested negative for influenza A(H5N6) virus by RT-PCR test. Of 146 environmental swabs collected in the case’s living places and relevant poultry markets, 38 were tested positive for influenza A(H5N6) virus by RT-PCR test. Results From Nov 1, 2015 to May 31, 2016, 2812 ILI cases were sampled and tested for influenza type A and subtypes of seasonal influenza. Those samples tested positive for influenza type A could be further subtype to seasonal A(H3N2) or A(H1N1), therefore no sample from ILI case was tested for influenza A(H5N6) virus. Serological surveys among poultry workers were conducted twice, for the first survey 186 poultry workers were recruited in Oct 2015, for the second survey 195 poultry workers were recruited in Jan 2016. Blood sample were collected and tested for HI antibody of influenza A(H5N6) virus. 2 individuals had H5N6 HI antibody titer of 1:40, 5 individuals had H5N6 HI antibody titer of 1:20, rest of them had H5N6 HI antibody titer of &lt;1:20. According to the WHO guideline, HI antibody titer of ≥1:160 against avian influenza virus were considered positive. From Nov 1, 2015 to May 31, 2016, of 1234 environmental swabs collected in poultry markets, 339 (27.5%) were tested positive for influenza A(H5N6) virus by RT-PCR test. Each of the ten districts had poultry markets which was contaminated by influenza A(H5N6) virus. Conclusions In 2015-2016 winter, three cases of infection with influenza A(H5N6) virus were identified in Shenzhen, all of them were young individuals with average age of 27.3 years and developed severe pneumonia soon after illness onset, two cases died. For acute and severe disease, early detection and treatment is the key measure for patient’s prognosis. H5N6 virus was identified in poultry market and other places where patient appeared, implying poultry market probably was the source of infection. Despite the high contamination rate of H5N6 virus in poultry market, we found that the infection with H5N6 virus among poultry workers was not prevalent, with infection rate being 0/381. Human infection with H5N6 virus seemed to be a sporadic occurrence, poultry-human transmission of H5N6 virus might not be very effective.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
To address the limitations of traditional static surveillancereporting by developing in-house infrastructure to create and maintaininteractive surveillance dashboards.

Introduction
Traditionally, public health surveillance departments collect, analyze, interpret, and package information into static surveillancereports for distribution to stakeholders. This resource-intensive production and dissemination process has major shortcomings that impede end users from optimally utilizing this information for public health action. Often, by the time traditional reports are ready for dissemination they are outdated. Information can be difficult to find long static reports and there is no capability to interact with the data by users. Instead, ad hoc data requests are made, resulting in inefficiencies and delays. Use of electronic dashboards for surveillance reporting is not new. Many public health departments have worked with information technology (IT) contractors to develop such technically sophisticated products requiring IT expertise. The technology and tools now exist to equip the public health workforce to develop in-house surveillancedashboards, which allow for unprecedented speed, flexibility, and cost savings while meeting the needs of stakeholders. At Alberta Health Services (AHS), in-house, end-to-end dashboard development infrastructure has been established that provides epidemiologists and data analysts full capabilities for effective and timely reporting of surveillance information.

Methods
An internal assessment of the available resources and infrastructure within AHS was conducted to iteratively develop a new analytics model that provides a foundation for in-house dashboard development capacity. We acquired SAS® and Tableau® software and conducted internal training for skills development and to transition staff to the new model. This model is highlighted below using our respiratory virus surveillance (RVS) dashboard as an example. For the RVS dashboard, stakeholder engagements were conducted to understand the end users’ needs. Next, data access was improved, where possible, by securing direct access to source data (e.g. emergency department visits for influenza like illness (ILI), Health Link calls, hospital admissions, etc.) on existing database servers. SAS® code was written for routinely connecting with multiple data sources, data management and analysis, data quality assurance, and posting summary data on a secure Oracle® server. The Tableau® dashboard development application was then used to connect to the summary data on the Oracle® server, create the interactive dashboards and publish the final products to the AHS Tableau server environment. Key users were consulted in the iterative development of the interface to optimize usability and relevant content. Finally, the product was promoted to stakeholders with a commitment to use their feedback to drive continuous improvement.

Results
In-house generated surveillance dashboards provide more timely access to comprehensive surveillance information for a broad audience of over 108,000 AHS employees; within as little as 3 hours of all data being available. They facilitate user-directed deep dives into the data to understand a more complete surveillance picture as well as stimulating hypothesis generation. Additionally they enhance productivity of personnel, by significantly reducing response times for ad hoc request and to generate reports, freeing up more time to respond to other emerging public health issues. Looking specifically at the RVS dashboard, its ability to bring all relevant surveillance information to one place facilitates valuable discussions during status update meetings throughout the influenza season. Among other things it has allowed Medical Officers of Health, emergency department staff, epidemiologists and others to make informed decisions pertaining to public messaging, the need for reallocating resources, such as staffing and handling the burden of ILI patients, as well as determining the necessity of opening influenza assessment centers.

Conclusions
Surveillance dashboards can facilitate public health action by assembling comprehensive information in one place in a timely manner so that informed decisions can be made in emerging situations.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the Georgia Department of Public Health’s (DPH) mosquito surveillance capacity before and after Zika virus was declared a public health emergency, review and compare mosquito surveillance results from 2015 to 2016, and evaluate the risk of autochthonous vector transmission of Zika virus based on 2016 surveillance data of Aedes aegypti and Aedes albopictus mosquitoes. Introduction Zika virus was declared an international public health emergency by the World Health Organization on February 1, 2016. With Georgia hosting the world’s busiest international airport and a sub-tropical climate that can support the primary Zika virus vector, Aedes aegypti, and secondary vector, Aedes albopictus, the CDC designated Georgia as a high risk state for vector transmission. Faced with a lack of mosquito surveillance data to evaluate risk of autochthonous transmission and a few counties statewide that provide comprehensive mosquito control, the DPH rapidly scaled up a response. DPH updated existing mosquito surveillance and response plans targeted for West Nile Virus (WNV) and expanded capacity to areas that lacked previous surveillance targeting the Zika virus vector. Methods Mosquito surveillance data provided by DPH was analyzed for years 2015 and 2016 to date. The geographical distribution of counties conducting surveillance, total number and percentage by mosquito species collected in 2015 were compared to 2016 data. The distribution of counties conducting surveillance was mapped using ArcMap 10.4.1 for pre and post Zika response. Autochthonous vector transmission risk was evaluated based on the overall numbers and percentages of Aedes aegypti and Aedes albopictus mosquitoes collected for 2016. Results In 2015, Georgia had 14 counties conducting mosquito surveillance, with a DPH entomologist providing direct surveillance in 4 of these counties. In 2016, DPH expanded surveillance capacity to 34 counties, a 142% increase, geographically dispersed across the State in urban and rural areas. A total of 76,052 mosquitoes were trapped and identified in 2015 compared to 91,261 mosquitoes trapped in 2016, representing a 20% increase. A total of 37 mosquito species were identified in both years with Culex quinquefasciatus, Georgia’s primary WNV vector, representing the highest percentage (2015-79.45% and 2016-70.41%) of mosquitoes trapped overall. In addition, Aedes aegypti represented only 0.108% and 0.007% of the total mosquitoes trapped respectively each year and was found in one county. Aedes albopictus represented only 1.50% and 1.82% of the total mosquitoes trapped respectively each year and was found in one county. Conclusions DPH was able to rapidly expand its surveillance capacity statewide by maximizing existing grant funds to hire new surveillance staff, while also collaborating with academic institutions, military bases, Georgia Mosquito Control Association, and local health departments to provide training and funding for surveillance and data sharing. This expanded surveillance network provided a clearer picture of the types of mosquitoes potentially exposing the public to mosquito-borne disease risks. Historical data for the primary vector of Zika virus, Aedes aegypti, has been isolated to just two counties in Georgia. Expanded surveillance in 2016 confirmed a lower abundance of Aedes aegypti, suggesting the primary vector for Zika has been displaced by Aedes albopictus. This may suggest a reduced risk of autochthonous transmission of Zika virus in Georgia due to Aedes albopictus’ affinity for feeding on both humans and animals. This should be interpreted with caution due to limitations in the data related to standardized reporting techniques for each county. DPH is working with all counties to improve the quality of data collected and reported and continues to educate the public on ways they can reduce their individual risk of mosquito bites, which in turn reduces the risk of other mosquito-borne diseases such as WNV. In conclusion, DPH’s response to Zika virus allowed it to rapidly increase its surveillance footprint and with new data, make sound public health decisions regarding mosquito-borne disease risks.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective This session will explore the role of the Houston Health Department (HHD) in the City of Houston’s response to the threat of Zika. The panelists will provide perspective from the roles of Bureau Chief, informatician, and epidemiologist and provide insight into lessons learned and strategic successes.

Introduction Zika virus spread quickly through South and Central America in 2015. The City of Houston saw its first travel-related Zika cases in December of 2015. On January 29th, the City held the first planning meeting with regional partners from healthcare, blood banks, petrochemical companies, mosquito control, and others. Additionally, the City activated Incident Command Structure (ICS) and designated the Public Health Authority as the Incident Commander.

Initial steps taken by HHD included expanding the capability and capacity of the public health laboratory to test for Zika virus; expand surveillance efforts; created an educational campaign around the “3Ds” of Zika defense (Drain, Dress, DEET) which were then disseminated through several means, including a mass mailing with water bills; and provided DEET to mothers through the WIC program. The Houston Health Department took the lead in authoring the City’s Zika Action Plan. In this 3 goals and 6 strategies were identified. Goals included 1) Keep Houstonians and visitors aware of the threat of Zika; 2) minimize the spread of the virus; and 3) protect pregnant women from the virus. The 6 strategies employed were to A) develop preparedness plans; B) implement ICS within the City; C) ensure situational awareness through surveillance; D) Increase community awareness; E) reduce opportunities for Zika mosquito breeding grounds; and F) provide direct intervention to reduce the threat of Zika. HHD was responsible for many of the action items within the plan. We conducted several community outreach events, where we disseminated educational materials, t-shirts, DEET, and other give-aways. These events allowed frequent engagement with the public for bidirectional communication on how to approach the threat.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Introduction

The ICD-9 codes for acute respiratory illness (ARI) and pneumonia/influenza (P&I) are commonly used in ARI surveillance; however, few studies evaluate the accuracy of these codes or the importance of ICD-9 position. We reviewed ICD-9 codes reported among patients identified through severe acute respiratory infection (SARI) surveillance to compare medical record documentation with medical coding and evaluated ICD-9 codes assigned to patients within influenza detections.

Methods

The Minnesota Department of Health (MDH) conducted SARI surveillance at three hospitals. All hospitalized patients with submission of a physician-ordered upper respiratory specimen (e.g., sputum, throat or nasopharyngeal swabs) were enrolled. A medical chart review was conducted to identify those meeting SARI criteria, defined as patients admitted to an inpatient ward with new onset of respiratory symptoms or acute exacerbation of chronic respiratory conditions. Enrolled patients who did not meet the SARI criteria were categorized as non-SARI. Residual material from the upper respiratory specimens were submitted to MDH for influenza testing by RT-PCR. Demographic and clinical data, including up to eight ICD-9 codes, were collected through the medical record review. Patients with an ICD-9 code indicating ARI (460 to 466) or P&I (480 to 488) were defined as having an ARI/P&I code. We compared the frequency of ARI/P&I codes by SARI clinical criteria and influenza detection and evaluated the position of the reported ARI/P&I code.

Results

From May 2013 through August 2015, we enrolled 5,950 patients, of which 4,449 (75%) met SARI criteria and 1,501 did not (non-SARI). An ARI/P&I code in any position was found in 61% (2,705) of SARI vs. 16% (241) of non-SARI patients (odds ratio [OR] 8.1, 95% confidence interval [CI] 7.0-9.4); an ARI/P&I code in the first position was found in 40% of SARI vs. 7% of non-SARI patients (OR = 8.6, 95% CI 7.0-10.5). Among SARI patients with at least one ARI/P&I code, 66% had their first or only ARI/P&I code in the 1st position, 25% in the 2nd position, and 6% in the 3rd position. For identification of SARI, sensitivity/specificity was 61%/84% for ARI/P&I codes in any position and 40%/93% for ARI/P&I codes in the 1st position. Among SARI patients, codes for pneumonia (486) and acute bronchiolitis (466.11, 466.19) were commonly reported. The most frequent codes among SARI patients without an ARI/P&I code were fever (780.6), acute respiratory failure (518.81), and asthma (493.92) (Table). Influenza was detected among 8% (351) of SARI patients. An ARI/P&I code in any position was more common in influenza-positive vs. influenza-negative SARI patients (77% vs 59%, OR 2.4, 95% CI 1.8-3.1). An ARI/P&I code in the 1st position was slightly more common in influenza-positive vs. -negative patients though not significant (44% vs 40%).

Conclusions

Among patients from whom a respiratory specimen was collected, administrative data identified those meeting SARI with moderate sensitivity and high specificity, and with lower sensitivity but greater specificity when limited to the 1st ICD-9 position. Pneumonia and acute bronchiolitis ICD-9 codes were frequent ARI/P&I codes among SARI patients. Further investigation is needed to determine the value of including additional ICD-9 codes, such as respiratory distress and acute asthma exacerbation, in identifying SARI.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
This study assessed the transmission of low pathogenic avian influenza in live poultry market setting, using paired fecal and drinking water samples from a longitudinal surveillance program. The relative contribution of transmission via direct fecal-oral route versus drinking water will be determined.

Introduction
Live poultry markets (LPMs) continue to operate in many Asian countries. Low pathogenic avian influenza (LPAI) viruses are often endemic in the poultry, and LPM presents the opportunity for human-poultry interactions and potential human infections with avian influenza viruses. As a series of interventions to control avian influenza transmission in Hong Kong LPMs, local health authority implemented market rest days once every month since mid-2001, and an additional rest day every month since 2003, during which all unsold poultry were slaughtered and the stalls cleaned and disinfected. Rest days were found to effectively reduce avian influenza A(H9N2) isolation rate to baseline level for a few days following the rest days. However, H9N2 isolation rate was still observed to be increasing between therest days, indicating the existence of efficient transmission in spite of rapid turnover of poultry. In LPMs, poultry are usually stored in cages where drinking water is shared among poultry. This is analogous to environmental contamination in the wild, but transmissibility may even be higher due to the dense environment. The use of drinking water for avian influenza surveillance in LPM setting was suggested to be more sensitive than fecal samples (1). However, the relative contribution of direct fecal-oral versus water transmission routes in the LPM setting was not yet understood. This study aimed to determine their role, which will have implications in the control of avian influenza transmission.

Methods
We analyzed 7,321 paired fecal and drinking water samples from a longitudinal surveillance programme during the period with 2 monthly rest days in the LPMs. Samples were collected from chicken cages and subsequently cultured. Positive isolates were subtyped by hemagglutination-inhibition tests and neuraminidase inhibition test. Data were aggregated by sampling occasion and days after the rest days. A compartmental transmission model which incorporated turnover and overnight stay of poultry, virus contamination and decay in drinking water was fitted to the data (Figure 1). A 12-hour trading day was assumed. Based on the parameterized model, we simulated the scenario that water transmission was prohibited to assess the role of transmission via drinking water.

Results
H9N2 isolation rates ranged from 0-25% for fecal samples and 0-56% for drinking water samples. A clear increasing trend can be seen over days after the rest days (Figure 2). The estimated parameter for water transmission is higher than the parameter for direct fecal-oral transmission. Simulation results show that transmission via drinking water plays a major role in the amplification of LPAI in the LPM setting (Figure 2).

Conclusions
Our study showed that drinking water has a major role in the transmission and amplification of LPAI H9N2 in LPMs, compared to direct fecal-oral transmission route. Given the relatively low prevalence of H9N2 in chicken, direct transmission is governed by chance events, while chickens are consistently exposed to viruses in drinking water if contaminated. Drinking water could be targeted for intervention to control LPAI transmission in LPM. The use of drinking fountain or frequent disinfection of drinking water may be considered. Avian influenza viruses (e.g. H5N1) may differ in their pattern of virus shedding via oral versus fecal routes and thus extrapolation of these results to other viruses needs to be done with caution. However, H7N9 viruses are similar to H9N2 viruses by being shed primarily via the respiratory/oral route (2) and it is reasonable to assume that these conclusions would apply to H7N9 virus which is of major public health concern. However, our model could not differentiate the effect of direct fecal-oral transmission through contamination of drinking water by droppings versus contamination through drinking.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To study the immune response in chicken on the administration of LPAIV isolated from the natural reservoir. Influenza is a serious problem for the health of people, animals and birds. Therefore, comprehensive study of influenza virus, its natural reservoir, pathogenesis and immune response will provide further opportunity to ensure protection for animals, birds and people from this infection.

Methods Four-week-old commercial chickens were intranasally inoculated with a H4N6 LPAIV A/Garganey/Chervonooskillske/4-11/2009 (H4N6), isolated from the cloacal swab of clinically healthy garganey in 2009 in Ukraine. Cecum, spleen, lung, and trachea samples were collected from infected chickens on 1 - 14 dpi and examined by immunohistochemical and virology techniques. On these days we collected blood samples for serological analysis. Detection of antibodies to avian influenza virus subtype H4 was performed with chicken serum samples by HI test and ELISA. The studies were done according to IACUC.

Results Upon intravenous and intranasal infection with this virus (A/Garganey/Chervonooskillske/4-11/2009), no clinical signs were observed in chickens and no pathological changes were found at necropsy. Infection of poultry with this virus provoked an antibody response at 10 days after intranasal inoculation which ranged from 1:8 to 1:32 serum antibody titers. Only 2 of 5 chickens were positive for the HI test and 3 of 5 were positive by ELISA at intranasal inoculation. All 10 chickens were positive both by HI test and by ELISA after intravenous inoculation. Specific antibodies (HI test) to influenza virus H4 were detected in titer ranges of 1:128 to 1:1024. In immunohistological studies, the respiratory tract organs (lungs and trachea) showed higher level of humoral immunity (IgM, IgG, IgA-expressing cells) in the lung compared to the trachea. Also, indicators of cell mediated immunity as measured by the CD4 and macrophage markers were higher in LPAIV-infected chickens in the lungs at 14 days post infection compared to uninfected chickens. Lymphocytes expressing CD8 were increased starting 7 dpi. The chickens in the infected group showed 2 times higher levels of CD8 cells compared to the control chickens. IFN-γ transcripts were observed in the AI-infected chickens starting at 7 dpi that coincides with the increasing level of CD4 cells. The number of lymphocytes which secrete IL-2 and IL-15 in AI-infected chickens were in general 1.5 to 2 times higher compared to the uninfected chickens. In AI-infected chickens, the level of cells expressing IFN-γ, IL-2, and IL-15 increased at 7 days after infection. The peak time coincided with a period of increasing CD8 cells. However, there was no significant difference in these cytokine levels between the AI-infected and uninfected groups. In the cecum, lower levels of CD4 cells were seen on 5 dpi but levels slowly increased from 7 dpi to 14 dpi following AIV infection. In the ceca, a significant increase in the number of cells expressing IgM and IgG was found. LPAIV infection induced an increase in macrophages and lymphocytes expressing CD4 and CD8 in the spleen throughout the period examined in this study indicating their role in host response to viral infection. The levels of macrophages in chickens of AI-infected group were 2 times higher than the control after 1 dpi. Conclusions Although infection with a LPAIV did not cause obvious clinical disease, viral replication was detected in the trachea and spleen and both local and systemic cellular and humoral immune responses were elicited in these LPAIV-infected chickens. Our results indicate the potential possibility for infection of poultry with viruses isolated from wild birds. But currently it is not completely known why some viruses from wild birds can cause infection in poultry, while others cannot. Further study of the immune response will enable us to determine the features of the pathogenesis of low pathogenic avian influenza.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Improve disease reporting and outbreak management. Introduction Specific communicable diseases have to be reported by law within a specific time period. In Ohio, prior to 2001, most of these disease reports were on paper reports that were reported from providers to local health departments. In turn the Communicable Disease Nurse mailed the hardcopies to the Ohio Department of Health (ODH). In 2001 the Ohio Disease Reporting System (ODRS) was rolled out to all local public health agencies in Ohio. ODRS is Ohio’s portion of the National Electronic Disease Surveillance System. ODRS should not be confused with syndromic surveillance systems that are for detecting a disease outbreak before the disease itself is detected. Chronic disease surveillance system data has been evaluated for long term trends and potential enhancements. However, the use of communicable disease reports vary greatly. The export data has not routinely been used for quality improvement purposes or the disease reporting process itself. In December 2014, Greene County Public Health (GCPh) began a project to improve reporting of communicable diseases and the response to disease outbreaks. Methods Initial efforts were to understand the current disease reporting process: Quantitative management techniques including creating a logic model and process map of the existing process, brainstorming and ranking of issues. The diseases selected to study included: Campylobacteriosis, Cryptosporidiosis, E. coli O157:H7 & shiga toxin-producing E. coli, Giardiasis, Influenza-associated hospitalization, Legionnaires’ disease, Pertussis, Salmonellosis, and Shigellosis. The next steps included creating a data collection and analysis plan. An updated process map was created and the pre- and post-process maps were compared to identify areas to improve. The median number of days were compared before and after improvements were implemented. Modeling of the impact of the process improvements on the median number of days reported was conducted. Estimation of the impact in healthy number of days derived from the reduction in days to report (if any) were calculated. Results Process improvements identified: Ensure all disease reporters use digital reporting methods preferably starting with electronic laboratory reporting directly to the online disease reporting system, with other methods such as direct web data entry into system, faxing lab reports, secure emailing reports, with no or little hard copy mailing; Centralize incoming email and fax reports (eliminating process steps); Standardize backup staffing procedures for disease reporting staff; Formalize incident command procedures under the authorized person in charge for every incident rather than distribute command between environmental and clinical services; and place communicable disease reporting under that single authority rather than clinical services. The days to report diseases were reduced from a median of 2 to under 0.5 days (p<0.001). All the diseases were improved except for cryptosporidium due to an outlier report two months late. The estimated societal healthy days saved were valued at $52,779 in the first eight months after implementation of the improvements. Conclusions Improvements in disease reporting decreased the reporting time from over 2 days to less than 1 day on average. Estimated societal healthy days saved by this project during the first 9 months was $52,779. Management of early command and control for outbreak response was improved.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: We seek to integrate multiple streams of geo-coded information with the aim to improve public health surveillance accuracy and efficiency. Specifically for vector-borne diseases, knowledge of spatial and temporal patterns of vector distribution can help early prediction of human incidence. To this end, we develop joint modeling approaches to evaluate the contribution of vector or reservoir information on early prediction of human cases. A case study of spatiotemporal modeling of tularemia human incidence and rodent population data from Finnish health care districts during the period 1995-2013 is provided. Results suggest that spatial and temporal information of rodent abundance is useful in predicting human cases.

Introduction: An increasing number of geo-coded information streams are available with possible use in disease surveillance applications. In this setting, multivariate modeling of health and non-health data allows assessment of concurrent patterns among data streams and conditioning on one another. Therefore it is appropriate to consider the analysis of their spatial distributions together. Specifically for vector-borne diseases, knowledge of spatial and temporal patterns of vector distribution could inform incidence in humans. Tularemia is an infectious disease endemic in North America and parts of Europe. In Finland, tularemia is typically mosquito-transmitted with rodents serving as a host; however, a country-wide understanding of the relationship between rodents and the disease in humans is still lacking. We propose a methodology to help understand the association between human tularemia incidence and rodent population levels.

Methods: Data on rodent population levels are collected around the country by the Finnish Natural Resources Institute. Human Tularaemia cases are recorded as laboratory-confirmed and reported to the National Infectious Disease Register (NIDR). Human cases and rodent data were aggregated to match the 20 Finnish health districts over the period 1995-2013 [1]. We develop our methodology in a Bayesian setting. The counts of human cases for each health district in a given year are assumed to follow a Poisson distribution and the rodent data are assumed to have a categorical likelihood. The linear predictors linked to the human and rodent likelihood functions are then decomposed additively into spatial, temporal, and space-time interaction random effects. We then link the two likelihoods via the interaction term by assuming that the human spatiotemporal variation is dependent on the rodent activity with a one-year lag. In the case of the rodent data, we also included two additional spatial and non-spatial contextual terms to better model ecological effects associated with rodent population levels as described before [2]. We then finally develop indicators on the scale 0 to 1, to quantify the association between human incidence and a rodent vector.

Results: Results suggest that spatial and temporal information of rodent abundance is useful in predicting human cases.

Conclusions: Future modeling directions are recommended to include environmental and epidemiological factors. To the best of our knowledge, this is the first time that rodent data, captured for non-health related purposes, is used to better inform the human risk of tularemia in Finland.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Introduction Syndromic surveillance is an alternative type of public health surveillance which utilises pre-diagnostic data sources to detect outbreaks earlier than conventional (laboratory) surveillance and monitor the progression of illnesses in populations. These systems are often noted for their ability to detect a wider range of cases in under-reported illnesses, utilise existing data sources, and alert public health authorities of emerging crises. In addition, they are highly versatile and can be applied to a wide range of illnesses (communicable and non-communicable) and environmental conditions. As a result, their implementation in public health practice is expanding rapidly. This scoping review aimed to identify all existing literature detailing the necessary components in the defining, creating, implementing, and evaluating stages of human infectious disease syndromic surveillance systems.

Methods A full scoping review protocol was developed a priori. The research question posed for the review was “What are the essential elements of a fully functional syndromic surveillance system for human infectious disease?” Five bibliographic databases (Pubmed, Scopus, CINAHL, Web of Science, ProQuest) and eleven websites (Google, Public Health Ontario, Public Health England, Public Health Agency of Canada, Centers for Disease Control and Prevention, European Centre for Disease Prevention and Control, International Society for Disease Surveillance, Syndromic Surveillance Systems in Europe, Eurosurveillance, Kingston Frontenac, Lennox & Addington Public Health (x2)) were searched for peer-reviewed, government, academic, conference, and book literature. A total of 1237 unique citations were identified from this search and uploaded into the scoping review software Covidence. The titles and abstracts were screened for relevance to the subject material, resulting in 142 documents for full-text screening. Following this step, 55 documents remained for data extraction and inclusion in the scoping review. Two independent reviewers conducted each step.

Results The scoping review identified many essential elements in the defining, creating, implementing, and evaluating of syndromic surveillance systems. These included the defining of “syndromic surveillance”, classification of syndromes, data quality and completeness, statistical methods, privacy and confidentiality issues, costs, operational challenges, management composition, collaboration with other public health agencies, and evaluation criteria. Several benefits and limitations of the systems were also identified, when comparing them to other public health surveillance methods. Benefits included the timeliness of analyses and reporting, potential cost savings, complementing traditional surveillance methods, high sensitivity, versatility, ability to perform short- and long-term surveillance, non-specificity of the systems, ability to fill gaps of under-reported illnesses, and the collaborations which are fostered through its platform; limitations included the potential resources and costs required, inability to replace traditional healthcare and surveillance methods, the false alerts which may occur, non-specificity of the systems, poor data quality and completeness, timelags in analyses, limited effectiveness at detecting smaller-scale outbreaks, and privacy issues with accessing data.

Conclusions Over the past decade, syndromic surveillance systems have become an integral part of public health practice internationally. Their ability to monitor a wide variety of illnesses and conditions, detect illnesses earlier than traditional surveillance methods, and be created using existing data sources make them a valuable public health tool. The results from this scoping review demonstrate the benefits and limitations and overall role of the systems in public health practice. In addition, this study also shows that a complete set of key elements are required in order to properly define, create, implement, and evaluate these systems to ensure their effectiveness and performance.


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Abstract

Objective(1) Early detection of Aedes-borne arboviral disease; (2) improved data on Ae. aegypti and Ae. albopictus distribution in the United States (U.S.); and (3) education of clinicians and the public. Introduction Zika, chikungunya, and dengue have surged in the Americas over the past several years and pose serious health threats in regions of the U.S. where Ae. aegypti and Ae. albopictus mosquito vectors occur. Ae. aegypti have been detected up to 6 months of the year or longer in parts of Arizona, Florida, and Texas where mosquito surveillance is regularly conducted. However, many areas in the U.S. lack basic data on vector presence or absence. The Zika, dengue, and chikungunya viruses range in pathogenicity, but all include asymptomatic or mild presentations for which individuals may not seek care. Traditional passive surveillance systems rely on confirmatory laboratory testing and may not detect emergent disease until there is high morbidity in a community or severe disease presentation. Participatory surveillance is an approach to disease detection that allows the public to directly report symptoms electronically and provides rapid visualization of aggregated data to the user and public health agencies. Several such systems have been shown to be sensitive, accurate, and timelier than traditional surveillance. We developed Kidenga, a mobilephone app and participatory surveillance system, to address some of the challenges in early detection of day-biting mosquitoes and Aedes-borne arboviruses and to enhance dissemination of information to at-risk communities. Methods Kidenga sends a weekly push notification prompting users to report symptoms, travel history, and day-biting mosquito activity. If an individual reports through Kidenga that they or a family member have had symptoms consistent with Zika, dengue, or chikungunya, they receive an email with educational information about the diseases, prevention strategies, and treatment/testing information for clinicians. Upon registration, users can opt in to have additional follow-up via email. At any time, users may also view maps of aggregated user reports, confirmed case counts by county from public health partners in pilot areas, Aedes distribution maps, information about prevention and control strategies, and news on the diseases and vectors from a curated newsfeed. Users in select pilot areas may also receive press releases issued by their state or local public health department related to the diseases and their vectors. University of Arizona owns and maintains the app and its data. Local and state health departments that want more detailed information on user symptoms and mosquito activity may request and monitor the data at no cost. A marketing campaign to recruit a broad user base is being implemented in Arizona, Texas, and Florida. Results Kidenga was developed with significant input from public health stakeholders and launched in September 2016, accompanied by English and Spanish radio public service announcements in select Arizona markets, press releases, and a social marketing campaign. A Spanish version of the app is under development. We will describe the results of user registration and survey submissions, challenges identified during development and deployment of this novel surveillance system, plans for data use and evaluation, and collaborations with public health partners. Conclusions The utility of Kidenga as a surveillance system will depend on broad and consistent participation among diverse user populations, particularly in low-risk areas; strategies to integrate health reports for high-risk populations who may not have smartphones; validation of data and development of sensitive and specific algorithms for taking public health action, and buy-in from public health departments to use the data and advocate for this novel surveillance tool. Kidenga’s secondary function as an education tool on Aedes-borne viruses is less dependent upon a large user base and can be evaluated separately. Participatory surveillance systems that specifically monitor Aedes-borne pathogens are relatively new, and the challenges associated with their early detection may differ from those of other diseases.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Introduction
There is no safe level of lead in the body, and elevated lead in children can lead to decreased Intelligence Quotients (IQ) and behavioral problems. The American Academy of Pediatrics recommends lead testing of children with a positive risk assessment. Children who live in low socioeconomic areas may be at higher risk for lead exposure. As recent events have shown, having an elevated lead poisoning surveillance system can be critical to ensure that there is not a community-wide lead exposure. To reach the children that may not have been screened by a primary care physician, on March 1, 2016 the Sedgwick County Health Department Women, Infants, and Children (WIC) program began offering lead screenings to all children in the WIC program and their mothers. Per Centers for Disease Control and Prevention (CDC) guidelines, the Sedgwick County Health Department Epidemiology program (Epi) investigates anyone who has an elevated blood lead test (5 μg/dL or greater). There are two types of lead tests – screening (capillary finger stick) and confirmatory (venous blood draw).

Methods
Sedgwick County WIC clients are offered screening lead testing at their WIC appointments. Education to reduce lead exposure is provided at the time the test is performed. The filter papers used in the testing are sent to the Kansas Health and Environmental Laboratories (KHEL) for analysis, and the results are reported to Epi. Epi reports the lead testing results to WIC, who track the results in their patient charts. Epi receives KHEL results of ≤ 5 μg/dL via fax and results of ≥ 5 μg/dL via electronic laboratory reporting in the EpiTrax disease investigation software maintained by the Kansas Department of Health and Environment. Epi notifies any WIC clients with results of ≥ 5 μg/dL, while WIC staff notify all other clients about their results. Education is provided to the client a second time by Epi staff and/or WIC nurse or dietician. For clients with elevated blood lead tests, Epi interviews the case or guardian using an enhanced blood lead exposure questionnaire which asks about potential lead exposures, both in the home and at other locations (work, hobbies, etc.). If only a screening test was performed, Epi recommends confirmatory testing. WIC lead testing program measures, including types of exposures identified, are monitored over time using data obtained from EpiTrax.

Results
Between March 1 and July 21, of the 2,150 WIC clients offered lead testing, 89% self-reported never having received a lead test previously. Of the 1,427 clients with WIC lead screening results, seven cases of elevated blood lead were identified. Of the seven, five did not have a previous elevated lead test in EpiTrax. The average screening test result was 8.6 μg/dL (range 6.8 to 13.4). The average age of the cases was 2 years (range 1-4). Of the seven cases, two (29%) were confirmed as 10.0 and 11.0 μg/dL through venous testing at their primary care provider’s office. The remaining five cases havenot received confirmatory testing. One of the three cases interviewed reported that their babysitter lived in an old home, which could be the source of lead exposure. While interviewing a child’s guardian about an elevated 2016 test (7.9 μg/dL), Epi discussed a previous 2015 elevated lead test (6.0 μg/dL) of which the client’s guardian was unaware.

Conclusions
The ease of access to lead testing in the Sedgwick County WIC program and the joint effort between WIC and Epi to implement an enhanced lead poisoning surveillance system identified six children with elevated lead levels whose guardians did not know they had elevated lead levels. This new surveillance program educates WIC parents about lead, determines the lead levels in children for guardian knowledge (low level) and further follow-up (elevated level), and identifies lead exposures of WIC children with elevated lead tests.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To retrospectively identify initial emergency department (ED) and urgent care center (UCC) visits for Florida’s Middle East respiratory syndrome coronavirus disease (MERS-CoV) patients under investigation (PUIs) in the Florida Department of Health’s (DOH) syndromic surveillance system, the Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE-FL), using information gathered from PUI case report forms and corresponding medical records for the purpose of improving syndromic surveillance for MERS-CoV. The results of this study may be further utilized in an effort to evaluate the current MERS-CoV surveillance query.

Introduction Human MERS-CoV was first reported in September 2012. Globally, all reported cases have been linked through travel to or residence in the Arabian Peninsula with the exception of cases associated with an outbreak involving multiple health care facilities in the Republic of Korea ending in July 2015. While the majority of MERS-CoV cases have been reported in the Arabian Peninsula, several cases have been reported outside of the region. Most cases are believed to have been acquired in the Middle East and then exported elsewhere, with no or rare instances of secondary transmission. Two cases of MERS-CoV were exported to the United States and identified in May 2014. One of these cases traveled from Saudi Arabia to Florida. DOH conducts regular surveillance for MERS-CoV through the investigation of persons with known risk factors. PUIs have most often been identified by physicians reporting directly to local health departments and by DOH staff regularly querying ED and UCC chief complaint data in ESSENCE-FL. ESSENCE-FL currently captures data from 265 EDs and UCCs statewide and has been useful in identifying cases associated with reportable disease and emerging pathogens.

Methods From 2013-2015 DOH identified and investigated 62 suspected cases of MERS-CoV, including one confirmed case in May 2014. Specimens were collected from all 62 patients under investigation (PUIs) and 61 were ruled out. Of the 61 PUIs who were ruled out, ten were part of the contact investigation initiated following the identification of MERS-CoV in May 2014 and were not included in this analysis. DOH utilizes a MERS-CoV PUI case report form to collect data regarding demographics, clinical presentation, and risk factors. Retrospectively, additional documents including medical records and discharge summaries were gathered and utilized to evaluate PUIs identified in ESSENCE-FL. Name of the facility where PUIs presented, date and time of visit, age at event, and sex were identified using PUI case report forms and corresponding medical records and discharge summaries. Visit details for each of the identified facilities were queried in ESSENCE-FL and pulled for all visits with corresponding age at event and sex for the patient’s visit date. Additional PUI information including chief complaint, discharge diagnosis, ZIP code, race, and ethnicity were gathered for the purpose of matching corresponding ESSENCE-FL data fields. ESSENCE-FL visit details were narrowed by ZIP code (or lack of ZIP code for residents of other countries) and match details were recorded and evaluated. The fields examined were not always complete in ESSENCE-FL. Visits were considered matches when all available data in the fields examined were consistent with information obtained in the PUI case report form and available medical records and discharge summaries. Results Of the 52 PUIs included in this analysis, 39 sought treatment at facilities participating in ESSENCE-FL at their time of visit. Comparing information obtained from PUI documents with data provided in ESSENCE-FL, 30 ED visits were successfully matched to PUIs, including an initial ED visit for the patient with a confirmed case of MERS-CoV. Conclusions Following preliminary identification, all matches are to be confirmed with the appropriate hospitals. Future work to examine the chief complaints associated with patients’ initial ED visits identified in ESSENCE-FL will serve as a way to validate and improve upon the query currently being used as a surveillance tool for MERS-CoV. Detailing these methods also has value in the replication of this study for other diseases and in the development and validation of other disease-specific queries. Summarizing the reasons why PUIs were unable to be matched to ESSENCE-FL visits is also useful in improving system robustness.

Abstract

Objective: The purpose of this article was to quantitatively analyze the spatial variability and temporal variability of influenza-like illness (ILI) by a three-level Poisson model, which means to explain the spatial and temporal level effects by introducing the random effects.

Introduction: The early detection of outbreaks of diseases is one of the most challenging objectives of epidemiological surveillance systems. In order to achieve this goal, the primary foundation is using those big-data surveillance data for understanding and controlling the spatiotemporal variability of disease through populations. Typically, public health’s surveillance system would generate data with the big data characteristics of high volume, velocity, and variety. One common question of big data analysis is most of the data have the multilevel or hierarchy structure, in other words the big data are non-independent. Traditional multilevel or hierarchical model can only deal with 2 or 3 hierarchical data structure, which bound health big data further research for modeling, forecast and early-warning in the public health surveillance, in particular involving complex spatial and temporal variability of Infectious Diseases in the real-life.

Methods: All the data based on the ISSC project from April 1, 2012 through March 31, 2014 in China. We adopted Markov Chain Monte Carlo algorithm (MCMC) in Bayesian hierarchical (multilevel) model, which means to explain the spatial and temporal level effects by introducing the random effects. In order to calculate the geographical variations and temporal variation of ILI cases during two years surveillance, we constructed spatial and temporal model of three levels, which was day-in-months $\rightarrow$ months-in-two-year $\rightarrow$ Monitoring Units (Fig-1). Level one was repeated measures within every month, which was referred as day-in-months and the maximum value was 31 days. Level two was the variation tendency of months which was 24 months. Level three was the effect of spatial distribution of monitoring units, which took the spatial heterogeneity into account rather than dependence. This model was then adopted to evaluate and improve the early warning capacity of syndromic surveillance.

Results: We adopted multilevel spatio-temporal model (day-in-months $\rightarrow$ months-in-two-year $\rightarrow$ Monitoring Units) to analyze the points data collected from 2 counties in China, including two hospitals at county-level, 15 central hospitals at township level and 152 health care units in the villages. The analysis of totally 108,163 pieces of point data on ILI case indicated there are significant spatial and temporal variation among these cases. Among two thirds of the variation attributes to the difference of geographical locations of these monitoring sites. Theremaining one third of the variation attributes to the time dimensions, such as seasonal effect.

Conclusions: The variation of monitoring data collected from health care units mainly attributes to the difference of geographic locations from monitoring sites, yet only one third of the change attribute to the time change, such as seasons, holidays and festivals. Therefore, it is critical to select the location of monitoring site, which is more rational to select the hotspots with representative characters rather than try to cover the whole monitoring area.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveCase and cluster identification of emergency department visits related to local transmission of Zika virus. Introduction The first travel-associated cases of Zika virus infection in New York City (NYC) were identified in January 2016. Local transmission of Zika virus from imported cases is possible due to presence of Aedes albopictus mosquitoes. Timely detection of local Zika virus transmission could inform public health interventions and mitigate additional spread of illness. Daily emergency department (ED) visit surveillance to detect individual cases and spatio-temporal clusters of locally-acquired Zika virus disease was initiated in June 2016. Methods ED visits were classified into two Zika syndromes based on chief complaint text and the International Classification of Diseases version 9 and 10 diagnosis codes for patients ≥ 6 years old: 1) fever and 2) Zika-like illness. Zika-like illness was defined as visits with mention of Zika; symptoms of rash, fever, and either joint pain or conjunctivitis; diagnosis of Guillain-Barré syndrome; or diagnosis of rare and non-endemic arboviral infection. We applied the prospective space-time permutation scan statistic in SaTScan daily since June 2016 to the fever syndrome, selected as a single representative symptom, to detect clusters by hospital or zip code of patient residence. The maximum spatial cluster size is 20% of observed visits, and the maximum temporal cluster size is 14 days – reflecting the incubation period. The study period is 90 days. Statistical significance is determined using Monte Carlo simulations (N = 999). Any cluster with a recurrence interval ≥ 365 days is summarized in a map and line-list of contributing visits. The map depicts the zip codes of the cluster with an overlay of census tracts at highest risk for human importation of Zika virus, as estimated by a zero-inflated Poisson regression model developed at NYC DOHMH that is updated regularly to reflect the most recent available data on confirmed cases. Zika-like illness syndrome visits are output in a daily line-list. DOHMH staff contact the EDs that patients visited to determine travel to Zika-affected country, clinical suspicion of Zika infection, and laboratory testing. Results During June 1–August 16, 2016, we observed a mean of 253 (range: 202–299) ED visits for the fever syndrome per day. Sixteen spatio-temporal fever syndrome clusters have been detected. Of these, 2 clusters were during testing and optimization of scan parameters, 13 were due to data quality issues, and 1 was dismissed due to the large geographic range of the cluster, spanning 3 boroughs. During June 1–August 16, 2016, we observed a mean of 2.7 (range: 0–7) ED visits for the Zika-like illness syndrome. Daily counts ranged from 0–3 visits from June 1–June 16 and 1–7 visits since June 16. Nineteen visits that occurred from July 31–August 4 were further investigated to establish a protocol for follow-up. Of those, eleven patients reported recent travel to countries with local transmission, one had travel over 3 months ago and an alternate diagnosis, six had unknown travel history due to incomplete follow-up, and one reported no travel. The one without travel had a diagnosis inconsistent with Zika virus disease. Subsequently, analysts contacted EDs only for the subset of Zika-like illness syndrome visits with no indication of travelor without an alternate discharge diagnosis. Findings from this effort will be presented. Conclusions The fever syndrome provides a means to monitor for clusters using ED data. Prospective cluster detection signal volume was manageable and has not identified clusters requiring additional investigation. The Zika-like illness syndrome can be used for case finding. Contacting EDs helps to supplement information missing in the syndromic system, such as travel history as well as Zika testing and diagnosis. As Zika-like illness syndrome counts are low and disease is emergent, contacting EDs is feasible and helpful in ruling out local Zika virus transmission. No visits or clusters to-date have indicated local transmission.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
Weekly numbers of deaths are monitored to increase the capacity to deal with both expected and unusual (disease) events such as pandemic influenza, other infections and non-infectious incidents. The monitoring information can potentially be used to detect, track and estimate the impact of an outbreak or incident on all-cause mortality.

Introduction
The mortality monitoring system (initiated in 2009 during the influenza A(H1N1) pandemic) is a collaboration between the Centre for Infectious Disease Control (CIb) and Statistics Netherlands. The system monitors nation-wide reported number of deaths (population size 2014: 16.8 million) from all causes, as cause of death information is not available real-time. Data is received from Statistics Netherlands by weekly emails.

Methods
Once a week the number of reported deaths is checked for excess above expected levels at 2 different time-lags: within 1 and 2 weeks after date of death (covering a median 43% and 96% of all deaths respectively). A weekly email bulletin reporting the findings is sent to the Infectious Disease Early Warning Unit (at CIb) and a summary of results is posted on the RIVM website (National Institute for Public Health and the Environment). Any known concurrent and possibly related events are also reported. When excess deaths coincide with hot temperatures, the bulletin is sent to the Heat Plan Team (also at RIVM). Data are also sent to EuroMOMO which monitors excess mortality at a European level. For the Dutch system baselines and prediction limits are calculated using a 5 year historical period (updated each July). A serfling-like algorithm based on regression analysis is used to produce baselines which includes cyclical seasonal trends (models based on historical data in which weeks with extreme underreporting have been removed. Also periods with high excess mortality in winter and summer were removed so as not to influence the baseline with previous outbreaks).

Results
Increased mortality occurred during the entire influenza epidemic and up to three weeks thereafter (weeks 1-14 of 2016), except for adrop in week 7 (figure 1). Excess mortality was primarily observed in persons 75 or older. Additionally, in several weeks mortality was increased in 65-74 year olds, (week 4-6; peaking in week 4 with 564 deaths, when 468 baseline deaths were predicted). Also, in week 4, mortality in the 25-34 year-old age group was significantly increased (25 deaths, while 14 were expected as baseline). Cumulative excess mortality was estimated at 3,900 deaths occurring during the 11 weeks of the 2015/2016 influenza epidemic and at 6,085 during the total winter season (44 weeks running from week 40 up to week 20).

Conclusions
In terms of number of deaths during the winter season (weeks 40-20) and during the influenza epidemic (weeks 1-11), the 2015/2016 season in the Netherlands was of moderate severity compared with the previous five years (and was of similar magnitude as the 2011/2012 winter). Notable was the short three-week time span with a higher peak in mortality in 65-74 year olds than has been observed in recent years. Although the influenza epidemic reached its peak in week 7, the mortality data showed a dip in week 7. The reason for the temporary decrease is unknown but there was a partial overlap with public holiday.

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Abstract

Objective To determine if all-cause and cause-specific school absences improve predictions of vireologically confirmed influenza in the community.

Introduction School-based influenza surveillance has been considered for real-time monitoring of influenza, as children 5-17 years old play an important role in community-level transmission.

Methods The Allegheny County Department of Health provided vireologically confirmed influenza data collected from all emergency departments and outpatient providers in the county for 2007 and 2011-2016. All-cause school absence rates were collected from nine school districts within Allegheny County for 2010-2015. For a subset of these schools, in addition to all-cause absences, influenza-like illness (ILI)-specific absences were collected using a standard protocol: 10 K-5 schools in one school district (2007-2008), nine K-12 schools in one school district (2012-2013), and nine K-12 schools from threeschool districts (2015-2016). We used negative binomial regression to predict weekly county-level influenza cases in Allegheny County, Pennsylvania, during the 2010-2015 influenza seasons. We included the following covariates in candidate models: all-cause school absences rates with different lags (weekly, 1-3 week lags, assessed in separate models using all other covariates) and administrative levels (county, school type, and grade), week and month of the year (assessed in separate models), average weekly temperature, and average weekly relative humidity. Separately, for the three districts for which ILI-specific and all-cause absences were available, we predicted weekly county-level influenza cases using all-cause and ILI-specific absences with all previously stated covariates. We used several cross-validation approaches to assess models, including leave 20% of weeks out, leave 20% of schools out, and leave 52-weeks out.

Results Overall, 2,395,020 all-cause absences were observed in nine school districts. From the subset of schools that collected ILI-specific absences, 14,078 all-cause and 2,617 ILI-related absences were reported. A total of 11,946 vireologically confirmed influenza cases were reported in Allegheny County (Figure 1). Inclusion of 1-week lagged absence rates in multivariate models improved model fits and predictions of influenza cases over models using week of year and weekly average temperature (change in AIC = -4). Using grade-specific all-cause absences, absences from lower grades explained data best. For example, kindergarten absences explained 22.1% of model deviance compared to 0.43% using 12th grade absences in validation. Multivariate models of week-lagged kindergarten absences, week of year, and weekly average temperature had the best fits over other grade-specific multivariate models (change in AIC = -6 comparing K to 12th grade). The utility of ILI-specific absences compared to total absences is mixed, performing marginally better, adjusting for other covariates, in 2 years, but markedly worse in 1 year. However, these results were based on a small number of observations. Conclusions Our findings suggest models including younger student absences improve predictions of vireologically confirmed influenza. We found ILI-specific absences performed similarly to all-cause absences; however, more observations are needed to assess the relative performances of these two datasets.

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Abstract

Objective Using active surveillance approaches to investigate the transmission dynamics of rabies on Pemba Island and across Southern Tanzania, whilst a large-scale dog vaccination program was underway, to gain a greater understanding of the dynamics of infection as the disease is driven towards elimination. Introduction Rabies is endemic in Tanzania and has circulated on Pemba Island since the late 1990s. In 2010, an elimination programme was initiated in Southern Tanzania to demonstrate that human rabies deaths can be eliminated through mass dog vaccinations. We used active surveillance approaches to investigate the dynamics of rabies across the area where this programme was implemented. Methods Government census data and post-vaccination transects were used to estimate the dog population and coverages achieved by vaccination campaigns. Routine surveillance of animal bite injuries using a mobile phone-based surveillance system and active contact tracing were used to identify animal rabies cases and human exposures. Epidemic trees were constructed using spatiotemporal distances between cases and used to estimate the effective reproduction number (Re). We examined factors affecting rabies incidence and transmission using generalized linear mixed models. Results We estimated a small dog population of 4095 and low dog:human ratio on Pemba (1:105). Overall island-wide vaccination coverage increased from 16.8% in 2011 to 68.2% in 2014. We found a further 48 human exposures (343%), who either were not reported or did not obtain post-exposure prophylaxis (PEP). Routine surveillance was found to detect less than 10% (~8.75%). There was a rapid decline in cases detected on Pemba, from 42 before mass dog vaccinations were implemented in 2011, to 2 cases in 2014 (Figures 1). Since May 2014, no rabies cases have been detected. Similarly, Re declined from 1.02 to 0 and a significant relationship was found with rabies cases decreasing with increasing vaccination coverage (p = 0.013, Figure 2). Across seven other districts on the Tanzanian mainland we also observed major declines in rabies cases with very few cases of rabies in dogs detected in 2016 (Figure 3). Conclusions We conclude that rabies has been eliminated from domestic dog populations on Pemba over the five years since vaccination campaigns have been implemented. Continued surveillance and investigations of any bite incidents are therefore needed to ensure any subsequent incursions are controlled and freedom from rabies is maintained. On the Tanzanian mainland, it has taken longer to control rabies, however trajectories look promising with several districts close to eliminating the disease. However, detection of some wildlife cases in the last 12 months in these districts indicates the need to further investigate remaining foci and the role of wildlife in maintenance.

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Abstract

ObjectiveTo examine the baseline influenza-like illness (ILI) rates in the emergency departments (ED) of a large academic medical center (AMC), community hospital (CH), and neighboring adult and pediatric primary care clinics.

IntroductionThe primary goal of syndromic surveillance is early recognition of disease trends, in order to identify and control infectious disease outbreaks, such as influenza. For surveillance of influenza-like illness (ILI), public health departments receive data from multiple sources with varying degrees of patient acuity, including outpatient clinics and emergency departments. However, the lack of standardization of these data sources may lead to varying baseline levels of ILI activity within a local area.

MethodsGeographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) – a syndromic surveillance program – was used to automate ILI detection using free text chief complaint/reason for visit fields and vital signs for a large AMC - ED, CH - ED, and neighboring outpatient clinics during the summer (June 15, 2016 to August 18, 2016) in order to create a baseline. The GUARDIAN system defined ILI as fever (temperature ≥ 100°F) and cough and/or sore throat. Descriptive analysis of the observed ILI rates along with bivariate ANOVA with post hoc Bonferroni and t-test were utilized to examine the difference within the settings.

ResultsThe average ILI rate for EDs is higher than the clinics by at least 0.39%. The CH- ED had 4.23% baseline ILI rate as compared to 1.35% for AMC- ED. While the AMC – Clinics have 0.96% baseline ILI rate as compared to 0.25% for CH – Clinics. The CH- ED and AMC – Clinics represented higher variations. Based on bivariate test, CH – ED was significantly different than AMC – ED, AMC - Clinics, and CH – Clinics (F = 10.58, df = 1238, p < 0.05). For the AMC - Clinics, the average ILI rate for clinics providing services to adult patients was 0.66% (SD: 4.5%) as compared to 2.03% (SD: 10.81%) for pediatric clinics, which was not statistically significant.

ConclusionsThe CH - ED has higher baseline ILI rates compared to the othersettings, as well as the CDC Region 5’s baseline (1.9% for 2015-2016). Based on previous studies, this is likely due to providers’ use of chief complaint free text fields. Thus, the CH – ED will have higher thresholds for widespread ILI activity. In addition, differences in baseline ILI rates between AMC - ED, AMC - Clinics, and CH - Clinics may result in different thresholds for widespread ILI activity (i.e., Average + 3 Standard Deviations). The CH – ED and AMC – Clinics had higher baseline standard deviations, indicting variations in underlying patient populations. In addition, pediatric clinics have higher baseline ILI activity but also higher variations, indicating the unique characteristics of pediatric patients. Thus, due to the above findings, there is a need to closely monitor the ILI rates at various healthcare sites for both timing of onset, as well as the intensity of ILI activity.


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Abstract

Objective
To estimate mortality attributable to influenza adjusted for other common respiratory pathogens, baseline seasonal trends and extremetemperatures. Introduction
Assigning causes of deaths to seasonal infectious diseases is difficult in part due to laboratory testing prior to death being uncommon. Since influenza (and other common respiratory pathogens) are therefore notoriously underreported as a (contributing) cause of death in death-cause statistics modeling studies are commonly used to estimate the impact of influenza on mortality.

Methods
Using primary cause of death (Statistics Netherlands) we modeled weekly timeseries of 1) respiratory deaths (ICD10 codes J00-J99) and 2) circulatory deaths (ICD10 codes I00-I99). We used regression models with an identity link and Poisson error to relate mortality to counts of influenza A & B diagnoses. We adjusted for other common respiratory pathogens (all pathogen data was at population level from the national laboratory surveillance), temperature (from the Dutch Royal Meteorological Institute), and baseline linear and cyclical (i.e. seasonal) trends. To account for the yearly variation in the severity of the main circulating influenza A strain we used time dependent variables for influenza A (fixed at lag 0 – assuming a direct effect of influenza. For influenza B and the confounding pathogens we considered a 0 to -4 time lag (thus allowing infection to precede death for up to 4 weeks). We performed the analyses separately per death cause group and by 3 different age groups (0-64, 65-74, 75+ years) over a 14-year time-period (mid 1999-mid 2013, thus 14 complete winter seasons).

Results
In the Netherlands on average 2,636 all cause deaths occur per week varying by season (lower in summer min: 2,219 and higher in winter max: 3,564) with yearly incidence ranging from 20/10,000 in 0-64 year olds to 885/10,000 in 75-plus year olds. Circulatory mortality (31% of total deaths) was higher than respiratory mortality (10% of total deaths) and both showed clear seasonality in all age-groups. Overall, 0.14% of all deaths were actually coded as influenza deaths. Preliminary model estimates showed that the proportion of respiratory deaths attributable to influenza A were quite similar for 0-64 and 65-74 year olds but higher in 75+ (5.1%, 5.7%, 7.0% respectively) while this proportion was stable across age-groups for circulatory deaths (approximately 1.5% in all age groups for influenza A). Influenza B was significantly associated with respiratory and circulatory deaths in the oldest age group of 75+ years (with proportions of 0.7% and 0.2% respectively) while in the 65-74 year olds it was associated only with circulatory deaths (0.2%). Influenza B was not significantly associated with either respiratory or circulatory mortality in the 0-64 year age group. On average, yearly in the 75+ age group 70/10,000 respiratory deaths and 39/10,000 circulatory deaths were attributable to influenza A. For influenza B the incidences were 7 to 10 fold lower (7/10,000 and 6/10,000 respectively). Conclusions
Influenza A was significantly associated with respiratory and circulatory mortality in all age groups while influenza B was significantly associated with respiratory and circulatory mortality in the elderly only.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To improve timeliness and sensitivity of legionellosis cluster detection in New York City (NYC) by using all addresses available for each patient in one analysis. Introduction The Bureau of Communicable Disease (BCD) at the NYC Department of Health and Mental Hygiene performs daily automated analyses using SaTScan to detect spatio-temporal clusters for 37 reportable diseases. Initially, we analyzed one address per patient, prioritizing home address if available. On September 25, 2015, a BCD investigator noticed two legionellosis cases with similar work addresses. A third case was identified in a nearby residential facility, and an investigation was initiated to identify a common exposure source. Four days later, after additional cases living nearby were reported, the SaTScan analysis detected a corresponding cluster. In response to this signaling delay, we implemented a multiple address (MA) analysis to improve upon single address (SA) analyses by using all location data available on possible exposure sites. Methods Positive Legionella latest results for NYC residents are reported to BCD with patient demographic and address data. BCD interviews all cases to elicit additional locations of potential exposure and enters the addresses into a disease surveillance database (Maven). Addresses are assigned X/Y coordinates in near real-time via integration with ageocoding webservice. We used the prospective space-time permutation scan statistic in SaTScan, enabling the advanced input feature on the spatial neighbor tab to “include location ID in the scanning window if at least one set of coordinates is included.” This option considered a case as included in a given cluster if any of the case’s addresses were within the cluster. The case file included: unique case ID (as the location ID), number of cases, onset date, and day of week. The coordinate file included: case ID and X/Y coordinates for each address per case, resulting in one or more rows per case. We searched for alive clusters with a temporal range of 2 to 30 days and a maximum spatial size of 50% of observed cases. The study period was 1 year. Monte Carlo simulations (N=999) were used to determine statistical significance. We mimicked prospective surveillance to determine when the September 2015 cluster would have been detected had this analysis been in place, by performing daily SA and MA analyses from September 21 (when the first outbreak-linked case was reported) to September 29 (when the initial SaTScan analysis signaled). Any cluster with a recurrence interval (RI) ≥ 100 days was summarized in a map and linelist. Prospective, automated analyses were launched in April 2016 and run daily using Microsoft Task Scheduler, SAS 9.4, and SaTScan 9.4.1. Signals through July 2016 were summarized. Results In mimicked prospective analysis, the SA and MA SaTScan analyses identified clusters of 13 and 11 cases, respectively, starting September 27, 2015. The MA cluster was more spatially focused (2.11 km vs. 5.42 km) and more unlikely to occur by chance alone (RI of 16,256 days vs. 8,758 days). In prospective analyses, a MA cluster of 6 cases was identified on July 5, 2016 with a radius of 1.69 km (RI=100 days). On July 6, the MA cluster case count increased to 7 and maintained the same radius (RI=685 days), while a cluster of the same 7 cases was identified by the SA analysis with a larger radius (1.97 km) and lower RI (292 days). The RI for both clusters peaked on July 7 (MA: 2348 days, SA: 713 days). Conclusions In preliminary evaluation, the MA analysis facilitated cluster detection using non-residential possible exposure sites, such as workplaces. Timeliness was slightly improved, but the larger practical benefit was identifying more spatially focused clusters. Smaller clusters are useful for more precisely targeting legionellosis infections source identification and remediation activities, especially in urban environments with high population and building densities.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To assess whether the change in death swabbing policy in Sierra Leone has begun to affect community death reporting, we analyzed trends in death reporting before and after the policy change.

Introduction Stems from the 2014-6 Ebola virus disease (EVD) outbreak, community event based surveillance (CEBS) was implemented in Sierra Leone using community health workers to generate alerts for trigger events suggestive of EVD transmission. Through September 30, 2015 (last month of active EVD transmission), the majority (86%) of alerts reflected community deaths; this was beneficial as Ebola-related deaths were detected with delay during the epidemic’s peak. The Government had implemented a policy of mandatory swabbing and testing of all dead bodies. The policy changed on June 30, 2016 wherein only swabbing of deaths deemed to be high-risk for EVD is required. To assess whether this policy change has begun to affect community death reporting, we analyzed trends in death reporting before and after the policy change.

Methods This analysis was conducted using data from nine districts during period 1 (January-June 2016) and period 2 (July 2016). Weekly changes in the reporting of death alerts during the two periods were assessed. An interrupted time series analysis (ITS) with a segmented linear regression was also used to assess the immediate impact of the policy change.

Results During period 1, monthly changes in death alerts across districts were variable (-8% to 16%). Comparison of the weekly average between periods 1 and 2 showed a 33% reduction in death alerts. During period 1 (before the policy change), there was an overall significant increase of 3.2 death alerts per week (p=0.00) and no immediate impact or changes in the trend afterwards. At the district level, on average 354 death alerts were generated weekly in June, compared to 237 in July (33% reduction); Moyamba district experienced the largest drop in death alerts from 46 to 16 (65%).

Conclusions Community death reporting provides early warning of EVD transmission by rapidly capturing death alerts where vital registration is not fully functional. Although we have one month of data post-policy change, this preliminary analysis suggests that the change in swabbing policy may have halted an observed increase in death reporting. Further community mobilization efforts and training are warranted to prevent a drop in death reporting.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Describe how the Georgia Department of Public Health (DPH) uses syndromic surveillance to initiate review by District Epidemiologists (DEs) to events that may warrant a public health response (1). Introduction DPH uses its State Electronic Notifiable Disease Surveillance System (SendSS) Syndromic Surveillance (SS) Module to collect, analyze and display results of emergency department patient chief complaint data from hospitals throughout Georgia. Methods DPH prepares a daily SS report, based upon the analysis of daily visits to 112 Emergency Department (EDs). The visits are classified in 33 syndromes. Queries of chief complaint and discharge diagnosis are done using the internal query capability of SendSS-SS and programming in SAS/BASE. Charting of the absolute count/percentage of ED visits by syndromes is done using the internal charting capability of SendSS-SS. A daily SS report includes the following sections: Statewide Emergency Department Visits by Priority Syndromes (Bioterrorism, BloodyRespiratory, FeverRespiratory, FeverChest, FeverFluAdmit, FeverFluDeaths, VeryIll, and PoxRashFever, Botulism, Poison, BloodyDiarrhea, BloodyVomit, FeverGI, IllFlu, RashFever, Diarrhea, Vomit). Statewide Flag Analysis: Is intended to detect statewide flags, by using the charting capability in SendSS-SS. Possible cases with presumptive diagnosis of potentially notifiable diseases: Is intended to provide early warning to the DEs of possible cases that are reportable to public health immediately or within 7 days using queries in the Chief Complaint and Preliminary Diagnosis fields of SendSS-SS. Possible clusters of illness: Since any cluster of illness must be reported immediately to DPH, this analysis is aimed at querying and identifying possible clusters of patients with similar symptoms (2). Possible travel-related illness: Is intended to identify patients with symptoms and recent travel history. Other events of interest: Exposures to ill patients in institutional settings (e.g. chief complaint indicates that other children in the daycare have similar symptoms). Trend Analysis: Weekly analysis of seasonality and trends of 14 syndromes. Finally, specific events are notified to and reviewed by the 18 DEs, who follow up by contacting the Infection Preventionists of the hospitals to identify the patients using medical records or other hospital-specific identification numbers and follow up the laboratory test results. Results Since 05/15/2016, 12 travel-related illnesses, 29 vaccine-preventable diseases, 14 clusters, and 3 chemical exposures have been notified to DEs. For instance, a cluster of chickenpox in children was identified after the DE contacted the Infection Preventionist of a hospital, who provided the DE with the laboratory results and the physician notes about the symptoms of the patients. These actions have resulted in earlier awareness of single cases or cluster of illness, prompt reporting of notifiable diseases, and successful interaction between DEs and health care providers. In addition, SS continues to track the onset, peak, and decline of seasonal illnesses. Conclusions The implementation of SS in the State of Georgia is helping with the timely detection and early responses to disease events and could prove useful in reducing the disease burden caused by a bioterrorist attack.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe how the state syndromic surveillance system (NC DETECT) was used to initiate near real time surveillance for endocarditis, sepsis and skin infection among drug users. Introduction Recreational drug use is a major problem in the United States and around the world. Specifically, drug abuse results in heavy use of emergency department (ED) services, and is a high financial burden to society and to the hospitals due to chronic ill health and multiple injection drug use complications. Intravenous drug users are at high risk of developing sepsis and endocarditis due to the use of a dirty or infected needle that is either shared with someone else or re-used. It can also occur when a drug user repeatedly injects into an inflamed and infected site or due to the poor overall health of an injection drug user. The average cost of hospitalization for aortic valve replacement in the USA is about $165,000, and in order for the valve replacement to be successful, patients must abstain from using drugs. Methods We examined temporal trends of drug-related visits to hospital EDs, as well as drug-related related ED admissions complicated with endocarditis, bacteremia and sepsis. Results The trends in Endocarditis/Sepsis and drug-related related admissions appear to echo overdose related ED admissions increase. Patients ED return visits and hospitalizations for the same problem are also growing compared to the previous years. We will discuss the NC DETECT case definition used to monitor drug overdose/dependence and infection, case definition transition from ICD-9 to ICD-10 codes, and will share surveillance analysis results. Conclusions NC DETECT’s system flexibility has been important in rapidly establishing surveillance of infections among drug users. Near real-time analysis on hospital, county and state levels can be performed using NC DETECT system reports to provide state officials, hospitals and LHDs with situational awareness. Limitations: Syndromic surveillance ED data contains less accurate information about the diagnosis codes, procedures, length of stay, and severity compared to the hospital discharge data.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

ObjectiveTo estimate the velocity of Zika virus disease spread in Brazil using data on confirmed Zika virus disease cases at the municipal-level.

IntroductionLocal transmission of Zika virus has been confirmed in 67 countries worldwide and in 46 countries or territories in the Americas (1, 2). On February 1, 2016 the World Health Organization declared a Public Health Emergency of International Concern due to the increase in microcephaly cases and other neurological disorders reported in Brazil (2). Several countries issued travel warnings for pregnant women travelling to Zika-affected countries with Brazil, Colombia, Ecuador, and El Salvador advising against pregnancy (3-7). The risk of local transmission in unaffected regions is unknown but potentially significant where competent Zika vectors are present (8) and also given the additional complexities of sexual transmission and population mobility (9, 10). Despite the rapid spread of Zika virus across the Americas and global concerns regarding its effect on fetuses, little is known about the pattern of spread. Knowledge of the direction and the speed of movement of disease is invaluable for public health response planning, including the timing and placement of interventions.

MethodsData for this analysis were obtained from the Brazil Ministry of Health and consisted of confirmed cases of Zika virus disease. The centroids of the municipalities were taken in meters from the shapefiles and used to perform a surface trend analysis. Surfacetrend is a spatial interpolation method used to estimate continuous surfaces from point data. The continuous surface of time to infection was estimated by regressing it against the X and Y coordinates. Time was in days and X and Y coordinates were meters. Parameters were estimated using least squares regression and velocity (in km per day) was obtained by inverting the final magnitude of the slope.

ResultsData provided from the Brazil Ministry of Health on May 31, 2016, indicated that Zika had been confirmed in 316 of the 5,564 municipalities in Brazil representing 26 states, with six additional municipalities identified from other reporting sources. Our models indicated a southward pattern of introduction of Zika starting from the northeast coast towards the southeastern coastal states of Rio de Janeiro, Espírito Santo, and São Paulo. There was also a pattern of western movement towards Bolivia. Overall, the average speed of diffusion was 42.1 km/day across all models, 6.9 km/day to a maximum of 634.1 km/day. The municipalities in the Northeast and North regions had the slowest speeds whereas the municipalities in the Central-West and Southeast regions had the highest speeds. This is due to proximity of cases in time and space, with more cases having occurred closer in time and over larger areas in South, Southeast, and Central-West regions resulting in faster rates of introduction.

ConclusionsThe average speed of spread was 42 km per day and it took approximately five to six months for Zika to spread from the northeastern coast to the southeastern coast and western border of Brazil. The rapid spread of Zika can help us understand its possible future directions and the pace at which it travels, which are key for targeted mosquito control interventions, public health messaging, and travel advisories. A multi-country analysis is needed to understand the continental spatial and temporal patterns of dispersion of Zika virus.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The objective is to discuss two decades of international experience in health information and disease surveillance systems strengthening and synthesize lessons learned as applicable to implementation of the Global Health Security Agenda (GHSA).

Introduction RTI International has worked on enhancing health information and disease surveillance systems in many countries, including the Democratic Republic of the Congo (DRC), Guinea, Indonesia, Kenya, Nepal, Philippines, Tanzania, Zambia, and Zimbabwe. Strengthening these systems is critical for all three of the Prevent, Detect and Respond domains within the Global Health Security Agenda. We have deep experience in this area, ranging from implementing District Health Information Software (DHIS), electronic medical records, health facility registries, eHealth national strategies, electronic Integrated Disease Surveillance and Response system (eIDSR), mobile real-time malaria surveillance and response, national weekly disease surveillance, patient referral system, and community-based surveillance. These experiences and lessons learned can inform work being done to advance the GHSA.

We will discuss several examples, including activities in Zimbabwe and Tanzania. RTI has been working in Zimbabwe for over six years to strengthen the national health information system. This work has included the configuration and roll-out of DHIS 2, the national electronic health information system. In doing so, RTI examined and revitalized the weekly disease surveillance system, improving disease reporting timeliness and completeness from 40% to 90%. Additionally, RTI has integrated mobile technology to help more rapidly communicate laboratory test results, a laboratory information management system to manage and guide test sample processing, and various other patient level systems in support of health service delivery at the local level. This work has involved capacity building within the ministry of health to allow for sustainable support of health information systems practices and technology and improvements in data dissemination and use practices.

Similarly, RTI has worked for more than five years to help strengthen the National HIS in Tanzania. These activities have included stakeholder coordination, developing national eHealth strategy and enterprise architecture, harmonizing indicators, redesigning routine reporting instruments, national DHIS 2 roll-out, information technology infrastructure management and user helpdesk support, reducing the number of parallel information systems, data dissemination and use, development of district health profiles, development of the national health facility registry, and supporting roll-out of the electronic integrated disease surveillance system.

Methods We will profile selected projects and synthesize critical lessons learned that pertain to implementation of the GHSA in resource-constrained countries. Results We will summarize our experience and lessons learned with health information and disease surveillance systems strengthening. Topics such as those that relate to advancing the GHSA RealTime Surveillance and Reporting Action Package areas will be discussed, including: indicator and event based surveillance systems; interoperable, interconnected, electronic real-time reporting system; analysis of surveillance data; syndromic surveillance systems; systems for efficient reporting to WHO, FAO and OIE; and reporting network and protocols in country.

Conclusions Our experience working over the past 14 years in 9 countries on different HIS and disease surveillance system strengthening projects has led to a deep understanding of the challenges around implementation of these systems in limited resource settings. These experiences and lessons learned can inform initiatives and programs to advance the GHSA.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: To assess essential support functions for Integrated Disease Surveillance and Response (IDSR) in the Kingdom of Swaziland and make recommendations for a national IDSR Roadmap.

Introduction: Implementation of the IDSR framework for fulfillment of the International Health Regulations (2005) ([IHR 2005]) has been challenging in Swaziland due to distribution of IDSR functions across units within the Strategic Information Department (SID) and other external departments within the Ministry of Health. We conducted a qualitative assessment and a Strength, Weaknesses, Opportunities and Threats (SWOT) analysis of current public health surveillance (PHS) support structures to inform implementation of IDSR.

Methods: Key informant interviews, focus group discussions, and a desk review were performed. Participants were personnel at essential units, departments and programs at the national level as well as at health facilities and clinics at regional and local levels. Transcripts were coded into SWOT matrices using MAXQDA for each building block of PHS: structures, workforce, resources, processes (detect, report, assess/analyze, respond, feedback), and informatics.

Results: Selected Strengths included existence of immediate notifiable disease reporting through the Epidemic and Pandemic Response unit (EPR) and reporting of summary health facility data to the Health Management Information System (HMIS) unit and laboratory network. Weaknesses included lack of clear roles and responsibilities for IDSR among SID units, limited coordination between SID units, lack of data sharing, lack of Standard Operating Procedures (SOPs), uncoordinated case investigations and response, minimal analysis conducted for public health surveillance and limited feedback for reporters. Identified opportunities were political will for establishing roles and responsibilities and mechanisms for coordination and data sharing. Threats were limited data access, limited funding for feedback, lack of analysis for IDSR and paper-based reporting.

Conclusions: Currently there is limited use of surveillance data for decision making due to lack of coordination. Findings were presented at a dissemination meeting to representatives of relevant departments, and there was consensus on the need to clearly define the roles and responsibilities of different programs for IDSR. In March 2016, a consensus meeting was held to designate roles and responsibilities for IDSR, a direct result of this assessment. Additional resources and funding is needed to support these highly important initiatives to ensure the safety and health security of the Swazi nation.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective

To identify Cause of deaths among children below age of 5 years from a prospective cohort of women in one urban and four peri-urban settings of Karachi, Pakistan

Introduction

Pakistan ranks 26th in Childhood mortality rates, globally. Pakistan, with other 4 countries is responsible for about half of the deaths of children age under 5. Despite such burden vital registration system is not well established, health facilities are not easily accessible and mostly deaths occur at home, making identification of cause of death (COD) difficult.

Methods

From Jan 2007-Dec 2012 under-5 mortality was identified by CHWs during their 3-monthly visits. A Research Assistant conducted Verbal Autopsies (VA). Each VA form was analyzed by 2 physicians, independently, and assigned a cause. VA is analyzed by a third physician in case two physicians do not agree on a cause. Cause Specific Mortality Fractions (CSMF) were calculated for each identified COD. Results 833 (58%) neonatal deaths and 591 (42%) Under-5 deaths (excluding neonates) were identified. Among neonates, most common CODs were perinatal asphyxia (30.4%), neonatal sepsis/meningitis (28%), pre-term birth complication (11%) and neonatal pneumonia (6%). For Post-neonatal deaths, most common CODs were sepsis (19%), diarrheal disease (17%), Pneumonia (17%) and meningitis (8%).

Conclusions

We describe the CSMF for different CODs among neonates and children under 5. Strategies for prevention of most common causes and making health facilities easily accessible will decrease this burden.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective In the spring of 2014, people from vulnerable households in allmarzes of Armenia were examined with the aim of active surveillance. Brucellosis is a serious disease caused by bacteria of the Brucella genus. It principally affects ruminants but may be transmitted to humans. Registration of cases in cattle farms causes considerable economic losses and creates favorable conditions for mass infection among humans. In Armenia the expansion of animal industries and urbanization are the main reasons for occurrence and development of brucellosis.

Methods Blood was sampled from people on farms reported as having infected animals. Blood samples were tested by the Wright-Huddleston method. The standard case definition of brucellosis was used for diagnosis. A questionnaire-based interview was carried out among the population to identify the form of contact with animals and to analyze epidemiological links. During the investigation provisions were followed in governmental decree RA 19.01.2006 N480-N on brucellosis prevention, epidemiology, diagnosis, treatment, preventive measures.

Results A total of 11160 people from 1054 households were enrolled in the study, of which 3625 (32.5%) underwent a laboratory examination. Nearly 6% (641) refused to be tested. Over 6% of those tested (226) were positive for antibodies to Brucellae. Of these, 129 (3.5%) had chronic brucellosis. Those testing positive for brucellosis were treated appropriately. These included 203 (90%) adults and 23 (10%) below 14 years old; 147 (65%) were male and 79 (35%) were female. Of those diagnosed with brucellosis, working in animal husbandry accounted for 46.6% (106), while those who harvested milk accounted for 37.6% (85) and those using raw milk made up 15.4% (35).

Conclusions Cases were most frequently reported among people 20-55 years of age; the highest percentage of positives were among 41-45 year old males who had contact with infected animals. The main risk factor for acquiring brucellosis is animal husbandry.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

IntroductionEpiCore draws on the knowledge of a global community of human, animal, and environmental health professionals to verify information on disease outbreaks in their geographic regions. By using innovative surveillance techniques and crowdsourcing these experts, EpiCore enables faster global outbreak detection, verification, and reporting. Methods Through a secure online platform, members are able to easily and quickly provide local information to expedite outbreak verification. EpiCore volunteer applications are vetted to ensure that they possess the public health and epidemiologic expertise necessary to contribute to the platform. Results EpiCore currently has over 1600 members that span 135 countries. During the first 8 months of EpiCore’s launch, 172 requests for information to volunteers have been posted with an average response rate of over 80%. Conclusions With its geographical distribution of members and high response rate, EpiCore is poised to enable the world to verify potential outbreak signals faster. By improving situational awareness, de-escalating rumors or false information, and corroborating using other existing sources, EpiCore is able to reduce the signal to noise ratio in disease surveillance. Hence, by detecting and verifying outbreaks faster, health officials can generate early responses that can curb epidemics and save lives.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the process of operation of the system and assess its key attributes, to determine the effectiveness and efficiency of the surveillance system and make appropriate recommendations to stakeholders for its improvement. Introduction Malaria is a parasitic disease caused by Plasmodium falciparum. About 3.2 billion people worldwide are at risk of malaria. Children and pregnant women are particularly vulnerable to the disease. Sub-Saharan Africa carries a high share of the global malaria burden. Effective malaria surveillance system is essential in the control and elimination of malaria. Worldwide, there were an estimated 198 million cases of malaria in 2013 and 584,000 deaths. Methods This study was conducted using the “CDC’s Updated Guidelines for Evaluating Public Health Surveillance System, 2001”. Keystakeholders and Malaria Focal Persons were interviewed. Integrated Disease Surveillance and Response case summary data from January to December 2014 was reviewed. Data analysis was done using Microsoft Excel 2016 and Epi-info 7. Results The system provides information on malaria trends, morbidity and mortality. Case definitions are well understood by participants. All Malaria focal persons (MFPs) were willing to continue using the system. Standardized data collection tools are available in 91% of Health Facilities (HF). The system was rated flexible by 91% of MFPs. The system was however not representative because data were essentially from public health facilities only. The system has an average timeliness of 37.7% and completeness of 59.4%, both parameters were below the State’s 80% target. About 91% MFPs had refresher training, while 78% MFPs received supportive supervision. Main challenges identified were lack of commodities in all HFs, and inadequate mobile facilities in 70% of HFs. Conclusions The Kaduna state Malaria surveillance system is meeting its objectives. However, challenges are observed in its timeliness, representativeness, and data quality. Efforts should be made to integrate tertiary and private health facilities into the system. MFPs need more training on malaria reporting to improve timeliness and data quality. There is the need to improve on the supply of malaria treatment commodities to all health facilities within Kaduna state.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: The session will discuss strategies for outbreak prevention, detection, and response for global health security and explore how these activities inform both domestic and international initiatives. Innovations in epidemiology, laboratory, informatics, investment, and coordination for disease surveillance will be discussed.

Introduction: Multiple agencies are involved in global disease surveillance and coordination of activities is essential to achieve broad public health impact. Multiple examples of effective and collaborative initiatives exist. The WHO/AFRO developed Integrated Disease Surveillance and Response (IDSR) framework, adopted by 43 of the 46 AFRO member states and applied in other WHO regions, was the first framework designed to strengthen national disease surveillance and response systems. The WHO International Health Regulations (IHR) 2005 are an agreement between 196 countries to prevent, detect, and respond to the international spread of disease. In 2013 CDC worked with Uganda and Vietnam to demonstrate the development of surveillance, laboratory, and emergency response center capacity and link data systems for six outbreak-prone diseases. More recently, the Global Health Security Agenda (GHSA) was launched with the support of 28 countries, WHO, OIE, and FAO just as Ebola was beginning to emerge in West Africa. This panel brings together CDC, local implementing partners, academic technical partners, and international non-government donor to discuss current and evolving strategies for prevention, detection, and response activities needed for global health security.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective We present lessons learned from over a decade of HIV bio-behavioral risk study implementation and capacity-building in African militaries. Introduction Circumstances within the military environment may place military personnel at increased risk of contracting sexually transmitted infections (STI) including HIV. HIV bio-behavioral risk studies provide a critical source of data to estimate HIV/STI prevalence and identify risk factors, allowing programs to maximize impact by focusing on the drivers of the epidemic. Methods Since 2005, RTI has provided technical assistance (TA) to support HIV/STI Seroprevalence and Behavioral Epidemiology Risk Surveys (SABERS) in 14 countries across Sub-Saharan Africa and Asia. SABERS are cross-sectional studies consisting of a survey to assess knowledge, attitudes and behaviors related to HIV, coupled with rapid testing for HIV and other STIs. RTI tailored each survey instrument to be culturally appropriate in content and methodology, trained military personnel to serve as data collection staff, and provided logistical support for study implementation. Results Key lessons learned are summarized below: Data collection mode varied from paper-based to computer-assisted surveys, depending on country preference, in-country staff capabilities, and the country’s technological capacity. Computer-assisted data collection systems were preferable because they improved data quality through the use of programmed skip patterns, range, and consistency checks. By eliminating the need for data entry, computer-assisted systems also saved program resources and enabled faster access to the data for analysis. Survey administration method varied from self-administered to interviewer-administered surveys. Literacy rates, technological familiarity, and confidentiality concerns were key drivers in determining the best data collection method. Self-administered surveys such as computer-assisted self-interview (CASI) were preferable due to the high-level of confidentiality they provide, but required a high-level of literacy and computer familiarity. If confidentiality was a big concern in low-literacy settings, audio computer-assisted self-interview (ACASI) was used if the population had some computer familiarity. Interviewer-administered surveys such as computer-assisted personal interview (CAPI) were used in low-literacy settings. Tailoring the survey instrument and administration for cultural appropriateness was vital to the acquisition of sound, viable data. Sexual behaviors and the definition of “regular sexual partner” and other terms varied according to local custom. The sensitivity of the survey questions also impacted survey administration operationally. The preference for same-sex or opposite-sex interviewers varied by country and military setting. It was imperative to pre-test the survey. A skilled workforce and staff retention are essential to provide high-quality data. Literacy levels, technological familiarity, HIV knowledge, and time commitments must all be considered when selecting data collection staff. Retention of staff throughout the duration of data collection activities can be a major issue especially among military personnel who were often called away from study activities to perform military duties. Host military ownership was integral to the success of the SABERS program. By engaging military leadership early and involving them in all decision-making processes we ensured the partner military was invested in the study and its success and found value in the resulting data and findings. Host militaries were actively involved in SABERS by providing staff for data collection, leading sensitization activities, and monitoring data collection activities in the field. Inclusion of capacity building elements during study implementation led to increased host military buy-in. Capacity building included staff trainings and practical experience in survey methodology, use of electronic data collection instruments, study logistics and data monitoring. Confidentiality of survey data and HIV test results was of increased concern given that these studies were conducted in a workplace environment. For this reason, it was imperative to assure participants that disclosures of drug or alcohol use and positive HIV/STI test results would remain confidential and would not affect their military employment. Conclusions Based on our experience, the following are required for the successful implementation of an HIV Bio-behavioral Risk Study in resource-poor military settings: (1) selection of a data collection mode and survey administration method that is context-appropriate, (2) utilization of local wording and customs, (3) a skilled workforce, (4) local buy-in/partnership, (5) inclusion of capacity building elements, and (6) assurance of confidentiality.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective
We aim to assess the implementation of malaria prevention, diagnosis and treatment strategies, to assess implementation trends from 2011 to 2014 and if surveillance targets were met. An introduction to malaria is a preventable disease but 3.4 billion people at risk globally with 207 million cases and 627 deaths reported in 2013. Africa accounts for 80% of cases and 90% of all malaria deaths. Nigeria accounts for 25% of malaria burden in Africa. The goal of malaria control is to reduce malaria–related transmissions, cases and deaths to a level where it is no longer a public health concern. Methods
Kaduna state, north western Nigeria with estimated population of 7.3 million has 23 districts and 1252 health facilities. Of these 461 sent malaria surveillance data to National Health Management Information System monthly. Data from January 2011 to December 2014 was analysed. We evaluated variables related to malaria interventions strategies such as malaria diagnosis, malaria treatment, malaria prevention in pregnancy. Frequencies, proportions and trend analysis were done and odd ratios for associations between variables were calculated with confidence interval set at 95%. Epiinfo statistical software was used for the analysis. Results
Data completeness was 89.8%. Of the 1,008,728 people that visited health facilities, 56.6% presented with fever. Among the fever cases, 34.2% was tested with rapid diagnostic test (RDT) and 5.5% with microscopy. Artemisinin based combination therapy was given to 361,464 of which 36.4% had confirmed malaria. Those aged < 5 years with suspected fever were 1.28 (95% confidential interval (C.I), 1.27-1.29; p<0.01) more likely not to be tested with either RDT or microscopy and they are 2.62 (95% C.I., 2.63 – 6.67;p<0.01) times more likely to have ACT for confirmed malaria. ACT prescription to presumptive malaria increases from 31.8% in 2013 to 200.2% in 2014. There is a progressive increase of long lasting insecticidal net distribution and access to second dose of Intermittent Preventive Therapy (IPT-2) for pregnant women. Conclusions
Generally, progress in malaria control transition to Elimination in Kaduna State, Nigeria is favorable with malaria prevalence at 36.4%. Some targets were met within the period and recommend strengthening of these malaria control strategies with focus on vulnerable groups and prevent uncontrolled ACT prescription for presumptive malaria.

Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective The study was carried out to determine physicians' knowledge of notifiable reporting and to identify the barriers to reporting in Grenada. Introduction Despite the significance of disease reporting to any health system, Grenada like most countries struggle with underreporting of notifiable diseases by physicians. In order to improve the national disease surveillance system in Grenada, it is critical to understand the reasons for any underreporting. The study was conducted to determine physicians' knowledge of notifiable reporting and to identify the barriers to reporting. Methods The Grenada Medical and Dental Council identified a total of 129 registered and practicing physicians. A cross-sectional study design was developed to obtain information from all registered and practicing physicians. The survey tool included questions on demographics, training history and medical practice details, as well as knowledge, practice, and barriers to reporting notifiable diseases. The survey was administered to physicians in both paper-based and electronic formats. Results To date only 13 surveys have been returned. Preliminary data show that 61.5% of respondents rated their knowledge of which diseases are reportable on an “average” level, and of those only 46% knew where to obtain a list of notifiable diseases (NDs). Fifty-three percent (53%) of respondents said that they have reported NDs to the relevant authorities in the past. Thirty-eight percent (38.5%) believed it should be the responsibility of nurses to report NDs and 30.8% stated it should be the physician. The major barriers to reporting identified by the respondents were being too busy, too much time required, and lack of infrastructure or reporting systems. When asked about ways to improve reporting, 38.5% identified improvements to the reporting form, and 30.8% identified education of physicians on reporting protocol and importance. Conclusions While this is still preliminary data, the majority of the physicians surveyed had some knowledge of reporting NDs. The barriers to reporting identified were being too busy and lack of infrastructure. Future improvements to the reporting system in Grenada should focus on making forms electronic and less lengthy, and on educating physicians on the importance and protocol of reporting NDs.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To identify and address gaps in acute flaccid surveillance for polio eradication in Buchar state

Introduction Poliomyelitis a disease targeted for eradication since 1988 is still pose public health challenge. The Eastern Mediterranean and African Regions out of the six World Health Organization (WHO) Regions are yet to be certified polio free. The certification of the WHO Africa region is largely dependent on Nigeria, while the WHO Eastern Mediterranean is dependent on Pakistan and Afghanistan. Surveillance for acute flaccid paralysis (AFP) is one of the critical elements of the polio eradication initiative. It provides the needed information to alert health managers and clinicians to timely initiate actions to interrupt transmission of the polio disease and evidence for the absence of the wild polio virus. Good and completed documentation is the proxy indication of the quality of the system while poor documentation translates to possibilities of missing wild poliovirus in the past. We evaluated the performance of the AFP surveillance system in Buchar, which is among the 11 high-risk states for wild polio virus in Nigeria to identify and address gaps in the surveillance system.

Methods We conducted a cross-sectional study in Buchar State. We assessed the material and documentation on AFP surveillance in eighteen of the twenty Local Government Areas (LGAs). We assessed the knowledge of the clinicians at focal and non-focal sites on case definition of AFP, the number and method of stool specimen collection to investigate a case and types of training received for AFP surveillance. We verified AFP case investigations for the last three years: The caregivers (mothers) were interviewed to authenticate the reported information of AFP cases, the method used for stool specimen collection and feedbacks. Community leaders’ knowledge on AFP surveillance was also assessed. Data was entered and analyzed in Excel spreadsheet.

Results Review of the expected deliverables of 18 out of the 20 LGA disease surveillance and notification officers (DSNO) revealed that only 2 (11%), 5 (28%), 6 (33%) and 7 (39%) had evidence of polio outbreak investigation, supervisory reports, minutes of meeting and surveillance work plan respectively. Of the 31 AFP cases investigated, correct and complete information was 39% for birth day, 26% for birth month of the child, 23% for date of onset of paralysis and 23% for date of investigation. Contacts of informants, AFP 001-3 were deficient in the focal and non-focal sites. The non-focal also lacked guidelines for integrated disease surveillance and response (IDSR) and terms of reference for surveillance focal person. Knowledge of case definition of AFP was 71% and 30% among clinicians at the focal and non-focal sites, respectively and 88% and 55% for method of stool collection among clinicians at focal and non-focal sites. Among the 38 caregivers (mothers) interviewed 16 (42%) did not remember the day or month the investigation for the AFP was conducted, 36 (95%) gave the correct number of stool samples, 15 (40%) mentioned that the stool samples were collected 24 hours apart and only 12 (32%) received feedbacks. Majority (79%) of the community leaders interviewed were aware of AFP and knew that stool was the specimen for investigation of the AFP but 21% did not know whom to report a case of AFP in their community.

Conclusions Our study revealed knowledge and documentation gaps in AFP surveillance for certification of polio-free in Nigeria. The state ministry of health and the WHO consultants in the polio eradication unit should update the knowledge of the health care workers at the operational levels on AFP surveillance. The state ministry of health and the WHO consultants should also provide all essential documents required for quality AFP surveillance and ensure their judicious use.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective: The objective of this survey was to study vaccination coverage and quality in dogs in Georgia through the detection of post-vaccination antibodies. Introduction: Rabies is endemic in Georgia with up to 100 confirmed cases in animals per year. There is an estimated 350,000 domestic and stray dogs/cats in Georgia. The prophylactic vaccination of domestic animals against rabies was reestablished in Georgia in 2013. Each year since 2013, coverage has increased aiming to cover approximately 70% of the total population of dogs/cats in Georgia. Methods: Only vaccinated dog populations were included in the sero-survey. Using random selection, five locations were selected. The survey was conducted over a period of 4-8 weeks after vaccination. In order to study vaccination coverage, the total dog population was registered. Samples were taken only from vaccinated dogs (confirmed by vaccination papers) and samples were sent to the Laboratory of the Ministry of Agriculture where they were tested for the presence of antibodies using ELISA. Epidemiological information and GPS coordinates were recorded in the electronic integrated disease surveillance system (EIDSS) and geographic information system (GIS). Results: Out of 572 dogs in sampled villages, 373 animal’s vaccination was confirmed leading to 65% vaccination coverage. Out of 255 samples, 241 were suitable for testing; 237 samples (98.3%) were positive for the existence of antibodies. Antibody titer was not measured. Conclusions: Based on the results of the survey, it can be seen that vaccination coverage is generally not high (65%) and needs improvement. The vaccination quality (as determined through the existence of antibodies) is good (98.3%). In further surveys, antibody titers must be measured in order to extract more information regarding vaccination quality.

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Abstract

Objective To determine burden, timing and causes of stillbirths in a prospective cohort of pregnant from a low income community setting in peri-urban Karachi. Stillbirth remained a neglected issue absent from mention in Millennium Development Goals. An estimated 2.6 million babies are stillborn every year with highest rate in Pakistan, 43.1 stillbirths/1000 births. There is lack of good quality prospective population-based data in Pakistan regarding burden, timing and causes of stillbirths.

Methods From Jan – Dec 2012, Community Health Workers (CHWs) identified pregnant women through 3 monthly household visits. Pregnant women were then followed up till end of their pregnancy. In case of a stillbirth, a detailed verbal autopsy (VA) interview was undertaken 2 weeks after the outcome by a research assistant. VA forms were then reviewed by 2 independent physicians who assigned a cause for stillbirth. In case of disagreement, VA form was reviewed by a third physician. A consensus between two physicians was required for a definitive cause.

Results There were a total of 273 stillbirths (3.04%) reported. Stillbirth rate was 30.7/1000 births. Distribution of antepartum and intrapartum stillbirths was 83% and 17%. Three most common causes of stillbirths included pregnancy induced hypertension (37%), antepartum hemorrhage (10%) and obstructed labor (6%) (fig. 1).

Conclusions We have reported a high burden of stillbirths that take place during the intrapartum period. This reemphasizes need for good quality antenatal care in these settings. Appropriate measures need to be taken targeting most common causes of stillbirths, focusing on improved antepartum health care facilities.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To determine the IgM and IgG antibodies of rubella virus circulating among pregnant women in Kaduna State Nigeria. Rubella virus causes “German measles,” also known as “three-day measles.” This is usually a milder disease than red measles. Red/Hardmeasles or just measles is caused by Rubeola virus. The result of acute infection of the virus is a benign systemic rash which is significantly pathogenic to humans. This virus is a, positive-strand RNA virus that replicates in the cytoplasm of the infected cell. (Brooks et al., 2007). If placental infection of the virus spread during 8-10 weeks gestation it causes a chronic infection of the fetus leading to the development of congenital rubella syndrome (CRS) (Matthews et al., 2011) The effect of the infection of the several organ systems which include the eyes, ears, heart, brain, and endocrine system is known as congenital rubella infection (CRI) (Chantler et al., 2001) Rubella is endemic in Nigeria. Studies among women of childbearing age in Nigeria put seroprevalence at 66.6% in Imo, 77% in Lagos and 93.5% in Oyo (8-10). Thus as part of the control measure, the availability of an effective vaccine to prevent Rubella infection and therefore CRS, is necessary to evaluate the burden of disease in a country where MMR vaccine is not covered in the immunizations schedule or in vaccination strategy.

Methods A cross-sectional study carried out on pregnant women attending ante-natal clinic from the three different senatorial district in Kaduna state. Blood samples were screened for rubella IgM & IgG antibody using commercially produced enzyme linked immunosorbent assay (ELISA). Questionnaires were administered to obtain demographic information and possible risk factors associated with rubella virus. Data was analyzed using Epi Info 6 Version 3.5.3. Results Of the 900 pregnant women screened, 572 (63.3%) were positive for rubella IgG. The prevalence of rubella IgG was highest among the age group 21-25 with 198 (34.6%) and IgM was highest among the age group 21-25 (51.3%). The IgG test results shows that 317 (66.0%) pregnant women tested positive for their first trimester, while the IgM positive results shows 17 (33.3%) for their first trimester. Although the southern senatorial district had the highest seroprevalence 14 (35.9%) among the three centres, the differences were not statistically significant (p>0.05). Only 3 people claimed to have been vaccinated against rubella virus. Acquisition of primary education and being a housewife were insignificantly associated with raised titres. (p>0.05).

Conclusions The serological evidence of rubella virus found in pregnant women among age group &amp; their first trimester in this study is an indication that rubella is prevalent in Nigeria. It is however still necessary to immunize seronegative women against rubella before they get pregnant.

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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To describe the challenges and lessons learned for public health and providers to successfully implement public health Meaningful Use readiness guidelines and navigate from intent to submission of production data while simultaneously upgrading surveillance systems.

Introduction The Syndromic Surveillance Consortium of Southeast Texas (SSCSeT) consists of 13 stakeholders who represent 19 counties or jurisdictions in the Texas Gulf Coast region and receives health data from over 100 providers. The Houston Health Department (HHD) maintains and operates the syndromic surveillance system for the Gulf Coast region since 2007. In preparation for Meaningful Use (MU) the HHD has adapted and implemented guidance and recommendations from Centers for Disease Control and Prevention, Office of National Coordinator for Health Information Technology and others. HHD's goal is to make it possible for providers meet MU specification by facilitating the transmission of health related data for syndromic surveillance. The timing of the transition into MU overlaps with the change in syndromic surveillance systems.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective Our primary goal is to move towards establishing a causal link between binge drinking, mental health, employment and income.

Introduction One of the key questions in health economics is what is the direction of causality: does poverty cause poor health outcomes; does slow education cause poor health outcomes; does poor health result in lack of productivity; does poor health cause poor educational and income outcomes; and how is this all related to mental health if at all. We are used to breaking down data into fragments as researchers: an investigator who is predominantly focused on health outcomes will approach the problem with disease as the dependent variable and income as the conditioning variable. However, if we are interested in income inequality we will reverse the direction and income will be the dependent variable with health status as the conditioning variable. The representation above allows us to visualize data as a function of multiple fragments. For example if we want to understand how depression is related to income, one can look at the figure to observe that with lower income there is a higher likelihood of being depressed. With this simple illustration we can see that establishing causal links can be very tricky, if not incredibly challenging.

Methods Two methods are: applied descriptive analysis and estimation. We approach this without causality in mind, but with an intention to explore how behavior responds to income, education, labor and health. Our descriptive approach looks at trends in binge drinking and mental health as it affects key economic outcomes such as education, employment, and income. For each outcome we then run a simple probit model controlling for a variety of characteristics. The key co-variates in these models are income, employment and health. It is very useful to look at these simple probits because often it is hard to separate the effects of income on health, employment on income, health on employment, education on employment, health and income, and finally income, employment, health and education on mental health and substance abuse.

Results Our estimated results are rather interesting. Examining the marginal probits, e.g. figures 1.3, and 1.5, we show that there isn’t a significant income effect, nor do we find significant education or employment effects associated with binge drinking. In fact we find that in Wisconsin binge drinking is a health burden for those who are eligible to drink irrespective of education and that the effect is significant; we also find that higher levels of education increase the probability of being unemployed but not significantly. The second set of probit estimates, e.g. figure 1.7, show that poor health is indeed associated with outcomes lower employment as compared to other groups, and higher probability of depression. The last set of probits, e.g. figure 1.1, show that retired, self employed and employed ares less likely to be depressed but not significantly so, and those who are unable to work have a higher estimated probability to be depressed. Income doesn’t appear to have a significant estimated effect on depression.

Conclusions Our analysis provide insights into the question of socio-economic status (SES), binge drinking, and depression in three important ways. First, we explore the relationship between SES and binge drinking, and we find that binge drinking is SES invariant. Second we find that depression is not associated with income as it does have a strong relationship with employment status. We are in the process of unpacking the effects of SES, binge drinking and depression to move beyond associational inferences to causal inferences.


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Roles of Health Literacy in Relation to Social Determinants of Health and Recommendations for Informatics-Based Interventions: Systematic Review

Abstract

Objective To analyze tobacco use in Georgia to influence policy, systems, and environmental changes as tools to reduce its burden on health outcomes. Introduction Tobacco use is the leading cause of preventable illness and death in Georgia. About 10.1% of deaths among adults in Georgia are linked to smoking-related illnesses. Most first use of cigarettes occurs by age 18 (87%), with nearly all-first use by 26 years of age (98%). Although cigarette smoking has declined significantly since 1964, very large disparities in tobacco use remain across different sub-groups of the population. Multiple environmental, psychological, and social factors have been associated with tobacco use, including race and ethnicity, age, SES, educational accomplishment, gender, and sexual orientation. These factors within the social environment have a huge influence on motivation to begin and to continue using tobacco products for not just the individual but also certain community groups within the population. Established in 2000, Georgia Tobacco Use Prevention Program (GTUPP) is a program designed to meet the overall goal of reducing the health and economic burden associated with tobacco use for all members of the community. By working with various partners, GTUPP plans, implements and evaluates policy, systems, and environmental changes designed to reduce tobacco-related illnesses and deaths. Best practice strategies focus on the following goals: preventing the initiation of tobacco use among young people; promoting quitting among young people and adults (e.g., Georgia Tobacco Quit Line (GTQL)); eliminating exposure to secondhand tobacco smoke; and identifying and eliminating the disparities related to tobacco use among various population groups. Methods The following data collection tools were used to educate community members, local coalition groups, and policy decision-makers on the burden of tobacco use in Georgia: Youth Tobacco Survey (YTS), Youth Risk Behavioral Survey (YRBS) and Behavioral Risk Factor Surveillance System (BRFSS). These tools allow public health professionals to create messaging needed to reach different stakeholders. The following are examples of key data points that were used to influence policy, systems, and environmental change: 27,000 of middle school students and 79,000 of high school currently use tobacco (cigarettes, smokeless tobacco or cigars). Approximately 32,400 of middle school students and 72,900 of high school students say they have tried smoking electronic cigarettes (e-cigarettes). Smoking prevalence among adult males 740,000 is significantly higher than among females 510,000, and the overall smoking prevalence is highest among adults’ ages 25-34 years 292,000. Results Currently, the following policies have been adopted as a result of using surveillance to educate policy decision makers and multi-sector groups in the community at large: 116 school districts are 100% tobacco-free, 28 parks and recreation are 100% tobacco/smoke-free, 46 colleges/universities are tobacco-free, 6 cities in Georgia have a comprehensive smoke-free air law, 65 multi-unit housing (private/public) are smoke free, and 132 hospitals are tobacco free. Between June 2015 and July 2016, over 15,000 Georgia tobacco users used the GTQL services to make a quit attempt, and healthcare providers through a systems change referral approach referred 13% of the users to the GTQL. Conclusions Working with schools (K-12), parks, colleges/universities, hospitals, worksites, and municipalities to adopt tobacco-free policies and promote cessation services provides an opportunity for all members of the community to be tobacco-free. As tobacco use is associated with chronic diseases it is imperative to engage all members of the community in tobacco-free living. Removing avoidable structural and social barriers and equally implementing tobacco use prevention programs and policies is essential.

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