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Contents



#### Abstract

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## Abstract

This paper describes a public health alerting approach that has the potential to improve patient care during a public health outbreak and reduce healthcare costs, streamline the process of public health alert management and dissemination, and heighten the crucial feedback loop between public health officials and clinicians. The approach ties public health alerts into the diagnostic process and allows clinicians to more easily determine when an observed medical condition may be related to a more widespread disease outbreak. A prototype Alert Knowledge Repository (AKR) service using this approach was demonstrated within the Health Information and Management Systems Society (HIMSS) and the Public Health Information Network (PHIN) interoperability showcases in April and September 2009, respectively.

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#### Abstract

Chlamydia trachomatis is the most prevalent infectious disease in the United States. Complications include pelvic inflammatory disease (PID), ectopic pregnancy, and infertility. The cost of PID in 1998 was estimated at greater than \$1.9 billion. Screening intervention strategies are often consumed by those at low risk. The objective of this study is the development of a more cost-effective intervention strategy by employing Geographic Information Systems and Census Bureau demographic data in selected Local Health Departments in Illinois.

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## Abstract

There is a current and pressing need for a test bed of electronic medical records (EMRs) to insure consistent development, validation and verification of public health related algorithms that operate on EMRs. However, access to full EMRs is limited and not generally available to the academic algorithm developers who support the public health community. This paper describes a set of algorithms that produce synthetic EMRs using real EMRs as a model. The algorithms were used to generate a pilot set of over 3000 synthetic EMRs that are currently available on CDC's Public Health grid. The properties of the synthetic EMRs were validated, both in the entire aggregate data set and for individual (synthetic) patients. We describe how the algorithms can be extended to produce records beyond the initial pilot data set.

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