

Advanced Querying Features for Disease Surveillance Systems

Mohammad Hashemian, MS¹, Wayne Loschen, MS¹,
Joseph Lombardo MS¹, Colleen Martin, MSPH², Sanjeev Thomas, MPH³, Jerome I.
Tokars, MD, MPH², Jacqueline Coberly, PhD¹

¹Johns Hopkins University Applied Physics Laboratory, Laurel, Maryland

²Centers for Disease Control and Prevention and SAIC, Atlanta GA

³Science Applications International Corporation, Atlanta GA

BACKGROUND

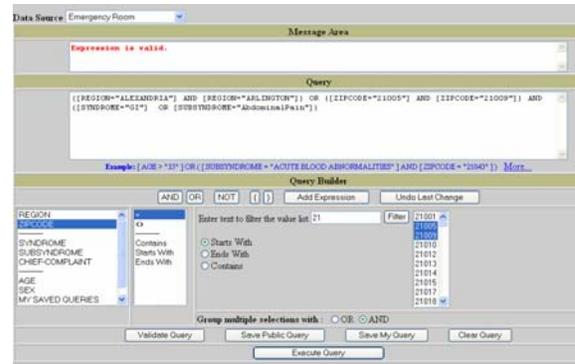
Automated disease surveillance systems that analyze data by syndrome categories have been used to look for outbreaks of disease for about 10 years. Most of these systems notify users of increases in the prevalence of reports in syndrome categories and allow users to view patient level data related to the increase. For most situations this level of investigation is sufficient, but occasionally a more dynamic level of control is required to properly understand an emerging illness in a community. During the SARS outbreak, for example, the respiratory syndrome was defined too broadly to allow users to track SARS. However, some systems, allowed users to build dynamic queries that allowed them to search their data by using the SARS case definition [1]. Users could perform free-text queries that identified records containing specific keywords in the chief complaint or specific combinations of ICD9 codes. This advanced querying capability has proven to be one of the most used features used by monitors of disease surveillance systems.

OBJECTIVES

The objective of this project is to build a new, more flexible query interface that allows users to define and build their query as if they were writing a logical expression for a mathematical computation. The interface is designed so that it can be easily adapted to fit into nearly any syndromic surveillance system. The interface will be evaluated in future versions of the ESSENCE and BioSense Systems.

METHODS

Teams from CDC and JHUAPL created prototype interfaces for the new query tool independently. Both prototypes were reviewed by the whole working group, the BioSense User's Group, and the ESSENCE working group. All of the groups provided valuable feedback that was used to create the design, requirements, and feature sets of the new interface. Figure 1 provides an example of the prototype interface.



RESULTS

The design incorporates the creation and verification of logical expressions for the user to extract and group data for analysis using all of the data elements available within the surveillance system. The next phase of the project is to evaluate the prototype tool in BioSense and ESSENCE. After the tool has been evaluated and recommendations for enhancements included, it will be made available to the surveillance community.

CONCLUSIONS

Dynamic querying features are invaluable when using existing surveillance systems to investigate outbreaks of newly emergent diseases. The AQT allows users to develop and investigate, save and share complex new case definitions. It provides a flexible interface that accommodates both advanced and novice users, checks the validity of the expression as it is built, and marks errors for users. This new tool improves the ability of electronic disease surveillance systems to detect and track user-defined case definitions.

REFERENCES

1. J. S. Lombardo, D. Buckeridge *et al.* "Disease Surveillance: A Public Health Informatics Approach." Wiley-Interscience, 2007.

Further Information : Mohammad Hashemian
mohammad.hashemian@jhuapl.edu