COACTION PUBLISHING

Disease profile development methodology for syndromic surveillance of biological threat agents

Julio Silva[1], Dino Rumoro[1], Marilyn Hallock[1], Shital Shah[1], Gillian Gibbs[1]* and Michael Waddell[2]

[1]Department of Emergency Medicine, Rush University, Chicago, IL, USA; [2]Pangaea Information Technologies, Chicago, IL, USA

Objective

The objective of this study is to outline and demonstrate the robust methodology used by Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) surveillance system to generate and validate biological threat agent (BTA) profiles.

Introduction

Detection of BTAs is critical to the rapid initiation of treatment, infection control measures and public health emergency response plans. Due to the rarity of BTAs, standard methodology for developing syndrome definitions and measuring their validity is lacking.

Methods

BTA profile development consisted of the following steps.

Step 1: Literature scans for BTAs: articles found in a literature review on BTAs that met predefined criteria were reviewed by multiple researchers to independently extract BTA-related data including physical and clinical symptoms, epidemiology, incubation period, laboratory findings, radiological findings and diagnosis (confirmed, probable or suspected).

Step 2: Data analysis and transformation: articles were randomly divided, taking into account reported diagnosis and sample size, to generate detection (75% of articles), and testing (25% of articles) profiles. Statistical approaches such as combining frequencies, weighted mean, pooled variance, min of min and max of max were utilized for combining the data from articles to generate the profiles.

Step 3: Missing data analysis: based on generated statistical and clinical judgment, specific reasonable assumptions about the missing values for each element (i.e., always reported, never reported, representative and conditionally independent) were applied to the profile. Imputed case analysis (ICA) strategies (1) used these data assumptions to fill in missing data in each meta-analysis of the summary data.

Step 4: Translation: the generated profiles and synthetic positive BTA cases were reviewed (via clinical filters and physician reviews) and programmed into GUARDIAN.

Step 5: Prior probability determination: using archived, historical patient data, the probabilities associated with each element of the profile were determined for the general (non-BTA) patient population.

Step 6: Validation and testing: multiple mutually exclusive samples of ED cases along with synthetic/real positive BTA cases were utilized to perform 10-fold cross-validation as well as testing to generate statistical measures such as positive predicted value, negative predicted value, sensitivity, specificity, accuracy and receiver operating characteristic curve (ROC) for each BTA. To demonstrate the applicability and usability of BTA methodology, severe acute respiratory syndrome (SARS) was chosen since differentiating SARS symptoms from regular influenza is difficult and presents challenges for even robust surveillance systems.

Results

Literature scan yielded 34 articles with 4265 cases and 90 unique signs, symptoms and confirmatory features (frequency data = 68 and continuous data = 22) for SARS. After combining the data and assigning the assumptions, there were 18 representative, 63 conditionally independent and 9 confirmatory features.

Applying the BTA methodology for SARS, the positive predicted value, negative predicted value, sensitivity, specificity and accuracy based on 10-fold cross-validation were 55.7%, 94.6%, 74.8%, 88.1% and 85.8%, respectively. An ROC curve analysis revealed an area under the curve of 0.929. The main features contributing toward identifying the positive SARS cases were fever, chills/rigors, nonproductive cough, fatigue/malaise/lethargy and myalgias. The identified features were in agreement with clinicians' judgment.

Conclusions

The GUARDIAN BTA profile development methodology provides a sound approach for creating disease profiles and a robust validation process even in a BTA (e.g., SARS) that may closely resemble regularly occurring diseases (e.g., influenza). The BTA profile development methodology has been successfully applied to other BTAs such as botulism, brucellosis and West Nile virus, with high sensitivity and specificity.

Keywords

Biological threat agents; real-time surveillance; surveillance methodology

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*Gillian Gibbs
E-mail: Gillian_Gibbs@rush.edu

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COACTION PUBLISHING

Surveillance in New Jersey—from anthrax to automation

Teresa Hamby*, Stella Tsai and Lisa McHugh

NJ Department of Health and Senior Services, Trenton, NJ, USA

Objective

To describe the improvements in New Jersey's Emergency Department surveillance system over time.

Introduction

In the summer of 2001, New Jersey (NJ) was in the process of developing surveillance activities for bioterrorism. On September 11, 2001, the United States suffered a major terrorist attack. Approximately a month later, anthrax-laced letters were processed through a NJ Postal Distribution Center (PDC). As a result of these events, the state instituted simplistic surveillance activities in emergency departments (EDs). Over time, this initial system has developed into a broader, more streamlined approach to surveillance that now includes syndromic data, e.g., Influenza-like illness (ILI), as well as the use of technology (automated surveys, real-time data connections and alert analysis), to achieve surveillance goals and provide daily information to public health partners in local health departments and DHSS response colleagues.

Methods

Daily response rates over time were analyzed to determine whether enhancements to surveillance produced any improvement in participation by EDs. During the timeframe used for the study, the total number of EDs varied due to facility closures and reorganizations and, therefore, daily response was measured by using the percentage of facilities responding each day versus the actual number. The study was broken into three different time periods: (1) December 2001, which is when the state's surveillance began, to August 2004, prior to updates in anticipation of the Republican National Convention in nearby New York City; (2) August 2004, when a more technologically advanced method was introduced, to April 2009; and (3) April 2009 when the Novel H1N1 Influenza A outbreak occurred and more sophisticated data collection mechanisms were implemented to present day.

Results

With each implementation of a new form of data collection and more advanced analysis, the response rate increased (see Fig. 1). In addition, the time involved for surveillance activities decreased for DHSS staff since increased automation led to fewer errors and a reduced need for follow up.

Conclusions

As automation in surveillance activities has increased, participation rates of facilities improved as well. Hospital staff became more engaged when there was a more defined purpose to reporting ED visits and admissions (e.g., The Republican National Convention and the H1N1 Novel Influenza A outbreak). Based on the improvements observed, the state is undertaking a project to move all NJ EDs into a real-time, syndromic surveillance system. This implementation is expected to further enhance data reporting and increase response rates beyond the current 86.4%.

Keywords

Surveillance; emergency department; participation

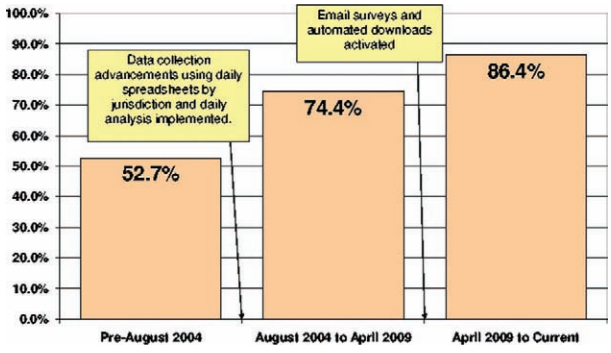

Fig. 1. Facility response rates over time.

Acknowledgments

NJ regional epidemiologists; Hospital infection control and ED staff; HMS, Inc.; DHSS OITS staff.

***Teresa Hamby**
E-mail: Teresa.Hamby@doh.state.nj.us

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COACTION PUBLISHING

Cloud computing for syndromic surveillance

Frank Hardisty*

The Pennsylvania State University, University Park, PA, USA

Objective

To describe how use of cloud computing resources can improve the timely provision of disease surveillance analyses.

Introduction

Two significant barriers to greater use of syndromic surveillance techniques are computational time and software complexity. Computational time refers to the time for many methods (for example, scan statistics and A Multidirectional Optimum Ecotope-Based Algorithm [AMOEBA] statistics) to create reliable results. Software complexity refers to the difficulty of setting up and configuring suites of software to collect data, analyze it and visualize the results. Both of these barriers can be partially surmounted by the use of cloud computing resources.

Methods

We used Amazon's EC2 (Elastic Compute Cloud) services to experiment with cloud computing for syndromic surveillance. We applied two cloud service models: Infrastructure as a Service (IaaS) and Software as a Service (SaaS).

Our first goal was to apply cloud computing technologies in order to reduce computational time needed for syndromic analyses. Scan statistics, due to their reliance on Monte Carlo simulation to find confidence levels, are particularly well suited to being improved by parallel computation. We used the R package DCluster to calculate scan statistics and combined that with the SNOW (Simple Network of Workstations) package. We also experimented with using cloud computing to parallelize the AMOEBA approach to cluster detection.

Our second goal was to determine the practicality of easing the barrier of software complexity. To that end, we created software packages that include data import, analysis and visual presentation of results and released them as freely available virtual machines, or images, for the public to use. The GeoViz Toolkit was one of the software packages delivered in this manner (Fig. 1).

Fig. 1. The GeoViz Toolkit is shown with multiple views of rates of ILI. The spatiotemporal clustering algorithms in the GeoViz Toolkit, as well as the multiple view visualizations, are examples of syndromic analytic functions that can be improved using cloud computing.

Results

We found that both Infrastructure as a Service and Software as a Service cloud computing service models can help reduce barriers to effective use of sydromic surveillance methods. Easy provision of many computers allowed us to speed up the computational times by an order of magnitude. The creation of integrated software services to perform disease surveillance is the easiest way to deliver complex functionality.

Conclusions

We conclude that, in the future, cloud computing can and should play a more prominent role in disease surveillance.

Keywords

Cloud computing; scan statistics; informatics

Acknowledgments

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***Frank Hardisty**
E-mail: hardisty@psu.edu

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COACTION PUBLISHING

Natural disasters and use of syndromic surveillance: Austin, Texas Metro Area 2011

Judy Henry[1]*, Patrick Murphy[2], Janet Pichette[1], David Andersen[2] and Heather Cooks-Sinclair[1]

[1]Austin/Travis County Health and Human Services Department, Austin, TX, USA; [2]Austin/Travis County Emergency Medical Services, Austin, TX, USA

Objective

Using case studies of three natural disasters that occurred in the Austin, Texas Metro area in 2011, demonstrate the role syndromic surveillance and emergency medical services (EMS) data played during the response to each different type of disaster.

Introduction

Emergency management during a disaster entails innumerable challenges. Each disaster uniquely shapes the types and timing of information needed both to manage the disaster and to measure the impact on available resources, the environment and community systems. Traditional public health surveillance methods typically preclude providing a real-time, comprehensive estimate of public health impacts related to the disaster while the disaster is unfolding. Traditional methods can also be resource intensive and costly, require active cooperation of medical systems involved in a disaster response and are often conducted postdisaster.

Syndromic surveillance of emergency department (ED) chief complaints and over-the-counter (OTC) medication sales was reinstituted in the Austin area in the fall of 2010. In 2011, the Austin area was hit with three natural disasters: a winter ice storm; a summer of extreme heat/extended drought; and a week of significant wildfires. Each disaster varied greatly in type, size, intensity and duration. The Austin/Travis County Health and Human Services Department (A/TCHHSD), in partnership with Austin/Travis County EMS (ATCEMS), was able for the first time to provide near-real time data to emergency managers on the potential health impact during each of the 2011 disasters using the syndromic and EMS electronic data systems. The data were used to provide situational awareness and guide selected response actions during the course of the disaster, as well as document potential areas for future mitigation efforts.

Methods

A/TCHHSD uses two syndromic surveillance systems: (1) Real-time Outbreak and Disease Surveillance (RODS) system— utilizes chief complaint data from emergency department visits in 14 Austin Metro area hospitals; and (2) National Retail Data Monitor (NRDM)— utilizes OTC medications sales data. ATCEMS has an automated system to track the types of calls to EMS and transport to area hospitals. All three systems also provide data on patient age, sex, home zip code and receiving hospital. Information on the use of syndromic surveillance and EMS systems for each natural disaster (ice, extreme heat and fire) will be presented. Each case study will provide information on: (1) salient features of the natural disaster; (2) rationale for the type(s) of surveillance resources employed; (3) data analysis; (4) results; (5) data dissemination; (6) advantages and limitations; (7) lessons learned; and (8) process improvements.

Results

Ice storm: Piloted the use of 'keyword' surveillance in our jurisdiction. Local hospitals were asked to include the word 'weather' in the chief complaint of patients presenting to the ED. The major trauma hospital in the Austin area implemented keyword surveillance within 4 hours of the request. Keyword surveillance provided insight into the impact of injuries during the ice storm. This approach was essentially resource neutral, both for the health department and the hospitals. The RODS system was also used to track chief complaints of hyperthermia and exposure. Data were reported twice a day during the ice event.

Drought/heat: This is an ongoing surveillance effort. We will present RODS data and EMS data from May through September 2011 which describe the pattern of heat-related illness over time. The pattern of heat-related illness diverged over time from the heat index. These data were reported to emergency management daily during the most extreme heat index days and weekly for the rest of the summer.

Wildfires/smoke incident: We were asked to provide an estimate of the impact of air quality from the wildfires. We examined ED chief complaint data, OTC medication sales and EMS data. These data are still being analyzed.

Conclusions

Syndromic surveillance/EMS data systems are extremely valuable in providing situational awareness during an emergency incident. Use of electronic data systems are essentially resource neutral and can provide near real-time data. These systems do not replace the need for traditional disease/injury surveillance but can help fill a need during a crisis. Response partners must be educated as to the limitations of the systems.

Keywords

Syndromic surveillance; EMS; emergency management; natural disaster; public health

***Judy Henry**
E-mail: judy.henry@austintexas.gov

COACTION PUBLISHING

Application of event-based biosurveillance to the 2011 *E. coli* outbreak in Germany

Emily Iarocci*, Ersi Polakis, Oliver Thalen, Noele Nelson and David Hartley

Georgetown University Medical Center, Washington, DC, USA

Objective

To demonstrate how event-based biosurveillance, using direct and indirect indications and warning (I&W) of disease, provides early warning and situational awareness of the emergence of infectious diseases that have the potential to cause social disruption and negatively impact public health infrastructure, trade, and the economy (1). Specifically, tracking of I&W during the 2011 enterohemorrhagic *Escherichia coli* (EHEC) O104:H4 outbreak in Germany and Europe was selected to illustrate this methodology.

Introduction

Argus is an event-based, multilingual surveillance system, which captures and analyzes information from publicly available Internet media. Argus produces reports that summarize and contextualize I&W of emerging threats and makes these reports available to the system's users (1). The significance of the EHEC outbreak analyzed here lies primarily in the fact that it raised epidemiological questions and public health infrastructure concerns that have yet to be resolved, and required the development of new resources for detecting and responding to newly emerging epidemics (2).

Methods

Argus reports meeting the following inclusion criteria were reviewed: (1) entities: *E. coli* and food/crop contamination, (2) location: Germany and the European Union (EU), (3) time period: May–July 2011. The reports were reviewed for relevant I&W with the primary goal of identifying factors that inhibited effective control of the outbreak and resulted in public health infrastructure strain. Geospatial visualizations of the Argus outbreak reports were created as the event unfolded.

Results

On May 23, a surge in EHEC infections was reported at hospitals mainly in northern Germany; the outbreak was unusual in that it caused atypically severe symptoms in adult females. By May 26, state health authorities had identified over 600 EHEC cases, including 214 severe cases with hemolytic uremic syndrome (HUS), and confirmed the causative agent as a highly virulent HUS-associated EHEC 41 strain belonging to serotype O104:H4. Faced with a rapidly growing number of cases, health authorities notified the EU of a potential public health emergency of international concern and implemented new surveillance systems (2). Media reports suggested that the public health infrastructure was strained to a breaking point, as hospitals in northern Germany issued appeals for blood donations and transferred cases to hospitals in neighboring states. These problems were compounded by the lack of an effective HUS treatment, causing health officials to resort to an emergency experimental treatment instead. As the outbreak continued to spread, up to 130 cases primarily associated with travel were detected in 13 other European countries (3). The EU responded by implementing a new case definition twice over the course of 1 month, to allow for effective surveillance and treatment of cases (3, 4). By June 29, an investigation launched by the European Food Safety Agency (EFSA) had determined that contaminated fenugreek seeds imported from Egypt were the most probable source of the outbreak (3, 5). Previous efforts to locate the source of infection had failed, resulting in strained trade relations and major economic losses among EU member states (3). On July 26, Germany's Robert Koch Institute (RKI) declared the outbreak over and reported a cumulative total of 4321 EHEC cases, including 852 HUS cases and 52 fatalities (6).

Conclusions

This study highlights the challenges faced in providing a timely response to a rapidly spreading infectious disease outbreak and the role that event-based biosurveillance can play in quickly identifying areas for public health intervention. Argus reporting identified that the EHEC outbreak fundamentally challenged the public health system in Germany, by exposing deficiencies in infectious disease surveillance. More importantly, it evidenced that even a strong public health system must be able to adapt rapidly to challenges posed by the changing epidemiology of infectious diseases (2). To that end, an interdisciplinary approach to event-based biosurveillance that allows for the timely detection of outbreaks and astute analysis of pertinent I&W is of paramount importance.

Keywords

Event-based biosurveillance; infectious disease; social disruption; *E. coli* O104:H4; food contamination

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***Emily Iarocci**
E-mail: iarocci@isis.georgetown.edu

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COACTION PUBLISHING

Unstructured free-text data and Meaningful Use

Charles Ishikawa[1]*, Michele E. Day[3], Wendy Chapman[3], Laura Streichert[1] and David L. Buckeridge[2]

[1]International Society for Disease Surveillance, Brighton, MA, USA; [2]McGill University, Montreal, QC, Canada; [3]University of California, San Diego, San Diego, CA, USA

Objective

To better inform health IT standardization practices, specifically related to Meaningful Use, by describing how US public health agencies use unstructured, free-text EHR data to monitor, assess, investigate and manage issues of public health interest.

Introduction

In 2010, as rules for the Centers for Medicaid and Medicare Electronic Health Record (EHR) Incentive Programs (Meaningful Use) (1) were finalized, ISDS became aware of a trend toward new EHR systems capturing or sending emergency department (ED) chief complaint (CC) data as structured variables without including the free-text. This perceived shift in technology was occurring in the absence of consensus-based technical requirements for syndromic surveillance and survey data on the value of free-text CC to public health practice.

On January 31, 2011, ISDS, in collaboration with the CDC BioSense Program, recommended a core set of data for public health syndromic surveillance (PHSS) to support public health's participation in Meaningful Use. This study was conducted to better support a requirement for ED CC as free-text, by investigating the relationship between the unstructured, free-text form of CC data and its usefulness in public health practice.

Methods

PHSS analysts from 40 public health agencies that contribute syndromic data to the ISDS Distribute project were asked to take an online survey.

The survey, developed in consultation with state- and local-level syndromic surveillance experts and implemented using SurveyMonkey®, consisted of 15 questions, which were crafted to obtain data in four areas: (1) basic system design and coverage; (2) CC data formatting and classification practices; (3) CC data use; and (4) impact of codifying CC on PHSS capabilities.

Participants had 2 weeks to complete the survey. ISDS staff contacted nonrespondents to encourage participation 7 and 3 days before the end of the survey period. Qualitative survey data from open-ended questions were reviewed and grouped into themes or categories.

Results

PHSS epidemiologists or analysts from 87.5% (35 out of 40) of the Distribute-contributing health authorities completed the survey. Within the respondent group, 9 cover local jurisdictions, 25 state jurisdictions, and one was from CDC BioSense. Combined, the 35 agencies captured EHR data from 1344 ED.

Survey results revealed that 97% of participants receive ED patient CC data in free-text (Fig. 1). ED triage staff presumably capture these data in an EHR, based on a patient's presenting condition as an open-ended, unstructured memo. Some survey participants also reported receiving ED CC in coded formats, either as ICD-9 codes (34%) or as text from a drop-down menu (20%).

A majority of survey respondents (74%) reported having used free-text CC to monitor public health in over 17 different emergencies over the past 2-3 years. Most frequently, free-text CC was used to monitor the impact of H1N1, heat waves, infectious disease outbreaks, and winter storms.

Conclusions

Through a national survey of PHSS epidemiologists, ISDS identified that public health agencies benefit from free-text CC data, and this format needs to be maintained. ISDS also learned that as newly certified EHR systems are switching CC from free-text to a structured format, the advantages for making this transition are not fully known to public health practitioners.

Keywords

Syndromic surveillance; Meaningful Use; free-text; EHR

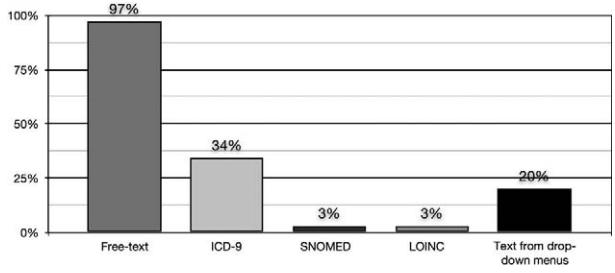

Fig. 1. Data formats in which ED CC are received by public health authorities for syndromic surveillance. Most syndromic surveillance practitioners (97%) receive and use ED CC data in a free-text format. A significant number of survey respondents also report receiving these data as ICD-9 (34%) or as text from a drop-down menu (20%).

Acknowledgments

Mr. Aaron Kite-Powell, Dr. Joseph Gibson and Ms. Julia Gunn provided valuable insight on early survey iterations.

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***Charles Ishikawa**
E-mail: cishikawa@syndromic.org

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COACTION PUBLISHING

Improving syndromic surveillance for nonpower users: NC DETECT dashboards

Amy Ising[1]*, Meichun Li[1], Lana Deyneka[2], Heather Vaughan-Batten[2] and Anna Waller[1]

[1]Emergency Medicine, UNC Chapel Hill, Chapel Hill, NC, USA; [2]North Carolina Division of Public Health, Raleigh, NC, USA

Objective

To describe the development, implementation and preliminary evaluation of new dashboard interfaces in NC DETECT, designed primarily for infrequent users of NC DETECT at local health departments.

Introduction

NC DETECT provides near-real-time statewide surveillance capacity to local, regional and state-level users across NC with twice daily data feeds from 117 (99%) emergency departments (EDs), hourly updates from the statewide poison center and daily feeds from statewide EMS runs and select urgent care centers. The NC DETECT Web application provides access to aggregate and line listing analyses customized to users' respective jurisdictions. The most active users are state-level epidemiologists (DPH) and hospital-based public health epidemiologists (PHEs). The use of NC DETECT is included in PHE job descriptions, and functionality has been developed specifically to meet their surveillance needs, including data entry of aggregated laboratory results for flu and respiratory panels. Interviews of local health department (LHD) users completed as part of an evaluation project have suggested that functionality specifically tailored to LHDs may increase their use of the NC DETECT Web application (1). As of June 2011, there were 139 LHD users with active NC DETECT accounts (out of 384 total users with active accounts).

Methods

Initial information-gathering sessions were held with DPH stakeholders on April 7 and 12, 2011. Mock-ups based on these meetings were discussed with LHD focus groups on April 13 and 14 via Web conference. A later version of the prototype was shown in person at a health department epidemiology team meeting on May 13, and feedback from that meeting was incorporated into the initial release of the dashboards, which were made available to LHD users on June 14, 2011. On June 21, 2011, drill down functionality was added to the dashboards, and on June 30, 2011, the dashboards were made available to DPH users. The dashboards were developed in Java to integrate with our existing Web application using Java and jQuery.

Results

The dashboards are organized by tabs; current tabs include Overview (Fig. 1), Hot Topics, Heat, Animals/Vectors, Hurricane, Foodborne, PHE Weekly Report summary and users comments on signals and events investigations. The tabs will change in subject in the fall and winter months, e.g., including a Flu tab. The average number of LHD logins into the NC DETECT Web application has not increased significantly since the release of the dashboards (Fig. 2).

Conclusions

Average LHD logins per week for June and July 2011 (n = 15) are significantly lower than for PHEs (45 per week on average for 12 total PHE level users). Dashboard interfaces may be particularly beneficial and used more during large scale events of public health significance monitoring, e.g., the 2012 Democratic National Convention in Charlotte, NC. We will continue to work with LHD users to design easy-to-use reports to meet their surveillance needs.

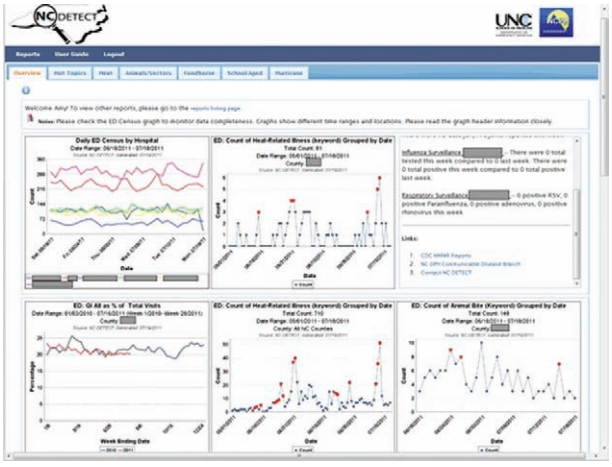

Fig. 1. Screenshot of NC DETECT overview tab on the dashboard interface.

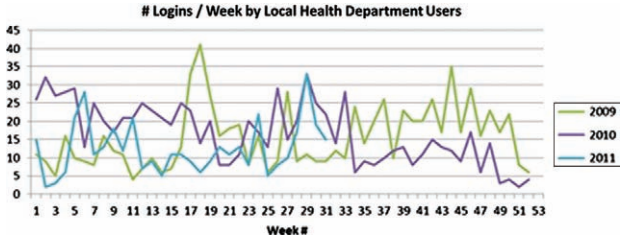

Fig. 2. Number of logins per week by local health department users of NC detect (2009–2011).

Keywords

Dashboards; all-hazards surveillance; user interface design

Acknowledgments

The authors wish to thank Clifton Barnett for his assistance in compiling user login information.

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*Amy Ising
E-mail: ising@ad.unc.edu

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COACTION PUBLISHING

The exploration of various methods for *Shigella* outbreak detection

Xin Jin*, Jian-Hua Chen, Charlene Weng, Bryon Backenson, Dina Hoefer and Hwa-Gan Chang

New York State Department of Health, Albany, NY, USA

Objective

To explore the possibility of using statistical methods to detect Shigella outbreaks, assess the effectiveness of the methods to signal real outbreaks, provide manageable information for follow-up activities and avoid unnecessary surveillance work.

Introduction

Shigella remains highly infectious in the United States, and rapid detection of Shigella outbreaks is crucial for disease control and timely public health actions. The New York State Department of Health (NYSDOH) implemented a Communicable Disease Electronic Surveillance System (CDESS) for local health departments (LHDs) to collect clinical and laboratory testing information and supplement epidemiologic information for the patients from New York State, excluding New York City, with infectious diseases. The CDESS includes reported cases that are involved in outbreaks and which constituted the base for identifying any outbreak. The selection of a fitted outbreak detection method would play a critical role in enhancing disease surveillance.

Methods

Weekly case numbers were obtained from CDESS and counted patients with Shigella who had diagnosis or specimen collection dated between January 1, 2006, and December 31, 2010. Six statistical models were applied to the weekly case numbers in generating signals to identify outbreaks, and signals were compared to the actual outbreak to evaluate their detection powers. Outbreak-related cases from CDESS were removed for the modeling purpose except for the cumulative sum-related methods, which used all cases. The sensitivity (SE), specificity (SP), positive predictive value (PPV) and negative predictive value (NPV) were calculated to evaluate the performance of each method.

General Linear method (GL)

$Yt = a + \Sigma bi\ ct, i, i = 1 \ldots 52$, where Yt is the expected number of cases in week t, ct,*i* is the dummy value which equals 1 if the week of the year for Yt is the same as *i*, else it equals 0.

Poisson method (PO)

It applies the same statistical procedure as GL except for the assumption that the case numbers follow Poisson distribution.

Time Series method (TS)

$Yt = a + bt + c1\sin(2\pi t/52) + c2\sin(4\pi t/52) + c3\sin(6\pi t/52) + d1\cos(2\pi t/52) + d2\cos(4\pi t/52) + d3\cos(6\pi t/52) + at$, where Yt is the expected number of cases in week t, and at is the random error.

A signal was generated when the case number exceeded the 95% confidence limit for the prediction value from the above three methods.

Cumulative Sum method (CuSum)

A signal was created when the case number exceeded the baseline mean, i.e., mean of previous two weeks, plus three standard deviations.

Historical Limit method (HL)

Similar procedures applied as CuSum except that data for the prior 8 weeks of the last year were used as the baseline.

Negative Binomial CuSum method (NBC)

Prior 8 weeks of data excluding current week were used to calculate the baseline mean and variance, which derived the NBC parameter. A signal occurred when the parameter exceeded the threshold value.

For the purpose of evaluations, an outbreak week was defined as any week that had over two outbreak-related cases during the study period.

Results

Fourteen outbreak weeks were identified to evaluate the detection ability of the six methods. The table below summarizes the measures of each method.

Model	*SE*	*SP*	*PPV*	*NPV*	*Total No signals*
GL	50%	98%	63%	97%	11
PO	93%	82%	23%	99%	57
TS	50%	97%	50%	97%	14
CuSum	7%	99%	33%	95%	3
HL	64%	90%	27%	98%	33
NBC	43%	80%	11%	96%	56

The SPs did not vary much across six methods while the SE of the PO method was higher than the rest. The PPV ranged from 11% to 63%, and the NPV did not vary greatly. The total numbers of signals generated from the PO and NBC methods were higher than the rest.

Conclusions

Among the above six methods, the PO method had the ability to detect a high percentage of true outbreaks. However, the high number of signals and the relatively low PPV indicated the limitations of the PO method. Other information such as geographical clusters should be considered in determining further public health investigations as needed.

***Xin Jin**
E-mail: xxj01@health.state.ny.us

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COACTION PUBLISHING

Linking informatics and cross-programmatic public health strategic objectives

Geraldine Johnson*, Sarah Goff, Drew Hanchett, Hope Plavin, and Guthrie Birkhead

New York State Department of Health, Office of Public Health, Albany, NY, USA

Objective

To develop strategic objectives necessary to optimize the collection, integration and use of information across public health programs and internal and external partners for improving the overall health and safety of people and their communities.

Introduction

There is national recognition of the need for cross-programmatic data as well as system coordination and integration for surveillance, prevention, response and control implementation. To accomplish this, public health must develop an informatics competency and create an achievable roadmap, supported by performance measures, for the future. Within the New York State Department of Health, Office of Public Health (OPH), a cross-organizational and cross-functional Public Health Information Management Workgroup (PHIM-WG) was formed to align public health information and technology goals, objectives, strategies and resources across OPH. In June 2011, the OPH Performance Management Initiative, funded by the Centers for Disease Control and Prevention's National Public Health Improvement Initiative, offered strategic planning workshops, funded by the Association for State and Territorial Health Officials (ASTHO), to PHIM-WG.

Methods

Senior management of the major programmatic areas within OPH including, Communicable and Chronic Disease, Family Health, HIV/AIDS, Environmental Health and Wadsworth Center Laboratory, identified representatives to participate in PHIM-WG. Informatics, information technology (IT) and information management (IM) literature was reviewed to determine a framework upon which to build the strategy (1). Words and concepts with multiple interpretations were identified and agreed-upon definitions were used for planning discussion. An assessment of the as-is and desired state formed the basis of the strategic objectives and destinations. A community-balanced scorecard (CBSC) approach (2), grounded in the Public Health Accreditation Board Essential Services (PHAB-ES), is being used to guide the development of a strategic plan, to include performance metrics.

Results

PHIM-WG includes physician, epidemiology, program management, policy and planning, IT, quality improvement and project management representatives. IM, composed of the integration of program, processes, policy and technology, was the selected framework. An initial informatics lexicon was developed. Using CBSC, identified strategic destinations were aligned with PHAB-ES objectives, which were then adapted and aligned with the IM framework. An IM vision and strategy map, including strategic objectives and destinations, were produced. Public health IM desired state, objectives, and activities were linked to the PHAB-ES within four major community perspectives; health status, implementation, process and learning, and assets. PHIM-WG is working to produce a more-fully developed strategy and implementation plan, including engaging internal and external partners, defining associated performance metrics to measure progress to the desired state and aligning with NYSDOH strategic planning efforts.

Conclusions

As a cornerstone of public health, IT/IM should be and can be aligned with or directly linked to the public health essential services. The development and promotion of a common informatics lexicon and workforce engagement and training are critical to public health, especially for advancing data analysis, use, and dissemination capabilities. PHAB-ES-based IM strategic planning can be an essential first step for community collaborators to define the vision, objectives and measurable activities to advance the technology, research and practice of public health surveillance.

Keywords

Informatics; information management; strategic planning; public health; cross program

Acknowledgments

NYSDOH OPH Public Health Information Management Workgroup, Nancy Schultz Consulting, ASTHO and Results That Matter (RTM) Team

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***Geraldine Johnson**
E-mail: gsb03@health.state.ny.us

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COACTION PUBLISHING

Using syndromic surveillance to assist in a meningitis outbreak investigation

Monica Luarca, Emily Kajita*, Cheryl Faustino, Megan Jones and Bessie Hwang

Acute Communicable Disease Control Program, Los Angeles County Department of Public Health, Los Angeles, CA, USA

Objective

To describe the complementary usage of electronic emergency department (ED) data, coroner deaths and 911 dispatch call center data in a bacterial meningitis outbreak.

Introduction

Beginning on March 13, 2011, ACDC experienced an unusual increase in reported bacterial meningitis cases in Los Angeles (LA) County. Early in the investigation, there were few epidemiological links between the cases. Three cases were homeless; two resided at the same Skid Row shelter in downtown LA. ACDC assessed its syndromic surveillance databases to help gauge the scope of the outbreak and detect potentially overlooked cases.

Methods

Electronic ED chief complaints (CC) from January 1, 2011, to April 10, 2011. were queried from eight EDs within an 11-mile radius of Skid Row. Only visitors with resident zip codes that corresponded to Skid Row or that were blank to account for homelessness were included. Visits were reviewed if CC included keywords based on common meningitis symptoms and also those of confirmed cases.

Coroner deaths from the same time period were reviewed for location of death and homeless status. Real-time LA City emergency dispatch calls were also reviewed if they were made from the same homeless shelter in which the two confirmed cases resided.

Results

Two hundred and thirty-eight ED visits met the meningitis syndrome definition; however, there was no substantial increase (Fig. 1). Within the same zip code catchment area, there were no ED visitors with mention of homelessness or shelter residence in their CC.

There was no overall increase in the total number of homeless coroner deaths. Two of 45 deaths took place in shelters—one death in January from 'cardiomyopathy' that occurred at the homeless shelter of interest, and another nonspecific shelter death in March from 'strep pneumonia'.

Forty-one 911 ambulance calls were made from the homeless shelter associated with the confirmed meningitis cases. While there was no overall increase in call volume, one call matched a confirmed case fatality.

Conclusions

One limitation of ED data in this investigation is that they do not contain patient resident addresses, making restriction to the homeless or shelter residents impossible. While no additional cases were found, the absence of an increase provides validation that a large countywide outbreak had not occurred.

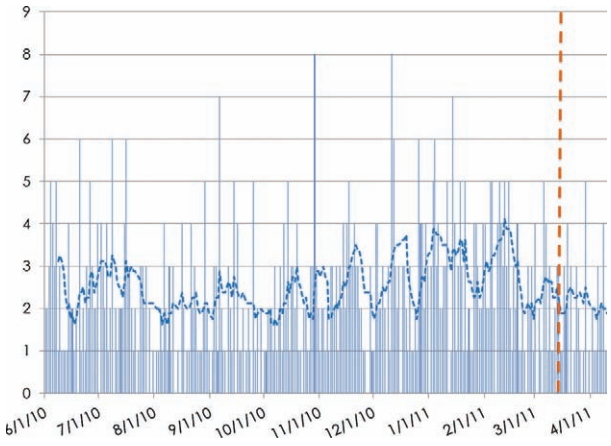

Fig. 1. ED visits per day in customized meningitis syndrome category. Dotted vertical line indicates date of first confirmed case.

Both coroner and 911 call databases were more flexible than ED data, containing fields facilitating focused queries on the key epidemiological links of homelessness and shelter residence. Coroner data are limited, however, in that there is a 2-day reporting lag. While many homeless deaths were found, few had precisely reported death locations.

Many 911 calls were reported from the shelter of interest. While medical information was vague, additional details enabled ACDC to match one call to a confirmed case. Follow-up for diagnosis information is possible when ED transportation information is present. Precise caller locations make 911 calls particularly useful for investigations with a strong emphasis on location such as point source outbreaks. Querying preestablished ED visit, coroner death, and 911 call feeds can provide a relatively quick supplement to traditional outbreak investigations.

Keywords

Coroner; 911 call; dispatch; emergency department; outbreak

Acknowledgments

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***Emily Kajita**

E-mail: ekajita@ph.lacounty.gov

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COACTION PUBLISHING

Automated chronic disease surveillance and visualization using electronic health record data

Michael Klompas[1,2*], Chaim Kirby[3], Jason McVetta[4], Paul Oppedisano[5], John Brownstein[2,3], Kenneth Mandl[2,3] and Richard Platt[1,2]

[1]Harvard Pilgrim Health Care Institute, Boston, MA, USA; [2]Harvard Medical School, Boston, MA, USA; [3]Children's Hospital Informatics Program, Boston, MA, USA; [4]Heliotropic, Inc., Los Angeles, CA, USA; [5]Massachusetts Department of Public Health, Boston, MA, USA

Objective

Develop methods for automated chronic disease surveillance and visualization using electronic health record (EHR) data.

Introduction

Chronic diseases are the leading causes of mortality and morbidity for Americans but public health surveillance for these conditions is limited. Health departments currently use telephone interviews, medical surveys and death certificates to gather information on chronic diseases but these sources are limited by cost, timeliness, limited clinical detail and/or poor population coverage. Continual and automated extraction, analysis and summarization of EHR data could advance surveillance in each of these domains.

Methods

We leveraged the Electronic medical record Support for Public Health (ESP) surveillance platform to create a chronic disease surveillance module. ESP is an open source software (esphealth.org) that reads structured EHR data, analyzes them for events of public health interest and communicates findings to public health agencies. We created algorithms to identify diabetes types using a combination of diagnosis codes, laboratory tests and medication prescriptions. We then applied these algorithms to the ESP installation in Atrius Health, a multisite, ambulatory practice with over 700,000 patients. We programmed ESP to create patient level linelists each night that detail patients' demographics (age, sex, race/ethnicity and zip code), vitals (body mass index, blood pressure and pregnancy status), key laboratories (hemoglobin A1C and cholesterol levels), diabetes type and care (medications and medical nutrition counseling). De-identified linelists are transmitted nightly to a secure website called the 'RiskScape' that automatically maps selected health indicators and stratifies results by age group, race/ethnicity, year of diagnosis and body mass index. Users can customize indicators and stratifications displayed by RiskScape.

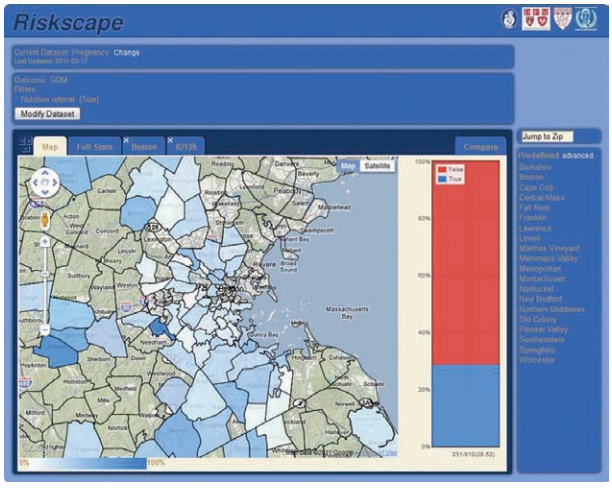

Fig. 1. Automatic mapping of disease prevalence.

Fig. 2. Automatic stratification by region, age, and race/ethnicity.

Results

The RiskScape presents a timely, clinically rich picture of the health of large populations using EHR data that is refreshed nightly. Examples of RiskScape views and report options are shown in Fig. 1 and 2. Fig. 1 maps the rate of nutrition referrals by zip code amongst women with gestational diabetes. Fig. 2 stratifies these results by age and race/ethnicity within the greater Boston area and compares them to statewide averages.

Conclusions

Automated analysis and presentation of EHR data can provide a rich, timely picture of chronic disease prevalence, care and complications for large populations. This technology has a great potential to advance public health practice by highlighting specific populations with gaps in care that merit targeted interventions.

Keywords

Chronic disease; surveillance; electronic health records; visualization; diabetes

***Michael Klompas**
E-mail: mklompas@partners.org

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COACTION PUBLISHING

Multistream influenza surveillance for situational awareness

Eric Lau*, Benjamin Cowling, Lai-ming Ho and Calvin Cheng

School of Public Health, The University of Hong Kong, Hong Kong

Objective

This paper describes the use of multiple influenza surveillance data for situational awareness of influenza activity.

Introduction

Much progress has been made on the development of novel systems for influenza surveillance (1, 2) or explored the choices of algorithms for detecting the start of a peak season. The use of multiple streams of surveillance data has been shown to improve performance (3) but few studies have explored its use in situational awareness to quantify level or trend of disease activity. In this study, we propose a multivariate statistical approach, which describes overall influenza activity and handles interrupted or drop-in surveillance systems.

Methods

A multivariate dynamic linear time series model was fitted to data on influenza-like illness (ILI) rates among networks of public and private general practitioners and school absenteeism rates, plus drop-in fever count data from designated flu clinics (DFC) that were created during the pandemic. The data streams were assumed to follow an underlying latent process with local linear trend. The estimated level and trend of the latent process reflect the magnitude and direction of influenza activity, which are then combined to infer an overall influenza activity index. Correlations between the estimated influenza level from the model and laboratory isolation rate were calculated to assess its performance before and during the 2009 pandemic.

Results

ILI rates from public outpatient clinics and the estimated influenza level from the multivariate model had the highest correlations with laboratory isolation data before the 2009 pandemic ($\rho = 0.57$ and 0.58, respectively) but the former was interrupted during the pandemic period due to activation of the DFC. The estimated influenza level from the multivariate model captured the influenza level well during the pandemic period ($\rho = 0.76$), significantly better than the best surveillance data in the same period (p-value $= 0.03$). The inferred influenza activity index is able to reflect the influenza activity (Fig. 1).

Conclusions

The use of a multivariate method to integrate information from multiple sources of influenza surveillance data can improve situational awareness of influenza activity, with the advantage of maintaining performance when data streams are interrupted or supplemented by additional systems during certain critical periods such as the 2009 influenza pandemic.

Keywords

Sentinel surveillance; influenza; multivariate analysis; pandemic

Acknowledgements

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***Eric Lau**
E-mail: ehylau@hku.hk

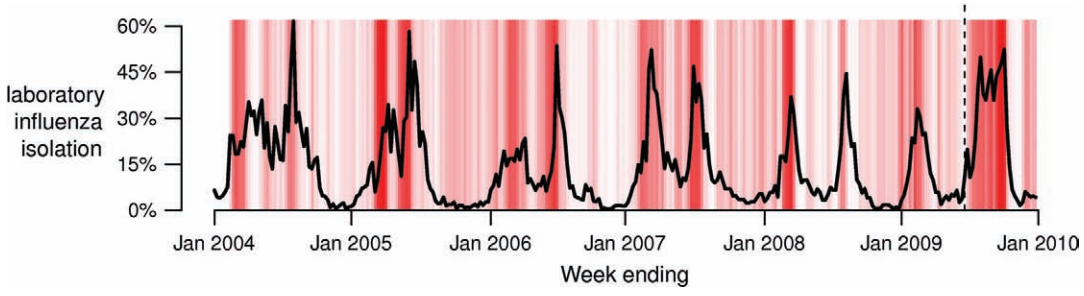

Fig. 1. Laboratory influenza detection rates from January 2004 through December 2009. The inferred influenza activity index was superimposed and color-coded from white (low) to red (high) in each panel. The vertical dashed line indicates the start of the pandemic period.

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COACTION PUBLISHING

Use of the National Poison Data System after the 2011 Japan radiological incident for surveillance of incident-related exposures in the United States

Royal Law[1,2]*, Josh Schier[2], Colleen Martin[2], Richard Thomas[3], Alvin Bronstein[3] and Arthur Chang[2]

[1]TKC Integration Services, Herndon, VA, USA; [2]Centers for Disease Control and Prevention, Chamblee, GA, USA; [3]American Association of Poison Control Centers, Alexandria, VA, USA

Objective

To describe how the National Poison Data System (NPDS) was used for surveillance of individuals with potential incident-related exposures in the United States resulting from the Japan earthquake radiological incident of 2011. Our secondary objective is to briefly describe the process used to confirm exposures identified through NPDS-based surveillance.

Introduction

NPDS is a national database of detailed information collected from each call, uploaded in near real-time, from the 57 participating regional poison centers (PCs) located across the United States. NPDS is owned and operated by the American Association of Poison Control Centers (AAPCC). Since 2001, scientists from the Centers for Disease Control and Prevention collaborated with AAPCC to use NPDS for surveillance of chemical, poison and radiological exposures. In March 2011, a 9.0 magnitude earthquake and tsunami damaged the reactors at the Fukushima Daiichi nuclear power plant in Japan, causing a radiological incident classified as a 'major accident' according to the International Nuclear Event Scale. The incident resulted in the release of radioactive iodine (I–131) into the global environment, which was detected in precipitation in parts of the United States. While no adverse health effects were expected, concerned citizens contacted public health officials at the local, state and federal levels. Many started to acquire and use potassium iodide (KI) and other iodide-containing products intended for thyroid protection from I–131, even though this was not a public health recommendation by state and federal public health agencies. Shortly after international media coverage began, regional PCs began receiving calls regarding the Japan radiological incident. State and federal health officials were interested in identifying health communication needs and targeting risk communication messages to address radiation concerns and KI usage recommendations as part of the public health response. This was done in part through NPDS-based surveillance.

Methods

A new, unique event code was created for staff of all 57 regional PCs to use for coding calls related to this incident. This enabled CDC and AAPCC to track incident-related information requests and exposure calls using NPDS. Calls involving either information requests or reported exposures to radiation, potassium iodide and other iodide-containing products were identified, reviewed and tabulated daily. For each exposure call, individual PCs were then contacted by AAPCC officials to obtain additional data not uploaded to NPDS. CDC epidemiologists and toxicologists reviewed these data daily using set criteria to determine if a true exposure had occurred. Aggregate NPDS data were reported daily to CDC's Emergency Operations Center leadership to enhance situational awareness.

Results

During the time period that the CDC Emergency Operations Center (EOC) was activated for this response (March 11 to April 18), there were 404 calls nationally regarding the Japan radiological incident. Three hundred and forty (84%) were calls requesting information about KI, iodide/iodine containing products or radiation associated with the Japan radiological incident. The remaining 64 calls (16%) were potential incident-related exposure calls. Of these, KI (n = 20), other iodide-containing products (n = 17) and radiation (n = 15) were reported most frequently. The number of information calls peaked on March 16 (n = 54), and the number of exposure calls peaked on March 17 (n = 9). Thirty-four (53%) of exposure calls were confirmed KI and iodide/iodine containing product exposures, 23 (36%) were calls regarding incident-related exposures, which were unable to be confirmed, and 7 (11%) were determined to be nonexposures.

Conclusions

Collaboration between CDC, AAPCC and PC staff were crucial to surveillance efforts during the Japan radiological incident response. National surveillance using NPDS demonstrated utility for conducting near real-time human health effects and exposure surveillance associated with a known public health emergency. Surveillance efforts identified confirmed exposures to KI and iodide-containing products. The CDC used this information, along with other media sources, to identify health communication needs and implement appropriate health messaging.

Keywords

Japan; radiation; surveillance

*Royal Law
E-mail: hua1@cdc.gov

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COACTION PUBLISHING

U.S. destinations of newly arrived immigrants and refugees with suspect TB, 2009–2010

Deborah Lee*, Richard Chang, Kevin Liske, Sharmila Shetty, Heather Burke, Rossanne Philen and John Painter

CDC, Atlanta, GA, USA

Objective

To conduct preliminary assessment of the U.S. destination locations among newly arriving immigrants and refugees with tuberculosis (TB) classifications.

Introduction

Immigrants and refugees are required to undergo TB screening before entering the United States (1). Nearly 700 overseas panel physicians designated by the U.S. Department of State perform these screenings (2). Over 450,000 new immigrants and nearly 80,000 refugees arrive in the United States each year with their medical documentation (3). Those with culture positive or smear positive TB are treated prior to arrival in the United States; those with radiographic or symptomatic TB but negative smears and culture may enter the United States with Class B TB (4). After arrival, CDC's Electronic Disease Notification system (EDN) notifies the health departments of the results of overseas examinations.

Methods

We assessed destination information from the EDN system for immigrants and refugees arriving during 2009 and 2010 with TB disease (Class A TB with waiver) or a radiographic TB without positive smear or culture for TB (Class B1), or LTBI (Class B2), or contact with a TB case. The destination information was mapped with ArcGIS software to the county level and aggregated at the national level. Data were categorized by region according to the 10 Agency for Toxic Substances and Disease Registry (ATSDR) regions (5). Since the change of location after arrival can be entered into the EDN system by the health department, this information was assessed for the system's ability to provide secondary migration information.

Results

The EDN system provided 23,348 and 24,707 notifications with TB classifications during 2009 and 2010, respectively. The largest number of notifications occurred in the region comprising Arizona, California, Hawaii and Nevada (ATSDR Region 9); these increased by 8.2% from 9,058 in 2009 to 9,802 in 2010. Over 80% of these notifications are for people whose birth countries are the Philippines, Mexico and Vietnam. Notifications of persons born in Mexico decreased by 10.8% from 2009 to 2010 in ATSDR Region 9 whereas those born in the Philippines and Vietnam increased by 2.8% and 72.9% respectively. Information on secondary migration was reported to the EDN system by health departments on 1,307 (5.6%) and 1,880 (7.6%) records for 2009 and 2010, respectively. The median number of days from arrival to updated location was 115 in 2009 and 70 in 2010.

Conclusions

Over one third of immigrant and refugee arrivals with TB notifications were in the region comprising Arizona, California, Hawaii and Nevada. The increase in TB notifications in this region was attributed to those born in Vietnam. Secondary migration data were available, but the relatively early change in locations may indicate corrections to initial destination data rather than true secondary migration.

Keywords

Tuberculosis; immigrants; refugees; electronic disease notification; EDN

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***Deborah Lee**
E-mail: DLEE1@cdc.gov

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COACTION PUBLISHING

In silico surveillance: highly detailed agent-based models for surveillance system evaluation and design

Bryan Lewis[1]*, Stephen Eubank[1], Allyson Abrams[2] and Ken Kleinman[2]

[1]Virginia Tech, Blacksburg, VA, USA; [2]Harvard, Boston, MA, USA

Objective

To create, implement and test a flexible methodology to generate detailed synthetic surveillance data providing realistic geospatial and temporal clustering of baseline cases.

Introduction

Modern public health surveillance systems have great potential for improving public health. However, evaluating the performance of surveillance systems is challenging because examples of baseline disease distribution in the population are limited to a few years of data collection. Agent-based simulations of infectious disease transmission in highly detailed synthetic populations can provide unlimited realistic baseline data.

Methods

Dynamic social networks for the Boston area (4.1 million individuals) were constructed based on data for individuals, locations and activity patterns collected from the real world. We modeled a full season of endemic influenza-like illnesses (ILI), healthcare seeking behavior and a surveillance system for outpatient visits. The resulting in silico surveillance data contain the demographics and complete history of disease progression for all individuals in the population; those who are in a specified surveillance system create a data stream of ILI visits. Outbreaks of influenza are artificially inserted into this surveillance data. Outbreak detection using space-and-time scan statistics was used to analyze the background with and without the inserted outbreaks. The performance of the algorithm was assessed under different levels of coverage and catchment distributions. One hundred unique baseline data sets were generated. Twelve artificial outbreaks were inserted in each. Six different surveillance system designs were assessed.

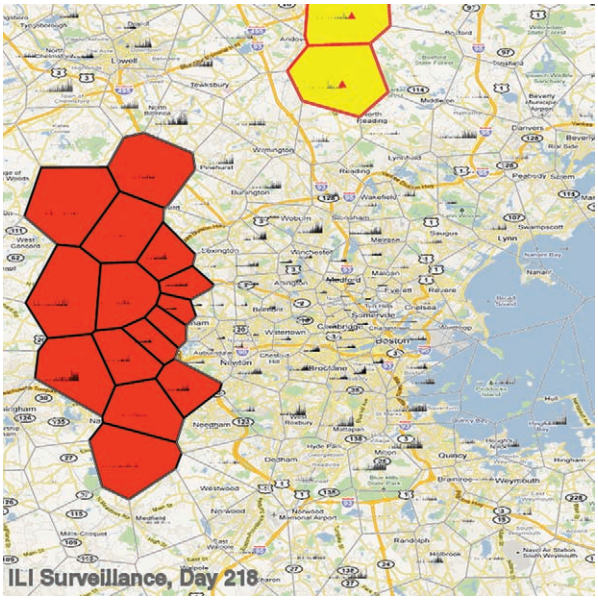

Fig. 1. Simulated ILI surveillance data for downtown Boston as captured by simulated surveillance system. Surveillance counts per day centered in each zip code location are shown as histograms within each zip code. Detection of an inserted test outbreak (red triangle) is indicated by red-bordered zip codes and a false-positive outbreak by blackbordered zip codes.

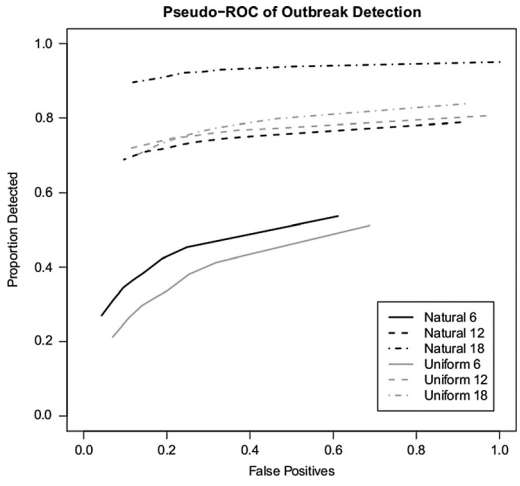

Fig. 2. Pseudo-ROC curves of outbreak detection. Proportion detected for each surveillance system vs. proportion of all false-positives identified.

Results

We present a robust framework for using highly detailed simulations to provide the foundation for evaluating and designing a surveillance system's ability to detect outbreaks. A small demonstration study shows that detection rates varied from 17% to 80% across the different surveillance systems. Increased coverage did not linearly improve detection probability for all surveillance systems. Surveillance systems with uniform coverage of the population did not perform better than one based on a real-world system with nonuniform coverage. Higher coverage improved the timeliness of detection but, for most cases, by only 1 or 2 days on average. Additional results can be found online (http://ndssl.vbi.vt.edu/insilicoSurveillance/).

Conclusions

Highly detailed simulations of infectious disease transmission can be configured to represent nearly infinite scenarios, making them a powerful tool for evaluating the performance of surveillance systems and the methods used for outbreak detection.

Keywords

Computer simulation; surveillance evaluation; outbreak detection; SaTScan

*Bryan Lewis
E-mail: blewis@vbi.vt.edu

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COACTION PUBLISHING

Utilizing the 'crowd trial' for pharmacovigilance: a case report

Itzchak Lichtenfeld[1], Limor Bar-Hai[2]*

[1]Analytics, First Life Research, Yehud, Israel; [2]Medical Informatics, First Life Research, Yehud, Isreal

Objective

The 'wisdom of the crowd' or the 'crowd trial' is a process of taking into account the collective intelligence of a large population sharing experiences regarding health issues and treatments online via social media platforms [Health 2.0], generating novel data sets comprising massive unstructured user-generated content of health reports.

Unlike regulated formal postmarketing reports, the crowd trial takes place spontaneously, continuously and on a very large scale. This crowd trial provides a snapshot of health trends and has become a proxy of postmarket clinical trials of medications and other therapies.

The purpose of this case report is to demonstrate how applying an additional data source originated from e-patient reports helps support drug surveillance and pharmacovigilance processes.

Introduction

Singulair (Montelukast Sodium) is a leukotriene receptor antagonist, indicated to prevent asthma attacks in adults and children. It is also used to relieve allergies in adults and children.

Singulair was approved by the FDA in February 20, 1998. In March 2008, the FDA informed healthcare professionals of investigating the possible association between Singulair usage and behavior/mood changes, suicidality and suicide.

First Life Research (FLR) identifies, analyzes, indexes and aggregates user-generated content by collecting billions of testimonials from social networks. It utilizes cutting edge technologies for massive data aggregation and applies advanced natural language processing (NLP) techniques for continuous analyses, in order to convert this unstructured data into refined information.

Methods

With the proliferation of social networks, the web has become a warehouse of patient discussions and reports, estimated at 10 billion records and growing at a rate of 40 percent per year. These reports are spread across more than 150,000 (and growing) English-language sites, forums and blogs. FLR has searched and mapped thousands of these sites and indexed hundreds of millions of posts (currently 800M) and is engaged in refining statistical methods of signal detection that enables investigation of health trends. FLR can look at large samples and discover small changes, such as drug side effects, which may not be discovered by other means for years.

Results

In this case, FLR detected the mentioned FDA alerts and related clinical manifestations prior to the official alert by 'listening' to the 'crowd trial', in that case, the Singulair users. Fig. 1 displays the first statistical peak (2004–2005) of reports mentioned Singulair usage, generated by the e-patients, discussing sleep disturbances and hallucinations. The second peak (2006) of reports discussed mood alterations and suicidal-related ideations. While the earliest manufacturer label modification took place in September 2007, and soon after (March 2008) FDA publication regarding ongoing safety review of Singulair, FLR demonstrated a drug surveillance and early detection capability few years earlier.

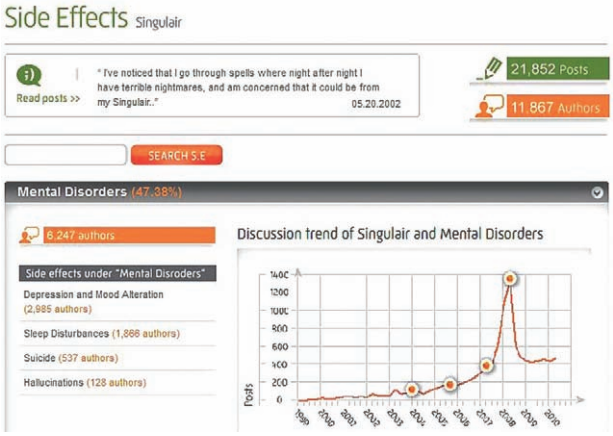

Fig. 1. FLR signal detection in the Singulair discussions trend overtime.

Conclusions

This report shows that by 'listening' into the social web, unforeseen phenomena may be revealed. Specifically, it is evident that advanced technological solutions and signal detection algorithm were able to detect neuropsychiatric events (side effects) in the case of Singulair, more than 2 years prior to any official warning by the regulator or the manufacturer.

'Crowd trial' provides a dashboard of health trends and grants feedback on medications, drug safety, side effects, interactions and drug comparisons.

The insights gained and demonstrated as aforementioned can be used to support and enable better informed decision making processes, both for patients and healthcare providers.

Keywords

Drug surveillance; user generated content; crowd trial; adverse drug reaction

Acknowledgments

The emerging 'wisdom of the crowd' analytics potentially represents a new phase and eventually new tools using data evaluations based on large scale population inputs, and it will benefit greatly all public health environment.

*Limor Bar-Hai
E-mail: limor@firstliferesearch.com

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COACTION PUBLISHING

S&I public health reporting initiative – building the future of harmonized biosurveillance systems

Nikolay Lipskiy[1]*, Anna Orlova[2] and Riki Merrick[3]

[1]OSELS, CDC, Atlanta, GA, USA; [2]PHDSC, Baltimore, MD, USA; [3]APHL, Silver Spring, MD, USA

Objective

The objective of this presentation is to evaluate progress on harmonization of public health electronic data exchange through the Public Health Reporting (PH-R) Standards and Interoperability (S&I) Framework activity.

Introduction

The American Recovery and Reinvestment Act (ARRA) initiated a broad range of national implementation activities. In order to support the critical activities of meaningful use (MU), ONC established the S&I Framework. In the beginning of 2011, the Laboratory Reporting Interface (LRI) Public Health (PH) Work Group (WG) was formed as a subworking group of the S&I Framework LRI activity. This LRI PH WG, besides providing PH required data elements to the LRI, assessed a need for documentation of the broad landscape of public health data exchange transactions. As a result, this WG recommended to participants and leadership of the ONC S&I that a new initiative, the ONC S&I PH-R activity should be established. In July 2011, a team of PH practitioners (co-authors of this presentation) started working on a charter and proposed deliverables for the group.

Methods

1. Assessment of a process toward development of interoperable PH related electronic data exchange across PH domains. 2. Assessment of priorities for the S&I PH-R initiative.

Results

Findings by ONC S&I LRI PH WG demonstrated that there are significant gaps in development of (a) functional requirements for PH-R and (b) interoperable standards-based specifications that support PH-R electronic data exchange from clinical care to public health and within public health. In order to strengthen PH-R, the S&I PH-R activity defined the following priorities: (1) Compile the full picture of all aspects of PH reporting; (2) Review and define public health and patient safety business processes and functional requirements and develop – HIT interoperability specifications; (3) Align public health objectives in MU Stage 1 with the needs of other public health domains and programs that were not explicitly mentioned in MU Stages 1; (4) Develop a roadmap for aligning public health, patient safety and clinical objectives in MU with regards to HIT standards, development, harmonization, testing and certification; (5) Develop a roadmap for deploying standard-based certified HIT applications in PH agencies and for patient safety reporting.

Conclusions

Even though practical tasks of the S&I PH-R initiative are at the initial stage, this activity will evolve into an important national forum that embraces stakeholders critical for improvement of population health tasks including system vendors, clinical care and public health professionals. Addressing gaps in interoperability of data exchange between clinical and population care should foster progress in situational awareness, PH emergency response and quality of population care.

Keywords

Public health reporting; ONC S&I; informatics

***Nikolay Lipskiy**
E-mail: dgz1@cdc.gov

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COACTION PUBLISHING

Electronic tracking of influenza-like illness incidence in an outpatient population

Steve Di Lonardo*, Michael Buck, Claudia Pulgarin and Winfred Wu

Health Care Access and Improvement, New York City Department of Health and Mental Hygiene, Queens, NY, USA

Objective

Evaluate the use of an electronic health record (EHR) network to track influenza-like illness (ILI) incidence in an outpatient population and, using laboratory testing, identify influenza cases by subtype as well as other respiratory viruses.

Introduction

Using an EHR system, we tracked an outpatient population from a series of primary care providers to identify ILI as part of a multistate effort directed by the Centers for Disease Control and Prevention. From these patients, we also collected de-identified project-specific information and symptoms using an electronic template to evaluate possible differences among patient groupings as well as longitudinal population patterns.

Methods

We selected a series of providers using NYC DOHMH's EHR network, from which we could obtain practice characteristics (i.e., number of patient visits, type of practice and age distribution) and evaluation score developed to rate a practice's ability to use EHRs. We then set up an electronic template at each practice and scheduled the transmission of a report with de-identified patient characteristics and patient counts. Nasopharyngeal samples were collected from each patient presenting with ILI to test for influenza subtypes including influenza A (H1, H3 and H1N1) and influenza B by RT-PCR. Samples negative for influenza were tested for other respiratory viruses including rhinovirus, metapneumovirus (MPV), respiratory syncytial virus (RSV), parainfluenza virus (PIV) and adenovirus by RT-PCR by Luminex. We analyzed the data for completeness to evaluate the success of electronic surveillance. We also compared the data by gender, age group, symptoms as well as evaluated virus frequency over time.

Results

Compared to paper-based records, EHR-based tracking reduced time and manpower requirements by the automation of data acquisition from each practice and improved capabilities for determining ILI incidence by reporting a patient denominator along with the number of ILI cases. Proper training and selecting the right practice played a large role in that success. Some initial challenges included providers overlooking the symptomology associated with ILI in the CDC guidelines, which led to failing to identify ILI cases and unfamiliarity with the electronic template. This was especially an issue in a larger practice that had a large number of rotating staff. The results of PCR testing for influenza subtypes evolved from almost exclusively H1N1 in 2009–2010 to the cocirculation of H1N1, seasonal H3 and influenza B in 2010–2011. Luminex testing was only performed in 2010–2011, and we found that rhinovirus and MPV were most common and were present over most of the season. Other viruses showed peaks at certain times of the year.

Conclusions

This project demonstrates that EHRs can improve surveillance capabilities by streamlining and standardizing reporting. This can help to establish a more sophisticated reporting tool using gold standard methods on a larger scale, which will in turn improve public health by providing information on the most common circulating virus at the time of diagnosis, and especially in the event of outbreaks such as pandemic H1N1. In addition, longer term longitudinal use of EHRs for this type of surveillance can determine whether the pattern observed one season is repeated the next.

Keywords

Electronic health record system; influenza-like illness; surveillance; influenza

Acknowledgments

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***Steve Di Lonardo**
E-mail: sdilonardo@health.nyc.gov

COACTION PUBLISHING

Mining intensive care vitals for leading indicators of adverse health events

Rajas Lonkar*, Artur Dubrawski, Madalina Fiterau and Roman Garnett

Carnegie Mellon University, Pittsburgh, PA, USA

Objective

To present a statistical data mining approach designed to: (1) Identify change points in vital signs, which may be indicative of impending critical health events in intensive care unit (ICU) patients and (2) Identify utility of these change points in predicting the critical events.

Introduction

The status of each ICU patient is routinely monitored, and a number of vital signs are recorded at subsecond frequencies (1), which results in large amounts of data. We propose an approach to transform this stream of raw vital measurements into a sparse sequence of discrete events. Each such event represents significant departure of an observed vital sequence from the null distribution learned from reference data. Any substantial departure may be indicative of an upcoming adverse health episode. Our method searches the space of such events for correlations with near-future changes in health status. Automatically extracted events with significant correlations can be used to predict impending undesirable changes in the patient's health. The ultimate goal is to equip ICU physicians with a surveillance tool that will issue probabilistic alerts of upcoming patient status escalations in sufficient advance to take preventative actions before undesirable conditions actually set in.

Methods

To generate potentially informative events from vital signs, we first segment each data channel into sequences of k consecutive measurements. We then perform Fourier transformation to obtain spectral profiles of each segment of raw signal. Multiple spectral profiles, extracted from periods of observation that are considered medically benign, are then assembled to form a k-dimensional flat table. We apply principal component analysis to this, and the top p components are considered further. These p components form a null space model of the expected normal behavior of the given vital sign. We build one null space model for each channel separately; this concludes the learning stage of the process.

Each newly observed set of k consecutive measurements is then processed through Fourier transform and projected onto the p principal components of the corresponding null space models. Over time of observation, these projections produce p time series per measurement channel. We apply a cumulative sum (CuSum) control chart to each of these time series and mark the time stamps at which CuSum alerts are raised. These moments correspond to circumstances in which the observed spectral decomposition of a vital sign does not match what is expected. We consider each such event as potentially informative of near-future deteriorations in the patient's health status. We quantify the predictive utility of each type of these automatically extracted events using training data, which contain actual health alerts, in addition to the vital signs data. To accomplish the task, we perform an exhaustive search across all pairs of CuSum event types (inputs) and alert types (outputs) and identify pairs with high values of the lift statistic (2). Input-output pairs with lifts significantly greater than 1.0 can be expected to enable prediction of health status alerts.

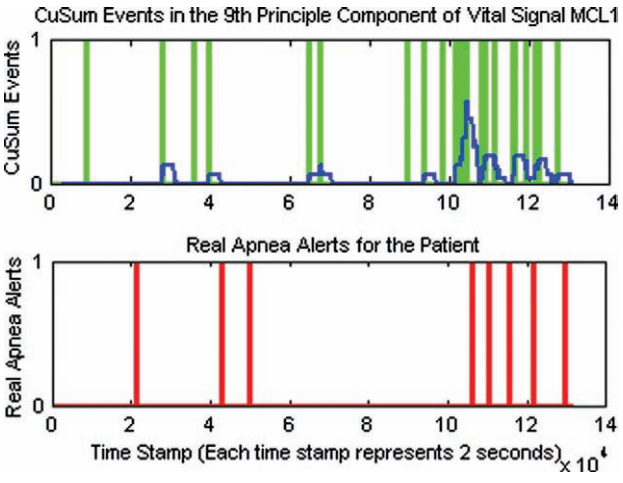

Fig. 1. Increased frequency of CuSum events (top) typically precedes the real apnea alerts (bottom).

Results

Fig. 1 depicts an example result obtained with the presented method. The CuSum Events (green spikes) obtained for the 9th principal component of Modified Chest Lead 1 (MCL1) signal, and the alerts (red spikes) are critical apnea conditions. We can see that, for this patient, the CuSum events most of the time precede apnea alerts, and they can potentially be used to predict an upcoming apneas.

Conclusions

We have outlined a method of processing vitals collected routinely at the bed side of ICU patients. It identifies signals that can be predictive of upcoming adverse health events.

Keywords

Critical care; event detection; data mining

Acknowledgments

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***Rajas Lonkar**
E-mail: rlonkar@andrew.cmu.edu

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COACTION PUBLISHING

Monitoring Twitter content related to influenza-like illness in Spanish-speaking populations

Arturo López-Pineda*, Charalampos Floudas, Fernando Suárez Obando, Gerald Douglas and Nara Um

Biomedical Informatics, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA

Objective

Identify the potential of Twitter as a source for monitoring and visualizing content regarding influenza-like illness (ILI) in Spanish-speaking populations for biosurveillance purposes.

Introduction

Influenza is a recurrent viral disease that requires timely and accurate detection. The use of Twitter as a source for biosurveillance has been shown useful (1). However, these efforts target messages in English, omitting from surveillance the part of users that speaks other languages, such as Spanish.

Methods

We implemented a system that builds upon existing technologies and services. The open source platform Ushahidi (2) was used to automatically search for content. An initial query report was generated from Twitter, includes username, content and timestamp. The city of each user was extracted from their profile and a query to GoogleMaps gave us the coordinates. At the end, this new information was uploaded to Ushahidi. We used the keyword 'gripa' (Spanish for flu) and scheduled hourly updates of the search.

Results

The prototype website operated for a pilot period of 1 month starting April 11h, 2011. A total of 473 unique occurrences worldwide were captured, of which 29% are located in Mexico (138/478) and 52% in Colombia (244/473).

Conclusions

We observed a higher number of incidences in Colombia relative to Mexico (Fig. 1a). When comparing these findings with the data on the reported cases of influenza (Fig. 1b) from the World Health Organization Flunet Biosurveillance (3), the results were consistent.

Our approach has promising potential for timely detection of ILI-related incidences in the areas previously underrepresented. Future work is to include different linguistic and contextual representations.

Keywords

Biosurveillance; influenza; twitter; open source; spanish

Acknowledgments

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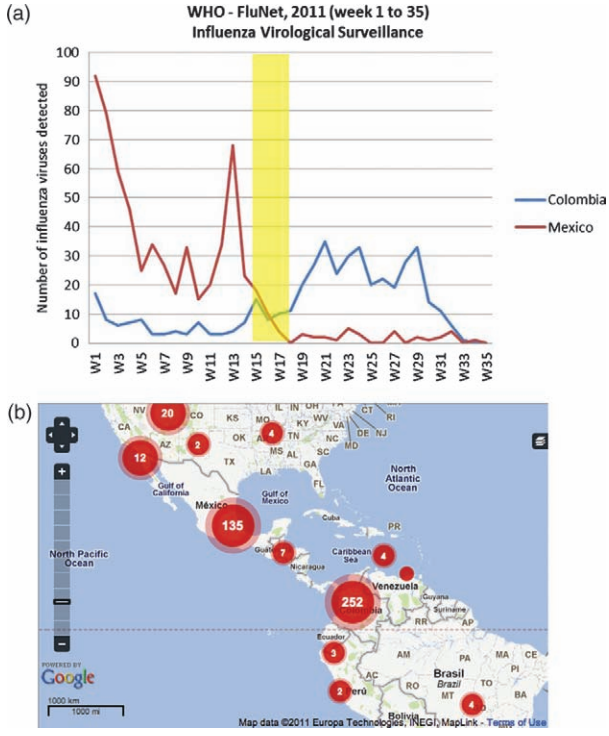

Fig. 1. (a) Screen-capture of the visualization interface for the reports aggregated in the system. (b) Influenza virological surveillance data extracted from the Flunet site by WHO.

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***Arturo López-Pineda**
E-mail: arl68@pitt.edu

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COACTION PUBLISHING

A demonstration of meaningfully using the ISDS-recommended data elements

Joseph Lombardo[1], William Stephens[2], Taha Kass-Hout[3], Wayne Loschen[1]* and Richard Wojcik[1]

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Tarrant County Public Health, Fort Worth, TX, USA; [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

This project represents collaboration among the CDC BioSense Program, Tarrant County Public Health and the ESSENCE Team at the Johns Hopkins University APL. The objectives of the project are to: develop reusable meaningful use messaging software for ingestion of health information exchange data available in Tarrant County, demonstrate the use of this data for supporting surveillance, demonstrate the ability to share data for regional and national surveillance using the messaging guide model and demonstrate how this model can be proliferated among health departments that use ESSENCE by investigating the potential use of cloud technology. The presentation will outline the steps for achieving this goal.

Introduction

National Health IT Initiatives are helping to advance the state of automated disease surveillance through incentives to health-care facilities to implement electronic medical records and provide data to health departments and use collaborative systems to enhance quality of care and patient safety. While the emergence of a standard for the transfer of surveillance data is urgently needed, migrating from the current practice to a future standard can be a source of frustration.

Methods

This project will investigate tools that can be used to support ingestion and translation of public health meaningful use data in the HL7 formats. Open source tools, such as Mirth, have been identified as early candidates to support this function. After the necessary translations have been made, this project will investigate transfer methods to move the meaningful use data from a public health department to a cloud environment. With data available in the cloud, the project will then investigate methods for putting the ESSENCE system in a cloud environment as well. This will provide the collaborative team a platform to evaluate the utility of both the meaningful use data and potentially the value of having regional and national data sharing aspects available to the public health users. Finally, the team will determine the scalability and performance of a cloud environment for disseminating these tools to other jurisdictions across the country.

Results

Early research for this project has already shown the need to redesign aspects of the ESSENCE system to support the additional meaningful use data fields. These changes involved modifications to the database design and the utilization of a more flexible configuration system. We fully expect additional modifications to be made to better support the cloud environment. These findings and the results of the public health evaluation of the system will be presented.

Conclusions

Public health departments will soon be flooded with mountains of new data. Having tools that can translate, transfer and utilize these new data sets effectively will be necessary. This collaborative team will research and put into practice solutions that can be used throughout the country.

Keywords

Electronic medical records for public health; meaningful use; interoperability; cloud

***Wayne Loschen**
E-mail: wayne.loschen@jhuapl.edu

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COACTION PUBLISHING

Confusing standards: common misconceptions about disease surveillance standards

Wayne Loschen*

Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

This talk will point out the inconsistencies and misunderstandings of the word 'standard'. Specifically, it will discuss HL7, syndrome definitions, analytical algorithms and disease surveillance systems.

Introduction

Domains go through phases of existence, and the electronic disease surveillance domain is no different. This domain has gone from an experimental phase, where initial prototyping and research tried to define what was possible, to a utility phase where the focus was on determining what tools and data were solving problems for users, to an integration phase where disparate systems that solve individual problems are tied together to solve larger, more complex problems or solve existing problems more efficiently. With the integration phase comes the desire to standardize on many aspects of the problem across these tools, data sets and organizations. This desire to standardize is based on the assumption that if all parties are using similar language or technology, then it will be easier for users and developers to move them from one place to another.

Normally the challenge to the domain is deciding on a vocabulary or technology that allows seamless transitions between all involved. The disease surveillance domain has accomplished this by trying to use some existing standards, such as Health Level 7 (HL7), and trying to develop some of their own, such as chief complaint-based syndrome definitions. However, the standards that are commonly discussed in this domain are easily misunderstood. These misunderstandings are predominantly a communication and/or educational issue, but they do cause problems in the disease surveillance domain. With the increased use of these standards due to meaningful use initiatives, these problems will continue to grow and be repeated without improved understanding and better communication about standards.

Methods

After reviewing presentations and participating in many discussions at conferences and with public health officials, a number of topics were identified that many believe use or are standards. These topics included HL7, syndrome definitions, analytical algorithms definitions and the definition of what is or is not a disease surveillance system. Next, the common understandings of each were compiled and compared with actual definitions and real world experiences from users of the standards. From this, a list of misunderstandings or poorly communicated aspects of each topic was derived.

Results

The results of this process have pointed out a number of inconsistencies with general assumed knowledge and actual truth related to many standards. The HL7 standard is just one example of a standard that is misunderstood in many aspects. Many believe that HL7 is a transport protocol, others believe that is a file format, others believe that it defines specific locations for data elements and still others believe that HL7 'set the language, structure and data types required for seamless integration from one system to another' (1). Each of these beliefs has nuggets of truth in them but do not explain the full story of HL7. Those that believe an HL7 message from one hospital can be fully read and understood in the exact same way as a second hospital may also be mistaken. Even though this is the hope of a standard, to have a standards-based tool that can be used over and over in different situations, real world experience tells us a different story about this so-called standard. Similarly, each topic has beliefs that are partially true, but by not understanding the whole truth, the standards can lead to complications.

Conclusions

Standards are highly beneficial to a domain. They provide efficiency in tool development and promote interoperability between organizations. Sadly, fully understanding a standard can sometimes be difficult, and misunderstandings can allow decisions to be made on untrue assumptions about a standard. The word standard has a meaning attached to it that can easily confuse someone into believing a capability exists that actually does not. Through improved education and communication, we can benefit from these standards without getting caught in their traps.

Keywords

Standards; HL7; syndrome definition; detector interfaces; system definition

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***Wayne Loschen**
E-mail: wayne.loschen@jhuapl.edu

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COACTION PUBLISHING

The evolution of ESSENCE

Wayne Loschen*, Sheryl Happel Lewis, Richard Wojcik, Howard Burkom and Joseph Lombardo

Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

This talk will describe the history and events that influenced the design and architecture decisions of the Electronic Surveillance System for Community-based Epidemics (ESSENCE) (1). Additionally, it will discuss the current functionality and capabilities of ESSENCE and the future goals and planned enhancements of the system.

Introduction

In development for over 14 years, ESSENCE is a disease surveillance system utilized by public health stakeholders at city, county, state, regional, national and global levels. The system was developed by a team from the Johns Hopkins University Applied Physics Laboratory (JHU/APL) with substantial collaborations with the U.S. Department of Defense Global Emerging Infections Surveillance and Response System (DoD GEIS), U.S. Department of Veterans Affairs (VA) and numerous public health departments. This team encompassed a broad range of individuals with backgrounds in epidemiology, mathematics, computer science, statistics, engineering and medicine with significant and constant influence from many public health collaborators.

Methods

We created a timeline of events, such as a particular partner's need (Florida Department of Health's desire to detect outbreaks based on patient time of arrival) or a public health outbreak (SARS) and correlated each one with design and architecture decisions that influenced ESSENCE. We used these events to describe the epidemiology, technology, analytical, administrative, political, legal and monetary factors that were considered at each point. Looking historically and critically at each decision point, we analyzed the benefits and costs of each decision. These benefits and costs were described from many different points of view, including those of the developer, user, administrator and others.

After walking through the historical timeline, we described the current architecture and feature set of ESSENCE. We also were able to point out the unique features between different instances of ESSENCE.

Based on user feedback, understanding outside influences and internal research, the ESSENCE team is always looking to improve the system. Part of this presentation will be to describe the future plans for the ESSENCE system from both architecture and feature stand points.

Results

Public health user needs and preferences have strongly influenced and prioritized the growth of ESSENCE, sometimes in unforeseen directions. Conversely, the evolving domain of syndromic and disease surveillance has broadened the situational awareness, perspectives and sometimes the responsibilities of public health monitors. The ESSENCE system has provided those monitors with the tools to help detect and investigate public health situations in their communities.

Conclusions

The utility of the ESSENCE system can be traced back directly to the influence of public health users and to the design decisions of the ESSENCE team. Understanding the history of disease surveillance in this context can help clarify current situations faced by today's public health practitioners as well as prepare them for tomorrow.

Keywords

ESSENCE, disease surveillance, system architecture

Acknowledgments

The ESSENCE system could not have been built without the support of many sponsors, numerous collaborators, perceptive users and all of the dedicated members of the ESSENCE team.

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***Wayne Loschen**
E-mail: wayne.loschen@jhuapl.edu

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COACTION PUBLISHING

Inpatient data: a new frontier in Veterans Affairs biosurveillance and public health monitoring from the electronic health record

Cynthia Lucero*, Patricia Schirmer, Gina Oda and Mark Holodniy

Department of Veterans Affairs, VHA Office of Public Health, Palo Alto, CA, USA

Objective

To describe the utility of inpatient data in the Veterans Affairs (VA) ESSENCE biosurveillance system.

Introduction

VA ESSENCE analyzes ICD-9 diagnosis codes and demographic data from outpatient and emergency department (ED) visits using complex aberrancy-detection algorithms (1). In 2010, a new instance was stood up (VA Inpatient ESSENCE), which receives weekly feeds of inpatient data from all VA acute care hospitals starting October 1, 2009. Data include demographics, admission/discharge data (including ICD-9 diagnosis codes), diagnosis-related group (DRG), bedsection, procedure and surgery data.

Methods

For this demonstration, we selected one disease for which we currently perform routine outpatient/ED ESSENCE surveillance (influenza) and one HAI of interest [*C. difficile* infection (CDI)]. First, we queried VA Inpatient ESSENCE for hospitalizations with an influenza diagnosis code (ICD-9: 487, 488). These data were compared to CDC's AHDRA hospitalizations, a voluntarily reporting system for laboratory-confirmed influenza-associated hospitalizations. Second, we queried VA Inpatient ESSENCE for hospitalizations with the CDI diagnosis code (ICD-9: 008.45) as well as total monthly discharges. Monthly rates for CDI were then calculated per 1000 total discharges. CDI rate per 100,000 population for FY 2010 was calculated using the total enrollees in VA Health Care in FY 2010 (8.343 million) as the denominator. Previous analysis from a non-VA hospital demonstrated good correlation between the CDI code and positive toxin assay (2).

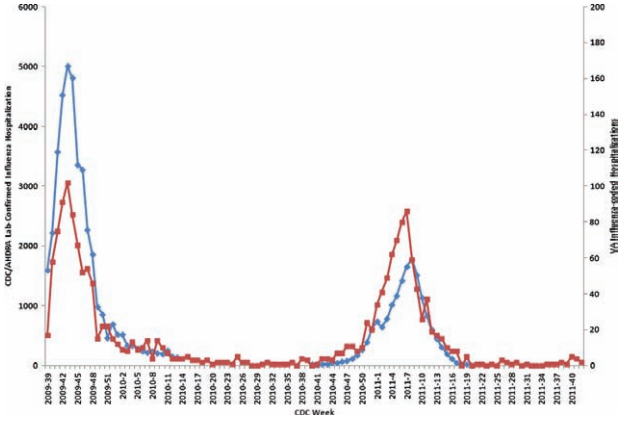

Fig. 1. VA Inpatient ESSENCE influenza-coded hospitalizations and CDC/AHDRA Laboratory-confirmed influenza hospitalizations, by CDC Week.

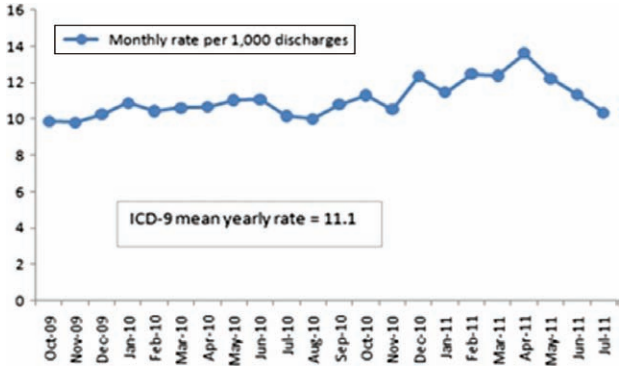

Fig. 2. VA Inpatient ESSENCE monthly rates of *Clostridium difficile* Infection by ICD-9 diagnosis code, October 2009–July 2011.

Results

Alerts for influenza were observed on multiple consecutive days during the fall wave of the H1N1 pandemic as well as during the peak of the 2010–2011 influenza season. Peaks in weekly influenza hospitalizations appeared to correlate well temporally between the VA and CDC's AHDRA data (Fig. 1). From October 1, 2009 to July 31, 2011 more than 12,500 CDI codes were identified among nearly 1.13 million hospitalizations with a calculated mean CDI rate of 11.1 per 1000 discharges (Fig. 2). The CDI rate for FY10 was 78/100,000 population.

Conclusions

Inpatient data provide robust and valuable information for VA beyond what was previously available in outpatient ESSENCE data or through manual methods. Inpatient data can be monitored year-round, which provides more complete situational awareness for planning and response. Future plans include (1) developing inpatient-specific alerting algorithms, (2) establishing a single VA ESSENCE application that combines both outpatient and inpatient data and (3) imsproving timeliness of inpatient data receipt and adding additional data elements to improve system specificity.

Keywords

Inpatient surveillance; influenza; healthcare-associated infections; *Clostridium difficile* infection; electronic health record

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***Cynthia Lucero**
E-mail: cynthia.lucero@va.gov

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COACTION PUBLISHING

Use of laboratory drug sensitivity tests and prescription practices in Malawi

Rudia Lungu*, Benson Chilima, Abel Phiri, James Kaphiyo and Ambonishe Mwalwimba

CHSU Public Health Laboratory, Ministry of Health, Lilongwe, Malawi

Objective

Assessment of routine use of drug sensitivity test results to guide treatment choices in district hospitals in Malawi.

Introduction

Of the 13 million people in Malawi (1) 85% are rural and the country has high burden of under-five morbidity and mortality due to preventable infectious diseases. Respiratory, febrile and diarrhea diseases are the top 3 morbidity and mortality illnesses in most developing countries (2). Acute medical care has greatly improved these conditions, but widespread and uncontrolled use of antibiotics threatens to reverse gains achieved so far. Drug sensitivity tests are a prerequisite to guide prescription practices.

Methods

An evaluative study on all 28 district hospital laboratories in all regions of Malawi. The data are routine quarterly assessments covering from October 2009 to April 2011. The main focus was on performance of culture procedures, drug sensitivity testing practice, documentation and demand and use of drug sensitivity results by clinicians.

Results

Malawi has 29 district hospital laboratories of which only 12 (41%) are currently able to perform culture procedures. Only four (14%) of the laboratories performing culture procedures are able to perform drug sensitivity cultures, which should inform prescription practices.

There is lack of demand and reliance on drug sensitivity tests by the prescribing clinician. Clinicians sited the lack of laboratory capacity and also the delays that go with culturing procedures.

Inadequate laboratory performance of drug sensitivity tests coupled with syndromic clinical diagnosis are the culprits of antimicrobial resistance and treatment access in Malawi.

There is no laboratory-based data forming sensitivity profiles of most antibiotics used to treat common infectious diseases.

Conclusions

Malawi is one of the many low income countries that can claim no substantive laboratory-based data on antimicrobial susceptibility. Laboratory surveillance of antimicrobial resistance is a prerequisite to guide informed selection and purchase of drugs for local use based on scientific proof. This is more cost effective and may lead to modification of treatment procedures as necessary.

Keywords

Drug sensitivity tests; prescription practices; clinicians; laboratory -based data.

Acknowledgments

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***Rudia Lungu**
E-mail: rglungu@gmail.com

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COACTION PUBLISHING

The spatial and temporal anatomy of seasonal influenza in the United States, 1972–2007

Bianca Malcolm* and Stephen Morse

Epidemiology, Columbia University Mailman School of Public Health, New York, NY, USA

Objective

To study the seasonality of influenza in the United States between 1972 and 2007 through the evaluation of the timing, velocity and spatial spread of annual epidemic cycles.

Introduction

Seasonality has a major effect on the spatial and temporal (i.e., spatiotemporal) dynamics of natural systems and their populations (1). Although the seasonality of influenza in temperate countries is widely recognized, interregional spread of influenza in the United States has not been well characterized.

Methods

We used weekly pneumonia and influenza (P&I) mortality data from the National Vital Statistics System (NVSS) (1972–1988) and the Centers for Disease Control and Prevention (CDC) 121 Cities Mortality Reporting System (1996–2008) to construct weekly time series of P&I mortality for each year and Census Bureau Division. The timing of each seasonal wave was determined by identifying a significant increase and subsequent decrease in P&I mortality plus a lead-in and a lead-out week. Average time to death ($[\Sigma[(t)(nt)]]/N$; where N = total P&I deaths for all weekly periods in the season, t = week of season (e.g., 1, 2, etc.), and nt = total P&I deaths for week t) was used to determine the timing and velocity of each seasonal influenza wave. Ordinary least squares regression was used to develop trend lines and spread vectors for annual influenza epidemics in order to determine the directionality of annual influenza waves. Average time to national spread, average time to national peak P&I mortality and average P&I mortality were also determined and compared between influenza subtypes.

Results

For the years 1972–1988 and 1996–2008, annual influenza epidemics needed an average of 7.9 weeks to spread across the country and lasted an average of 22 weeks. Seasons where H3N2 was the dominant influenza subtype (N = 13) were, on average, significantly shorter (20.3 vs. 26.7 weeks $p = 0.0049$) and spread quicker (time to death: 10.3 weeks vs. 13.8 weeks, $p = 0.0053$) than seasons with H1N1 as the dominant subtype (N = 3). There was also a significant difference in the average time to national spread between H3N2-dominant seasons and H1N1-dominant seasons (6.1 vs. 13 weeks, $p = 0.0253$) (Table 1). Moreover, an average seasonal traveling wave of influenza began in the East North Central region then took two routes: (1) eastward then southward along the Atlantic coast and (2) westward to the Pacific coast.

Conclusions

Preliminary results of this analysis suggest that certain temporal patterns of influenza seasons vary by influenza subtype. Future analyses will focus on determining the temporal characteristics for influenza seasons between 1989 and 1996 (and for seasons between 1996 and 2007, using complete NVSS mortality sets) and assessing the intercounty spread of epidemic influenza. Accurately identifying spatiotemporal patterns could improve epidemic prediction and prevention as well as aid the creation of efficient containment policies for pandemic influenza (2). This analysis will aid public health in developing more effective and efficient strategies to decrease morbidity and mortality associated with seasonal influenza in the United States.

Keywords

Pandemic preparedness; spatial dynamics; geographic synchrony

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***Bianca Malcolm**

E-mail: blm2115@columbia.edu

Table 1. ANOVA analysis of the means of seasonal parameters of epidemic influenza in the United States, 1972–1988 and 1996–2008, by dominant circulating influenza subtype

Influenza subtype (No. seasons)	*Total seasonal P&I mortality*	*Average time to death†*	*Season length†*	*Time to national spread†*	*Time to peak P&I mortality*
B (3)	29344	10.5	20	8	7
B/H1N1 (4)	26784	13.7	26.5	10	7.8
B/H3N2 (4)	22285	11.7	22.5	9	10.8
H1N1 (3)	28408	13.8	26.7	13	10.7
H1N1/H3N2 (1)	26937	8.3	16	3	7
H3N2 (13)	26335	10.3	20.3	6.1	8.1

†$p < 0.05$.

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COACTION PUBLISHING

Education as a mechanism to reduce spread of brucellosis among at-risk populations in Uzbekistan

Adkhamjon Mamatkulov[1]*, Aybek Khodiev[1], Lisa Strelow[2] and Victor Del Rio Vilas[2]

[1]Science Department, Technology Management Company, Tashkent, Uzbekistan; [2]Bechtel National, Inc., Tashkent, Uzbekistan, Uzbekistan

Objective

To outline the mechanism of a pilot educational brucellosis prevention program among selected high-risk groups in an endemic region of Uzbekistan.

Introduction

One goal of the Biological Threat Reduction Program (BTRP) of the US Defense Threat Reduction Agency (DTRA) is the enhancement of surveillance of especially dangerous pathogens of both humans and animals within countries of the former Soviet Union. One of the diseases of interest to the program is brucellosis, which is a life-threatening condition and constitutes a major health and economic challenge around the world. This is also true for Uzbekistan (UZ), where brucellosis is endemic in a number of regions. In the Samarqand region of UZ, for example, studies have reported a 9.3%, and 3.6% seroprevalence for humans and farm animals, respectively (1). The lack of awareness about brucellosis in at-risk populations, shepherds, veterinarians and people who handle raw milk is believed to significantly contribute to the spread of disease from animals to humans. Here, we suggest mechanisms to evaluate awareness about the disease and the impact of an educational intervention in at-risk groups.

Methods

The intervention and two control groups will include subjects from the at-risk groups in the Samarqand region. In all three groups, the selection of study subjects will be done from non-brucella-related visits to primary care centers by at-risk patients with no previous history of brucella. At-risk subjects within the intervention and first control group will be asked to complete a questionnaire to assess their awareness about brucellosis, specifically about its clinical presentation and risk for exposure in people. At-risk subjects in the second control group will not receive any questionnaire. The educational intervention procedures will consist of briefings to a group of healthcare professionals, delivered through BTRP regular training events, together with printed materials to be explained by the physicians to patients in the intervention group. The briefings and materials will show practical ways of preventing the spread of brucellosis targeted at common practices within the at-risk groups. The seasonality of the disease in endemic regions like Samarqand dictates that the best timing for the intervention program is in the fall (Sept–Dec), before lambing season (Feb–Jun). Our measurable outcome is the number of newly acquired human brucellosis cases among the three study groups registered after the intervention. Registration of brucellosis cases will follow existing protocols within the Uzbek healthcare system. Additionally, the questionnaire administered to the intervention and one control group will provide an insight of the baseline awareness about the disease. Adequate sample size and analysis of the data will allow comparisons between the three study groups and between strata within the groups, e.g., veterinarians and farmers. The control group not exposed to the questionnaire will allow an assessment of the impact of possible increased awareness as a result of our interventions.

Results

Disease awareness questionnaires, educational materials and further details of our study design will be presented at the conference.

The anticipated increase in knowledge about risk practices associated with the transmission of brucellosis from animals in at-risk populations should lead to a reduction in human cases of brucellosis in the intervention group, compared to control groups.

Conclusions

The epidemiology of brucellosis among humans and animals is well-characterized. Preventive measures for the diseases are well known; yet, applying this knowledge in resource-poor countries remains a constant challenge. Having effective health education programs is a vital component in efforts to reduce the disease burden by reducing the animal-to-human transmission rate.

Keywords

Brucellosis; education; brucellosis prevention; brucellosis at-risk population; education effectiveness

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***Adkhamjon Mamatkulov**
E-mail: amamatku@bechtel.com

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COACTION PUBLISHING

Aiding the practice of tuberculosis control: a decision support model to predict transmission

Hiroshi Mamiya*, Kevin Schwartzman, Aman Verma, Christian Jauvin, Marcel Behr and David Buckeridge

McGill University, Montreal, QC, Canada

Objective

To develop and validate a prediction model that estimates the probability of a newly diagnosed tuberculosis (TB) case being involved in ongoing chain of transmission, based on the case's clinical and sociodemographic attributes available at the time of diagnosis.

Introduction

A new TB case can be classified as: (1) a source case for transmission leading to other, secondary active TB cases; (2) a secondary case, resulting from recent transmission; or (3) an isolated case, uninvolved in recent transmission (i.e., neither source nor recipient). Source and secondary cases require more intense intervention due to their involvement in a chain of transmission; thus, accurate and rapid classification of new patients should help public health personnel to effectively prioritize control activities. However, the currently accepted method for classification, DNA fingerprint analysis, takes many weeks to produce the results (1); therefore, public health personnel often solely rely on their intuition to identify the case who is most likely to be involved in transmission. Various clinical and sociodemographic features are known to be associated with TB transmission (2). By using these readily available data at the time of diagnosis, it is possible to rapidly estimate the probabilities of the case being source, secondary and isolated.

Methods

A multinomial logistic regression model was developed based on the information of 1552 TB cases reported on the island of Montreal between 1996 and 2007. The predictor variables were age, sex, area of residence in Montreal, country of origin, presence of cavitary lesion in chest X-ray, sputum smear result, HIV infection, illicit drug use, living in apartment, history of TB diagnosis, being alcoholic, and coughing. DNA fingerprint analysis was used as the reference standard to define the dependent variable of the model. The data were multiply imputed, and model selection was performed by Bayesian Model Averaging. Cross-validation was performed on each of the imputed datasets to measure the predictive performance of the model using the area under the receiver operating curve (AUC).

Results

A total of 1552 cases comprising 107(6.9%) source cases, 207(13.4%) secondary cases and 1238 (79.8%) isolated cases were available to train the model. The AUCs of the model to discriminate source, secondary and isolated case are shown in Table 1. HIV infection (odds ratio [OD] 3.72, 95% confidence interval [CI] 2.10; 6.59) and the interaction of living in apartment and presence of cavitary lesion (OD 3.19, 95% CI 1.71; 5.96) were found to be significant predictors of being a source, while being Canadian-born (OD 2.87, 95% CI 1.94; 4.26) and being Haitian-born (OD 3.09, 95% CI 1.99; 4.78) were significant predictors of being a secondary case.

Table 1. Discriminative performance of the prediction model

Outcome to be predicted	*AUC (95% CI)*
Source	0.62 (0.57; 0 67)
Secondary	0.64 (0.61; 0.66)
Isolated	0.65 (0.65; 0.66)

Abbreviations: CI, confidence interval, AUC, area under curve

Conclusions

Performance of the prediction model was promising as it was significantly better than random prediction (i.e., the AUCs were higher than 0.5). Small proportions of source and secondary cases in the available data may have limited performance. However, the model can be an effective decision support tool if its ability to identify a case likely to be involved in transmission is superior to the intuition of public health officials. Thus, further evaluation of the model in the context of TB control program should be conducted. If effective, the model would be particularly useful when incidence of TB increases in a resource limited setting, in which efficient prioritization of investigation is desired. Overall, the current study has important implications in promoting the approach of evidence-based practice in control of TB.

Keywords

Tuberculosis; transmission; prediction model; public health; decision support

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***Hiroshi Mamiya**
E-mail: hiroshi.mamiya@mail.mcgill.ca

COACTION PUBLISHING

Applications of syndromic surveillance in resource poor settings: a series of case studies

Larissa May*, Rebecca Katz, Elissa Test and Julia Baker

Department of Emergency Medicine, The George Washington University, Washington, DC, USA

Objective
The aim of this study is to demonstrate how syndromic surveillance systems are working in low-resource settings while identifying the key best practices and considerations.

Introduction
Particularly in resource-poor settings, syndromic surveillance has been proposed as a feasible solution to the challenges in meeting the new disease surveillance requirements included in the World Health Organization's International Health Regulations (2005).

Methods
Information on established syndromic surveillance systems was collected from peer-reviewed articles (found in MEDLINE, Scopus and Google Scholar), proceedings from all ISDS Conferences and other conferences and searches through reference lists of papers. In addition, web pages of international health organizations, surveillance networks and Ministries of Health were explored. Identified syndromic surveillance systems were categorized by country, resource level and surveillance methodology, among other features. Eight systems were selected and examined in detail to extract transferable information.

Results
The literature demonstrates the many diverse, yet successful, syndromic surveillance efforts being implemented at the national and regional levels. Existing systems utilize a variety of data sources, data transmission techniques and analysis methodologies, ranging from low-tech, highly manual systems to automated, electronic systems. Frequently, syndromic surveillance systems are a coordinated effort among several partners, supplement existing systems, incorporate both specific and nonspecific disease detection and are used in conjunction with laboratory-based surveillance.

Conclusions
Though not without challenges, syndromic surveillance has the potential to serve as a valuable disease detection tool in resource-limited settings. Further examination and evaluation of these systems will benefit global disease surveillance capacity.

Keywords
Biosurveillance; syndrome; developing countries

***Larissa May**
E-mail: larissa.may@gmail.com

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COACTION PUBLISHING

Changes in alcohol-related travel behavior due to an under 21 ordinance

Tina McCarty*, Eric Foster, Alberto Segre and Philip Polgreen

University of Iowa, Iowa City, IA, USA

Objective

To study alcohol-related arrests during the time surrounding the introduction of an alcohol-related ordinance in the Iowa City, IA, area.

Introduction

Alcohol abuse is one of the major leading causes of preventable mortality in the United States (1). Binge drinking or excessive alcohol consumption, categorized as a pattern of drinking that brings a person's blood alcohol concentration (BAC) to 0.08 (2), has become a major cause for concern, especially in the 18- to 20-year-old population. Iowa City is home to the University of Iowa, a large public university of 30,000 students. On June 1, 2010, the city council enacted a new ordinance prohibiting persons under 21 from entering or remaining in bars (establishments after 10:00 PM whose primary purpose is the sale of alcoholic beverages) after 10:00 PM (3). Prior to the ordinance, Iowa City was the only municipality in the region where underage patrons were allowed on premises. The new ordinance was enacted largely in response to public safety concerns, including perceptions of increased violence and sexual assaults, especially at bar closing time.

Our hypothesis is that the under 21 ordinance also resulted in changes to travel behavior, where prior to the ordinance, the campus bar culture constituted an 'attractive nuisance', attracting a volatile mix of college students and nonlocals of all ages.

Methods

Arrest records were obtained from the University of Iowa Police Department containing all alcohol-related citations from January 1, 2004 to June 26, 2011. As the University of Iowa Police Department is one of the 4 local law enforcement agencies (Iowa City Police, Coralville Police and Johnson County Sheriff), these 7002 records represent a sample of alcohol-related arrests, albeit one focused on the downtown bar area frequented by college students. Each record contains the date of the arrest as well as the age and home address of the offender, allowing us to compare 'in town' offenders (i.e., from within Iowa City, Coralville and transients) with 'out of town' offenders. Records corresponding to football Saturdays, where some 50,000 people come to Iowa City to tailgate and attend the Big10 football game, were excluded from the analysis as not representative of the usual bar culture. A total of 1490 alcohol-related arrest records remained in the analysis.

A Fisher's exact test was used to test the hypothesis of whether the proportion of arrests of out of town patrons versus in town patrons is independent of the under 21 ordinance.

Results

Data analysis confirms that, following the ordinance, the proportion of arrests involving out of town patrons to in town patrons was significantly reduced (Fisher's exact test, $p \leq 0.0001$). Similar results were obtained for only under 21 arrests (Fisher's exact test, $p = 0.0095$) and over 21 arrests (Fisher's exact test, $p = 0.0058$), suggesting that the campus bars were equally attractive to all age groups prior to the ordinance.

Conclusions

Immediately following the ordinance, the average weekly number of alcohol-related arrests increased from 9.3 to 16.3. Since over 21 arrests also increased, the change cannot be attributed solely to the new ordinance; indeed, additional police resources were deployed in a deliberate attempt to change the drinking culture. Of course, since the arresting officer cannot generally detect residency prior to arrest, arrest data still represent a geographically unbiased sample of bar patrons and can be used to explore changes in the mix of patrons.

We hypothesize that the changes detected in the proportion of arrests of in town and out of town patrons reflect a more homogeneous student clientele, where town-gown tensions are less likely to arise. Of course, any reduction in out of town patrons also corresponds to a reduction in the risk of DUI-related fatalities, since students walk to the bars.

There are several shortcomings to this study. First, our data are incomplete as data from other enforcement agencies was not available. Second, we were unable to directly confirm the link with violence or sexual assault, as additional data would be required to do so: these are our next steps.

Keywords

Alcohol; binge drinking; college binge drinking

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*Tina Mccarty
E-mail: tina-mccarty@uiowa.edu

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COACTION PUBLISHING

Enhancing surveillance for infectious disease in the United States–Mexico border region of Arizona

Orion McCotter*, Catherine Golenko, Shoana Anderson, Laura Erhart, Robert Guerrero and Ken Komatsu

Arizona Department of Health Services, Phoenix, AZ, USA

Objective

To establish and maintain an active binational sentinel hospital-site surveillance system and to enhance border region epidemiology and laboratory infrastructure.

Introduction

The Border Infectious Disease Surveillance (BIDS) program was established in 1999 by the Centers for Disease Control and Prevention and Mexico Secretariat of Health, following mandates from the Council of State and Territorial Epidemiologists (CSTE) and the United States–Mexico border health association to improve border surveillance. The BIDS program is a binational public health collaboration to create an active sentinel-site surveillance of infectious disease among the United States–Mexico border. It is a collaborative effort between local, state, federal and international public health agencies throughout both countries in the border region. This project is aimed at using the best aspects of both countries surveillance system.

Methods

We established a network of sentinel clinic and hospital sites along the geographical United States–Mexico border region. We utilized a shared syndromic case definition that is compatible between both countries. Standardized data collection instruments allows for exchange of surveillance data. We increased the laboratory capacity for to test for diseases of public health importance.

Results

This effort has been successful at building a regional surveillance system. In the 2010, three pilot hospital sites were enrolled to conduct severe acute respiratory infection (SARI) surveillance. These patients were tested for viral, bacterial and important fungal infections that cause respiratory disease. Fig. 1 includes results of the 74 hospitalized SARI patients who were enrolled in the 2010–2011 influenza season. The SARI patients were 54% (n = 40) male and had a median age of was 62.5 years (range, 0–87 years). The expansion of this surveillance system requires additional sentinel hospital-sites and additional syndromes. A syndrome of acute diarrheal illness will be the focus of surveillance at one new pilot sentinel site, with potential to expand in the future.

Conclusions

A surveillance system using syndromic and CSTE case definitions allows for comparison of morbidity in the United States/Mexico border region, increased communication and bidirectional sharing of information across the border. Creating and expanding a regional surveillance system that crosses an international boundary requires coordination and collaboration from all agencies involved. These surveillance data allow for examination of the border region as one epidemiologic unit. Consistent communication with clinicians and hospital staff helps to build credibility and interest. Simplicity in surveillance procedures encourages compliance. These surveillance efforts can guide vaccine allocation planning and efficiency in evaluating illnesses that maybe vaccine preventable. Systems to share information between various states in the United States–Mexico border region are important to develop binational control strategies.

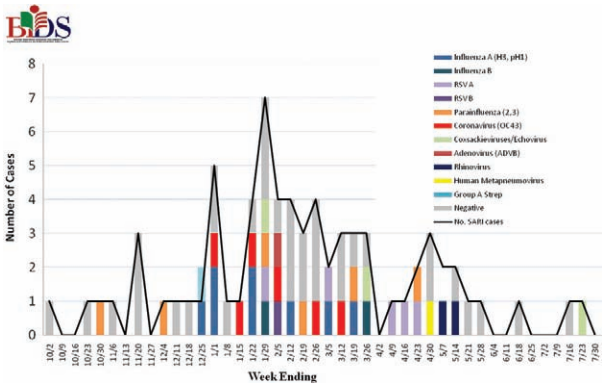

Fig. 1. RT-PCR Test Results Among SARI Cases from All Sites by Week, October 2010 to August 2011.

Keywords

Surveillance; syndromic; border; binational; Mexico

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***Orion McCotter**
E-mail: orion.mccotter@azdhs.gov

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COACTION PUBLISHING

Novel conceptual framework and toolset for country-wide assessments of opportunities and challenges for public health interventions

Scott McNabb[1]*, Joseph Wamala[2], Anila Naz[1], Anna Hartrampf[1], Dan Samoly[1], David Mutonga[3] and Meeyoung Park[1]

[1]Hubert Department of Global Health, Emory University, Rollins School of Public Health, Atlanta, GA, USA; [2]Uganda Ministry of Health, Kampala, Uganda; [3]Kenya Ministry of Public Health and Sanitation, Nairobi, Kenya

Introduction

Imbalances in wealth, education, infrastructure, sociopolitical leadership, healthcare and demographics create opportunities and challenges when implementing public health interventions. Understanding these, while embracing 'smart power', one can objectively assess a country's receptivity for support. Therefore, we developed a novel conceptual framework and toolset that objectively measured opportunities and challenges to inform decision-making, specifically about future implementation of the Electronic Integrated Disease Surveillance System (EIDSS)—a computer-based system for national reporting and monitoring of reportable human and veterinary infectious diseases—in East Africa and the Middle East.

Methods

After conceptualizing and designing the toolset architecture, we gathered objective data to calculate indicators using a systematic approach from published reports; articles from peer-reviewed journals; and websites of international organizations and national Ministries in each country. We also interviewed stakeholders. Indicators were weighted to reflect the level of impact on elements and domains, and standardized baselines were established to uniformly measure outcomes. Outcomes for each element and domain were then calculated based on the weighted, indicator data.

Results

One hundred twenty-four indicators were identified that measured 16 elements that defined 7 domains of country-specific opportunities and challenges: political will, stakeholder involvement, culture, public health functionality, healthcare, laboratory and communication infrastructure. Thirty (24%) of the 124 indicators were chosen from the reporting requirements of the 2005 International Health Regulations. In the pilot, we found various positive and negative implementation characteristics in Uganda, Kenya, Tanzania, Afghanistan, Iraq and Pakistan.

Conclusions

We conceived a new and useful approach to objectively analyze opportunities and challenges for public health interventions within a country. With respect to introducing EIDSS, we piloted the toolset and described a balanced view of the opportunities and challenges. Application of this novel framework should be useful for other public health interventions, and validation and further testing of the toolset should be performed.

Keywords

Public health evaluation; assessment; SWOT; smart power

*Scott McNabb
E-mail: scottjnmcnabb@emory.edu

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COACTION PUBLISHING

Mobile technology systems for surveillance in low resource settings

Donna Medeiros[1]*, Ray Ransom[2] and John Boos[1]

[1]RTI International, Raleigh, NC, USA; [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

To present the prevailing global public health informatics landscape in developing countries highlighting current mobile system requirements and usage for disease surveillance and revealing gaps in the technology.

Introduction

Mobile technology provides opportunities to monitor and improve health in areas of the world where resources are scarce. Poor infrastructure and the lack of access to medical services for millions have led to increased usage of mobile technology for health-related purposes in recent years. As adoption has increased, so has its acceptance as a viable technology for health data collection. The ability to provide timely, accurate and informed responses to emerging outbreaks of disease and other health threats makes mobile technology highly suitable for use in surveillance data collection activities and within the arena of global health informatics overall. The American Public Health Association (APHA) defines global health informatics as the application of information and communication technologies to improve health in low-resource settings, which include the following:

- linking disparate sources of data together through natural language processing;
- use of mobile health technologies for disease surveillance;
- use of telemedicine to manage chronic disease;
- use of digital libraries to increase knowledge and awareness of public health events.

Methods

Based on donor-funded global health projects, systems requirements were gathered and existing mobile systems were evaluated for use in surveillance in low-resource settings. In advance of the tools evaluation, literature reviews were performed, and informatics experts at the Centers for Disease Control and Prevention (CDC), the World Health Organization (WHO) and various global nongovernmental organizations (NGOs) and associations were consulted and then recommendations were formulated. Systems were evaluated based on minimum requirements, which included maturity, usage, scalability, interoperability, functional features related to data collection and attributes that enable country ownership and generate high data quality.

Results

In our evaluation, no single system was found to meet the needs of all the surveillance requirements. Mobile technology standards and guidelines were searched for, with none being found. An open-source, end-to-end software solution that is readily available and able to meet the needs of health surveillance was not identified, although several systems were deemed promising and have garnered significant use. Key features of an end-to-end mobile surveillance system would include the following:

- easily adoptable;
- open source or public domain;
- able to support multiple mobile platforms;
- form design environment;
- enumeration, case selection and case management;
- multilingual and Unicode functionality;
- client-server deployment (local and cloud based);
- SMS enabled;
- rational database system data storage;
- data extraction to statistical file formats;
- embedded analysis and report capability;
- GIS/GPS enabled, with global mapping capability;
- geospatial analytic capability;
- data visualization.

Conclusions

Mobile technology has emerged as a key component of global health informatics. With the expansion of this technology, a plethora of tools and systems have materialized. With so many systems, it is difficult to know which tools to apply. To add to the confusion, no standards or guidelines currently exist. Additionally, there is a clear need for an end-to-end, open-source, scalable mobile system that incorporates functionality for questionnaire design, data management, analysis and reporting.

These gaps must be addressed in order for mobile surveillance technologies adoption to advance adequately.

Keywords

Mobile technology; informatics; open source; low resource settings; surveillance systems

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*Donna Medeiros
E-mail: donna_d_medeiros@yahoo.com

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COACTION PUBLISHING

Game-theoretic surveillance approaches for hospital-associated infections

Aaron Miller*, Philip Polgreen and Linnea Polgreen

University of Iowa, Iowa City, IA, USA

Objective

To analyze optimal disease screening in strategic multiunit settings and determine how the level of unit autonomy may effect screening decisions.

Introduction

Disease screening facilitates the reduction of disease prevalence in two ways: (1) by preventing transmission and (2) allowing for treatment of infected individuals. Hospitals choosing an optimal screening level must weigh the benefits of decreased prevalence against the costs of screening and subsequent treatment. If screening decisions are made by multiple decision units (DU; e.g., hospital wards), then they must consider the disease prevalence among admissions to their unit. Thus, the screening decisions made by one DU directly affect the disease prevalence of the other units when patients are shared.

Because of this interdependent relationship, one DU may have an incentive to "free-ride" off the screening decisions of others as the disease prevalence declines. On the other hand, DUs may find it futile to invest in screening if they admit a large number of infected patients from neighbors who fail to screen properly. This problem is important in determining the optimal level of unit autonomy, since increasing a unit's level of autonomy in screening effectively increases the total number of DUs.

Methods

We develop a theoretical model that incorporates the two channels through which screening may reduce prevalence. The model is based on a hospital composed of N treatment units (e.g., ICU and ER) divided into n DUs, that transfer patients between one another and an outside population. Disease prevalence in each DU is determined by an SIS model based on the multi-institutional framework of Smith, et al. (1,2). A DU's prevalence is a function of its own screening level (s) and that of their neighbors (š).

We develop a cost structure similar to Armbruster and Brandeau that incorporates the various costs to screen for and treat a disease. (3) Given these costs, a single DU chooses the screening level that minimizes its net present value of discounted future costs. We solve for the symmetric, pure-strategy Nash equilibrium.

Results

As the rate of recovery following treatment (τ) increases relative to screening and treatment costs, the DU's best response curve transitions from an inverted-U pattern to one that is monotonically decreasing (Fig. 1). Additionally, the equilibrium screening value is monotonically decreasing in the number of DUs (Fig. 2). Here the best response curves intersect the line of equal screening values.

Conclusions

When treatment is less effective, free-riding is less severe and a DU's optimal screening may actually increase with its opponents level. However, as treatment becomes more effective, optimal screening levels are strictly decreasing in the other DU's allocation: free-riding takes full effect. As the number of DUs increases, so does the opportunity to free-ride. This means optimal screening will decrease and disease prevalence will increase as the number of DUs increases. Therefore, in a purely symmetric environment increasing unit autonomy may adversely affect disease prevalence: authority for screening should be centralized.

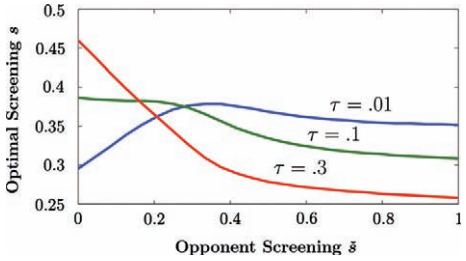

Fig. 1. Best Responce Function.

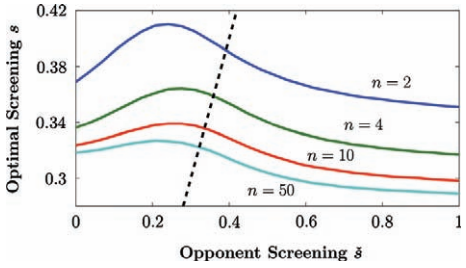

Fig. 2. Equilibrium Values.

Keywords

Game theory; screening; infectious disease

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***Aaron Miller**
E-mail: aaron-miller@uiowa.edu

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COACTION PUBLISHING

Can we identify 'bellwether' states with respect to syphilis incidence?

Mauricio Monsalve*, Sean Tolentino, Sriram Pemmaraju and Philip Polgreen

Computational Epidemiology Group, The University of Iowa, Iowa City, IA, USA

Objective

(i) To forecast syphilis cases per state in the United States to support early containment of outbreaks. (ii) For each state, to determine which states are most correlated, to find 'bellwether' states to inform surveillance efforts. (iii) To determine a small collection of states whose syphilis incidence patterns are most closely correlated with all the states.

Introduction

The time series of syphilis cases has been studied at the country and state level at the yearly basis (1, 2), and it has been found that syphilis has a periodicity of approximately 10 years (2). However, to inform prevention efforts, it is important to understand the short-term dynamics of disease activity.

Methods

We used data from the MMWR. It contains weekly syphilis counts per state. We consider the time period from 1995 to 2009. We removed week 53 when present, due to inconsistencies in reporting. We considered 53 locations: the 50 states plus Puerto Rico, and the cities of New York City and Washington DC. To predict disease activity in each state, we constructed a series of linear lagged regression models that used several states as covariates. To benchmark our models, we constructed a basic ARIMA model with one autocorrelation term. All the models were constructed to forecast 4 weeks in advance. Prediction at week t was performed by fitting the models using all past data prior to week t–4. To identify bellwether states, we proceeded as follows. First, we repeatedly fitted 2-covariate models to forecast each state and obtained the top 5 most frequent bellwether states for each state. Then, we obtained the most frequent bellwether states from the above lists.

Results

We found that forecasting states using less than 10 states as covariates is better than using more or the state itself as covariate (ARIMA), as shown in Fig. 1. An example of out of sample prediction is shown in Fig. 2, for New York City.

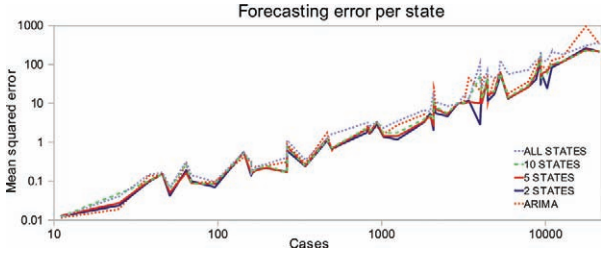

Fig. 1. Mean squared error in out of sample forecasting per number of covariates used. Plotted in log-log scale. States were sorted by their historical number of cases. Solid lines illustrate the methods with the smallest errors (using 2 and 5 states).

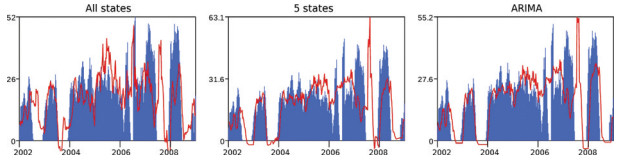

Fig. 2. Forecasting New York City one month in advance.

We also found that the 10 most frequent states in models with two covariates are California, Virginia, Florida, New York City (treated as state), Alabama, Ohio, Tennessee, North Carolina, New Hampshire and New Mexico. The first 5 are covariates of 40 states, and the amount increases to 50 when adding the later.

Conclusions

Using several states as covariates in models seem to improve their forecasting power. This suggests that these models 'learn' the dynamics of syphilis between different states. In addition, we have identified the existence of specific bellwether states. By using these bellwether states, it is possible to forecast syphilis cases in almost all the states in the country.

Several limitations undermine the quality of the predictions. First, cases are counted at reporting time instead of acquisition time (3). Second, the MMWR file supposedly contains cumulative numbers within a year, but this is not always true. Third, some states exhibit strong yearly periodicity, which seems to be due to patterns in disease reporting.

Keywords

Syphilis time series; forecasting; disease surveillance

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***Mauricio Monsalve**
E-mail: mauricio-monsalve@uiowa.edu

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COACTION PUBLISHING

Application of event-based biosurveillance to disease emergence in isolated regions

Wai-Ling Mui*, Brian White, Emily Iarocci, Aimee Reilly, Noele Nelson and David Hartley

Division of Integrated Biodefense, Georgetown University Medical Center, Washington, DC, USA

Objective

To demonstrate how event-based biosurveillance can be utilized to closely monitor disease emergence in an isolated rural setting, where medical information and epidemiological data are limited, for the purpose of identifying areas for public health intervention improvements.

Introduction

Argus is an event-based surveillance system, which captures information from publicly available Internet media in multiple languages. The information is contextualized, and indications and warning (I&W) of disease are identified. Reports are generated by regional experts and are made available to the system's users (1). In this study a small-scale disease event, plague emergence, was tracked in a rural setting, despite media suppression and a low availability of epidemiological information.

Methods

Argus reports meeting the following inclusion criteria were selected retrospectively: (1) disease: plague, (2) location: Peru, (3) time period: April–October 2010. The reports were reviewed for relevant I&W of plague infection, with the goal of identifying factors that contributed to disease spread and ineffective public health response.

Results

From the time period specified, media reported on a human plague outbreak in northern Peru where all 3 clinical forms of plague were identified (septicemic, pneumonic and bubonic); in one area, bubonic plague was registered for the first time in over a decade while pneumonic plague was reported for the first time ever in the country, according to an official (2).

The first human case of bubonic plague was reported in April, followed by a 2-month reporting lull from May to July. Subsequently, new media information revealed ongoing human plague cases, including nosocomial pneumonic infections which had spread from one patient to medical staff and one relative, as well as a severe lack of biosafety personal protective and laboratory equipment (3).

Retrospective review of Argus reports later identified 3 key factors that limited the effectiveness of disease management in the region: (1) a lack of government leadership and accountability, (2) poor sanitation leading to an inability to decrease the vector population and (3) an inadequate regional healthcare infrastructure (4). Media sources recognized discrepancies in medical information provided by health officials and the medical community, and as the outbreak continued, protests erupted over poor sanitary conditions and insufficient medical resources as observed by healthcare workers. In August, the Minister of Health (MOH) declared that the outbreak had been 'controlled'; however, the media continued to report human plague cases and noted concern regarding the potential danger of plague spreading to urban markets. Travel restrictions were applied and reports later speculated that the World Health Organization (WHO) would close ports and issue a national quarantine if plague extended into coastal export areas (5, 6). Further, officials declared a latent risk of disease transmission to bordering countries. At the end of the study reporting timeframe, media continued to identify the confirmation of new human bubonic plague cases, the implementation of vector control efforts, and the ongoing risk to residents despite attempted disease management efforts.

Conclusions

The use of an event-based methodology provided detailed insight into a localized, small-scale disease situation where limited medical and epidemiological information was available. Argus documentation of this event allowed for a retrospective review, which identified deficiencies in the current disease management system in Peru and drew attention to the potential negative impact of social and political context on public health efforts.

Keywords

Surveillance; plague; emergence; intervention; isolated

Acknowledgments

Members of the Georgetown Medical Center Project Argus team, including but not limited to, Denise McAnany, Sarah Riedl and Carlos Balhana.

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***Wai-Ling Mui**
E-mail: mui@isis.georgetown.edu

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COACTION PUBLISHING

Assessing the use of syndromic surveillance data to identify and track heat illness in Nebraska, 2010–2011

Eryn Murphy[1,2]* and Thomas Safranek[1]

[1]Division of Epidemiology, Nebraska Department of Health and Human Services, Lincoln, NE, USA; [2]University of Nebraska Lincoln, Lincoln, NE, USA

Objective

The purpose of this study was to develop methodology to accurately identify and track heat illness in a timely manner using syndromic surveillance data.

Introduction

Heat waves have serious health impacts such as heat exhaustion, heat stroke, dehydration and death. Heat illness morbidity and mortality can be reduced with the identification of vulnerable populations and targeted public health interventions. In June and July of 2011, a heat wave occurred in Nebraska in which 28 days reached 90 F or higher. Syndromic surveillance data were used to describe heat-related illness emergency department (ED) visits during this time.

Methods

Eight hospitals currently submit syndromic surveillance ED data to Nebraska Department of Health and Human Services (NeDHHS), representing approximately 18% of all ED visits for the state. Five hospitals reported complete data for the selected study period, June 1, 2010–August 10, 2011. The three hospitals not reporting complete data for the study period were excluded. These records represent approximately 15% of all ED visits in the state for June–August. Cases of heat-related illness were identifiedusing ICD9CM diagnostic and external cause of injury codes: 992, 705.1, 708.2 and E900. Additional cases were identified from the chief complaint field using the SAS INDEX function to locate the following words within the text field: 'HEAT', 'HEATED', 'DEHYDRATED' and 'HYPERTHERMIA'. Each record returned from these searches was examined to confirm the presence of heat illness. Chief complaint fields containing keywords but not involving heat-related illness, i.e., 'applied heat to swollen ankle', were eliminated.

Results

A total of 21,906 and 23,222 total ED records were available from five Nebraska ED facilities during June 1, 2010–August 10, 2011. ICD9CM codes identified 182 heat-related illness records in 2010 and 227 records in 2011. Searching the chief complaint field for keywords identified 119 and 188 records in 2010 and 2011, respectively. After reviewing records to confirm presence of heat illness, 64 chief complaint-identified records were excluded in 2010, and 100 chief complaint-identified records were excluded in 2011. In 2010 and 2011, there were 220 and 293 ED records, respectively, indicating heat-realted illness from ICD9CM codes or chief complaint key words. Preliminary results suggest crude rates for heat-related illness are slightly higher in 2011 than 2010. Heat-related illness visits were found in 10.0 records per 1000 visits in 2010 and 12.6 records per 1000 visits in 2011. Combining 2010 and 2011 data, patients with heat-related ED vists were 55% male (n = 273) with a median age of 34 years. Further analyses will assess correlation between heat index and heat illness in Nebraska.

Conclusions

The rate of heat-related illness ED visits was slightly higher in the summer of 2011 than in 2010. This system provides an effective method to identify and track heat illness. Timely identification of patients with heat illness using this system can facilitate rapid and focused public health response and reduce heat*related morbidity and mortality.

Keywords

Syndromic surveillance; heat illness; heat wave

Acknowledgments

Tom Safranek, MD; Jennifer Marcum, DrPh.

***Eryn Murphy**
E-mail: eryn.murphy@nebraska.gov

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COACTION PUBLISHING

Detecting previously unseen outbreaks with novel symptom patterns

Yandong Liu and Daniel B. Neill*

Event and Pattern Detection Laboratory, Carnegie Mellon University, Pittsburgh, PA, USA

Objective

We propose a new text-based spatial event detection method, the semantic scan statistic, which uses free-text data from emergency department chief complaints to detect, localize and characterize newly emerging outbreaks of disease.

Introduction

Commonly used syndromic surveillance methods based on the spatial scan statistic (1) first classify disease cases into broad, preexisting symptom categories (prodromes) such as respiratory or fever, then detect spatial clusters where the recent case count of some prodrome is unexpectedly high. Novel emerging infections may have very specific and anomalous symptoms, which should be easy to detect even if the number of cases is small. However, typical spatial scan approaches may fail to detect a novel outbreak if the resulting cases are not classified to any known prodrome. Alternatively, detection may be delayed because cases are lumped into an overly broad prodrome, diluting the outbreak signal.

Methods

We propose a new approach to detect emerging patterns of keywords in the chief complaint data. Our semantic scan statistic has three steps: automatically inferring a set of topics (probability distributions over words) from the data using Latent Dirichlet Allocation (2), classifying each chief complaint to the most likely topic, and then performing a spatial scan using the case counts for each topic. We compare three variants of the semantic scan: static (topics are learned from historical data and do not change from day to day), dynamic (topics are recalculated each day using the most recent two weeks of data) and incremental (not only using the static topics but also learning additional 'emerging' topics that differ substantially from the static topics).

Results

We compared the three semantic scan methods to the standard, prodrome-based spatial scan using synthetic disease outbreaks injected into real-world emergency department data from Allegheny County, PA. We first considered 55 different outbreak types, corresponding to all distinct ICD-9 codes with at least 10 cases, which were mapped to one of the existing prodromes. For each outbreak type, we generated spatially localized injects with chief complaints sampled from the cases with that ICD-9 code (Fig. 1). The static, dynamic and incremental methods required an average of 7.7, 7.1 and 6.9 days, respectively, to detect and were able to precisely characterize the outbreak based on the detected topic (e.g., top keywords for ICD-9 code 569.3 were 'rectal', 'bleed', and 'bleeding'). The prodrome method achieved more timely detection (5.0 days to detect) but with much less precise characterization (e.g., 'hemorrhagic' for ICD-9 code 569.3). Next, we considered both randomly selected, unmapped ICD-9 codes and synthetically generated unprecedented events, such as an outbreak that makes the patient's nose turn green. The prodrome method required 10.9 days to detect these outbreaks, while the semantic scan was able to achieve much faster detection. For example, for the green nose outbreak, the static, dynamic and incremental methods detected in 6.4, 5.3 and 5.6 days, respectively. The dynamic and incremental methods correctly identified the emerging topic (keywords 'green', 'nose', 'nasal', etc.), while the static method did not, since the outbreak did not correspond to any of the topics learned from historical data.

Conclusions

The semantic scan statistic can successfully capture emerging spatial patterns in free-text chief complaint data, enabling more timely detection of novel emerging outbreaks with previously unseen patterns of symptoms. Other advantages include more accurate characterization of outbreaks (identifying a set of keywords that precisely describe the disease symptoms) and the ability to detect outbreaks without preexisting syndrome definitions. Additionally, our methods have the potential to achieve more timely detection by incorporating free-text data sources, such as Twitter and other social media tools, into the surveillance process.

Keywords

Text mining; event detection; semantic scan

Acknowledgments

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***Daniel B. Neill**
E-mail: neill@cs.cmu.edu

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COACTION PUBLISHING

Optimal sequential management decisions for measles outbreaks

Jarad Niemi[1]* and Michael Ludkovski[2]

[1]Iowa State University, Ames, IA, USA; [2]University of California-Santa Barbara, Santa Barbara, CA, USA

Objective

Development of general methodology for optimal decisions during disease outbreaks that incorporate uncertainty in both parameters governing the outbreak and the current outbreak state in terms of the number of current infected, immune and susceptible individuals.

Introduction

Optimal sequential management of disease outbreaks has been shown to dramatically improve the realized outbreak costs when the number of newly infected and recovered individuals is assumed to be known (1, 2). This assumption has been relaxed so that infected and recovered individuals are sampled, and therefore the rate of information gain about the infectiousness and morbidity of a particular outbreak is proportional to the sampling rate (3). We study the effect of no recovered sampling and signal delay, features common to surveillance systems, on the costs associated with an outbreak.

Methods

We develop a stochastic compartment model for disease populations consisting of susceptible (S), infected (I), recovered (R) and deceased (D) individuals. This model contains four parameters determining the rates of these transitions: $S \rightarrow I$, $I \rightarrow R$, $I \rightarrow D$ and $S \rightarrow R$ (vaccination). While all vaccination and death transitions are observed completely, the infected and recovered transitions are observed through sampling possibly with a delay between the transition and when the information can be used in a decision.

Sequential inference of parameters is performed using Bayesian updating, which is available in closed form when independent gamma priors are assumed, and the current system state is known. For the two sampled transitions, the associated parameters are updated in a manner that is consistent with how information is gained during sampling so that the rate of information gain is proportional to the sampling rate.

A cost structure is developed to weigh the outbreak morbidity and mortality versus the cost of active outbreak control (isolation, vaccination and increased sampling). The morbidity cost is quadratic to account for increased costs that occur when many individuals are sick simultaneously. Control costs include fixed and running costs, which are a function of the current number of infected individuals (3).

The effect of recovered sampling and delay is primarily assessed by running separate scenarios that have combinations of sampling and delay and calculating the average outbreak cost under these scenarios. In addition, allowing recovered sampling in a control allowed analysis of how often and when the optimal outbreak management utilized this sampling.

Results

As a case study, we use a recent measles outbreak in Harare, Zimbabwe, as our basis. At outbreak onset, we assume 20,000 susceptible individuals ($\sim$1% of total population in accordance with vaccination coverage rates) and 20 infected individuals. Priors for outbreak parameters are vague but informative, e.g., a 95% interval for infectiousness is 4 to 11 days.

Relative to the base-case scenario where immediate sampling is performed on both newly infected and recovered individuals, the following results are observed. Eliminating recovered sampling increases average costs by 5%, a one-period delay between transitions and control action increases costs 6%, a two-period delay increases costs 14% and eliminating all sampling increases costs by 34%.

When allowing increased sampling as a possible outbreak control measure, the optimal decision was to utilize sampling of infected and recovered individuals about 20% of the time.

Conclusions

Typical syndromic surveillance systems have taken the first step, which is to provide a measure of the number of newly infected individuals. Costs being equal, this research suggests this was the best investment for surveillance. We hope future research with different diseases and surveillance possibilities will elucidate where money should be spent in improving surveillance practices.

Keywords

Optimal control; Bayesian; basic reproductive number; time series; statistical model

Acknowledgments

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*Jarad Niemi
E-mail: niemi@iastate.edu

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COACTION PUBLISHING

An exploratory analysis of the 2010 measles outbreak in Zimbabwe

Jarad Niemi*

Iowa State University, Ames, IA, USA

Objective

To systematically organize the World Health Organization data on the 2010 measles outbreak in Zimbabwe. To perform a post hoc exploratory analysis to understand how the outbreak spread geographically and evaluate the effectiveness of a mass vaccination campaign.

Introduction

This report describes an exploratory analysis of the 2009–2010 Zimbabwe measles outbreak based on data publicly available in the World Health Organization's Zimbabwe cholera epidemiological bulletin archive. As of December 12, 2010, the outbreak appears to have ended after it is suspected to have caused 13,783 infections, 693 of those being confirmed IgM positive and 631 deaths (1).

Methods

Data were extracted from the weekly Zimbabwe cholera epidemiological bulletins available in the World Health Organization's Zimbabwe cholera epidemiological bulletin archive (2). The focus of the data collection was on the tables titled 'Distribution of Measles IgM Positive by Age group and District of residence', which typically contained both cumulative and new cases of IgM-confirmed measles cases by district and age categories. Although not entirely consistent, the age categories were younger than 9 months, 9–11 months, 1–4 years, 5–14 years, and 14 years and older.

The statistical software R (3) was used for data cleaning (an extensive process) and exploratory analysis. The maptools package (4) was used to generate maps of the geographical disease progression.

Results

Fig. 1A provides an example time series for the cumulative-confirmed measles cases in Harare, the capital of Zimbabwe, where all age categories have been combined. Indicated in green is the mass vaccination campaign that took place between May 24 and June 2.

Fig. 1B provides an example map displaying the geographical distribution of confirmed measles cases upon extinction of the outbreak. The darker color indicates a higher attack rate (number of confirmed cases divided by total population); the darkest red area is Harare.

Conclusions

This exploratory analysis questions the utility of the mass vaccination campaign since the campaign came after the peak of the outbreak in the hardest hit district in Zimbabwe. But since Harare was one of the earliest districts affected, perhaps the campaign prevented further spread to other districts. In addition, it is possible that suspected cases in Harare were more likely to become confirmed cases due to geographical proximity of testing laboratories, thereby inflating the relative attack rate.

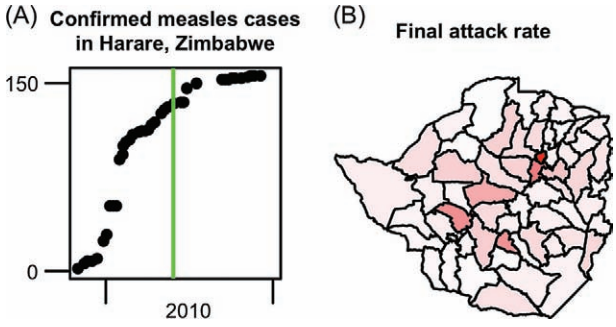

Fig. 1. (A) Cumulative confirmed cases for the 2010 measles outbreak in Harare, Zimbabwe, with mass vaccination campaign (green). (B) Raw district-specific attack rates (confirmed cases divided by population, darker indicates higher) in Zimbabwe as of Dec 12, 2010.

Keywords

Measles; Zimbabwe; exploratory analysis; geographical; R

Acknowldgements

Thank you to the team of undergraduates at the University of California, Santa Barbara who collated the data: Alexandra Ackroyd, Kari Davis, Yang Gao, Aashish Khanal, Mark Marcos, Emily Marlow, Jaclyn Ong and Diwen Song.

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***Jarad Niemi**
E-mail: niemi@iastate.edu

COACTION PUBLISHING

Operation of the evacuation site surveillance for the Great East Japan Earthquake in 2011

Yasushi Ohkusa*, Tamie Sugawara, Yoshinori Yasui, Kazutoshi Nakashima, Tomimasa Sunagawa, Yuichiro Yahata, and Kiyosu Taniguchi

National Institute of Infectious Diseases, Shinjuku, Japan

Objective

For an early detection and control of an infectious disease outbreak, we developed and have been operating syndromic surveillance for evacuation sites 'evacuation site surveillance'.

Introduction

In March 11, 2011, the big earthquake attacked eastern Japan followed by huge tsunami and nuclear plant accident. Consequently, a lot of people could not help living in evacuation sites. Since those evaluation sites have high density of population and were not necessarily good in sanitary condition, outbreaks of influenza, norovirus or other infectious diseases were concerned.

Methods

We developed a web-based evacuation site surveillance system with 8 syndromes including acute gastroenteric symptoms; influenza or influenza-like-illness; acute respiratory symptoms other than influenza; rash and fever; neurologic symptoms including tetanus, meningitis and encephalitis; cutaneous symptoms; wound-related infectious diseases; icterus and death. Age of the patients was classified into three categories: younger than 5 years, 5 to 64 years and 65 years old or older. Analysis by evacuation site was performed automatically, and if some aberrations were found, the system showed an alert sign on the screen of a computer. The information on patients was shared with the public health center and the local government office simultaneously.

Results

Evacuation site surveillance started in Fukushima prefecture on March 25, 2011, and in Miyagi prefecture on May 8, 2011. About 400 sites in Miyagi prefecture were covered until the end of May. When the surveillance found an aberration, the public health center investigated the site and started taking an action for control.

Conclusions

This system raised awareness of infectious diseases and provided good information for risk assessment. Before the earthquake, the pharmacy surveillance and the school surveillance (only in Miyagi prefecture), which are nationwide syndromic surveillance in Japan, were operating, and these played a complementary role for evacuation site surveillance and the official surveillance. Our experience showed that it would be too late to start to develop the system from the scratch after a disaster occurred. Thus, it is essential to make a plan on activation of the system in advance in case a severe disaster occurs and to prepare and stockpile the hardware that is necessary for an early activation of evacuation site surveillance. The necessary hardware, for example, includes battery and communication tool even if electronic power, internet and (mobile) phone network are shut down. This is the next challenge.

Keywords

Earthquake; evacuation site; disaster

***Yasushi Ohkusa**
E-mail: ohkusa@nih.go.jp

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COACTION PUBLISHING

Adopting a common influenza-like illness syndrome across multiple health jurisdictions

Don Olson[1]*, Atar Baer[2], Marc Paladini[3] and Howard Burkom[4]; ISDS Distribute Working Group[1]

[1]International Society for Disease Surveillance, New York, NY, USA; [2]Public Health—Seattle & King County, Seattle, WA, USA; [3]New York City Department of Health & Mental Hygiene, Queens, NY, USA; [4]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

Assess the feasibility and utility of adopting a common influenza-like illness (ILI) syndrome across participating jurisdictions in the ISDS Distribute project.

Introduction

Syndromic surveillance systems were designed for early outbreak and bioterrorism event detection. As practical experience shaped development and implementation, these systems became more broadly used for general surveillance and situational awareness, notably ILI monitoring. Beginning in 2006, ISDS engaged partners from state and local health departments to build Distribute, a distributed surveillance network for sharing de-identified aggregate emergency department (ED) syndromic surveillance data through existing state and local public health systems (1). To provide more meaningful cross-jurisdictional comparisons and to allow valid aggregation of syndromic data at the national level, a pilot study was conducted to assess implementation of a common ILI syndrome definition across Distribute.

Methods

Six jurisdictions provided 4 years of baseline ED data using a common ILI definition comprising 3 subsyndrome components defined by a formal code-set (Fig. 1). Distribute sites were invited to participate in the assessment based on geography, jurisdiction size and ED coverage. Invited sites were asked to provide historical data consisting of total and ILI-related daily visit counts by age group (<2, 2–4, 5–17, 18–44, 45–64 and 65+ years). The common ILI syndrome and subsyndrome case definitions for the pilot were defined from coded or free text ED patient electronic chief complaint data as 'fever and cough', 'fever and sore throat', and 'flu'. Evaluation included comparison of syndrome time-series, subsyndrome and age-specific distribution of visits and signal-to-noise measures.

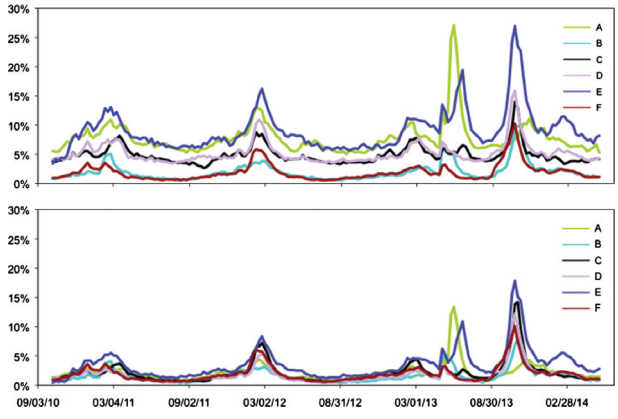

Fig. 1. Time-series of percent of total ED visits: locally preferred ILI (top) and common ILI (bottom) syndromes for six Distribute jurisdictions.

Results

We found less variation between jurisdictions in weekly ratios using the common ILI definition (mean 2%; range 1.5–3.1%) than locally preferred syndromes (mean 4.9%; range 1.8-8.4%), and influenza epidemic signal-to-noise ratios were comparable for most jurisdictions during the study period. The findings suggest that the common syndrome improves comparability without an overall cost in terms of epidemic signal discrimination.

Conclusions

The results of this common ILI assessment suggest that disparate local systems can adopt a harmonized syndrome definition allowing for meaningful comparisons and national aggregation while maintaining the ability to use local systems and definitions. The common ILI syndrome provided more directly comparable time-series, both during baseline periods and epidemics. Use of the common syndrome did not have an overall or systematic cost in terms of epidemic signal discrimination. Where the signal-to-noise ratio was not improved, differences were usually minimal. Also, the use of the common syndrome did not restrict the use of the locally defined syndromes for local detection. This collaborative pilot was useful in synthesizing local experience in the creation of a nationally harmonized ILI syndrome definition.

Keywords

Influenza; surveillance; epidemiology; syndrome standard; emergency department

References

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*Don Olson
E-mail: drolson@gmail.com

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COACTION PUBLISHING

Monitoring winter-seasonal acute gastroenteritis emergency department visits by age

Don Olson[1]*, Ian Painter[2] and ISDS Distribute Working Group[1]

[1]International Society for Disease Surveillance, New York, NY, USA; [2]University of Washington, Seattle, WA, USA

Objective

We describe the initial phase of the ISDS Distribute pilot for monitoring acute gastroenteritis (AGE) syndromic emergency department (ED) visits and present preliminary analysis of age-specific trends documenting a dramatic shift in AGE consistent with US rotavirus vaccine policy and use.

Introduction

Epidemic AGE is a major contributor to the global burden of morbidity and mortality. Rotavirus and norovirus epidemics present a significant burden annually, with their predominant impact in temperate climates occurring during winter periods. Annually, epidemic rotavirus causes an estimated 600,000 deaths worldwide and 70,000 hospitalizations in the United States, primarily among children younger than 5 years (1). The U.S. burden from norovirus is estimated at 71,000 hospitalizations annually, with the impact more generally across age groups (2). Changes in rotavirus vaccine use have significantly reduced the impact of epidemic rotavirus (3).

Methods

The Distribute project began in 2006 as a distributed, syndromic surveillance effort networking state and local health departments to share aggregate ED based influenza-like illness (ILI) syndrome data (4). The AGE pilot was conducted to assess the feasibility of generalizing the Distribute model from ILI trends to monitoring other syndromes. Distribute participating jurisdictions were asked to submit diarrheal and vomiting AGE syndrome ED data, following a commonly used syndrome definition. Of the 10 Distribute participating jurisdictions that submitted AGE data, 6 provided historical baseline data going back to January 2006 or earlier. Of these, 3 were state, 3 large city or county jurisdictions, located in Northeastern, Mid-Atlantic, Midwestern and Western U.S. surveillance regions. Syndrome time-series ratios [(weekly AGE syndrome count)/(total ED visit count)] were assessed by jurisdiction and age group. To aid comparison of seasonal trends across jurisdictions, time-series were normalized around their baseline as a measure of relative increase [(weekly AGE ratio)/(weekly lower-quartile)]. Rotavirus vaccine 2006 pre- and postlicensure periods were compared.

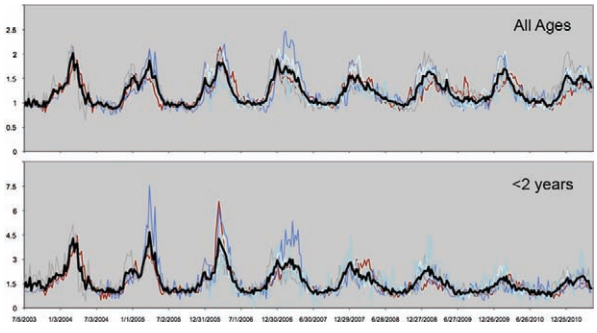

Fig. 1. Distribute jurisdiction AGE trends, July 2003 to May 2011, shown normalized as a measure of relative increase for 6 jurisdictions (thin lines) and as a composite mean ratio (thick black lines). The top graph shows relative increase for ED visits among all age groups. The bottom shows relative increase only for those aged younger than 2 years.

Results

All jurisdictions submitting AGE data to Distribute presented seasonal trends with predominant winter peaks. Across the pilot jurisdictions, seasonal peaks from 2003/04 to 2005/06 occurred during Mar–Apr, while 2006/07 to 2009/10 seasonal trends peaked predominantly in Dec–Feb. Overall, epidemic timing was similar across age groups; however, the shifting pattern in impact after the 2006/07 season presented a greater drop among young children. (Fig. 1).

Conclusions

The results of the pilot suggest the Distribute model can be successfully generalized to monitoring AGE trends, specifically the age-specific timing and impact of winter-seasonal epidemic rotavirus and norovirus. The case study of 2006 rotavirus vaccine implementation and subsequent shift in timing and impact of AGE trends suggest that syndromic ED data can potentially provide a useful surveillance indicator of population-level vaccine effect.

Keywords

Gastroenteritis; norovirus; rotavirus; epidemiology; emergency department

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*Don Olson
E-mail: drolson@gmail.com

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COACTION PUBLISHING

Gossamer Health: a meaningful, open-source approach to shared surveillance software

Bill Lober, Ian Painter*, Blaine Breeder and Debra Revere

University of Washington, Shoreline, WA, USA

Objective

The goal of this work is to make available to the public health community an open source system that makes available in a standards-based, modular fashion the basic tools required to conduct automated indicator-based population health surveillance. These tools may be deployed in a flexible fashion on health department servers, in the Amazon EC2 cloud, or in any combination, and are coupled through well-defined standards-based interfaces.

Introduction

Cost-effective, flexible and innovative tools that integrate disparate data sets and allow sharing of information between geographically dispersed collaborators are needed to improve public health surveillance practice. Gossamer Health (Good Open Standards System for Aggregating, Monitoring and Electronic Reporting of Health), http://gossamerhealth.org, is an open source system, suitable for server or 'cloud' deployment, which is designed for the collection, analysis, interpretation and visualization of syndromic surveillance data and other indicators to monitor population health. The Gossamer Health system combines applied public health informatics research conducted at the University of Washington (UW) Center for Public Health Informatics and Washington State Department of Health, in collaboration with other state and local health jurisdictions, the International Society for Disease Surveillance and the Centers for Disease Control and Prevention.

Methods

Gossamer combines work on (1) methods for automated surveillance based on summarized clinical data, such as the influenza and visit counts used in the Distribute project (1), (2) methods developed for the modularization of surveillance processes developed for the Shoki project (2), (3) methods developed for the automated processing of Health Information Exchange data (HIE) as part of the CDC HIE initiative (3) and (4) standard industry server virtualization and deployment techniques (4).

Results

Gossamer uses code developed at UW and additional open source components. Most components are distributed under the '3-clause BSD license', permitting free use, modification and redistribution. Automated modules include (1) HL7 message receipt, processing and storage, (2) compilation of line listing data from HL7 Minimum Biosurveillance Data Set (MBDS) and Meaningful use (under development) messages, (3) classification of cases into syndromes and compilation of syndrome data into indicators, (4) receipt, storage, aggregation and management of indicator data, and (5) analysis, visualization and reporting (AVR) of indicator data. Modules may be deployed locally or in the EC2 cloud and communicated using standard protocols to let deployment strategies be mixed across the system to support both sharing and shared use of components, as well as load balancing and optimization. This presentation will talk about the goals of the open source system and give underlying details of the technical implementation using virtual machines. As an example, we will discuss an application of the Gossamer system instance developed to let a state public health agency disseminate summarized laboratory test results for multiple (14) respiratory viruses (see Fig. 1).

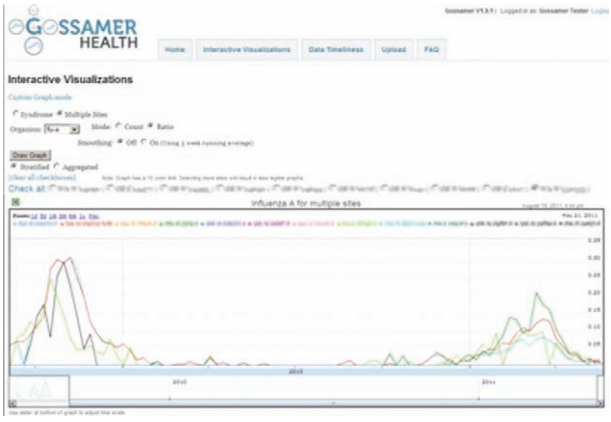

Fig. 1. Gossamer Health Screenshot showing timeseries graph of positive test rates for multiple respiratory viruses.

Conclusions

To support existing and emergent surveillance needs, the UW has worked with local and state health jurisdictions to identify features that allow for user-defined indicators of chronic and infectious disease surveillance. An important aspect of the Gossamer Health vision is its support for public health agencies to collaborate in cross-jurisdictional surveillance efforts through both on-demand and automated sharing of standards-based data feeds.

Gossamer is a work in progress, but it is a community work. All are welcome to participate in its development.

Keywords

Surveillance; open source; architecture; cloud; software

***Ian Painter**
E-mail: ipainter@uw.edu

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COACTION PUBLISHING

Rapid ad hoc cross-jurisdictional sharing of syndrome data using Distribute technology

Ian Painter[1]*, Don Olson[2] and Bill Lober[1]

[1]University of Washington, Shoreline, WA, USA; [2]International Society for Disease Surveillance, Brighton, MA, USA

Objective

To demonstrate how rapid ad hoc sharing of surveillance data can be achieved through informatics methods developed for the Distribute project.

Introduction

Cross-jurisdictional sharing of public health syndrome data is useful for many reasons, among them to provide a larger regional or national view of activity and to determine if unusual activity observed in one jurisdiction is atypical. Considerable barriers to sharing of public health data exist, including maintaining control of potentially sensitive data and having informatics systems available to take and view data.

The Distribute project (1,2) has successfully enabled cross-jurisdictional sharing of ILI syndrome data through a community of practice approach to facilitate control and trust and a distributed informatics solution.

The Gossamer system (3) incorporates methods used in several UW projects including Distribute. Gossamer has been designed in a modular fashion to be hosted using virtual or physical machines, including inside cloud environments. Two modules of the Gossamer system are designed for aggregate data sharing and provide a subset of the Distribute functionality.

The Distribute and Gossamer systems have been used for ad hoc sharing in three different contexts: sharing of common ILI data for research into syndrome standardization, sharing syndromic data for specific events (2010 Olympics) and for pilot regional sharing of respiratory laboratory results. Two additional projects are underway to share specific syndromes of recent interest: alcohol-related and heat-related ED visits.

Methods

The Distribute system was initially designed to share 4 syndromes (broad and narrow ILI, and GI syndromes). To reduce barriers to entry, the Distribute project does not impose strict syndrome definitions. This lack of standardization introduces variability between jurisdictions and a pilot has been undertaken to compare sites with preferred definitions and to develop a common ILI definition. To enable the addition of a common syndrome considerable modifications to the structure of the Distribute system were required. The approach taken allowed for the use of arbitrary indicators and stratification ranges.

The Gossamer system uses a similar data storage architecture to that of the current version of Distribute, though Gossamer is more modular and better able to use external services. These features make it useful for moving beyond specific political structures or disease content areas.

Results

The expanded data model has now been used to support the ILI standardization effort through comparison of newly contributed 'ILI-S' syndrome data. Distribute was also used to develop a site to allow Washington State DoH to share specific syndromic data with British Columbia during the 2010 Olympics. An instance of Gossamer demonstrated sharing laboratory results for 14 viral isolates between two states. In addition to community-driven comparisons of ILI and GI syndromes, the data model has been applied at the design level to two additional syndrome types for ad hoc data sharing: alcohol intoxication-related visits and heat exposure-related ED visits.

While built around similar data models, each system has strengths and weaknesses for ad hoc sharing of data. Advantages of the Distribute system for sharing additional data include making use of the existing trust and community that is based around the system, which reduces many barriers to sharing data and facilitates adding more community members. In addition, data feeds and administrative details are already in place.

Disadvantages of using Distribute include limitations in the common data transmission format, limitations in stratifiers and limitations in compartmentalization.

The implementation of the very similar data model in Gossamer is able to address some of these issues by various strategies including virtualization and modular architecture, while extending the flexibility which supports new applications of the data collection, quality and analysis methods developed for use with influenza syndromes in Disribute.

Conclusions

The 5 examples illustrate the strengths of the community of practice approach to sharing data. The Distribute and Gossamer systems illustrate how lightweight systems can be designed to easily facilitate ad hoc sharing between jurisdictions.

Keywords

Informatics; surviellance; architecture; data sharing; public health practice

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3. www.gossamerhealth.org.

*Ian Painter
E-mail: ipainter@uw.edu

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COACTION PUBLISHING

How good is your data?

Ian Painter[1]*, Julie Eaton[1], Don Olson[2], Debra Revere[1] and William Lober[1]

[1]University of Washington, Seattle, WA, USA; [2]International Society for Disease Surveillance, Boston, MA, USA

Objective

The goal of this session will be to briefly present two methods for comparing aggregate data quality and invite continued discussion on data quality from other surveillance practitioners and to present the range of data quality results across participating Distribute sites.

Introduction

Distribute is a national emergency department syndromic surveillance project developed by the International Society for Disease Surveillance (ISDS) for influenza-like illness (ILI) that integrates data from existing state and local public health department surveillance systems. The Distribute project provides graphic comparisons of both ILI-related clinical visits across jurisdictions and a national picture of ILI.

Unlike other surveillance systems, Distribute is designed to work solely with summarized (aggregated) data, which cannot be traced back to the unaggregated 'raw' data. This and the distributed, voluntary nature of the project create some unique data quality issues, with considerable site to site variability. Together with the ISDS, the University of Washington has developed processes and tools to address these challenges, mirroring work done by others in the Distribute community.

Methods

University of Washington together with the ISDS has undertaken a comprehensive analysis of the quality of the data being received by Distribute, primarily using visual methods, examining data quality characteristics within and between sites. This process included basic exploratory analysis of data quality problems and analytical analysis of specific aspects of data quality, including the relationship between timeliness, completion and accuracy.

Results

Considerable variability was seen between sites in terms of timeliness and completion, and completion rates did not necessarily correlate with accuracy. In our talk, we will present results comparing the quality of data between sites (sites will be unidentified), in particular comparisons between timeliness, completion and accuracy. We will also examine the types of observed relationships between timeliness, completeness and accuracy exhibited across the sites.

The purpose of this talk is to facilitate discussion between Distribute participants around data quality and the role that the ISDS can play in ensuring data quality. We will show prototypes of two features that could be hosted on the Distribute restricted site. The first feature would allow each site to compare the quality of their data (identified only to them, with site linked to the id of the user) with the remaining sites (each unidentified). The second feature would allow each site to see time series of their data together with prediction intervals for the accuracy of the ILI ratio for recent dates where the data are incomplete (see Fig. 1).

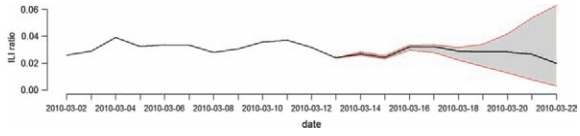

Fig. 1. ILI ratio timeseries calculated from incomplete data with superimposed 95% prediction interval for the complete data value for a representative site.

Conclusions

Our goal is to spark discussion on data quality with respect to syndromic surveillance data and, in particular, how the Distribute project can be leveraged to improve the quality of aggregate data produced by participating sites.

Keywords

Data quality; surveillance; public health practice; data quality

*Ian Painter
E-mail: ipainter@uw.edu

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COACTION PUBLISHING

Visualizing data quality: tools and views

Ian Painter[1]*, Julie Eaton[1], Don Olson[2], William Lober[1] and Debra Revere[1]

[1]University of Washington, Shoreline, WA, USA; [2]International Society for Disease Surveillance, Brighton, MA, USA

Objective

To present exploratory tools and methods developed as part of the data quality monitoring of Distribute data and discuss these tools and their applications with other participants.

Introduction

Distribute is a national emergency department syndromic surveillance project developed by the International Society for Disease Surveillance for influenza-like illness (ILI) that integrates data from existing state and local public health department surveillance systems. The Distribute project provides graphic comparisons of both ILI-related clinical visits across jurisdictions and a national picture of ILI.

Unlike other surveillance systems, Distribute is designed to work solely with summarized (aggregated) data, which cannot be traced back to the unaggregated 'raw' data. This and the distributed, voluntary nature of the project creates some unique data quality issues, with considerable site to site variability. Together with the ISDS, the University of Washington has developed processes and tools to address these challenges, mirroring work done by others in the Distribute community.

Methods

The University of Washington together with the ISDS has undertaken a comprehensive analysis of the quality of the data being received by Distribute, primarily using visual methods, examining data quality characteristics within and between sites. Several visualization tools were developed to assist in analyzing and characterizing data quality patterns for each site: upload pattern graphs (Fig. 1), stacked lag histograms and arrays of lagged time series graphs. Upload pattern graphs are heat maps comparing upload dates with encounter dates (an example figure is given below for three sites). Stacked lag histograms provide a succinct view of the complete distribution of data timeliness for a particular site. Arrays of lagged time series graphs provide an in-depth look at how timeliness patterns manifest in time series graphs. Implementation of the latter two visualizations required implementing a specific database architecture to enable reconstruction of the data at any prior upload date.

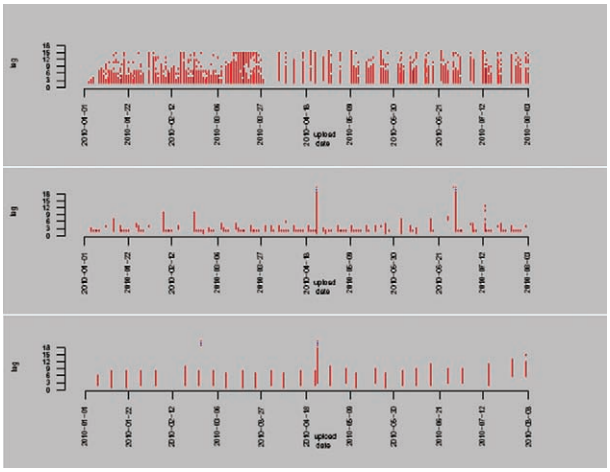

Fig. 1. Upload pattern plots for three sites. Each point represents an encounter date contained with in an upload file. The x-axis represents the date of the file upload and the y-axis represents the number of days prior to the upload date the encounter date was. The graph is truncated at 16 days prior to the upload date.

Results

In our talk, we will present these visualizations and demonstrate how they can be used to discover several common and some unusual data quality patterns and issues. We will also discuss the underlying architecture that allows us to reconstruct prior views and discuss the importance of examining data quality in terms of prior data views.

Keywords

Visualizations; data quality; surveillance

*Ian Painter
E-mail: ipainter@uw.edu

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COACTION PUBLISHING

Utilization of EMR data for public health surveillance and situational awareness during the 2010 Haiti Earthquake: a preliminary assessment

Dina Passman* and Jennifer Olsen

ASPR/OPEO, HHS, Washington, DC, USA

Objective

To describe some uses of EMR data for surveillance and situational awareness during disaster response.

Introduction

During responses, an electronic medical record (EMR) allows federal emergency response staff to view and evaluate near real-time clinical encounter data. Analysis of EMR patient data can enhance situational awareness and provide decision advantage for headquarters' staff during both domestic and international events. The EMR was utilized by field medical personnel during the response to the Haiti earthquake.

Methods

During the U.S. response to the Haiti Earthquake in January 2010, patient demographic and clinical treatment data were collected by ESF-8 responders through the EMR. Data were collected throughout the patient experience during registration, triage, treatment and discharge. Inclusion criteria for encounter records in the main analysis were entered into the EMR between January 18, 2010, and February 22, 2010, encounter occurred at one of the HHS sites in Haiti and data downloaded no later than February 23, 2010. Data were then analyzed in order to identify potential emerging conditions and operational medical needs during the entire response.

Results

We analyzed 8925 patient encounter records entered into the EMR between January 18 and February 22, 2010. Of those records, 4612 (51.8%) were coded as female, 3995 (44.8%) as male and 303 (3.4%) were not specified. Additionally, 1444 (16.2%) of the encounters were coded as less than 6 years old, 1638 (18.3%) were coded as 6–18 years old, 4352 (48.8%) were coded as 19–49 years old, 1004 (11.2%) were coded as 50–65 years old, 283 (3.2%) were coded as more than 65 years old and 204 (2.3%) were not specified. Mean age was 27.1 (SD = 19.1) years with a minimum of 1 day and a maximum of 100 years. Additionally, 6575 (75.1%) records were coded as nonurgent, 1889 (21.6%) as urgent and 295 (3.3%) as emergent. Daily surveillance of the records resulted in the identification many of suspected or confirmed symptom and disease occurrences. They included 8 cases of chicken pox/herpes zoster, 46 cases of conjunctivitis, 1 case of hemorrhagic fever, 23 guns shots wounds, 15 cases of malaria, 1 case of measles, 3 cases of meningitis, 2 cases of mumps, 53 cases of acariasis (including scabies), 1 case of typhus, 3 cases of tetanus, 3 cases of tuberculosis and 7 cases of pneumonia. We also detected 714 instances of fever and 550 instances of diarrhea.

Conclusions

During the 2010 earthquake response in Haiti, knowledge of the medical encounters through EMR data in the field provided indications of need for patient care. The surveillance of suspected and confirmed condition and diseases of concern allowed for timely decisions on adjustments to the response. Event burden could be quickly assessed through electronic reporting. EMR data can enhance and inform emergency response decision-making during domestic and international events and may be a useful tool for field public health and medical surveillance and situational awareness during future disaster responses.

Keywords

Surveillance; disaster response; electronic medical records

***Dina Passman**
E-mail: dina.passman@hhs.gov

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COACTION PUBLISHING

Pandemic H1N1-related ICU rates according to race/ethnic groups in Massachusetts

Hilary Placzek[1]* and Lawrence Madoff[2]

[1]Clinical and Population Health Research Department, University of Massachusetts Medical School, Worcester, MA, USA; [2]Division of Epidemiology and Immunization, Massachusetts Department of Public Health, Jamaica Plain, MA, USA

Objective

(1) Investigate 2009 H1N1-related ICU admissions in Massachusetts (MA) by race/ethnic group; (2) Investigate the association between ICU stay and race/ethnic group adjusted for socioeconomic status (SES).

Introduction

Epidemiological data suggests that there have been disproportionate numbers of non-White persons hospitalized due to 2009 pandemic influenza (H1N1) in MA. Population-based statewide descriptions of H1N1-related hospitalizations according to race/ethnic group and SES have not been described.

Methods

We identified those discharged from any MA hospital during the H1N1 pandemic in the Hospital Discharge Database (HDD) with ICD-9 diagnosis codes correlating highly with positive viral specimens (1). Using five-digit zip codes as an identifier, we linked census data to the HDD population to provide a measure of SES indicator through aggregate levels of affluence. We used random-effects multivariate logistic regression models to explore the above objectives.

Results

9737 individuals met inclusion criteria, and 1529 individuals (16%) were admitted to the ICU. Hispanics had the lowest rates of ICU stay (11% Hispanics in the ICU had the highest length of stay (8.1 days), the youngest mean age (26 years), nearly a third (32%) were <18 years, 52% were from the lowest SES group, and 58% were female (Table 1). Differences between race/ethnic groups and SES exist (Table 1). Results from multivariate regressions indicate that Hispanics are at 27% lower risk for ICU stay compared to Whites (OR =0.73, p <0.001—data not shown).

Conclusions

Hispanics were particularly vulnerable to exposure and susceptibility to H1N1 (2). However, Hispanics had the lowest rates of H1N1-related ICU admission and significantly lower risk of having H1N1-related ICU visits. Logistic regression models indicate that these differences are not explained by the large differences in SES. This is contrary to other reports and could be related to the low mean age of this group. Future work should address how lower age among Hispanics influences H1N1-related ICU stay – especially in young Hispanic women.

Keywords

Pandemic H1N1 influenza; epidemiology; disparity research; race/ethnicity

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*Hilary Placzek
E-mail: hilary.placzek@umassmed.edu

Table 1. Study population by race/ethnic group and ICU stay

	White		Hispanic		Black		Other	
Independent Variables n(%)	ICU n=1,116	No ICU n=5,648	ICU n=130	No ICU n=1,042	ICU n=174	No ICU n=916	ICU n=109	No ICU n=602
Gender								
Male	631 (57)	2887 (51)	55 (42)	549 (53)	100 (58)	444 (48)	53 (49)	321 (53)
Female	485 (43)	2761 (49)	75 (58)	493 (47)	74 (42)	472 (52)	56 (51)	281 (47)
Age Groups								
Mean (SD)	47 (17.6)	41 (20.8)	31 (21.6)	26 (22.4)	33 (21.0)	31 (22.4)	33 (23.4)	25 (33.0)
<18 years	108 (10)	1053 (19)	42 (32)	450 (43)	48 (28)	292 (32)	39 (36)	288 (48)
18–44 years	239 (21)	1335 (24)	41 (32)	303 (29)	55 (32)	291 (32)	22 (20)	134 (22)
45–64 years	713 (64)	3064 (54)	44 (34)	277 (27)	69 (40)	325 (36)	48 (44)	171 (28)
SES Group by zip code								
0–4.9%	329 (30)	1,728 (31)	3 (2)	52 (5)	15 (9)	79 (9)	28 (25)	142 (24)
5.0–9.9%	388 (35)	2,001 (35)	10 (8)	120 (12)	26 (15)	115 (12)	27 (25)	142 (24)
10.0–19.9%	308 (28)	1,528 (27)	50 (38)	386 (37)	70 (40)	356 (39)	41 (37)	207 (34)
≥20%	92 (8)	390 (7)	68 (52)	483 (46)	62 (36)	367 (40)	14 (13)	110 (18)
No. of deaths	116 (10)	63 (1.1)	8 (6.2)	4 (0.4)	9 (5.2)	2 (0.2)	11 (10)	5 (0.8)
Admitted through ED	690 (62)	3089 (55)	74 (57)	413 (40)	106 (61)	520 (57)	59 (54)	254 (42)
Length of Stay, days mean (SD)	7.7 (8.0)	3.7 (3.6)	8.1 (9.0)	3.3 (3.3)	7.3 (6.2)	3.3 (3.3)	6.5 (6.1)	3.1 (3.5)

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COACTION PUBLISHING

Using spatial analysis for estimation of the stage of HIV epidemic

Oleksandr Postnov[1]*, Oleksandr Neduzhko[1], Nina Slavina[1], Tetiana Gerasimenko[1], Stanislav Servetskiyy[2] and Yurii Farion[3]

[1]Ukrainian State Anti-Plague Research Institute, Odessa, Ukraine; [2]Odessa Regional Center for AIDS Prevention and Control, Odessa, Ukraine; [3]Ukrainian Institute of Geography, Kyiv, Ukraine

Objective

To investigate the utility of spatial analysis in the tracking of the stages of the HIV epidemic at an administrative territory level, using the Odessa region, Ukraine, as an example.

Introduction

Detection of the signs of HIV epidemic transition from concentrated to generalized stage is an important issue for many countries including Ukraine. Objective and timely detection of the generalization of HIV epidemic is a significant factor for the development and implementation of appropriate preventive programs. As an additional method for estimating HIV epidemic stage, the spatial analysis of the reported new HIV cases among injection drug users (IDU) and other populations (due to sexual way of transmission) has been recommended.

For studying new HIV cases in small societies, relative risk (RR) rates are preferred over incidence indicators. Spatial clustering based on the calculation of RR rates allows us to locate the high-risk areas of HIV infection with greater accuracy.

In our opinion, in the process of epidemic generalization, the spatial divergence of epidemic will be observed as well. In particular, clusters with high RR of sexual HIV transmission independent from the clusters with high RR of injection HIV transmission may appear.

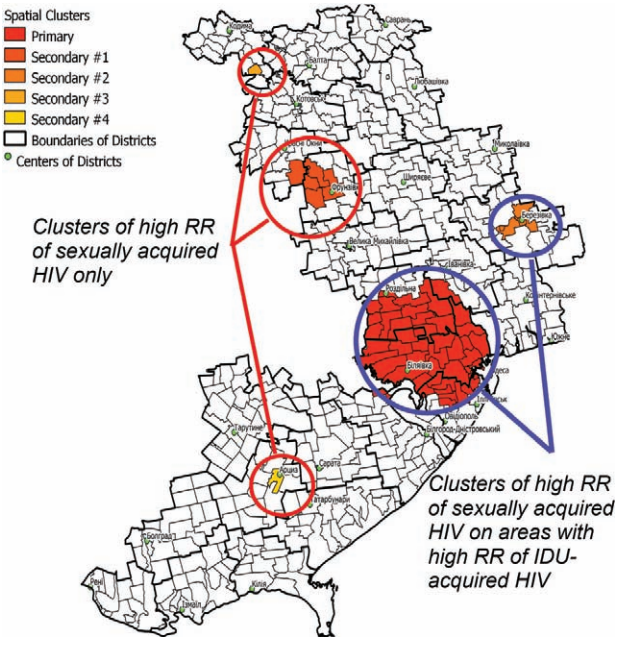

Fig. 1. Spatial clusters of high RR of sexual acquired HIV in the Odessa region in 2005–2009.

Methods

We used spatial clustering based on reported HIV cases acquired through IDU and sexual transmission from 1994 to 2009 in the smallest administrative units (called Radas) in the rural territory of the Odessa region, Ukraine. For the formal spatial clustering, we used Kulldolf Spatial Statistics, realized in the SatScan program. Clustering was conducted by the Poisson model. We used the circle window and set the cluster size limit empirically at 15% of the at-risk population. The study was done in clusters with high RR.

Visualization was carried out on QuantumGIS.

Results

With clustering, the HIV incidence due to IDU and sexual intercourse were mostly identical in the 1994–1999 and 2000–2004 periods. However, three spatial clusters of sexually acquired HIV emerged in the 2005–2009 period (RR = 3.44, $p = 0.0005$; RR = 10.60, $p = 0.011$; RR = 2.18, $p = 0.0265$), which did not correspond to an increased RR of IDU-acquired HIV (see Fig. 1).

Proportion of Radas, simultaneously included in the clusters of both types of HIV transmission, decreased from 64.58% in 2000–2004 to 48.33% in 2005–2009.

To test the effectiveness of the method, we compared the number of Radas where HIV cases were registered due to sexual transmission only and were not detected due to IDU. In the 2005–2009 period, we observed an increase in the number of Radas reporting sexually acquired HIV cases but not IDU-acquired HIV cases.

Conclusions

The spatial clustering of the HIV epidemic in the rural areas of the Odessa region showed a divergence in the spatial distribution between IDU and sexually transmitted HIV. We believe this finding may indicate the generalization tendencies of HIV epidemic. Our hypothesis has been supported by other epidemiological characteristics, such as: increase in number of sexual HIV cases and their proportion in the total number of HIV cases; increase in proportion of Radas reporting sexually acquired HIV cases but not IDU-acquired HIV cases; increase in the proportion of sexual HIV cases reported in these Radas; HIV seroprevalence among pregnant women in the region accounted in average to 0.9–1.1%.

To estimate HIV epidemic stage, additional methods of epidemiological analysis like spatial analysis of morbidity can be used.

Keywords

HIV epidemic; spatial analysis; GIS

*Oleksandr Postnov
E-mail: apostnovmd@gmail.com

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COACTION PUBLISHING

Marketing a syndromic surveillance system to hospital emergency departments

Melissa Powell* and Kyle Ryff

Oregon Health Authority, Portland, OR, USA

Objective

Encourage hospitals to participate in the Oregon Health Authority (OHA) emergency department (ED) syndromic surveillance system, Oregon ESSENCE.

Introduction

OHA, in collaboration with the Johns Hopkins University Applied Physics Laboratory, implemented a syndromic surveillance system, Oregon ESSENCE. A critical component to developing and growing this statewide system is obtaining buy-in and voluntary participation from hospital EDs. This process involves approval at multiple levels within a hospital facility from administration to information technology (IT) staff responsible for sending electronic ED data to the Oregon ESSENCE system. Therefore, developing marketing materials that appeal to a wide range of recruitment audiences is a key step in obtaining stakeholder buy-in. OHA adopted the ISDS and CDC syndromic surveillance standards for the public health objective of the Center for Medicaid and Medicare Services (CMS) Meaningful Use Programs. However, Oregon hospitals will not receive financial incentive to participate in Oregon ESSENCE from CMS until 2014 during stage two of Meaningful Use. Consequently, this project's early years will focus on obtaining voluntary participation from hospitals.

Methods

OHA developed a recruitment packet to provide information to hospital Chief Executive Officers, Chief Information Officers, Infection Preventionists, Meaningful Use coordinators and IT staff. The packets will be distributed in a number of ways: primarily, during face-to-face meetings with hospital and public health stakeholders, and also during other forums such as meetings of the Oregon Association of Hospitals and Health Systems as well as broader Meaningful Use seminars. Recruitment folders include a brief overview of syndromic surveillance and the ESSENCE system (Welcome to Oregon ESSENCE); a description of utility (Oregon ESSENCE: Real-time Data for Public Health Action); a list of the requested variables (Oregon ESSENCE Data Fact Sheet); examples of effective uses of ESSENCE (ESSENCE success stories); a visual diagram of the data flow process (Oregon ESSENCE data flow); and a list of action steps to begin participation (Let's Roll).

Results

We developed an informative packet of materials for a variety of audiences that is both appealing and concise. Oregon's hospitals come in all shapes and sizes, each with unique approval processes for engaging in data sharing, prioritization of voluntary public health projects, coordination of Meaningful Use efforts and IT support. Therefore, we expect that the breadth and depth of the marketing materials will be a critical component to successful recruitment of hospitals.

Conclusions

We developed appealing and concise information packets for a variety of audiences. While each individual may not need the full breadth of the information we are providing, depending on their role at the hospital, we anticipate that the recruitment packet provides a useful overview of Oregon ESSENCE and syndromic surveillance to a variety of hospital and public health stakeholders.

Keywords

Emergency departments; data exchange; marketing

***Melissa Powell**
E-mail: melissa.e.powell@state.or.us

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COACTION PUBLISHING

Surveillance of poison center data using the National Poison Data System web service

Melissa Powell[1]*, Kyle Ryff[1] and Sandra Giffin[2]

[1]Oregon Health Authority, Portland, OR, USA; [2]Oregon Poison Center, Portland, OR, USA

Objective

Enhance Oregon ESSENCE by integrating data from the Oregon Poison Center (OPC) in a cost-effective manner.

Introduction

Oregon Health Authority (OHA), in collaboration with the Johns Hopkins University Applied Physics Laboratory, recently implemented Oregon ESSENCE, an automated, electronic syndromic surveillance system. One way to strengthen syndromic surveillance is to include data from multiple sources. We are integrating data from emergency departments, state notifiable conditions and vital statistics and the Oregon Poison Center (OPC). Implementing ESSENCE in Oregon provided the opportunity to automate poison center surveillance, which was previously done manually. In order to achieve this, OHA needed a daily data feed of OPC data to upload into Oregon ESSENCE servers. For OPC to do this directly, they would have incurred significant costs to develop the necessary electronic infrastructure to query and send the data; furthermore, OPC does not employ IT staff. OHA does not currently have funding available to support IT system interoperability with Oregon ESSENCE; so, we sought a low-cost solution that would build upon existing systems that utilized the National Poison Data System (NPDS) web service.

Methods

OPC facilitated OHA access to the NPDS web service, which OHA could use free of charge. Access to the web service consisted of requesting approval from the local poison center and adhering to an NPDS web service data use agreement between OPC and OHA. We use FileMaker, a commercial off the shelf database application, to automatically query the NPDS web service on a daily basis. The queried data are then automatically sent from a local database temporarily storing the information to the ESSENCE servers. OHA already uses FileMaker for managing notifiable conditions data (i.e., communicable disease reporting); so, there were no new licensing costs associated with this method.

Results

OPC data are available within the ESSENCE application to OHA syndromic surveillance staff. Sending OPC data into ESSENCE allows OHA staff to monitor timely OPC data in an automated, routine manner. When alerts are generated within the ESSENCE system, they are first assessed by syndromic surveillance staff. Those that require follow-up trigger a call between OHA and OPC. Oregon is the first state to use the NPDS web service to upload poison center data into ESSENCE.

Conclusions

OHA previously monitored OPC data using two methods: (1) through the NPDS system using a web-based interface; and (2) through ToxiTrack, poison center database software. ToxiTrack software is a companion software to Toxicall®, the data collection software system utilized by OPC. Data from Toxicall were transferred via VPN to OHA, where ToxiTrack software was used to view data. Although both of these systems provide unique capabilities for viewing summarized case data, there are limitations in their functionality for situational awareness. ESSENCE offers OHA the ability to easily analyze and report on these data and geospatial graphing capabilities without having to use additional statistical and GIS software.

Integration of poison center data into Oregon ESSENCE supports the initiative to develop a statewide syndromic surveillance system that includes a variety of data sources. It also addresses the need for improved, timely communication between OPC and OHA that was identified following Oregon's response to the 2011 Japanese Earthquake and Radiation event. Because OPC data are integrated into ESSENCE, OHA staff members are able to develop an understanding of expected call volumes and types during day-to-day operations. This is an important component of ongoing situational awareness as we learn what to expect and also how to interpret data from OPC. This resource-effective solution can be applied to jurisdictions that use a variety of applications to monitor their poison center data.

Keywords

Poison center; web service; integration across data sources; resource-limited settings

***Melissa Powell**
E-mail: melissa.e.powell@state.or.us

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COACTION PUBLISHING

Comparison of ED and urgent care ILI surveillance data from the 2009 H1N1 outbreak

Robert Redwood* and Marc Bellazzini

Division of Emergency Medicine, University of WI School of Medicine and Public Health, Madison, WI, USA

Objective

To compare the proportion of patients presenting with influenza-like illness (ILI) to urgent care centers versus the emergency department (ED) during the 2009 Fall Novel H1N1 outbreak.

Introduction

Syndromic surveillance of health care data such as the International Classification of Diseases, Ninth Revision (ICD-9), codes related to ILI, was used to track the progression of the 2009 Fall Novel H1N1 outbreak in the Madison area (1). Early studies focused on prediction of an outbreak; however, further investigation of patient resource utilization would be helpful in developing an action plan for addressing community and patient needs during future outbreaks. There is a paucity of research comparing ED and urgent care utilization rates during the 2009 Novel H1N1 pandemic, though there are regional data suggesting that urgent care centers bore a larger portion of the burden of H1N1 influenza than EDs (2). Furthermore, one group found that ILI-related phone calls to urgent care centers predicted influenza outbreak at least 1 week ahead of peaks in the ILI hospital care consultation rates (3). ED data on its own have proven useful for public health disease surveillance (4, 5), and many studies group urgent care and ED care together. The literature is lacking subgroup analysis of these two very different care environments. Understanding the correlation between urgent care and ED utilization rates will provide a more in depth understanding of the stress that the 2009 Fall Novel H1N1 placed on community resources in our geographic region.

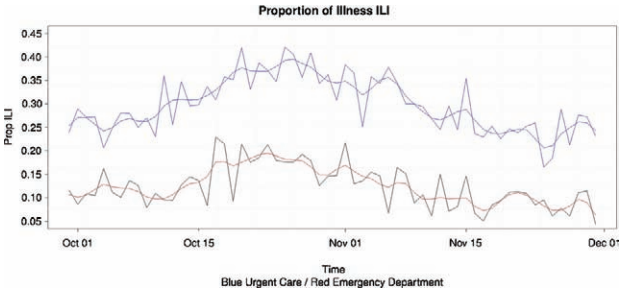

Fig. 1. Urgent care utilization for ILI (blue) versus ED utilization for ILI (red).

Methods

This study is a cross-sectional retrospective analysis of ED vs. urgent care utilization rates for ILI in the greater Madison area from October 2009 to December 2009. The proportion of ILI encounters was calculated for two university-based urgent care centers (grouped) and compared with the ED data from the same university-based system. Proportions were calculated from ICD-9 and total daily encounter volume data.

Results

The average proportion of encounters for ILI at urgent care centers was 0.298 in comparison with 0.125 for ED visits during the 2009 Fall Novel H1N1 influenza outbreak. Graphical trends in illness were comparable.

Conclusions

Patients in our geographic region were 2.4 times more likely to seek care at urgent care centers for ILI during the Fall wave of the H1N1 influenza pandemic. Neither care site predicted the outbreak more effectively than the other.

Keywords

H1N1; urgent care; ED; ILI; syndromic surveillance

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***Robert Redwood**
E-mail: rredwood@uwhealth.org

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COACTION PUBLISHING

Smart homes and novel indicators to inform an evidence-based population health intervention for aging in place and design of a community health registry

Blaine Reeder* and George Demiris

University of Washington, Seattle, WA, USA

Objective

This study aims to (1) characterize the state of smart homes research as a population health intervention to support aging in place through systematic review and classification of scientific literature using an evidence-based public health (EBPH) typology and (2) identify novel indicators of health captured by monitoring technologies to inform design of a community health registry.

Introduction

The critical need for population-level interventions to support the health needs of the growing population of older adults is widely recognized (1). In addition, there is a need for novel indicators to monitor wellness as a resource for living and a means for prediction and prevention of changes in community health status (2). Smart homes, defined as residential infrastructure equipped with technology features that enable passive monitoring of residents to proactively support wellness, have the potential to support older adults for independence at the residence of their choice. However, a characterization of the current state of smart homes research as a population health intervention is lacking. In addition, there is a knowledge translation gap between the smart homes research and public health practice communities.

The EBPH movement identifies three types of evidence along a continuum to inform population health interventions: Type 1 (something should be done), Type 2 (this should be done) and Type 3 (how it should be done) (3). Type 2 evidence consists of a classification scheme for interventions (emerging, promising, effective and evidence based) (3). To illustrate typology use with an example: the need for population health interventions for aging populations is well known (Type 1 evidence), many studies show that smart home technologies can support aging in place (Type 2 evidence), but there are few, if any, examples of smart homes as population health interventions to support aging in place (Type 3 evidence).

Our research questions for this systematic review are as follows:

1) What categories of Type 2 evidence from the scientific literature uphold smart homes as an EBPH intervention?
2) What are the novel health indicators identified from smart home studies to inform design of a community health registry that supports prediction and prevention of negative changes in health status?
3) What stakeholders are reported in studies that contribute Type 2 evidence for smart homes as an EBPH intervention?
4) What gaps exist between Type 2 and Type 3 evidence for smart homes as an EBPH intervention?

Methods

Our search methodology includes searches of MEDLINE, CINAHL and IEEE conference proceedings databases to provide coverage across a literature that is found in many disciplines and is not well-indexed. As the term 'smart home' is not well-defined, our search terms also include 'telemedicine', 'telehealth', 'e-health', 'health monitoring', 'gerontechnology' and 'gerotechnology' in combination with 'older adult', 'elderly', 'aging', 'ageing', 'community-dwelling' and 'senior'. Our inclusion criteria include any study that describes a technology designed for an older adult audience to support wellness management through social, spiritual, physical or cognitive means (4). Our exclusion criteria include smart homes designed for efficiency and nonhealth-related surveillance technologies.

Results

Initial search results indicate many studies that can be classified as Type 2 evidence along the continuum of emerging, promising, effective and evidence-based smart home interventions. Initial findings are that Type 3 evidence is lacking and public health policy makers are underrepresented.

Conclusions

Early analysis of complete search results will be presented for (1) categorizations of evidence according to the evidence-based public health typology, (2) enumeration of stakeholders reported in included studies and (3) identification of novel indicators of health to inform design of a standards-based community health registry for older adults.

Keywords

Smart homes; population health; aging in place; older adults; informatics

Acknowledgments

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***Blaine Reeder**
E-mail: breeder@uw.edu

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COACTION PUBLISHING

Syndromic surveillance for bicycle-related injuries in Boston, 2007–2010

Marcus Rennick[1]*, Julia Gunn[1], Michael Donovan[1], Snehal Shah[1], M. Anita Barry[1], Howard Burkom[2,3], Soyoun Park[4], Peter Hicks[2] and Stephen Benoit[2]

[1]Boston Public Health Commission, Boston, MA, USA; [2]Centers for Disease Control and Prevention, Atlanta, GA, USA; [3]Johns Hopkins University Applied Physics Lab, Laurel, MD, USA; [4]SRA International, Atlanta, GA, USA

Objective

To quantify the injury burden and to identify possible risk factors using bicycle-related injury (BRI) visits at Boston emergency departments (EDs).

Introduction

In May 2001, Boston released a strategic transportation plan to improve bicycle access and safety (1). According to the Boston Transportation Department, ridership has increased 122% between 2007 and 2009 (2). A collaborative public health and public safety task force was initiated in 2010 to foster a safe and healthy bicycling environment.

Methods

The Boston Public Health Commission (BPHC) syndromic surveillance system receives information from ED visits from all 10 acute care hospitals in Boston every 24 hours. Data received include visit date, demographics, ZIP code of residence, chief complaints and ICD-9 CM-coded final diagnosis. Disposition information was reported from 9 of these hospitals in 2010. BPHC collaborated with CDC's BioSense Program to specify a BRI syndromic case definition that combined chief complaint and ICD-9 CM-coded information and excluded motor cycle only related events. Subsyndromes were used to assess the type of injury and severity based upon 47 standard BioSense subsyndromes and 21 subsyndromes developed for this study.

The data sample used for this study included over 2 million visits between 2007 and 2010. Injury visits were categorized at the neighborhood level using a standard ZIP code of residence-to-neighborhood mapping. Results were stratified by age, patient neighborhood of residence, race/ethnicity, gender and disposition (2010 data only).

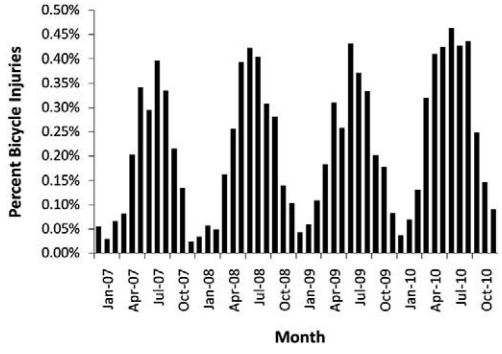

Fig. 1. Percentage of visits at Boston EDs involving bicycle injuries: 2007–2010.

Results

Over the study period, a total of 4510 ED visits were classified as BRIs (0.22%). The percentage of BRI visits increased from 0.18% in 2007 to 0.27% in 2010. The majority of injuries (69%) occurred between May and September (Fig. 1) and likely corresponds to increased bicycling activity during those months.

Seventy-five percent of persons presenting with BRIs were male and 60% reported race/ethnicity as white. Persons aged 18–25 years represented 28% of visits and those aged 6–17 years accounted for 17%. Boston residents accounted for 52% of BRI visits; 15% were from bordering communities. One Boston neighborhood with the highest BRI rate by patient residence also has a large college student population.

Throughout the entire study period (2007–2010), nearly one quarter (1082) of BRI visits were associated with fractures and dislocations; whereas less than 10% of visits were for sprains or strain injuries. Head injuries were associated with 84 (1.9%) of BRI visits.

In 2010, 149 (11%) of the 1411 BRI visits resulted in admission, most commonly for fractures and dislocations. Twenty-two percent were among individuals aged between 50 and 59 years; 21% were among persons aged 18–24 years. Fifty-four percent of all BRI admissions were associated with fractures and dislocations. Thirty-one (2.2%) BRI visits in 2010 were associated with head injuries; of which 11 (35%) were admitted for care. For BRI visits involving falls, 8% were admitted versus 17% for BRI visits associated with a motor vehicle.

Conclusions

Syndromic surveillance can be used to monitor and track BRI and to inform targeted prevention activities such as education and outreach to select at-risk populations (e.g., college students). Presently, information on the environmental context of injuries, such as the precise location of the accident, is limited. As bicycle use increases, improved methods to combine syndromic surveillance, emergency medical services and public safety information are needed to identify accident 'hot spots' to guide implementation of preventive measures.

Keywords

Injury; prevention; emergency; bicycle; syndromic surveillance

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*Marcus Rennick
E-mail: mrennick@bphc.org

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COACTION PUBLISHING

Animal bite surveillance using NC DETECT

Sarah Rhea[1]*, Amy Ising[1], Anna Waller[1], Lana Deyneka[2], Heather Vaughan-Batten[2] and Marilyn Goss Haskell[2]

[1]University of North Carolina, Chapel Hill, NC, USA; [2]North Carolina Division of Public Health, Raleigh, NC, USA

Objective

We describe the use of emergency department (ED) visit data collected through the North Carolina Disease Event Tracking and Epidemiologic Collection Tool (NC DETECT) for surveillance of animal bites in NC. Animal bite surveillance using ED visit data provides useful and timely information for public health practitioners.

Introduction

Animal bites may have potentially devastating consequences, including physical and emotional trauma, infection, rabies exposure, hospitalization and, rarely, death (1). NC law requires animal bites be reported to local health directors (2). However, methods for recording and storing bite data vary among municipalities. NC does not have a statewide system for reporting and surveillance of animal bites. Additionally, many animal bites are likely not reported to the appropriate agencies (3).

NC DETECT provides near-real-time statewide surveillance capacity to local, regional and state-level users with twice daily data feeds from NC EDs. Between 2008 and 2010, 110 to 113 EDs were submitting visit data to NC DETECT. Several animal bite-related online reports are available and provide aggregate and visit-level analyses customized to users' respective jurisdictions. The NC DETECT ED visit database currently provides the most comprehensive and cost-effective source of animal bite data in NC.

Methods

Several NC DETECT animal bite-related reports were developed based on chief complaint and triage note keyword searches and ICD-9-CM codes. Using the Animal Bite Keyword Report, statewide ED visit data were extracted for 2008–2010. ED visit records in NC DETECT were examined manually to assess the performance of case definition keywords. Using the Animal Bite ICD-9-CM Code Report, statewide ED visit data were extracted for 2008–2010. The following ICD-9-CM injury codes are included in this report: E906.0 (dog bite), E906.1 (rat bite), E906.3 (bite of other animal except arthropod) and E906.5 (bite by unspecified animal). The burden of ICD-9-CM–coded animal bite visits to total ED visits was examined by age group and gender.

Results

Review of Animal Bite Keyword Report data revealed several additional case definition inclusion and exclusion keywords. This knowledge has led to continued development of keyword reports. The Animal Bite ICD-9-CM Code Report indicated a total of 33,294 ED visits for animal bite from 2008 to 2010. For each year, the highest proportion of ICD-9-CM–coded animal bite ED visits to total ED visits were for 5–9 year olds (Fig. 1). Across all 3 years, males had a slightly higher proportion of animal bite-coded ED visits to total ED visits (0.28%) compared to females (0.23%).

Conclusions

Case definition development for the Animal Bite Keyword Report is an iterative process. Sensitivity and specificity of keyword reports must be considered, and case definitions should depend on the report's intended use. Evaluation of the Animal Bite ICD-9-CM Code Report showed 5–9 year olds and males have the highest proportion of animal bite-coded ED visits in NC. A snake bite report and animal bite incidence rate reports are under development. NC DETECT is a valuable source for animal bite surveillance in NC.

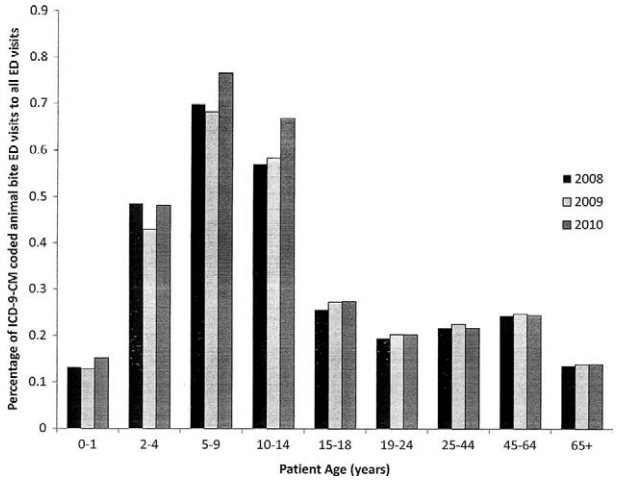

Fig. 1. Percentage of ICD-9-CM*–coded animal bite ED visits to all ED visits by patient age and year, 2008–2010, NC DETECT. *E906.0, E906.1, E906.3 and E906.5.

Keywords

Animal bite; surveillance; emergency department

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*Sarah Rhea

E-mail: srhea@email.unc.edu

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COACTION PUBLISHING

Identification of a measles case using syndromic surveillance in Salt Lake County, Utah

Jenny Robertson* and Mary Hill

[1]Salt Lake Valley Health Department, Salt Lake City, UT, USA

Objective

To detect measles cases during an outbreak using syndromic surveillance.

Introduction

In March–April 2011, Salt Lake Valley Health Department (SLVHD) investigated an outbreak of measles (N = 9) resulting from a single imported case from Europe. Syndromic surveillance was used to identify measles-like illness (MLI) and enhance early case detection, which is crucial for proper public health intervention (1).

Methods

Daily text-based chief complaint data, March 23–May 5, 2011, from 15 syndromic sites were obtained from EpiCenter (2) (funds provided by Utah Department of Health), mapped to 5 MLI syndromes (Table 1) and summarized using the Early Aberration Reporting System (EARS) (3). Events of interest included all 'rash' events that contributed to an alert or had a concerning chief complaint (e.g., eye pain), all 'febrile rash' events that had a concerning chief complaint, all 'prodrome' events that had a concerning chief complaint, all 'case definition' events April 7, 2011 onward (date after which public health intervention was still possible) and all 'measles/testing' events. Visit notes, laboratory tests and results were obtained daily for each event of interest and reviewed for MLI. Summary findings, including diagnoses, laboratory results, rash descriptions and suspect exposures, were documented and non-MLI events were ruled out. Events of high suspicion for measles were further investigated via patient interview by phone and/or home visit.

Results

Ninety-seven events of interest (of 2365 events captured in MLI syndromes) were identified: 32 rash, 58 febrile rash, 1 prodrome, 12 case definition and 8 measles/testing (14 were categorized in > 1 syndrome). Eighty-four events of interest were ruled out based on chart findings. Thirteen events of high suspicion for measles required further investigation. Twelve events were ruled out based on negative measles IgM results, evidence indicating other diseases (fifth disease and Kawasaki syndrome), vaccine reaction or inaccurate documentation of clinical symptoms. One event was found to be confirmed by positive measles IgM (Fig. 1).

Table 1. Measles-like illness (MLI) syndrome definitions

Syndrome	*Definition*
Rash	Rash and not chronic and not pregnancy and not medications and not exclude
Febrile rash	Fever and rash
Prodrome	Fever and (malaise or cough or runny nose or conjunctivitis)
Clinical case definition	Fever and rash and (cough or runny nose or conjunctivitis)
Measles/ testing	Measles

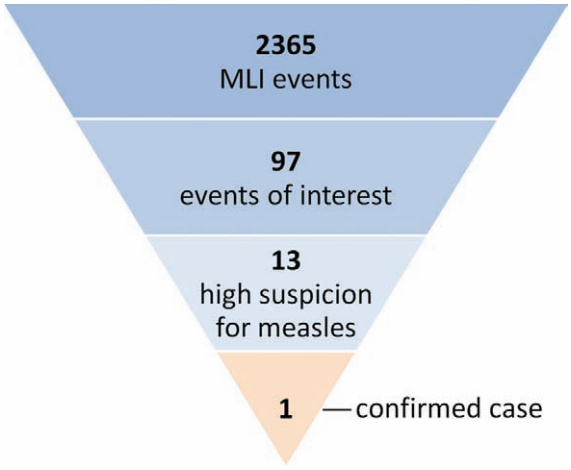

Fig. 1. Identification of 1 confirmed case of measles from 2365 measles-like illness (MLI) syndromic events.

Conclusions

Early identification of a measles case using syndromic surveillance during an outbreak was crucial in reducing contact exposures, preventing additional cases and reducing the cost associated with proper public health intervention. We estimate that early detection of the remaining 8 confirmed cases by syndromic surveillance could have reduced the direct cost of the outbreak by 82%. Syndromic surveillance played a significant role in curtailing the outbreak as a valuable tool to supplement active surveillance.

Keywords

Measles; syndromic surveillance; early detection; outbreak; cost

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*Jenny Robertson
E-mail: jrobertson@slco.org

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COACTION PUBLISHING

The validity of emergency department influenza-like illness (ILI) for laboratory-confirmed influenza in children

Carla Rodriguez[1]*, Janet Baseman[1], Danielle Zerr[1,3], Janet Englund[1,3], Ian Painter[1], Atar Baer[1,2], Thomas Koepsell[1], David Yanez[1] and Jeffrey Duchin[1,2]

[1]Department of Epidemiology, University of Washington, Seattle, WA, USA; [2]Public Health-Seattle & King County, Seattle, WA, USA; [3]Seattle Children's, Seattle, WA, USA

Objective

Estimate and compare the accuracy of various ILI syndromes for detecting lab-confirmed influenza in children.

Introduction

Syndromic surveillance systems use electronic health-related data to support near-real time disease surveillance. Over the last 10 years, the use of ILI syndromes defined from emergency department (ED) data has become an increasingly accepted strategy for public health influenza surveillance at the local and national levels. However, various ILI definitions exist and few studies have used patient-level data to describe validity for influenza specifically.

Methods

A retrospective design was used to evaluate clinical records for a predictive model of lab-confirmed influenza. Children who presented to the ED at Seattle Children's Hospital between January 1, 2001 and May 31, 2005 were eligible for inclusion in the study. The accuracy of four syndrome definitions were compared for identifying lab-confirmed influenza: (1) ILI from chief complaint (CC) or diagnoses codes ("ILI"); (2) ILI from CC alone; (3) febrile illness from CC or diagnoses ("Febrile"); and (4) febrile illness from CC alone. We evaluated syndrome validity over two distinct time periods: (1) the "discrete" 2003–04 influenza season, which had relatively less co-circulation of influenza and respiratory syncytial virus (RSV) compared to most years, and (2) the "concomitant" 2000–05 influenza seasons (excluding 2003–04), when influenza and RSV co-circulation was high. Analyses during the concomitant years were further stratified by age <5 years and ≥ 5 years. Multiple imputation was used to address missing viral lab results. The imputation model was based on testing guidelines in place at the hospital during the time of study.

Results

We studied approximately 14,000 visits during the discrete year and 32,000 visits during concomitant years. Viral results were unavailable for approximately 75% of respiratory visits and multiple imputation was used to impute values. During the discrete year, sensitivity and specificity were 0.49 (95% Confidence Interval [CI]: 0.30, 0.68) and 0.72 (CI: 0.70, 0.74) respectively, for the "Febrile" definition and 0.29 (CI: 0.13, 0.54) and 0.89 (CI: 0.87, 0.90) for the "ILI" definition. ILI sensitivity was 2.05 (CI: 1.08, 3.91) times greater and its false positive fraction 44% (CI: 37%, 49%) lower in concomitant years compared to the discrete year. Greater sensitivity and false positive fractions (1-specificity) tended to be produced by the febrile definitions than by the ILI definitions; and by definitions derived from CC or diagnoses as compared to those from CC alone. The false positive fraction of all syndrome definitions was higher in younger children compared to older children.

Conclusions

Although the sensitivity of syndromic ILI definitions was not high by clinical standards, our interest was to understand the proportion of influenza cases in the community being captured by the system. ED ILI may provide a more robust estimate of the burden of disease than laboratory surveillance, which captures only a subset of patients seen by a healthcare provider and who were tested. The higher specificity of the ILI definitions suggests it is best used for situational awareness during influenza outbreaks and for distinguishing influenza from other viral agents. The use of several definitions throughout the season may be most appropriate in some settings. Public health practitioners should bear in mind that syndrome performance may vary by season and year. Higher syndrome specificity among older children suggests specificity in adults should be higher than that observed for younger populations. However, the generalizability of these results to adult populations and other hospitals is uncertain and should be further studied.

Acknowledgments

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*Carla Rodriguez
E-mail: carlarod@uw.edu

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COACTION PUBLISHING

Trends in emergency department visits for influenza-like illness and antiviral medication transactions

Anikah Salim*, Zachary Faigen, Isaac Ajit and Sherry Adams

Office of Preparedness and Response, Maryland Department of Health and Mental Hygiene, Baltimore, MD, USA

Objective

To examine the trends in prescription antiviral medication transactions and emergency department (ED) visits for influenza-like illness (ILI) and the relationship between these trends.

Introduction

The electronic surveillance system for the early notification of community-based epidemics (ESSENCE) is the web-based syndromic surveillance system utilized by the Maryland Department of Health and Mental Hygiene (DHMH). ESSENCE utilizes a secure, automated process for the transfer of data to the ESSENCE system that is consistent with federal standards for electronic disease surveillance. Data sources in the Maryland ESSENCE system include ED chief complaints, poison control center calls, over-the-counter (OTC) medication sales and pharmaceutical transaction data (specifically for antibacterial and antiviral medications). All data sources have statewide coverage and are captured daily in near real-time fashion.

Methods

Forty-six EDs, two major pharmacy chains, two poison control centers and the Centers for Disease Control and Prevention (through a pilot partnership), all contribute data to ESSENCE on a daily basis. Data reported from June 1, 2009, through January 1, 2011, were used to examine the relationships between ED visits for ILI and antiviral (M2 inhibitors and neuraminidase inhibitors) prescription medication transactions in the state of Maryland. ArcGIS 9.2 was used to spatially evaluate these relationships. Data for the total population of Maryland by jurisdiction were obtained from the U.S. Census Bureau, Census 2010 PL94-171 release and prepared by the Maryland Department of Planning, Projections and Data Analysis/State Data Center, April 2011.

Results

Generally, jurisdictions with the highest populations also had the highest number of ILI ED visits and the highest numbers of antiviral prescription medication transactions. These results did not vary based on type of antiviral medication. There was one exception to the general trend: County 14 had the lowest percent of ILI ED visits (0.45%) but the highest percentage of antiviral prescription medication transactions (1.26%). Spatial analysis showed that the highest number of ILI ED visits were in the National Capital Region (NCR) and Central Maryland while the highest numbers of antiviral prescription medications were in the NCR Region.

Conclusions

The trends seen in this analysis follow what is to be expected; the counties with the larger populations had higher numbers of ILI ED visits and higher antiviral prescriptions. These larger counties have more hospitals, which allows for greater access to EDs. County 14 has only one hospital that contributes data to the ESSENCE system; thus, residents may have traveled to an ED in another county but filled a prescription in their home county. This could account for why County 14 had the lowest number of ILI visits and the highest number of antiviral prescriptions. This county also has a very high median income; thus, it is possible that ED visits were lower because more individuals sought medical attention from primary care physicians. Other counties may follow these same trends.

The ESSENCE system has been a useful tool in the tracking and monitoring of diseases such as influenza. It is also used as an indicator to local health departments to begin preparation for flu season. DHMH will continue to use syndromic surveillance on a daily basis for early detection of seasonal and pandemic influenza.

Keywords

Influenza; syndromic surveillance; prescription medication; ESSENCE

***Anikah Salim**
E-mail: asalim@dhmh.state.md.us

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COACTION PUBLISHING

MNCH surveillance response systems strengthening in Indonesia

Rossi Sanusi*

Center for Health Service Management, GadjahMada University School of Medicine, Yogyakarta, Indonesia

Objective

To evaluate the efficacy of the Maternal, Neonatal and Child Health (MNCH) Surveillance-Response (S-R) systems strengthening approach used by the Center for Health service Management (CHSM), GadjahMada University School of Medicine (GMU SM).

Introduction

During 2007–2010, the CHSM conducted training and consultations to strengthen the MNCH S-R Systems of 10 districts and 5 municipalities of 5 provinces in Indonesia (Bali, Sulawesi Tengah, Bengkulu, Riau and Yogyakarta). These districts and municipalities represent a mix of high and low Fiscal Capacity of the local governments and high and low Economic Capacity of the population.

MNCH S-R Systems strengthening was carried out by means of two 2-day training sessions (of approximately 1 year apart) at the District/Municipal Health Offices (D/M HOs) and consultations via electronic telecommunication. The subject matter of the training sessions courses and consultations consisted of: (1) controlling MNCH priority diseases; (2) applying S-R core and support functions by the D/M HO and health service providers; (3) managing a S-R Support Unit at the D/M HO; and, (4) setting up a D/M HO internet website and publishing S-R electronic bulletins (1, 2).

Methods

Evaluation was conducted through electronic telecommunication with the disease control staff of the D/M HOs and checking of websites and S-R electronic bulletins.

Results

Together with the staff of the Sardjito Hospital (teaching hospital of the GMU SM), local D/MHOs and the GMU MS Department of Public Health, the CHSM developed Standard Operating Procedures for S-R core and support functions of MNCH priority diseases (e.g., postpartum bleeding, preeclampsia/eclampsia, LBW and pneumonia) as well as of other major diseases (e.g., malaria, TB, DM and hypertension). The training sessions and consultations were effectively executed in the target districts and municipalities. Based on the performance of the electronic bulletins, however, only one DHO has a functioning S-R support unit. Efficacy of the S-R Systems strengthening approach used by the CHSM could not be evaluated by way of on-the-spot interviews, observation and review of S-R records/reports due to financial constraints.

Conclusions

A more intensive strengthening method is required to ensure sustainable operation of core and support functions of S-R Systems. The MoH is considering to post at least one Field Epidemiology Training Program (FETP) graduate at the D/M HOs. These FETP graduates, and students, could be used to build and enhance S-R systems for priority diseases and to conduct valid monitoring-evaluation.

Keywords

Surveillance-response; MNCH; strengthening; Indonesia

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***Rossi Sanusi**
E-mail: rossi_sanusi@yahoo.com

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COACTION PUBLISHING

Use of cell phones to strengthen malaria surveillance-response systems of Bangka/Belitung, Indonesia—a proposal

Rossi Sanusi*

Center for Health Service Management, Gadjah Mada University School of Medicine, Yogyakarta, Indonesia

Objective

To seek collaboration with international research institutions and funding agencies.

Introduction

The Government of Indonesia (GoI) aims to eliminate malaria by 2030 in 4 stages (1). To reach the elimination phase, High Case Incidence (HCI) areas go through a preelimination phase. The aim of the proposed project is to support one of the Stage 3 provinces in reaching the preelimination phase by 2015 and to assist its HCI districts and municipalities in reorienting their programs to malaria elimination. The preelimination phase can be attained by following these evidence-based technical strategies: (1) prompt and accurate diagnosis of cases; (2) prompt treatment with effective medicines, including intermittent preventive treatment in pregnancy (IPTp); (3) selective, targeted and integrated vector control; and (4) emergency and epidemic preparedness (2).

These strategies can only be properly carried out if the District/Municipal Health Offices (D/M HOs) have a timely, useful and reliable malaria surveillance-response (S-R) system. The use of computers and electronic telecommunication networks has sped up the flow of institution-based case surveillance data to the D/M HO.

To increase its usefulness, however, the S-R system must include data of cases detected in the community along with data of the disease agent and environment. The proposed project will include the collection of all these surveillance data in order to be useful for the implementation of malaria control strategies. Furthermore, to increase timeliness and reliability, the project will support the malaria S-R systems of the Bangka Belitung Province, Sumatera, by means of cell phone (CP) applications through the following activities:

1) To develop a CP software for a malaria S-R system and to set up a malaria S-R central data bank (CDB) that will be placed at a commercial hosting server.
2) To set up a village CP network in each HCI village for demographic data and home malaria management (HMM) data reporting by households.
3) To train village midwifes or village malaria workers (VM/MW) to provide HMM, to administer IPTp to pregnant members, to send diagnosis, treatment and IPTp data to the CDB and to obtain blood films for microscopic examination by the HC parasitology microscopist.
4) To train HC parasitology microscopists to perform microscopic examinations, to use a microscopy-enabled CP for sending microscopy images to the Provincial Lab for reliability testing and to send data to the CDB.
5) To train HC coassistant entomologist, D/M HO assistant entomologist and Provincial HO entomologist to collect vector and environment data, to use a CP for sending vector control targets data to the CDB and to use a microscopy-enabled CP for sending microscopy images to the Provincial Lab for reliability testing.
6) To provide consultations, training and resources for the D/MHOs to facilitate the utilization of CP applications for reporting demographic and HMM data and drug and insecticide resistance/efficacy sentinel surveillance and to facilitate sector and intersector surveillance-based rapid and planned response decision making.

To ensure the attainment of project objectives, the GMU CHSM and collaborating institutions will (1) obtain endorsements from the heads of the District/Municipal and Provincial Governments; (2) engage MoH Directorate of Malaria and GMU Medical School staff in workshops and technical guidance; (3) engage malaria program managers of the District/Municipal and Provincial HOs as project field coordinators; and, (4) recruit experienced technicians as on-the-job trainers in parasitological microscopy, entomology and information technology and experienced experts as trainers and consultants in public health surveillance and management.

Methods

Poster presentation at the ISDS 10th Annual Conference 2011.

Conclusions

Benefits of the project: (1) elimination of malaria in Bangka, Sumatera; and, (2) recommendations for expansion of the project/model to other districts/municipalities of Sumatera, Nusa Tenggara Barat, Kalimantan and Sulawesi.

Keywords

Malaria; elimination; surveillance-response; cell-phone application; Indonesia

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***Rossi Sanusi**
E-mail: rossi_sanusi@yahoo.com

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COACTION PUBLISHING

Distributing countermeasures for all hazards events and reporting their utilizations

Michele Renshaw[1], Sanjeeb Sapkota[1]*, Stephanie Dulin[1], Guy Faler[2], Benjamin Erickson[1], Sarah Waite[3], Leslie Han[3], Caroline Westnedge[3], Jeanne Tropper[1] and Barb Nichols[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Northrop Grumman Information Technology, Atlanta, GA, USA; [3]SRA International, Inc., Atlanta, GA, USA

Objectives

To describe the Centers for Disease Control and Prevention (CDC) Countermeasure Tracking Systems (CTS) and the impact of its four closely related informatics components toward enhancing federal, state and local public health capacity to track and manage medicine and other medical or nonmedical supplies during daily operations and all hazards public health events.

Introduction

Description: CDC works to save lives and protect people during major public health events. In an effort to support these processes, CDC established CTS, which is maintained within the Division of Informatics Solutions and Operations (DISO), in the Public Health Informatics and Technical Program Office (PHITPO). CTS consists of four system components, which interoperate to improve communications and event response efficiency while still functioning independently, recognizing the unique requirements and use cases for each system. Collectively, the data consolidated from these systems can show population coverage, numbers of untreated individuals, drug and equipment shortages, need for resupply and more. The web-based applications are deployed centrally at CDC and use the CDC's secure data access method for security.

The first of these components is the Inventory Management and Tracking System (IMATS), currently under development. IMATS provides state and local public health providers with a tool to track medical and nonmedical countermeasure inventory and supplies during daily operations or an event. The solution tracks quantities of inventory, monitors reorder thresholds and facilitates warehouse operations including receiving, staging and storing of inventory.

The Communications Portal is a web-based content management system in development, which consolidates important event response details into one place and will provide timely and adequate information to states and other jurisdictions. This system is complementary to the IMATS as it manages communications related to, but not limited to, Emergency Use Authorization (EUA), Investigational New Drug (IND) and recall notices.

Conclusions

Preparing for the future of public health surveillance also requires innovative and appropriate informatics systems that provide timely and accurate response to all-hazards events. CTS and its components are developed to assist in all types of surveillance needs.

Keywords

Countermeasure; all hazards; public health; inventory; tracking

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*Sanjeeb Sapkota
E-mail: ssapkota@cdc.gov

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COACTION PUBLISHING

Use of syndromic surveillance in decision making during the H1N1 pandemic in Ontario, Canada

Anna Chu[1], Rachel Savage[1]*, Natasha S. Crowcroft[1,2,3], Laura C. Rosella[1,2], Donald J. Willison[1,2,4] and Ian Johnson[1,2]

[1]Public Health Ontario, Toronto, ON, Canada; [2]University of Toronto, Dalla Lana School of Public Health, Toronto, ON, Canada; [3]University of Toronto, Department of Laboratory Medicine and Pathobiology, Toronto, ON, Canada; [4]McMaster University, Hamilton, ON, Canada

Objective

To describe if and how syndromic surveillance data influenced public health decisions made during the 2009 H1N1 pandemic within the context of other existing public health surveillance systems.

Introduction

For public health surveillance to achieve its desired purpose of reducing morbidity and mortality, surveillance data must be linked to public health response. While there is evidence of the growing popularity of syndromic surveillance (1, 2), the impact or value added with its application to public health responses is not well described (3).

Methods

Ontario's 36 public health units, the provincial ministry of health and federal public health agency completed a web survey in 2010 to identify surveillance systems used routinely and during the pandemic and to describe the perceived utility of systems for monitoring pandemic activity and informing decision making. Follow-up semi-structured interviews were conducted with key informants to elucidate drivers for specific public health actions taken during the pandemic and, specifically, to understand the role syndromic data played in influencing decisions among those who had access.

Results

The web survey identified 20/38 (53%) organizations which use at least one syndromic surveillance system; key informant interviews identified another 2 organizations, for a total of 22/38 (58%) syndromic surveillance 'users'. Mirroring routine surveillance, traditional surveillance systems, specifically laboratory and reportable disease data (iPHIS) and school absenteeism data were the most frequently used sources during the pandemic (Fig. 1). Laboratory data were considered the most useful data source for monitoring the epidemiology (71% of organizations perceived it as 'essential') and informing decision making (76%), while emergency department screening data were considered the most useful syndromic surveillance source (52% and 70%). Syndromic data were found to support two specific public health actions taken during the pandemic: influenza assessment centers and communications, including recommendations to the public. Informants felt that syndromic data provided confidence to decide whether and when to open/close influenza assessment centers and when/what to communicate to the public. Non-syndromic users utilized stakeholder consultations and traditional surveillance data to support these decisions. Syndromic surveillance did not appear to have a role in supporting decisions around immunization clinics, school closures or recommendations to health care professionals; rather vaccine availability and ministerial guidance acted as drivers for these decisions.

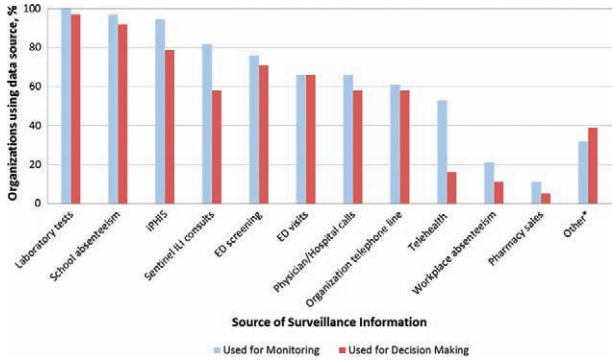

Fig. 1. Data sources used by organizations to monitor the epidemiology of the 2009 H1N1 pandemic and inform decision making, Ontario. *Other includes EMS/paramedic activities, hospital admission, intensive care unit and ventilator use data, immunization visits, flu assessment centre visits and provincial surveillance bulletins and teleconferences.

Conclusions

While traditional surveillance systems were considered most essential for monitoring the pandemic locally and informing decisions, syndromic surveillance was found to support several public health actions taken during the pandemic. Understanding how syndromic surveillance systems are valued, utilized and linked to public health action is necessary to inform investments to build surveillance capacity.

Keywords

Public health surveillance; syndromic surveillance; pandemic influenza; evaluation

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*Rachel Savage
E-mail: rachel.savage@oahpp.ca

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COACTION PUBLISHING

Crowdout: when do other events hinder informal disease surveillance?

David Scales*, Emily Chan and John Brownstein

Computational Epidemiology Children's Hospital Boston, Boston, MA, USA

Objective

Reporting about large public health events may reduce effective disease surveillance by syndromic or informal surveillance systems. The goal is to determine to what extent this problem exists and characterize situations in which it is likely to occur.

Introduction

Informal surveillance systems like HealthMap (HM) are effective at the early detection of outbreaks (1, 2). However, reliance on informal sources such as news media makes the efficiency of these systems vulnerable to newsroom constraints, namely high-profile disease events drawing reporting resources at the expense of other potential outbreaks and diminished staff over weekends and holidays. To our knowledge, this effect on informal or syndromic surveillance systems has yet to be studied.

Methods

Using HM's English-language global infectious disease database events (3), we identified expected periods of decreased reporting of infectious disease due to newsroom constraints between July 1, 2008, and August 31, 2011. Crowdout events were defined as averaging greater than five events per day for at least 2 weeks, plus making up at least 50% of daily events. Meeting these criteria were H1N1/swine flu (two instances), Haiti's cholera epidemic, 2010, and the *E.coli* outbreak in Germany, 2011. The December holiday period, when most of the newsroom is off duty, was also tested. We examined whether the average number of noncrowdout events differed significantly from the average daily HM events at baseline, defined as similarly structured periods without holidays or high-profile epidemic events. Baselines were measured before and after the crowdout period, plus during the same time period in other applicable years. Means were compared using paired *t* tests with unequal variances.

Results

The two instances where H1N1 met inclusion criteria both resulted in average numbers of daily events significantly lower than similar periods before, after and parallel to the time period in question (Fig. 1). See Table 1 for more results. On average, the greatest number of daily events occurs on Thursdays, least on Sundays. The outbreaks of cholera in Haiti and *E. coli* in Germany showed no significant crowdout effect at both global and regional levels. A reduction in the average events per day during the December holiday period was not significant.

Conclusions

Informal surveillance has limitations that are exacerbated by newsroom constraints. During the global H1N1 pandemic, significantly fewer infectious disease events were recorded by HM's informal surveillance system. Crowdout poses a risk for epidemiological surveillance since decreased relative surveillance may postpone reporting of outbreaks. Moreover, crowdout during H1N1 showed that this phenomenon can endure for long time periods. However, regional outbreaks like cholera in Haiti or *E. coli* in Germany do not appear to affect informal surveillance on a global or regional scale.

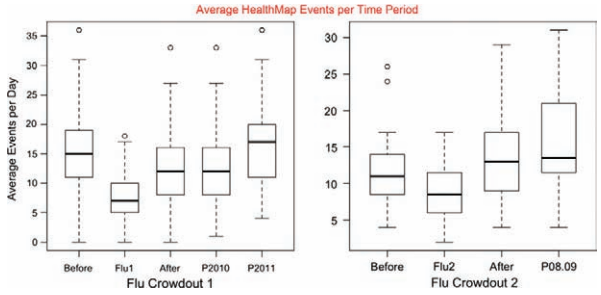

Fig. 1. Boxplots showing average daily HealthMap events during two separate periods when H1N1 met crowdout criteria. Flu1 and Flu2 represent respective crowdout periods. Before and after are of the same length and structure as the crowdout period. P2010, P2011 and P08.09 are parallel time periods, i.e., the same dates as the crowdout period but during different years.

Table 1. Means comparison of average daily events

Crowdout period	*Period*	*Difference*	*95% CI (low)*	*95% CI (high)*
Flu 1	Before	7.79	7.0	8.57
Flu 1	After	4.83	4.09	5.57
Flu 1	Parallel 1	4.89	4.24	5.54
Flu 1	Parallel 2	8.74	7.51	9.98
Flu 2	Before	2.81	1.06	4.56
Flu 2	After	4.56	2.55	6.57
Flu 2	Parallel	7.0	4.74	9.26

Keywords

Informal surveillance; syndromic surveillance; infectious disease; epidemics; media

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***David Scales**
E-mail: david.scales@childrens.harvard.edu

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COACTION PUBLISHING

Use of CDC's epidemic information exchange system as a disease surveillance tool

James Schwendinger*, Eric Lahr, Jonathan Lynch, Molly McCollom and Amanda Evanson

Epi-X, CDC, Atlanta, GA, USA

Objective

To evaluate the usability and usefulness of *The Epidemic Information Exchange* (*Epi-X*) system, a secure online information exchange provided by the Centers for Disease Control and Prevention (CDC), in assisting with case finding in response to infectious disease outbreaks and clusters that involve, or have the potential to involve, cases in multiple state-level jurisdictions within the United States.

Introduction

Epi-X is an internet-based secure website for the exchange of information regarding developing public health events. Reports are exchanged with state epidemiologists, state health officers and other key public health officials. Provisional and secure information is regularly posted on *Epi-X*. The *Epi-X* user base is restricted to public health officials at the local, state, federal and international levels. Private healthcare practitioners who do not otherwise hold a government position are not given access to *Epi-X*. As of August 2011, *Epi-X* has approximately 6000 users, of which approximately 1600 are authorized to directly contribute reports regarding developing public health events. *Epi-X* is frequently used to seek reports of cases of illness related to an outbreak, cluster or increased occurrence of a specific infectious disease. The usability and usefulness of *Epi-X* in this capacity have not previously been assessed.

Methods

A total of 52 case-seeking reports were posted on *Epi-X* during calendar year 2010, all of which were used to seek cases of infectious disease. *Epi-X* staff were successful in eliciting contributor feedback in regards to 30 of these reports. Four questions were asked that assessed the motivation behind posting a case-seeking report on *Epi-X*, the practicality of posting a case-seeking report on *Epi-X*, the successfulness of finding related cases by posting a case-seeking report on *Epi-X* and if the contributor intends to use *Epi-X* for this purpose in the future.

Results

Of the 52 case-seeking reports posted on *Epi-X* during calendar year 2010, all were posted with the intent of seeking cases of illness caused by infectious disease. One report was broad based and also sought cases of illness caused by injury. These reports were categorized by type of infectious agent, depending upon commonality of symptoms and routes of transmission. *Epi-X* contributors posted case-seeking reports for 19 individual confirmed or suspected infectious agents in 2010. The top four infectious agents for which case-seeking reports were posted on *Epi-X* in 2010 were *Salmonella* (10 reports), *Legionella* (9), hepatitis A virus (4) and measles virus (4). Other infectious agents included *Influenza*, *Bordetella*, *Cryptosporidium*, *Escherichia coli* and *Listeria*. Three reports were posted for which the infectious agent was unknown.

The 52 reports were contributed by 44 contributors. *Epi-X* staff were able to elicit feedback from contributors for 30 reports. In regards to usability, the system was considered practical for 28 of the 30 reports for which feedback was elicited. In regards to case-seeking usefulness, 2 of the 30 case-seeking reports for which feedback was elicited were considered not successful; eight were considered moderately successful, and 15 were considered fully successful. For five reports, the contributor was unable to rank the success. Of the 30 respondents, 28 stated their intent to use *Epi-X* for this purpose in the future.

Conclusions

Epi-X case-seeking reports were considered at least moderately successful in 23 of 30 reports for which feedback was elicited. In some instances, investigators expected to find no other related cases but posted their reports to make sure they had been thorough. Some investigators regarded their report(s) as successful, despite not finding any additional cases. Investigators may become more confident that all related cases have already been identified if they do not find additional cases as a result of posting on *Epi-X*.

Epi-X has become a standard method of identifying related cases. For investigators seeking additional cases in other state-level jurisdictions, posting case-seeking reports on *Epi-X* is a practical method. Increased use would likely strengthen the public health response to emerging infectious-disease events.

Keywords

The Epidemic Information Exchange; *Epi-X*; surveillance; secure; case finding

***James Schwendinger**
E-mail: bnz2@cdc.gov

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COACTION PUBLISHING

Hepatitis A surveillance evaluation in Mafraq Health Directorate, Jordan 2010

Ghazi Sharkas[1,2*], Sami Sheikh-ali[1,3] and Sultan Abdulla[1,4]

[1]Ministry of Health, Amman, The Capital, Jordan; [2]FETP Alumni, Amman, The Capital, Jordan; [3]Focal Point Viral Hepatitis, Amman, The Capital, Jordan; [4]Head of Surveillance Department, Amman, The Capital, Jordan

Objective

The study aims to assess HAV surveillance in Mafraq Health directorate and to determine whether the increase in reporting is related to a public health issue or is a result of a relatively good surveillance.

Introduction

Hepatitis A virus (HAV) infection is usually mild in childhood but more severe in adolescents and adults. An estimated 1.4 million cases of HAV infection occur annually in the world. The case-fatality rate among patients of all ages is approximately 0.3% but tends to be higher among older persons (approximately 2% for 40 years or older). HAV is a notifiable disease on weekly basis where health centers and hospitals report cases to the health directorates, which in turn report electronically to the Communicable Diseases Directorate, with subsequent paper reporting of detailed epidemiological description. The due time is Tuesday next week. Diagnosis is clinically based and depends on case definition. A previous study in Jordan revealed that reporting rate increased from 6.4 in 2004 to 7.9 in 2008/100,000, the highest reporting rate was in the North region, mainly Mafraq.

Methods

Ten health centers and one hospital were randomly selected; 13 weeks were also selected randomly from the year 2009. The reporting process was reviewed in the three levels for the number of reported cases of HAV in the selected weeks: the peripheral level by reviewing the reporting forms, notifiable logbooks of the reporting sites; the intermediate level in the health directorate by reviewing the specific notification forms(SNF) from each reporting site, and the comprehensive forms from all reporting sites; and the central level by reviewing the electronic and paper reporting to the communicable diseases directorate.

Results

The SNF were found for only 15% of reported HAV from Health Directorate in 2009. All the selected reporting sites had commitment in reporting. The sensitivity of reporting from reporting sites to health directorate was 96%; nevertheless, 38% of the reporting sites reported zero cases. HAV surveillance in Mafraq was evaluated upon application of CDC criteria for evaluation of surveillance system (as demonstrated in Table 1).

Conclusions

The increased number of HAV-reported cases in Mafraq is not related to a public health hazard; it is probably a result of relatively reasonable surveillance system. The reporting protocol is not well implemented, it is mostly phone based, and this will weaken the sensitivity of surveillance system; therefore, paper-based reporting should be enhanced.

Keywords

Hepatitis A; surveillance; evaluation; Mafraq, Jordan

Table 1. Evaluation of surveillance by application of CDC criteria

Simplicity	*Flexibility*
The diagnosis is clinically based and does not depend on laboratory test. Surveillance does not require complex training, equipments or fulltime working personnel. Reporting procedure is telephone based and 'regular mail' based, which is affordable to all reporting centers	The sureveillance system for HAV is clinically based, it includes also suspect and probable cases, and the reporting is according to available facilities. Case definition could be easily modified to cope with any addition
Acceptability Almost 38% of the reporting sites did not report any case in 2009; also, 23% of the reporting sites reported three cases or less, this could reflect that the surveillance for hepatitis A is not well accepted	*Timeliness* Almost all reporting centers reported to the health directorate in exact time by telephone, this is followed by paper reporting. Only 42% of the reports from Mafraq health directorate to the Communicable Diseases Directorate were done electronically; about 90% of the electronic reporting was done on time, 'Tuesday' the next week
Representativeness HAV surveillance is considered representative as monthly reports give detailed epidemiological information	*Data quality* The SNFs were found for only 15% of reported HAV cases from Health Directorate; none of HAV cases were investigated. Discrepancies were observed in the reported numbers, as 7% in excess was found in the reporting centers registry in comparison with the original reporting center SNFs; while 6% less was observed between the numbers of reported HAV cases in health directorate registry in comparison with reporting center registry
Sensitivity The percentage of reported cases to the truly existing cases (sensitivity) was 96% according to our case definition	

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*Ghazi Sharkas
E-mail: ghazisharkas@yahoo.com

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COACTION PUBLISHING

Inferring travel from social media

Alessio Signorini*, Philip Polgreen and Alberto Segre

Computer Science, University of Iowa, Iowa City, IA, USA

Objective

To use sequential, geocoded social media data as a proxy for human movement to support both disease surveillance and modeling.

Introduction

The spread of infectious diseases is facilitated by human travel. Disease is often introduced by travelers and then spread among susceptible individuals. Likewise, uninfected susceptible travelers can move into populations sustaining the spread of an infectious disease.

Several disease-modeling efforts have incorporated travel and census data in an effort to better understand the spread of disease. Unfortunately, most travel data are not fine grained enough to capture individual movements over long periods and large spaces. Alternative methods (e.g., tracking currency movements or cell phone signals) have been suggested to measure how people move with higher resolution but these are often sparse, expensive and not readily available to researchers.

FourSquare is a social media application that permits users to 'check-in' (i.e., record their currentlocation at stores, restaurants, etc.) via their mobile telephones in exchange for incentives (e.g., location-specific coupons). FourSquare and similar applications (Gowalla, Yelp, etc.) generally broadcast each check-in via Twitter or Facebook; in addition, some GPS-enabled mobile Twitter clients add explicit geocodes to individual tweets.

Here, we propose the use of geocoded social media data as a real-time fine-grained proxy for human travel.

Methods

Sixty-eight million geocoded entries (tweets and check-ins) from 3.2 million users were collected from the Twitter streaming API for the period from September 11, 2010 through January 28, 2011. The Twitter API provides a random sample of tweets; non-geocoded tweets or tweets originating from outside the United States were discarded. In addition, users with fewer than 6 records, or those who check in too frequently (more than once in 5 seconds) or travel too quickly (faster than 1800 km/hr) were removed to exclude automated bots or other location spam.

Results

We analyzed a 5-week subset of the data (September 11, 2010 through October 26, 2010) consisting of 3 million record intervals from 165,000 users.

We display intrastate travel by aggregating each user's consecutive records within each state and plotting only transitions between states (Fig. 1). The denser edges represent more frequent transitions, illustrating the pattern of travel on a national scale. We also constructed a heat map representation of Manhattan (Fig. 2) by aggregating users' check-ins with 500 m resolution. A larger bubble represents a denser set of records in that geographic area.

By linking each individual users' consecutive location records together, we computed the statistical distribution of time interval and distance traveled between records. About half of the checkins are less than 6 hr and no more than 1km apart from each other.

Conclusions

We show that social media location data can be used as multiscale proxy for travel at the national, state and urban level. These data are inexpensive and easily obtained. Furthermore, they can be used not only to understand historical travel but also to monitor in real-time changes in travel behavior to help inform disease surveillance.

Future work, currently underway, will validate this source of information against other sources of travel data and will investigate its value to better understand the spread of infectious diseases for disease monitoring and surveillance purposes.

Keywords

Social media; travel; modeling; surveillance; twitter

***Alessio Signorini**

E-mail: alessio-signorini@uiowa.edu

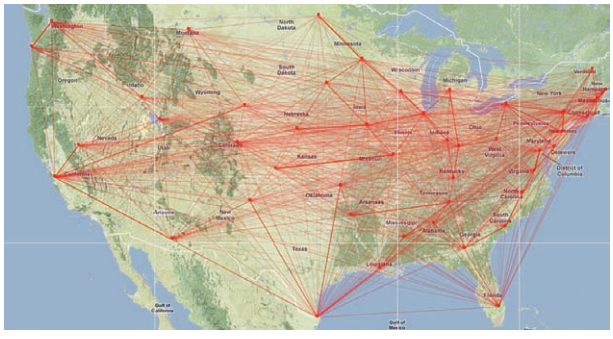

Fig. 1. User Transitions between U.S. States.

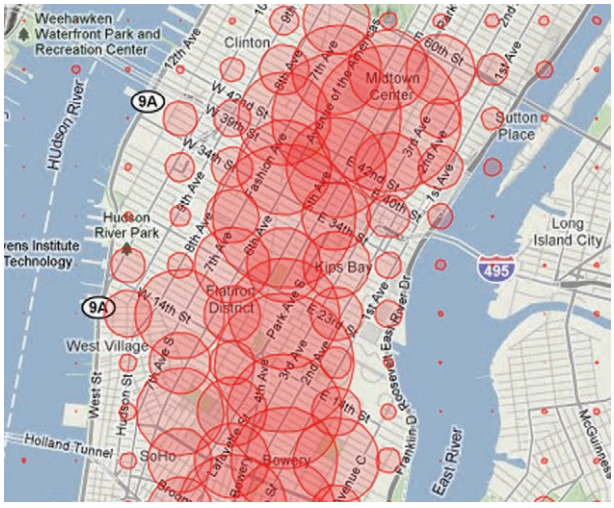

Fig. 2. Density of Check-ins over Manhattan, New York City, NY.

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COACTION PUBLISHING

Adverse drug events: 'Insights' from Google search volume

Jacob Simmering*, Chao Yang, Eric Foster, Linnea Polgreen and Philip Polgreen

University of Iowa, Iowa City, IA, USA

Objective

To investigate the use of search volume data from Google Insight for the detection and characterization of adverse drug events.

Introduction

Adverse drug events (ADEs) are a major cause of morbidity and mortality (1, 2). However, postmarketing surveillance systems are passive, and reporting is generally not mandated (2). Thus, many ADEs go unreported, and it is difficult to estimate and/or anticipate side effects that are unknown at the time of approval. ADEs that are reported to the FDA tend to be severe, and potentially common, but less serious side effects are more difficult to characterize and document.

Drugs with a high risk of harm outweighing the therapeutic value have recently been subjected to a greater level of interest with the Food and Drug Administration's Risk Evaluation and Mitigation Strategies (REMS) (3). However, no rapid method to detect if the REMS produce the desired effect and assessment of the impact is conducted by the drug manufacturer.

Increasingly, Americans have been turning to the internet for health-related information, largely by the use of search engines such as Google. The volume of searches for drugs and ADEs provides a unique insight about the interest in various medications and side effects as well as longitudinal changes.

Methods

We generated a list of the 179 most commonly used drugs in the United States in 2008 based on the Agency for Healthcare Research and Quality's Medical Expenditure Panel Survey (MEPS). Using this list of drugs, we consulted MicroMedex, a drug database, for information regarding possible ADEs for each drug. Next, we then obtained search volume data from Google Insight for all possible pairs of drugs and ADEs.

Using a set of searches restricted to only the known ADEs for a given drug, we coded each ADE as either common or other as listed by MicroMedex. Based on this categorization, we conducted a Wilcoxon two-sample signed rank test. Finally, we constructed a negative binomial model to explain the number of ADEs found by Google Insights. The total number of detected ADEs was modeled using the number of common ADEs in MicroMedex, the number of other ADEs in MicroMedex and the number of prescriptions for the drug based on 2008 data from MEPS as covariates.

A second list of 149 drugs with REMS was obtained from the FDA and search volume as collected for each of the drugs. We fit a generalized linear model to the data starting 1 year before and ending 1 year after the initial REMS approval date. The model included a dummy variable indicating if the month occurred before or after the initial approval of the REMS. The interaction between this variable and the time covariate was used to determine if the REMS had any impact on interest as measured by search volume.

Results

Both the Wilcoxon signed rank test and the negative binomial model indicate that Google Insight more readily detected common ADEs compared to the other ADEs. The Wilcoxon rank sum test indicated a shift toward more complete detection for the common ADEs compared to other ADEs ($p < 0.001$).

The negative binomial had similar results. The marginal increase in the number of ADEs detected by Google at the median for both the common and other ADEs was similar at 1.27 and 1.29, respectively. However, the median values were 7 and 39, respectively.

Only 40% (59/149) of drugs with a REMS approval demonstrated a change in slope with 90% confidence. The remaining 60% (90/149) indicated no significant change in interest over the time frame.

Conclusions

Our data help validate the use of Google Insights and search volume as a means to estimate the relative incidence of ADEs. In addition, internet search volume can be used as a rapid means for detecting new or changing ADEs after approval. Finally, the severity and frequency of ADEs may vary within a particular drug class, and search volume may provide additional information for guiding clinicians to select a given drug within a class.

The release of the REMS failed to create a change in search volume for the majority of the drugs. This may be due to prior elevated interest as the result of previous safety alerts or may be an indication that the REMS fails to create increased awareness of the risks of the drug. Further analysis of FDA safety alerts or change point analysis may provide a greater understanding of the effect of various risk management methods.

Keywords

adverse drug events, Google Insights, post-marketing surveillance

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***Jacob Simmering**
E-mail: jacob-simmering@uiowa.edu

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COACTION PUBLISHING

An evaluation of mobile phone technology use for Integrated Disease Surveillance Project (IDSP) in Andhra Pradesh, India

Vivek Singh[1]*, B Madhusudan Rao[2] and Jagan Mohan[2]

[1]Indian Institute of Public Health (IIPH)—Hyderabad, Hyderabad, Andhra Pradesh, India; [2]State Surveillance Unit, Directorate of Health, Hyderabad, Andhra Pradesh, India

Objective
To assess the impact of use of mobile phones use on the efficiency and effectiveness of the Integrated Disease Surveillance Project (IDSP) in the state of Andhra Pradesh (AP).

Introduction
Public health surveillance systems are constantly facing challenges of epidemics and shortage in the healthcare workforce. These challenges are more pronounced in developing countries, which bear the greatest burden of disease and where new pathogens are more likely to emerge, old ones to reemerge and drug-resistant strains to propagate. In August 2008, a mobile phone-based surveillance system was piloted in 6 of the 23 districts in the state of AP in India. Health workers in 3832 hospitals and health centers used mobile phones to send reports to and receive information from the nationwide Integrated Disease Surveillance Project (IDSP). Like in many other states, the IDSP in AP is facing many operational constraints like lack of human resource, irregular supply of logistics, hard to reach health facilities, poor coordination with various health programs and poor linkages with nonstate stakeholders. The mobile phone-based surveillance system was an attempt to tackle some of the barriers to improving the IDSP by capitalizing on the exponential growth in numbers as well as reach of mobile phones in the state. Promising results from the pilot of the system led AP state to extend it to about 16,000 reporting units in all 23 districts. This study evaluates how the system has affected the efficiency and effectiveness of IDSP in the state.

Methods
Key informant interviews, focus group discussions, record reviews and surveillance data analysis were conducted at the District Surveillance Units (DSUs), Primary Health Centers(PHCs)and Health Subcenters (HSCs). Five out of the 23 districts were selected for the evaluation using a probability proportion to size sampling strategy. Six PHCs were selected randomly from each of these 5 districts and 1 HSC was selected randomly from each of the PHCs. A total of 30 PHCs and HSCs were visited for evaluation.

Results
The mobile phone-based system was being used only by 20 to 60% of the reporting units. Since the start of the system, there was an increase of 10 to 25% in completeness of IDSP reports. There were significant gains (12–30%) in timeliness of reports. The system was saving time and money on logistics when compared to paper-based reporting. Public health workers in the field were enthusiastic about the system but were not using it as widely or extensively as was possible, because of lack of clear directives for implementation; lack of guidelines for usage and lack of systematic training of workforce for using the system.

Conclusions
Use of mobile phone technology has the potential to enhance the overall efficiency and effectiveness of the IDSP but will require clear policy directives and guidelines for deployment and usage, systematic training plans and adequate resources for the technology to be accepted and used universally in the state. Our evaluation findigs suggest that to maximize the potential benefits of mobile technology in health systems, its use should be based on evidence from operational, technical and technological feasibility studies. This study will prove useful for scaling up such strategies toward disease surveillance systems in countries with similar operational challenges and ready access to mobile phones.

Keywords
Integrated disease surveillance; mobile technology; surveillance quality; feasibility; policy

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*Vivek Singh
E-mail: vivek.singh@iiphh.org

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COACTION PUBLISHING

Ten years after Amerithrax: have improvements to our bioterrorism and influenza surveillance networks enhanced our preparedness?

Alan Siniscalchi*

State of Connecticut, Department of Public Health, Hartford, CT, USA

Objective

The 2001 U.S. anthrax mailings, which followed a week after the tragic events of September 11, highlighted the nation's vulnerability to bioterrorist attacks. This event, known by its FBI code name 'Amerithrax', resulted in 22 known infections and 5 deaths in various east coast locations, including Connecticut (1). These cases enforced the need for an effective, federal, state and locally integrated biosurveillance system network that can provide early warnings to reduce casualties, as called for in U.S. Homeland Security Presidential Directive (HSPD)-21 and emphasized in recent CDC reports (2). This presentation reviews several post-2001 anthrax cases and the roles played by various biosurveillance systems in their identification. Recommendations for the use of modeling and the development of regional and national coordinated surveillance systems are also discussed.

Introduction

The use of syndromic surveillance systems by state and local health departments for the detection of bioterrorist events and emerging infections has greatly increased since 2001. While these systems have proven useful for tracking influenza and identifying large outbreaks, the value of these systems in the early detection of bioterrorism events has been under constant evaluation (3, 4).

Methods

Several U.S. anthrax infections have been identified since the 2001 Amerithrax attacks. These cases were investigated by a number of local, state and federal agencies, and most were subsequently associated with exposure to imported animal hides contaminated with anthrax spores of natural origin (5–7). Each incident presented a unique diagnostic challenge since all three forms of the disease (inhalation, cutaneous and gastrointestinal) were identified. All of the cases were reviewed to determine which laboratory and surveillance systems were used to first identify possible cases and the number of days required to confirm the diagnosis of anthrax. The role of syndromic surveillance and other advanced surveillance systems in identifying these cases and searching for additional cases was evaluated. Efforts to coordinate surveillance and communication efforts among the various jurisdictions involved in the investigation of these cases were also noted.

Results

A review of these post-Amerithrax incidents revealed that all the cases were identified by astute clinicians using improved laboratory techniques. The time required to suspect and confirm the diagnosis of anthrax decreased with each subsequent incident, with increased awareness of animal sources of anthrax combined with improved compliance with laboratory reporting protocols. While syndromic surveillance systems did not identify the initial patients, these systems were used to search for additional cases. These efforts were enhanced when they were well coordinated among all jurisdictions.

Conclusions

The single local sources of exposure in most of these cases limited the value of these incidents to test the ability of syndromic surveillance systems to detect potential bioterrorist attacks. However, each incident provided valuable experience in the use of advanced laboratory and syndromic surveillance systems in the identification of anthrax cases. Although 10 years of surveillance system development has enhanced our nation's preparedness, use of outbreak modeling exercises in conjunction with regional and national multijurisdictional public health working groups, such as the Distribute Community of Practice, can further test and develop our ability to respond to bioterrorist attacks and emerging disease.

Keywords

Anthrax; syndromic surveillance systems; disease detection; modeling

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***Alan Siniscalchi**
E-mail: alan.siniscalchi@ct.gov

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COACTION PUBLISHING

Sufficient reduction methods for multivariate surveillance

Sawaporn Siripanthana* and Eleanor Stillman

School of Mathematics and Statistics, The University of Sheffield, Sheffield, United Kingdom

Objective

To reduce the dimensionality of p-dimensional multivariate series to a univariate series by deriving sufficient statistics, which take into account all the information in the original data, correlation within series (CWS) and correlation between series (CBS).

Introduction

Parallel surveillance, separate monitoring of each continuous series, has been widely used for multivariate surveillance; however, it has severe limitations. First, it faces the problem of multiplicity from multiple testing. Also, the ignorance of CBS reduces the performance of outbreak detection if data are truly correlated. Finally, since health data are normally dependent over time, CWS is another issue that should be taken into account. Sufficient reduction methods are used to reduce the dimensionality of a simple multivariate series to a univariate series, which has been proved to be sufficient for monitoring a mean shift in multivariate surveillance (1, 2). Having considered the sufficiency property and the nature of health data, we propose a sufficient reduction method for detecting a mean shift in multivariate series where CWS and CBS are taken into account.

Methods

Wessman (1) and Frisén et al (2) proposed a sufficient reduction method used for monitoring a mean shift in multivariate series where observations are assumed independent. Also, the former allows for CBS while the latter does not. In this study, we further develop sufficient reduction methods by taking CWS and CBS into account. At each time point, data from p-dimensional multivariate series are used to calculate sufficient statistics derived from the likelihood ratio between out of control and in control states. The evaluation of this method is by simulation study, where bivariate series are generated daily from different sets of parameters (whether or not CWS and/or CBS are present) (3). Detection of a mean shift, which is 2, 3 or 4 times standard deviation of background data, is investigated. A EWMA chart is used to monitor the resultant series of sufficient statistics, and the conditional expected delays (CED) and false alarm rates (FAR) (4) from four methods are compared.

Results

Three examples from our simulation study are shown in Table 1. Data are generated from three different sets of parameters (CWS (φ) and CBS (ρ)), and the aim is to detect a shift in mean of 2s.d. Dataset 1 has no CWS and CBS ($\varphi = 0$ and $\rho = 0$). Dataset 2 includes CWS ($\varphi = 0.4$), while dataset 3 presents both CWS and CBS ($\varphi = 0.4$ and $\rho = 0.3$). For all datasets, the parallel method gives longer delays compared with other methods. In the case of dataset 1 (no CWS and CBS), the last three methods perform similarly. When CWS is present (dataset 2), the proposed method performs better than the others with slightly lower delay and much lower FAR. This pattern is repeated when CBS is incorporated (dataset 3).

Conclusions

When CWS is present, CWS should be taken into account to the sufficient reduction method as ignoring CWS delays detection and gives more false alarms. Sufficient reduction methods derived for independent observations (1, 2) do not take CWS into account; therefore, the effect of CWS is still present in their derived series of sufficient statistics. This effect violates the assumptions of EWMA chart, for which data are assumed to be independent and then produces a high FAR. Although the sufficient reduction method proposed by Wessman (1) allows for CBS, it does not allow CWS. Incorporating both CWS and CBS in our proposed sufficient reduction method substantially improves the performance in detecting a mean shift in multivariate surveillance data.

Keywords

Sufficient statistics; multivariate surveillance; autocorrelation

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***Sawaporn Siripanthana**
E-mail: smp08ss@sheffield.ac.uk

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COACTION PUBLISHING

Fast graph structure learning from unlabeled data for outbreak detection

Sriram Somanchi* and Daniel B. Neill

Event and Pattern Detection Laboratory, Carnegie Mellon University, Pittsburgh, PA, USA

Objective

Our goal is to learn the underlying network structure along which a disease outbreak might spread and use the learned network to improve the timeliness and accuracy of detection.

Introduction

Disease surveillance data often have an underlying network structure (e.g., for outbreaks that spread by person-to-person contact). If the underlying graph structure is known, detection methods such as GraphScan (1) can be used to identify an anomalous subgraph, indicative of an emerging event. Typically, however, the network structure is unknown and must be learned from unlabeled data, given only the time series of observed counts (e.g., daily hospital visits for each zip code).

Methods

Our solution builds on the GraphScan (1) and Linear Time Subset Scan (LTSS) (2) approaches, comparing the most anomalous subsets detected with and without the graph constraints. We consider a large set of potential graph structures and efficiently compute the highest-scoring connected subgraph for each graph structure and each training example using GraphScan. We normalize each score by dividing by the maximum unconstrained subset score for that training example (computed efficiently using LTSS). We then compute the mean normalized score averaged over all training examples. If a given graph is close to the true underlying structure, then its maximum constrained score will be close to the maximum unconstrained score for many training examples, while if the graph is missing essential connections, then the maximum constrained score given that structure will be much lower than the maximum unconstrained score. Any graph with a large number of edges will also score close to the maximum unconstrained score. Thus, we compare the mean normalized score of a given graph structure to the distribution of mean normalized scores for random graphs with the same number of edges and choose the graph structure with the most significant score given this distribution.

Results

We generated simulated disease outbreaks that spread based on the zip code adjacency graph with additional edges added to simulate travel patterns and injected these outbreaks into real-world hospital data. We evaluated detection time and spatial accuracy using the learned graphs for these simulated injects (Fig. 1). This figure also shows the detection performance given the true (adjacency plus travel) graph, the adjacency graph without travel patterns and the average performance given randomly generated graphs. We observe that the learned graph achieves comparable spatial accuracy to the true graph, while the adjacency graph has lower accuracy. Additionally, the learned graph is able to detect outbreaks over a day earlier than the true graph and 1.5 days earlier than the adjacency graph. Thus, our method can successfully learn the additional edges due to travel patterns, substantially improving detection performance.

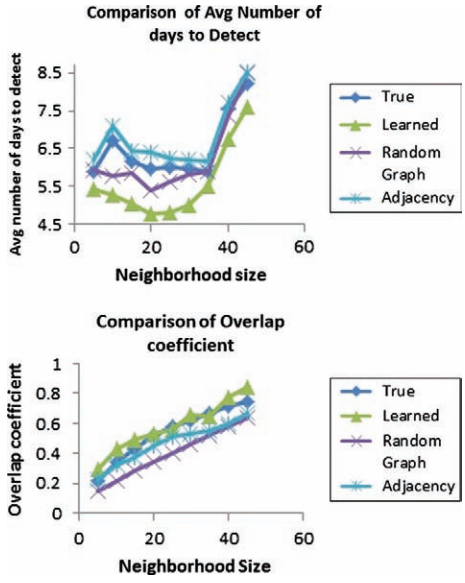

Fig. 1. Comparison of detection performance of the true, learned and adjacency graphs.

Conclusions

We proposed a novel framework to learn graph structure from unlabeled data. This approach can accurately learn a graph structure, which can then be used by graph-based event detection methods such as GraphScan, enabling more timely and accurate detection of outbreaks, which spread based on that latent structure. Our results show that the learned graph structure is similar to the true underlying graph structure. The resulting graph often has better detection power than the true graph, enabling more timely detection of outbreaks, while achieving similar spatial accuracy to the true graph.

Keywords

Event detection; biosurveillance; graph learning

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*Sriram Somanchi
E-mail: somanchi@cmu.edu

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COACTION PUBLISHING

Digital surveillance of the illegal wildlife trade: identifying hot-spots for emerging zoonoses

Amy Sonricker Hansen[1,2]*, Annie Li[3], Damien Joly[4] and John Brownstein[2]

[1]Department of Epidemiology, State University of New York at Albany, Albany, NY, USA; [2]Informatics Program, Children's Hospital Boston, Boston, MA, USA; [3]City University of Hong Kong, Kowloon, Hong Kong; [4]Wildlife Conservation Society, Vancouver, BC, Canada

Objective

We aim to develop an automated, real-time, comprehensive, global system for monitoring official and unofficial reports of illegal wildlife trade activity and to determine potential hot-spot regions for emerging zoonotic pathogens along commonly utilized illegal wildlife trade routes.

Introduction

The illegal wildlife trade is a multifaceted, clandestine industry that has led to the disruption of fragile ecosystems, facilitated the spread of pathogens and led to the emergence of novel infectious diseases in humans, domestic animals and native wildlife (1, 2). The trade is as diverse as it is large, with live and dead wildlife, representing multiple species sold to satisfy human demands for food, medicine, pets and trophies. Wildlife are harvested at astonishing numbers and used for such things as exotic pets, ornamental jewelry and clothing and traditional Chinese medicine (3). An estimated 75% of recently emerging infectious diseases originated from animals (4), which can include both live animals and animal products.

Methods

Freely available RSS feeds from official sources, such as organizations dedicated to ending the illegal wildlife trade to include TRAFFIC, WildAid and the Coalition Against Wildlife Trafficking (CAWT), were used to obtain information on illegal wildlife and wildlife product confiscations. In addition, information was obtained from freely available, disparate Internet sources (including discussion forums, mailing lists, news media outlets and blogs) by utilizing specific keyword search strings. For a 1-year period beginning August 1, 2010, English-language reports were collected on the illegal wildlife trade and interception points were analyzed (Fig. 1). When available, the origin and intended destinations of illegal wildlife products were also collected to aid in the development of proposed wildlife trade routes and hot-spot regions. Lastly, a comprehensive list of commonly traded species was compiled along with the potential zoonotic diseases that could be spread from traded animals to humans.

Fig. 1. The wildlife trade website (http://www.healthmap.org/wildlifetrade) showing time period from August 1, 2010 to July 31, 2011. Pins show locations of interceptions of illegally traded wildlife, as provided in reports received through the automated system.

Results

From 858 reports collected, elephants (n = 107, 12.5%), rhinoceros (n = 103, 12.0%), tigers (n = 68, 7.9%), leopards (n = 54, 6.3%), and pangolins (n = 45, 5.2%) were among the most commonly intercepted species (to include live animals and wildlife products). Zoonotic diseases associated with these species include rabies, cowpox, echinococcosis, anthrax, and tuberculosis. Countries with the most illegal wildlife product interceptions included India (n = 146, 15.6%), the United States (n = 143, 15.3%), South Africa (n = 75, 8.0%), China (n = 41, 4.4%), and Vietnam (n = 37, 4.0%).

Conclusions

Available at http://www.healthmap.org/wildlifetrade, the digital wildlife surveillance tool is freely available to both wildlife conservation officials as well as members of the general public and shows real-time reports of illegal wildlife trade activity worldwide as an interactive visualization. The system combines official and unofficial reports with an overall goal of providing a greater understanding of the global wildlife trade network in addition to providing a jumping-off point for the identification of hot spot regions where enhanced surveillance should be implemented for emerging zoonoses.

Keywords

Zoonoses; wildlife; digital surveillance; wildlife trade; zoonotic diseases

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*Amy Sonricker Hansen
E-mail: alhansen@albany.edu

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COACTION PUBLISHING

Evaluation of the Connecticut hospital emergency department syndromic surveillance system for monitoring of community gastrointestinal illness

Kristen Soto*, Jaime Krasnitski, Quyen Phan, Therese Rabatsky-Ehr and Matthew Cartter

Epidemiology, Connecticut Department of Public Health, Hartford, CT, USA

Objective

To evaluate the utility of the Connecticut hospital emergency department syndromic surveillance system (HEDSS) to monitor gastrointestinal (GI) illness in the community.

Introduction

The HEDSS system was implemented in 2004 to monitor disease activity (1). Twenty of 32 emergency departments (ED) and 1 urgent care clinic provide data. Chief complaints are routinely categorized into 8 syndromes.

Although previous studies have shown that ED syndomic surveillance is not useful for early detection of GI outbreaks (2), it has demonstrated utility in monitoring trends in seasonal norovirus activity (3). An evaluation to assess the utility of HEDSS to characterize endemic and outbreak levels of GI illness has not been previously conducted in Connecticut.

Methods

In Connecticut, *Campylobacter*, *Cryptosporidium*, *Cyclospora*, shiga toxin-producing *Escherichia coli* (STEC), *Giardia*, *Listeria*, *Salmonella*, *Shigella*, *Vibrio* and *Yersinia* are laboratory reportable findings. Aggregate hospital admissions data are reported daily by all hospitals. Facility and community GI outbreaks are also reportable events. Weekly percentage of HEDSS GI syndrome visits (combined GI, vomiting, diarrhea and bloody diarrhea) were compared to the number of GI hospital admissions, number of facility and community GI outbreaks and reportable enteric diseases using correlation coefficients. GI syndrome ED visits were also examined by geographical region and age.

Results

Vomiting and diarrhea were each highly correlated with the combined GI syndrome ($r = 0.99$, $p < 0.0001$; $r = 0.93$, $p < 0.001$, respectively), although vomiting has a greater magnitude than diarrhea. ED GI visits were correlated with GI hospital admissions ($r = 0.73$, $p < 0.0001$). Similar results were also seen when comparing HEDSS GI data to the number of total reported outbreaks ($r = 0.76$, $p < 0.0001$) and facility outbreaks ($r = 0.71$, $p < 0.0001$) but not community outbreaks alone ($r = 0.09$, $p = 0.23$). The combined GI syndrome was inversely correlated with laboratory confirmed cases of *Giardia* ($r = -0.18$, $p = 0.02$), *Campylobacter* ($r = -0.45$, $p < 0.0001$), STEC ($r = -0.32$, $p < 0.0001$), *Listeria* ($r = -0.23$, $p = 0.004$), *Salmonella* ($r = -0.41$, $p < 0.0001$), *Shigella* ($r = -0.19$, $p = 0.01$), *Vibrio* ($r = -0.36$, $p < 0.0001$). No significant positive correlations were detected when controlling for seasonality or using a narrower syndrome definition. There was no significant geographic variation in GI illness by region. Children younger than 5 years had a proportion of ED visits for GI illness that was consistently higher than all other age groups.

Conclusions

There is a strong and consistent association between ED visits for GI illness and facility outbreaks, the majority of which are suspected to be caused by norovirus (4,5). The strength of observed associations was similar when using a vomiting, diarrhea or combined GI syndromes; no significant correlations were observed when using the narrow bloody diarrhea syndrome. HEDSS GI syndromes were inversely correlated with illness caused by bacterial enteric pathogens, even when using the bloody diarrhea syndrome to identify more severe illness or controlling for seasonality. The HEDSS system is a critical tool for situational awareness of community gastrointestinal illness, particularly that which is caused by norovirus. Since norovirus is not a reportable condition in Connecticut, this system is used as the primary source of monitoring community GI illness.

Keywords

Syndromic surveillance; gastrointestinal; public health practice; evaluation

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***Kristen Soto**
E-mail: kristen.soto@ct.gov

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COACTION PUBLISHING

Determinants of asthma length of stay in London hospitals: individual versus area effects

Ireneous Soyiri[1,2]*, Daniel Reidpath[2] and Christophe Sarran[3]

[1]University of Ghana, Legon, Accra, Ghana; [2]MONASH University, Sunway Campus, Malaysia; [3]Met Office, Exeter, UK

Objective
To identify predictors of length of stay (LOS) of asthma admissions in London and to model their area and individual effects.

Introduction
Asthma is a chronic condition of public health concern associated with morbidity, mortality and healthcare utilisation. It disproportionately affects certain ethnic and demographic groups.

Methods
Asthma admission records in London (2001–2006) were used. Negative binomial regression was used to model the effect of demographic (*sex, age & ethnic group*), diagnostic (*primary & secondary diagnosis, method of admission*) and temporal (*day of the week, meteorological season & year of admission*) factors on the LOS, accounting for the random effects of each patient's attendance, as model 'I' and again for area of residence, model 'A'. Akaike information criterion (AIC) was used to compare the two models.

Table 1. Summary statistics of asthma-related hospital admissions in London, 2001–2006

Characteristics	N (%)
Age (years)	
< 5	12,420 (12.4)
5–14	10,700 (10.7)
15–44	16,612 (16.6)
45–59	7,029 (7.0)
60–74	5,698 (5.7)
≥ 75	4,309 (4.3)
Ethnic Group	
White	26,230 (46.2)
Black	6,604 (11.6)
Asian	6,382 (11.2)
Mixed/Other	5,780 (10.2)
Not stated	11,782 (20.8)
Secondary Diagnosis	
Other diseases of URT	25,053 (44.1)
Influenza and Pneumonia	692 (1.2)
Other acute lower respiratory infections	6,256 (11.0)
Acute upper respiratory infections	70 (0.1)
Chronic lower respiratory infections	1,207 (2.1)
Lung diseases due to external agents	1,519 (2.7)
Other diseases of respiratory system	378 (0.7)
Other Non-respiratory system diseases	15,227 (26.8)
Missing Values	6,376 (11.2)
Method of Admission	
Accident and emergency services	52,074 (91.7)
General Practitioner (GP)	2,602 (4.6)
Bed bureau	41 (0.1)
Consultants out patient clinic	577 (1.0)
Other means	1,484 (2.6)
Meteorological Season	
Summer	12,340 (21.7)
Spring	13,453 (23.7)
Autumn	16,800 (29.6)
Winter	14,185 (25.0)

Results
The median and mean asthma LOS over the period of study were 2 and 3 days, respectively. Admissions increased over the years from 8308 (2001) to 10,554 (2006), but LOS declined within the same period. Fewer males (48%) than females (52%) were admitted and, the latter had longer LOS compared to males. Only 5% were primarily diagnosed as *predominantly allergic*, whilst >94% were classified as '*asthma, unspecified*'. Younger people were more likely to be admitted than elderly, but the latter had higher LOS ($p < 0.001$). The secondary diagnosis and method of admission were important diagnostic determinants of length of stay, with very marginal differences between the two statistical models ('I' & 'A'). Again, all the temporal factors were significant determinants of LOS. Overall the patient cluster model (AIC=239394.8) outperformed the area model (AIC=247899.9).

Conclusions
Asthma LOS is best predicted by demographic, diagnostic and temporal factors with individual patients as a random effect.

Keywords
Asthma; length of stay; spell duration; risk factors; hospital admission

*I. Soyiri
E-mail: soyiriin@yahoo.com

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COACTION PUBLISHING

Scalable detection of irregular disease clusters using soft compactness constraints

Skyler Speakman*, Edward McFowland III, Sriram Somanchi and Daniel B. Neill

Event and Pattern Detection Laboratory, Carnegie Mellon University, Pittsburgh, PA, USA

Objective

We present a new method for efficiently and accurately detecting irregularly shaped outbreaks by incorporating 'soft' constraints, rewarding spatial compactness and penalizing sparse regions.

Introduction

The spatial scan statistic (1) detects significant spatial clusters of disease by maximizing a likelihood ratio statistic F(S) over a large set of spatial regions, typically constrained by shape. The fast localized scan (2) enables scalable detection of irregular clusters by searching over proximity-constrained subsets of locations, using the linear-time subset scanning (LTSS) property to efficiently search over all subsets of each location and its $k-1$ nearest neighbors. However, for a fixed neighborhood size k, each of the 2^k subsets are considered equally likely, and thus the fast localized scan does not take into account the spatial attributes of a subset. Hence, we wish to extend the fast localized scan by incorporating soft constraints, which give preference to spatially compact clusters while still considering all subsets within a given neighborhood.

Methods

For a given local neighborhood with center location s_c and size k, we place a bonus or penalty $\triangle_i = h(1 - 2d_i/r)$ on each location s_i, where d_i is that location's distance from the center, r is the neighborhood radius and h is a constant representing the strength of the compactness constraint. Each $\triangle_i$ can be interpreted as the prior log-odds that s_i will be affected, and thus the center location ($d_i = 0$, $\triangle_i = h$) is e^h times as likely as its $(k-1)$th nearest neighbor ($d_i = r$, $\triangle_i = -h$). We demonstrate that the penalized score function $F'(S) = F(S) + \Sigma s_i \in S \ \triangle_i$ can be efficiently maximized over all subsets S for each neighborhood. To do so, we show that F(S) can be written as an additive function (sum over locations) conditioned on the relative risk in region S, and therefore F'(S) is additive given the risk as well. We then jointly maximize F′(S) over all subsets S and all values of the risk.

Results

The penalized subset scan was evaluated using emergency department (ED) data from 97 Allegheny County zip codes. We compared detection power and spatial accuracy, with and without compactness constraints, on synthetic, spatially localized outbreaks injected into the ED data. Our results show that including compactness constraints allows the penalized subset scan methods to detect outbreaks earlier and improve spatial accuracy, as compared to the unpenalized fast localized scan and circular scan, over a wide range of neighborhood sizes (Fig. 1). Without compactness constraints, the method averaged 7.6 days to detect and an overlap coefficient of 54.9% for neighborhood size of $k = 10$, but detection performance degraded rapidly for smaller or larger values of k. Performance of the compactness-constrained methods was less dependent on neighborhood size, requiring 7.4 days to detect and achieving an overlap coefficient of 59.3% for well-chosen parameter values.

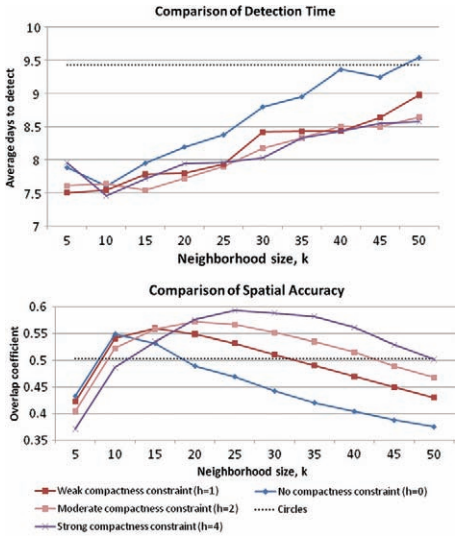

Fig. 1. Comparison of detection performance for methods with and without soft compactness constraints.

Conclusions

Our results demonstrate that the incorporation of soft compactness constraints substantially improves the timeliness and accuracy of outbreak detection. Our new approach based on additive linear-time subset scanning enables efficient maximization of penalized scan statistics over subsets of the data, thus improving detection of irregular clusters.

Keywords

Outbreak detection; spatial scan; penalized subset scan

Acknowledgments

This work was partially supported by NSF grants IIS-0916345, IIS-0911032, and IIS-0953330.

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***Skyler Speakman**
E-mail: skylerspeakman@gmail.com

COACTION PUBLISHING

A systematic approach to building and sustaining a regional and local biosurveillance community of practice

Bill Stephens[1] and Michael Coletta[2]*

[1]Tarrant County Southwest Center for Advanced Public Health Practice, Arlington, TX, USA; [2]NACCHO, Washington, WA, USA

Objective

To explore the lessons learned from the Advanced Practice Center methodology regarding the implementation of syndromic surveillance while considering what it takes to create, enhance and sustain relationships between hospitals, public health practitioners and the community.

Introduction

Although the advent of the ONCs 'meaningful use' criteria has added significant new incentives for healthcare organizations to provide the necessary data for implementing syndromic surveillance, incentives alone are not sufficient to sustain a robust community of practice that engages public health and healthcare practitioners working together to fully achieve meaningful use objectives. The process for building a successful community of practice around syndromic surveillance is primarily applicationagnostic. The business process has many of the same characteristics regardless of application features and can be incrementally customized for each community based on the unique needs and opportunities and the functional characteristics of the application. This presentation will explore lessons-learned in the north central Texas region with BioSense 1 and ESSENCE over the past 6 years and will describe the multiphase process currently underway for BioSense 2.0. Key program process steps and success criteria for public health and healthcare practitioners will be described. This road map will enable other local health department jurisdictions to replicate proven methodologies in their own communities. The presentation will also highlight what it takes for an existing community of practice with a home-grown system to move processes and protocols to the cloud.

Methods

The NACCHO Advanced Practice Centers (APC) Program is a network of local health departments whose mission is to promote innovative and practical solutions that enhance the capabilities of all local health departments and the public health system to prepare for, respond to, and recover from public health emergencies. Real world practice situations are supported and evaluated, resulting in the creation of tools designed to export and scale roll outs of lessons learned to other jurisdictions.

Results

Several products or tools specific to biosurveillance, disease detection and investigation were created through the APC Program methodology. Highlighted in this talk will be the Building a Public Health Community of Practice—A Biosurveillance Resource Compendium is a CD toolkit intended to help public health agencies implement an effective, comprehensive biosurveillance program. Providing approximately 40 resources, the CD includes a series of articles on implementing biosurveillance initiatives, materials defining and discussing the development of a public health community of practice, specific examples of real-world tools and resources that have proven beneficial in North Texas (including system response protocols) and a research report on biosurveillance system efficacy. The CD can help public health agencies strengthen partnerships with stakeholders at the federal, state and local levels and with the medical community, law enforcement, first responders and schools; it details how Tarrant County Public Health accomplished those goals and shares tools that were instrumental to the agency's success.

Conclusions

Lessons learned from a systematic approach to building and sustaining a regional and local biosurveillance community of practice have been documented in a meaningful way. These lessons can and should be leveraged as more of the country engages in syndromic surveillance through meaningful use incentives and the BioSense 2.0 infrastructure. The NACCHO sponsored north central Texas APC and tools derived from their work is a proven method to provide such assistance to local health departments across the country.

Keywords

Informatics; advanced practice centers; sustained relationships

*Michael Coletta
E-mail: mcoletta@naccho.org

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COACTION PUBLISHING

Evaluating the relationship between heat-related ED visits and weather variables

Bill Storm* and Brian Fowler

Bureau of Infectious Diseases, Ohio Department of Health, Columbus, OH, USA

Objective

Correlation and linear regression analyses were completed to evaluate the relationship between a heat-related illness (HRI) classifier using emergency department (ED) chief complaint data and specific weather variables as predictors, in Ohio.

Introduction

The ability to estimate and characterize the burden of disease on a population is important for all public health events, including extreme heat events. Preparing for such events is critical to minimize the associated morbidity and mortality (1,2). Since there are delays in obtaining hospital discharge or death records, monitoring of ED visits is the timeliest and an inexpensive method for surveillance of HRI (1). Aside from air temperature, other environmental variables are used to issue heat advisories based on the heat index, including humidity and wind (3). The purpose of this study was to evaluate the relationship between HRI ED visits and weather variables as predictors, in Ohio.

Methods

Syndromic surveillance data from ED visits were collected and analyzed from Ohio's syndromic surveillance application, Epi-Center, for July 2011. Since the physical effects of HRI can vary greatly and affect multiple body systems, a specific classifier was created to query ED visits that were likely related to HRI and was defined as chief complaints referencing heat 'exhaustion or exposure', dehydration or hyperthermia. Measurements for weather variables included temperature, dew point, humidity, pressure and wind speed. The average daily values of these variables were calculated from seven geographically representative cities in Ohio and used as a surrogate for statewide data. These data were obtained from Weather Underground, which collects data from Automated Surface Observations System (ASOS) stations located at airports throughout the United States. These data were analyzed via time-series analyses and stratified by age group and gender. Correlation and linear regression analyses were performed, using SAS v 9.2 to determine which weather variables were the best predictors of HRI, as defined by ED chief complaint data.

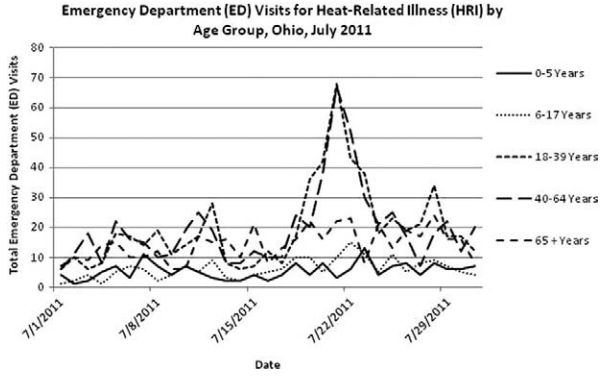

Fig. 1.

Results

During the third week of July 2011, Ohio experienced a heat wave with multiple heat advisories throughout its various cities. The total ED visits related to HRI peaked on July 21 (n = 170, 107 males, 63 females), which was also the day with the highest maximum temperature (97.4 F). A time-series chart of these ED visits by age group is shown below. The data show that the most sensitive populations (ages 0-5 and 65 and older) were the least affected and likely were adhering to the heat advisories. The 18–39- and 40–64-year-old age groups were most affected by the heat. Pearson correlation showed a strong relationship between HRI visits and mean temperature and dew point ($r = 0.76$ and $r = 0.66$), $p < 0.0001$. Multiple linear regression analyses were completed to determine which weather variables were the best predictors with HRI. The best model showed that for every 1 unit increase in ED visits, there was a 3.88 unit increase in mean temperature, independent of mean humidity and wind speed, $p < 0.0001$. The addition of mean dew point caused the model to have a high colinearity and was removed from the model.

Conclusions

These results suggest the advisories provided to the public during the heat wave in Ohio were most adhered to by the sensitive populations (very young and elderly). Middle-aged males were most susceptible to HRI during the peak of the heat wave. Temperature and dew point showed a strong relationship with HRI and were modeled as significant predictors of HRI. Additional analyses should be completed to further evaluate this relationship. Finally, obtaining patient diagnosis records from the hospital EDs would provide strength in validating the observed results.

Keywords

Heat-related illness; weather; predictor; classifier; correlation

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*Bill Storm
E-mail: William.Storm@odh.ohio.gov

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COACTION PUBLISHING

Building meaningful use reporting infrastructure in NH through partnerships

David Swenson[1]*, Christopher Taylor[1], Brook Dupee[1], Gerald Bardsley[1], Trico Hightower[2], Art Ramos[2], Jeff Proulux[2] and Drew Ivan[2]

[1]DHHS, State of NH, Concord, NH, USA; [2]Orion Health, Santa Monica, CA, USA

Objective

To describe steps used to build the required infrastructure to meet Public Health Meaningful Use (MU) reporting requirements for electronic syndromic surveillance, Electronic Lab Reporting (ELR) and immunization data in NH Division of Public Health Services (NH DPHS).

Introduction

Under the Electronic Health Record (EHR) Incentive Program Rule, hospitals are eligible to receive incentive payments from the Centers of Medicare and Medicaid Services (CMS) provided they meet certain requirements including MU. Demonstrating MU requires meeting a core and menu set of objectives including the capability to submit electronic syndromic surveillance, ELR and immunization data in accordance with state law and practice. NH is building a NH Heath Information Exchange (HIE) to serve all NH's MU needs including those of public health. This not only represents a huge opportunity for public health to collect more data to enhance disease detection and control, improve safety, and reduce health disparities, but also presents an integration challenge.

Methods

In 2011, NH DPHS initiated a project with Orion Health to build a Rhapsody integration engine (1) portal to receive the three types of Public Health data. A Syndromic surveillance pilot was chosen since 25 of 26 hospitals were already sending real-time data in HL7 format to the statewide syndromic surveillance system. NH DPHS collaborated with the NH Regional Extension Center (REC) to host MU guidance and brokered with Orion Health, the Office of the National Coordinator (ONC), and CMS to offer hospitals the option to use a modular certification for MU public health measures by selecting the Orion Health module (2). Selecting this module allows hospitals to send data to the NH DPHS Rhapsody portal in whatever format they choose; then, the NH DPHS Rhapsody system converts these messages to the approved ONC standards for public health reporting.

Orion Health contractors set up the Rhapsody server, configured data routes and built validation, filtering, and mapping logic. Mapping to HL7 2.5.1 was performed, but additional mapping to 2.3.1 was done before sending data to the syndromic surveillance application. Hospitals were directed to reroute data transmissions to the new Rhapsody VPN IP address and port, and Rhapsody was configured to pass traffic to the original surveillance application address and port. Additionally, data was sent through the normal VPN connection to compare the accuracy and performance of the new path.

Results

This MU project generated more hospital participation than was realized prior to initiating the Rhapsody integration. Negligible syndromic surveillance processing time degradation was realized with the added Rhapsody processing. This processing allowed NH DPHS to implement its last acute care hospital into the existing syndromic surveillance application (using Rhapsody mapping), filter existing hospital syndromic surveillance transmissions on specific patient types (preventing unwanted types), receive MU ELR and immunization data prior to expected timelines, increase hospital MU certification reimbursement without additional MU expenditure and decrease the hospital laboratory staff reporting burden, which previously was manual.

Conclusions

NH DPHS was able to take advantage of opportunities and resources beyond the State of NH. The brokered Orion Health Rhapsody MU certification solution provided a lower cost certification solution to hospitals (as compared to purchasing Rhapsody or certifying their EHR). NH DPHS was able to build an expandable public health MU infrastructure easily integrated with the NH HIE. The MU REC website provided guidance, FAQs, state rules and allowed NH DPHS to communicate effectively with hospital partners and the NH REC, to take advantage of REC expertise, and keep all partners informed.

Keywords

Informatics; disease surveillance; Meaningful Use

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*David Swenson
E-mail: dswenson@dhhs.state.nh.us

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COACTION PUBLISHING

Ten years of syndromic surveillance in New Hampshire: innovation, experience and outcomes

David Swenson[1]*, Xiaohui Zhang[2], Stephanie Miller[1], Kenneth Dufault[1], Christopher Taylor[1], Kim Fallon[1] and Elizabeth Daly[1]

[1]State of NH, DHHS, DPHS, Concord, NH, USA; [2]Scientific Technology Corporation, Tucson, AZ, USA

Objective

To illustrate development of syndromic surveillance in NH, share innovation experience with the public health community and contribute to the syndromic surveillance body of knowledge in the new public health information technology landscape.

Introduction

In response to the terrorist attack of September 11, 2001, the NH Department of Health and Human Services (NH DHHS) engaged state and external partners in the design of an early warning surveillance system to support bioterrorism and emergency preparedness. Initially, NH DHHS began collecting four syndrome counts from 13 hospital emergency departments (EDs) by fax. Automation began in 2002, when an over-the-counter (OTC) syndromic surveillance pilot system was implemented by Scientific Technologies Corporation (STC). In 2003–2004 this system, the Syndromic Tracking and Encounter Management System (STEMS), was expanded to include school absentee and occupational health reports. Over time, an internal death data application was automated to query vital record deaths, and in 2005, a real-time ED surveillance pilot, the Automated Hospital ED Data System (AHEDD), was developed by STC to replace manual ED surveillance. Over the past decade, NH continued to expand the original concept with innovative approaches to identify undetected or underreported disease outbreaks.

Methods

NH's surveillance consists of assessing individual but compatible surveillance systems for (1) rapid detection of a covert bioterrorism attack and (2) early detection of naturally occurring outbreaks (i.e., influenza).

The OTC pharmaceutical system was implemented with automated data processing and alerting within an enterprise architecture. Modified Shewhart charting was developed with dynamic system modeling using a knowledge base technique. Community health status was charted with a set of state syndrome variables and dynamic processes, where baselines, thresholds, trend analysis and alerts from historic data were automatically charted (1). This technical framework was implemented in STEMS with OTC data, school absentee data and occupational health data, then later in AHEDD. The AHEDD system also used the Real-Time Outbreak and Disease Surveillance CoCo chief complaint classifier with electronic data feeds from four hospitals. AHEDD was later expanded to include drill down custom querying for all 26 acute care hospitals (allowing NH to realize statewide ED surveillance).

Over time, custom querying included data mining techniques adapted from the death data application, (2) to detect narrowly defined chief complaint health conditions and cluster activity. This together with a 'Google'-like query tool allow NH surveillance staff to quickly assess any situation. Recently, a single portal infrastructure, based on AHEDD, was created to receive all external syndromic surveillance, Electronic Lab Reporting and immunization transmissions, helping hospital partners meet Meaningful Use (MU), which paves the way for integration with a statewide Health Information Exchange.

Results

Over the past 10 years, the usefulness of NH's surveillance systems has been demonstrated repeatedly. STEMS detected influenza and school norovirus outbreaks (3), and AHEDD tracked H1N1 and acute respiratory illness during the flu season, detected anthrax exposures during a gastrointestinal anthrax investigation and identified reportable disease occurrences (i.e., Lyme disease) and nonreportable clusters (i.e., carbon monoxide). These narrowly defined chief complaint queries have been found to be more useful than broad-based queries in detecting daily illness and heath risks. Results of individual surveillance systems assessed together validate individual system detections (i.e., increased sales of OTC antiviral medication and increased school ILI absenteeism validate ED flu spikes).

Conclusions

Ten years of NH syndromic surveillance tool development has established a critical biosurveillance infrastructure with emergency preparedness response capability during disease outbreaks and natural disasters. These syndromic surveillance tools are now integral to the daily efforts of epidemiologists and public health professionals.

Keywords

Informatics; disease surveillance; Meaningful Use

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*David Swenson
E-mail: swensd@comcast.net

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COACTION PUBLISHING

The association of influenza vaccination with influenza-like illness among adults aged 65 years and older in the United States

Mayuko Takayama[1,2*], Catherine Wetmore[1] and Ali Mokdad[1]

[1]Institute for Health Metrics and Evaluation, University of Washington, Seattle, WA, USA; [2]Department of Health Promotion Science, University of Tokyo, Bunkyo-ku, Tokyo, Japan

Objective

To explore the association of influenza vaccination with influenza-like illness (ILI) among adults aged 65 years and older

Introduction

After the 2009 H1N1 influenza pandemic, CDC initiated community-based surveillance of self-reported influenza-like illness (ILI) (1), defined as the presence of fever with cough or sore throat. Although ILI is frequently attributed to other pathogens, including rhinovirus, routine surveillance of ILI at the population level does aid in the detection of nascent influenza outbreaks. In the United States, approximately 90% of influenza-related deaths occur among adults aged 65 years and older (2). We explored the association of influenza vaccination with ILI, among this vulnerable age group.

Methods

Self-reported survey data from the 2010 Behavioral Risk Factor Surveillance System (BRFSS) was analyzed. Because the relationship between ILI and influenza infection is strongest during the influenza season, we limited the study sample to adults aged 65 years and older who participated between January and March 2010 (N = 35,628). We adjusted for three categories of individual-level factors: sociodemographics, health behaviors, and history of chronic disease diagnoses. We used stratified, weighted multivariable logistic regression to estimate the association between receipt of the influenza vaccine in the past year and report of ILI in the past month via adjusted odds ratios (aOR) and 95% confidence intervals (95% CI).

Results

Recent ILI was reported by 3.37% (95% CI: 3.02–3.73%) of responders. 67.7% (95% CI: 66.8–68.6%) reported receiving the influenza vaccine in the past year. After adjusting for sociodemographics, health behaviors, and chronic disease diagnoses, receipt of influenza vaccination was significantly associated with recent ILI, with vaccine recipients being more likely to report ILI (aOR = 1.50, 95% CI: 1.01–2.24). Persons who are underweight (BMI < 18.5, compared with normal weight) (aOR = 3.21, 95% CI: 1.19–8.65), and those diagnosed with asthma (aOR = 2.45, 95% CI: 1.65–3.62), coronary heart disease (aOR = 1.77, 95% CI: 1.17–2.65), and stroke (aOR = 1.75, 95% CI: 1.07–2.87) were also more likely to report ILI.

Conclusions

Our study showed an association between influenza vaccination and influenza-like illness among persons aged 65 years and older. This is a counterintuitive finding as vaccines are known to reduce the burden of influenza. Although our study is cross-sectional and we cannot determine a causal pathway, it is possible that individuals with greater susceptibility to influenza infection (e.g., persons with chronic diseases) were more likely to get vaccinated. Indeed, these findings suggest the success of targeted public health messaging regarding the importance of vaccination among high risk individuals.

Keywords

Influenza; vaccination; influenza-like illness; surveillance

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*Mayuko Takayama
E-mail: mayukot@u.washington.edu

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COACTION PUBLISHING

Changes in the spatial distribution of syphilis

Sean Tolentino[1]*, Sriram Pemmaraju[1], Philip Polgreen[2], Anson Tai YatHo[1], Mauricio Monsalve[1] and Alberto Segre[1]

[1]Department of Computer Science, Computational Epidemiology, University of Iowa, Iowa City, IA, USA; [2]University of Iowa Hospitals and Clinics, Iowa City, IA, USA

Objective

To study the spatial distribution of syphilis at the county level for specific states and nationally and to determine how this might have changed over time in order to improve disease surveillance.

Introduction

Public health officials and epidemiologists have been attempting to eradicate syphilis for decades, but national incidence rates are again on the rise. It has been suggested that the syphilis epidemic in the United States is a 'rare example of unforced, endogenous oscillations in disease incidence, with an 8–11-year period that is predicted by the natural dynamics of syphilis infection, to which there is partially protective immunity' (1). While the time series of aggregate case counts seems to support this claim, between 1990 and 2010, there seems to have been a significant change in the spatial distribution of the syphilis epidemic. It is unclear if this change can also be attributed to 'endogenous' factors or whether it is due to exogenous factors such as behavioral changes (e.g., the widespread use of the internet for anonymous sexual encounters). For example, it is pointed out that levels of syphilis in 1989 were abnormally high in counties in North Carolina (NC) immediately adjacent to highways (2). The hypothesis was that this may be due to truck drivers and prostitution and/or the emerging cocaine market (1). Our results indicate that syphilis distribution in NC has changed since 1989, diffusing away from highway counties (see Fig. 1).

Methods

Using CDC data for syphilis, we construct county-level syphilis distribution maps for NC and Florida and time series (1990-2010) of spatial distributions of syphilis for Florida. Additionally, for comparison, we construct county-level (from 2004 to 2010) and state-level (from 1995 to 2010) syphilis distribution time series.

Results

Maps of cases (per 100,000) in NC show that the disease has spread into rural counties and is no longer concentrated along the highway (see Fig. 1). In Florida, along with the overall decrease in syphilis incidence, the distribution of cases becomes more concentrated from 1990 to 1998. When, in 1999, syphilis incidence rates begin to increase again, the distribution again widens and spreads to more rural communities (see Fig. 2).

Fig. 1. Syphilis incidence rates in 2010 are no longer concentrated along I95.

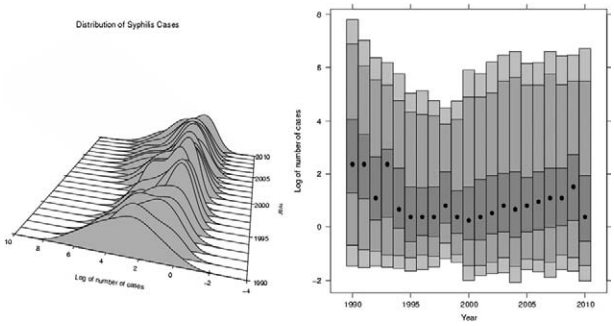

Fig. 2. Distribution of syphilis incidence in Florida from 1990 to 2010.

The time series of national state-level syphilis distribution indicates an increase in the number of states at the extremes of the distribution (i.e., with very high or very low case counts). However, at the same time, the national county-level distribution remains stationary. This indicates that counties with high case counts are clustering in states with high case counts and similarly counties with low case counts are clustering in states with low case counts.

Conclusions

The county-level spatial distribution of syphilis has changed significantly since 1990 and in ways that may depend on exogenous factors. Higher prevalence of syphilis in states seems more due to an increase in syphilis in counties that earlier had a low incidence of the disease. County-level syphilis data present a rather nuanced picture of how syphilis incidence has changed over the years and may form the basis for effective interventions.

Keywords

Spatial distributions; time-series analysis; syphilis

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*Sean Tolentino
E-mail: seanluciotolentino@gmail.com

COACTION PUBLISHING

A review of automated text classification in event-based biosurveillance

Manabu Torii*, Jeffrey Collmann, David Hartley and Noele Nelson

Georgetown University Medical Center, Washington, DC, USA

Objective

The objective of this literature review is to identify current challenges in document classification for event-based biosurveillance and consider the necessary efforts.

Introduction

Event-based biosurveillance monitors diverse information sources for the detection of events pertaining to human, plant and animal health using online documents, such as news articles, newsletters and blogs (1). Machine learning techniques have been successfully used for automated document classification, an important step in filtering source information (2–15).

Methods

We review studies on document classification using machine learning for event-based biosurveillance and comparatively summarize them for close examination.

Results

Table 1 lists relevant studies we identified. These studies differ in target regions, languages, event types and surveillance criteria, as well as classification methods. This diversity illustrates the complementarity of all the approaches.

Conclusions

Common challenges shared by these methods include detection of rare events and practical evaluation of the employed methods. The comparative advantages of each method remain unclear because of the lack of benchmark data. A community effort is necessary to develop an event ontology and benchmark corpora.

Table 1. Selected studies

Program	*Reference*	*Primary source*	*Methods*
Argus I	Lehner et al. (10)	News	NB
Argus II	Torii et al. (12)	News	NB, SVM
Biocaster	Conway et al. (4)	News	DT, NB, SVM
	Doan et al. (6)	News	NB, SVM
EpiSpider	Tolentino et al. (11)	ProMed	NB
GPHIN	Blench (3)	News	'proprietary'
Healthmap	Freifeld et al. (8)	News	NB
InSTEDD	http://instedd.org/evolve	News	NB, SVM
-	Aramaki et al. (2)	Twitter	SVM
-	Culotta (5)	Twitter	LR
-	von Etter et al. (7)	News	NB, SVM
-	Lampos et al. (9)	Twitter	Bolasso
-	Signorini et al. (15)	Twitter	SVM
-	Zhang et al. (14)	News	kNN, NB, SVM
-	Zhang and Liu (13)	ProMed	NB, SVM

Abbreviations: NB, naive Bayes.

Keywords

biosurveillance; text classification; machine learning

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***Manabu Torii**
E-mail: manabu.torii@gmail.com

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COACTION PUBLISHING

Defining emergency department asthma visits for public health surveillance

Debbie Travers*, Kristen Hassmiller Lich, Steven Lippmann, Anna Waller, Morris Weinberger and Karin Yeatts

University of North Carolina, Chapel Hill, NC, USA

Objective

Determine operational definition of emergency department (ED) visits attributable to asthma for public health surveillance.

Introduction

Tracking ED asthma visits is an important part of asthma surveillance, as ED visits can be preventable and may represent asthma control failure (1). When using limited clinical ED datasets for secondary purposes such as public health surveillance, it is important to employ a standard approach to operationally defining ED visits attributable to asthma. The prevailing approach uses only the primary ICD–9–CM diagnosis (Dx) for the ED visit (2); however, doing so may underestimate the public health impact of asthma. We conducted this pilot study to determine the value of including ED visits with asthma-related Dx in secondary or tertiary positions. For example, for an ED visit with a primary Dx of upper respiratory infection and secondary Dx of asthma, it is possible that the infection triggered the asthma exacerbation and the visit could be attributed to both infection and asthma.

Methods

We utilized all ED visit data for 2008–2009 from the state public health surveillance system (3), accounting for 99.5% of the visits to North Carolina EDs. Included were visits with an ICD-9-CM diagnosis code for asthma (493.xx) in any Dx position (1–11). We then grouped asthma visits into 11 strata based on the Dx position containing the asthma code. We identified the most frequent chief complaint and primary Dx categories for each of the 11 asthma Dx positions. We also grouped procedure codes (ICD–9–CM and CPT) for potential asthma (e.g., nebulized medications) and cardiac (e.g., electrocardiogram) conditions for each Dx position.

Results

350,341 (4.0%) of the 8.7 million ED visits had a diagnosis of asthma in 1 of the 11 Dx positions. The most common chief complaints for visits with asthma were: Dx positions 1 and 2- dyspnea and asthma, and Dx positions 3–5- injury. 69,877 (19.9%) of the asthma visits had at least 1 procedure code assigned, those with asthma or cardiac procedure code are shown in Fig. 1.

Conclusions

Restricting the definition of an asthma-related ED visit to the first diagnosis position may miss a substantial proportion of the asthma-related public health burden. Further analysis is in progress to evaluate the validity of these preliminary findings.

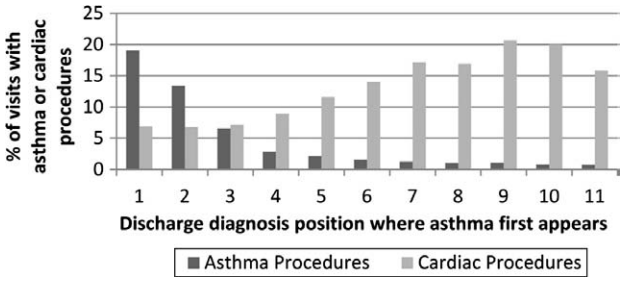

Fig. 1. Procedures by diagnosis position where asthma first appears.

Keywords

Public health surveillance; ED data; asthma

Acknowledgments

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***Debbie Travers**
E-mail: dtravers@email.unc.edu

COACTION PUBLISHING

Data requests for research: best practices based on the North Carolina DETECT experience

Heather Vaughan-Batten[1]*, Lana Deyneka[1], Amy Ising[2] and Anna Waller[2]

[1]Communicable Disease Branch, N.C. Division of Public Health, Raleigh, NC, USA; [2]University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Objective

To describe the process by which researchers request access to data sets of emergency department data from NC DETECT, the history of this process and the resulting best practices and lessons learned.

Introduction

The North Carolina Division of Public Health (NC DPH) has been collecting emergency department data in collaboration with the Carolina Center for Health Informatics in the UNC Department of Emergency Medicine (CCHI) since 1999. As of August 2011, there are 113 of 115 emergency departments sending data electronically at least once daily to NC DETECT. Data elements include disposition, initial vital signs, up to 11 ICD-9-CM final diagnosis codes, up to five external causes of injury codes (E-codes), as well as the arrival date and time, patient sex and age, patient zip and county and chief complaint. As of January 2008, NC DETECT emergency department data covered 99% of the NC population and captures approximately 4.5 million ED visits each year. As a result, requests for data from researchers continue to increase. Use of the data for public health purposes is covered by the mandate requiring hospitals to submit their emergency department data to NC DPH.

Methods

Data requesters must use the ED data in NC DETECT for public health-focused studies. Data requests from commercial entities are not approved. The data request process occurs primarily via paper and e-mail, although we have implemented a centralized tracking system to store all documentation for data requests and track changes to them over time. To initiate the process, requesters view a presentation on https://www.ncdetect.org/ReportsPortal/public/dataRequest.do and then enter information on the study purpose, the researchers involved, any grants covering the research and the specific data requested—specifically the data elements, time frame and file format. Researchers must get approval from their home institution's Institutional Review Board and sign a Data Use Agreement (DUA) with NC DPH. The DUA outlines data use requirements such as securing the data during the study, presenting data in aggregate form only (in a manner in which an individual cannot be identified), sharing materials with NC DPH prior to presentation or publication and destroying data upon completion of the study. Data requests within NC DPH typically do not require a DUA and are exempt from this process. In addition, researchers who need to determine the feasibility of a study before submitting a full data request can go through an exploratory process that requires a DUA but no IRB. While data requests are ongoing, a small Data Oversight Committee (DOC) meets once monthly to review these requests and to discuss status and outstanding issues. The NC DETECT DOC includes representatives from the NCDPH, CCHI, NC Hospital Association (NCHA) and DPH legal personnel (as needed).

Results

We currently have 31 data requests in our online tracking system. Each data request represents multiple e-mails and phone calls, iterative revisions to the data request and multiple data pulls from the NC DETECT database. Requests can be delayed when researchers request data elements that are not collected by NC DETECT, submit unclear requirements, change requirements, do not understand the challenges of processing free text data and/or add/change researchers who will be accessing the data. Requesters have used NC DETECT data to publish manuscripts on topics including the health effects of wildfires, ED visits for cancer patients, tick-borne illness and asthma, and comparison of NC ED visit data to national data, among others. Because the ED visit data are collected under a state mandate and in collaboration with the NCHA, their release and use for research is thoroughly evaluated by the DOC. The complexity of the data requests over time has resulted in changing of data use restrictions, as well as revisions of the DUA wording. We do not have enough resources to closely monitor the use of the data once they are provided to researchers. However, researchers are expected to abide by all provisions detailed in their DUA and by signing acknowledge the potential penalties for violation of the terms the agreement.

Conclusions

Data requests can take a considerable amount of time and iterative discussions with the requester, even with a well-defined process and clear documentation. Understanding the administrative and technical time commitments involved is important when considering making syndromic surveillance data available to external users for research.

Keywords

Data sharing; data use agreements; data requests

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*Heather Vaughan-Batten
E-mail: heather.vaughan-batten@dhhs.nc.gov

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COACTION PUBLISHING

Applications of the ESSENCE Desktop Edition for outbreak detection in a resource-limited setting

John Mark Velasco[1]*, Vito Roque Jr.[2], Jacqueline Coberly[3], Richard Wojcik[3], Charles Hodanics[3], June Corpuz[2], Sheri Lewis[3] and In-Kyu Yoon[1]

[1]Department of Virology, United States Army Medical Component—Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand; [2]National Epidemiology Center, Department of Health, Manila, Philippines; [3]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

To determine system usefulness of the ESSENCE Desktop Edition (EDE) in detecting increases in the number of dengue cases in the Philippines.

Introduction

Recent events have focused on the role of emerging and reemerging diseases not only as a significant public health threat but also as a serious threat to the economy and security of nations. The lead time to detect and contain a novel emerging disease or events with public health importance has become much shorter, making developing countries particularly vulnerable to both natural and manmade threats. There is a need to develop disease surveillance systems flexible enough to adapt to the local existing infrastructure of developing countries but which will still be able to provide valid alerts and early detection of significant public health threats.

Methods

In collaboration with the Philippine National Epidemiology Center (NEC) and the Philippines-AFRIMS Virology Research Unit, Armed Forces Research Institute of Medical Sciences, the EDE program, which was developed by Johns Hopkins University–Applied Physics Lab, was introduced in the Philippines to augment the data analysis capability of the Philippine Integrated Disease Surveillance and Response (PIDSR) System. Reported significant increases in the number of suspect dengue cases/outbreaks at the municipality, provincial and regional level, which were reported to and investigated by NEC from July 1, 2011, to August 31, 2011, were used as a reference point. A defined period, 30 days prior to the date when the event was officially reported, was retrospectively analyzed. The day when an EDE alert was first triggered and the number of EDE alerts detected during this period were described. Since NEC analyzes data by morbidity week, municipalities that were detected to be above the NEC alert or epidemic threshold during a randomly selected morbidity week (week 31; reporting date of August 6, 2011) were compared with the number of EDE alerts triggered during the past 7 days before the report date of morbidity week 31.

Results

Retrospective analysis done during the past 30 days before the event was officially reported showed that EDE Alerts were already triggered as early as 30 days (median of 27.5 and range 14–30 days) prior to the date of the NEC report. The number of days associated with EDE 'alerts' out of the 30 days prior to the NEC official report date had a median of 9.5 days (range of 3–14 days). A total of 17 municipalities had reported dengue cases above the alert or epidemic threshold with 8/17 of these municipalities having at least 1 day in the previous week with a case count of more than 5 while 9/17 had case counts of 5 or less for all 7 days in the past week. For municipalities with at least 1 day with a case count of 5 or more for the previous 7 days, the median of the number of days with associated EDE alerts was 5 (range 0–7 days). For municipalities with case counts of 5 or less for all 7 prior days, no alerts were usually generated (median 0 and range 0–2 days).

Conclusions

A surveillance system's usefulness for outbreak detection should be correlated with its ability to increase the lead time in detecting outbreaks of public health significance, which should subsequently lead to a more timely intervention. Analysis of currently available data seem to show promising applications of EDE in early warning alert capability of impending increases in dengue cases in the Philippines though when case counts are 5 or less, alert results may not be very reliable. Validity of alerts generated by EDE for early detection of outbreaks should be further investigated using other diseases, prediagnostic/nonclinical/nontraditional data and syndromes, taking into consideration effect of seasonality, weekly trends or holidays.

Keywords

Surveillance, outbreak, dengue, predictive, validity

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*John Mark Velasco
E-mail: VelascoJM@afrims.org

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COACTION PUBLISHING

Integrated approach of nonspecific surveillance in Réunion Island

Pascal Vilain[1]*, Arnaud Bourdé[2], Pierre-Jean Marianne Dit Cassou[3], Philippe Morbidelli[4], Yves Jacques-Antoine[5], Brigitte Ristor[6] and Laurent Filleul[1]

[1]Regional Office of French Institute for Public Health Surveillance of Indian Ocean, Saint Denis, Reunion; [2]Regional Hospital Center, Saint Denis, Reunion; [3]Regional Hospital Center, Saint Pierre, Reunion; [4]Hospital Center, Saint Paul, Reunion; [5]Hospital Center, Saint Benoît, Reunion; [6]National Health Insurance, Saint Denis, Reunion

Objective

To demonstrate that the different surveillance systems allow to establish complementary indicators.

Introduction

In Réunion Island, the nonspecific surveillance was developed since 2006 and was based on the activity of only one hospital emergency department and on mortality. To respond to the threat of influenza A(H1N1) pandemic emergence, this surveillance system was significantly enhanced (1,2). All hospital emergency departments of the island have been included as well as the emergency medical service regulation center (3). In 2010, a new surveillance was implemented from National Health Insurance data.

Methods

For the influenza A(H1N1) pandemic 2009, several indicators were monitored:

- number of consultations for influenza-like illness (ILI) to emergency departments of the four hospitals;
- number of call phone for ILI to the emergency medical service regulation center;
- number of consultations and home visits by general practitioners.

These indicators and their trends were described and compared to the data of sentinel network practitioners who reported the percentage of consultations for ILI.

Results

Whatever the data's source, we observed the peak of epidemic on week 35 (Fig. 1). Furthermore, trends observed were concordant for the four indicators.

Conclusions

These indicators show various levels of gravity of the influenza pandemic (phone calls, practitioner consultations and emergency consultations). These complementary data produced by these surveillance systems are widely sent to the public health network (clinicians, hospitals, etc.) and give essential pieces of knowledge about the health situation to crisis management authorities. To make a decision in terms of health planning and communication without having a quantified estimate of the risk is an unpredictable situation for the health authorities.

Keywords

Integrated approach; nonspecific; Réunion Island

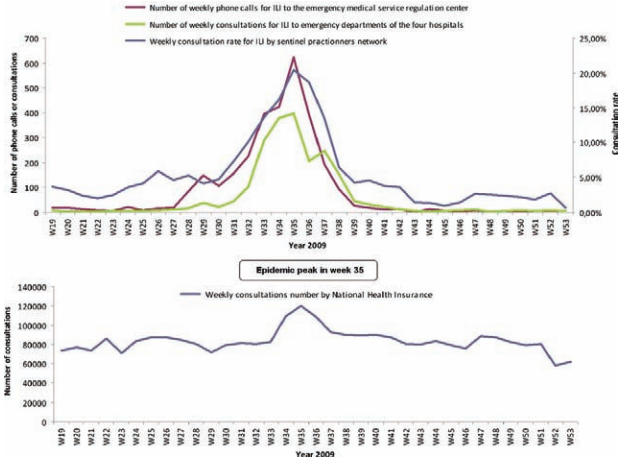

Fig. 1. Trends of different indicators during the influenza A(H1N1) pandemic in Réunion Island, 2009.

Acknowledgments

We are thankful to all the sentinel network practitioners, the practitioners of the adult and pediatric emergency departments. We thank all clinicians for providing their assistance and all patients for their participation in providing clinical data.

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***Pascal Vilain**
E-mail: Pascal.VILAIN@ars.sante.fr

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COACTION PUBLISHING

National Health Insurance: a new application for nonspecific surveillance in Réunion Island

Pascal Vilain[1]*, Nadège Caillère[2], Brigitte Ristor[3] and Laurent Filleul[1]

[1]Regional Office of French Institute for Public Health Surveillance of Indian Ocean, Saint Denis, Reunion; [2]French Institute for Public Health Surveillance, Saint Maurice, France; [3]National Health Insurance, Saint Denis, Reunion

Objective

To assess the ability to detect an unusual health event from National Health Insurance data.

Introduction

In Réunion Island, the nonspecific surveillance was mainly developed during A(H1N1) influenza pandemic in 2009 (1, 2). In March 2010, a new surveillance system was implemented from National Health Insurance data. This monitoring was based on the weekly consultation number and home visits by general practitioners.

Methods

The data based on the activity of general practitioners were transmitted on week W and covered the consultations and home visits carried out by the general practitioners in the week W − 1. These data were updated week by week according to the flow of repayments. The data received were aggregated, and no personal information was communicated.

The thresholds corresponding to the statistical alarms for the weekly numbers of all consultations were based on a calculation using adapted versions of two historical methods (log-linear regression model of Farrington and historical limit method) and CUSUM methods.

The surveillance period was spread over 134 weeks from week 1 of 2009 to week 29 of 2011. For the two historical methods, expected numbers of all consultations were calculated during these 134 weeks, using a training period of at least 3 years. A 95% confidence interval was calculated for each weekly expected number. A weekly count observed was considered significantly greater than the expected value if it was above the 95% upper confidence limit.

For the CUSUM methods, only few weeks were necessary to calculate a one-sided positive cumulative sum. An alarm was obtained if this cumulative sum was greater than a fixed decision value.

Results

The data covered 72% of the population of Réunion Island. Over the surveillance period, 11,048,739 consultations were recorded with an average of 82,453 consultations per week (min: 56,682; max: 120,432). An illustration of the results obtained with the historical limit method is presented in Fig. 1. The first alarms that occurred on week 34 to week 36 of 2009 corresponded to the influenza A(H1N1) epidemic with a peak in week 35. Statistical alarms observed on week 8 of 2010, and week 7 to 9 of 2011 were related to the season circulation of respiratory syncytial virus. These results were confirmed by the laboratory data. During the austral winter of 2010, one alarm was obtained in week 39 corresponding to the influenza epidemic.

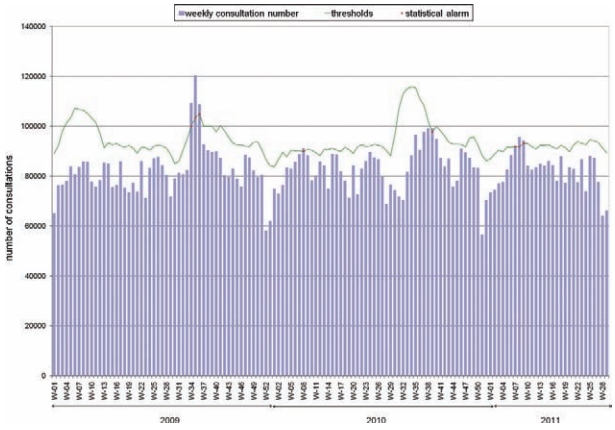

Fig. 1. Application of the historical limit method on National Health Insurance data, Réunion Island, 2009-2011.jpg.

Conclusions

This surveillance system based on the data of the National Health Insurance is a complementary tool to nonspecific monitoring in Reunion Island. Not only does it ensure the detection of unusual health events but it also allows to quantify a public health impact for major events. It brings information about the recourse to the so-called 'non emergency' cares that will allow public health authorities to implement adapted control measures. The major advantage of this system is its exhaustive data use that ensures a global view on all consultations carried out in the island and to have a denominator to calculate other indicators.

Keywords

National Health Insurance; nonspecific surveillance; Réunion Island

Acknowledgments

We are thankful to Mlle Baroux Noémie and Mlle Mérolle Marianne.

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***Pascal Vilain**
E-mail: Pascal.VILAIN@ars.sante.fr

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COACTION PUBLISHING

Opportunistic approaches to threat reduction efforts in resource-limited countries

Victor Del Rio Vilas*, Asatilla Sayitahunov and Yury Shlyonsky

Bechtel International Systems Inc., Tashkent, Uzbekistan

Objective

We describe approaches to the evaluation of threat reduction efforts in resource-limited countries. Specifically, we present an opportunistic approach to measure the success of efforts to improve on-farm biosecurity in Uzbekistan, which should lead to a reduction of disease transmission between animals and holdings, and to humans for zoonotic conditions.

Introduction

The Biological Threat Reduction Program (BTRP) of the U.S. Defense Threat Reduction Agency (DTRA) delivers interventions to enhance surveillance of especially dangerous pathogens of both humans and animals within countries of the former Soviet Union. The program targets the different stages at which threats or their impact can be reduced, for example, via (i) the reduction of exposure to threats or (ii) measures for the containment of the threat.

The program delivers training on surveillance-related subjects through regular events attended by representatives of the Ministry of Agriculture of Uzbekistan (UZ). This provides an opportunity to capture data and conduct simple interventions on specific subjects amenable to basic evaluation. Given the sensitive nature of pathogen-specific data, we focus on non-disease-specific interventions leading to the reduction of exposure to and release of any given hazard. Here, we present an opportunistic approach for capturing data, at no additional cost, to assess (i) baseline awareness of on-farm biosecurity measures among UZ veterinary officials and (ii) the impact of training on their awareness of biosecurity. We also discuss the conceptual design of a study to assess on-farm biosecurity practices in UZ.

Methods

We monitor four indicators to assess the effects of training (1): (i) reaction to training measured through structured feedback forms (FF); (ii) learning measured through pre- and posttraining tests; (iii) impact on the organization (i.e., how much the organizational practices change as a result of the trainings provided, measured, for example, through specific FFs); and (iv) return on investment (ROI), for which we are devising proxy measures to assess the improvement of traditional surveillance attributes (e.g., sensitivity). Here, we focus on impact. Specifically relating to biosecurity on farm, we aim to assess the impact at the training events through interactive presentations that allow the elicitation of trainees' views on what are the most common biosecurity breaches in their regions of origin, the measures they recommend and the barriers that prevent their implementation. At the end of the session, trainees discuss the most common biosecurity breaches to produce a check list that they can use the next time they visit farms.

Results

Collection of data at the training events is planned to start during the summer of 2011. We will present results of the data captured at the training events from that period onward. This will provide a baseline of biosecurity awareness within the surveillance workforce and suggested check lists for on-farm biosecurity assessments.

Conclusions

An on-farm assessment to identify biosecurity breaches against the check list developed at the trainings can be conducted during the visits by officials to farms as part of their regular duties. This will not require significant additional resources. A record of the number of breaches is made for every farm. This constitutes the baseline biosecurity status of the farm prior to the intervention. The intervention would be in the form of advice from the visiting official and the provision of a limited amount of materials to support the implementation of biosecurity measures (e.g., poster with biosecurity messages, log book, etc.). Later visits to the farm by the official will aim to record the number of breaches and allow comparisons with the baseline. Results from this study could be taken as a proxy measure of the ROI from the training efforts.

The model of opportunistic data collection at trainings can be extended to advise other nonsensitive areas, such as some of the technical attributes of the surveillance system (timeliness, etc.). Other extensions are possible by means of expanding generic frameworks, like the one discussed here, into disease-specific ones either to assess biosecurity or the risk pathways to the introduction of a pathogen into the country, a region or a farm.

Keywords

Especially dangerous pathogens; threat reduction; effect of training; biosecurity; resource-poor countries

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***Victor Del Rio Vilas**
E-mail: vdelriovilas@yahoo.co.uk

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COACTION PUBLISHING

Using cKASS to facilitate knowledge authoring and sharing for syndromic surveillance

Liqin Wang[1]*, Mingyuan Zhang[1], Mike Conway[2], Peter Haug[1] and Wendy Chapman[2]

[1]Biomedical Informatics, University of Utah, Salt Lake City, UT, USA; [2]University of California, San Diego, La Jolla, CA, USA

Objective

We describe cKASS (clinical Knowledge Authoring & Sharing Service), a system designed to facilitate the authoring and sharing of knowledge resources that can be applied to syndromic surveillance.

Introduction

Mining text for real-time syndromic surveillance usually requires a comprehensive knowledge base (KB), which contains detailed information about concepts relevant to the domain, such as disease names, symptoms, drugs and radiology findings. Two such resources are the Biocaster Ontology (1) and the Extended Syndromic Surveillance Ontology (ESSO) (2). However, both these resources are difficult to manipulate, customize, reuse and extend without knowledge of ontology development environments (like Protégé) and Semantic Web standards (like RDF and OWL). The cKASS software tool provides an easy-to-use, adaptable environment for extending and modifying existing syndrome definitions via a web-based Graphical User Interface, which does not require knowledge of complex, ontology-editing environments or semantic web standards. Further, cKASS allows for—indeed encourages—the sharing of user-defined syndrome definitions, with collaborative features that will enhance the ability of the surveillance community to quickly generate new definitions in response to emerging threats.

Methods

We have developed a web-based prototype of the cKASS system that allows individual users or collaborative communities to access the service anytime and anywhere, without a complex technical configuration process (Fig. 1). Two types of databases are used to support cKASS. First, a relational database is used to store user information and KB descriptors(e.g., KB domain and status). Second, KBs are stored as RDF triples using triple store and queried using SPARQL, an RDF query language, with the Jena SDB (SPARQL database,) providing robust and scalable storage. Existing resources stored in standard RDF and OWL formats can be easily loaded into the triple store and used as a basis for constructing new syndrome definitions.

The web interface is designed to support both individual and collaborative KB development. cKASS consists of two zones:

1. User workspace, where registered users can create, browse, modify and publish customized syndrome definitions constructed from either publicly available or user-created resources.
2. Community space, where anyone can browse and search shared KBs. Users who choose to share their KBs can make them available to the general community in this space.

cKASS also provides search/query capabilities at different levels. For example, the user can search within a specified domain or within a named KB for terms or concepts. Queries can either be simple strings or can consist of arbitrarily complex SPARQL and SQL queries. Further, users can import queried results into their syndrome definitions (for example, concept only, concept and its attributes or concept and all its subclasses). Finally, once created, KBs can be exported in standard formats, such as XML, CSV or RDF, for use with other tools.

Results

Currently, two existing syndromic surveillance oriented ontologies—Biocaster and ESSO—have been loaded into the cKASS triple store and can be used as a basis to construct new syndrome definitions. Both KBs can be queried using SPARQL and SQL.

Conclusions

cKASS offers public health professionals and clinicians an environment to support the extension and modification of existing KBs, without the need to use complex ontology editing environments and formalisms, allowing the user to rapidly develop or augment existing syndrome definitions and react quickly to the changing surveillance landscape.

Keywords

Syndrome surveillance; knowledge authoring; ontology

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*Liqin Wang
E-mail: liqin.wang@utah.edu

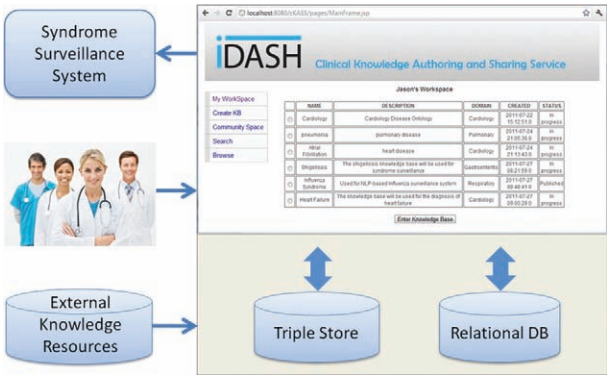

Fig. 1. The architecture of cKASS.

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COACTION PUBLISHING

Regional emergence of TB lesions in swine identified at slaughter

Wolf Weber[1]*, Jim Lowe[2,3] and Troy Bigelow[1]

[1]USDA APHIS Veterinary Services, Riverdale, MD, USA; [2]Carthage Veterinary Service, Ltd., Carthage, IL, USA; [3]College of Veterinary Medicine, University of Illinois, Urbana, IL, USA

Objective

This paper characterizes a regional outbreak of tuberculosis (TB) in market swine by combining local swine producer-based information on condemned stock at slaughter with geographically broader FSIS Animal Disposition Reporting System (ADRS) data. This study aims to obtain summary information on anomalous swine TB (STB) condemns at slaughter, compare critical outbreak time frames between outbreak areas and identify the geographical spread of abnormally high STB condemns.

Introduction

A case study presented at the November 2010 Iowa Annual Swine Disease Conference for Swine Practitioners detailed increases in STB lesions beginning January 2010 (1). Producers were informed of the problem by their swine processing facility. Tissue samples from affected producers were culture-positive for *Mycobacterium avium*. In the spring of 2010, USDA Veterinary Services (VS) began monitoring weekly ADRS STB carcass condemn data after a VS Staff Officer was made aware of unusual increases in STB condemns in another region. By June 2010, STB condemn rates in both of the affected areas decreased to typical seasonal levels; however, beginning January 2011, rates again rose beyond baseline seasonal highs, exceeding those seen in the 2010 outbreak.

Methods

The ADRS provides weekly condemn data to VS along with information on species and total number of animals slaughtered. June 2007–May 2011 ADRS market swine data were grouped by three major swine production areas (basins) to (1) identify preoutbreak condemn baselines, (2) quantify differences in the 2010 and 2011 STB outbreaks and (3) ascertain the geographical extent of the outbreaks. In addition, a fourth basin was created representing the remainder of U.S. market swine slaughter plants. To identify critical weeks of anomalous condemns, a modification of the 'C3' version of the Early Aberration Reporting System was applied to the STB condemn series (2). In addition to examining alerts by basin, the alerting algorithm was applied to individual plant data. Data processing was performed using SAS version 9.1 and an Excel-based 'Alerting Algorithms Tool' developed and published by Dr. Howard Burkom (3).

Results

Mean weekly swine TB condemn rates, which seasonally ranged from 5.7 to 21.4 per 100,000 between 2007 and 2009 (mean = 10.7, SD = 3.0), increased above typical levels beginning January 2010 and rose even higher beginning January 2011 (Fig. 1). Most of the increase was due to condemns in Basin 3, which experienced 670/100,000 weekly STB condemns at the height of the 2011 outbreak. Summary data for Basins 1, 2 and 4 indicate that condemn profiles remained at nonoutbreak levels over the 4-year data series. Retrospective analysis by individual facility suggests that while condemns in Basin 1 appeared to coincide with typical seasonal STB rates, the pattern of alerts for one facility may have signaled STB outbreaks in both outbreak periods.

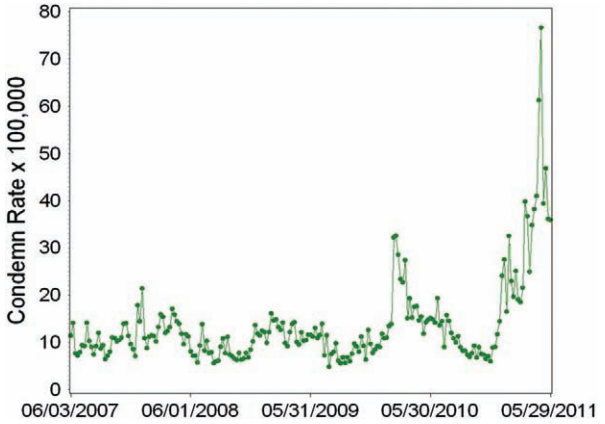

Fig. 1. Weekly swine TB condemn rates, four-year series.

Conclusions

By combining 'on-the-ground' practitioner-based information with geographically broader analysis of ADRS data, we identified an emerging disease situation involving TB lesions in swine. A preliminary epidemiological investigation suggests that likely principal risk sources are related to feed and ground water (1). Analysis of ADRS condemn data suggests that several lower Midwest slaughter facilities in addition to the affected plant used by producers involved in the investigation may have been affected by STB.

Keywords

Abattoir; surveillance; syndromic

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***Wolf Weber**
E-mail: wolf.d.weber@aphis.usda.gov

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COACTION PUBLISHING

Novel approach to hypoglycemia surveillance in an international online diabetes social network

Elissa Weitzman[1]*, Skyler Kelemen[1], Maryanne Quinn[1], Emma Eggleston[2] and Kenneth Mandl[1]

[1]Children's Hospital Boston, Boston, MA, USA; [2]Harvard Pilgrim Health Care Institute, Boston, MA USA

Objective

To measure the prevalence of hypoglycemic episodes and associated harms among participants in an international, online diabetes social network.

Introduction

Hypoglycemia is a serious sequel of diabetes treatment that is not tracked by current health surveillance efforts despite substantial related morbidity and mortality (1). We take a novel approach to hypoglycemia surveillance, engaging members of an international online diabetes social network (SN) in reporting about this issue as members of a consented, distributed public health research cohort.

Methods

We collected structured self-reported data about hypoglycemia and related harms using a software application called TuAnalyze that supports SN-mediated health research (2). Odds for harms were estimated controlling for demographics, diabetes type and health insurance.

Results

Of 2538 TuAnalyze users, 608 (24% response rate) completed two complementary surveys on hypoglycemia and diabetes care. Of these, 169 (27.8%) reported ≥1 severe low in the past 12 months. Harms were high; one in seven reported an accident or serious injury; over 40% reported high daily worry, and the frequency of reported withdrawal behaviors ranged from 20 to 50%. Experience of ≥1 past 12-month severe low was associated with added risk for each of the six harms, and for experiencing multiple harms. (Tables 1 and 2).

Conclusions

Hypoglycemia prevalence is high and exerts a considerable toll in terms of physical and social harms in this sample of predominantly type 1 or insulin-treated patients. Hypoglycemia surveillance is feasible using a novel approach that affords opportunity for bidirectional communication and tracking—capabilities important to ameliorating this problem.

Table 1. Sample demographics and disease indicators

Total sample (N = 608)	*N (%)*	*Average (median, range)*
Male	243 (40)	–
White	546 (90)	–
U.S location	523 (86)	–
Type 1 and LADA	483 (79.4)	–
Insulin user	541 (89)	–
Health insurance	560 (92.1)	–
Age (yr)	–	44.8 (46, 14–83)
Severe lows/past 12 months	–	4 (0, 0–400)
Diabetes duration (yr)	–	17.9 (15, 0–67)

Table 2. Prevalence of recent and severe hypoglycemia and associated risks for harms

	Total N (%)	*N (%) ≥1 severe event*	*N (%) 0 severe events*	*OR (95% CI) ≥1 severe event†*
Total sample	608 (100)	169 (27.8)	439 (72.2)	
Harms, including withdrawal behaviors (6):				
History of accident or injury	89 (14.7)	47 (28.1)	42 (9.6)	3.6 (2.2, 5.9)***
Worry about hypo affects daily life	254 (41.8)	107 (63.3)	147 (33.5)	3.3 (2.2, 4.9)***
Limit driving	215 (35.4)	91 (53.9)	124 (28.3)	2.6 (1.8, 3.9)***
Stay home more than would like	137 (22.5)	62 (36.7)	75 (17.1)	2.9 (1.9, 4.4)**
Avoid exercise	305 (50.2)	107 (63.3)	198 (45.1)	1.9 (1.3, 2.8)**
Avoid sex	126 (20.7)	47 (27.8)	79 (18)	1.8 (1.1, 2.7)*
Multiple adverse outcomes (≥2 of 6)	303 (49.8)	119 (70.4)	184 (41.9)	3 (2, 4.5)***

*$p < .05$ **$p < .01$ ***$p < .0001$.
†Adjusted for age, sex, race, diabetes type, health insurance

Keywords

Diabetes; hypoglycemia; surveillance; social networking

Acknowledgments

This work was supported by P01HK000016 and P01HK000088-01 from the Centers for Disease Control and Prevention (CDC).

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***Elissa Weitzman**
E-mail: elissa.weitzman@childrens.harvard.edu

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COACTION PUBLISHING

Another type of cluster monitoring: detection of groups of anomalous patient residence locations

Aaron Wendelboe[1,2]*, Howard Burkom[3], Cynthia Lucero[2] and Mark Holodniy[2]

[1]University of Oklahoma Health Sciences Center, College of Public Health, Oklahoma City, OK, USA; [2]Department of Veterans Affairs, Office of Public Health, Palo Alto, CA, USA; [3]Johns Hopkins University, Applied Physics Laboratory, Baltimore, MD, USA

Objective

To develop an algorithm to identify disease outbreaks by detecting aberrantly large proportions of patient residential zip codes outside a healthcare facility catchment area.

Introduction

The Veterans Health Administration (VHA) uses the Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE) to detect disease outbreaks and other health-related events earlier than other forms of surveillance (1). Although Veterans may use any VHA facility in the world, the strongest predictor of which healthcare facility is accessed is geographic proximity to the patient's residence. A number of outbreaks have occurred in the Veteran population when geographically separate groups convened in a single location for professional or social events. One classic example was the initial Legionnaire's disease outbreak, identified among participants at the Legionnaire's convention in Philadelphia in the late 1970s (2). Numerous events involving travel by large Veteran (and employee) populations are scheduled each year.

Methods

An H1N1 influenza outbreak was identified at a Veteran Benefits Administration (VBA)-sponsored conference in Baltimore, MD, in July 2009 in which affected VBA employees (both local and from out-of-town) sought healthcare at the VA Maryland Health Care System—Baltimore Medical Center. Using ESSENCE, daily counts of ICD-9 codes related to influenza diagnoses (as defined by VA ESSENCE influenza-like illness [ILI] syndrome group) were collected from the VHA Baltimore Medical Center from March 01, 2009, to September 12, 2009. Data included case status (as defined by ICD-9 code and chart review), date and location of visit and patients' zip code of residence. We also accessed data from the VA Planning System and Support Group to determine whether the patients' residential ZIP code fell within the Baltimore VA Medical Center's catchment area. Using SAS, a p-chart (where the denominator was the daily number of patient ILI encounters) was run to determine days during which an aberrant proportion of patients from out-of-catchment zip codes were encountered.

Results

An aberrant proportion of out-of-catchment zip code ILI encounters signaled an out-of-control process (or alert) on July 23, 2009, 2 days later than the beginning of the influenza outbreak at the facility (Fig. 1) on the date when the majority of affected participants were evaluated for flu symptoms. (The alert on July 26, 2009, was a part of this same outbreak.) Using this algorithm, there were two other days in the 7-month period during which the chart signaled that the process was out-of-control: March 21, 2009, and September 6, 2009. Investigations are being conducted to determine the nature of these other signals.

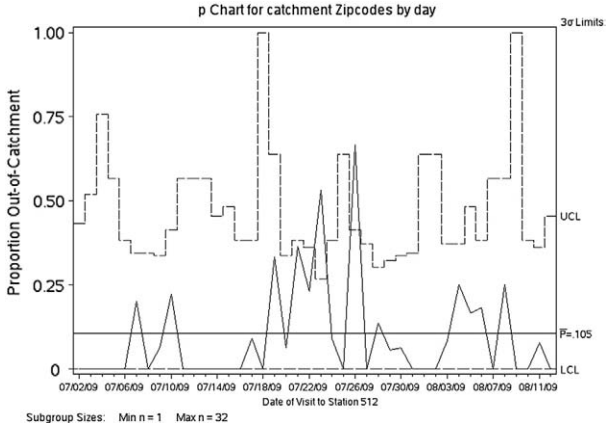

Fig. 1. ILI encounter dates of patients' whose residential zip code is out of the Baltimore VA Medical Center's catchment area. The jagged solid line exceeding the dashed line (the upper confidence limit) indicates an aberrantly large proportion of out-of-catchment events over the surveillance period.

Conclusions

Using p-charts to detect unusual clusters of patients' residential zip codes that fall outside of facilities catchment area is likely a method of detecting disease outbreaks previously not utilized. Future work includes running this algorithm in all VA Medical Centers to prospectively identify disease outbreaks involving increased proportions of patients residing outside of the medical center's catchment area.

Keywords

Surveillance; p-chart; algorithm; signal detection; outbreak

Acknowledgments

We are grateful to Gina Oda, Eugene Elbert, and Vivian Hung for their help with this project.

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*Aaron Wendelboe
E-mail: aaron-wendelboe@ouhsc.edu

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COACTION PUBLISHING

Severe influenza pneumonia surveillance: clinical and translational epidemiology

Timothy Wiemken[1–3]*, Paula Peyrani[1], Kristina Bryant[1,4], Forest Arnold[1], Raul Nakamatsu[1,5], Jennifer Simms[6], Sheryl Stockton[7], Rich Pinson[8], Colleen Jonsson[9] and Julio Ramirez[1]

[1]Division of Infectious Diseases, University of Louisville School of Medicine, Louisville, KY, USA; [2]Department of Health Promotion and Behavioral Sciences, University of Louisville School of Public Health and Information Sciences, Louisville, KY, USA; [3]University of Louisville Center for Health Hazards Preparedness, Louisville, KY, USA; [4]Kosair Children's Hospital, Louisville, KY, USA; [5]Robley Rex Veterans Affairs Medical Center, Louisville, KY, USA; [6]Spring View Hospital, Lebanon, KY, USA; [7]Trover Regional Medical Center, Madisonville, KY, USA; [8]Highlands Regional Medical Center, Prestonsburg, KY, USA; [9]University of Louisville Center for Predictive Medicine, Louisville, KY, USA

Objective

To present the development and implementation of the SIPS project, a statewide, hospital-based surveillance system for severe community-acquired pneumonia (sCAP) in Kentucky.

Introduction

The threat of epidemics due to nonhuman strains of influenza A viruses is ever present (1). Surveillance is a critical aspect of pandemic preparedness for early case detection (2). Identification of the index cases of a pandemic virus can trigger public health mitigation efforts (3). To develop an appropriate surveillance process, it is important to understand the two possibilities of pandemic evolution. A new pandemic may begin with mild cases, during which surveillance should be concentrated on work/school absenteeism and in physician offices. The other possibility begins with severe cases, characterized by sCAP, respiratory failure and ICU admission. As the syndrome of pneumonia is not reportable to health agencies for public health surveillance, a year-round, hospital-based surveillance mechanism may be an important tool for early case detection in the event of an epidemic of sCAP. To fill these gaps, we developed a statewide, hospital-based surveillance network for sCAP surveillance in Kentucky.

Methods

All acute care hospitals in Kentucky were invited to participate in the project. A case of sCAP was defined as a patient admitted to an ICU with the physician diagnosis of CAP. Upon patient identification, demographic and clinical characteristics were entered into an Internet-based data collection form. All patients had a nasopharyngeal swab sent to the University of Louisville Infectious Diseases Reference Laboratory for identification of viral pathogens. The Luminex xTAG respiratory viral panel multiplex PCR was used for viral identification. Clinical cultures were utilized to identify bacterial and fungal causes of sCAP. Statistical Process Control (SPC) charts were used to identify outbreaks. Chloropleth maps were used for spatial analysis. Each analytical mechanism was provided in real-time via the study website.

Results

Surveillance for sCAP began in December 2008, prior to the 2009 H1N1 influenza A pandemic. Six facilities representing all areas of the state, both rural and metropolitan were included. The website, www.kyflu.net was developed for study coordination. From December 1, 2008, through August 2011, 458 cases of sCAP were identified. There were multiple areas of special-cause variance on the SPC charts, though there were no unusual clusters upon spatial evaluation of the maps. The most common virus identified in patients with sCAP was rhinovirus (n = 39, 20%), followed by 2009 H1N1 influenza A virus (n = 34, 18%). These viruses were cultured in chicken eggs, genetically analyzed and further studied in mouse and ferret models to determine viral evolution and virulence mechanisms. One influenza virus was found to be hypervirulent compared to other strains.

Conclusions

The SIPS project is an ongoing effort that has thus far successfully identified patients with sCAP of viral etiology. Surveillance for sCAP is important not only for the early detection of cases in the event of a pandemic of influenza but for other etiologies as well. Furthermore, through translational research activities, we were able to identify novel strains of influenza and are working to further characterize the evolution of these viruses in our state.

Keywords

Influenza; respiratory virus; outbreak; pandemic; epidemic

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*Timothy Wiemken
E-mail: tlwiem01@louisville.edu

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COACTION PUBLISHING

Early detection of adverse drug events using the full text of letters to the editor

Chao Yang*, Jacob Simmering, Padmini Srinivasan, Linnea Polgreen and Philip Polgreen

The University of Iowa, Iowa City, IA, USA

Objective

Our objective was to explore the intuition that letters to the editor in leading medical journals contain early signals about adverse drug events. We explored this with letters in two leading journals.

Introduction

Adverse drug events (ADEs) are a significant source of morbidity and mortality. The majority of postmarketing surveillance for ADEs is passive. Information regarding ADEs is reported to the medical community in peer-reviewed journals. However, in most cases, there is significant lag in the publication of peer-reviewed articles concerning ADEs. Within medical journals, our intuition is that letters to the editor may provide the earliest reports of ADEs. They often report single case reports or a collection of cases and usually precede more formal investigations and reports.

Although these letters may contain useful and timely information, the challenge is that letters to the editor may be 'buried' inside print journals. Furthermore, they may be more difficult to find and access even when using electronic searches because unlike other published reports, there is no corresponding abstract to view. Due to the lack of an abstract, detection depends almost exclusively upon words in a title or manually applied Medical Subject Headings (MeSH). We propose that searching the full text of letters to the editor can provide a faster and perhaps more complete detection of ADEs compared to searches based on MeSH terms or titles alone.

Methods

We first identified a list of the most commonly used 179 drugs in 2008 based on the Agency for Healthcare Research and Quality compiled Medical Expenditures Survey. We then used MicroMedex, a commercial drug information service, to find a list of key publications describing ADEs for these drugs. Next, we obtained the text for the majority of letters to the editor published in *The Lancet* (6558 from 1967 to date; 82% of total) and *The New England Journal of Medicine* (3524 from 1966 to date; 75% of total). We restricted the letters to those that had the MeSH term 'adverse effect' in the indexing data. We also eliminated the letters with label 'Comment' to avoid searching letters specifically referencing a previously published paper in each journal, respectively. The resulting dataset contained 2166 letters for *The Lancet* and 1449 for *The New England Journal of Medicine*.

We then compared the results from two different search strategies. In the first, an emulation of a PubMed search, we only examined the MeSH terms and the title for the letter. Our second approach included a search of the full text of the letters in addition to the title. Using these two strategies, we were able to determine the 'earliest' letter in these two journals for a given drug/ADE pair. We compared this date against the date of the citation referenced by MicroMedex to determine which search method provided the earliest detection.

Results

Both search strategies, with and without full text, were able to find the particular drug/ADE pair mentioned in letters before the corresponding Micromedex reference. However, using full-text search outperformed title/MeSH-based search, not only based on the number of drug/ADE pairs found but also on the time of detection. The percentage of letters in the dataset that are not related to specific articles is 0.6% using title/MeSH, 2.1% using title/full-text. Furthermore, we found that MeSH terms are not always reliable. For example, some of the letters had MeSH terms like "Adverse Effect" but no mention of adverse effects in the letter. Not surprisingly, since MeSH is a controlled vocabulary, some of these terms do not appear in the full text of the letters. These findings are shown in Table 1.

Table 1. The results of two search strategies (title/mesh vs. title/full-text)

	Title/ MeSH	*Title/full-text*
No. specific drug/ADE letters found	23	77
Distinct No. drug/ADEs pairs found	10	35
Average time prior to the year cited by Micro-Medex	5.291	6.901
Standard Deviation (year)	4.846	5.291

Conclusions

Our results suggest that the full texts of the letters to the editor provide a potential stream of information regarding early warnings for ADEs. Future work will need to expand the number of journals considered and, furthermore, consider the potential for 'false positive' warnings.

Keywords

Adverse drug events; letters to the editor; signal detection

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***Chao Yang**
E-mail: chao-yang@uiowa.edu

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COACTION PUBLISHING

Analysis of zero-inflated and overdispersed time series: an application to syphilis surveillance in the United States

Ming Yang[1]*, Joseph Cavanaugh[1] and Philip Polgreen[2,3]

[1]Department of Biostatistics, College of Public Health, University of Iowa, Iowa City, IA, USA; [2]Division of Infectious Diseases, Department of Internal Medicine, Carver College of Medicine, University of Iowa, Iowa City, IA, USA; [3]Department of Epidemiology, College of Public Health, University of Iowa, Iowa City, IA, USA

Objective

The purpose of this study is to develop novel statistical methods to analyze zero-inflated and overdispersed time series consisting of count data.

Introduction

Time series data involving counts are frequently encountered in many biomedical and public health applications. For example, in disease surveillance, the occurrence of rare infections over time is often monitored by public health officials, and the time series data collected can be used for the purpose of monitoring changes in disease activity. For rare diseases with low infection rates, the observed counts typically contain a high frequency of zeros (zero-inflated), but the counts can also be very large (overdispersed) during an outbreak period (1). Failure to account for zero-inflation and overdispersion in the data may result in misleading inference and the detection of spurious associations.

Methods

Under the partial likelihood framework (2), we develop a class of regression models for zero-inflated and overdispersed count time series based on the conditional zero-inflated negative binomial (ZINB) distribution with probability mass function defined as follows:

$$f(y_t; k,\ \mu_t, \pi_t | \mathcal{F}_{t-1}) = \pi_t I(y_t = 0) + (1-\pi_t)\frac{\Gamma(k+y_t)}{\Gamma(k) y_t!}\left(\frac{k}{k+\mu_t}\right)^k \left(\frac{\mu_t}{k+\mu_t}\right)^{y_t}$$

The ZINB distribution is very general; it is a two-component mixture of the NB distribution with a point mass at zero. It reduces to the NB distribution when the zero-inflation parameter is zero and the zero-inflated Poisson (ZIP) distribution as the dispersion parameter goes to infinity.

Results

We applied the methodologies proposed above to monthly syphilis data in the United States from 1995 to 2009 (http://www.cdc.gov/mmwr/). During the study period, a high proportion of zeros and some large positive counts were observed in most of the 66 surveillance locations. Among the four candidate distributions (Poisson, NB, ZIP and ZINB), we find that the ZINB distribution is most frequently favored in terms of Akaike's information criterion (AIC) (3). In contrast, we find that the Poisson distribution is never selected for any of the surveillance locations (Table 1).

Conclusions

Although the Poisson distribution has been used widely in public health practice, its performance becomes unreliable in the presence of zero-inflation and overdispersion. The ZINB distribution is an attractive alternative to the Poisson distribution, as it provides a unified approach to model zero-inflated and overdispersed count time series in a variety of disciplines.

Table 1. Model selection results for the 66 surveillance locations

Distribution	*Poisson*	*Negative binomial*	*Zero-inflated Poisson*	*Zero-inflated negative binomial*
Frequency	0	11	6	49

Keywords

Syphilis surveillance: time series; zero-inflation

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***Ming Yang**
E-mail: ming-yang@uiowa.edu

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COACTION PUBLISHING

Using injury surveillance to assess sport- and recreation-related heat illness

Ellen Yard[1]*, Julie Gilchrist[1], Dawn Comstock[2,3], Tadesse Haileyesus[1] and Matt Murphy[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Center for Injury Research and Policy, Nationwide Children's Hospital, Columbus, OH, USA; [3]College of Public Health, The Ohio State University, Columbus, OH, USA

Objective

To examine the incidence and characteristics of heat illness during sports and recreation.

Introduction

Although heat illness is preventable, it is a leading cause of death among U.S. high school and college athletes (1). Despite this, the total burden of heat illness during sports and recreation is unknown. With over 250 million U.S. residents reporting occasional participation in sports or recreational activities (2), there is a large population at risk.

Methods

We used two national injury surveillance systems to examine heat illnesses in two different U.S. population subsets. We used the National Electronic Injury Surveillance System-All Injury Program (NEISS-AIP) to examine heat illness incidence and characteristics among sports and recreation participants of all ages from 2001 to 2009, and we used the National High School Sports-Related Injury Surveillance Study (High School RIO™) to examine heat illness incidence and characteristics among high school-aged athletes from 2005 to 2009 (Table 1).

NEISS-AIP, operated by the U.S. Consumer Product Safety Commission, monitors consumer product-related injuries treated in a nationally representative sample of 66 U.S. hospital emergency departments (EDs) (3). Trained coders enter demographics, a brief narrative and consumer product information for each injury presenting to their ED. High School RIO™, operated by the Center for Injury Research and Policy at Nationwide Children's Hospital (Columbus, OH), monitors sports injuries in a nationally representative sample of 100 high schools (4). Certified athletic trainers at participating schools report exposure and injury data electronically.

Results

Using NEISS-AIP, we calculated an estimated 5946 (95% confidence interval [CI] = 4194–7698) ED visits for sports- and recreation-related heat illnesses occurred annually from 2001 to 2009. Incidence was highest among males (72.5%) and among persons aged 15–19 years (35.6%) and occurred most commonly during football (24.7%) and exercise (20.4%). Using RIO™, we calculated an estimated 9237 (95% CI = 8357–10,116) heat illnesses resulting in time lost from participation occurred during high school sports annually from 2005 to 2009, most commonly during football (70.7%).

Conclusions

National injury surveillance systems provide a unique opportunity to examine heat illness in sports and recreational settings. NEISS-AIP and High School RIO™ demonstrate different approaches to studying this problem. Results from both analyses indicate that heat illness causes substantial morbidity among sports and recreation participants. We need to find new ways to target effective heat illness prevention messages to those at greatest risk to reduce morbidity and prevent mortality. Continued surveillance is also warranted to monitor trends and evaluate interventional activities.

Keywords

Injury; surveillance; heat illness; NEISS; RIO™

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***Ellen Yard**
E-mail: eyard@cdc.gov

Table 1. Description of sports- and recreation-related heat illness data collected by two national injury surveillance systems

System	*Reporting institutions*	*Population*	*Heat illness definition*	*Data collected*
NEISS-AIP(3)	66 nationally representative U.S. hospital EDs	Entire U.S. population	Nonfatal ED visits with a reference to heat illness (e.g., "heat exhaustion", "dehydration", etc.) in the narrative description, occurring during a sport or recreational activity	Demographics, brief narrative, consumer product information
High School RIO™ (4)	100 nationally representative U.S. high schools	High school athletes	Dehydration or heat exhaustion/stroke during a practice or competition, assessed by a medical professional, and resulted in ≥1 days of time loss from athletic activity	Exposure, demographics, illness characteristics, event characteristics

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COACTION PUBLISHING

A spatio-temporal Bayesian model for syndromic surveillance: properties and model performance

Jian Zou[1]*, Alan Karr[2], David Banks[3], Matthew Heaton[4], Gauri Datta[5], James Lynch[6] and Francisco Vera[7]

[1]Department of Mathematical Sciences, Indiana University-Purdue University Indianapolis, Indianapolis, IN, USA; [2]National Institute of Statistical Sciences, RTP, NC, USA; [3]Duke University, Durham, NC, USA; [4]National Center for Atmospheric Research, Boulder, CO, USA; [5]University of Georgia, Athens, GA, USA; [6]University of South Carolina, Columbia, SC, USA; [7]Escuela Superior Politecnica del Litoral, Guayaquil, Ecuador

Introduction

Syndromic surveillance uses syndrome (a specific collection of clinical symptoms) data that are monitored as indicators of a potential disease outbreak. Advanced surveillance systems have been implemented globally for early detection of infectious disease outbreaks and bioterrorist attacks. However, such systems are often confronted with the challenges such as (i) incorporate situation specific characteristics such as covariate information for certain diseases; (ii) accommodate the spatial and temporal dynamics of the disease; and (iii) provide analysis and visualization tools to help detect unexpected patterns. New methods that improve the overall detection capabilities of these systems while also minimizing the number of false positives can have a broad social impact.

Methods

In this paper, we propose an inference model for determining the location of outbreaks of epidemics in a network of nodes. In our setting, the network is the NC counties where the basic model incorporates spatial geographical relationships between the counties. The model is epidemiological, by choice, to process daily flu counts from the counties in order to infer when an outbreak of flu is present in a county that is distinguishable from background counts. The methodology incorporates Gaussian Markov random field (GMRF) and spatio-temporal conditional autoregressive (CAR) modeling.

Results

The methodology has some nice features including timely detection of outbreaks, robust inference to model misspecification, reasonable prediction performance as well as attractive analytical and visualization tool to assist public health authorities in risk assessment. Based on extensive simulation studies and synthetic data generated from a dynamic SIR model, we demonstrated that the model is capable of capturing outbreaks rapidly, while still limiting false positives.

Conclusions

In this paper, we have presented a new methodology that adapts the existing GMRF class of models to deal with spatio-temporal surveillance data. When the data are mainly spatial and coarsely discretized in time, simple models such as the CAR model will continue to be valuable for descriptive analysis. However, when data have a fine resolution in both the spatial and temporal dimensions, our model, which explicitly incorporates the directional nature of time by conditioning future events on past outcomes, is likely to be more insightful.

Keywords

Syndromic surveillance; spatio-temporal; Markov random field; conditional autoregressive

Acknowledgments

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***Jian Zou**
E-mail: zoujian@iupui.edu

COACTION PUBLISHING

Subsidized laboratory testing as an incentive for improved livestock disease reporting

Kathy Zurbrigg*

Veterinary Science and Policy, OMAFRA, Elora, ON, Canada

Objective

To evaluate free diagnostic testing as an incentive for compliance with a livestock disease surveillance program.

Introduction

Livestock owners normally pay the full cost of disease testing. As a result the number of laboratory submissions is dependent on the owner's perception that testing is beneficial. This decreases the likelihood of an accurate diagnosis and biases the number and type of samples received by a laboratory. Despite these limitations, laboratory data are commonly used for passive disease surveillance.

The Ontario Farm-call Surveillance Project (OFSP) analyzed disease-related farm call data supplied by livestock veterinarians. Project goals were to provide a new data source for livestock disease monitoring and to improve the quality of laboratory data. As an incentive for participation, veterinarians were not charged when diagnostic samples were sent to the Animal Health Laboratory (AHL), University of Guelph.

Methods

The OFSP veterinary clinics were a convenience sample of food-production and equine clinics in Ontario. Clinics participating in OFSP were offered two incentives: (1) free diagnostic testing at the AHL and (2) $175.00 per farm call if postmortems (PMs) were performed and farm call data were received within 10 days of the call. The first incentive was offered for the duration of the project; the second was available from October 2010 to June 15, 2011.

The average number of days from farm call completion to data submission was compared pre- and post-PM incentive.

The rate at which a veterinarian submitted samples for diagnostic testing to the AHL was calculated (total number of submissions/total number of farm calls). Only 20/28 OFSP clinics were enrolled in the study pre-PM incentive. A comparison of the number of submissions to the AHL for those clinics pre- and post-PM incentive was performed. Submissions of animals for necropsy or tissue for histology were classified as 'pathology' submissions. The proportion of livestock pathology submissions that were from the OFSP were compared to the total livestock pathology submissions pre- and postcommencement of the PM incentive. AHL reporting rates of livestock zoonotic diseases were compared pre- and post-commencement of the OFSP (total number of positive livestock zoonotic disease laboratory submissions/total number of livestock laboratory submissions).

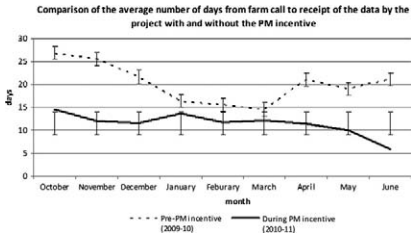

Fig. 1. A comparison of the timeliness of data before and after the start of the Post Mortem Incentive.

Results

One hundred and eight veterinarians from 28 livestock clinics contributed data to the surveillance project between April 2009 and June 2011. No clinics withdrew from the study.

Fig. 1 illustrates the timeliness of reporting before and after the PM incentive.

Veterinarians participating in OFSP submitted a sample to the AHL 11% of the time they completed a disease-related farm call. A comparison of 20 OFSP clinics revealed that 458 more cases were submitted to the AHL while those clinics were participating in the OFSP than the year prior to participation. OFSP clinics represented 19% (28/147) of the clinics submitting pathology samples during the time period the PM incentive was offered. OFSP pathology submissions represented 36% (712/1984) of the total pathology livestock submissions for the same time period. For the same period, the previous year (pre-PM incentive) OFSP pathology submissions accounted for 7.7% (141/1822) of the total pathology submissions.

The proportion of laboratory submissions from OFSP clinics positive for a zoonotic disease increased from 4.3% prior to participation in the project to 7.7% while part of the OFSP.

Conclusions

Incentives are needed to ensure adequate compliance with a surveillance program. The OFSP incentives were considered a key factor in the number of veterinarians participating in the study as well as the 0% drop out rate.

Receiving data quickly is critical when monitoring for new or emerging diseases. Animals found dead or moribund are an important group to monitor for livestock disease surveillance but producers often do not want to pay the cost of a PM. The ability to provide better client service made the incentives offered by OFSP appealing to veterinarians.

The OFSP incentives increased submissions to the laboratory, improved the laboratory data for passive surveillance and, specifically, increased zoonotic disease reporting.

Keywords

Incentives; surveillance; livestock

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***Kathy Zurbrigg**
E-mail: kathy.zurbrigg@ontario.ca

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