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Using Health Helpline Mediated Self-Swabbing as a Surveillance Tool for Influenza

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Objective
Explore the use and feasibility of self-swabbing mediated by a telephone health helpline (THHL) as a complementary tool for surveillance of influenza and other common respiratory viruses in Ontario, Canada.

Introduction
Currently, three main sources of data are used to monitor the prevalence of influenza in Ontario: Public Health Agency of Canada’s (PHAC) FluWatch, Ontario’s Acute Care Enhanced Surveillance (ACES) data and Public Health Ontario’s (PHO) traditional laboratory data. However, a limitation of these data sources is that it typically underestimates the burden of infection in populations living in remote communities and/or populations with less severe symptoms. This study describes a self-swabbing surveillance system mediated by a THHL that uses syndromic surveillance tools to recruit and monitor participants with influenza-like illness. The intent of this system is not to replace, but rather to complement other surveillance systems and clinical based testing for influenza, thereby extending the reach of surveillance through the use of self-swabbing. An additional rationale for this type of surveillance system is that it can reduce transmission of infection by limiting the number of visits to emergency departments or doctors’ offices, thereby reducing contact with the young and elderly populations, who are at most risk for infection.

Methods
Recruitment and System Operation: Participants were recruited through a THHL available to all residents of Ontario. Callers were triaged based on assessment by a registered nurse and deemed eligible to partake in the study if classified under the “referral” or “self-care” categories. Participants must also be at least 2 years old, and have one of the following symptoms: fever, cough, sore throat, or coryza. Upon agreeing to participate, participant information was collected and a self-swabbing package, including a swabbing kit, consent form, questionnaire, and description of the study with instructions for participation, was sent out the next business day. The participant completed the documentation, used the nasal swab to obtain a specimen, and returned them to the laboratory. Data was then collected and the swab was tested for influenza viruses.

Analyses and evaluation: The questionnaire data and laboratory results were used to evaluate the feasibility of the surveillance system. Evaluation included a descriptive analysis of the population captured by these methods and a basic assessment of the operational aspect of the system. Detection of respiratory viruses using the self-swabbing methodology was reported based on the molecular test results. Furthermore, the timely detection of influenza emerging in Ontario was compared to other surveillance systems that are routinely used in the province via peak comparison methods.

Results
A total of 2431 participants were successfully sent a package and 666 (27.40%) returned a package with consent, thus their samples were tested. The mean and median number of days between the time of call to the THHL and the time a package was received at the laboratory was approximately 10.4 and 8.6 days, respectively. The time between swab collection and package reception was 4.9 days on average, or a median of 4 days. Given these timelines, self-swabbing proved to be a viable method of detecting influenza and other respiratory viruses as 279 (42%) specimens tested positive for a virus by molecular methods. In terms of early detection, this surveillance system adequately captured the 2014 influenza B season in a timely manner when compared to data generated by FluWatch, ACES, and PHO’s traditional laboratory data; however, it did not necessarily detect the emergence of influenza B any earlier than alternative sources. Surveillance of influenza A by our system was also evaluated; however, the number of cases of influenza A peaked approximately two weeks after that reported by PHO’s data.

Conclusions
This study demonstrated the potential a THHL-mediated self-swabbing surveillance tool has for capturing data on a population that is not typically included in existing surveillance methods, and for the timely detection of influenza for surveillance purposes. Certain limitations of this study made for a challenging evaluation of the system. Despite these challenges, this surveillance system was able to obtain viable specimens for laboratory testing and capture seasonal patterns of influenza B in time with the aforementioned alternative surveillance systems.

Keywords
influenza; self-swabbing; surveillance; respiratory viruses; health helpline

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A Bayesian Hierarchical Model for Estimating Influenza Epidemic Severity

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Objective
To use multiple data sources of influenza epidemic severity to inform a model which can estimate and forecast severity for the current influenza epidemic season by accounting for the bias from each source.

Introduction
Timely monitoring and prediction of the trajectory of seasonal influenza epidemics allows hospitals and medical centers to prepare for, and provide better service to, patients with influenza. The CDC’s ILINet system collects data on influenza-like illnesses from over 3,300 health care providers, and uses this data to produce accurate indicators of current influenza epidemic severity. However, ILINet indicators are typically reported at a lag of 1-2 weeks. Another source of severity data, Google Flu Trends, is calculated by aggregating Google searches for certain influenza related terms. Google Flu Trends data is provided in near-real time, but is a less direct measurement of severity than ILINet indicators, and is likely to suffer from bias. We create a hierarchical model to estimate epidemic severity for the 2014 - 2015 epidemic season which incorporates current and historical data from both ILINet and Google Flu Trends, allowing our model to benefit both from the recency of Google Flu Trends data and the accuracy of ILINet data.

Methods
To forecast for the 2014 - 2015 influenza epidemic season, we provide our model with both ILINet and GFT data from previous seasons, starting with the 2004 - 2005 epidemic season, and going through the 2013 - 2014 epidemic season. Our model has a hierarchical structure, which allows ILINet and GFT data from previous seasons to inform epidemic severity prediction in the current season. ILINet data is modeled as being an unbiased but noisy estimate of the true, unknown influenza severity. GFT severity measurements, on the other hand, are influenced by external factors such as media coverage. These factors could consistently bias GFT severity estimates to over or under-estimate the true epidemic severity depending on the intensity of media influenza coverage in a season. To account for this potential bias in GFT data, we include an autoregressive error term, which allows over or under-predictions made by GFT data in one week to carry over into the next. Estimation is performed using the Bayesian statistical software Stan (http://mc-stan.org/).

Results
We also evaluated each model’s ability to forecast epidemic severity one week into the future. Figure 1 shows a comparison of the week ahead forecasting abilities of these models.

Conclusions
Combining up-to-date Google Flu Trends data with accurate ILINet data improves epidemic severity forecasting ability significantly. Additional data sources, such as data from Twitter or Wikipedia, could likely further benefit forecasting.

Keywords
Influenza; Google; Model; Bayesian; Hierarchical

References

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CDCPlot: an Application for Viewing Weekly CDC MMWR Disease Count Data

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Objective
To demonstrate the current features and functionality of the CDCPlot application, and to introduce potential new features of the application.

Introduction
The CDC provides data on incidences of diseases on its website (https://data.cdc.gov/). Data is available at national, regional, and state levels, and is uploaded to the CDC’s website on a weekly basis. The CDCPlot web application (available at https://michaud.shinyapps.io/CDCPlot/), built using the Shiny package in R, provides a quick and user-friendly method of visualizing this data. Users are able to select timeframes, locations, and diseases which they wish to view, and plots are produced. There is an optional alert threshold, which will alert users when a disease increases significantly from one week to the next. In addition, CDCPlot provides visualizations of CDC data on Pneumonia and Influenza mortality.

Methods
An integral feature of CDCPlot is automated weekly updating. Every Thursday, a script is run which scrapes data for individual diseases from the https://data.cdc.gov/ website. This individual disease data is reformatted and combined into a single data file which contains counts for all diseases, across all locations. For each disease and location, we compute alert thresholds, and set alerts when the weekly disease counts surpass these thresholds. Alert thresholds are calculated using a moving average technique.

The Shiny R package lets us create menus which allow users to specify diseases, locations, and time ranges to plot. Data can be plotted as weekly counts or cumulative counts, with the option to overlay multiple year’s worth of data for comparison. Plots are made using the ggplot2 R package. Source code for the app is available at https://github.com/NLMichaud/WeeklyCDCPlot.

The app can also be run locally from within R by a call to: runGitHub('NLMichaud/WeeklyCDCPlot')

Results
CDCPlot can be used to quickly compare disease counts across locations and time periods, simplifying the process of obtaining and viewing data. The different geographical scales that the app provides can also be used to easily identify specific locations that are giving rise to high disease counts. For example, looking at Legionellosis data for the whole country shows a spike in cases in mid-August of 2015. Refining our plots to look at individual regions shows that most of these cases came from the Mid-Atlantic region. Refining further still to look at all states and locations within the Mid-Atlantic region reveals a large spike in cases in New York City, which was experiencing an outbreak of Legionellosis at that time.

Conclusions
Potential future additions to the app include:
• Tables displaying data counts for user-selected diseases and time ranges.
• Additional methods for calculating alert thresholds.
• Maps displaying geographical distributions of disease counts.

Keywords
CDC; Disease; Visualization

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Using Laboratory Data to Aid Early Warning in Prospective Influenza Mortality Surveillance

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Objective
To demonstrate use of routine laboratory-confirmed influenza surveillance data to forecast predicted influenza-attributable deaths during the current influenza season. We also assessed whether including information on influenza type produced better surveillance forecasts.

Introduction
Several countries prospectively monitor influenza-attributable mortality using a variation of the Serfling seasonal time series model that uses sinusoidal terms for seasonality.1-4 Typically, a seasonal model from previous years is used to forecast current expected mortality. Using laboratory surveillance time series data in the model may enhance interpretation of the surveillance information.

Methods
We fit a Serfling-type, robust linear regression, time series model5 to weekly, all-age counts of influenza and pneumonia deaths for Australia, 2007-2011. Weekly laboratory-confirmed influenza counts were included as covariates; one model using total influenza was compared with a model including influenza type A and B. The two model forecasts of weekly deaths during 2012 were compared against observed deaths using root mean squared error (RMSE). An indicator variable was used to adjust for inflated testing during the 2009 pandemic year and laboratory data was lagged by two weeks.

Results
Both models provided a reasonable forecast for 2012 (Figures 1 and 2). RMSE for the 2012 forecasts were 12.08 and 9.37, for the total influenza and type A and B models, respectively; the influenza type A and B model had a better fit. The total influenza model predicted that an increase of 100 total influenza notifications in a week was associated with an increase of 0.4 (95%CI: 0.02-0.9) deaths two weeks later. The influenza type A and B model predicted that an increase of 100 type A notifications in a week was associated with an increase of 1.2 (95%CI: 0.7-1.8) deaths two weeks later. However, parameter estimate for influenza type B was negative.

Conclusions
We demonstrated a laboratory data-based time series model that may improve prospective mortality surveillance to assess the current season’s influenza impact. The model would allow week to week forecast of expected deaths as new laboratory data is received. Also, the observed deaths could be compared with the forecast influenza-attributable deaths and if the observed deaths were higher than the forecast by a threshold amount, then we could signal a more virulent influenza strain or a more susceptible population than expected. Some statistical challenges remain.

Keywords
influenza; surveillance; statistical models; mortality

Acknowledgments
Data were provided by the Australian Institute of Health and Welfare and the Australian Department of Health.

References

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Surveillance Systems that Include Deprivation Indices & Social Determinants of Health

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Objective
This roundtable will provide a hands-on workshop to learn about three surveillance systems developed and used by the Emergency Department Syndromic Surveillance Team at KFL&A Public Health. It will be an opportunity to address issues relevant to syndromic surveillance including: equity, emergency response, health preparedness, and health systems management. Additionally, participants will be able to apply new knowledge on improving health equity, and its relationship to social determinants of health, in their own jurisdictions.

Introduction
In 2012, Canada and other World Health Organization Member States endorsed the Rio Political Declaration on Social Determinants of Health, a global commitment to address health inequities by acting on the social, economic, environmental, and other factors that shape health. The Public Health Informatics team at KFL&A Public Health works on various surveillance projects to better support vulnerable populations, and prepare for emergency situations.

Description
The facilitators will present three of the surveillance tools used at KFL&A Public Health: Public Health Information Management System (PHIMS), Social Determinants of Health (SDOH) Mapper, and South Eastern Health Integrated Information Portal (SHIIP). The goals of the facilitators are: to teach participants to use these tools and apply them to their own jurisdictions, and to achieve high-quality outcomes for syndromic surveillance and emergency response systems so as to improve health equity.

PHIMS aims to enable the visualization and spatial analysis of environmental data with underlying population based indicators. PHIMS consists of layers of environmental information across Ontario and allows users to view maps demonstrating environmental or demographic data as they apply to specific geographic areas. This is useful for observing where environmental events are occurring, detecting potential emergency situations, and identifying areas with vulnerable populations.

SDOH Mapper allows users to customize maps demonstrating social determinants of health as they apply to specific geographic areas within the province of Ontario, and visualize graphs with access to seven layers related to the marginalization and deprivation levels for specified populations. This is useful for observing trends in marginalization and deprivation across dissemination areas in Ontario, and for examining health inequities in an area over time.

SHIIP is a portal-based technology solution that enhances individual patient care while providing real-time feedback and summarized data to help plan care. The primary objective of SHIIP is to develop an Integrated Portal with core functionalities that will facilitate the sharing of information and enable person-centred care coordination. SHIIP is designed to identify and assist in the delivery of care for complex/high needs patients, and will facilitate reporting, performance monitoring and quality improvement efforts.

Audience Engagement
The facilitators will provide demonstrations of the three surveillance tools (PHIMS, SHIIP, and the SDOH Mapper) and will teach participants how to use the tools and apply them to their own jurisdictions. Participants will be given access to the PHIMS and the SDOH Mapper tools at the workshop so that they may take part in interactive demonstrations. Each tool will be presented for 20 minutes, after which participants will be asked to take part in an open discussion and to comment on benefits and potential improvements for each tool. Participants may also ask questions regarding the use and/or application of each tool at this time. Participants will be required to bring a laptop with a wireless connection and Google Chrome so that they can access the web-based tools. The end result of the roundtable will be a list of functionality and enhancements requirements to be considered by KFL&A’s Syndromic Surveillance Team, as well as having promoted surveillance and response systems that include the use of deprivation indices and social determinants of health to stakeholders, in hopes of improving health equity.

Keywords
equity; GIS; maps; deprivation; marginalization

* E-mail:
Tracking Trends in Marginalization and Deprivation Across Ontario with SDOH Mapper

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**Objective**

To describe how the Social Determinants of Health (SDOH) Mapper is used by KFL&A Public Health to enhance real-time situational awareness of vulnerable populations across Ontario by facilitating the inclusion of information relating to marginalization and deprivation indices.

**Introduction**

Geographic Information System (GIS) technology provides visual tools, through the creation of computerized maps, graphs, and tables of geographic data, which can assist with problem solving and inform decision-making. One of the GIS tools being developed by KFL&A Public Health is the Social Determinants of Health (SDOH) Mapper. The SDOH Mapper consists of layers of information related to deprivation and marginalization indices across Ontario. The SDOH Mapper facilitates the inclusion of information related to vulnerable populations with the use of both age and social determinants of health data into the GIS portal. This is useful for observing trends in marginalization and deprivation across dissemination areas in Ontario, and for examining health inequities in an area over time. The SDOH mapper will, in this way, improve knowledge transmission on the effects of poverty and marginalization on outcomes.

**Methods**

The SDOH Mapper allows users to customize maps demonstrating social determinants of health as they apply to specific geographic areas within the province of Ontario. The tool allows the user to visualize graphs with access to seven layers related to the marginalization and deprivation levels for a specified population so that they may better understand the health outcomes related to poverty, and thereby make informed decisions relating to health equity.

Deprivation layers are derived from the Deprivation Index of Health developed by the Quebec Public Health Institute (INSPQ). The deprivation social and material deprivation, as well as material and social deprivation combined. Marginalization data is obtained from the Ontario Marginalization Index (ON-Marg) developed by the Centre for Research on Inner City Health. The marginalization layers include residential instability, material deprivation, dependency, and ethnic concentration, which are derived from 18 indicators reflecting inequality and marginalization in Canada from both the 2001 and 2006 Census of Canada.

The SDOH Mapper encompasses a number of different functions and tools. Users can choose from several basemaps that identify different geographic features, such as topography, streets, or public venues, to best meet their needs. Users can apply seven deprivation and marginalization layers to the selected basemap, which allows for the appropriate visualization of social determinants of health as they apply to a specific geographic area. A legend is displayed that identifies the colour-coded quintiles for the marginalization and deprivation layers. Using the population summary tool, users are able to visualize graphs demonstrating the marginalization and deprivation layers for specific populations. Users can also measure the distance between two locations, as well as the perimeter and area of specified geographic locations using the draw and measure function.

**Conclusions**

The Public Health Informatics Team at KFL&A Public Health is working to develop, in an ongoing systematic manner, a single access point to the GIS portal that will visualize multiple environmental and population based data sets in real-time. The single GIS portal will include the SDOH Mapper along with two other GIS applications developed by KFL&A Public Health: the Public Health Information Management System (PHIMS) and the Tobacco Module. By providing available real-time data from multiple partners into the GIS portal, the Public Health Informatics team intends to assist with identifying health events earlier than traditional public health methods. Including the SDOH Mapper in the GIS portal provides an important social determinants of health lens through which environmental data, underlying population based indicators, and health events of interest can be examined and visualized, to provide users with an understanding of the effects of poverty on health outcomes.

**Keywords**

poverty; marginalization; deprivation; map; GIS

E-mail:
Real-Time Surveillance of Environmental and Demographic Data in Ontario with PHIMS

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Objective
To describe how the Public Health Information Management System (PHIMS) tool is used by KFL&A Public Health to enhance real-time situational awareness and assist with evidence informed decision-making to help protect the health of the population.

Introduction
Geographic Information System (GIS) applications are increasingly being used for public health purposes. GIS technology provides visual tools – through the creation of computerized maps, graphs, and tables of geographic data – that can assist with problem solving and inform decision-making. PHIMS aims to enable visualization and spatial analysis of environmental data with underlying population based indicators. PHIMS displays many layers of environmental information across Ontario, and users can view maps demonstrating environmental or demographic data as they apply to specific geographic areas. This is useful for observing where environmental events are occurring, detecting potential emergency situations, and identifying areas with vulnerable populations. By displaying available, real-time, environmental data from multiple partners through PHIMS, public health events can be identified earlier to better prevent, prepare for, and respond to emergencies.

Methods
PHIMS collects and compiles environmental and demographic data, and uses web-based mapping applications, spatial analytic functionality, and third party libraries to achieve map visualization of the information collected. The data collected by PHIMS is derived from various sources. Some of these sources include: Statistics Canada, Environment Canada, Ministry of the Environment, U.S Geological Survey, Ministry of Natural Resources, Canadian Nuclear Safety Commission, the Ontario Marginalization Index, and Standard Public Health Service data (e.g. Tap into Kingston, Cool Down and Warm Up Centres, Immunization Sites, etc.).

PHIMS encompasses several tools and functions that can be accessed through a web-based user interface. PHIMS users can choose from several basemaps to visualize their map with different geographic features. Users have the ability to apply demographic layers related to age, deprivation, and marginalization to the selected basemap, which allows for colour-coded visualization of the social determinants of health as they apply to different geographic locations. These options enable users to easily view where the most vulnerable populations reside, which will help prepare and prioritize resources in the event of a public health emergency. PHIMS also enables map visualization of real-time environmental conditions, because environmental layers related to weather radar data, weather conditions, stream gauges, and heat information can also be added to the basemap. PHIMS includes several layers which visualize other pertinent public health data, such as: forest fires, wildfire smoke forecasts, well water uranium levels, nuclear reactor locations, earthquake information, and various factors relating to the Air Quality Index, wind strength and direction, as well as plume dispersion of pollutants and toxins.

Conclusions
Having a GIS tool, such as PHIMS, to visualize environmental and population based data in real-time on virtual maps, facilitates identification of emergencies earlier than through traditional public health methods. PHIMS, therefore, enhances public health situational awareness to better predict and prepare for extreme weather events and other environmental emergencies. Additionally, PHIMS can provide insight into where vulnerable populations are located, so that resources can be properly allocated in the case of an emergency.

Keywords
GIS; map; environmental; geographic; demographic

* E-mail:
Facilitating the Sharing of Patient Information Between Health Care Providers

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Objective
To describe how the South Eastern Integrated Information Portal (SHIIP) will support the Health Links program with the delivery of care for patients, by facilitating reporting, performance monitoring and quality improvement efforts. The portal-based technology that SHIIP uses to integrate all of a patient’s clinical care information into summarized data and to provide real-time feedback will also be explained.

Introduction
In the current state of the health care system there is uneven access to primary care, and too many people struggling to navigate the system are receiving care in the hospital for issues that would be better dealt with in the community, and then are being readmitted to the hospital only days after leaving. To address these issues and improve efficient continuum of care, the Health Links program provides a new model of care at the clinical level in Ontario. In this model all of the patient’s health service providers in the community, including primary care, hospital, and community care, work together to create a coordinated care plan for the patient. The initial focus of Health Links is on high-cost users.

Health Links, and primary care as a whole, require comprehensive data analysis to effectively support patients and providers. SHIIP is a portal-based technology solution that enhances individual patient care while providing real-time feedback and summarized data to help plan care. The primary objective of SHIIP is to develop an Integrated Portal with core functionalities that will facilitate the sharing of information and enable person-centred care coordination. SHIIP aims to assist the success of Health Links by providing consistent maintenance and sharing of patient records, timely communication and collaboration between a patient’s multiple health care providers, and removing physical barriers through the virtualization of care processes. SHIIP is designed to identify and assist in the delivery of care for complex/high needs patients, and will facilitate reporting, performance monitoring and quality improvement efforts. Some of the anticipated benefits of SHIIP include: enhanced patient experience, reduced workflow duplication, improved access to information at point of care, more efficient clinical documentation, and improved health outcomes. Ultimately, SHIIP helps to improve access and quality of healthcare, and consequently health equity, especially for complex/high-needs patients.

Methods
SHIIP provides the technology to enable collaborative, multi-agency care processes. The SHIIP system collects patient demographic and clinical data from hospital databases. Most of the data is captured from its sources in real-time or near real-time, with an emphasis on unidirectional flow of information from hospitals to primary care providers. Through this process, primary care providers are supplied with timely access to various clinical data. Algorithms developed in the system use the information collected to identify complex/high needs patients. SHIIP also uses the collected data to notify, in real-time, primary care providers, Health Links coordinators, and other health care providers of patient encounters and transitions, and enables tracking of patients within the health system. In addition, as more data becomes available after patient discharge, the complex patient identification algorithms are updated to continuously enrich the patient’s profile. Expansion of SHIIP to additional health care providers is scheduled for future phases.

In order for end-users to access the information collected, SHIIP has a single centralized web interface for all primary care providers in the SELHN. The web-based graphical user interface allows primary care providers to view their patients’ Emergency Department, Acute Inpatient, and Outpatient clinic visits and related information. The interface highlights key patient characteristics useful to primary care providers, such as: current admissions, visit history, chief complaints, complex/high needs flags, interventions, patient flow and other risk factors. This functionality enhances awareness of patient needs and improves communication among different health care providers to enable better care coordination planning and more efficient delivery of health care.

Results
SHIIP is currently in use in the SELHN (a population of approximately 500,000 people), with an evaluation anticipated in 2 years.

Conclusions
The use of SHIIP will improve the access to and quality of care, especially for complex/high-needs patients. These improvements, which will enable person-centered care coordination, will be achieved through the consistent maintenance and sharing of patient records between health care providers.

Keywords
portal; primary care; real-time

E-mail:

* E-mail:
Ensuring the Week Goes Smoothly - Improving Daily Surveillance Visualization

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Objective
To develop smoothing techniques for daily syndromic surveillance data that allow for the easier identification of trends and unusual activity independent of day of the week and holiday effects.

Introduction
Real-time syndromic surveillance requires daily surveillance of a range of health data sources. Most real-time data sources from health care systems exhibit large day of the week fluctuations as service provision and patient behaviour varies by day of the week. Regular day of the week effects are further complicated by the occurrence of public holidays (usually 8 per year in England), which can limit the availability of certain services and affect patient behaviour. Simple seven day moving averages fail to provide a smoothed trend around public holidays and can lead to false alarms or potentially delays in detection of outbreaks.

Methods
Data were used from four national syndromic surveillance systems (a non-emergency medical number, emergency department records, and information from family doctor in hours and unscheduled care consultations) coordinated by Public Health England. Day of the week effects were modelled in the absence of public holidays by calculating the percentage of a week’s activity that occurs on each day of the week for a range of different syndromic indicators and syndromic surveillance systems. Simple statistical t-tests were used to check for the significance of differences between days of the week.

Syndromic data were examined to test how public holidays impacted on day of the week effects. Days immediately preceding and following holidays were also examined to identify any significant changes. Differences between public holidays based on the time of year and the number of holidays within a single year were also examined.

Smoothing techniques for different syndromic systems were developed to remove artificial spikes around public holidays in simple seven day moving averages.

Results
The impact of day of the week effects were found across all syndromic surveillance systems. Unsurprisingly GP in hours data reported very little activity at weekends and on holidays, whilst GP unscheduled care and telephone help line data activity was roughly double at weekends and holidays. Day of the week effects were much less clear in emergency department attendances but significant differences were still demonstrable.

Public holiday activity was similar to weekend activity in most cases, although activity on 25th December, Christmas day was considerably less than other holidays. Evidence was seen both of increased activity immediately prior to public holidays and on the first working day after a public holiday.

Seven day moving averages that are adjusted for bank holidays

Conclusions
Improved understanding of day of the week and public holiday effects enables improved modelling of baselines used in statistical detection algorithms, for instance 25th December should not be treated as having the same impact as other public holidays. Future work will also consider condition-specific differences where the case mix varies by day of the week and during holidays.

These improved smoothing techniques have enabled improved data visualization tools, enabling investigators to easily identify unusual activity during daily surveillance.

Example of improved smoothing for daily rates of Herpes Zoster consultations.

Keywords
Surveillance; visualisation; smoothing

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Using Scenarios and Simulations to Validate Syndromic Surveillance Systems

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Objective
To devise a methodology for validating the effectiveness of syndromic surveillance systems across a range of public health scenarios, even in the absence of historical example datasets.

Introduction
Whilst the sensitivity and specificity of traditional laboratory-based surveillance can be readily estimated, the situation is less clear cut for syndromic surveillance. Syndromic surveillance indicators based upon presenting symptoms, chief complaints or preliminary diagnoses are designed to provide public health systems with support to detect multiple potential threats to public health. There is however, no gold standard list of all the possible ‘events’ that should have been detected. This is especially true in emergency response where systems are designed to detect possible events for which there is no directly comparable historical precedent.

Methods
A scenario template specification was created to identify the information needed to validate syndromic systems. In order to estimate the number of extra cases presenting to syndromic systems two types of information were required; a model for the numbers of people affected each day, and a series of parameter estimates to determine if those affected would be captured by the surveillance system.

Results
Scenario templates enabled the collection of the relevant information and estimates for each scenario, using previous research, historical examples and public health expert knowledge. A number of parameters were identified as being required, including: the number of people who become symptomatic, the proportion of these who would seek health care, the population coverage of syndromic systems and the proportion of patients with a diagnosis linked to a syndromic indicator (see figure).

Conclusions
The scenario approach has been combined with simulations to evaluate existing detection algorithms. The approach of identifying key parameters for estimation enables uncertainty to be quantified and combined to give a joint inference for the probability of detection based on both random noise and uncertainty due to modelling and parameter estimation. Scenarios can be easily modified to identify how changes in any aspect of the scenario or the syndromic system would affect detection rates.

Keywords
Simulation; Syndromic surveillance; Scenarios

Acknowledgments
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ISDS 2015 Conference Abstracts

The Burden of Seasonal Respiratory Pathogens on a New National Telehealth System

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Objective
We compared weekly laboratory reports for a number of seasonal respiratory pathogens with telehealth calls (NHS 111) to assess the burden of seasonal pathogens on this syndromic surveillance system and investigate any potential for providing additional early warning of seasonal outbreaks.

Introduction
Seasonal rises in respiratory illnesses are a major burden on primary care services. Public Health England (PHE), in collaboration with NHS 111, coordinate a national surveillance system based upon the daily calls received at the NHS telehealth service. Daily calls are categorized according to the clinical ‘pathway’ used by the call handler to assess the presenting complaints of the caller e.g. cold/flu, diarrhoea, rash.

Methods
Multiple linear regression models were used to identify significant contributions from respiratory pathogens to seasonal variation in NHS 111 calls for respiratory symptoms, including cold/flu, cough, difficulty breathing and sore throat. Children under 5, aged 5-14 and adults 65+ were examined separately and time lags of up to four weeks introduced in the models to investigate any potential early warning provided.

Results
Respiratory pathogens explained over 47% of the variation in calls for cold/flu, cough and difficulty breathing. The most sensitive signal for influenza virus was NHS 111 cold/flu calls; whilst for RSV the most sensitive signal was cough calls. The models illustrated that NHS 111 calls for cold/flu and cough peaked a week before the specimen date of laboratory reports for RSV and influenza.

Conclusions
Daily surveillance of NHS 111 telephone calls can provide early warning of seasonal rises in influenza and RSV compared with traditional laboratory surveillance methods.

Selected regression models

<table>
<thead>
<tr>
<th>Syndrome</th>
<th>Cold/Flu</th>
<th>Cough</th>
<th>Difficulty breathing/Sore throat</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>56.7</td>
<td>56.7</td>
<td>56.7</td>
</tr>
<tr>
<td>&lt;5 140-64 All</td>
<td>56.7</td>
<td>56.7</td>
<td>56.7</td>
</tr>
<tr>
<td>Adjusted R square (%)</td>
<td>75.5</td>
<td>75.5</td>
<td>75.5</td>
</tr>
<tr>
<td>Percentage of calls due to significantly correlated pathogen</td>
<td>75.5</td>
<td>75.5</td>
<td>75.5</td>
</tr>
<tr>
<td>Coronavirus</td>
<td>8</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>Human metapneumovirus (HMPV)</td>
<td>6</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>Influenza A</td>
<td>14</td>
<td>15</td>
<td>24</td>
</tr>
<tr>
<td>Influenza B</td>
<td>7</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>Parainfluenza</td>
<td>12</td>
<td>13</td>
<td>8</td>
</tr>
<tr>
<td>Respiratory syncytial virus (RSV)</td>
<td>12</td>
<td>15</td>
<td>24</td>
</tr>
<tr>
<td>Rhihovirus</td>
<td>18</td>
<td>18</td>
<td>18</td>
</tr>
<tr>
<td>Invasive streptococcus pneumoniae</td>
<td>5</td>
<td>5</td>
<td>5</td>
</tr>
</tbody>
</table>

Where significant positive correlations with pathogens were found the estimated burden of calls due to the pathogen are shown (Sept 2013 - July 2015).

Keywords
Syndromic surveillance; Respiratory; Regression

Acknowledgments
The authors would like to acknowledge support from: NHS 111 and HSCIC. Also the help of all the ReSST team, including Sue Smith, Paul Loveridge, Helen Hughes and Leandro Carrilho. RAM, AJE and GES receive support from the National Institute for Health Research Health Protection Research Unit in Emergency Preparedness and Response. The views expressed are those of the authors and not necessarily those of the NHS, the NIHR, the Department of Health or Public Health England.

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Identifying Depression-Related Tweets from Twitter for Public Health Monitoring

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Objective
We aim to develop an annotation scheme and corpus of depression-related tweets to serve as a test-bed for the development of natural language processing algorithms capable of automatically identifying depression-related symptoms from Twitter feeds.

Introduction
Major depressive disorder has a lifetime prevalence of 16.6% in the United States. Social media platforms – e.g. Twitter, Facebook, Reddit – are potential resources for better understanding and monitoring population-level mental health status over time. Based on DSM-5 [1] diagnostic criteria, our research aims to develop a natural language processing-based system for monitoring major depressive disorder at the population-level using public social media data.

Methods
In this pilot study, three annotators - two psychology undergraduates (A1, A2) and a postdoctoral biomedical informatics researcher (A3) - annotated 900 tweets using a linguistic annotation scheme based on DSM-5 depression criteria (e.g. anhedonia – “I don’t enjoy singing anymore”) [2]. We report agreement between annotator pairs computing F-score, a surrogate for kappa. Finally, we trained and tested three machine learning classifiers – support vector machine, naïve bayes, and decision tree – for predicting two depression-related classes: 1) whether a tweet represents clinical evidence of depression or not and 2) if the tweet is depression-related, whether it is classed as low mood, fatigue or loss of energy, or problems with social environment. We trained and tested each classifier using the Weka toolkit (v.3.6.8) with 10-fold cross validation using unigram features, and then reported classifier performance compared against 884 adjudicated tweets with sensitivity and positive predictive value.

Results
We observed high agreement between annotator pairs: A1/A2: 81%, A1/A3: 76%, and A2/A3: 78%. Of the 884 adjudicated tweets, the majority of tweets represented no clinical evidence of depression (n=635; 72%) then clinical evidence of depression (n=249; 28%). The skewed distribution of the most frequent 3 clinical evidence of depression symptoms/stressors ranged from low mood (n=114; 13%), fatigue or loss of energy (n=51; 6%), and problems with social environment (n=36; 4%). Overall, we observed comparable sensitivities and positive predictive values among classifiers for discerning whether a tweet represented clinical evidence of depression or not (Table 1). No clinical evidence of depression and fatigue or loss of energy can be more accurately identified than low mood, problems with social environment, and other types of clinical evidence of depression by all three classifiers. No one classifier performs with both superior sensitivity and positive predictive value for any one symptom/stressor, suggesting that different approaches may be necessary for reliable classification.

Conclusions
Automatically identifying depression-tweets with a moderate degree of accuracy is feasible. We are actively improving our training models leveraging a corpus of ~10,000 tweets, expanding symptoms/stressors being detected, and experimenting with richer features for symptom/stressor detection (e.g. gender, age).

Table 1. Classification performance using unigrams. SVM=Support Vector Machine; NB=Naïve Bayes; DT=Decision Tree; Sens=sensitivity; PPV=positive predictive value

<table>
<thead>
<tr>
<th></th>
<th>SVM</th>
<th>NB</th>
<th>DT</th>
</tr>
</thead>
<tbody>
<tr>
<td>clinical evidence of depression or not</td>
<td>Sens</td>
<td>PPV</td>
<td>Sens</td>
</tr>
<tr>
<td>no clinical evidence of depression</td>
<td>75</td>
<td>74</td>
<td>75</td>
</tr>
<tr>
<td>clinical evidence of depression</td>
<td>84</td>
<td>81</td>
<td>83</td>
</tr>
<tr>
<td>low mood</td>
<td>51</td>
<td>56</td>
<td>56</td>
</tr>
<tr>
<td>fatigue or loss of energy</td>
<td>33</td>
<td>41</td>
<td>37</td>
</tr>
<tr>
<td>problems with social environment</td>
<td>88</td>
<td>73</td>
<td>84</td>
</tr>
</tbody>
</table>

Keywords
social media; mental health; Twitter; public health; natural language processing

Acknowledgments
This work was funded by a grant from the National Library of Medicine (R00LM011393) and was granted an exemption from review by the University of Utah Institutional Review Board (IRB 00076188).

References

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Socio-Demographic Inequalities in HIV Testing and Prevalence Among Older Adults in Rural Tanzania, 2013

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Objective
This study aimed to estimate socio-demographic inequalities in HIV testing and prevalence among adults aged 50+ years, living in Ifakara town, Tanzania, in 2013

Introduction
Like in other African countries, most HIV research in Tanzania focuses on adults 15-49 years, ignoring persons aged 50 years and above. In Tanzania, the HIV testing rate (ever tested) for 15 - 49 year olds has increased from 37% to 62% for women and 27% to 47% for men between 2008 and 2012. Limited data is available on HIV testing and prevalence among older adults specifically. Some studies in Sub-Saharan Africa have, however, reported a high HIV prevalence among older people.

Methods
This is a cross-sectional study using data from the baseline measurement of the Ifakara MZIMA cohort study conducted in 2012/13. Consenting participants were interviewed and tested for HIV. Information on prior testing behaviour, age, marital status, occupation, gender, ethnicity, religion, education (PROGRESS framework indicators) was retrieved from the interviewer administered questionnaires. Multivariable logistic regression analysis was used to establish associations between HIV testing and prevalence with the socio-demographic indicators.

Results
Among the 1,643 adults 50+ years included in the study, HIV prevalence and the HIV testing rate (ever tested) were 6% and 11.4% respectively. Multivariable analysis showed that the HIV testing rate was lower for older people (OR=0.19 (95%CI 0.09-0.41 for 75+ versus 50-54); those separated/divorced/widowed had higher odds of testing than those married (OR=1.46; 1.02-2.10); and “other Christians” had a higher odds than Muslims (OR=1.95; 1.06-3.58). With respect to HIV prevalence, it is higher for older people (OR=0.27; 0.11-0.66 for 75+ versus 50-54); and Catholics have a lower odds compared to Muslims (OR=0.54; 0.34-0.85).

Conclusions
These results are valuable as they provide insight into the sociodemographic inequalities among older adults. The high HIV prevalence among this group and the low HIV testing behaviour call for more efforts on HIV prevention, treatment and care. Also the older adults should be included in the national surveillance systems like DHS and THMIS as they are also the HIV risk population. Furthermore, the government should establish elder friendly services and strengthening the capacity of the health system to deliver quality services for HIV and other diseases in the country. Additionally, the findings of this study also warrant further research on the HIV prevalence and testing behaviour of older adults, including studies on the sexual behaviour of older adults.

Keywords
HIV; Older adults; Testing; prevalence; social economic inequalities

Acknowledgments
This study was supported by health information systems grant from Global Fund round 9; the author would like to acknowledge the support from the Ministry of Health and Social Welfare (MoHSW), Kilombero district, IHI staff, and the local community of Ifakara.

References

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A Timeliness Study of Disease Surveillance Data Post ELR Implementation in Houston

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Objective
Review 5 years of surveillance data post electronic lab reporting (ELR) implementation and 8 years of data prior to ELR, to evaluate timeliness and completeness of disease surveillance.

Introduction
Since 2009, Houston Health Department (HHD) uses an electronic disease surveillance system (Maven) to receive ELRs from reporting facilities in the Houston jurisdiction. Currently, two large hospital systems, a blood bank, two large commercial labs, and two public health labs are sending ELRs to Maven. The overall percentage of disease reports received via ELR was over 50%. We hypothesize that the implementation of ELR has improved the timeliness and completeness of disease surveillance.

Methods
The data are from two sources, Maven and Casefile, Maven’s predecessor. Nearly half of disease reports in Maven are manually entered, and thus we group reports in three groups: Casefile (all manually entered cases 2000-2008), Interactive (manually entered cases in Maven 2009-2014) and Batch (cases in Maven automatically populated by ELRs 2009-2014). We select campylobacter infection, Hepatitis A infection, legionellosis, bacterial meningitis and salmonellosis to represent reportable conditions with different reporting priorities. Variables were selected to evaluate the timeliness and completeness of case reporting and investigation. Variables were selected for patient demographics.

For case reporting, the timeliness is evaluated using the difference between onset date and reporting date, whereas case investigation is evaluated only for reportable (confirmed or probable) cases by the difference between reporting date and investigation close date. For each selected variable, the completeness is evaluated by the percentage of cases without missing observations.

Results
The annual case volume increased substantially post the ELR implementation. Prior to ELR, on average the HHD received 1167 cases per year, and the number increased to 2797 cases per year post-ELR. After ELR implementation, the percentage of disease reports received via ELR increased rapidly by year, and in 2014 the percentage of ELR was around 70% (chart1):

Post ELR, the number of reportable cases conditions also substantially increased. Pre ELR, on average 400 reportable cases per year were reported to HHD, whereas post-ELR approximately 700 reportable cases per year were reported to HHD (chart1).

In terms of timeliness of case reporting, on average, Batch showed improvement over Interactive cases (Kruskal-Wallis chi-squared= 357.7, p-value < 0.01) and over cases in Casefile (24.4, p<0.01) (Table1). By comparing Interactive cases with cases in Casefile, Interactive cases were more complete on reporting variables, and reported in more timely manner than the cases in Casefile (76.0, p<0.01). Moreover, the overall differences were also statistically significant (405.9, p<0.01):

Conclusions
Post the ELR implementation the annual number of cases (including reportable cases) in Houston jurisdiction increased substantially (chart1); prior to the ELR it took longer to receive a case report, and the use of electronic disease surveillance system and the implementation of ELR improved the Houston disease surveillance system capacity of early case detection (table1); however, post ELR implementation, probably due to the increase in case volume, it took longer to complete a case investigation (table2); moreover, for patient information, no substantial differences were found between cases pre and post ELR implementation, but cases populated by ELRs were less complete with case reporting information (table3).

Keywords
Disease surveillance; electronic lab reporting; timeliness; Completeness

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Correlation Between Influenza-Like Illness Reported by ILINet and NSSP, Kansas, 2014-2015

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Objective

Measure the correlation between Influenza-like Illness (ILI) data collected by the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) and the National Syndemic Surveillance Program (NSSP) in Kansas for the 2014-2015 influenza surveillance period.

Introduction

Influenza is not a notifiable disease in Kansas; patient-level influenza data is not reported to the Kansas Department of Health and Environment (KDHE). Kansas’ primary method of influenza surveillance is the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet), a collaboration between the Centers for Disease Control and Prevention (CDC) and state health departments. During the 2014-2015 influenza surveillance period (September 28, 2014 through May 16, 2015), 35 health care providers (20 family practice clinics, nine hospital emergency departments, four university student health centers, and two pediatric clinics) served as ILINet sites. Providers were instructed to report the previous week’s influenza-like illness (ILI) data, including the number of patients who met the ILI case definition and the total number of patients seen, by 11:00 AM each Tuesday. An average of 16 providers (45%) met the deadline each week.

Kansas’ method of syndemic surveillance is the National Syndemic Surveillance Program (NSSP). During the 2014-2015 surveillance period, 98 of 129 Kansas hospital emergency departments (EDs) automated submission of electronic health record data to NSSP. Twenty-three EDs submitted data at least once per day throughout the season; the remaining EDs were still undergoing testing and validation to meet minimum data quality standards, and therefore were prone to erratic data submission and indeterminate data quality.

Methods

The weekly proportion of ILINet provider patients who met the ILINet ILI case definition (Fever ≥100°F with cough or sore throat) were compared to the weekly proportion of NSSP-enrolled emergency department patients who met the NSSP Syndrome Definitions Work Group ILI syndrome definition (ILI-S). Patients were included in ILI-S if influenza-related symptoms or diagnosis codes were present in the chief complaint, diagnosis code, or diagnosis text portions of their NSSP record.

ILI providers that also submitted data to NSSP were removed from the ILINet data set to ensure those seven emergency departments did not influence correlation.

ILI and NSSP data submitted before the weekly ILINet deadline were compared to evaluate if NSSP could be used as a proxy for accurate situational awareness in Kansas, given NSSP’s automatic, daily data submission and the reporting delays seen with ILINet.

Pearson correlation coefficients (rho) were calculated using SAS 9.3 (SAS Institute Inc., Cary, NC, USA)

Results

ILI and NSSP ILI data were highly correlated, both when comparing all data submitted during the surveillance period (rho=0.91, P<0.001; Figure 1) and data submitted prior to the weekly ILINet deadline (rho=0.69, P<0.001; Figure 2).

Conclusions

Despite the differences in ILI definitions applied to each surveillance system, variation in the number of sites submitting data each week to each system, and differences in the type, geographic distribution, and total number of reporting sites, the weekly proportions of ILI patients reported to ILINet and NSSP were highly correlated. The correlation was higher when comparing all data collected during the surveillance period than when comparing only data submitted before the weekly ILINet deadline. Applying the ILI-S syndrome definition to NSSP data may provide useful situational awareness for states whose ILINet providers do not routinely meet the weekly data submission deadline.

Keywords

Influenza like illness; Syndemic surveillance; NSSP; ILINet; Influenza

Acknowledgments

The authors wish to thank CDC’s Influenza Division and the NSSP Syndrome Definitions Workgroup for their assistance.

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Surveillance of the Naural Foci of Especially Dangerous Infections in Southern Ukraine

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Objective

Comprehensive ecological, epidemiological and microbiological investigations of natural foci of EDI in southern Ukraine were carried out.

Introduction

Surveillance of the natural foci of Especially Dangerous Infections (EDI) is necessary due to their etiological, epidemiological, and clinical diversity, their global spread and overall negative impact on public health. Some EDI pathogens with natural foci are also potential agents for biological weapons. Study of the EDI characteristics is important for development of an effective epidemiological protection system. Francisella tularensis is one of the most virulent human microorganisms and a critical Category A biological agent. In Ukraine, tularemia natural foci are registered in 23 of the 25 regions. We conducted integrated ecological-epidemiological and microbiological research on the EDI natural foci for the past 20 years.

Methods

We studied ecological-epidemiological data (using retrospective analyses) and isolated F. tularensis strains by molecular-genetic (PCR, VNTR-Analysis), bacteriological, immunological, environmental-epidemiological, statistic methods.

Results

We detected favorable conditions for formation and long-term functioning of EDI natural foci of various etiologies in ecosystems of southern region of Ukrainian. Here tularemia natural foci were registered in Kherson and Odessa regions, and the largest outbreak of tularemia in humans in Ukraine occurred – 100 people fell ill in 1998 in the Odessa and Mykolaiv regions. The sources of infection were small mammals (forest and field mice), and hare. In our serological study of tularemia vectors, positive field data results confirmed the stability of tularemia natural foci. Seventeen strains of F. tularensis subsp. holarctica were isolated from different sources (rabbits, rodents, ticks, water). We conducted VNTR-analysis of the natural isolates, identified 9 genotypes, and constructed genetic passports of individual F. tularensis strains. In some Ukrainian southern regions, habitats containing natural foci revealed circulation of various EDI pathogens (tularemia, psittacosis, leptospirosis, arboviruses), which requires a polynozological approach to their monitoring, considering the overlap of vectors.

Conclusions

Eco-epidemiological and microbiological research in southern Ukraine have established the widespread presence of EDI of various etiologies. The presence of overlapping natural foci indicates that the southern region is an area with high risk of epizootic and epidemic complications. Use the molecular genetic research methods promote a science-based system for confirming areas containing EDI-specific territories and optimize the potential for prevention of infections near natural foci.

Keywords

EDI natural foci; strains genotyping; diagnosis; monitoring; prevention

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Surveillance of the Naural Foci of Especially Dangerous Infections in Southern Ukraine

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Mechnikov I.I. Ukrainian Research Antiplague Institute of the Ministry of Health of Ukraine, Odessa, Ukraine, Odessa, Ukraine

Objective
Carry out comprehensive ecological, epidemiological and microbiological investigations of natural foci of EDI in southern Ukraine.

Introduction
Surveillance of the natural foci of Especially Dangerous Infections (EDI) is necessary due to their etiological, epidemiological, and clinical diversity, their global spread and overall negative impact on public health. Some EDI pathogens with natural foci are also potential agents for biological weapons. Study of the EDI characteristics is important for development of an effective epidemiological protection system. *Francisella tularensis* is one of the most virulent human microorganisms and a critical Category A biological agent. In Ukraine, tularemia natural foci are registered in 23 of the 25 regions. We conducted integrated ecological-epidemiological and microbiological research on the EDI natural foci for the past 20 years.

Methods
We studied ecological-epidemiological data (using retrospective analyses) and isolated F. tularensis strains by molecular-genetic (PCR, VNTR-Analysis), bacteriological, immunological, environmental-epidemiological, statistic methods.

Results
We detected favorable conditions for formation and long-term functioning of EDI natural foci of various etiologies in ecosystems of southern region of Ukrainian. Here tularemia natural foci were registered in Kherson and Odessa regions, and the largest outbreak of tularemia in humans in Ukraine occurred – 100 people fell ill in 1998 in the Odessa and Mykolaiv regions. The sources of infection were small mammals (forest and field mice), and hare. In our serological study of tularemia vectors, positive field data results confirmed the stability of tularemia natural foci. Seventeen strains of F. tularensis subsp. holarctica were isolated from different sources (rabbits, rodents, ticks, water). We conducted VNTR-analysis of the natural isolates, identified 9 genotypes, and constructed genetic passports of individual F. tularensis strains. In some Ukrainian southern regions, habitats containing natural foci revealed circulation of various EDI pathogens (tularemia, psittacosis, leptospirosis, arboviruses), which requires a polynozological approach to their monitoring, considering the overlap of vectors.

Conclusions
Eco-epidemiological and microbiological research in southern Ukraine have established the widespread presence of EDI of various etiologies. The presence of overlapping natural foci indicates that the southern region is an area with high risk of epizootic and epidemic complications. Use the molecular genetic research methods promote a science-based system for confirming areas containing EDI-specific territories and optimize the potential for prevention of infections near natural foci.

Keywords
EDI natural foci; strains genotyping; diagnosis; monitoring; prevention

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A Tool to Improve Communicable Disease Surveillance Data

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Objective

Improved methods for user analysis of communicable disease surveillance data in New York State (NYS), excluding New York City (NYC).

Introduction

NYS (excluding NYC) has a very robust Communicable Disease Electronic Surveillance System (CDESS). This system provides disease specific modules, as well as a tracking system for contacts, and a perinatal infant tracking system. This system provides an easy way for users to quickly download a file with all of their data. NYS (excluding NYC) tracks, on average, 300 infants of hepatitis B surface antigen (HBsAg) positive mothers annually. CDESS provides an infant tracking module for local health departments (LHDs) to enter and monitor vaccine information, add multiple infants per mother, and track patient movement and loss to follow-up. The tool allows LHDs to analyze infants’ data by birth year cohort, with all of their current vaccination and serology information available in one record.

In 2013 and 2014, more than 13,000 cases of gonorrhea were reported to CDESS in NYS (excluding NYC). From November 2013 through May 2014, only 61% of cases were adequately treated with a regimen recommended by the Centers for Disease Control and Prevention (CDC) STD Treatment Guidelines for Gonorrhea\(^1\), and 29% were missing treatment information. The CDESS system allows the LHDs to track patients who have inadequate and/or missing treatment information.

Methods

The infant’s birth information, mother’s information, and the provider information in CDESS are prepopulated from newborn screening for each infant born to an HBsAg positive mother. LHDs enter the infant’s vaccination record and the infant’s serology record. To access the infant’s data on CDESS, the LHD needs to know the mother’s information: either the unique identifier or complete name and date of birth.

Gonorrhea investigations are automatically created by CDESS by data from the Electronic Clinical Laboratory Reporting System (ECLRS). Demographic, provider, and laboratory information is prepopulated by ECLRS. LHDs create the case upon review and perform follow-up and update the case supplemental form with information regarding risk, treatment, and additional provider data. The CDESS data resides in Oracle tables. Using SAS V9.3, the complex relational data is collated into one record per infant for the perinatal data, and one record per patient for the gonorrhea data. This data is then converted to one comma separated values (CSV) file for each county and birth year cohort for perinatal, and county and case year for gonorrhea. These CSV files are pushed to the Oracle database by using the Oracle SQL*Loader utility. This loads the CSV files as a Character Large Object (CLOB) into an Oracle table in the CDESS database.

SAS runs automatically every night and sends the updated CSV files to CDESS. The updated CSV files are immediately available for download by the LHDs. Using these files county users can filter their data by provider, treatment, vaccine dosage, and age to be more proactive in protecting the health of New Yorkers.

Results

The simplicity of accessing one file removes multiple steps in finding the perinatal infants’ vaccination and serology information. Using these CSV files, we can easily see that there are 259 babies currently being followed in the 2014 birth cohort. Twenty babies of the original 285 birth cohort moved out of jurisdiction, while six cannot be located. Of the 259, five did not receive HBIG at birth and four did not receive their first dose at birth. By eight months of age, 219 (85%) had received three Hepatitis B vaccinations. Thirty-eight percent have already had their PVST.

Using the gonorrhea files, the LHDs can assess who is in need of treatment. From November 2014 through May 2015, 92% of cases received adequate treatment, with only 2.6% missing data. Twenty percent fewer patients were considered to be inadequately treated because they received only one treatment in 2014-2015 than in 2013-2014.

Conclusions

Removal of multiple steps in data retrieval saves time for the LHDs. The LHDs now have an easy way to analyze their own data and be more proactive on their follow-up with physicians and families. All infants and patients within a jurisdiction can be monitored simultaneously. User-friendly systems and simple data analysis processes improve the overall quality of data collection.

Keywords

surveillance; communicable disease; gonorrhea treatment; perinatal hepatitis tracking

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\(^1\) Centers for Disease Control and Prevention. Update to CDC’s Sexually Transmitted Diseases Treatment Guidelines 2010: Oral Cephalosporins No Longer a Recommended Treatment for Gonococcal Infections. MMWR 2012;61(31): 590-94.

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Flea-Borne Rickettsiae in Almaty Oblast, Kazakhstan

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Introduction

Flea-borne diseases in Kazakhstan have been a significant health risk to inhabitants and visitors for ages, particularly plague. Flea-borne rickettsial disease threats are unknown in Kazakhstan, we therefore initiated a study to detect and identify flea-borne rickettsiae among fleas collected in the Almaty Oblast, in southeastern Kazakhstan.

Methods

Fleas (n=248) were collected by members of the Taldykorgan anti-plague station from live captured rodents (i.e. the Great Gerbil-Rhombomys opimus) and from the rodent burrows collected at five Rayons (districts) within Almaty Oblast (province) during 2015. Fleas were identified morphologically by entomologic keys and then pooled together (1-50 fleas/pool) by species and host/rodent burrow. DNA was extracted from triturated fleas (PrepMan Ultra kit) and tested by genus- (Rickettsia), group- (R. felis genogroup), and species- (Rickettsia typhi, Rickettsia felis and Candidatus Rickettsia asemboensis) specific quantitative real-time PCR (qPCR) assays, Rick17b, RfelG, Rtyph, and Rasemb, respectively. With GPS coordinates and GIS (ArcGIS) a distribution map was developed.

Results

Of 248 fleas (Coptopsylla lamellifer 45, Echidnophaga oschanini 1, Nosopsyllus laeviceps 10, Nosopsyllus tarus 1, Nosopsyllus turkmenicus 1, Paradoxopsyllus tereifrons 2, Xenopsylla conformis 1, Xenopsylla gerbilli 87, Xenopsylla hirtipes 26, and Xenopsylla skrjabini 74) assessed by qPCR 56 were identified as having: Rickettsia spp. only n=20, R. felis genogroup n=8, R. felis n=1, and Ca. R. asemboensis n=27. X. gerbilli was the flea most frequently found to be infected with a rickettsiae (44 of 87;50.6%) and 25 of the 44 rickettsia-infected fleas (56.8%) were infected by Ca. R. asemboensis. X. hirtipes was the next most commonly infected flea (4 of 26; 15.4%). One flea was infected with R. felis, and none were infected with R. typhi. R. felis and R. typhi cause flea-borne spotted fever and murine typhus, respectively.

Conclusions

Fleas captured from R. opimus or at their burrows were infected with rickettsiae. Most commonly found rickettsia-infected flea species was X. gerbilli and the most commonly found rickettsia was Ca. R. asemboensis. Future studies may include testing these and other fleas samples for the presence of other disease agents including Bartonella spp. and Yersinia pestis.

Keywords

flea-borne disease; rickettsiae; Kazakhstan

Acknowledgments

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* E-mail:
Denver County *Clostridium difficile* Trends and Associated Risk Factors 2011-2013

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**Objective**

Identify population-based *Clostridium difficile* infection (CDI) incidence stratified by Health Care Facility Onset (HCFO), Community Onset-Healthcare Facility Associated (CO-HCFA), and Community Onset-Community Associated (CO-CA) CDI in Denver County from 2011 - 2013 and describe demographic, health care facility exposure, and medication use risk factors.

**Introduction**

*Clostridium difficile* (CD), a gram-negative, anaerobic, spore-forming bacterium causes symptoms ranging from mild to severe diarrhea and may result in death.1 Approximately 75% of CDI cases have symptom onset outside of health care settings.2 Annual US costs of treatment and infection containment have surpassed $4.8 billion.3 Risk factors for CDI include recent broad-spectrum antibiotic exposure, advanced age, severe underlying morbidities, immunocompromised status, long-term hospital stays, and residence in long-term-care facilities.4 Nationally, CO-CA cases have increased from 2.8/100,000 person in 1993 to 14.9/100,000 person in 2005.5

**Methods**

A retrospective chart review studied CDI cases from 2011 through 2013 with incident (no positive test in the previous 8 weeks) stool specimen (CDI positive toxin or molecular assay) reported to the state health department, among Denver County residents older than 1 year. Cases were randomly selected for chart review. Cases were stratified by epidemiologic classification (HCFO, CO-HCFA or CO-CA) and analyzed for associations with: age, gender, antibiotic exposure, underlying disease, and exposure to high risk areas (e.g., long-term care facilities and hospitals). Rates were calculated using State Demography Office-Department of Local Affairs information. Descriptive statistics (means and frequencies) were used to describe CDI trends by year, demographic group, epidemiologic classification, and risk factors.

**Results**

Between 2011 and 2013, 2503 CDI cases were reported and 892 cases were chart reviewed (22%) and identified as CO-CA (339), CO-HCFA (175), or HCFO (44). Denver CDI incidence rate increased from 129/100,000 residents in 2010 to 139/100,000 residents in 2013. Incidence rates of cases classified as HCFO and CO-HCFA remained stable over the study period. Rates of CO-CA cases decreased from 50.4/100,000 residents in 2011 to 46/100,000 residents in 2013. The mean age for HCFO cases was 67 years, 49 years for CO-CA cases, and 56 years for CO-HCFA cases. HCFO was more common among men; there were no gender disparities for CO-CA or CO-HCFA. During the study period, the presence of underlying morbidities increased in all onset types with over half of CO-CA and CO-HCFA cases reporting underlying morbidities in 2013 (CO-CA: 65%; CO-HCFA: 69%). Antibiotic exposure substantially increased between 2011 and 2013, in cases classified as CO-HCFA (29% to 70%), and CO-CA (18% to 50%).

**Conclusions**

Rates of CO-CA CDI rose during the study period. Our study reflects national trends in age and antibiotic exposure by epidemiologic classification.6 The frequency of antibiotic exposure and underlying morbidities increased from 2011 to 2013 in both CO-CA and CO-HCFA cases. Denver CO-CA cases had more underlying morbidities compared to recent reports.7

**Keywords**

Clostridium difficile; healthcare associated infections; community acquired infections; Infectious disease

**References**


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Evaluation of National Influenza Sentinel Surveillance System in Nigeria, Jan-Dec 2014

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Objective
To assess the performance of the surveillance system and identify factors affecting the performance.

Introduction
National Influenza Sentinel Surveillance (NISS) was established in Nigeria in 2006 to monitor influenza occurrence in humans in Nigeria and provide a foundation for detecting outbreaks of novel strains of influenza. Surveillance for influenza-like illness (ILI) and severe acute respiratory infection (SARI) is carried out in 4 sentinel sites. Specimens and epidemiological data are collected and transported 4 days a week from the sentinel sites to the National Influenza Reference Laboratory. At the laboratory, they are tested for influenza A and B viruses and further subtyped if positive for influenza A virus.

Methods
Surveillance facilitators from the 4 functional sentinel sites were interviewed via telephone while oral interviews were conducted with laboratory staff. Information on NISS structure and management of data and specimens were collected. NISS protocol was reviewed, and surveillance data from January to December 2014 were analysed using Epi Info software. CDC Updated guidelines for evaluating public health surveillance systems was used to guide the evaluation.

Results
NISS activities are funded through a cooperative agreement with the US Centres for Disease Control and Prevention (CDC). Of specimens sent from the sentinel sites, 68% reached the laboratory within 48 hours. Specimen processing in the laboratory took an average of 23 days. Reasons given for the delay include late distribution of supplies from the laboratory to sentinel sites and stock-out of working materials at the laboratory. Surveillance activities were disrupted in the month of July 2014 because of health workers’ strike. The predictive value positive was 8.7%. Of submitted case investigation forms, 73.7% were completely filled. The testing algorithm and NISS protocol have been reviewed (addition of more variables on co-morbidities, age classification of patients seen daily at the sentinel health facilities, and analysis of more influenza subtypes at the laboratory) over the years.

Conclusions
The NISS is useful in characterizing influenza epidemiology in Nigeria. It is simple, flexible, and acceptable to the stakeholders. However, there was delay in sending of specimens to the laboratory and timely processing of specimens received. The observed delay may undermine its ability to detect early unusual patterns of morbidity and mortality due to influenza or signal the beginning of influenza season. The overdependence of the surveillance activities on donor-funding is a threat to its sustainability. We recommend improvement of logistics management and encouragement of local partnerships for sustainability.

Keywords
sentinel surveillance; influenza; Nigeria

Acknowledgments
We wish to express our gratitude to the National Influenza Sentinel Surveillance team and other stakeholders who made this evaluation possible

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Ebola Virus Disease Outbreak in Lagos, Nigeria; 2014: an Epidemiological Investigation

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Objective
To describe the socio-demographic characteristics of Ebola virus disease (EVD) patients and their contacts, magnitude of the outbreak and factors associated with outcome in patients.

Introduction
West Africa recently experienced the most persistent epidemic of EVD recorded in history. The reported morbidity and mortality of the highly virulent, emerging zoonotic filovirus infection is far larger than all previous epidemics combined1. Its spread to Nigeria (Africa’s most populous country) and to densely populated Lagos (a city in Nigeria with approximate combined population of Guinea, Sierra Leone, and Liberia) raised significant public health concern2. The Federal Ministry of Health was notified of a suspected case of viral haemorrhagic fever on the 22nd July, 2014. A 40-year old male Liberian presented in a private health facility on account of fever, vomiting and diarrhea. On the 23rd July, the index case was confirmed to have EVD and on 25th July, he died.

Methods
An Emergency operation centre was set up on 25th July, 2014. We adapted case and contact definitions from the World Health Organization (WHO) guidelines. Active case search in health facilities, communities, religious centers and various ports of entry into the country was done by well-trained epidemiologists and surveillance officers. We traced EVD contacts by contact identification, listing and active follow-up; taking daily temperature measurements and monitoring of symptoms to identify suspected cases. Laboratory confirmation of cases was done by reverse transcriptase-polymerase chain reaction. Prompt case management was commenced for positive cases with strict adherence to infection prevention and control measures. Data on socio-demographic characteristics, clinical symptoms and disease outcomes was collected using contact listing, contact follow-up, case listing forms and Open Data Kit (ODK) for real time data collation. Univariate and bivariate analysis was done.

Results
Fourteen out of the 16 cases identified (87.5%) were contacts under follow-up. From these cases, 293 contacts were identified. None of the contacts was lost to follow-up. The mean age of cases and contacts were 39.1 ± 11.9 years and 33.2 ± 13.9 years respectively. Majority of the cases (43.8%) and contacts (33.0%) were aged 30 – 39 years. Of the 16 cases, 8 (50.0%) were females and 10 (62.5%) were health workers. Of the 293 contacts 150 (52.0%) were females and 138(47.0%) were health workers. Of the 15 cases traced to the index case, 13 (86.7%) were first generation cases while 2(13.3%) were second generation cases. The case reproduction number for the outbreak was 1.3 and the secondary attack rate was 4.4%. The most reported symptom was fever (85.7%). Case fatality rate (CFR) among all the cases was 37.5% (6/16), while CFR among health workers was 40.0% (4/10). Health workers proportional mortality rate was 66.7% (4/6). The epidemic curve revealed a common source pattern at the early phase and a propagated pattern thereafter. Average duration of illness from onset of symptoms to survival and death was 16 ± 4.8 days and 11.6 ± 5.0 days respectively. There were no statistically significant association between the duration of illness and the outcome of disease (odds ratio (OR) = 1.14, 95% CI = 0.08 - 16.95), and between occupation of cases (health workers versus non-health workers) and outcome (OR = 1.33, CI = 0.16 - 11.08)

Conclusions
Health care workers and the active age group were more affected during the outbreak. The outbreak was contained through effective contact tracing and surveillance. Duration of illness and occupation were not significantly associated with outcome.

Figure: Epidemic curve of EVD in Lagos State, July to September, 2014

Keywords
Ebola virus disease; outbreak investigation; disease outcome; Lagos State

References

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Cancer Health Disparities in Southeastern Wisconsin

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Objective
To assess health disparities in all-site cancer incidence and mortality rates, and stage of specific cancer diagnosis (female breast cancer and colorectal cancer) compared between African American and white populations of southeastern Wisconsin during 2007-2011.

Introduction
Advanced cancer treatments and research have been helping reduce cancer mortality nationally and in Wisconsin. However, chronic health disparities in cancer remain a major public health concern as not all population subgroups have equal access to these healthcare benefits [1, 3]. Previous cancer studies showed that cancer health disparities persisted among racial populations had primarily focused on the entire state of Wisconsin [2]. The southeastern region Wisconsin, the greater Milwaukee metropolitan area, is home to 83% of Wisconsin’s African American population, and includes one of the most segregated metropolitan areas in the United States [1]. Because of this, better understanding of cancer trends in the southeastern Wisconsin region can assist in targeting a focal point to more effectively use resources to eliminate health disparities in Wisconsin.

Methods
Cancer incidence data were obtained from the Wisconsin Cancer Reporting System (WCRS) for the period 2007-2011. Cancer mortality data was assessed from the National Center for Health Statistics (NCHS) for the period 2007-2011. For absolute disparities, trends in cancer incidence, mortality, and the stage of diagnoses for African Americans and whites were calculated. Ratios of African American rates and white rates were used to measure changes in relative disparities [2].

Results
During 2000-2011, African Americans had higher cancer incidence rates and mortality rates than whites, except for breast cancer incidence rates were lower for African American women than for white women (Figures 1, 2, 3, and 4). Sex affected the trends in disparities and the magnitude of change for incidence rates (Table 1). In 2010, African American female breast cancer incidence rate was 8 cases per 100,000 population fewer than white rates. African American women tend to be diagnosed at a late stage of breast cancer with a rate ratio of 1.03 in 2000 and 1.29 in 2011. For colorectal cancer, African American men were more likely to be diagnosed with an advanced stage than white men with a slight decrease in disparity. The ratio between African American and white rates were 1.44 in 2000 and 1.40 in 2011.

Conclusions
Reducing cancer burden and eliminating cancer health disparities will need further research. But this study has shown that the at-risk population in the southeastern Wisconsin is a good starting point for public health professionals and policy markers to utilize their resources and prioritize effectively to reduce racial health inequity in cancer in Wisconsin.

Keywords
cancer; Registry; Health equity

Acknowledgments
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References


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Methods to Measure Socio-Economic Inequalities in Health for Indian Adolescents

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Objective
To identify and validate methods and scales measuring determinants of social inequalities in health in context to Indian adolescents.

Introduction
Health inequalities are major global public health problem and varies within and between countries [1]. LMICs particularly India, are undergoing a phase of rapid economic development leading to an increase in informal settlements or urban slums [2]. These settlements exhibit extreme poverty and suffers from adverse health outcomes. The worst affected are the adolescents because it is a crucial and most vulnerable age when health behaviours and lifestyle choices are established which affects their current and future health [3]. The current health system in many of the developing countries are outdated and have either rudimentary health statistics or none. There is lack of standardized and reliable questionnaires to capture various behavioural aspects of subjective health of the population in India. Thus, we aim to identify various measures of determinants of social inequalities relevant to the Indian adolescent population context.

Methods
We adopted scales and questions from internationally validated questionnaires, and conducted reliability and validity tests through a cross sectional study on 1386 adolescents residing in diverse areas of residence (slums, middle class and resettlement colonies) and standardized them to be used on Indian adolescent population. Questionnaire included important determinants of health: degree of neighbourhood social capital, level of social support, health related behaviours, self-rated health and key socio-demographic of adolescents. The social capital scale was adapted from an adolescent social capital scale used by Gage et al (2005) [4] and showed a reasonable internal consistency (Cronbach’s Alpha = 0.63) when tested on Indian adolescents. Social support scale was adapted from the adolescent social support scale developed by Seidman et al (1995) [5] and showed excellent internal consistency (Cronbach’s Alpha = 0.86) when tested on study population. Questions on health related behaviours were taken from WHO HBSC survey which is a survey of school children undertaken periodically in more than 40 countries of the world [6].

Results
A social gradient in health inequalities was observed with a sequentially detrimental health outcome at each lower level of areas of residence.

Conclusions
The questionnaire was observed sensitive to LMICs setting and consistent with both international as well as Indian adolescents context. Studying both clinical and subjective health outcomes in a population can provide important insights about different explanations of various indicators of health, highlighting the complex nature of inequalities. The questionnaire is useful in identifying social inequalities in health to advance health equity among adolescents.

Keywords
Social Inequalities; Methods; Adolescents

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References

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Investigating a Syndromic Surveillance Signal with Complimentary Data Systems

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Objective
To investigate a communicable disease syndromic surveillance signal using multiple data sources.

Introduction
From June 4-8, 2015, the New York City (NYC) syndromic surveillance system detected five one-day citywide signals in sales of over-the-counter (OTC) antidiarrheal medications using the CUSUM method with a 56-day moving baseline. The OTC system monitors sales of two classes of antidiarrheal medications, products with loperamide or bismuth, from two NYC pharmacy chains. To determine if this increase reflected a concerning cluster of diarrheal illness, we examined multiple communicable disease surveillance data systems.

Methods
We evaluated the OTC sales data using emergency department chief complaint, school nurse visits, enteric reportable diseases, nosocomial reports, clinical laboratory, water quality, and social media (Table) for 30 days prior to the first signal through one week following the last signal (May 12-June 15).

Results
We compared weekly counts of antidiarrheal sales during this period for 2014 and 2015. Bismuth sales were slightly higher in June 2015. Loperamide sales were similar between the two years. Promotional sales for both classes of medications were identified before and during the signals.

We observed no temporal or spatial diarrheal signals in our ED system during this period. The ratio of diarrheal to all ED visits decreased, suggesting declining diarrheal illness. A diarrheal signal on June 1 was observed in the school nurse system, but there were no specific increases by grade or neighborhood.

Weekly trend analyses of giardiasis, cryptosporidiosis, salmonellosis, and shigellosis identified five spatial and one borough level signal for giardiasis. The magnitude and location of the signals did not correlate with the OTC sales increase. Campylobacteriosis diagnoses increased in mid-May and early June but this was consistent with seasonal trends. A signal in clinical laboratory submissions was identified on June 10 but volume was not unusual and the baseline was low. No gastrointestinal illness outbreaks were reported through the NORA or sentinel nursing home systems.

Findings from DEP identified one coliform positive, E. coli negative event at a station on June 8. Routine pathogen monitoring for giardia and cryptosporidium showed no abnormal findings, and screening for viruses was negative.

Water quality complaints were within the expected range, and there was no increase in mentions of gastrointestinal illness on social media. Google Trends for gastrointestinal illness did not appear to increase compared with the previous year.

Conclusions
There were five one-day signals indicative of possible diarrheal illness from our syndromic systems over a five day period in early June 2015. After further investigation of syndromic and other systems, findings possibly reflected sales promotions but did not suggest increased diarrheal illness in NYC. Using multiple complementary systems can provide useful situational awareness when investigating disease signals.

Data Sources

<table>
<thead>
<tr>
<th>Data System</th>
<th>Contributors</th>
<th>Detection Criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>OTC pharmacy</td>
<td>2 NYC pharmacy chains</td>
<td>Sale of antidiarrheal products (loperamide or bismuth) or child electrolyte solution; Direct calls to chains internet searches to identify sales promotions for antidiarrheal products</td>
</tr>
<tr>
<td>Emergency department</td>
<td>51 NYC hospitals</td>
<td>Chief complaint mention of diarrhea or ICD-9 code 787.81</td>
</tr>
<tr>
<td>School nurse</td>
<td>NYC public and charter schools</td>
<td>Visit for stomachache or diarrhea</td>
</tr>
<tr>
<td>Reportable disease</td>
<td>NYC healthcare providers and laboratories</td>
<td>Report of giardiasis, cryptosporidiosis, salmonellosis, shigellosis, campylobacteriosis; Sentinel reporting system</td>
</tr>
<tr>
<td>Nosocomial Reports NORA/sentinel nursing homes</td>
<td>NYS Article 28 reporting system</td>
<td>Pathogen monitoring report for giardia or cryptosporidium; coliform event; boil water alert; distribution system water chemistry sample for turbidity and residual chlorine</td>
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<tr>
<td>Clinical laboratory submissions</td>
<td>NYC laboratories</td>
<td>Stool submission for culture and sensitivity</td>
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<td>Water quality indicators</td>
<td>Department of Environmental Protection</td>
<td>Pathogen monitoring report for giardia or cryptosporidium; coliform event; boil water alert; distribution system water chemistry sample for turbidity and residual chlorine</td>
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<td>Water quality complaints</td>
<td>311 calls</td>
<td>Complaint for dirty water, issues with quality/taste, and color or water access/supply</td>
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<tr>
<td>Social media</td>
<td>Twitter, blogs, internet posts, Google Trends</td>
<td>Mention of key words (diarrhea, loperamide, bismuth, water quality); Internet result from key word search (diarrhea, loperamide, bismuth, antidiarrheal)</td>
</tr>
</tbody>
</table>

Keywords
Syndromic; Signal; Investigation

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Use of Electronic Health Records to Determine the Impact of Ebola Screening

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Objective
To present methods of screening chief complaints and laboratory orders to find patients who presented for Ebola Virus Disease (EVD) screening, in order to determine the impact Ebola concern had on the Military Health System (MHS).

Introduction
Since the largest epidemic of Zaire ebolavirus (EBOV) in recorded history began in Guinea in December 2013, the epidemic has spread to neighboring countries of Liberia and Sierra Leone resulting in an estimation of over 27,000 total cases and over 11,000 deaths to date (1). In response to the widespread social disruption caused by this epidemic in West Africa, President Obama committed approximately 2,000 US service members to deploy to the region and provide humanitarian aid. US military physicians were called upon to evaluate service members returning from West Africa (WA) to rule out EVD. The US military also has a considerable number of beneficiaries who travel to WA to visit friends and relatives placing them at risk for exposure to EBOV and the development of illness upon returning to the US.

We are conducting an expanded surveillance program that employs a standard questionnaire that all providers can use when evaluating a patient at-risk for EVD that will also capture information from historical encounters. The data collected from the questionnaire will be used to assess the frequency with which clinicians are called to evaluate patients for EVD and the resources required. However, we realize that many encounters may not be captured with this method, especially those that are not high enough risk to require consultation with infectious disease (ID) specialists, and are developing ways to screen the Electronic Health Record (EHR) to find additional patients.

Methods
The Department of Defense’s (DoD) Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE) has the capability to screen the “reason for visit” field in the EHR for any combination of words. Previous to this study, we determined text strings that best captured potential EVD patients. Screening for these words, we can scan the entire EHR in ESSENCE from January 2014 until the termination of the outbreak to determine the number of times patients presented for EVD screening, basic demographic information on their age, gender, location, military status (active duty, retiree, family member), if they presented to the emergency department or outpatient clinic for care, any laboratory tests that were performed and the results and the ICD-9 diagnosis given.

We will also query the EHR for evidence of EBOV laboratory testing to identify all patients who had EBOV-specific tests administered. Currently, only PCR is used by the MHS to detect EBOV. Comprehensive SQL and SAS algorithms for the electronic HL7 data were developed to identify patients with EBOV laboratory tests performed. Algorithms were validated against clinical care records. For these patients, we will determine the laboratory results, whether they were hospitalized, associated diagnoses, and basic demographic information.

Results
Early in the DoD response to the EVD epidemic, we found 76 patients who presented at 27 military treatment facilities for rule-out EVD from 1 Aug 14 through 17 Oct 14. The majority (58%) were post-deployment EVD screening, but many were single concerned individuals. For laboratory testing, from June 2014 through July 2015, 13 tests were documented on 10 patients at 4 different locations. Upon review of the EHR, 2 “patients” appeared to be testing the lab system with 8 others having suspicion of exposure. No EVD cases have been detected in the MHS to date. The final results of what we are able to obtain from the EHR will be presented.

Conclusions
We have determined that various elements of the EHR, either through an existing syndromic surveillance system or through a specifically-derived method, can provide useful information on the impact of outbreaks on a health system. For EVD, we found patients that did not come to the attention of the ID specialists due to low risk, but still utilized MHS resources. Use of these methods to find patients of concern could be expanded to other outbreaks.

Keywords
Ebola; Electronic health record; Screening; Laboratory tests; Chief complaints

References

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Prospective Spatio-Temporal and Temporal Cluster Detection by Salmonella Serotype

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Objective
To prospectively identify serotype-specific clusters of salmonellosis in New York City (NYC).

Introduction
Nontyphoidal Salmonella, consisting of >2,500 distinct serotypes, is the leading bacterial agent of foodborne illness in the U.S., causing an estimated 1 million infections per year. In NYC, interviews of all case-patients (N=1,100 annually) are attempted to support outbreak investigation and control. Salmonella clusters in NYC are typically identified either by notification from PulseNet, CDC, or other health departments or by a weekly analysis using the historical limits method. More systematic and timely cluster detection could inform resource prioritization and improve the effectiveness of public health interventions. We initiated daily analyses in May 2015 to detect spatio-temporal clusters by serotype among cases since February 23. In July 2015, an analysis was added to detect purely temporal clusters among cases since May 1.

Methods
Salmonella isolates for NYC residents are serotyped by the city and state public health laboratories and reported to the Bureau of Communicable Disease of the NYC Department of Health and Mental Hygiene. An automated process assigned a standardized serotype to each salmonellosis case. Each case’s residential address at time of report was geocoded in near real-time and assigned a census tract. Each case was also assigned an “event date,” representing the illness onset date.

We used the prospective space-time permutation scan statistic to detect and evaluate clusters. A spatio-temporal analysis, with a maximum spatial size of 50% of observed episodes, was run for each serotype with a case reported in the past 60 days. A temporal analysis was run for all serotypes, replacing “space” in the space-time permutation scan statistic with “serotype” and setting the maximum spatial size to 0. For all analyses, the temporal cluster size range was 2 to 60 days. A 14-day lag was implemented to allow for data accrual. The baseline period was 1.5 years. Monte Carlo simulations (N=999) were used to determine statistical significance. Automated analyses were run each morning using Microsoft Task Scheduler, SAS 9.2, and SaTScan 9.4.1.

Any cluster with a recurrence interval (RI) ≥45 days was summarized in a map and linelist. Foodborne disease epidemiologists assessed clusters to determine if cases were linked by a common exposure and/or by pulsed-field gel electrophoresis (PFGE) of isolates.

Results
With event dates February 23–July 29, 2015, 391 Salmonella cases of 48 serotypes were reported, and 7 spatio-temporal clusters were identified for 5 serotypes. With event dates May 1–July 29, 254 cases of 42 serotypes were reported, and 5 temporal clusters were identified for 5 serotypes. The most unusual clusters were citywide temporal clusters of S. Poona (N=9, RI=14.5 years), S. Oranienburg (N=4, RI=4.3 years), and S. Berta (N=13, RI=3.0 years), and a spatio-temporal S. Heidelberg cluster (N=5, RI=456 days), which at the time of signaling corresponded to clusters already identified and under investigation. A cluster of S. Muenchen, first identified by our temporal (RI=67 days), then by our spatio-temporal analyses (RI=59 days) 8 days later, ultimately included 6 cases whose isolates were indistinguishable by PFGE. The investigation is ongoing.

Conclusions
In the first few months of prospective, automated cluster detection analyses by serotype, a manageable number of clusters were detected. The purely temporal analysis was sensitive to rare serotypes. All clusters either prompted new investigations or corresponded to ongoing investigations, complementing NYC’s existing enhanced Salmonella surveillance system. These methods could be useful for other health departments to adopt for primary or confirmatory cluster detection.

Keywords
Salmonella; foodborne illness; outbreak detection

Acknowledgments
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References

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Factors Influencing the Stability and Quality of the French ED Surveillance System

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Objective
Identification of the main factors influencing the stability and the quality of the French Emergency departments (ED) syndromic surveillance system.

Introduction
Since 2004, the French syndromic surveillance system Oscour® has been implemented by the national institute for public health surveillance (InVS) and is daily used to detect and follow-up various public health events all over the territory [1].

Beginning with 23 ED in 2004, the coverage and data quality have permanently been increasing until including about 650 ED in August 2015. Initially based on a voluntary participation of ED, a mandatory transmission has been decided in July 2013, with major modification on the structural organization of the data transmission in some regions and on coding practices of the new ED.

Besides this juridical context, the system is based on automatically data collection by ED physicians without recording added information for public health surveillance. This represents the main theoretical condition to ensure stability and quality, even in case of occurrence of major public health events susceptible to drastically increase the workload [2].

Methods
Four evaluation criteria on essential characteristics for a syndromic system were daily supervised during 19 consecutive months (from May 2014 to November 2015) through a dashboard [3]:

1/ stability and 2/regularity of data transmission at D+1 (expected delay), evaluated by a prospective calculation of the proportion of ED having transmitted their data on time,
3/ the data transmission delay during a 7-day period, when data are not transmitted at D+1,
4/ the data quality of medical information (ICD10 codes).

Three main factors influencing these criteria have been analyzed: 1/ temporal factors (day of week, day-off, vacations), 2/ health events occurring in 2015 (the exceptional influenza epidemic from January to March and a major heat wave in July), 3/ the influence to move from a voluntary to a mandatory system on data quality and transmission.

Results
Every day, about 40,000 attendances recorded in 550 ED are transmitted to InVS, corresponding to 82% of the total number of attendances expected from the ED including in the network. From May 2014 to November 2015, this number increase of 27% (+12,000 attendances) due to the introduction of 150 new ED related to the move to a mandatory system (Figure 1).

In 2015, the two major health events occurring in France did not impact negatively the data transmission (Figure 1).

Conclusions
The setting-up of the daily analysis of data transmission indicators allowed identifying frailty issues. Efficient solutions with IT unit and ED were implemented, enabling a better stability and regularity in a 3-months delay.

Finally the follow-up of such indicators in routine is an added-value for the reactivity of actions when technical difficulties occur. It is also crucial for supporting the epidemiological analysis and interpretation of data. Such indicators are included in the daily bulletins and dashboards published weekly at national and regional levels.

Keywords
Evaluation analysis; syndromic system; OSCOUR system; Lesson learned

Acknowledgments
To emergency department data providers and all InVS regional unit for their substantial contribution to the system.

References

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Monitoring Media Content About Vaccines in the United States: Data from the Vaccine Sentimeter

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Objective
The current analysis describes the scope and trends in United States content from the Vaccine Sentimeter’s results, while seeking to examine any possible links between media content, vaccine coverage, and reported vaccine adverse events in the country.

Introduction
The success of public health campaigns in decreasing or eliminating the burden of vaccine-preventable diseases can be undermined by media content influencing vaccine hesitancy in the population. A tool for tracking and describing the ever-growing platforms for such media content can help decide how and where to invest in campaigns to increase public confidence in vaccines. The Vaccine Sentimeter, developed from the Healthmap project, aims to assist public health practitioners in maintaining or improving vaccine coverage through a real-time, online visualization tool of global media content on vaccines.

Methods
The Vaccine Sentimeter collected over 9,552 online articles covering US events from 2012 to 2014, from sources such as news aggregators, government reports, and blogs. The sources were searched every hour using key terms related to vaccines, such as brand names, adverse events, or vernaculars (e.g. “shots”). Through both manual and automated curation, articles were classified by date, location, vaccine, category (topic such as “outbreaks”, “research”, “costs”, etc.), and overall article sentiment (positive, neutral/unclear, or negative). Data on vaccine coverage rates were obtained online from the results of the Center for Disease Control’s National Immunization Survey (NIS), the Behavioral Risk Factor Surveillance System (BRFSS), and the National Health Interview Survey (NHIS). Reports of adverse events were collected from online data of the Vaccine Adverse Event Reporting System (VAERS). National coverage for 12 vaccines for which sufficient reporting was found in the Vaccine Sentimeter articles were examined for possible links to the sentiment of media content on each vaccine. Finally, the categories of media content were compared to that of the VAERS to examine whether the media content about adverse events and other topics followed similar patterns as those reported in the public.

Results
The three most frequently reported states in the media were California, New York, and Texas with, respectively, 760, 517, and 393 classified reports. Most frequently reported vaccines included Influenza/H1N1 vaccines (n=2750), human papillomavirus vaccines (HPV) (n=1678), vaccines of the mumps, measles, and/or rubella family (MMR) (n=1363), vaccines of the diphtheria, pertussis, and/or tetanus (DPT) family (n=847), and polio-related vaccines (n=450). Across the US, 10.2% of vaccine media content was classified as being of an overall negative sentiment, while 86.4% were positive and 3.4% neutral/unclear. Most frequent classified categories included policy recommendations (n=1365), delivery strategies (n=907), outbreaks (n=756), and vaccine effectiveness (n=617). National coverage for vaccines of interest ranged from 57% (HPV) to 92.9% (polio vaccines). The percentage of negative sentiment for these vaccines ranged from 1.6% (meningococcal vaccines) to 21.5% (Hepatitis B vaccines). National vaccine coverage was negatively but not significantly correlated (r = -0.47, p = .122) with percentage of negative media sentiment for the 12 vaccines of interest.

Conclusions
These and future findings emphasize the importance of the Vaccine Sentimeter as a valid tool for public health agencies. This tool may allow them to track any loss of confidence in a variety of vaccines, at either the national or state level, at an early enough stage to allow effective policy implementation.

Funding for development of the Vaccine Sentimeter was provided by Sanofi-Pasteur

Keywords
Media content; Vaccine; HealthMap; Vaccine coverage; Vaccine Sentimeter

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Law, Policy, and Syndromic Disease Surveillance: A Multi-Site Case Study

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Objective

Explore the impact of law and government policy on the practice of syndromic disease surveillance (SyS) in the United States.

Introduction

SyS systems have great potential to prevent morbidity, injury, and mortality by monitoring population health and providing real-time data to inform public health department decisions. Electronic health information technology and federal, state and local incentives and investments have helped to facilitate their rapid and widespread implementation. As a result, SyS systems operate in the context of laws and regulations that determine their success. An understanding of the effects of this legal environment is crucial to insuring that SyS systems fulfill their potential.

Methods

We conducted semi-structured, in-depth interviews with 55 SyS stakeholders (e.g., state/local health department officials, legal counsel, health care facility personnel) from six jurisdictions and facilitated focus groups with national SyS stakeholder organizations. All interviews and focus groups were audio-recorded, transcribed, and analyzed by two coders using thematic content analysis and NVivo software. We also identified and conducted a content analysis of relevant legal documents.

Results

Four main findings emerged. First, SyS was largely conducted under the same legal authority as ‘traditional’ (e.g., notifiable disease) public health surveillance. In some jurisdictions, statutes and administrative rules have been amended to include “disease clusters” and “syndromes” as notifiable conditions or to mandate reporting of emergency department data. In some jurisdictions, these regulations were promulgated at the request of health care facilities reporting SyS data that saw them as a legal safeguard.

Second, requirements for “Meaningful Use” of electronic health records promulgated under the Health Information Technology for Economic and Clinical Health Act have eased health care facilities’ SyS-related legal concerns and injected funding that has substantially increased the number of facilities that send SyS data to state public health agencies and generally obviated the need for data use agreements. However, many public health agencies lack the staff to maximize the analytic potential of these data receive data only from emergency department and urgent care settings. Some public health professionals explained that Meaningful Use regulations lack a mechanism to maintain the quality of SyS data and that the incentive to satisfy Meaningful Use requirements has prompted some to outsource SyS reporting to third party vendors, weakening inter-personal relationships between health department and hospital personnel and hindering follow-up investigations as a result.

Third, very few legal concerns were expressed related to the federal BioSense program. Some jurisdictions participate in BioSense because they do not have the resources to conduct their own data collection and analysis, others do so to obtain financial resources for surveillance activities and to enhance the robustness of a national surveillance system. Officials in several jurisdictions that do not participate cited the indemnification clause of the BioSense data use agreement, which holds states liable in the event of a data breach. Others cited concerns regarding deidentification of the data.

Finally, we found that the primary barriers to maximizing the public health potential of SyS systems were technical issues and limited health department resources, not legal concerns. Although public health professionals, health care personnel, and public health legal professionals were aware of the legal context in which SyS practice operates, legal barriers were viewed as surmountable and secondary to limited information technology and epidemiology resources. In particular, few concerns were expressed regarding legal requirements for protecting data privacy, including those issued under the Health Insurance Portability and Accountability Act.

Conclusions

SyS has become an integral component of public health surveillance in the United States. Federal Meaningful Use electronic health record incentives and state public health statutes that mandate submission of data have facilitated the growth of these systems. They have also alleviated most of the legal concerns that had been raised when these systems were first established. The jurisdictions that participate in BioSense benefit from the financial and technical resources available through this program.

Keywords

Meaningful Use; BioSense; Law; Policy

Acknowledgments

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**Susceptibility Profile of Drug-Resistant *Streptococcus pneumoniae* Based on ELR**

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**Objective**

Our objective is to report the antimicrobial susceptibilities of *Streptococcus pneumoniae* received from a local safety net hospital via electronic laboratory reporting (ELR), and compare susceptibility percentages with those of the Centers for Disease Control and Prevention’s Active Bacterial Core surveillance (ABCs) program.

**Introduction**

Since November 2014, the Houston Health Department has been receiving antimicrobial resistance information for *Streptococcus pneumoniae* from a safety net hospital via electronic laboratory reporting (ELR). Antimicrobial characteristics and vaccination rates of pneumococcal disease are of public health interest due to potential implications in treatment and prevention. Ten states participate in the CDC’s Active Bacterial Core surveillance (ABCs) program. Texas, which represents a different and diverse demographic compared to other states, is not an ABCs participating state. No studies have compared local antimicrobial susceptibility percentages to those of the ABCs. The aim of this study is to 1) report the antimicrobial susceptibility of *S. pneumoniae* in a local cohort, 2) characterize the demographics of the cohort including the use of pneumococcal vaccine, and 3) compare antimicrobial susceptibility percentages of the local cohort to the 2013 ABCs program.

**Methods**

Selected local antimicrobial susceptibility results received between November 2014 and July 2015 were compared to the ABCs susceptibilities using binomial methods. The data source for the local information is susceptibility ELRs submitted from the local safety net hospital lab, and the data source for the ABCs information is the 2013 ABCs report. The local study cohort consisted of individuals who had positive blood cultures and reported susceptibilities for *S. pneumoniae* at a safety net hospital in Houston (N=27). The susceptibility characterization of *S. pneumoniae* from ELR includes percentages susceptible, intermediate, and resistant by antimicrobial drug.

**Results**

From November 2014 to July 2015, there were 27 individuals with pneumococcal disease with reported susceptibilities. Of the 27 patients, 9 (33%) had been vaccinated. The racial breakdown is 44% African American, 41% Hispanic or Latino, and 15% Caucasian. About 59% were aged 50-64 years, while 26% were aged 25-49 years at the time of disease onset. We found that erythromycin shares a similar percentage susceptible as its 2013 ABCs counterpart (p=0.206; 95% confidence interval 0.335 to 0.797), while penicillin has a significantly different percentage susceptible than the 2013 ABCs penicillin (p < 0.01; 95% confidence interval 0.224 to 0.612). The susceptibility profile of *S. pneumoniae* in the local hospital cohort is displayed in Table 1 below.

**Conclusions**

Statistical comparison of pneumococcal disease in a local safety net hospital cohort to ABCs statistics can identify differences in the susceptibility profile and use of pneumococcal vaccine. Erythromycin has a similar percentage susceptible in both cohorts, while penicillin has a significantly different percentage susceptible. The limitations of the study include the small sample size and potential biases due to multiple comparisons. The automated retrieval of susceptibility information via ELR is an important tool for public health surveillance. These findings, which are not population-based, can inform the design and development of enhanced population-based surveillance of pneumococcal disease based on ELR.

**Table 1. Susceptibility profile of *S. pneumoniae* in a local hospital cohort, Houston, TX, November 2014 - July 2015**

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>Susceptible</th>
<th>Intermediate</th>
<th>Resistant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penicillin</td>
<td>11</td>
<td>53.6</td>
<td>2</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>17</td>
<td>49.5</td>
<td>15</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>11</td>
<td>37.9</td>
<td>-</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>19</td>
<td>100.0</td>
<td>-</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>8</td>
<td>100.0</td>
<td>-</td>
</tr>
</tbody>
</table>

**Keywords**
electronic lab reporting; antimicrobial resistance; pneumococcal; *Streptococcus pneumoniae*; vaccination

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Predicting Facility-Level Carbapenem-Resistant Enterobacteriaceae (CRE) Incidence Based on Social Network Measures

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Objective
To enhance CRE surveillance and communication by incorporating social network measures to quantify patient sharing between facilities.

Introduction
CRE are multidrug-resistant bacteria associated with up to 50 percent mortality in infected persons (1). CRE are increasingly problematic in Illinois healthcare facilities, especially long-term acute care hospitals (LTACHs); therefore, Illinois implemented the eXtensively Drug-Resistant Organism (XDRO) registry (www.xdro.org). Mathematical models have identified patient sharing between healthcare facilities as a mechanism for regional spread (1), and the importance of each facility within a network can be quantified using social network analysis (2). Degree centrality is a measure representing the number of facilities with which a facility has shared at least one patient, and hence, a measure of “risk” of receiving a CRE colonized patient. Eigenvector centrality is more sophisticated in that it quantifies how well a given node is connected to other “well-connected” nodes (3). We expect that facilities that have high degree and/or eigenvector centrality – and, thus, higher “risk” of encountering a CRE colonized patient – will have higher incidence of CRE, as will facilities that share patients with LTACHs. Understanding facility-level characteristics that predict higher CRE rates will enhance the XDRO registry’s usefulness as a surveillance tool.

Methods
We obtained facility-level CRE cases from the XDRO registry and characteristics from the 2013 Illinois Department of Public Health (IDPH) Annual Hospital Questionnaire. The network analysis was done using IDPH hospital discharge data, and centrality measures were generated using UCINET (Harvard Analytic Technologies 2002). Centrality, number of beds, number of patients shared with LTACHs, and proximity to Chicago were considered as predictors of higher CRE rates. Multivariable negative binomial regression was used to compare incidence rate ratios; we constructed separate models for the state, and stratified by Chicago region.

Results
Higher centrality and sharing patients with an LTACH was associated with higher CRE rates. These associations hold true for the state and after restricting analysis to the Chicago region (Figure 1). After controlling for number of beds, city proximity, and LTACH sharing, the highest quintile of eigenvector centrality was associated with an over two-fold higher CRE incidence compared to the other quintiles combined (IRR 2.3 95% CI: 1.2-4.7); the association remained when analyzing facilities near Chicago (3.0, 1.6-5.4). Degree centrality did not predict a higher CRE rate for the state, but did for the Chicago region (1.5, 1.2-2.1). Sharing patients with LTACHs was a significant predictor in the Chicago eigenvector model (2.0, 1.03-4.0) and the statewide degree model (2.5, 1.1-5.8).

Conclusions
There is strong evidence that a facility’s centrality and sharing patients with LTACHs predicts higher CRE rates. Combining a surveillance tool such as the XDRO registry with social network measures is a powerful way to understand the geographic spread of antibiotic resistant bacteria. Quantifying patient sharing using the principles of social network analysis allows public health agencies to identify facilities likely to contribute to the spread of antibiotic resistant bacteria, and plan focused interventions.

Figure 1: 111 facilities in the Chicago region

Keywords
Surveillance; Healthcare; Social Network Analysis; HAI

Acknowledgments
IDPH CRE Taskforce

References

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The Public Health Community Platform: Implementing Electronic Case Reporting

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Objective
To inform the community on the progress of electronic case reporting (eCR) utilizing the shared infrastructure and applications of the Public Health Community Platform (PHCP).

Introduction
The PHCP is a community-led initiative to provide shared infrastructure, services, and applications to the public health community as solutions for complex public health informatics problems. The project has progressed by establishing a governance structure led by an executive committee representative of the public health practice community. The executive committee has established the strategic path for the continued development of the PHCP and prioritized eCR as the initial use case for implementation.

Case reporting from clinical providers still requires forms to be manually filled out and sent via mail or fax to the public health agency (PHA). Reporting requirements vary among PHAs and providers may be unaware of reporting requirements and mechanisms in their practicing jurisdiction.

The complexities of case reporting from clinical providers have resulted in inconsistent, incomplete, inaccurate, and delayed reporting of persons that are of interest to public health. This impacts the overall ability of PHAs to interpret surveillance data and take informed action to minimize the population burden of these conditions. The eCR solution coincides with expected Meaningful Use Stage 3 rules that will include case reporting as a public health option.

Methods
eCR includes the design, development, and implementation of a common electronic infrastructure (i.e., content, platform, and tools) to leverage EHRs so clinical care can more efficiently send standards-based, secure, and confidential case reports for reportable conditions to state, territorial, local, and tribal PHAs.

There are several components needed to achieve eCR, including:
• Standard data extractions from EHRs
• Data transaction and transportation protocols
• Trigger codes to filter clinical encounters and identify those most likely to include a reportable condition
• Decision support rules and logic defined by each jurisdiction to determine if a filtered patient encounter is reportable in the relevant jurisdiction
• Web forms and forms managers to collect additional data elements for public health

The PHCP is currently coordinating the development, integration, and deployment of these components. This includes the successful completion of an HL7® standard for an initial case message and implementation and integration of a production version Reportable Conditions Knowledge Management System (RCKMS) under development by CSTE [1] (integral to providing jurisdictionally defined rules for decision support logic). The information flow is illustrated in Figure 1.

The process is designed for PHA customization due to the variability in state and local reporting requirements. Centrally locating customization on the PHCP relieves the burden on EHR systems to account for all permutations of PHA differences, allowing PHAs to modify their data collection based on emerging needs. Furthermore, PHCP-located resources decreases the need for PHAs to locally create duplicative services and applications to support eCR.

Results
Pilot teams consisting of PHAs, EHR vendors, and clinical providers are being formed to test this information flow and integration with the PHCP and RCKMS.

Conclusions
As data collection becomes automated with eCR, it is expected that the PHA workforce will be redirected toward data analysis, interpretation, response, and prevention (rather than focusing on the completion of case report forms). As that data is transformed into knowledge, public health will be able to provide greater input into the Learning Health System and improve health outcomes in the population.

Figure 1. Transactional information flow for eCR.

Keywords
eCR; case reporting; Public Health Community Platform; interoperability

Acknowledgments
The PHCP Executive Committee: Art Davidson (NACCHO co-chair), J.T. Lane (ASTHO co-chair), Bill Brand, Jim Collins, Mark Conde, Rebecca Coyle, & Bryant Karras.

CDC/CSELS

References

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An R Script for Assessment of Data Quality in the BioSense Locker Database

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Objective
To describe an R script developed to assess and produce reports on data quality in the BioSense locker database.

Introduction
Syndromic surveillance requires reliable, accurate, and complete healthcare encounter data to assess patterns of illness and respond to public health events. Illinois implemented syndromic surveillance statewide in response to Meaningful Use reporting objectives. To address the need for continuous, automated assessment following initial on-boarding of facility Emergency Department data, we developed an R script to assess the quality of data in the private BioSense locker database.

This script builds upon and adapts from scripts previously developed for syndromic surveillance1,2 and data quality assessment3.

Methods
This R script examines identifying variables in the HL7 messages from the locker, aggregates messages into ED visits based on these identifiers, processes the aggregated data to calculate metadata for each visit, and computes various data quality metrics. Results are displayed in the console and written to an HTML file.

Given a user-specified time period and list of contributing facilities, this R script assembles a MySQL query and executes it to retrieve messages from the database meeting the specified criteria.

This script first examines the identifiers Unique_Visiting_ID, Patient_Visit_ID, Unique_Patient_ID, and FacilityID_UUID. It calculates the number of distinct values of UVID, PVID, and (FID, PVID) which appear, then calculates the number of UVID corresponding to each (FID, PVID) pair and vice versa. Finally, it finds instances of more than one PVID matching a single (FID, PID) pair on a single date and tallies the number of such occurrences at each facility.

This script aggregates messages into patient visits based on the ordered pair (FacilityID_UUID, Patient_Visit_ID); this pair of HL7 data elements as defined in the PHIN messaging guide uniquely identifies patient visits using a facility-generated identifier. Any distinct values present in a single field in different messages from the same visit are concatenated to ensure capture of new or revised information submitted throughout the patient visit. In addition, several metadata variables are calculated: the first and last values of key date fields are determined, and the longest and latest entries in reason-for-visit data elements (Chief_Complaint, Triage_Notes, diagnosis variables) and the date of the first non-null diagnosis and disposition are identified. Indicator variables reflecting multiple values (within a single visit) for age, PID, MRN, UVID, and admit date are also created.

A new data table of these aggregated visits and visit-level metadata variables is saved as an R object and exported as a pipe-delimited text file.

Finally, the R script produces an HTML file which displays message-level and visit-level data quality metrics. At the message level, results on the identifier variables are provided. Several tables displaying visit-level data quality results by facility are provided, including a table of percent completeness of several key demographic and clinical variables, a table displaying percent of visits having multiple values of demographic and clinical variables that should be single-valued, and frequency tables of visits by age group and patient class. The script can also be easily extended to calculate and display other results or additional data quality metrics that may be developed in the future.

This script was developed with input from the BioSense Data Quality workgroup and was demonstrated on conference calls that led to the sharing among jurisdictions of results regarding identifiers.

Results
Since January 2013, Illinois has performed on-boarding and validation to incorporate 156 hospitals into the BioSense Platform. This data quality assessment script, scheduled to run quarterly, produces a facility-level report that is shared with hospital and vendor contacts to support re-engagement and improvements following initial onboarding validation.

Conclusions
Moving forward, IDPH will utilize this script in its local HL7 integration project to improve data quality and facility monitoring on a continuous basis.

Keywords
R programming; data quality; syndromic surveillance

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Characterizing Public Health Actions in Response to Syndromic Surveillance Alerts

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Objective
To describe results of a prospective study to assess the impact of using a standard process by which public health units (PHUs) investigate syndromic surveillance alerts for respiratory illness.

Introduction
Public health in Ontario, Canada has no standardized system for carrying out syndromic surveillance. Previous research had demonstrated wide variation in the implementation of syndromic surveillance.

Methods
We recruited 15 PHUs that routinely accessed syndromic data (9 intervention, 6 control). Many already received alerts of aberrant events directly from their system. Both intervention and control groups were encouraged to continue standard practices to receiving and responding to these alerts, but in addition, intervention PHUs received alerts from a standard statistical algorithm designed by the study team to maximize specificity, and were asked to implement an evidence-based protocol for investigating all alerts. Data collection forms (“logbooks”) collected qualitative and quantitative information about the alerts and follow-up. Logbook data were grouped into themes, and tabulated to determine how frequently they occurred.

Results
Between October 2013 to February 2015, 15 PHUs received 1,969 alerts for respiratory and influenza-like illness syndromes from emergency department visit data. Of these alerts, 942 alerts were for the intervention units and 1,027 were for the control health units. Two hundred and twelve (24%) of the intervention alerts were generated by the study. PHUs in the intervention group checked alerts three times more frequently than control health units for alternate explanations as specified in the protocol. Control health units performed 20% more epidemiological investigations of aberrant events they received. Figure 1 illustrates the types of actions taken. For control health units, 549 (53%) of the alerts were deemed to warrant a response but 341 (33% of all alerts) of these responses were described as “watchful waiting”. In contrast, for intervention health units the numbers were 165 (18%) and 119 (13%) respectively. Overall, less than 10% of the alerts led to internal and external notifications. The high percentage of alerts warranting a response in the control group is partially due to one control health unit having a low threshold for designated that action was warranted. Next steps include adjusting for repeated measures by health units in calculating statistical significance.

Conclusions
The use of a standard protocol appears to have altered the approach to verification and validation of alerts. However, the large number of alerts translated into few tangible public health actions. Syndromic surveillance of emergency department visits appeared mainly to be used for “watchful waiting” and situational awareness.

Keywords
Syndromic surveillance; Evaluation; Response; Public Health

Acknowledgments

References

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The Impact of Standardized Decision Support on Syndromic Surveillance in Alberta

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Objective
The objective of this study was to carry out a mixed-methods evaluation of the ability of standardized supports to improve the usefulness of school absenteeism syndromic surveillance for public health in Alberta.

Introduction
Syndromic surveillance uses pre-diagnostic data to inform communicable disease prevention and control. Among health zones in the province of Alberta, Canada, practices employed by public health when using elementary school illness-cause absenteeism data vary widely.

Methods
The Alberta Real Time Surveillance System Network (ARTSSN) collects, analyzes and reports on school absenteeism data for all schools in participating health zones across Alberta. The two largest health zones in Alberta, Edmonton Zone and Calgary Zone, participate in ARTSSN and further agreed to participate in a study where one health zone was randomly allocated (flip of a coin) to receive the standardized supports intervention, or to continue with their regular practice. The intervention consisted of (1) a cumulative sum aberration detection algorithm applied to the ARTSSN data and (2) a protocol outlining how to investigate and follow up on aberrant events. The zone receiving the intervention additionally continued with their regular practices to ensure they could meet their required public health responsibilities. Staff in both intervention and control zones used electronic data collection forms, known as “logbooks” to document and track alerts received, any subsequent investigations done, and any public health action as a result of the alert. At the end of the data collection period, semi-structured interviews were conducted to understand more fully their alert investigation method, rationale for public health action, and their uptake of the study intervention. Frequencies of logbook elements were generated for numeric or categorical data to compare descriptive statistics between intervention and control groups, and logbook free-text elements and qualitative data collected through semi-structured interviews were analyzed thematically. The analysis was performed using Excel, and SAS statistical software.

Results
The Edmonton (intervention) Zone relied heavily on the regular ARTSSN alerts and study generated alerts. Between February 2014 and February 2015, the intervention zone investigated 246 alerts. In comparison, the Calgary (control) Zone relied on public health nurses communicating regularly with school principals to detect outbreaks in the schools. During the same time period, the control zone investigated 20 alerts. The intervention health zone resulted in the detection of 19 outbreaks, while the control zone resulted in 16 outbreaks detected. In terms of public health actions, there were 39 instances where the intervention health unit provided advice on environmental cleaning as a method of infection control. These actions increased in the second year of the study after 4 hours per week of dedicated nursing time were assigned. While many of the outbreaks in the control health zone were monitored, follow-up actions such as advice on environmental cleaning were not reported.

Conclusions
These study findings suggest that using automated processes to analyze school absenteeism data results in more frequent alerts than traditional systems relying on principal-nurse interactions. The response to the syndromic surveillance was augmented by the presence of standardized processes, particularly with respect to public health actions such as advice on environmental cleaning, and frequent hand washing. This increase in response only occurred once sufficient human resources were provided to investigate the alerts.

Keywords
Syndromic surveillance; public health; school absenteeism; Evaluation

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Syndromic Surveillance Evaluation of Influenza Activity in At-Risk Sub-Populations

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Objective
To determine if emergency department (ED) based syndromic surveillance can be utilized to characterize in near real-time influenza infection in three high-risk populations: a) adults > 65, b) pregnant women, and c) children < 5.

Introduction
Near real-time emergency department chief complaint data is accessed through Florida’s syndromic surveillance system: Electronic Surveillance System for the Early Notification of Community-based Epidemics-Florida (ESSENCE-FL). The Florida Department of Health relies heavily upon these data for timely surveillance of influenza and influenza-like illness (ILI). Hospital discharge data available from the Florida Agency for Health Care Administration (AHCA) captures information about influenza-associated ED visits and is considered complete. The delay in receiving the data (up to a year) hinders timely evidence-based decision making during the influenza season. Previous analyses (comparing the complete AHCA hospital discharge data to the ESSENCE-FL ILI syndrome and Influenza sub-syndrome) have shown ESSENCE-FL is a timely, effective tool to monitor influenza activity in the state and that the Influenza sub-syndrome most closely approximates influenza season activity in Florida. Adults > 65, pregnant women and children < 5 are at increased risk for morbidity and mortality from influenza infection. This investigation aims to determine if syndromic surveillance can be used to characterize in near real-time influenza infection in adults > 65, pregnant women, and children < 5 by comparing ED visits for influenza and ILI in ESSENCE-FL to historical AHCA records of people who incurred ED charges at a Florida hospital with diagnosed influenza.

Methods
Florida AHCA data for hospital admissions and ED visits from 2008-2014 were queried for patients with diagnosed influenza (ICD9-CM Code: 487 or 488) in the following groups a) adults > 65, b) pregnant women and c) children < 5. In the AHCA dataset, pregnant women were identified by querying for women aged 14-49 with a diagnosis code of influenza and a pregnancy diagnosis code (ICD9-CM Code: v22 or v23). ESSENCE-FL ED chief complaint data for the three target populations categorized into the ILI syndrome or the Influenza sub-syndrome (or both) for the same time period. In ESSENCE-FL, ED visits in pregnant women were identified using a free text query for “preg” in the chief complaint field among women aged 14-49. A time series by week was used to compare the ESSENCE-FL ILI syndrome data and the Influenza sub-syndrome data to the influenza diagnosis data from AHCA for each of the three target populations. Subsequently, AHCA data were compared to ESSENCE-FL ILI syndrome data and the Influenza sub-syndrome (among each of the three target populations) by week to determine the correlation between the syndromic surveillance categories and AHCA discharge diagnoses.

Results
In the AHCA data set a) 29,503 adults > 65, b) 858 pregnant women, and c) 71,807 children < 5 with influenza diagnoses incurred ED charges from Florida hospitals. In the ESSENCE-FL dataset the ILI syndrome identified: a) 62,015 visits from adults > 65, b) 1,841 visits from pregnant women, and c) 288,033 visits from children < 5; use of the Influenza sub-syndrome identified: a) 36,345 visits from adults > 65, b) 1,217 visits from pregnant women and c) 25,858 visits from children < 5 years of age. In all three sub-populations, trend (season onset, duration, and end) and volume analyses showed that ED visits categorized into the ESSENCE-FL Influenza sub-syndrome best matched the ACHA data for approximating the impact of influenza in the target populations. Correlation analyses found that the ESSENCE-FL Influenza sub-syndrome had higher correlation coefficients than the ILI syndrome when compared to the AHCA data by week (albeit these gains were very small for the adults over 65 and pregnant women groups). None of the queries had a correlation coefficient lower than 0.76.

Conclusions
Syndromic surveillance can be used not only to monitor overall influenza trends, but is also effective for timely surveillance and estimation of influenza activity in three target populations: a) adults > 65, b) pregnant women, and c) children < 5 in Florida. While rich, complete AHCA data may be up to one year old, which does not allow for timely and informed decision-making and prioritization of resources during influenza season.

Keywords
influenza; syndromic; at-risk populations

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Epidemic Situation in Ukraine Related to the Quality of Drinking Water

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Introduction
The World Health Organization (WHO) puts a great emphasis on the study of diseases related to using or consuming poor-quality water and the absence of proper hygiene. Unfortunately, consumption of poor-quality water causes certain diseases in Ukraine.

Methods
The data of the official reports for 1997-2014 were used as the information basis for our study. We used theoretical and statistical methods of analysis. The purpose of the study was to obtain summary data regarding the outbreaks that occurred as a result of water consumption, to evaluate their scope, and the main causes of disease.

Results
70 outbreaks of severe enteric infections were registered among the population in 19 administrative territories in Ukraine over the past 17 years. The source of infection was poor-quality water. A total of 8265 people acquired an infection, 4140 of them were children.

Clinical manifestations of disease in the outbreaks can be divided into: viral hepatitis – 33 outbreaks (2947 people infected), dysentery – 18 outbreaks (1217 people infected), typhoid – 9 outbreaks (189 people infected), enteroviruses – 4 outbreaks (457 people infected), rotaviruses – 3 outbreaks (3353 people infected), opportunistic pathogenic microflora – 2 outbreaks (70 people infected) and yersiniosis – 1 outbreak (32 people infected).

Most patients (80%) had clinical manifestations of gastroenteritis of rotavirus etiology. It was verified by clinical and viral data. The age group of the disease included children of 1-6 years old (60% specific gravity).

The largest number of sick persons was registered in 2001 during the outbreak of rotavirus infection in Odesa. 3143 people were infected, 2277 of them were children.

Conclusions
Most outbreaks were related to the piped water contaminated by rotaviruses, as a result of emergencies in the water supply and sanitation systems.

The poor condition of the water supply in Ukraine is caused by the following factors: contamination of water supply reservoirs by untreated sewage; non-observance or absence of sanitary control zones of the water supply reservoirs; usage of old and ineffective techniques for water purification and decontamination; poor technical conditions of water supply plants and systems; and cutting-off water supply plants from the power supply system. The absence of the power for a long time allows bacterial contamination of the water in water supply systems.

Keywords
quality of drinking water; infectious disease; outbreak

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Acute Gastroenteritis: Contribution of SOS Médecins Network

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Objective
To illustrate the complementarity and added value of the GP’s emergency network “SOS Médecins” through an example of an epidemic of gastroenteritis (GE).

Introduction
In France, the surveillance of GE is performed by several complementary systems including specific and syndromic surveillance systems.

The GP’s emergency associations “SOS Médecins” are part of the French syndromic surveillance system SurSaUD since 2006. SOS Médecins functions as a liberal medical regulation. In 9 years, the network has become almost exhaustive and contribute to the surveillance of seasonal and non-seasonal health events at different geographical scales, in the fields of infectious diseases and environmental health. GE is one of the 50 indicators daily followed by the French Institute for Public Health Surveillance (InVS) syndromic surveillance unit.

Methods
In July 2015, 60 of the 62 associations (about 1000 GP’s) transmit daily data to InVS, representing an average daily volume of about 10,000 consultations. National coverage is nearly exhaustive and distribution is homogeneous all over territory including overseas. 80% of the population living in urban areas is estimated to potentially have access to this type of structure. At a national level, the mean proportion of coding for medical diagnoses is 84% in 2015 (only 60% in 2010).

The daily national analysis is performed based on the number of acts, 7 days moving average and the proportion of the tracking indicator among coded acts. Similar analysis are performed at regional level. Data analysis is performed daily and weekly using dashboards and control charts that are generated by a business intelligence application.

Results
In September 2014, an increase of the proportion of GE diagnoses in all-coded diagnosis was observed at a national level through daily dashboards. The regional analysis revealed that some regions were more impacted such as Normandie and Pays de la Loire (both West-North regions). The early signal was confirmed after querying practitioners of SOS Médecins associations in Basse-Normandie. The analysis of the specific surveillance data (GP’s in-hour nor laboratory testing) or the syndromic OSCOUR Emergency Department data did not showed any increase in their GE indicators. The syndromic network of Public Health England (PHE) was contacted and reported an increase in the number of cases of GE. The clinical presentation of GE observed in France and UK were mostly upper gastro-intestinal presentation with vomiting symptoms. This episode affected all age groups and particularly children under 15 years old and young adults.

Conclusions
SOS Médecins data was the only data source to identify an increase in GE in two French regions.

The clinical presentation did not fit with the various case definitions adopted. In fact, the specific monitoring systems could not detect the increase because they use a restrictive case definition only including acute diarrhea. Also, this outbreak has not been detected in the emergency because symptoms were not serious in all age groups. This episode allowed to discuss the relevance of the different case definitions used in France for GE surveillance. This data source is essential for syndromic surveillance system of InVS: data quality and geographical coverage of the network allows, in addition to emergency services, to obtain accurate analysis epidemic phenomena (eg flu or heat wave).

Keywords
acute gastro-enteritis; SOS Médecins; GP’s

Acknowledgments

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Which Sections of Electronic Medical Records Are Most Relevant for Real-Time Surveillance of Influenza-like Illness?

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Objective
To investigate which section(s) of a patient’s electronic medical record (EMR) contains the most relevant information for timely detection of influenza-like illness (ILI) in the emergency department (ED).

Introduction
Effective real-time surveillance of infectious diseases must strike a balance between reliability and timeliness for early detection. Traditional syndromic surveillance utilizes limited sections of the EMR, such as chief complaints and/or diagnosis. However, other sections of the EMR may contain more pertinent information than what is captured in a brief chief complaint. These other EMR sections may provide relevant information earlier in the patient encounter than at the diagnosis or disposition stage, which can appear in the EMR up to 24 hours after the patient’s discharge. Comprehensive analysis may identify the most relevant section of EMRs for surveillance of all major infectious diseases, including ILI.

Methods
This was a retrospective, cross-sectional study. The sample consisted of 100 randomly selected ED ILI-positive patients at an academic medical center. These patients came to the emergency department during the 2014-2015 ILI season (September 1, 2014 to April 30, 2015). Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) — a syndromic surveillance program — was used to identify the positive ILI patients by applying the Centers for Disease Control and Prevention case definition of ILI (i.e., fever with cough and/or sore throat) to the entire EMR.

For each patient, the presence or absence of each ILI symptom was documented by a board-certified emergency physician for each section of the EMR, specifically: registration/arrival complaints, triage chief complaints, flow sheet/vital signs data, history of present illness (HPI), review of systems (ROS), physical exam, assessment plan, diagnosis, free-text clinical notes, and discharge instructions, among others. In addition, efficacy of each EMR section in detecting ILI was documented.

Results
The ILI symptoms documented in the HPI section of the EMR captured 80% of ILI cases (Table 1). Thirty-nine percent of ILI cases had ILI symptoms documented in registration/arrival complaints, triage chief complaints, flow sheet/vital signs data, history of present illness (HPI), review of systems (ROS), physical exam, assessment plan, diagnosis, free-text clinical notes, and discharge instructions, among others. In addition, efficacy of each EMR section in detecting ILI was documented.

Conclusions
The HPI, ROS, and nursing notes sections of the EMR were information rich and the most relevant sections for ILI surveillance. Since 61% of cases reported ILI symptoms in areas of the EMR other than the commonly-used triage and registration sections, it is warranted that expanding ED syndromic surveillance to other areas of the EMR may increase sensitivity. Thus, reliable real-time syndromic surveillance systems need to be capable of processing both discrete and free-text data from various sections of the EMR.

Table 1: Percent of each section of EMR that meets the definition of ILI

<table>
<thead>
<tr>
<th>Sections(s) of EMR</th>
<th>% ILI Cases (n=100)</th>
</tr>
</thead>
<tbody>
<tr>
<td>History of present illness (HPI)</td>
<td>80%</td>
</tr>
<tr>
<td>Review of systems (ROS)</td>
<td>76%</td>
</tr>
<tr>
<td>Nurses</td>
<td>46%</td>
</tr>
<tr>
<td>Attending notes</td>
<td>32%</td>
</tr>
<tr>
<td>Assessment plan</td>
<td>24%</td>
</tr>
<tr>
<td>Screening questions</td>
<td>20%</td>
</tr>
<tr>
<td>Triage chief complaint (CC)</td>
<td>18%</td>
</tr>
<tr>
<td>Registration arrival complaints</td>
<td>8%</td>
</tr>
<tr>
<td>Diagnoses</td>
<td>3%</td>
</tr>
<tr>
<td>Physical exam</td>
<td>1%</td>
</tr>
<tr>
<td>Residents</td>
<td>1%</td>
</tr>
<tr>
<td>Others</td>
<td>1%</td>
</tr>
<tr>
<td>Nurse practitioner (NP) notes</td>
<td>1%</td>
</tr>
<tr>
<td>Flowsheet vital signs</td>
<td>0%</td>
</tr>
<tr>
<td>Flowsheet vital signs &amp; HPI &amp; ROS</td>
<td>91%</td>
</tr>
<tr>
<td>HPI &amp; ROS</td>
<td>81%</td>
</tr>
<tr>
<td>Registration arrival complaints &amp; Screening questions &amp; Triage CC &amp; Flowsheet vital signs</td>
<td>46%</td>
</tr>
<tr>
<td>Registration arrival complaints &amp; Screening questions &amp; Triage CC</td>
<td>39%</td>
</tr>
<tr>
<td>Attending &amp; Resident &amp; NP Notes</td>
<td>34%</td>
</tr>
</tbody>
</table>

Keywords
Influenza-like illness; GUARDIAN; Electronic Medical Records

Acknowledgments
GUARDIAN is funded by the US Department of Defense, Telemedicine and Advanced Technology Research Center, Award numbers W81XWH-09-1-0662 and W81XWH-11-1-0711.

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The Impact of Documentation Style on Influenza-Like Illness Rates in the Emergency Department

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Objective
To compare the influenza-like illness (ILI) rates in the emergency departments (ED) of a community hospital versus a large academic medical center (AMC).

Introduction
In recent years, the threat of pandemic influenza has drawn extensive attention to the development and implementation of syndromic surveillance systems for early detection of ILI. Emergency department (ED) data are key components for syndromic surveillance systems. However, the lack of standardization for the content in chief complaint (CC) free-text fields may make it challenging to use these elements in syndromic surveillance systems. Furthermore, little is known regarding how ED data sources should be structured or combined to increase sensitivity without elevating false positives. In this study, we constructed two different models of ED data sources and evaluated the resulting ILI rates obtained in two different institutions.

Methods
Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) – a syndromic surveillance program – was used to automate ILI detection using chief complaints with free text and vital signs (i.e., ILIv1), and the entire Electronic Medical Record (EMR) (i.e., ILIv2) for a large AMC and a community hospital during the 2014-2015 influenza season. The GUARDIAN system defined ILI as fever (temperature ≥ 100°F) and cough and/or sore throat.

The first step in our data analysis was to compute the daily ILI rates (i.e., the total number of ILI patients divided by the total ED census per day) and the 7-day moving average ILI rates (henceforth referred as the ILI rate). Thereafter, we performed graphical and statistical (i.e., descriptive and ANOVA with post hoc Bonferroni test) analyses and compared the results generated from the data obtained through the two ILI detection approaches.

Results
Compared to the AMC ILI rate for ILIv1, the community hospital had significantly higher ILI rates for both ILIv1 and ILIv2 (p<0.01), as shown in Table 1. For ILIv1, the community hospital had, on average, 3.84% higher ILI rates as compared to the AMC. In addition, ILIv2 yielded higher mean ILI rates than ILIv1 in both institutions, with a difference of 1.89% for the community hospital and 7.55% for the AMC. Figure 1 indicates that the ILI rates derived from ILIv1 and ILIv2 for the community hospital and the ILI rates derived from ILIv2 for the AMC are typically above 5%, while the ILI rates derived from ILIv1 for the AMC is below 5%. All pairs of ILI models vs. settings were significantly different from each other (F= 217.84, df = 949, p<0.01).

Conclusions
The community hospital had higher ILIv1 rates as compared to the AMC mainly due to frequent use of CC free-text fields by community hospital triage nurses. There are clinical, operational, and cultural differences between AMC and community hospital EDs.

With detailed clinical documentation at triage, surveillance systems can generate reliable probabilities/weights for early ILI detection. Since CC free-text fields are so data rich, surveillance systems that utilize natural language processors can improve ILI and other disease detection. In addition, depending on the setting, institutions similar to the AMC in this study should consider using the entire EMR for ILI surveillance.

Table 1: Comparison of ILI models between AMC and community hospital settings

<table>
<thead>
<tr>
<th>ILI Models</th>
<th>7 Day Moving Average ILI Rates (Mean ± Standard Deviation)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AMC</td>
</tr>
<tr>
<td>ILIv1</td>
<td>3.81% ± 1.76%</td>
</tr>
<tr>
<td>ILIv2</td>
<td>11.36% ± 3.08%</td>
</tr>
</tbody>
</table>

Figure 1. Comparison of ILI models between AMC and community hospital settings

Keywords
GUARDIAN; Influenza-like illness; Emergency department

Acknowledgments
GUARDIAN is funded by the US Department of Defense, Telemedicine and Advanced Technology Research Center, Award numbers W81XWH-09-1-0662 and W81XWH-11-1-0711.

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Natural Language Processing and Technical Challenges of Influenza-Like Illness Surveillance

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Objective
To review the natural language processing (NLP) and technical challenges encountered in an automated influenza-like illness (ILI) surveillance system.

Introduction
Processing free-text clinical information in an electronic medical record (EMR) may enhance surveillance systems for early identification of ILI outbreaks. However, processing clinical text using NLP poses a challenge in preserving the semantics of the original information recorded. In this study, we discuss several NLP and technical issues as well as potential solutions for implementation in syndromic surveillance systems.

Methods
This is a retrospective, cross-sectional study conducted at the EDs of a large urban academic medical center and community hospital. The study timeframe was October 1, 2014 to June 30, 2015. Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) – a syndromic surveillance program – received and processed HL7 messages in real-time and generated ILI surveillance reports. The sophisticated GUARDIAN NLP algorithm processed each patient chart component, consistent with a physician’s manual review [1].

A random sample of 10 ILI-positive cases detected by GUARDIAN was drawn each week for manual review to confirm the positive presence of the ILI case definition terms: fever, cough, and sore throat. False ILI-positive cases, and associated causes, were documented and categorized as shown in Table 1.

Results
Of the 519 ILI-positive charts reviewed, 56 cases were false positive, mainly due to NLP or programming errors (e.g., incorrect concept parsing due to certain punctuation and word combinations). Temporal relationships were found to be a challenge for NLP: examples included when a clinician noted a fever in the past or documented instructions to return for a fever. Physician documentation style was also a common and difficult problem: examples include the use of italics or bold text to represent a positive or negative symptom.

We identified new terms to add to the negation list and discovered a problem caused by the use of a long negation string. GUARDIAN was programmed to acknowledge negation strings up to 16 words since any more words than that decreased accuracy.

We found that temperatures were occasionally corrected in the EMR, while GUARDIAN had no way of knowing the original value was an error. Lastly, on occasion, there was also reception of incorrect inpatient vitals and truncated nurse notes.

With the modification of our system architecture and NLP engine, we were able to reduce the associated ILI false positives from 56 (10.8%) to 32 (6.2%).

Conclusions
The use of NLP can enhance the efficacy of syndromic surveillance systems. However, there are limitations to NLP processing loads. While many NLP errors can be corrected, yielding improved accuracy, some issues cannot be resolved. Sharing known technical and NLP issues, and their resolutions, can assist in minimizing errors to acceptable levels (<5%) leading to refinement of existing syndromic surveillance systems.

Table 1. Review of NLP and technical challenges in ILI surveillance.

<table>
<thead>
<tr>
<th>Issue</th>
<th>Examples</th>
<th>Prevalence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Temporal relationship</td>
<td>Historical symptoms noted; instructions to</td>
<td>26.8% (15)</td>
</tr>
<tr>
<td></td>
<td>return if symptoms persist</td>
<td></td>
</tr>
<tr>
<td>Programming error*</td>
<td>Punctuation caused concepts to be incorrectly</td>
<td>26.8% (15)</td>
</tr>
<tr>
<td></td>
<td>parsed</td>
<td></td>
</tr>
<tr>
<td>Text formatting</td>
<td>Physician used rich-text formatting to</td>
<td>16.1% (9)</td>
</tr>
<tr>
<td></td>
<td>indicate negative symptoms</td>
<td></td>
</tr>
<tr>
<td>Excessive negation string</td>
<td>More than 16 words long</td>
<td>10.7% (6)</td>
</tr>
<tr>
<td>length</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Context misrepresentation*</td>
<td>Unrelated symptoms, such as “hay fever”</td>
<td>8.9% (5)</td>
</tr>
<tr>
<td>Slippage of additional data</td>
<td>Incorrectly received inpatient vitals or partial</td>
<td>7.1% (4)</td>
</tr>
<tr>
<td>through filters</td>
<td>nurse note</td>
<td></td>
</tr>
<tr>
<td>Correction ambiguity</td>
<td>Temperature corrected by nurse</td>
<td>3.6% (2)</td>
</tr>
</tbody>
</table>

Note: *Issues were resolved by modifying the system architecture and NLP engine.

Keywords
Influenza-like illness; Natural language processing; Lessons learned

Acknowledgments
GUARDIAN is funded by the US Department of Defense, Telemedicine and Advanced Technology Research Center, Award numbers W81XWH-09-1-0662 and W81XWH-11-1-0711.

References

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One Health e-Surveillance for Early Detection of Gastrointestinal Disease Outbreaks

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Objective
To describe how a real-time surveillance system for early detection of gastrointestinal disease (GI) outbreaks in small animal and human health is being developed by collecting electronic health records (EHRs) from veterinary practitioners and a telephone-based 24-hour medical triage service in the UK.

Introduction
In human and animal health, conventional approaches to preventing and controlling GI have not reduced the overall disease burden. In order to understand and mitigate shared GI aetiologies between humans and animals it is necessary to develop One Health Surveillance approaches that integrate data-sources contributed to by human and veterinary healthcare. Such approach is described here.

Methods
Veterinary data were collected electronically in real-time by SAVSNET, the Small Animal Veterinary Surveillance Network, from 102 UK veterinary practices (total of 197 premises) using a compatible version of practice management software. The study sampling frame included all dog and cat EHRs recorded within the SAVSNET database between January 2014 and July 2015. Each record included the animal signalment (including species, breed, sex, age, etc.), clinical free text, owner’s postcode, treatment, syndrome information and results from a short questionnaire administered to veterinary surgeons and appended after ~25% of GI consultation. The owner’s postcode data were used to link each animal against veterinary surgeons and appended after ~25% of GI consultation. Veterinary data were collected electronically in real-time by SAVSNET, the Small Animal Veterinary Surveillance Network, from 102 UK veterinary practices (total of 197 premises) using a compatible version of practice management software. The study sampling frame included all dog and cat EHRs recorded within the SAVSNET database between January 2014 and July 2015. Each record included the animal signalment (including species, breed, sex, age, etc.), clinical free text, owner’s postcode, treatment, syndrome information and results from a short questionnaire administered to veterinary surgeons and appended after ~25% of GI consultation. The owner’s postcode data were used to link each animal against veterinary surgeons and appended after ~25% of GI consultation.

A Bayesian spatio-temporal mixed effects binary regression model was used to model the incidence of GI in dogs and cats as a proportion of all presentations. The model was fitted to data between 01/11/2014 and 15/11/2014 using a bespoke Markov chain Monte Carlo algorithm to generate samples from the predictive distribution of the underlying spatio-temporal incidence surface. These samples were then used to compute predictive probabilities for exceedance of policy-relevant relative risk thresholds; a high predictive probability at a particular time and place gives an early warning of a possible GI outbreak. To test the ability of the model to detect GI outbreaks, a data set it was created with a fictitious premise having an excessive number of fake GI cases. The synthetic data is based on a typical premise in the SAVSNET dataset to ensure it reflects the characteristics of the genuine data. This premise is placed 1.5km east and 3.9km south of the chosen genuine premise. The outbreak is defined throughout the fictitious premise as the eight days from Monday, 03/11/2014 to Monday, 10/11/2014 inclusive. We run the model using data from 01/11/2014 to 15/11/2014.

Conclusions
This is the first demonstration of the feasibility of real-time syndromic surveillance in UK small animal practices. In future work, we intend to adapt the model to early detection of human GI outbreaks, and to investigate the possible inter-dependence of spatio-temporal variations in GI risk between companion animals and people.

Keywords
One health surveillance; early detection; gastrointestinal disease; UK; SAVSNET

Acknowledgments
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Data Blindspots: High-Tech Disease Surveillance Misses the Poor

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Introduction

Evidence from over 100 years of epidemiological study demonstrates a consistent, negative association between health and economic prosperity (Farmer 2001; Marmot 2005). In many settings, it is clear that causal links exist between lower socioeconomic status and both reduced access to healthcare and increased disease burden (Shi et al. 1999; Liao et al. 2004). However, our study is the first to demonstrate that the increased disease burden in at-risk populations interacts with their reduced access to healthcare to hinder surveillance.

Despite overwhelming evidence for a causative relationship between poverty and disease, critical gaps exist in our understanding of how to design surveillance systems for these at-risk communities. Past work on infectious disease surveillance has focused at the state-level (Polgreen et al. 2009; Scarpino et al. 2012) or assumed that risk was evenly spread across well-mixed populations (Pelat et al. 2014). Surveillance studies focused on broader definitions of health and on chronic diseases have found similar disparities to the ones presented here (Liao et al. 2004; Kandula et al. 2007).

Methods

As a measure of situational awareness, we focus on a surveillance system’s ability to predict hospitalizations. To achieve this goal, we constructed generalized additive models. First, zip codes are partitioned into poverty quartiles. We then expanded each predictor in a third-order B-spline basis with six degrees of freedom to allow for non-linear effects. To avoid overfitting, we regularize the spline coefficients using a lasso penalty, with the regularization parameter chosen by cross-validation. We also evaluated out-of-sample Poisson log-likelihoods and performed least squares regressions. To test for the coherence of each poverty quartile, we calculated the pairwise correlation coefficient between all zip codes within a grouping. We confirmed these results using a principle component analysis. To determine significance, both for the correlation analysis and predictive performance, we randomly assigned zip codes to poverty groups 5000 times and repeated the analyses.

Results

We analyzed the effectiveness of an integrated surveillance system—one that combines data from Biosense 2.0, ILINet, Hospital Discharge Records, and Google Flu Trends. At higher levels of aggregation—e.g. at the state-level, or multiple counties within a state-level—we find that these data sources correlate well with seasonal influenza. We find strong evidence that these data sources work significantly better for affluent populations than for less affluent, at-risk populations. Furthermore, we find that these most at-risk zip codes are more synchronous with each other and have higher hospitalization rates for influenza.

Conclusions

Populations with lower socioeconomic status often experience higher hospitalization rates across a range of diseases. One causative mechanism for this increased burden is reduced access to healthcare (Shi et al. 1999). Our results suggest that this reduced access may also have profound public health consequences, by impairing situational awareness. Specifically, we find that an integrated, data-driven surveillance system can accurately predict one-week ahead inpatient influenza hospitalizations in wealthier, but not poorer, more at-risk zip codes. This indicates that the high-tech, integrated surveillance systems of recent focus in the literature have a data blindspot—these technology-driven systems miss at-risk populations.

Keywords

Disease Surveillance; Poverty; Influenza; Forecasting

References

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A Comparison of Clinical Surveillance Systems in New York City

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Objective
To compare two clinical surveillance systems in development in New York City, one built on a distributed query network of electronic health records (EHRs) and the other accessing data from a Health Information Exchange (HIE).

Introduction
The widespread adoption of Electronic Health Records and the formation of Health Information Exchanges has opened up new possibilities for public health monitoring. Since 2009, The New York City (NYC) Department of Health and Mental Hygiene (DOHMH) has been developing two public health surveillance systems for chronic diseases. The first is the NYC MacroScope, which is built on a distributed query network (the Hub) of 740 New York City ambulatory practices all using proprietary software from one EHR vendor (eClinicalWorks). The second model, Query Health, still in its initial phase, accesses data collected by Healthis, the largest NYC HIE. This study compares these two models for potential disease surveillance and public health application.

Methods
In the Query Health model, the data has already been collected and standardized by Healthis and is transmitted in HL7 C32 standards, one document per patient. Data is available from 100% of the facilities, but facilities are providing Healthis with varying areas of the record. For NYC MacroScope, queries are developed and executed nightly on each individual practice’s EHR. Because queries are being executed against the live practice database, individual practices may not send a response to every query, but all areas of the record are being accessed for each practice that does return data. Poor data documentation at certain practices is a challenge in both systems. Inclusion criteria for Hub data were applied such that annually each provider minimally has a) seen 10 adult patients, b) documented BMI or BP on >=50% of patients, c) prescribed a medication to >=20% of patients, and d) documented 1+ ICD-9 codes for >=80% of patients. Individual provider documentation has not yet been assessed for Query Health.

Results
The Hub had 6 million patients who ever had a visit at one of the 740 participating ambulatory practices, representing approximately 9% of the estimated over 8,000 NYC practices. This includes non-NYC residents and has not been de-duplicated for patients visiting multiple practices. Ninety-three percent (n=686) of Hub practices returned data for the NYC MacroScope queries. For 2013, 700,000 adult patients with an eligible visit to a primary care provider that met the inclusion criteria were included in the MacroScope.

The participating Query Health HIE had 26 of the 54 (48%) NYC hospitals, an additional 15 hospitals on Long Island, and 61 non-hospital facilities submitting patient demographic data for approximately 9 million patients with both in-patient and ambulatory visits. Current data coverage is variable with 94% of facilities submitting encounter data, 80% submitting diagnosis data, 65% submitting lab results, 39% submitting vital signs, and 24% submitting medications. Practice documentation will also be a factor for Query Health and inclusion criteria will be applied for future surveillance efforts.

Conclusions
The NYC MacroScope has provided a novel view for chronic disease surveillance on a scale not previously seen for the health of New Yorkers. This model allows more complete access to the medical record, but is limited to participating practices returning data nightly. Unlike the MacroScope, Query Health has access to data for all participating facilities, but not all areas of the patient record are currently available in Query Health. The areas in patient records currently available for Query Health have potential for estimating disease prevalence. As Query Health facilities have limited vital sign and medication data, the MacroScope may be a more complete system for disease treatment and control estimates. As HIEs expand and receive more areas of the patients’ record, Query Health has the potential to be a large scale source for public health surveillance. Continued work is needed with HIEs and to support improvement of data completeness and quality, especially for public health use cases, in NYC and beyond.

Keywords
Chronic disease surveillance; Surveillance system; Health Information Exchange

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Monitoring and Evaluation Mechanism for Multi-Center Capacity Building Gestational Diabetes Program for Physicians in India

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Objective
With implementation of program on all India level aim is to develop a robust monitoring and evaluation system to ensure quality assurance and standardized course delivery on all India level.

Introduction
International Diabetes Federation (IDF) estimates that 21.4 million women in 2013 had some form of hyperglycaemia in pregnancy and in India alone an estimated 4 million women have GDM. Recognizing the shortfall of trained manpower; Certificate Course in Gestational Diabetes Mellitus (CCGDM) was launched in 2012; since then it has spread across 17 states and 39 cities across 55 regional training centers and trained 2400 Primary care physicians (PCP) all across India.

Methods
Inadequate knowledge among PCPs is one of the major obstacles in the prevention and management of GDM therefore we developed a comprehensive 4 modular course to train PCPs which is a joint program of Public Health Foundation of India and Dr. Mohan’s Diabetes Education Academy(WHO Collaborating centre) with final approval of the course curriculum by national expert panel.A cadre of Observers who are eminent Public Health Professionals were the backbone. It incorporated on-site monitoring visits every month to Regional Centers for evaluation on the basis of standardized indicators and formats. Baseline survey was employed to assess Knowledge Attitude Practices of GDM among participants,SMS Real Time E- Monitoring System was used for meticulous and timely follow up, End Line Evaluation was planned at the end of program; by the means of face to face interviews information was received on structure of curriculum, teaching methods, session environment, knowledge improvisation, value addition.

Results
The analysis of data generated was subsequently published in reports and shared with stakeholders. The impeccable delivery of CCGDM has given it recognition from IDF and accreditation from South Asian Federation of Endocrine Society. The results of end line evaluation concluded with improved knowledge of PCPs (Pre-test & Post-test score, P<0.001), value addition to knowledge (98.5%), value addition to skills (96.8%), program enhanced routine treatment plan (95%); ideal for learning (96.1%), useful case studies (88.5%); interactive and informative sessions (98%), faculty competency (94%); professional network and referral (67.6%).

Conclusions
The launch of capacity building initiative is just the beginning but final success will depend on how effectively we monitor and evaluate it.

Keywords
Gestational Diabetes Mellitus; Monitoring & Evaluation; Pan India

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Prof. D. Prabhakaran, Dr. Sandeep Bhalla, Dr. V. Mohan, Dr. Ranjit Unnikrishnan

References
IDF Atlas 6th edition

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Avian Flu, Ebola, MERS, and Other Emerging Challenges for Influenza Surveillance Practitioners

Alan Siniscalchi and Brooke Evans

Objective
To continue efforts in characterizing the challenges experienced by influenza surveillance coordinators and other practitioners conducting surveillance for the presence of avian influenza, novel respiratory diseases, and other globally emerging viruses in an era of limited resources among public health agencies.

Introduction
Public health practitioners endeavor to expand and refine their syndromic and other advanced surveillance systems which are designed to supplement their existing laboratory testing and disease surveillance toolkit. While much of the development and widespread implementation of these systems was previously supported by public health preparedness funding, the reduction of these monies has greatly constrained the ability of public health agencies to staff and maintain these systems. The appearance of highly-pathogenic avian influenza (HPAI) H5N2v, and other novel influenza A viruses required agencies to carefully identify systems which provide the most cost-effective data to support their public health practice. The global emergence of influenza A (H7N9), Ebola virus strains, Middle East Respiratory Syndrome Coronavirus (MERS-CoV), and other viruses associated with high mortality, emphasize the importance of maintaining vigilance for the presence of emerging diseases.

Methods
This project included a review of data obtained from a survey of public health practitioners recruited among members of the International Society for Disease Surveillance (ISDS) Public Health Practice Committee (PHPC) during 2012 and 2013 (1, 2). In these surveys, questions were selected for discussion and additional responses collected from influenza surveillance coordinators using a web-based survey tool managed by ISDS staff on behalf of the PHPC. During 2014 and 2015, additional information was requested to assess efforts to identify highly-pathogenic avian and other novel influenza strains, MERS-CoV, and other emerging viruses (3). Special emphasis was made to obtain information on comparative approaches to cost-effective surveillance in response to an earlier ISDS policy paper (4). An early fall 2015 follow-up survey was prepared to obtain late-breaking data.

Results
The 2015 survey received an initial response from the majority (82%) of influenza surveillance coordinators practicing throughout the United States. This latest survey revealed that most jurisdictions continue to be challenged to be able to maintain the variety of surveillance systems needed for conducting emerging disease surveillance. A major challenge continues to be the recruitment and retention of well-trained and experienced public health and informatics staff to maintain these systems in an era of increasingly limited resources. Many public health practitioners are tasked with establishing new surveillance protocols for an increasing number of diseases associated with novel and emerging viruses including HPAI, influenza A (H3N2) infections associated with agricultural fairs and ruling out influenza A (H7N9), MERS-CoV, and even Ebola virus infections. Most jurisdictions continually struggle to determine which surveillance systems are the most cost-effective for providing the most valuable data in the face of decreasing funding.

Conclusions
Public health agencies continue to strive to develop and maintain cost-effective disease surveillance systems to better understand the burden of disease within their jurisdictions. The emergence of novel influenza, other respiratory viruses and other emerging diseases offer new challenges to public health practitioners. The importance of maintaining sufficient infrastructure and the trained personnel needed to operate surveillance systems for optimal disease detection and public health response readiness cannot be understated. Expansion of academic training programs and promotion of careers in public health surveillance will provide a pool of competent professionals to properly staff public health agencies.

Keywords
situational awareness; Ebola; MERS-CoV; novel influenza surveillance; resource limitations

References

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HIT Conformance Testing: Advancing Syndromic Surveillance System Interoperability

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Objective
Describe how the 2015 Edition of the National Institute of Standards and Technology’s (NIST) Syndromic Surveillance Messaging Validation Suite continues to support federal efforts to increase healthcare information technology interoperability for timelier public health surveillance in the US; and show how this tool is used to validate messages.

Introduction
Speed, reliability, and uniformity of data collection enable syndromic surveillance (SyS) systems to provide public health authorities (PHAs) with timely information about community health threats and trends. Increasingly, healthcare information technology (HIT) is being used to accelerate and automate data collection for more real-time surveillance, reducing irregularity in how SyS data are packaged and sent by healthcare providers. Continuing to focus on patient and population health outcomes, the on-going US federal program that certifies HIT to promote interoperability has mandated broader use of an updated standard for communication of SyS data. Under the Edition 2015 federal rule tied to Medicare and Medicaid reimbursement, hospitals, in addition to emergency departments and urgent care centers, are now required to provide SyS data to PHAs using HL7 2.5.1 messages that are in conformance with Release 2.0 of the CDC’s Public Health Information Network (PHIN) guide for SyS. To facilitate the intended application of this updated standard, a new version of conformance testing tools is being published, which will enable HIT developers to increase their probability of meeting the requirements outlined in the standard and lead to enhanced product interoperability and reliability.

Methods
To advance conformance to the standard and promote interoperability of HIT, the Office of the National Coordinator for Health Information Technology (ONC) has continued to maintain a voluntary HIT certification program. ONC certification testing provides the means to evaluate SyS data messages created by HIT against a mandated standard through use of a context-based validation method composed of a suite of publicly accessible, web-based tools developed by subject matter experts from NIST, ISDS, and the CDC. The updated Edition 2015 SyS Messaging Validation Suite (SyS-MVS) will support testing SyS data messages based on Release 2.0 of the PHIN Guide and includes test stories that set the clinical context, test SyS data, testing guidance, automated SyS message validation, and a forum for testers to ask questions or provide feedback about the suite. ONC-Accredited Testing Laboratories (ATLs) will use the suite to test HIT modules for certification, and HIT vendors can use them while developing their products. Healthcare providers and PHAs can download a version of the validation suite and use it locally to verify conformance of SyS messages containing real patient data for implementing SyS data exchange.

Results
As of August, 2015, the updated version of the Sys-MVS is being developed in anticipation of the publication of the ONC Edition 2015 HIT certification Final Rule due in Q3 2015. Several HIT vendors have been recruited to pilot test the draft SyS-MVS prior to release of the final version in December 2015. The ATLs are to begin using the SyS-MVS in January 2016, and local PHAs are anticipated to begin using the validation suite as part of their on-boarding process with their healthcare providers at that time. Feedback about the 2014 Edition of these tools was positive, indicating that the users: (1) were motivated to think through the steps for capturing/reporting syndromic data in more detail than before; (2) appreciated the subject matter expertise that generated the tools; and (3) used these tools locally to promote collection and reporting of standardized SyS data in a timely manner.

Conclusions
The 2015 Edition SyS-MVS, to be used nationally by the ATLs to test HIT for certification and locally by healthcare providers to validate electronic messages before sending their SyS data to PHAs, will help move the industry further toward true interoperability for efficient reporting and use of syndrome-based public health surveillance information.

Keywords
certification; healthcare information technology; interoperability; conformance; standards

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Objective
To describe Denver Public Health’s model for designing a business intelligence (BI) tool for HIV surveillance and outreach and the impact after implementation.

Introduction
Recently signed in Denver, the Paris Declaration demonstrates a collective resolution to end AIDS by continually monitoring these goals. However siloed data and in/out migration results in poor capacity to track population level care indicators for persons living with HIV (PLWH). Surveillance should not only enumerate PLWH but also support prevention and care programming (1). We designed and implemented the HIV Data to Care Tool to describe the continuum, from case finding to HIV care. This study describes a system to combine data sources to inform local HIV surveillance, outreach, and care. Development objectives included targeted community and clinical interventions and evaluation, user defined reports to identify subpopulation disparities, and a persistent data visualization readily available to stakeholders.

Methods
Existing local data sources were integrated into a common data infrastructure, including: CDC’s HIV surveillance system from Denver and 4 Denver-adjacent counties, US Census denominators and demographics, state mandated clinical measure reporting (viral load and CD4 counts), and HIV clinic encounter data (e.g., sexually transmitted infections, pharmacy and prevention measures). Denver Health, an integrated safety-net provider, serves 25% of Denver’s residents with electronic health record data for its patients. Collaborative requirements gathering defined needs and specifications, including wireframes, a data dictionary, and business needs. The web-based, custom developed business intelligence dashboard was built with MS-SQL Server Reporting Services and deployed after testing for quality assurance and usability.

Results
Requirements gathering identified six population health use cases (and dashboards) for integrated data analysis, within a BI environment: Diagnosis Summary, Linkage to Care, Retention in Care, Care Summary, Community Viral Load, and a Surveillance Summary Page. Three patient line lists were also developed to meet outreach worker needs. Users control content through configurable parameters including demographics, location of PLWH residence, care site, and transmission category, allowing custom reporting to identify disparities (i.e., black MSM incidence rates), see Figure 1.

Conclusions
The tool integrated existing regional data sources and permitted new, near real-time visualization of complex information. Utilized locally for program planning and patient management, it provided a more nuanced understanding of the local epidemic and benefited resource allocation. It has improved evaluation, assessment and quality improvement of linkage, reengagement, and clinical outcomes by subpopulations, including identification of those not in care. Additionally reporting has supplemented the Denver Community Health Assessment, grant applications, and strengthened regional relationships through collaborative development. New efforts are focused on extending the tool to serve adjacent counties and integrating new data sources for more comprehensive reporting. A jurisdiction may benchmark an HIV-infected individual’s or population’s movement through the care continuum (2), gauge intervention effectiveness, and generate timely, user driven reports. The tool’s development and implementation model have proven reusable and translatable to address other priorities (e.g., chronic disease and immunization coverage).

Keywords
Informatics; Visualization; HIV

References

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Extending an Uncertainty Taxonomy for Suspected Pneumonia Case Review

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Objective
We sought to classify evidence that supports, refutes, or contributes uncertainty when reviewing cases of suspected pneumonia. We extend an existing taxonomy of uncertainty to classify these phenomena with the goal of improving existing Natural Language Processing (NLP) algorithms.

Introduction
Natural language processing algorithms that accurately screen clinical documents for suspected pneumonia must extract and reason about whether these mentions provide evidence that supports, refutes, or represents uncertainty. Our efforts extend existing algorithms [1] and taxonomies [2] that can be leveraged by NLP tools for more accurate handling of uncertainty for suspected pneumonia case review.

Methods
We conducted an automated screening of all outpatient encounters occurring at the VA Salt Lake City Health Care system between 01/01/2009 and 01/01/2012 to identify a cohort of suspected cases of pneumonia. Screening criteria included: a) presence of ICD-9 code for pneumonia and b) presence of an electronic physician note and/or same day chest imaging report. We then selected a random sample of 200 cases, 457 documents (216 physician notes and 241 corresponding chest imaging reports).

All cases were reviewed by a pulmonologist, an internist, and six allied health professionals. Using an annotation tool called eHOST [3] and criteria based on the CDC pneumonia case definition, reviewers classified evidence into three semantic classes for words or phrases that a) support, b) refute, or c) are uncertain for suspected pneumonia. Three reviewers (A1, A2, A3) conducted a thematic review applying a clinical uncertainty taxonomy to map those snippets marked as uncertain (3,150 unique snippets) into 12 categories of uncertainty (Table 1). We report ranges of pair-wise inter-annotator agreement (IIA) and annotations for each semantic class. We also report IIA for mapping uncertain evidence snippets to our uncertainty taxonomy and distribution stratified by document source.

Results
A total of 30,872 annotations were generated for supports (20,477, 66.3%), refutes (6,688, 21.7%), and uncertain (3,707, 12.1%). Range for pair-wise IAA across all semantic classes was (0.40-0.73) and individually for supports (0.61-0.81), refutes (0.46-0.65), uncertain (0.19-0.47). We observed substantial IAA between reviewer pairs for mapping the uncertain evidence snippets into 12 categories of uncertainty (Table 1): A1/A2: 0.86, A1/A3: 0.89, A2/A3: 0.82.

Conclusions
We have extended an existing taxonomy of uncertainty and applied it to suspected pneumonia case review, deepening understanding of how uncertainty is expressed in clinical texts for suspected pneumonia. Despite substantial annotator variability in identifying supporting, refuting or uncertain evidence we observed high agreement for classification of evidence snippets to a taxonomy of uncertainty.

Table 1. Distribution of Evidence Snippets

<table>
<thead>
<tr>
<th>Uncertainty Category</th>
<th>Physician Notes/Chest Imaging Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Radiology Finding</td>
<td>N (91)</td>
</tr>
<tr>
<td>Radiology Interpretation/Diagnosis</td>
<td>56 (1.78)</td>
</tr>
<tr>
<td>Symptom</td>
<td>83 (2.63)</td>
</tr>
<tr>
<td>Physical Finding</td>
<td>5 (0.17)</td>
</tr>
<tr>
<td>Source</td>
<td>0 (0.00)</td>
</tr>
<tr>
<td>Anatomic Location</td>
<td>0 (0.00)</td>
</tr>
<tr>
<td>Indication for exam</td>
<td>0 (0.00)</td>
</tr>
<tr>
<td>Other</td>
<td>29 (0.92)</td>
</tr>
</tbody>
</table>

Keywords
Natural Language Processing; Chart Review; Pneumonia

Acknowledgments
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References

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Comparison of Exposure to Risk Factors for Giardiasis Among Endemic and Travel Cases

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Objective

The objective of our study was to determine how demographic and exposure factors related to giardiasis vary between travel (both international and domestic) and endemic cases, for residents of the Region of Waterloo, Ontario.

Introduction

Increasing immigration to Canada coupled with the increasing number of Canadians travelling domestically and abroad is expected to significantly impact the burden of illness due to enteropathogens, including Giardia, in Canada¹. When estimating this burden of illness, international travel cases are considered to be distinct from domestically acquired cases due to differences in control measures in other countries²,³. However, there is no distinction made between domestic travel-related cases and endemic cases. As such, there has been no published literature where domestic travel-related cases (DTRCs) have been analyzed separately from endemic cases (ECs). This represents a considerable knowledge gap, as risk factors for contracting giardiasis via domestic travel may be different from those associated with endemic giardiasis or international travel. In our study, we subsequently demonstrated that grouping DTRCs and ECs together for analysis is likely not appropriate due to differences in exposures to risk factors for giardiasis among these groups.

Methods

Public health inspectors gathered exposure and demographic data for giardiasis cases reported in the Region of Waterloo from 2006 to 2012, inclusive. Logistic regression models were fit to assess differences in exposure to risk factors for giardiasis between international travel-related cases and Canadian acquired cases while controlling for age and sex. Multinomial regression models were also fit to assess the differences in risk profiles between international and domestic travel-related cases and endemic cases.

Results

Over the six year study period, 472 giardiasis cases were reported to the Region of Waterloo, 191 (40%) cases were related to international travel, and 282 (60%) cases were acquired in Canada. Of the cases acquired in Canada, 29 (10%) were related to domestic travel, and the remaining were acquired within the Region of Waterloo. Travel-related cases (both international and domestic) were more likely to go camping or kayaking, and consume untreated water compared to endemic cases. Domestic travel-related cases were more likely to visit a petting zoo or farm compared to ECs, and were more likely to swim in freshwater compared to endemic cases and international travel-related cases. International travelers were more likely to swim in an ocean compared to both DTRCs and ECs.

Conclusions

Traditionally, domestic travel related cases and endemic cases are grouped together into a domestic category (i.e., Canadian acquired) in studies that examine the effect of travel on the burden of illness on a population. To the best of the authors’ knowledge, this is the first study to separate Canadian cases into ECs and DTRCs, instead of the traditional method. We found significant differences in exposures to various risk factors for giardiasis among the various case groups (international travel, domestic travel and endemic), including significant differences between ECs and DTRCs. Therefore, we suggest that in future studies, DTRCs and ECs should not be included together as this may result in missing important associations or risk factors. Distinguishing between these two case types will likely have an impact on public health policies. Perhaps, of greater significance, our findings are important for creating effective and targeted health promotion campaigns to prevent giardiasis in this region, by targeting activity-specific (e.g., endemic, domestic or international travel) risk activities.

Keywords

giardiasis; travel-related infection; endemic infection; Giardia; surveillance

Acknowledgments

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References


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African One Health e-Surveillance Initiative

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Objective

1) To establish One Health workgroups and conduct an e-Surveillance assessment to inform national strategic planning efforts in pilot countries. 2) To provide evidence for the African Surveillance Informatics Governance Board (ASIGB) to address its mission of establishing e-Surveillance.

Introduction

Information and Communication Technology (ICT) can enhance public health surveillance (PHS) by facilitating the digital exchange of information. Electronic surveillance (e-Surveillance) is the use of electronic systems to empower the digitization of PHS functions of prevention, detection, and response. E-Surveillance maximizes compliance with the International Health Regulations (2005), enables efficient Integrated Disease Surveillance and Response, and empowers One Health.

In Africa, e-Health is hindered by donor-funded, short-term projects known as “pilotitus.” Proactive national leadership is required to establish a sustainable e-Surveillance program; an assessment and a strategic plan are the first steps.

Therefore, the One Health e-Surveillance Initiative (OHSI) was conceived and piloted by Public Health Practice, LLC (PHP) and the African Field Epidemiology Network (AFENET), with support by the Defense Threat Reduction Agency and the U.S. Centers for Disease Control and Prevention (CDC).

Methods

OHSI was piloted in Burkina Faso, Cameroon, Kenya, Nigeria, and Uganda from 2013 – 2015. One Health country-level work groups (CLWGs) were established and composed of medical epidemiologists, veterinary epidemiologists, laboratory scientists, informaticians, and clinicians. CLWG members were current employees of the Ministries of Health and Agriculture/Wildlife and were supported by the World Health Organization Regional Office for Africa country representatives. Their scopes of work included conducting a national e-Surveillance assessment and advocating for One Health e-Surveillance within their countries. PHP, AFENET, and CDC provided training and technical support for these efforts.

As part of the e-Surveillance assessment, CLWGs collected, cleaned, and analyzed data. They also interpreted data collected and wrote reports. Public health and veterinary surveillance units, health facilities, and laboratories at all administrative levels were assessed.

Results

OHSI stimulated formation of an African Surveillance Informatics Governance Board (ASIGB), chaired by the World Health Organization Regional Office for Africa (WHO/AFRO). OHSI established a framework consisting of the formation and training of One Health CLWG teams who conducted an e-Surveillance assessment. Additionally, a transnational e-Surveillance assessment tool and protocol capturing the variance of ICT capacity for e-Surveillance were developed. Owned by national Ministries, the assessment data collected will inform national strategic planning efforts. CLWG members are now advocates for One Health e-Surveillance.

Conclusions

ASIGB and CLWG creation, engagement, and ownership of the OHSI process and outcomes allowed for an in-depth understanding of the variance of ICT capacity to support e-Surveillance. The data collected through the assessment will support evidence-based strategic planning, and OHSI created champions of One Health e-Surveillance who can support this process.

Challenges included multiple languages, poor Internet connectivity, and time constraints of CLWG members due to the Ebola outbreak.

National strategic planning should occur using the assessment data collected. After incorporating feedback on the pilot processes and assessment, the ASIGB should support similar One Health e-Surveillance assessments in other African countries. OHSI should be replicated in other regions to support establishment of One Health e-Surveillance.

Keywords
e-Surveillance; One Health; Africa; Strategic planning; Evaluation

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Strengthening Community Surveillance of Ebola Virus Disease in Sierra Leone

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Objective
Systematically assess and strengthen the capacity of communities and sections in Port Loko District, Sierra Leone to detect significant events related to the reporting of Ebola virus disease (EVD) such as sick persons, secret burials and deaths. The components of the enhanced surveillance system will be described.

Introduction
Communities and sections that are consistently underreporting both illness and death pose a significant risk to surveillance and their efficacy is dependent upon the reporting of community structures such as government structures (primary health units (PHUs), schools), EVD response structures (contact tracers, community events based surveillance (CEBS), social mobilization), and traditional structures (chiefs, traditional healers, village task forces, religious institutions).

All structures are required to report to the District Ebola Response Center (DERC) as depicted in Figure 1. Frequent and protocolized information sharing is central to the reporting efficacy within this structure to ensure early capture of all EVD-related incidents.

Methods
Underreporting in 162 sections and communities in Port Loko district was determined by using a proxy of standard mortality ratio (SMR = reported deaths/expected deaths). Port Loko estimated mortality data (17.1 deaths per 1000/year) and population figures from the Statistics Sierra Leone were used to calculate expected deaths. Reported deaths were gathered through the national 117 alert system and verified by surveillance teams and burial teams. Sections were categorized by reporting efficacy (ranging from 0% to 100+% of expected deaths reported). Sections with the lowest reporting efficacies were prioritized first. Systematic interviews with each community reporting structures (government, EVD response and traditional). Interviews were conducted using an Open Data Kit (ODK) smartphone based closed questionnaire, designed to cross-check EVD reporting statistics and actions recorded under each reporting structure. Responses will be compared for levels of consensus (weighted scales and kappa scores) to evaluate the efficacy of the communication network and frequency of information sharing between reporting structures. Data are being used to find the barriers to reporting (e.g. leadership structure, awareness campaigns and geographic boundaries) and identify areas of weakness to provide a tailored response to strengthening surveillance.

Results
The described active surveillance model was implemented on June 15, 2015. Sick and death alerts were compared 4 weeks before the implementation of the active surveillance model and 4 weeks after implementation. In the 4 week period before implementation, Port Loko had 136 sick alerts and 749 death alerts, compared with 334 sick alerts and 869 death alerts in the 4 weeks following, a 146% and 16% increase respectively, for an overall increase of 36%. This increase in reporting was particularly pronounced in sections that previously underreported.

Conclusions
Focusing active surveillance efforts on silent sections leads to increased reporting of significant EVD events and the development of an integrated section-level surveillance system to identify disease triggers. Finally, strengthening disease-reporting structures may also support the detection of other rare and rapidly propagating infectious diseases, which may improve the reporting capacity of more common endemic disease and thus have wider benefits on the health system.

Further analysis of the active surveillance questionnaires to assess consensus among reporting structures is still ongoing and central to maintaining the integrity of EVD surveillance.

Keywords
surveillance; ebola; Epidemiology

Acknowledgments
GOAL would like to acknowledge the contributions of the Port Loko District Health Medical Team, District Ebola Response Center, WHO, CDC, Unicef

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Surveillance of Anthrax Foci Across Pipeline Constructions in Georgia, 2003-2014

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Introduction
Anthrax is a widely distributed endemic infection in Georgia, affecting nearly the entire country. Many of the human cases that are annually registered are agriculturally acquired. Anthrax remains a public health risk due to active, resistant soil foci. More than 2,000 anthrax affected areas are registered in the country; around 10% of them are active. Recent reports have indicated an increase in the number of human cases as a result of contact with the environment, this is hypothesized to be due to expansion of affected foci, and this has raised concerns of the disease spreading to new areas.

The control of anthrax foci is one of the main goals of the public health and veterinary service’s in Georgia. A surveillance program of anthrax foci across pipeline constructions in Georgia has been ongoing since 2003. Field trips are conducted by National Center for Disease Control and Public Health mobile teams to investigate each possible affected area across pipeline constructions.

Methods
During 2003-2014, 9,296 soil samples were collected from 19 different regions of the country and screened for the presence of Bacillus anthracis using bacteriological and molecular methods. Laboratory investigations at NCDC were performed using Threat Agent Detection and Response (TADR) algorithms.

Results
The data shows that areas around several construction sites were contaminated, therefore, workers had a potential exposure risk. Overall, 40 isolates of B. anthracis were obtained from the soil samples. Phenotypic (DTRA approved algorithm) and genetic (e.g., SNP, MLVA) profile studies were conducted for strain characterization.

Conclusions
Affected territories were isolated and decontaminated, and material that provided education on how to prevent the spread of anthrax in construction zones was provided to appropriate populations. The data obtained from this study highlights the importance of surveillance programs on especially dangerous pathogens.

Keywords
Bacillus anthracis; anthrax; surveillance; pipeline; decontamination

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Objective

Create a flexible user-friendly geo-based social media analytic tool for local public health professionals. With the goal of increasing situational awareness, system has capability to process, sort and display tweets with text terms of potential public health interest. We continue to refine the Social Media and Research Testbed (SMART) via feedback from surveillance professionals.

Introduction

Introduction: Numerous methods using social media for syndromic surveillance and disease tracking have been developed. Many websites use Twitter and other social media to track specific diseases or syndromes. Many are intended for public use and the extent of use by public health agencies is limited. Our work builds on 4 years of experience by our multi-disciplinary team with a focus on local surveillance of influenza.

Methods

Tweets with key words of interest are collected continuously using customized geo-targeted Twitter APIs. Based on topic, different areas are monitored: Influenza- 32 North American cities; Ebola- 12 west African cities, U.S. 3 cities and 5 areas with airline hubs; HIV- 2 US states & worldwide; Vaccine Exemption- any location, California Wildfires -4 metro areas. Cities are described by a 17 m. radius from Twitter account location or coordinates. Collected tweets are processed using machine learning programs trained to filter and sort tweets. English tweets are coded for: geolocation; retweet; image or other media, hashtag(s), URL(s). Processed tweets are stored in a database and displayed as requested on the SMART dashboard built with Python®, JavaScript®, and Node.js®.

Results

The SMART dashboard allows selection of geographic subsets (cities, areas, countries) for each topic area. Figure 1. The top display provides a summary of all tweets in database (all points, daily, weekly, monthly). Other panels include: Scalable time trend; Word Cloud; top 10 for URLs, Hashtags, Mentions, Retweets, Media displayed and geocoding status. Each display panel allows sub-setting by (all, past 30 days, past week and yesterday). Raw and/or filtered tweets are displayed. Rates for selected tweets are calculated per appropriate denominator population, listed and displayed on selectable maps. For each display users can add a keyword for additional refinement and then display the raw tweets for their query. Permitted users can download samples of tweets to Excel for further examination.

Conclusions

Situational awareness can be enhanced by using geo-targeted social media analytics and GIS methods displayed in a user-friendly manner. The system provides a feasible method to track and monitor issues of public health concern. In the long term, utility of social media tracking and improvement of the SMART system depends on use by professionals and feedback to developers in this emerging field of syndromic surveillance.

Keywords

Social media; Twitter; Syndromic; Dashboard; Influenza

Acknowledgments

This study is partially supported by the National Science Foundation Grant #1416509, project titled “Spatiotemporal Modeling of Human Dynamics Across Social Media and Social Networks”. We especially thank Chris Allen, Jiue-An Yang, Su Han, Elias Issa, and Jessica Dozier for data analysis.

References


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Evaluation of Legionellosis Surveillance in Michigan Focusing on Diagnostic Testing

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Objective
To describe the strengths and weaknesses of Michigan’s legionellosis surveillance system and the influence of diagnostic methods on the temporal and geographic distribution of legionellosis cases in Michigan.

Introduction
In Michigan, both presentations of legionellosis, Pontiac Fever (PF) and Legionnaires’ Disease (LD), are reportable through the Michigan Disease Surveillance System (MDSS), a web-based electronic database. Legionella pneumophila serogroup 1 is responsible for 50-90% of cases.¹,² Several diagnostic tests are available with varying sensitivities and specificities. Urinary Antigen testing (UAg) is the most commonly used test but only reliably detects L. pneumophila-1. Culturing is the gold standard test but is limited by antibiotic interference, technical expertise, and time.³ The purpose of this study was to evaluate Michigan’s legionellosis surveillance system and to determine if diagnostic methods influenced case distribution.

Methods
Descriptive and quantitative analyses were conducted using suspect and confirmed legionellosis cases reported to the MDSS from 2004–2013. Michigan’s legionellosis surveillance system was evaluated according to the 2001 MMWR surveillance system evaluation guidelines focusing on data quality, timeliness, and sensitivity.⁴ A survey of local health departments (LHD) was used to assess data quality, acceptability, and usefulness. The median time between each step in the reporting system was calculated and compared with state reporting requirements. Data from 2013 hospitalized LD cases reported through the MDSS were compared with 2013 Michigan hospital discharge data for LD cases to estimate the system’s sensitivity. Clinical laboratories in Michigan were surveyed for their diagnostic techniques and procedures.

Results
From 2004–2013, 1,756 cases of legionellosis were reported. Average annual incidences of 1.44 and 0.07 per 100,000 were calculated for LD and PF, respectively. Annual legionellosis incidence between 2004 and 2013 increased from 1.23 to 2.75 per 100,000. The median time from diagnosis to reporting was 2 days, with a median of 14 days between case entry and completion. Among all reported cases, 13.8% of key variables had unknown or missing values; however, completeness improved by more than 20% over 10 years. Hospital discharge data recorded 284 LD cases in 2013, while the MDSS recorded 246 cases. Of these, 189 were able to be matched on birthdate and zip code, for a calculated reporting sensitivity of 67.5%. Overall, 87.8% of cases were confirmed via UAg, of which 30.5% were confirmed by additional testing. Cultures were performed on 67.5%. Overall, 87.8% of cases were confirmed via UAg, of which 30.5% were confirmed by additional testing. Cultures were performed on 67.5%. Overall, 87.8% of cases were confirmed via UAg, of which 30.5% were confirmed by additional testing.

Conclusions
Overall, the surveillance system showed moderate sensitivity and reporting times in excess of the 24-hour state requirements. However, key variable completeness increased more than 20% over 10 years. With few cases diagnosed by culture, linking cases to an environmental source, and therefore investigating outbreaks, is challenging. The high proportion of cases confirmed by UAg alone could lead to 10-50% of cases going undiagnosed. Further research is needed to develop standardized molecular diagnostic testing methods, e.g. PCR, that are rapid, noninvasive, and comprehensive to allow for linking cases with environmental sources.

Keywords
Surveillance evaluation; Waterborne disease; Legionellosis

Acknowledgments
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References

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Highway Emergency Response and Accident Mitigation Service (HERAM) – A Field Report

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Piramal Swasthya Management and Research Institute, Hyderabad, India

Objective

The objectives of this paper are
1. To describe the functioning of a highway emergency response and accident mitigation service and
2. To characterize the profile of the accidents and the victims served by this project

Introduction

The increasing frequency and severity of Road Traffic Accidents (RTA) in India have caused grave concern for road safety, posing serious challenge to transport policy makers, planners, regulators, police, engineers and civil society alike. With just 1% of world’s vehicles, India leads with 10% of world’s total Road Traffic Fatalities, resulting in untold misery to lakhs of people and costing about 3% of the GDP. Due to the impact of the RTA, the United Nations declared the current decade “the decade of action for road safety with a goal to save five million lives”. Post-crash response is very critical to reduce the mortality and morbidity due to accidents.

Piramal Swasthya in collaboration with the National Highways Authority of India and General Insurance Company set up the Highway Emergency Response and Accident Mitigation Service between Hyderabad and Vijayawada, as a pilot project to address the post-crash response.

Methods

We report a descriptive cross-sectional analysis of data pertaining to accidents that occurred on the stretch mentioned above, over a period of one year from June 1st 2014 to 30th May 2015. Any RTA on this stretch could be reported by calling 1033. and all such calls were attended by a trained individual at a 24x7 central 4-seater call center. A fully equipped trauma ambulance was despatched to the site immediately. The victim was attended to by well-trained paramedical workers stationed in the ambulance and then transported to the nearest health care facility.

Information regarding the accident was also transmitted to the nearest police official. Thus the entire service was integrated with the Police at the ground level, thus leading to a very robust network of emergency response. Data were entered on an android based hand held device by a trained paramedic and analysed using descriptive statistics.

Results

A total of 1379 calls were received reporting a total of 1311 accidents took place in the study period leading to injuries to 1489 people. Of the 1311 accidents, 774 (59.04%) were attended to by 1033 ambulance. An incoming call was answered within an average of four seconds. On an average, an ambulance was dispatched to the site of accident by one min & 19 sec. More than half the accidents were of the collision variety (55.42%) while the non-collision variety contributed about one-fifth of the accidents. Most commonly, accidents took place in the evenings between 4 pm and 8 pm (24.03%) followed by those in the afternoon (20.15%). The age of the victims ranged from 1 yr to 93 yrs with a mean age of 36.4 (±14.6) yrs. A majority of the accident victims were males (83.73%). More than half the accident victims were between 21 and 40 yrs of age (56.64%).

Conclusions

Highway emergency response and accident mitigation service with a dedicated call centre, ambulance and integration with the police force is an effective service to provide post-crash response to accident victims on the National Highway. This service attended to 60% of the accidents in the service area. Incidence of fatalities was 5.63%. We recommend this service at national level to provide emergency ambulance care service to accident victims on National Highways.

Time taken for specific critical activities after receiving the distress call

<table>
<thead>
<tr>
<th>Time taken</th>
<th>Average time taken (Duration in MM:SS)</th>
<th>Maximum time taken (Duration in HH:MM:SS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>To answer an incoming distress call</td>
<td>00:04</td>
<td>00:00:14</td>
</tr>
<tr>
<td>To dispatch help / ambulance</td>
<td>01:19</td>
<td>00:07:05</td>
</tr>
<tr>
<td>To reach the accident site from the time of answering the call</td>
<td>12:01</td>
<td>00:30:57</td>
</tr>
<tr>
<td>To reach the hospital from the time of answering the call</td>
<td>37:52</td>
<td>01:12:05</td>
</tr>
<tr>
<td>To reach the hospital from the time of dispatch</td>
<td>36:35</td>
<td>01:04:45</td>
</tr>
<tr>
<td>To reach the hospital from the accident site</td>
<td>22:38</td>
<td>00:57:48</td>
</tr>
</tbody>
</table>

Keywords

Emergency Response; Accident Mitigation; Ambulance; Call Centre; Road Traffic Injury

Acknowledgments

We are grateful to all the call centre officials who have been handling all the calls since the inception of the programme. We acknowledge the contributions of the staff members of Piramal Swasthya Management & Research Institute in helping us complete this paper.

References


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Enhancing Biosurveillance Specificity Using Praedico™, A Next Generation Application

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Objective
To compare syndromic surveillance alerting in VA using Praedico™ and ESSENCE.

Introduction
Many methods to detect outbreaks currently exist, although most are ineffective in the face of real data, resulting in high false positivity. More complicated methods have better precision, but can be difficult to interpret and justify. Praedico™ is a next generation biosurveillance application built on top of a Hadoop High Performance Cluster that incorporates multiple syndromic surveillance methods of alerting, and a machine-learning (ML) model using a decision tree classifier [1] evaluating over 100 different signals simultaneously, within a user friendly interface.

Methods
513 million VA patient records, incorporating over 5 years of syndromic surveillance, were analyzed for identical syndromic surveillance groupings from outpatient ICD-9 diagnosis codes. The Praedico™ ML layer was trained by utilizing hundreds of false positive and true positive syndromic alerts. To guarantee high detection recall, the Praedico™ algorithm leverages many known detection algorithms, including versions of CDC, CUSUM, EWMA, and regression models [2]. The ML model combines these models and uses additional time series features to detect anomalies and user feedback received on previous alerts (high confidence alerts). Low confidence alerts, which many not trigger an alert but show a natural increase or normal divergence from the mean in data distribution are presented for users review. To facilitate alert interpretation, a natural language interface provides human interpretable messages relaying event significance by comparing historical values collected from the same facilities. Praedico™ syndromic alerts were compared to those generated by VA ESSENCE for the period of June 2014 thru May 2015.

Results
Praedico™ alerts were significantly lower compared to ESSENCE generated alerts (Table 1). This was expected as Praedico™ leveraged user feedback to enhance anomaly detection and improve precision of outbreak detection. Both Praedico™ and ESSENCE categorized alerts as high and low confidence groups. In both systems, higher deviation levels from expected values resulted in high confidence alerts. 62% of Praedico™ alerts directly correlated with ESSENCE alerts, suggesting that although the total number of Praedico alerts was smaller, they were not simply a subset of ESSENCE alerts. Praedico™ demonstrated higher seasonal sensitivity, adjusting for seasonality using historical and seasonal information, while ESSENCE alerts were more uniformly distributed over the year (Figure 1). The increased December and January alerts were due to ILI syndrome alerts, likely due to elevated influenza activity. Respiratory, Fever, and ILI syndrome groups had the highest number of alerts, and were significantly higher with ESSENCE (Figure 2).

Conclusions
Praedico™ demonstrated improved precision of surveillance syndrome clusters compared to VA ESSENCE by reducing the number of alerts. By reducing alerting fatigue, users’ sensitivity to computer-generated alerts remain high, which in return results in further usage, feedback, and more gradual improvement in the algorithm’s output (specificity and sensitivity), adapting to the interest of users.

Table 1. Total number of VA syndromic alerts generated by Praedico Biosurveillance and ESSENCE

<table>
<thead>
<tr>
<th>Month</th>
<th>Praedico</th>
<th>ESSENCE</th>
</tr>
</thead>
<tbody>
<tr>
<td>June 2014</td>
<td>771</td>
<td>15,846</td>
</tr>
<tr>
<td>May 2015</td>
<td>3,452</td>
<td>21,502</td>
</tr>
</tbody>
</table>

Keywords
ESSENCE; biosurveillance; Veterans; Big Data

References

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Biosense and Violence: Progress Toward Violence Prevention Using Syndromic Surveillance

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Objective
Our objective was to measure the incidence and prevalence of intentional violent injury and death using Illinois’ syndromic surveillance system.

Introduction
Violence is now clearly recognized as a public health problem. Intentional injuries ranked among the top six leading causes of death for Illinois residents aged 1-44 in 2013. The Illinois Department of Public Health currently collects data on violent injuries and deaths from emergency medical services reports, death certificates, coroner/medical examiner reports, law enforcement reports, and crime lab reports. However, syndromic surveillance provides near real-time data on violence-related emergency department visits that would increase the timeliness and quality of data available for public health interventions.

Methods
We developed violence syndromes using text and ICD-9 codes in the chief complaint and diagnosis code data from Illinois emergency departments. These were defined as weapon-related (gunshots and stabbings) and other physical assaults. Legal interventions and emotional/psychological abuse were excluded from the analysis. The violence syndromes were used to describe the number and distribution of cases of injuries treated at Illinois hospitals in 2014 that were attributable to physical assaults, gunshots, and stabbings. The data was stratified by demographic (gender, race, age group), temporal (since January 2014), and spatial (county, regional CD) characteristics. These results were compared with prior-year data reported through the Emergency Medical Service Data System and the National Vital Statistics System, as an initial estimate of data quality.

Results
The violence query retrieved 13,179 reports for the year 2014. Of these reports, whites (60.2%), females (51.8%), and the 25-49 year old age group (33.8%) had the majority of incidents. Compared to the syndromic surveillance reports, Emergency Medical Service Data System data contained a lower proportion of females (35.4%) and whites (36.5%), and a higher proportion of incidents in Northeastern Illinois (70.8% vs. 42.0%). There was a similar proportion of 25-49 year olds (36.4%). Data from the National Vital Statistics System indicated a higher incidence of violent death in whites (68.1%) and victims aged 25-49 (43.7%), and lower incidence in females (20.4%), compared to syndromic surveillance reports.

Conclusions
Results obtained from the syndromic surveillance system were comparable to the data in emergency medical service and violent death reporting system for demographic and spatial characteristics. It was not possible to differentiate between new visits of violence-related injuries and repeat visits to EDs for conditions treated previously, but we assumed the rate of duplicacy was similar across emergency medical service and syndromic surveillance data. We also assumed that morbidity and mortality trends in Illinois would be similar, and this assumption may limit the generalizability of our analysis.

Syndromic surveillance has the potential to provide real-time data to inform timely and data-driven public health responses to violence.

Keywords
violence; syndromic surveillance; data quality

References
1. Dahlberg L, Mercy J. History of violence as a public health issue. AMA Virtual Mentor. 2009 February; 11(2).

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Situational Awareness for Unfolding Gastrointestinal Outbreaks Using Historical Data

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Objective

The objectives of this project are to identify properties that influence the progression of an outbreak, evaluate the ability of a property-based algorithm to differentiate between military and civilian outbreaks and different pathogens, and develop a decision support tool to enhance situational awareness during an unfolding outbreak.

Introduction

The CDC defines a foodborne outbreak as two or more people getting the same illness from the same contaminated food or drink. These illnesses are often characterized as gastroenteritis until the causative agent is identified (bacterial or viral). Due to the globally interconnected food distribution system, local foodborne disease outbreaks often have global impacts. Therefore, the rapid detection of a gastroenteritis outbreak is of utmost importance for effective control. Situational awareness is important for early warning or detection of a disease outbreak, and tools that provide such information facilitate mitigation actions by civil/military health professionals. We have developed the Surveillance Window app (SWAP), a web based tool that can be used to help understand an unfolding outbreak. The app matches user input information to a library of historical outbreak information and provides context. This presentation will describe our analysis of global civilian and military gastrointestinal outbreaks and the adaptation of the SWAP to enhance situational awareness in the event of such outbreaks.

Methods

We collected data on about 100 civilian and military outbreaks caused by five pathogens (E. coli, Salmonella spp., Campylobacter jejuni, Shigella spp. and Norovirus). Outbreak history (causative agent, location, time of year, environmental conditions, population at risk), time series, and methods of detection were compiled. By comparing civilian and military outbreaks and performing cross pathogen analysis, we identified properties that would distinguish between different types of outbreaks that could be used in an algorithm applied in the SWAP. Analyses were performed to understand the influence of identified properties on cumulative case numbers and duration of an outbreak.

Results

We identified five properties with a potential to distinguish between the different outbreak types. These properties are cumulative case count, time information, product or site/event (e.g. salad or wedding), source of contamination (e.g. cooked food, uncooked food, live animals), and season. Using these properties, we compared outbreaks occurring in civilian and military populations (Table 1). Similarly, these properties were used to differentiate between outbreaks caused by different pathogens. Figure 1 shows the outbreak trends for cumulative case count, duration, and time to peak for different pathogens. The epidemiological and biological reasons for these differences are discussed in the presentation. The SWAP based evaluation of outbreaks is ongoing. Initial analyses showed that when data for military outbreaks were used as input, more than 50% of the top matches were other military outbreaks. We are currently working on SWAP based analyses for identification of the pathogen.

Conclusions

The SWAP is a free web based tool that facilitates understanding of an unfolding outbreak in the context of a similar historical epidemic. Our research indicates that this tool may be used in identifying probable causes and pathogens associated with a gastrointestinal outbreak. An early and accurate identification of cause will aid public health officials during the surveillance of the outbreak and in developing appropriate control measures.

Table 1: A comparison of military and civilian outbreak properties

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Civilian</th>
<th>Military</th>
<th>Proposed cause</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cumulative case count</td>
<td>Varies</td>
<td>Smaller</td>
<td>Exposed population (population at risk) is small and homogeneous</td>
</tr>
<tr>
<td>and duration of an outbreak</td>
<td>based on</td>
<td>civilian</td>
<td></td>
</tr>
<tr>
<td>Pathogen</td>
<td></td>
<td>outbreaks</td>
<td>and similar across pathogens.</td>
</tr>
<tr>
<td>Time to peak</td>
<td>Varies</td>
<td>Military</td>
<td>A closely knit population</td>
</tr>
<tr>
<td>Pathogen</td>
<td>based on</td>
<td>outbreaks</td>
<td>within 1-2 weeks</td>
</tr>
<tr>
<td>Source of contamination</td>
<td>Nine</td>
<td>Contaminated cooked food causes majority of military outbreaks</td>
<td></td>
</tr>
<tr>
<td>Pathogen</td>
<td>possible</td>
<td>food</td>
<td></td>
</tr>
<tr>
<td>Season</td>
<td>Most cases occur in</td>
<td>Most military outbreaks occur in</td>
<td>New recruits</td>
</tr>
<tr>
<td></td>
<td>summer</td>
<td>autumn</td>
<td></td>
</tr>
</tbody>
</table>

Cross pathogen analyses - Mean

Keywords

Surveillance window app (SWAP); food borne outbreaks; decision support tools; situational awareness and surveillance; gastroenteritis

Acknowledgments

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References

http://swap.lanl.gov

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Interest of Prospective Spatio-Temporal Analysis from ED Data to Detect Unusual Health Events

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Objective
To present the implementation and the first results of a prospective spatio-temporal analysis from emergency department (ED) data in Reunion Island.

Introduction
Many syndromic surveillance systems use spatio-temporal analysis to detect local outbreaks such as gastrointestinal illnesses and lower respiratory infections [1, 2]. In Reunion Island, the syndromic surveillance system is based mainly on ED visits. Spatial analysis was first used in 2013 to validate retrospectively a cluster of viral meningitis [3]. At the end of 2014, the Regional Office of French Institute for Public Health Surveillance implemented a prospective computer-automated space-time analysis in order to launch daily analyses of ED visits.

Methods
To realize the prospective space-time analysis, a R program generate the parameter files of SaTScan™ and then run the software in batch mode. The space-time permutation model is used with the following parameters: the upper limit on the geographical size of the outbreak is a circle with a 5-km radius, the maximum temporal length is set at 1 and 7 days, the number of days included in the calculation of the expected number is 60 days and the number of replications is set at 999. If the recurrence interval of a signal is 2.7 years for a temporal window of 1 day (p<0.001) or 19.1 years for a temporal window of 7 days (p<0.001) then an investigation is carried out.

Results
Between January 1st and May 31, 2015, the prospective spatio-temporal analyses from ED data generated 13 cluster-signals for a temporal window of 7 days and 3 cluster-signals for a temporal of 1 day (Table 1). From 25 to 31 January 2015, several consecutive signals of gastroenteritis were generated. The epidemiological investigation allowed to confirm the outbreak nevertheless the source of contamination has not been identified. At the end of January 2015, the surveillance system detected a significant increase of conjunctivitis cases. During the investigation, the general practitioners (GPs) of the area confirmed this health event that remained localized. On April 2, 2015 a significant increase of bronchiolitis was detected but was not confirmed by GPs. In consequent the signal has been invalidated.

Conclusions
The implementation of a prospective computer-automated space-time analysis based on ED data allowed the early detection of several infectious diseases outbreak. Though the source of contamination is not always identified, it makes possible early implementation of control measures.

Table 1: Results of space times analyses from ED data, January 1 to May 31, 2015, Reunion Island

<table>
<thead>
<tr>
<th>Syndrome</th>
<th>Temporal window (days)</th>
<th>Signal date</th>
<th>Signal code</th>
<th>Number of observed cases</th>
<th>Number of expected cases</th>
<th>p-value</th>
<th>Recurrence interval (years)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gastroenteritis</td>
<td>7</td>
<td>1/25/2015</td>
<td>97209</td>
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</tr>
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<td>Bronchiolitis</td>
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</tr>
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</table>

Keywords
Syndromic surveillance; Emergency Department; Spatial analysis

Acknowledgments
All emergency departments of the Reunion Island

References

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Using Syndromic Surveillance to Identify Synthetic Cannabinoids or Marijuana Adverse Health Events in Virginia

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Objective
Use syndromic surveillance to identify and monitor adverse health events resulting from synthetic cannabinoid receptor agonists (SCRAs) or marijuana. Characterize the current trend of SCRAs and marijuana use among emergency department (ED) and urgent care center (UCC) visits in Virginia to determine whether findings align with utilization trends identified by other states from poison control center calls and ED visits.

Introduction
SCRAs are accessible and affordable, sold online, in gas stations, and in “head” shops for $5-30 per package.[1] While marijuana is a schedule 1 narcotic, unavailable for any use, SCRAs navigate the legal landscape with marketing as non-consumable and frequent modifications to the active ingredients that outpace lawmakers’ updates. When consumed, SCRAs bind the same receptor as the active ingredient in marijuana with 10-1000 times the affinity. Physical reactions to marijuana use include breathing problems, increased heart rate, hallucinations, paranoia, lower blood pressure, and dizziness. [2] Health departments have reported varying clinical presentations in response to SCRAs, including extreme agitation and tachycardia. Ongoing reports of SCRA reactions and rising marijuana legalization emphasize the imperative to leverage syndromic surveillance to monitor trends, detect emerging outbreaks, and observe changes in clinical presentations or user demographics.

Methods
A retrospective study was conducted using ED and UCC chief complaint visit data received by the Virginia Department of Health (VDH). A SCRA and marijuana query was developed using ESSENCE to search for relevant text strings within chief complaints based on nationwide media reports, public health alerts such as Epi-X notices, and consultation with syndromic surveillance practitioners in other states. Descriptive analyses were conducted on ED and UCC visits identified by chief complaint from January 2010 through July 2015.

Results
From January 2010-July 2015, 733 SCRA or marijuana related ED and UCC visits were identified in Virginia, of which 20% (147) occurred since January 2015. Visits peaked in September-October 2013 (43) and May-June 2014 (48), and continued to increase throughout 2015, with a peak in April 2015 (32). Of the 733 visits, 481 (66%) further identified adverse health events in the chief complaint. Most of the 481 visits indicated a nondescript drug reaction (195), while the remaining were grouped into the following 10 categories: cardiac (57), unresponsive (49), restlessness (49), gastrointestinal (31), fainting (24), weakness (24), mental health (22), dyspnea (18), seizure (11), or injury (7). Visits occurred predominantly in males 10-29 years of age (318, 43%), with a median age of 23 years. Males accounted for roughly twice as many visits as females, both overall and across adverse health event categories, except dyspnea and gastrointestinal which were distributed equally among males and females.

Conclusions
Syndromic surveillance identified SCRA or marijuana related ED and UCC visits in Virginia that corroborate findings from poison control center calls and ED visits in other states. Virginia temporal trends align with clusters in June 2014 in Washington, DC and April 2015 in Alabama, New York and New Jersey. Of the 10 Virginia identified adverse health event categories, 9 are represented in reports from New York and New Jersey, DC, New Hampshire, and CDC. Virginia additionally identified adverse health events relating to injury, specifically motor vehicle accidents. Study findings resulted in data sharing with Virginia poison control centers, presentations to the state fusion center and local public health, and distribution of a clinician letter for heightened awareness and notification of adverse health events from SCRA use. Continued surveillance will allow detection of fluctuations in trends and demographics resulting from the discontinuation of SCRA sales and regional marijuana legalization.

Keywords
synthetic cannabinoid; syndromic surveillance; marijuana

Acknowledgments
Keith Li, Jacqueline Reuben-DC DOH
Jonah Long-PA DOH

References

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Lessons Learned from the Transition to ICD-10-CM: Redefining Syndromic Surveillance Case Definitions for NC DETECT

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Objective
To describe lessons learned from the transition to ICD-10-CM.

Introduction
NC DETECT receives ICD-9-CM codes for emergency department (ED) visits and uses these codes in case definitions for syndromic surveillance (e.g. infectious disease, injury, etc.). Hospitals will begin using ICD-10-CM codes on October 1, 2015. As a result, preparations have been made to accommodate ICD-10-CM codes in NC DETECT for data transmission, receipt, processing and use in the NC DETECT Web Application.

Methods
Staff from the Carolina Center for Health Informatics (CCHI) at the University of NC at Chapel Hill (UNC-CH), the Injury Prevention Research Center (IPRC) at UNC-CH, and the NC Division of Public Health (NC DPH) reviewed existing case definitions. While other systems are planning to map ICD-10-CM codes back to ICD-9-CM codes, the approach in NC was to add ICD-10-CM codes to existing definitions. A variety of resources have been used for updating case definitions including: mapping resources, CDC input, and input from subject matter experts. The prioritization of case definitions was based on perceived need, frequency of usage, and ease with which the definitions could be updated. Case definition review has also provided the opportunity to streamline definitions where possible, rename definitions for clarity, add new definitions, and archive those that are no longer useful. In addition, once the transition to ICD-10-CM has taken place, NC DETECT ED data will be monitored for consistency in reporting. If needed, case definitions will be revised to meet surveillance goals.

Results
To date, 15 case definitions have been updated with ICD-10-CM codes, one new definition has been created, and one definition is awaiting approval from a content expert. Table 1 displays the updated case definition for heroin overdose and describes key differences between ICD-9-CM and ICD-10-CM. The original ICD-9-CM case definition contains one diagnosis code and one External Cause of Injury code (E-code). The ICD-10-CM case definition contains one diagnosis code and one External Cause of Injury code (E-code). The ICD-10-CM case definition for heroin overdose and describes key differences in ICD-10-CM, respectively. Another difference between ICD-9-CM and ICD-10-CM is the magnitude of codes available. While ICD-9-CM contains ~14,000 individual codes, ICD-10-CM contains ~70,000.

Since ICD-10-CM codes contain many codes that are not found in ICD-9-CM, direct mapping is difficult. Using the example displayed in Table 1, the ICD-10-CM case definition includes the code T40.1X3, “Poisoning by heroin, assault.” There is no direct match with this code in ICD-9-CM; the closest approximation would be E962.0, “Assault by drugs and medicinal substances.” Since the transition does not take place until October 1, 2015, results are not available for assessing the utility of the updated case definitions. Preliminary results will be discussed during the presentation.

Conclusions
The transition from ICD-9-CM to ICD-10-CM required extensive preparation prior to the implementation to ICD-10-CM on October 1, 2015, and equally extensive monitoring after the date of implementation. It is important that local, state, and national organizations involved in syndromic surveillance share lessons learned from the transition to assist other organizations that may be struggling with how to adapt to the coding changes.

References
4. NCIPC. Recommended Actions to Improve External-Cause of-Injury Coding in State-Based Hospital Discharge and Emergency Department Data Systems. CDC. Atlanta (GA); 2009.

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Table 1. Example of a NC DETECT Case Definition: Heroin Overdoses

<table>
<thead>
<tr>
<th>Key differences in ICD-10CM</th>
<th>Category</th>
<th>Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
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<td>ICD9CM</td>
<td>T40.1X3</td>
<td>Poisoning by heroin, assault.</td>
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<tr>
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<td>T40.1X3</td>
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</tr>
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</table>

Keywords
Syndromic surveillance; Lessons learned; Definitions

Acknowledgments
We would like to acknowledge NC DPH, IPRC, and UNC-CH. This project is supported by the CDC as part of its Core Violence and Injury Prevention Program.
Automating Ambulatory Practice Surveillance for Influenza-Like Illness

Andrew Walsh*

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Objective
To investigate the viability of using prediagnostic syndromic surveillance data from ambulatory practices for influenza-like illness surveillance

Introduction
Data submitted to ILINet from ambulatory practices are a primary feature of influenza-like illness (ILI) surveillance in the United States. Practices count relevant patient records and submit this data manually to ILINet. The ongoing data collection is useful for surveillance, and a significant amount of historical data has accumulated which is useful for research purposes and comparisons of the present season to the past. However, the tabulation of this data is costly, and retention of sentinel practices can be challenging as there is no mandate to submit data.

Increasingly, the EpiCenter syndromic surveillance system is receiving data from ambulatory practices. Syndromic surveillance data is sent automatically in near-realtime. Meaningful Use requirements incentivize practices to participate in ongoing data transmission. Syndromic surveillance data from ambulatory practices is thus a possible substitute for the current, more labor-intensive surveillance of ambulatory practices.

Methods
Chief complaints, triage notes and patient temperature were collected from 141 hospitals and 710 ambulatory practices for patients from 5 Philadelphia-area counties. An ILINet-compatible classification was defined using cough or sore throat in either the chief complaint or triage notes along with either mention of fever in one of those fields or a measured patient temperature over 100°F. The existing EpiCenter classification of ILI Specified, which looks for reference to influenza or ILI in the text fields, was also used. Registrations were classified using both criteria.

Results
A total of 1,497,521 ED registrations and 836,431 ambulatory registrations were collected from June 30, 2014 to June 28, 2015. Of these, 10,661 (0.71%) ED registrations and 2,359 (0.28%) ambulatory registrations were classified as ILINet compatible, while 18,363 (1.23%) ED registrations and 11,088 (1.33%) ambulatory registrations were classified as ILI specified. Figure 1 shows the weekly time series of the percentage of visits by classification. The registrations classified as ILI specified more closely matched the expected values, with a baseline around 2% of visits and a peak of 4%. The temporal pattern of these registrations was also most closely matched the expected pattern for flu season.

The percentage of ambulatory visits with an ILI specified increased earlier in flu season than the ED visits. This pattern was not consistent across all counties. Philadelphia County in particular exhibited minimal change in ILI visits at any point during flu season.

Conclusions
The current criteria used to define ILI-related visits for ILINet may not be applicable to patient-provided data. Although the ILINet criteria use symptoms that patients can identify and report, in practice those symptoms are not always individually recorded in chief complaints for ILI patients. A registrar is more likely to summarize multiple symptoms as “flu symptoms,” “URI” (for upper respiratory infection), or similar. In essence, the registrar is performing a first level of classification into an ILI category. If syndromic surveillance data is to be used for ILI surveillance, the criteria for classifying visits will need to account for this summarizing of symptoms by the data providers.

The ILI time series suggest different usage patterns of ambulatory practices and EDs at different points in the flu season. This may be indicative of access to ambulatory care; patients may seek treatment there earlier if they can, while those without ambulatory access will wait longer until their disease is severe enough to warrant visiting the ED. This could explain the geographic differences observed, but it cannot explain all of the temporal differences, as influenza does not typically span a month or more even without treatment. It may also be the case that other, milder respiratory illnesses circulate in the fall.

Keywords
ILINet; ambulatory; syndromic surveillance; influenza

Acknowledgments
We wish to thank the Pennsylvania Department of Health for funding support and data for this work.

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Enhancing EpiCenter Data Quality Analytics with R

Andrew Walsh*
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Objective
To demonstrate the broader analytical capabilities available by making the R language available to EpiCenter reporting

Introduction
The EpiCenter syndromic surveillance platform currently uses Java libraries for time series analysis. Expanding the data quality capabilities of EpiCenter requires new analysis methods. While the Java ecosystem has a number of resources for general software engineering, it has lagged behind on numerical tools. As a result, including additional analytics requires implementing the methods de novo.

The R language and ecosystem has emerged as one of the leading platforms for statistical analysis. A wide range of standard time series analysis methods are available in either the base system or contributed packages, and new techniques are regularly implemented in R. Previous attempts to integrate R with EpiCenter were hampered by the limitations of available R/Java interfaces, which were not actively developed for a long time.

An alternative bridge is via the PostgreSQL database used by EpiCenter on the backend. An R extension for PostgreSQL exists, which can expose the entire R ecosystem to EpiCenter with minimal development effort.

Methods
The PL/R extension version 8.3 was installed in PostgreSQL 9.2 using R version 3.2.1. Gaussian and Poisson regression models were fit using the base glm function. Negative binomial regression models were calculated using the R package MASS version 7.3.42.

Regression models were fit using covariates calculated from dates - day of week, hour of day, days since start of time series, and periodic variables with an annual period. Model fits were compared using root mean squared error (RMSE) and median average deviance (MAD). Out-of-range values were defined as observations outside the 99.9% confidence interval defined by the model distribution.

Predictions for periods with outages were generated from the date-based covariates and models fit to other data.

Results
A total of 16,028,901 emergency department (ED) registrations from 415 hospitals were collected from July 1, 2014 to June 30, 2015. Hospitals were grouped on whether known or obvious data quality issues existed in their data (N=71) or not (N=344). Model performance was assessed on data from hospitals without apparent data quality issues. Gaussian regression models were fit with no covariates, approximating EpiCenter’s moving average analysis method. Poisson and negative binomial regression models were fit using date-based covariates.

The Gaussian models had an average RMSE of 2.89; for the Poisson and negative binomial models it was 2.09. The MAD for the Gaussian models was 2.26; for the Poisson and negative binomial models it was 1.26.

Out-of-range values were generated comparing observations to the 99.9% confidence intervals calculated from the model fit. All detected issues were assumed to be false alerts, as no known or obvious data quality issues existed in this data. Figure 1 shows the number of false alerts relative to ED volume. False alerts from the Gaussian model decreased with increasing volume, while false alerts from the other two models showed the opposite trend.

Detection of known outages in the data from the 71 hospitals with known issues showed a similar performance profile between the modeling options.

Conclusions
The PL/R extension for PostgreSQL provides a convenient option for extending the data quality analytics of EpiCenter. By adding the resources of the R environment, new techniques can be implemented and deployed flexibly with minimal development effort. Future work will focus on integrating these methods into the main EpiCenter workflows.

ED volume data is not always well modeled with a Gaussian distribution, particularly at smaller facilities. Regression models can account for the structure in the data, such as the day-of-week effect, and also more accurately reflect the true distribution of the data, improving precision in detecting data quality problems. While the analysis presented here makes some over-broad simplifying assumptions (e.g. there are almost certainly unknown and subtle data quality issues in the data which was assumed to be reliable for the purposes of quantifying false alerts), it does demonstrate the advantage of expanded analytical capabilities.

Keywords
R; data quality; EpiCenter; syndromic surveillance

Acknowledgments
We wish to thank the New Jersey, Ohio, Pennsylvania and Wyoming Departments of Health for funding support and data for this work.

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Alcohol-Related ED Visits and Ohio State Football: Putting the O-H in ETOH

Kristen A. Weiss* and Andrew Walsh
Health Monitoring Systems, Inc, Pittsburgh, PA, USA

Objective
Identify any relationship between alcohol-related emergency department visits in Franklin County, Ohio and Ohio State University football games.

Introduction
According to the Center for Disease Control (CDC), binge drinking causes over half of the 88,000 excessive alcohol use deaths and costs approximately $149 billion dollars annually in the United States\(^1\). Additionally, excessive alcohol use can increase the risk of many other health problems, including injuries and cancer, placing a large burden on public health. In Franklin County, Ohio, The Ohio State University (OSU) football games are an occasion of binge drinking for the student body and Columbus population alike. The purpose of this study is to determine if the binge drinking population is significantly different during football games.

Methods
This study looked at emergency department (ED) registration data for Franklin County, Ohio for the past 5 years that was classified as alcohol-related using EpiCenter. Days that had a significantly elevated number of visits were identified as being two standard deviations above the yearly mean, and termed “high volume” (HV) days. These HV days were characterized by whether or not they occurred relative to an OSU football game or football-related tradition. Comparisons were drawn between total counts, gender distribution, and average age of football vs. non-football HV days.

Results
An average of 15 total HV days were found each year, ranging from 11 in 2011 to 19 in 2012 (Table 1). The total percentage of these HV days that can be correlated to OSU football games is 37%. This ranges by year, and seems to trend with the regular season football record. In 2011, the record was 6-6, and the percentage of HV days associated with OSU football dropped to 18%. By contrast, the record was either 11-1 or 12-0 the other 4 years, corresponding to higher percentages. A comparison of football to non-football HV days by year can be seen in Figure 1. The results were then broken down further, as seen in Table 2. There was no significant difference found between the number of visits on football vs. non-football HV days at the 95% confidence level (\(p\) value 0.054). Visits by females were significantly higher for football HV days than baseline (\(p\) value 0.002). The average patient age was significantly different between football and non-football HV days, at 36 and 40 years old respectively (\(p\) value 0.001). Additionally, the first football game of the season accounted for at least 1 HV day in 4 of the 5 years analyzed.

Conclusions
The binge drinking population is significantly different during football games in Franklin County. This population is comprised of significantly younger adults and more females. With this information in mind, public health may desire to do seasonal targeted awareness campaigns addressed to this population. Additionally, considering the consistency of binge drinking episodes that occur during the first football game of the season, public health may want to emphasize these dates for the campaigns.

Table 1

<table>
<thead>
<tr>
<th>Year</th>
<th># HV Football Days</th>
<th># HV Days Total</th>
<th>% Football</th>
<th>Regular Season OSU Football Record(^2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>4</td>
<td>13</td>
<td>30.77%</td>
<td>11-1</td>
</tr>
<tr>
<td>2011</td>
<td>2</td>
<td>11</td>
<td>18.18%</td>
<td>6-6</td>
</tr>
<tr>
<td>2012</td>
<td>10</td>
<td>19</td>
<td>52.63%</td>
<td>12-0</td>
</tr>
<tr>
<td>2013</td>
<td>5</td>
<td>18</td>
<td>27.78%</td>
<td>12-0</td>
</tr>
<tr>
<td>2014</td>
<td>7</td>
<td>14</td>
<td>50.00%</td>
<td>11-1</td>
</tr>
<tr>
<td>Total</td>
<td>28</td>
<td>75</td>
<td>37.33%</td>
<td>55.8</td>
</tr>
</tbody>
</table>

Table 2

<table>
<thead>
<tr>
<th>Year</th>
<th>Number of Visits (High Volume Days)</th>
<th>% Male</th>
<th>Average Age</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>37</td>
<td>77</td>
<td>59.46%</td>
</tr>
<tr>
<td>2011</td>
<td>19</td>
<td>91</td>
<td>52.63%</td>
</tr>
<tr>
<td>2012</td>
<td>102</td>
<td>88</td>
<td>59.80%</td>
</tr>
<tr>
<td>2013</td>
<td>75</td>
<td>153</td>
<td>57.33%</td>
</tr>
<tr>
<td>2014</td>
<td>109</td>
<td>103</td>
<td>60.55%</td>
</tr>
<tr>
<td>Total</td>
<td>342</td>
<td>512</td>
<td>59.06%</td>
</tr>
</tbody>
</table>

Keywords
Alcohol; EpiCenter; Binge Drinking; Football; Health Monitoring Systems

Acknowledgments
We wish to thank the Ohio Department of Health for the data for this work.

References

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Enhancing Syndromic Surveillance at a Local Public Health Department

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Objective

To demonstrate how a local public health department used the Centers for Disease Control and Prevention (CDC) Framework for Program Evaluation and a logic model to enhance its syndromic surveillance program.

Introduction

The mission of the Maricopa County Department of Public Health (MCDPH; Arizona) is to protect and promote the health and well-being of its residents and visitors. Surveillance efforts allow epidemiologists to quantify and characterize public health threats, but traditional methods take time. In an effort to enhance situational awareness, the Office of Epidemiology dedicated resources to begin developing a robust syndromic surveillance program. This abstract outlines steps for enhancing syndromic surveillance at a local public health department.

Methods

The CDC Framework for Program Evaluation was used to systematically improve MCDPH’s existing syndromic surveillance program. [1] First, stakeholders from the state and county syndromic surveillance programs were engaged. The MCDPH Syndromic Surveillance Strategic Planning and Development Workgroup was formed to identify existing resources, current challenges, and a unified mission. Meetings were arranged with Arizona Department of Health Services (ADHS) staff to exchange ideas for future projects. Second, a logic model was created to describe MCDPH’s existing and future syndromic surveillance efforts. The MCDPH logic model was influenced by the National Syndromic Surveillance Program’s logic model for enhancing syndromic surveillance capacity and practice. [2] Third, the scope of the program was focused by identifying five priority initiatives for the year. The remaining steps are in progress. Plans were established to measure outcomes of the program, evaluate progress for meeting goals, and share lessons learned.

Results

The MCDPH Strategic Planning Workgroup has been meeting bi-weekly since June 2015. The Workgroup identified goals and activities and organized them in a logic model (Figure). Using input from state and county public health officials, five priority syndromes were identified: heat-related illness, arboviral disease, drug overdose, influenza-like illness, and gastrointestinal illness. For each syndrome, Workgroup members began (1) developing technical guides for accessing and analyzing data, and (2) seeking collaborations with external entities. MCDPH is now actively involved with the following activities: CSTE Heat Syndrome Workgroup, ADHS Arboviral Syndromic Surveillance Use Case Project, and “Flu Near You” local use initiative. The Workgroup plans to review its progress quarterly and adjust activities that are not adequately achieving goals. By sharing MCDPH’s experience, the Workgroup is achieving a goal to contribute knowledge to the national community of practice.

Conclusions

In MCDPH’s experience, the CDC Framework for Program Evaluation was an effective tool for strategic planning, while the logic model helped focus efforts on the appropriate initiatives. In less than 3 months, the Workgroup collaborated with local, state, and national stakeholders, identified challenges faced by the existing program, prioritized goals, and launched activities to enhance surveillance for five priority syndromes. The immediate next steps will be to finalize technical guides, validate syndromic surveillance queries, evaluate progress of the program, and continue to share lessons learned with the community of practice. The authors hope that by sharing this experience, other public health practitioners will be encouraged to enhance syndromic surveillance at their local health departments.

Keywords

Strategic planning; Evaluation; Local level

Acknowledgments

The authors thank the MCDPH Syndromic Surveillance Strategic Planning Workgroup for its contributions.

References


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Using Syndromic Surveillance to Enhance Arboviral Surveillance in Arizona

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Objective
To develop a protocol for enhancing traditional arboviral surveillance with syndromic surveillance and to evaluate the protocol for accuracy, effectiveness, and timeliness.

Introduction
Arizona is facing multiple public health threats from arboviral diseases. State and local public health departments are monitoring two mosquito-borne outbreaks within its borders and two in adjacent territories. To prevent transmission, viremic patients must be identified in a timely manner and encouraged to avoid additional mosquito exposure and vector control actions must be implemented. Using traditional surveillance, however, health departments may not be alerted until the laboratory confirms and reports a positive result, which may take up to 14 days after specimen collection. The Arizona Department of Health Services (ADHS) partnered with local public health jurisdictions to enhance traditional arboviral surveillance by incorporating syndromic surveillance.

Methods
In collaboration, ADHS and county epidemiologists developed a protocol for identifying and responding to possible arboviral cases using chief complaint and diagnosis data from the National Syndromic Surveillance Platform. Arizona’s Arboviral Syndromic Surveillance Protocol outlines steps for both state and county public health staff. In phase 1, ADHS uses phpMyAdmin two times per week to extract emergency department and inpatient visit data. The query retrieves records that include variant spellings for chikungunya, dengue, West Nile virus, or St. Louis encephalitis. These records are posted to county-specific spreadsheets on a secure server. In phase 2, counties use a decision tree to determine whether patient visits warrant further investigation (Figure). For visits of interest, staff note whether the patient was previously reported via traditional surveillance and whether the medical record provides additional information to change the level of suspicion. Counties decide whether to contact the patient to gather more information, provide education, or alert their vector control department.

Results
This abstract was submitted 1.5 weeks after Arizona officially began using syndromic surveillance for enhanced arboviral surveillance (on 8/24/15). After 3 data extractions by ADHS, records for 12 visits from 11 unique patients were retrieved by the arboviral query. The patient records, from 2 Arizona counties, mentioned West Nile virus (10) and St. Louis encephalitis (1). Eight of the 11 patients were previously identified via traditional surveillance. Medical records from the remaining 3 patients were reviewed. Arboviral diseases were not confirmed by the medical records of these 3 patients. Dividing responsibilities between ADHS and county staff has been helpful for managing time and resources for this enhanced surveillance effort. ADHS plans to continue using syndromic surveillance for arboviral surveillance through January 2016. As data are collected, state and county epidemiologists will monitor the protocol’s effectiveness and timeliness and implement modifications if necessary. In January, a full evaluation will assess the query’s ability to identify true positive cases, the speed at which possible cases are identified compared to traditional surveillance, and the time dedicated by state and county staff for enhanced surveillance. As the evaluation continues, the authors will continue to share the findings.

Conclusions
In collaboration with county health departments, ADHS developed a protocol for identifying and responding to possible arboviral cases using syndromic surveillance. Initially, the query, which searches for records that specifically mention an arboviral disease, retrieved 11 unique patients from 2 counties. Dividing responsibilities between ADHS and county staff has been helpful for managing time and resources for this enhanced surveillance effort. ADHS plans to continue using syndromic surveillance for arboviral surveillance through January 2016. As data are collected, state and county epidemiologists will monitor the protocol’s effectiveness and timeliness and implement modifications if necessary. In January, a full evaluation will assess the query’s ability to identify true positive cases, the speed at which possible cases are identified compared to traditional surveillance, and the time dedicated by state and county staff for enhanced surveillance. As the evaluation continues, the authors will continue to share the findings.

Keywords
arboviral; syndromic; use case; collaborative

Acknowledgments
The authors thank the arboviral and syndromic teams at both ADHS and Maricopa County Department of Public Health for their contributions.

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Evaluating the BioSense Syndrome for Heat-Related Illness in Maricopa County, Arizona

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Objective
To evaluate the pre-defined “Heat, excessive” query in BioSense 2.0 using recent Maricopa County, Arizona data; quantify the number of cases retrieved by the query due to chief complaint terms rather than clinical diagnosis; and provide a list of terms to be considered for exclusion criteria while developing a custom query.

Introduction
Monitoring heat-related illness (HRI) is a public health priority in Maricopa County, Arizona. Since 2006, Maricopa County Department of Public Health has utilized data from hospital discharges, medical examiner preliminary reports, and death certificates to quantify heat-related morbidity and mortality, but these surveillance methods take time. Identifying HRI more quickly would improve situational awareness and allow public health officials to launch a more immediate response to extreme heat events. Arizona began using BioSense 2.0 in July 2014 to collect chief complaint and diagnosis terms for syndromic surveillance. The BioSense Front End Application uses a standard query definition for HRI (i.e., “Heat, excessive”), but this definition may perform differently for each jurisdiction.

Methods
We used BioSense 2.0 to produce a line list of patient records between 1/1/15 and 8/15/15 that met criteria in the “Heat, excessive” query definition. Records with a clinical diagnosis or injury code (992 or E900, respectively) were considered confirmed HRI cases. We manually reviewed the chief complaint fields of the remaining records and classified each as probable HRI case, HRI ruled out, or undetermined HRI status. We compiled a list of terms that were common among the ruled out cases and determined how the query would perform if we added these terms to the query as exclusion criteria. As a secondary analysis, we determined whether the exclusion criteria would perform differently depending on season.

Results
The “Heat, excessive” query retrieved 539 Maricopa County, AZ patient records between 1/1/15 and 8/15/15. Nearly half of the records had a clinical diagnosis for HRI, while 271 records (50.3%) required a manual review of the chief complaint data. We classified 148 records (27.5%) as probable HRI cases because they had symptoms consistent with HRI and 32 records (5.9%) as undetermined HRI cases. By manually reviewing the chief complaint data, we found that 17% of the records were not related to environmental heat exposure. The query could be more specific if exclusion criteria were added. Our next steps will be to continue evaluating data through 2015, determine whether additional terms should be added as inclusion and exclusion criteria, and validate our proposed query definition against both medical records and finalized hospital discharge data. As we refine our query definition for syndromic surveillance, we will increase our capacity to detect and characterize heat-related morbidity in the county.

Conclusions
The pre-defined “Heat, excessive” query in BioSense 2.0 allowed us to quantify Maricopa County’s HRI burden in a timely manner. The query retrieved 268 records with a clinical diagnosis for HRI and 148 additional cases that had symptoms consistent with HRI in their chief complaint data (i.e., probable HRI). By manually reviewing the chief complaint data, we found that 17% of the records were not related to environmental heat exposure. The query could be more specific if exclusion criteria were added. Our next steps will be to continue evaluating data through 2015, determine whether additional terms should be added as inclusion and exclusion criteria, and validate our proposed query definition against both medical records and finalized hospital discharge data. As we refine our query definition for syndromic surveillance, we will increase our capacity to detect and characterize heat-related morbidity in the county.

Keywords
BioSense; Evaluation; Heat-related illness; syndrome; query

Acknowledgments
The authors thank Arizona Department of Health Services for implementing BioSense 2.0 in Arizona.

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Table. Number of Maricopa County, Arizona records that included one or more of the potential exclusion terms

<table>
<thead>
<tr>
<th>Potential Exclusion Terms</th>
<th>%</th>
<th>Probable HRI</th>
<th>Undetermined HRI</th>
<th>HRI ruled out</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dairy pain and sensitivities to heat; oral AND conjunctival AND angioedema; pain AND jaw; heat rash; OR oral AND eye AND head AND ear AND face</td>
<td>10 (3.7%)</td>
<td>3</td>
<td>0</td>
<td>7</td>
</tr>
<tr>
<td>Misspecified “heart”</td>
<td>8 (2.5%)</td>
<td>0</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>Misspecified “head”</td>
<td>2 (0.7%)</td>
<td>0</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>Misspecified “feelings”</td>
<td>23 (6.5%)</td>
<td>1</td>
<td>2</td>
<td>20</td>
</tr>
</tbody>
</table>

Table. Potential exclusion terms included in the query definition.
Sensitivity and Specificity of the Fever Syndromes in BioSense and ESSENCE

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Objective
To objectively compare the BioSense and ESSENCE fever syndromes using recorded temperature as a gold standard.

Introduction
Syndromic surveillance refers to the monitoring of disease related events, sets of clinical features (i.e. syndromes), or other indicators in a population. Tennessee obtains emergency department data for syndromic surveillance in standardized HL7 format following the field and value set standards published by the Public Health Information Network. Messages contain information previously unavailable to syndromic surveillance systems, including quantitative values such as recorded temperature. Data are received daily and processed by a Tennessee ESSENCE application and the national BioSense platform.

These systems use chief complaint keywords, ICD9 codes, and other algorithms to assign syndromes for each record. The differences between the BioSense and ESSENCE syndrome assignments have not been well defined. Detailed comparisons of syndrome assignment across tools are difficult to perform due to the intensity of the manual review required. However, definitions of fever can be easily confirmed in HL7 messages when the recorded temperature is provided. Currently, both the BioSense and ESSENCE syndrome definitions exclude recorded temperature from consideration when assigning syndromes.

To compare the performance of the fever syndromes used by BioSense and ESSENCE, recorded temperature data was used as the gold standard.

Methods
Emergency department data from five Memphis area hospitals during 7/1/14 – 6/30/15 were used for this analysis. BioSense data were queried and extracted using the system supplied version of RStudio and analyzed using SAS 9.4. A “visit” was defined a record with a unique combination of facility and the BioSense created variable “analysis visit id”. Data lacking a syndrome assignment were excluded from the analysis. Temperature was determined by taking the maximum recorded temperature (Tmax) across all updates for each record.

ESSENCE overwrites records with each update, so recorded temperature at the last update was used as Tmax for this evaluation. A “true” fever was defined as any record with a Tmax of greater than 100 degrees Fahrenheit. Sensitivity, specificity, positive predictive value, and negative predictive value were calculated for the fever syndrome in BioSense and ESSENCE.

Results
There were 326,966 records assigned to a syndrome with recorded temperature identified in the BioSense data (18,744 observations were missing temperature) and 319,246 records identified in the ESSENCE data (27,237 missing temperature). Sensitivity and specificity are plotted month by month in Figure 1. Positive predictive value and negative predictive value were not substantially different.

Conclusions
The BioSense fever syndrome and the ESSENCE fever syndrome performed similarly. ESSENCE had higher sensitivity compared with the BioSense fever syndrome throughout the study period.

There were some discrepancies in both data sets. The small difference in total visit numbers across both systems is likely due to additional processing rules in the BioSense platform. Also, ESSENCE had a larger number of observations missing temperature, likely due to record updates overwriting existing temperature data with missing data. Theoretically, update messages sent via HL7 should contain all information sent previously, but this may not be true for recorded temperature data. Additional investigation is needed to see if the overwrites are true corrections by the submitting facility or attributable to another source.

Recorded temperature adds value to syndromic surveillance practice when sent consistently. Including recorded temperature data as a queryable variable would increase the sensitivity of the fever syndromes in both ESSENCE and BioSense.

Keywords
BioSense; ESSENCE; fever; syndrome

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Figure 1: Sensitivity and Specificity of the BioSense and ESSENCE Fever Syndromes from July 2014 through June 2015
Analysis of ED and UCC Visits Related to Synthetic Marijuana in ESSENCE-FL, 2010-2015

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Objective
One of the numerous functions of syndromic data has been the identification of visits of public health interest using customized free text queries. A specific query of syndromic data was created to search for and identify emergency department (ED) and urgent care center (UCC) visits possibly related to the use of synthetic marijuana to describe and quantify this public health issue in Florida.

Introduction
Illnesses related to synthetic marijuana use have been reported in many states, including Florida. Because these visits can present with a variety of symptoms, as well as be attributed to numerous diagnosis codes, it can be difficult to identify and quantify these visits. The Electronic Surveillance System for the Early Notification of Community-based Epidemics in Florida (ESSENCE-FL) receives chief complaint (CC) and discharge diagnosis (DD) data as free text allowing uncommon or new terms to be searched for within each patient visit. The main source of data for ESSENCE-FL is emergency department (ED) and urgent care center (UCC) data. There are currently 210 EDs and 33 UCCs throughout Florida that send their data to the ESSENCE-FL server. Using ESSENCE-FL, a free text query of patient CCs and DDs was used to identify visits related to synthetic marijuana use. This study is designed to analyze these identified visits for trends over time, geographical distribution and descriptive statistics and demographics.

Methods
News articles, publications and internet searches were used to develop a comprehensive list of all terms and names that could be used for synthetic marijuana (ie. Spice, K2, etc.). These terms, and their common misspellings, were used to create the free text query. The query attempted to identify visits related to synthetic marijuana, while minimizing the identification of unrelated visits. All identified visits from January 1, 2010 through June 30, 2015 were analyzed using Microsoft Excel and mapped using GIS.

The query used was written as:

\[ (\text{synth}^*, \text{andnot}^*, \text{synthroid}^*, \text{orphert}^*, \text{sint}^*, \text{or}^*, \text{fake}^*), \text{and}, \text{(pot}^*, \text{or}^*, \text{THC}^*, \text{or}^*, \text{weed}^*, \text{or}^*, \text{mari}^*, \text{or}^*, \text{mara}^*, \text{or}^*, \text{herb}^*, \text{or}^*, \text{bud}^*, \text{or}^*, \text{cannab}^*, \text{or}^*, \text{canibl}^*, \text{or}^*, \text{canab}^*, \text{or}^*, \text{canab}^*), \text{or}, (\text{spice}^*, \text{andnot}^*, \text{hospice}^*, \text{or}^*, \text{spicy}^*), \text{or}, \text{smoked K}^*, \text{or}^*, \text{smoking K}^*, \text{or}^*, \text{of k}^*, \text{or}^*, \text{from k}^*, \text{or}^*, \text{on k}^*), \text{or}, \text{Scobyby^*}, \text{or}^*, \text{nice guy}^*, \text{or}^*, \text{cloud nine}^*, \text{or}^*, \text{(used}^*, \text{or}^*, \text{smok}*, \text{or}^*, \text{inhale}^*), \text{and}, (\text{potpo}^*, \text{or}^*, \text{herb}^*, \text{or}^*, \text{incen}^*, \text{or}^*, \text{insen}^*, \text{or}^*, \text{insen}^*), \text{or}, \text{genie}^*, \text{or}^*, \text{Yucatan}^*, \text{or}^*, \text{solair flare}^*, \text{or}^*, \text{fire n ice}^*, \text{or}^*, \text{fire and ice}^*, \text{or}^*, \text{mamba}^*, \text{or}^*, \text{bombay}^*, \text{or}^*, \text{bad to the bone}^*, \text{or}^*, \text{dark night}^*, \text{or}^*, \text{berry blend}^*, \text{or}^*, \text{magma}^*, \text{or}^*, \text{budz}^*, \text{or}^*, \text{sativah}^*, \text{or}^*, \text{ultra chronic}^*, \text{or}^*, \text{zohai}^*, \text{or}^*, \text{funky green}^* \]

Results
This query identified 2545 visits between January 1, 2010 and June 30, 2015.

Conclusions
Utilization of this query provided key insights and information into the demographics, geographic distribution and trends of synthetic marijuana visits in Florida. The Tampa Bay Area - Hillsborough, Pasco, Pinellas, and Polk counties - had a substantial concentration of visits (37.1% of all identified visits). Visits were mostly male (75.2%) and with an average age of 26.8 years old (66% of visits were age 14-28). Additionally evident is the recent reemergence of this public health issue, The ability to identify visits related to drugs with numerous names and nicknames, as well as novel synthetic drugs, within specific demographics and geographic areas may be integral in the effective implementation of public health interventions.

Keywords
Synthetic; Marijuana; query; ESSENCE; Florida

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Comparison of Air Passenger Travel Volume Data Sources for Biosurveillance

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Objective

To evaluate different government and commercial air travel route and volume data sources for utility in determining likely points of arrival and subsequent spread of communicable diseases originating from outbreaks outside the United States.

Introduction

The National Biosurveillance Integration Center (NBIC) has the responsibility to integrate, analyze, and share the nation’s biosurveillance information provided from capabilities distributed across public and private sectors. The integration of information enables early warning and shared situational awareness of biological events to inform critical decisions directing response and recovery efforts.

Understanding travel trends and volumes is essential to managing public health and emerging infectious diseases as travelers move across today’s increasingly globalized world. Travel routes, seasonal trends, and general passenger flow volume help determine where communicable diseases are more likely to arrive and spread within the US.

This type of data is useful in informing policy decisions, especially with respect to resource allocation and border screening procedures. Accuracy in the underlying data is important to build better predictive models

Methods

We conducted extensive research into currently available government and commercial air passenger data sources to evaluate data quality, utility, and accessibility for the purposes of biosurveillance. The goal was to identify the most complete and accurate data source of air passenger counts and flight schedules. The scope was limited to commercial passenger air flights.

The commercial data sources were limited to two industry leaders: the International Air Transport Association (IATA) and the Official Airline Guide (OAG). Evaluation of their products included interviews with data users in government, interviews with company representatives and some of their analytics staff, system demonstrations and examination of the results of sample data queries. The search for government sources of data included interviews of personnel within DHS Customs and Border Protection (CBP), the Federal Aviation Administration (FAA), the Centers for Disease Control and Prevention (CDC), and Department of Defense (DoD).

Identical queries were made of each data source. Examination of the differences between the volume values then led to the exploration of how each data source defined its designated variables and derived its calculations.

The purpose and use of air travel data to support decision-making was strongly considered during evaluation. Some examples of these concerns include resource allocation of staff, communication or messaging of health advisories, or planning for border screening processes and training staff. This plays a role in determining what kind of questions to ask of the data and whether a data source is flexible in altering its parameters to allow that query.

Results

The following are preliminary findings:

Commercial data sources differ in multiple ways:

• Not all commercial sources provide passenger volume data.
• OAG volume data is based on booked seats as gathered from Global Distribution Systems (GDS) and, with data delay, from Computer Reservation Systems (CRS). IATA volumes are based on the Business Settlement Process (BSP) surrounding ticket purchasing.
• Comparison of the results of OAG and IATA system query results is difficult as both draw from different data systems and use proprietary algorithms to calculate results.
• Most single commercial sources appear to require additional estimations to fill data gaps.

Government data sources:

• Government sources are usually limited to flight schedules or volumes of passengers crossing US airspace or borders, unless their mission space is in intelligence.
• DHS Customs and Border Protection (CBP) US entry data systems are considered the gold standard as they contain complete arriving passenger data.
• The results of government data systems queries differ from that of commercial sources due to differences in parameter definition.

Conclusions

The commercial data often used by academia and private performers to build disease spread models can differ significantly from government data not only due to the methodology to derive the passenger volumes (i.e. tracking passenger arrivals as opposed to ticket sales estimations based on flight routes), but also due to differing parameter definitions.

Keywords

air travel; border screening; commercial and government data; translocation

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A Suggestion to Improve Timely Feedback of Infectious Disease Surveillance Data at a Provincial Level in South Korea

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Objective
This study will explore the timeliness of the Korean National Notifiable Disease Surveillance System (KNNDSS) at provincial level, and suggest a reasonable duration for publication the weekly reports to improve timely feedback of infectious disease surveillance data to physicians and community.

Introduction
In South Korea, the NNDSS is organized at three levels: local, provincial, and central. At the local level, physicians report the cases to the Public Health Center (PHC) and PHC conduct control measures. At the provincial level, the PHC reports the cases to the Department of Health (DOH) of the province and DOH obliged to report the cases to the Korea Centers for Disease Control and Prevention (KCDC) and feedback of the surveillance data to PHC and physicians. At the central level, the Disease Web Statistics System (http://is.cdc.go.kr/dstat/index.jsp) provides real-time data on 54 national notifiable infectious diseases [1]. Although there are variations according to the disease and surveillance step, the KNNDSS generally functions well in terms of timeliness and Yu et al. reported that 89.7% of mumps, one of the most incident contagious disease in South Korea, reported in 15 days after the physician’s notification [2]. To improve the timeliness of feedback at the provincial level, we explored the KNNDSS data and suggested an evidence based duration for publication of the weekly reports, in consideration of reducing the publication schedule.

Methods
We analyzed the reported infectious disease surveillance data (N=23,486) at Gyeonggi province in 2014. Time points recorded in the KNNDSS data include dates of onset, diagnosis, doctor’s notification to the PHC, PHC reporting to the DOH, and DOH reporting to the KCDC [2]. Using these dates, we defined the time lags in days from physician’s notification to central appraisal, and the number of cases reported last week was summarized by the days of notification and publication schedule.

Results
The average time lags were 9.6 days (SD = 30.3) from physician’s notification to central appraisal.
21,108(92.73%) of reported cases were finished central appraisal till next Friday. 96.82%, 92.17% and 90.86% of cases notified on Sunday, Wednesday and Saturday, respectively, could be covered on next Friday.
20,491(90.02%) of reported cases were finished central appraisal till next Wednesday. 96.13%, 90.47% and 83.60% of cases notified on Sunday, Wednesday and Saturday, respectively, could be covered on next Wednesday.
Otherwise, only 15,684(68.90%) of reported cases were finished central appraisal till next Monday. 95.16%, 80.91% and 4.54% of cases notified on Sunday, Wednesday and Saturday, respectively, could be covered on next Monday.

Conclusions
Our study suggested the utility of the assessment of time-lag distributions for the feedback strategies to improve surveillance and regional infectious disease controls.

Keywords
Korean National Notifiable Disease Surveillance System; Notifiable Disease; Timeliness; Weekly report

References

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Update on the CDC National Syndromic Surveillance Program

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Objective
Inform conference attendees about the CDC National Syndromic Surveillance Program (NSSP), various program-related projects and who is working on them, what was accomplished during the past year, and NSSP-development plans for the future.

Introduction
The Public Health Security and Bioterrorism Preparedness and Response Act of 2002 mandated establishing an integrated national public health surveillance system for early detection and rapid assessment of potential bioterrorism-related illness. In 2003, CDC created and launched the BioSense software program. At that time, CDC’s focus was on rapidly developing and implementing Web-based software to collect hospital emergency department data for analysis to detect and monitor syndromes of public health importance. During the ensuing decade, BioSense evolved and now is part of CDC’s renamed National Syndromic Surveillance Program (NSSP). The broader vision of NSSP aims to achieve two key goals: significantly improve technical capabilities for collecting and analyzing syndromic surveillance data, and to create and facilitate opportunities for collaboration among local, state, and national public health programs. Through NSSP, the syndromic surveillance community can be strengthened by access to improved technical capacity and to best-practices knowledge sharing among syndromic surveillance professionals. These NSSP initiatives can help the nation-wide public health community strengthen situational awareness and enhance response capability to hazardous events. NSSP encompasses people, partners, policies, information systems, standards, and resources. Session attendees will learn more about NSSP, its growing group of partners, what the program is doing now, and its future.

Description
The 2014 CDC Surveillance Strategy calls for modernizing its health surveillance systems. Through a host of improvements, CDC; its state, tribal, local, and territory public health partners; and the public health community-at-large will have better data and information to help inform decisions. The panel will discuss the BioSense Platform, formerly known simply as BioSense, which is one of the four national surveillance programs identified for transformation in the CDC Surveillance Strategy. The BioSense Platform is now a component of NSSP, which was launched last year by CDC’s Division of Health Informatics and Surveillance.

The panel will discuss how the NSSP staff is upgrading the BioSense Platform in three main areas:

1) Data Quality: Improving data management, quality, and representativeness
2) Technology: Upgrading BioSense Platform technological capacity with better tools for data collection, processing, and analyses
3) Partner Engagement: Strengthening the syndromic surveillance Community of Practice to promote data sharing that will further the science and practice of syndromic surveillance

The panel will consist of CDC staff members who are leading these efforts and representatives from the BioSense Governance Group (BGG), an organization representing public health jurisdictions participating in NSSP. The BGG collaborates with CDC to develop ways to improve BioSense Platform performance including the tools and services it hosts. The panel will provide updates on current and near-term NSSP activities, describe recent enhancements to the program, and engage the audience in discussions about ways to improve the utility of syndromic surveillance at all levels of the public health enterprise. Discussion topics might include the anticipated deployment of new tools on the BioSense Platform such as ESSENCE, SAS, and R Studio Professional; identifying technical assistance, training, and support needs of local and state programs; data workflow and ways to improve data quality; strengthening the NSSP Community of Practice initiative by increasing local-and state-level engagement; and ideas and topics for collaborations among jurisdictions and with CDC.

Audience Engagement
Director of CDC’s Division of Health Informatics and Surveillance Paula Yoon, ScD, will introduce the NSSP team (Program Manager, BioSense Platform Lead, Data Quality Lead, Partner Engagement Lead, and BioSense Governance Group (BGG) partners) and provide historical perspective on BioSense from inception in 2003 to its current role in NSSP. Then NSSP team members will describe work underway and goal accomplishments in the three modernization focus areas identified earlier. The NSSP program manager will offer a vision for the future. The BGG partners will describe their roles in representing the public health syndromic surveillance community. They also will facilitate an audience discussion intended to discover others’ viewpoints and recommendations.

Keywords
NSSP; BioSense Platform; CDC

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Use of Peripheral Health Units in Low-Transmission Ebola Virus Disease Surveillance

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Objective
A community-based EVD surveillance system with improved symptom recording and follow-up of malaria positive patients at PHUs was implemented during low EVD transmission. The rationale and methodology in implementing a PHU-focused approach to strengthen surveillance system sensitivity is described.

Introduction
Existing EVD surveillance strategies in Sierra Leone use a centralized live alert system to refer suspect cases from the community to Ebola treatment centers. As EVD case burden declined in Port Loko District, so did the number of reported alerts. As EVD presents similarly to malaria, the number of alerts reported are expected to remain consistent with malaria prevalence in malaria-endemic areas, irrespective of a reduction in true EVD cases. Declines in reported suspect cases from the community alluded to the possibility that individuals were returning to healthcare centers to seek treatment for malaria, and that PHUs were not adequately reporting suspect EVD cases. District surveillance officers (DSOs) were used to investigate the usage of PHUs by community members, as well as the mechanisms that health center staff used in recording patient visits.

Surveillance methods specific to PHUs were introduced to increase the number of reported EVD alerts, as well as establish the foundation for future integrated disease surveillance response strategies.

Methods
PHU surveillance methodology focused on 4 primary components:
• Initial Evaluation: PHU-specific evaluations were conducted to gauge the level of community use of primary health care structures as EVD case-load decreased. “Under-five”, OPD, and Triage registers were reviewed to investigate what disease recording mechanisms were used by healthcare staff.
• Case Definition Education: healthcare staff were educated on EVD case definition and protocol for reporting all suspect cases through the centralized live alert system.
• Improved Symptom Recording: a section in all patient registries was included specifically for recording symptoms of any patient upon arrival at a PHU. Recording of patient symptoms, as opposed to only presumed diagnosis, was introduced as a tool for surveillance of a greater range of diseases by allowing for easy review of demographic-specific trends in symptomatic presentations. Recording symptoms of individuals with a positive rapid diagnostic test (RDT) not only forms the foundation for a malaria patient follow-up system but also allows symptomatic groupings for differential EVD diagnosis.
• Malaria algorithm: a system was introduced to aid healthcare staff in eliminating possibilities of malaria and EVD co-infection among patients presenting at PHUs. As artemisinin combination therapy (ACT) is fast acting and can reduce parasitemia levels within 1-2 days, an algorithm was proposed for improved surveillance (fig. 1.)

Results
Initial PHU evaluations showed that the majority of community members weren’t actually returning to PHUs, and that the decrease in live alerts was a result of poor community reporting, unrelated to receipt of healthcare at PHUs. As a result, social mobilization and community engagement efforts were adapted to stress the importance of returning PHUs for primary healthcare needs. The PHU EVD surveillance system was used to implement several small, but effective changes to the recording of patient symptoms, follow-up of malaria confirmed patients, and contributed to an increase in community-reported live and death alerts in the district (fig. 2).

Conclusions
PHU attendance was gauged as an indicator of baseline disease in order to investigate the decrease in live alerts in the EVD reporting system. Low reporting could be correlated to low PHU attendance and indicated a need for social mobilization and community engagement.

Keywords
Ebola Virus Disease surveillance; Peripheral health unit; Sierra Leone; malaria

Acknowledgments
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Place Matters: Revealing Infectious Disease Disparities Using Area-Based Poverty

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Objective
The panel will describe applying the methods of Harvard’s Public Health Disparities Geocoding Project1 to a diverse collection of infectious disease surveillance data from 14 US states and New York City. This session will demonstrate the feasibility and utility of using US Census data to reveal sub-populations vulnerable to infectious diseases.

Introduction
Most public health surveillance systems in the United States do not capture individual-level measures of socioeconomic position. Without this information, socioeconomic disparities in health outcomes can be hidden. However, US Census data can be used to describe neighborhood-level socioeconomic conditions like poverty and crowding. Place matters. Neighborhood affects health independently of personal characteristics. Thus, important trends may be elucidated by linking geocoded public health surveillance data to area-based measures of socioeconomic position, such as the percentage of residents with incomes below the federal poverty level.

Description
Panel members will each share their experience using the methods of the Public Health Disparities Geocoding Project on an infectious disease surveillance dataset. Topics covered will include:
• Working with US Census data, both decennial population files and American CommunitySurvey estimates
• Accessing online methodological resources from the Council of State and Territorial Epidemiologists and the Public Health Disparities Geocoding Project at Harvard School of Public Health
• Identifying health department resources needed to complete similar analyses
• Establishing interdepartmental partnerships to carry out specialized methods (e.g., geocoding)
• Consulting subject matter experts to interpret results
• Communicating findings for use in public health policy and action

Specifically, the audience will hear from three epidemiologists who conducted similar independent analyses. The discussion will include successes and challenges in analyzing the incidence of 53 reportable communicable diseases by census tract-level poverty in New York City, an area of pronounced income inequality2. From Connecticut, analysis of reported Campylobacter infections from 1999-2009 will highlight the ability of this methodology to detect socioeconomic disparities within sub-groups and include interpretation of unexpected results. Finally, discussion of the analysis of influenza hospitalization data from over 70 counties in 14 states will help to illustrate the obstacles to and ultimate value of sharing data across jurisdictions. Audience members will learn how to conduct similar analyses with their own data and where to find detailed guidance.

Audience Engagement
Audience members will be asked to discuss barriers to implementing routine analysis of surveillance data within their own jurisdictions according to area-based poverty. Technical as well as conceptual questions will be answered. Audience recommendations for acting on the results of similar analyses in terms of policy and prevention measures to advance health equity will be encouraged.

Keywords
Health Disparities; Geospatial analysis; Poverty; Socioeconomic Status; Geocoding

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References

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Addressing Health Equity Through Data Collection and Linked Disease Surveillance

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Objective
Utilize existing data sets and data sources to address health equity and improve the management of chronic disease.

Introduction
In 2012, half of all adults in the US had one or more chronic health conditions; at least 25% had two or more chronic health conditions (1). Seven of the top ten causes of death in 2010 were chronic diseases; two of the seven chronic diseases, heart disease and cancer, account almost for over 50% of all deaths (2). Chronic disease is one of the most costly contributors in healthcare expenditures; once diagnosed many patients must be followed for a lifetime. In lower-income countries chronic disease is now the biggest contributor to mortality (3). Socioeconomic inequalities are a major driver of the chronic disease epidemic (4). Chronic disease in the US, such as cancer, heart disease, renal end stage disease and diabetes are tracked in national datasets but are not linked. Chronic diseases share many risk factors, major risk factors, e.g. tobacco, diet, alcohol, and physical inactivity are already known, their interactions with comorbidities are important and clinical practice indicates that the chronic disease epidemic may be addressed more effectively using a holistic approach. However, this approach has not yet been implemented in disease surveillance activities as data collection is still disease specific. Data collection is still one disease at a time, without connecting our disease surveillance efforts to get better, more complete and encompassing data. Health inequities result in lower quality of healthcare, worse healthcare outcomes for minority racial/ethnic populations and people with low socioeconomic status, increased direct and indirect healthcare costs, and decreased productivity (5).

Methods
We identified four chronic diseases that contribute to the majority of death and disease: cancer, diabetes, coronary heart disease, and renal end stage disease. We explored datasets related to each disease to identify comorbidities and other overlapping information and common factors present in all four datasets which allows to look at chronic disease as a whole. We describe the four datasets and the information that we have discovered using this approach and discuss how such information can improve outcomes and potentially reduce inequities. In addition, we demonstrate the advantage to link these data.

Results
There is an overlap in the data that are collected for the four chronic diseases that contribute to morbidity and mortality in the US and worldwide. We demonstrate that the method of combining datasets will not only enhance data completeness and quality but also increase accuracy for all four datasets and allow for additional research that would not be possible with dataset silos.

Conclusions
By looking at the four datasets, we were able to identify variations in different racial/ethnic populations, socioeconomic status and risk factors such as tobacco use, obesity and the presence of one or more than one chronic disease. By utilizing data that are already collected and linking datasets, we can capitalize on existing data to support studies that focus on one or more of the diseases and expand the use of previously isolated datasets associated with chronic conditions that contribute to the majority of disease and mortality in the US and worldwide. This approach also opens the door to explore possible connections between chronic diseases that may lead to better understanding of why they go hand-in-hand and to interventions that are culturally appropriate and action-oriented, and can be embedded in the community.

Keywords
Disease Surveillance; Chronic Disease; Data Linkage

References

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Epizootology and Molecular Diagnosis of Lumpy Skin Disease Among Livestock in Azerbaijan

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Introduction

Lumpy skin disease (LSD) is a cutaneous disease of livestock caused by a DNA-containing virus belonging to Poxviridae family called Lumpy Skin Disease Virus (LSDV). Another name of the virus is Neethling. The disease is characterized mainly by fever, and lesions appearing on the skin. The incubation period is 6-9 days. Mortality of the disease is about 10% [1, 2], however, secondary infection of lesions can increase the mortality rate. LSD was first recorded in Zambia, South Africa, then spread to Sudan, Nigeria and European countries. According to information provided by OIE, LSD outbreaks also have spread in Middle Eastern countries including Turkey, where it has been considered endemic since 2007-2008 [1]. An outbreak of LSD was also reported in Iran in 2013-2014 [1, 2].

Signs of LSD in Azerbaijan were recorded for the first time in the Region (rayon) of Bilasuvar in May of 2014 and reported to OIE [3]. LSD was quickly suspected, as Bilasuvar neighbors Iran which had recently reported LSD. The same clinical signs were subsequently recorded in cattle in the regions of Jalilabad, Aghdash and Udjar. Some of the cases resulted in death. A PCR assay was set up in the Republican Veterinary Laboratory in Azerbaijan in order to test livestock samples for the disease while an epizootological study was conducted to determine the extent of disease spread within the three affected rayons.

Methods

Samples from lungs and abdomen, and head and neck lesions were taken from animals in the regions of Aghdash, Udjar, Jalilabad and Bilasuvar were sent to the Republican Veterinary Laboratory (RVL) for testing. Suspensions were prepared from the samples, and extraction was performed using a DNeasy blood mini kit (Qiagen, Stanford, CA), following the manufacturer’s instructions.


Taq DNA Polymerase, 10X PCR buffer, 50 mM MgCl₂, and 10 mM dNTPs were used to prepare the master mix according to the protocol described [4]. Samples and negative and positive template controls were added to the prepared master mix, and the reaction was run on a Light Cycler 2.0 PCR instrument using the thermocycling conditions used by Balinsky et al. [4]

Results

The LSDV PCR set up by the virology department of the RVL was able to confirm the presence of LSDV in cases from Bilasuvar, Jalilabad, Udad and Aghdash. From 2822 susceptible cattle with LSD lesions, 33 animals died (1.2%). The 255 animals that tested were positive by PCR. The surviving 2567 animals were treated. Lesions of the animals exposed to LSDV were disinfected using detergent iodine. Appropriate preventative measures were put in place. The epizootological status is currently stable, and the virus is now considered endemic in the Azerbaijan Republic.

Keywords

LSD; PCR; lumpy skin diseases

Acknowledgments

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3. Report OIE LSDV in Azerbaijan 7 July 2014

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Exploring Usability of School Closure Data for Influenza-Like Illness Surveillance

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Objective
Evaluate usability of alternative data sources, such as public announcements of unplanned school closures, for additional insight regarding influenza-like illness (ILI) activity.

Introduction
School children are the primary introducers and significant transmission sources of influenza virus among their families and surrounding communities [1,2]. Therefore, schools play an important role in amplifying influenza transmission in communities. Using school-related data sources may be an informative addition to existing influenza surveillance. Unplanned school closures (USCs) are common, occur frequently for various reasons, and affect millions of students across the country [3]. Information about USCs is publicly available in real-time. For this study, we evaluated usability of applying USC data for ILI surveillance.

Methods
From August 1, 2011 through June 30, 2015, we conducted systematic daily searches of publicly available online data (via Google, Google News, and Lexis-Nexis) to identify USCs lasting ≥1 school day in the United States. We selected USCs for which infectious diseases, particularly respiratory illnesses, were indicated as the main reason for the school closures. We described these USCs and compared their temporal patterns with ILI data from outpatient provider visits (available via ILINet at http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html). We also evaluated the correlation (at alpha=0.05) between weekly occurrence of ILI, reported by ILINet, and respiratory illness-related USCs over the 4 school years, excluding summer breaks (weeks 26-31).

Results
Of the 396 USCs related to infectious diseases, 232 (59%) were due to respiratory illnesses; the duration of these closures ranged from 1-4 days (based on 135 USC for which these data were available). The patterns of respiratory illness-related USCs corresponded similarly with those of ILI activity observed via ILINet data regardless of the severity of influenza season (Figure 1). During the 2012-13 and 2014-15 influenza seasons, when ILI activity was high and peaked at around 6%, the number of USC’s nationwide peaked as well; combined, these 2 school years accounted for 191 (82.3%) of all respiratory illness-related USCs over the 4-year study period. In 2012-13, ILI activity was highest around the winter holiday break (at weeks 51-52). Following this winter break, a small increase in ILI activity at week 4 corresponded with a peak in USCs: more than 30 USCs were announced. Similar patterns characterized the 2014-15 influenza season. In 2011-12 and 2013-14 when the influenza seasons were milder and ILI activity lesser, USC patterns still corresponded to those of ILI activity with highest increase in USC’s on week 6 in 2012 and on week 2 in 2014. Overall correlation between USC and ILINet data was significant: R² = 0.54 with p-value <0.0001.

Conclusions
Our data demonstrated that the occurrence pattern of respiratory illness-related USCs is reflective of the national pattern of ILI activity. This suggests that monitoring USCs can be a useful addition to existing influenza surveillance systems, particularly useful during severe influenza seasons when respiratory illness-related USCs may occur more frequently. Also, other studies of USCs [4] indicated that the main reason for respiratory illness-related closures was increased student absenteeism; thus, usability of cause-specific student absenteeism data for monitoring local and state influenza activity should be evaluated via prospective studies.

Figure 1 Respiratory illness-related USCs and percentage of outpatient provider visits for ILI in the United States by week, August 2011 - June 2015
Note: Weeks 26-31 correspond with school summer breaks

Keywords
School closures; influenza; surveillance

References

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Efficient Surveillance of Childhood Diabetes Using Electronic Health Record Data

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Objective

The study goal was to develop an efficient surveillance approach for childhood diabetes across two large Southeastern US public academic health care systems, using electronic health record (EHR) data.

Introduction

Traditional surveillance methods, such as registries that require manual validation of every diabetes case or questionnaires, are resource intensive and associated with considerable delay in reporting results. An EHR-based surveillance system may be more efficient for sustained monitoring of the incidence and prevalence of childhood diabetes, so as to inform health care needs for this growing population.

Methods

The study population at the Medical University of South Carolina (MUSC) included all children <20 years of age as of December 31, 2012 who were seen by a health care provider for any reason between July 1, 2012 and December 31, 2012. At the University of North Carolina Health Care System (UNC-HCS), we included all children <20 years of age as of December 31, 2011 who were seen by a health care provider for any reason in 2011. EHR data included demographics, billing codes, outpatient medications prescription lists, laboratory test results and patient problem lists. Presumptive diabetes cases were identified as those having ≥1 of the following 5 indicators in the past 3.5 years, including elevated HbA1c, elevated blood glucose, diabetes related billing codes, diabetes related patient problem lists or outpatient medications. EHRs of the presumptive cases were manually reviewed, and true diabetes status and diabetes type were determined by the presence of a diabetes diagnosis in the EHRs written by health care providers. Algorithms for identifying diabetes cases overall and classifying type were either pre-specified or derived from classification and regression tree analysis. Surveillance approach was developed based on the best algorithms identified.

Results

We used pre-specified algorithms derived from billing codes only and targeted manual EHRs review to develop a stepwise surveillance approach (Figure 1A and 1B). The sensitivity and positive predictive value for this surveillance approach in both health care systems were generally ≥90% for ascertaining diabetes cases overall, and classifying cases with type 1 or type 2 diabetes (Table 1). This stepwise surveillance approach resulted in a >70% reduction in the number of cases requiring manual validation compared to traditional surveillance methods.

Conclusions

EHR data may be used to establish an efficient and accurate approach for large scale surveillance for childhood diabetes, although some manual effort is still needed.

Keywords

Childhood diabetes; Surveillance; Electronic health record
Acknowledgments

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