Tools and Apps to Enhance Situational Awareness for Global Disease Surveillance

June 29th, 2017
Situational awareness - The perception of elements in the environment within a given time and space, the comprehension of their meaning, and the projection of their status in the near future (Endsley, 1995)
LANL’s suite of decision support tools for biosurveillance

**Analytics**
An app to provide context and a frame of reference for disease surveillance information about an unfolding event, through matching of user input to a library of global historical disease outbreaks. ([http://aido.bsvgateway.org](http://aido.bsvgateway.org))

An analysis tool to provide early warning or detection of the re-emergence of an infectious disease at the *global* level, but through a regional lens. Facilitates long term public health planning.

**Databases**
A tool to; a) facilitate obtaining disease surveillance information. Contains information on disease surveillance resources worldwide, b) rapidly select appropriate epidemiological models for infectious disease prediction, forecasting and monitoring. ([http://brd.bsvgateway.org](http://brd.bsvgateway.org))

A data collection and visualization tool for notifiable disease data from around the world. ([https://epiarchive.bsvgateway.org](https://epiarchive.bsvgateway.org))
Funding support for BSV tools

- BRD, EPI Archive and RED Alert are funded by the Defense Threat Reduction Agency (DTRA)
  - CB 10027
- AIDO was developed with DTRA funds and is currently being enhanced through Department of Homeland Security (DHS) funding
  - DTRA - CB 10027
  - DHS - HSHQPM-16-X-00226
• Decision support tools offered through LANL’s Biosurveillance (BSV) gateway ([http://bsvgateway.org/](http://bsvgateway.org/)) and DTRA’s Biosurveillance Ecosystem (BSVE)
Analytics for Investigation of Disease Outbreaks

• Two functionalities
  • Understand your unfolding outbreak – analytic components
  • Learn about representative global historic outbreaks – library

• Contextualizes user input of an unfolding infectious disease outbreak using historical outbreak data

• Places a frame of reference for where a case count is during an outbreak

• Suggests additional information sources that could support effective consequence management of an outbreak

• Provides short term forecasts for unfolding situation using method of analogs

• Provides structured and categorized information about historical outbreaks
Understanding an unfolding outbreak

Outbreak comparison

AIDO offers a simple interface for viewing and interacting with a substantial outbreak library spanning many diseases. Users are able to search across this library to find outbreaks similar to what they are facing, allowing them to quickly identify historical outbreaks that may be significant to the ongoing event.

Short term forecast

In addition to the library of historical outbreaks, AIDO includes a forecasting feature that makes use of the method of analogs algorithm. This algorithm uses the data collected for each outbreak in the selected disease to make a simple forecast of cumulative disease incidence.

Access our data

AIDO provides a REST API through which external applications can run queries on our data. Currently, we provide access to our diseases, outbreak time series, and location hierarchy. Explore the API here.

Outbreak time series

Each outbreak in AIDO provides detailed information on how the disease progressed under the circumstances of that outbreak. All outbreak records display an interactive time series and are annotated with contextual information.

Outbreak groups

AIDO includes several major outbreaks that spread across multiple regions. The reports from each of these regions have been collected and added to AIDO, making it easy for users to gather data from the different governments and organizations that monitored the separate locations involved in the outbreak.

Select a disease

- Chikungunya
- Cholera
- Dengue
- Ebola
- Foot And Mouth Disease
- Gastroenteritis
- Campylobacteriosis
- Norovirus
- Salmonellosis
- Shiga Toxin-Producing E. Coli (STEC)
- Shigellosis
- Leptospirosis
- Malaria
- Measles
- Meningococcal Disease
- Novel Influenza A
- Plague
- Polio
- Q Fever
- Tularemia
- West Nile Virus
- Yellow Fever
Understanding an unfolding outbreak

**Polio facts**

**Pathogen**
Polio is caused by the poliovirus (genus Enterovirus) and is defined as a paralytic disease. Therefore, only people with paralytic infection are considered to have the disease. Polio outbreaks are caused by wild polio virus (WPV) and to a small extent by vaccine-derived polio virus (VDPV).

**Host and animal reservoir**
The pathogen is a human virus, there are no animal reservoirs.

**Transmission**
Poliovirus is highly contagious and spreads through person-to-person contact. The virus lives inside the throat and infection of the patients spreads through feces and droplets from sneezing and coughing. An infected person can transmit the virus through feces for many weeks; this is true for people without symptoms also. Fecal contamination of food and water increase the risk for people living under unsanitary conditions.

**Disease symptoms - onset, duration and characteristic features**
The incubation time can range from 3 to 35 days, but most commonly occurs between 8 to 20 days. Most people infected with poliovirus (72%) will not have any visible symptoms. 1 out of 4 infected people will experience flu-like symptoms that last 2 to 5 days. These symptoms include:
- Sore throat, fever, tiredness
- Nausea, headache, stomach pain

More severe symptoms of the disease include:
- Paralysis (feeling of pins and needles in the legs)
- Paralytic polio (infection of covering of brain and/or spinal cord)
- Paralysis

Paralysis occurs in 1/200 cases. Only people with paralysis are considered to have polio. Paralysis may occur in adults who have recovered from polio as children, 15 - 40 years later. This is known as post-polio syndrome. More details on post-polio syndrome can be found here.

**Epidemiology and risk factors**
Children less than 5 years of age are the most affected population. Polio is on the verge of eradication, cases have decreased by 99% since 1988. Only 76 cases were reported in 2015 worldwide. Of the three wild type polio strains, WPV-2 was eradicated in 1999 and only one case of type 3 was reported by Nigeria since 2012. WHO collects all information on polio outbreaks at this website. A world map depicting polio endemic, outbreak, key at risk and polio free countries is shown here.
Understanding an unfolding outbreak

<table>
<thead>
<tr>
<th>Disease</th>
<th>Cases</th>
<th>First case report</th>
<th>Location</th>
<th>Human development index</th>
<th>Country</th>
<th>Polio category</th>
<th>Outbreak pathogen</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polio</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Polio facts**

- **Pathogen**: Poliomyelitis, caused by the poliovirus (genus Enterovirus), is with paralytic infection are considered to have the disease. Polio and to a small extent by vaccine derived polio virus (vDPV).
- **Host and animal reservoir**: The pathogen is a human virus, there are no animal reservoirs.
- **Transmission**: Poliovirus can be transmitted from person to person through fecal-oral route. This is through people living under unsanitary conditions.
- **Disease symptoms - onset, duration and characteristic features**: The incubation period of polio is usually 8 to 20 days. Most people experience flu like symptoms. 1 out of 4 infected people will experience flu like symptoms. 1 out of 4 infected people will experience flu like symptoms. 1 out of 4 infected people will experience flu like symptoms.

**Country options**

- Niger
- Nigeria (Country)
- Imo, Nigeria (State)
- Jigawa, Nigeria (State)
- Ogun, Nigeria (State)
- Cross River, Nigeria (State)
- Yobe, Nigeria (State)
- Edo, Nigeria (State)
- Gombe, Nigeria (State)
- Zinder, Niger (State)

**Similarity score options**

- >0.8
- 0.7 - 0.8
- 0.55 - 0.7
- <0.55

**Polio free country**

- WPV
- vDPV
Polio: Outbreak comparison

- 85% | Pakistan (2012)
- 64% | Pakistan (2013)
- 49% | Sudan (2004)
- 48% | Madagascar (2001)
- 48% | Haiti (2000)

Polio: Pakistan (2012)

- 85% similar to your situation

Event features:
- Important dates: This outbreak report is from 2012.
- Index case: Polio is endemic in Pakistan; information on index case is not available.
- Species/genotype/serotype/type: Most of the cases in this outbreak were caused by wild polio virus type 1 (WPV1). A smaller portion of cases were caused by circulating vaccine derived polio virus type 2 (cVDPV2) and WPV3.

Contextual information:
- Case definition: Specific case definition was not provided in the referenced publication. The graph shows laboratory confirmed cases.
- Geographic/historic information: This outbreak report is from Pakistan one of endemic countries for WPV1. There was a surge in polio cases in 2013-2014.
Summary information included for every outbreak record in AIDO
**How was this outbreak scored?**

### Score breakdown

![Chart showing score breakdown](image)

<table>
<thead>
<tr>
<th>Property</th>
<th>Outbreak value</th>
<th>Score</th>
<th>Weight</th>
<th>Weighted score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Case count</td>
<td>93.4%</td>
<td>0.300</td>
<td>28.0%</td>
<td></td>
</tr>
<tr>
<td>Time</td>
<td>100%</td>
<td>0.300</td>
<td>30.0%</td>
<td></td>
</tr>
<tr>
<td>Country polio category</td>
<td>Endemic country</td>
<td>100%</td>
<td>0.133</td>
<td>13.3%</td>
</tr>
<tr>
<td>Human development index</td>
<td>0.5</td>
<td>100%</td>
<td>0.133</td>
<td>13.3%</td>
</tr>
<tr>
<td>Outbreak pathogen</td>
<td>WPV</td>
<td>---</td>
<td>0.133</td>
<td>---</td>
</tr>
</tbody>
</table>

**Total: 84.7%**  
**Max possible score: 86.7%**

### Identification

- **Name**: Disease Early Warning System (DEWS)
- **Short name**: DEWS
- **Status**: Active
- **Category**: System
- **Organizations**: 1) World Health Organization (WHO)
- **Update frequency**: Weekly
- **Created**: 2012-10-05 03:59:55+00:00
- **Modified**: 2016-03-04 22:21:48.121985+00:00

### Basic Information

**Overview**: The WHO, in collaboration with the Federal Ministry of Health, designed and set up DEWS. Its goal is to reduce morbidity and mortality by early detection and response to epidemic-prone diseases. Its objectives are to report weekly disease trends from country-wide sentinel sites, respond to alerts within 24 hours and control outbreaks through measures such as water quality and sanitation interventions, clinical case management and health promotion.

**Goals**:
1. Baseline awareness
2. Early detection
3. Situational awareness

**Year start**: 2008


**URL (alternate)**: [http://www.emro.who.int/pak/communication-resources/information-resources.html](http://www.emro.who.int/pak/communication-resources/information-resources.html)

### Disease and Geography

- **Locations**: 1) Pakistan
- **Geography**: No
Browsing the library

Dengue facts

Pathogen: The dengue viruses are members of the genus *Flavivirus* in the family *Flaviviridae*.

Host and animal reservoir: Disease occurs in humans and non-human primates. Symptoms are sub-clinical in primates.

Transmission: The transmission route is human to mosquito to human. The vector is *Aedes* mosquitoes. They are a tropical and subtropical species with geographical limits of 35N to 35S. This website can be used to view the global distribution of *A. aegypti* and *A. albopictus* mosquitoes.

Disease symptoms - onset, duration and characteristic features: The fever begins 4-7 days after infection. The illness lasts an average of 4.5 days after onset of symptoms. Dengue has a wide spectrum of clinical presentations, often with unpredictable clinical evaluation and outcome. Most patients recover following a self-limiting non-severe clinical course, but a small proportion progress to severe disease. Dengue fever (DF), dengue hemorrhagic fever (DHF), and dengue shock syndrome (DSS) denotes severe cases. Symptoms for the different categories are given below. More details are given here.

<table>
<thead>
<tr>
<th>Criteria for dengue</th>
<th>Warning signs</th>
<th>Criteria for severe dengue</th>
</tr>
</thead>
<tbody>
<tr>
<td>Provable dengue (DF)</td>
<td>Abdominal pain or tenderness</td>
<td>Severe plasma leakage</td>
</tr>
<tr>
<td>Fever and 2 of the following criteria:</td>
<td>Persistent vomiting</td>
<td>Leading to dengue shock syndrome (DSS)</td>
</tr>
<tr>
<td>- Nausea, vomiting</td>
<td>Clinical fluid accumulation</td>
<td>Fluid accumulation with respiratory distress</td>
</tr>
<tr>
<td>- Rash</td>
<td>Mucosal bleed</td>
<td></td>
</tr>
<tr>
<td>- Aches and pains</td>
<td>Lethargy, restlessness</td>
<td></td>
</tr>
<tr>
<td>- Leukopenia</td>
<td>Liver enlargement &gt;2cm</td>
<td></td>
</tr>
<tr>
<td>- Laboratory confirmation of dengue</td>
<td>Increase in hematocrit concurrent with rapid decrease in platelet count</td>
<td></td>
</tr>
</tbody>
</table>

Operated by Los Alamos National Security, LLC for NNSA
Browsing the library

Event features
- Important dates: Case numbers crossed the outbreak threshold in January of 2013. During the peak season in March, more than 100,000 cases were reported per week.
- Index case: Specific information on the index case is not available, but dengue is endemic in Brazil.
- Vector: The mosquito species, Aedes aegypti, is considered the most important vector.
- Species/genotype/serotype/type: This outbreak was caused by the DENV-4 serotype.

Contextual information
- Case definition: WHO case definitions for dengue and its complications were used. Probable cases of dengue are reported in the graph.
- Geographic/historic information: This outbreak affected about 1.5 million people in Brazil. The Ceilândia and Samambaia regions reported the most cases in 2013. Precipitation in Brazil is classified as winter dry (W).
- Risk factors: The large size of the outbreak was in part due to the fact that DENV-4 was fairly new to Brazil.
Interagency collaborations through AIDO (DTRA-DHS)

- Expand AIDO to include priority diseases for the National Biosurveillance Integration Center (NBIC)
- Expand existing AIDO outbreak library for NBIC selected diseases (9)
- Develop an anomalous event detecting algorithm for AIDO
- Refine AIDO UI and functionality to meet NBIC needs
- Operational evaluation and demonstration within the APEX program
An analysis tool that can be used to provide early warning or detection of the re-emergence of an infectious disease at the global level, but through a local lens

- Facilitate future planning of control and preventive measures
- Alert a user of local re-emergence of a disease and provide possible causes
- Facilitate hypothesis generation and therefore early warning/detection for global re-emergence
What is re-emergence?

“Any condition...that had decreased in incidence in the global population ... and began to resurge as a health problem due to changes in the health status of a susceptible population, e.g. Cholera, dengue, diphtheria, malaria, tuberculosis.”

-Segen's Medical Dictionary

“Re-emerging infectious diseases are diseases that once were major health problems globally or in a particular country, and then declined dramatically, but are again becoming health problems for a significant proportion of the population”

-NIH Curriculum Supplement
Understanding Emerging and Re-emerging Infectious Disease
A user is asked to:
- put in a case count or time series of a country-level event/outbreak
- add in the location of the outbreak, followed by the auto-population of some data
- select a historic duration of time to compare local disease incidence (e.g. 2000-2014)
RED Alert: About the tool

• RED Alert will:

  “Local”
  – Calculate historical trend/pattern analyses of disease incidence for the location of interest (temporal context)
  – Provide information about related countries (those with similar disease incidence) for geospatial context
  – Determine a subset of likely associated causes of re-emergence event through machine-learning algorithms (data-driven approach)

  “Global”
  – Provide interactive visuals of the global context which users can use to generate hypotheses of global re-emergence (VBI)

• RED Alert will not:
  – Provide insight for outbreak investigation of an ongoing event
  – Provide a user with direct, categorical classification of an event as “re-emergent” or not (YET)
RED Alert: Key features

• Ease of use
  • Minimal user input required

• Trend analysis is not readily available elsewhere
  • In disease incidence (historical populations/geographic components)

• Exportable graphics and data
  • Easy to add to reports/for documentation

• “Related indicators” offers informative statistical analysis without modeling/forecasting
  • Data can be used (open source APIs) for user’s own models
  • Facilitating analysis for decision support
RED Alert: About the tool

Multiple-tabbed interface

User input panel

RED Alert is an analysis tool that can provide early warning or indication of the re-emergence of an infectious disease at the global level, but through a regional lens. RED Alert offers the capability of enhancing situational awareness to facilitate in the prevention or mitigation of re-emerging diseases persisting at the global level.
Algorithm 1: Does my outbreak represent a re-emergence event?

Example: Measles in USA 2014, temporal incidence trends

User input transformed to disease incidence
Algorithm 1: Does my outbreak represent a re-emergence event?

Example: Measles in USA 2014, spatial/geographic incidence trends
Algorithm 2: What are associated causes of re-emergence in my location?

1. Herd Immunity (coverage >95%)
   - P (yes)
   - P (no)

2. Adequate vaccination coverage
   - P (yes)
   - P (no)

3. Pockets of unvaccinated communities
   - P (yes)
   - P (no)

4. Civilian cause (religious, social motivation)
   - P (yes)
   - P (no)

5. Majority of infected children too young for second dose of vaccine
   - P (yes)
   - P (no)

Terminus: Not re-emergence

Terminus: re-emergence

Terminus: re-emergence

Terminus: re-emergence

Terminus: re-emergence
## Measles re-emergence component causes

| Host | Lack of herd immunity | Children below vaccination age  
People receiving only MCV1 not MCV2  
Low vaccination coverage (specific communities or nationally) |
|------|-----------------------|--------------------------------------------------------------------------------|
|      | Vaccine failure        | Vaccine strategy (number of doses, age of vaccination)  
Vaccine stability and immunogenicity  
Handling and administration factors (injection technique, cold chain issues)  
Vaccine failed to elicit immune response |
|      | Weakened immunity      | HIV positive infants too young to be vaccinated |
| Pathogen | New serotype          | Replacement of endemic strains with new strains  
Introduction of new strains to non endemic regions |
| Environment | Inadequate public health infrastructure | Health system deficiency  
Poor surveillance  
Nosocomial transmission |
|        | Natural Environment    | Weather pattern  
Natural disaster |
|        | Human behavior         | Mistrust of healthcare/mis-information  
Migration (voluntary or involuntary)  
Mass gatherings  
Civil unrest/war  
Cultural practices |
This functionality explores a number of socioeconomic, health, and country-level infrastructural metrics in order to assess their correlations with disease incidence in a given location. Data mapping begins with a compilation of all notable disease-related features identified through a comprehensive literature review. These “indicators” are categorized into host, pathogen, or environmental factors for each disease and displayed in the interactive graphic below.

Please select an analytic in order to visualize your results: Sample Measles Tree
Algorithm 3: Is my outbreak connected to other recent ones and if so, is this global re-emergence?

Visualization of various disease relevant data layers that may connect global outbreaks.
LANL BSV tool team

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Thank you!

“Be the best you can be every day, for cholera beckons always.”
-James Madison