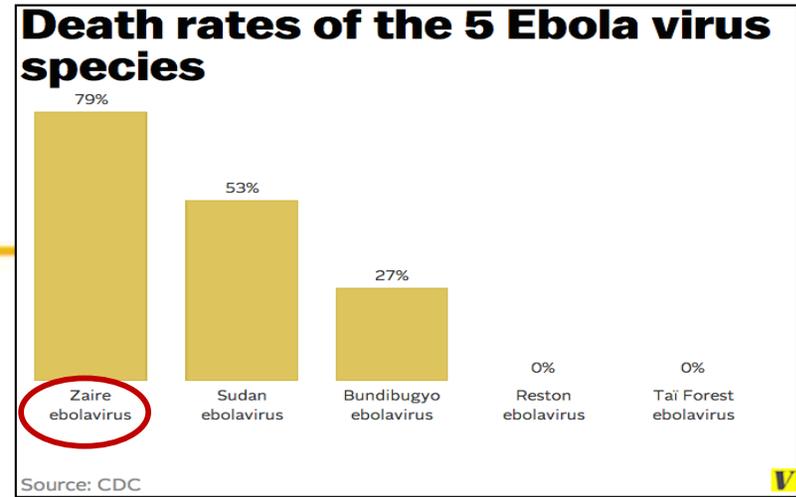
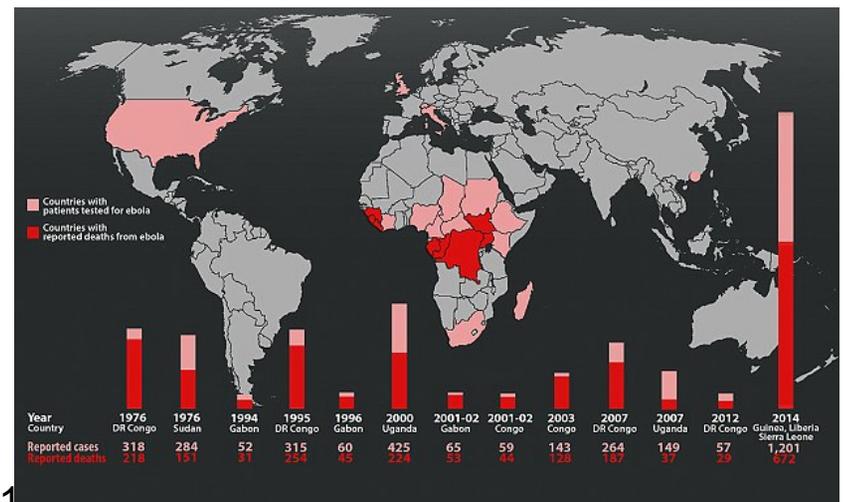
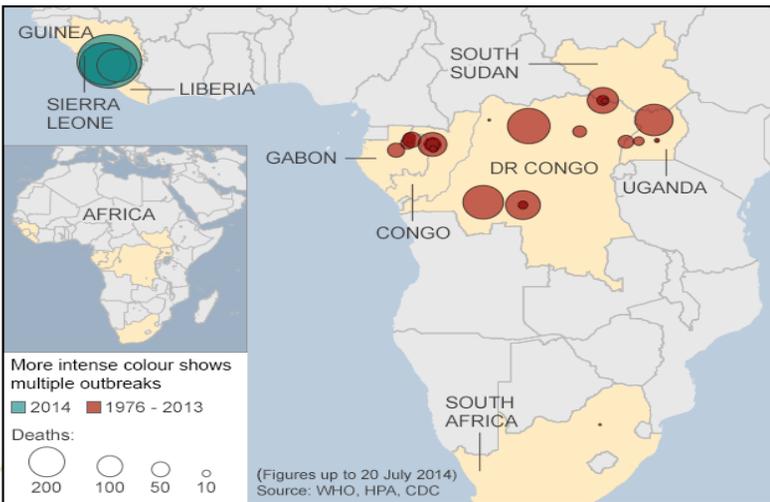


# Tools and Apps to Enhance Situational Awareness for Global Disease Surveillance

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)



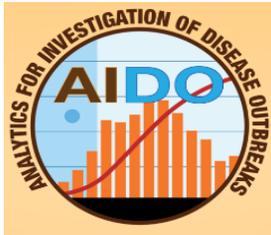
LA-UR-17-24721

Slide 2

# 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>)



→ 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>)



Epi  
Archive

A data collection and visualization tool for notifiable disease data from around the world. (<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

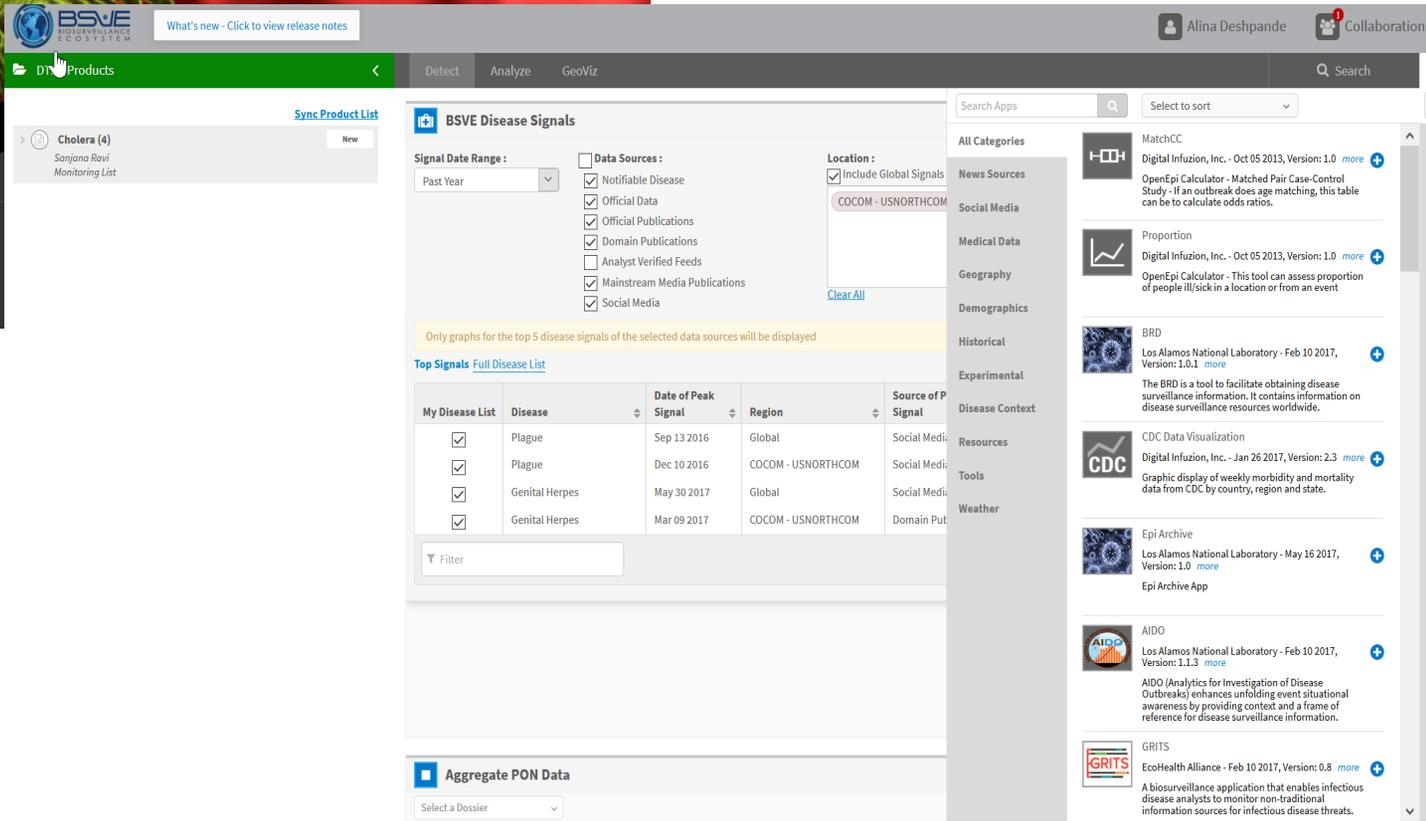
# Biosurveillance Gateway

Diagnostics, predictive modelling, and decision support for global and national security

ABOUT RESOURCES CAPABILITIES NEWS OUTREACH

Welcome to the  
**Biosurveillance Gateway**

The Biosurveillance Gateway serves as a centralized portal for all news, information, resources, and research related to biosurveillance at Los Alamos National Laboratory.



The screenshot displays the BSVE interface with the following components:

- Header:** BSVE BIOSURVEILLANCE ECOSYSTEM logo, a notification for "What's new - Click to view release notes", and user information for Alina Deshpande and Collaboration.
- Navigation:** "Products" menu, "Detect", "Analyze", and "GeoViz" tabs.
- Left Panel:** "Cholera (4)" monitoring list by Sanjana Ravi.
- Main Content:**
  - BSVE Disease Signals:** Includes filters for "Signal Date Range" (Past Year), "Data Sources" (Notifiable Disease, Official Data, Official Publications, Domain Publications, Analyst Verified Feeds, Mainstream Media Publications, Social Media), and "Location" (Include Global Signals, COCOM - USNORTHCOM).
  - Top Signals Table:**

My Disease List	Disease	Date of Peak Signal	Region	Source of P Signal
<input checked="" type="checkbox"/>	Plague	Sep 13 2016	Global	Social Media
<input checked="" type="checkbox"/>	Plague	Dec 10 2016	COCOM - USNORTHCOM	Social Media
<input checked="" type="checkbox"/>	Genital Herpes	May 30 2017	Global	Social Media
<input checked="" type="checkbox"/>	Genital Herpes	Mar 09 2017	COCOM - USNORTHCOM	Domain Publications
  - Aggregate PON Data:** Select a Dossier dropdown.
- Right Panel:** Search Apps, Select to sort, and a list of categories including MatchCC, Proportion, BRD, CDC Data Visualization, Epi Archive, AIDO, and GRITS.

- Decision support tools offered through LANL's Biosurveillance (BSV) gateway (<http://bsvgateway.org/>) and DTRA's Biosurveillance Ecosystem (BSVE)

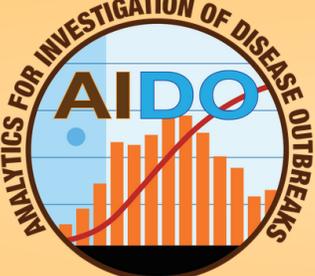
# Analytics for Investigation of Disease Outbreaks

---



- 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



**Analytics for Investigation of Disease Outbreaks**

AIDO is a tool designed to enhance situational awareness during unfolding disease outbreaks by providing the user with detailed background information on historical outbreaks.

Composed of over 450 outbreaks across a wide variety of diseases, the goal of AIDO is to give the user a representative sample of how each disease progresses under different circumstances.

*This tool was previously known as the SWAP (Surveillance Window Application).*

Tutorial      Frequently asked questions

Select a disease      Search

Tutorial  
FAQ  
Data Streams  
Feedback

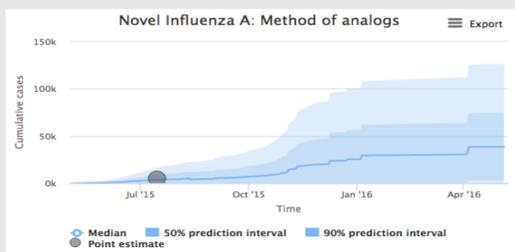
### Outbreak comparison

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.

Click [here](#) for more information.



### Outbreak time series

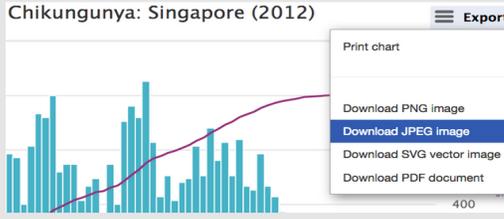
Each outbreak in AIDO provides detailed information on how the disease progressed under the circumstances of that outbreak. All outbreak records display an interactive time series and are annotated with contextual information.

Click [here](#) for more information.

### Chart export

AIDO provides visualizations for much of the data it uses. All plots displayed in AIDO can be quickly downloaded in various formats, allowing them to be easily included in reports.

Chikungunya: Singapore (2012)



### 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](#).

Click [here](#) for more information.

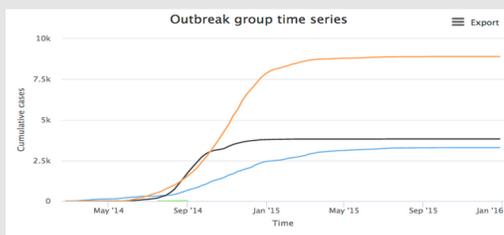
```

Allow: GET, OPTIONS
Content-Type: application/json
Vary: Accept

{
  "count": 455,
  "next": "https://aido.bsvstaging.lanl.gov/api/outbreaks/?page=2",
  "previous": null,
  "results": [
    {
      "url": "https://aido.bsvstaging.lanl.gov/api/outbreaks/991/",
      "id": 991,
      "disease": "https://aido.bsvstaging.lanl.gov/api/diseases/58/"
    }
  ]
}
    
```

### 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

**AIDO**

Select a Dossier

Content BSV Gateway

**\* Disease** Polio

**\* Sort by** Similarity score

**\* Cases**

**\* First case report**

**\* Last case report**

**Location** Enter location

**Human development index** -----  
Data source

**Country** -----  
**Polio category**  
Data source

**Outbreak pathogen** -----  
Help

**Restrict search**

**Search**

## Polio facts

**Pathogen** Poliomyelitis, caused by the poliovirus (genus Enterovirus) 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** Polio virus is highly contagious and spreads through person-to-person contact. The virus lives inside the throat and intestine of the patients and 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 6 to 20 days. Most people infected with polio virus (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, head ache, stomach pain

More severe symptoms of the disease include;

- Paresthesia (feeling of pins and needles in the legs)
- Meningitis (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, caseloads have decreased by 99% since 1998. 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](#) web site. A world map depicting polio endemic, outbreak, key at risk and polio free countries is shown [here](#).

# Understanding an unfolding outbreak

**AIDO**

Select a Dossier

**Polio facts**

**Pathogen** Poliomyelitis, caused by the poliovirus (genus Enterovirus) is characterized by paralysis. Polio with paralytic infection are considered to have the disease. Polio is caused by three types of poliovirus 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** Polio is transmitted from person-to-person, person-to-animal and droplet-to-person. This is true for all three types of poliovirus. Polio is most commonly transmitted to people living under unsanitary conditions.

**Disease symptoms - onset, duration and characteristic features** The incubation period for polio is most commonly between 6 to 20 days. Most people with polio experience flu like symptoms. 1 out of 4 infected people will experience flu like symptoms.

**Epidemiology and risk factors** Children under 5 years of age are at the highest risk of contracting polio. Polio is on the verge of eradication, caseloads were reported in 2015 worldwide. Of the three wild type polio virus types, only type 2 and case of type 3 was reported by Nigeria since 2012. WHO has a polio database and a site. A world map depicting polio endemic, outbreak, key at-risk countries is available.

**Sort by** Similarity score

**Location** Enter location

**Human development index**

**Country**

**Polio category**

**Outbreak pathogen**

**Similarity score**

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

**Polio free country**

**Endemic country**

**Outbreak country**

**Key at-risk country**

**WPV**

**vDPV**

**Niger**

- Niger (Country)
- 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)

**Restrict search**

**Search**

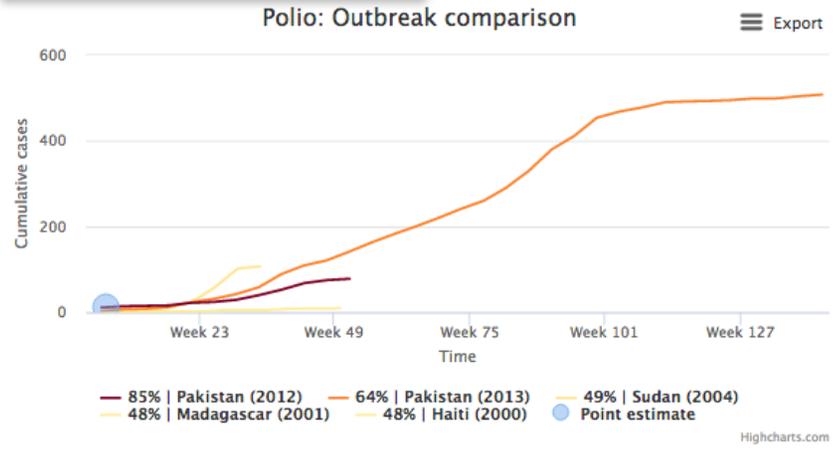
\* Disease: Polio  
 \* Sort by: Similarity score  
 \* Cases: 12  
 \* First case report: 01/29/2017  
 \* Last case report: 02/04/2017  
 Location: Pakistan (Country)  
 Human development index: <0.55  
 Country: Endemic country  
 Polio category: Polio  
 Outbreak pathogen: -----

Restrict search

Search

1 2 Next »

Outbreak comparison Method of analogs



Outbreak comparison

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

Outbreak comparison

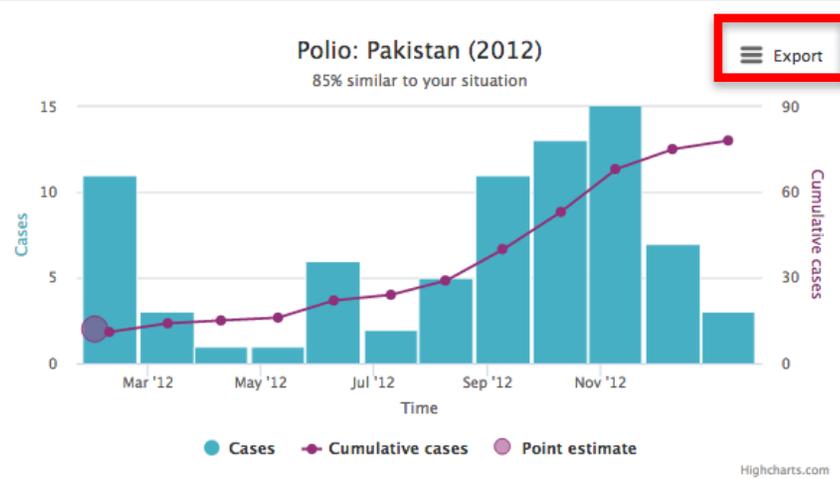
85% | Pakistan (2012)

64% | Pakistan (2013)

49% | Sudan (2004)

48% | Madagascar (2001)

48% | Haiti (2000)



Export

View related outbreaks

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.

Print chart

Download PNG image

Download JPEG image

Download SVG vector image

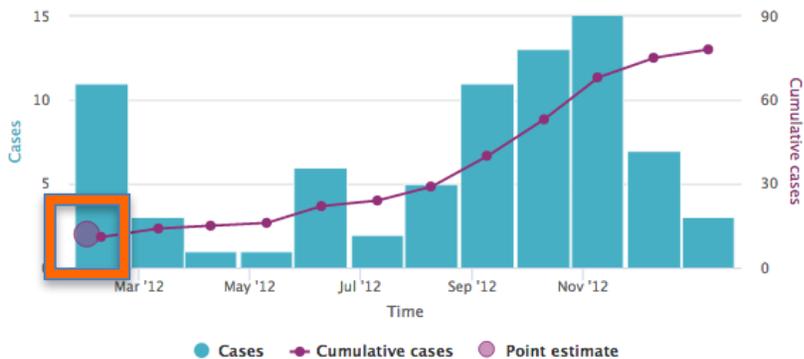
Download PDF document



## Polio: Pakistan (2012)

85% similar to your situation

Export



View related outbreaks

### 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.
- Risk factors: Wild polio virus still circulates in northern parts of Pakistan. Many areas were inaccessible for routine vaccination due to war and conflicts.

### Actions or control measures

- Vaccination of children in Pakistan-Afghanistan border regions remains a big challenge to world polio eradication efforts. The disease is very prevalent in these parts despite vaccination efforts.

### Related outbreaks

THIS OUTBREAK IS DIRECTLY RELATED TO THE FOLLOWING OUTBREAKS:

- Pakistan (2013)
  - Pakistan is one of the three countries where polio is still endemic.
  - A much larger outbreak occurred in 2013-2015.

### Data sources

- Morbidity and Mortality Weekly Report (MMWR). Progress Toward Poliomyelitis Eradication — Pakistan, January 2014–September 2015. Center for disease control; 2015; <http://www.cdc.gov/m...6445a4.htm>.

### Suggested early data streams

Clinic/health care provider records

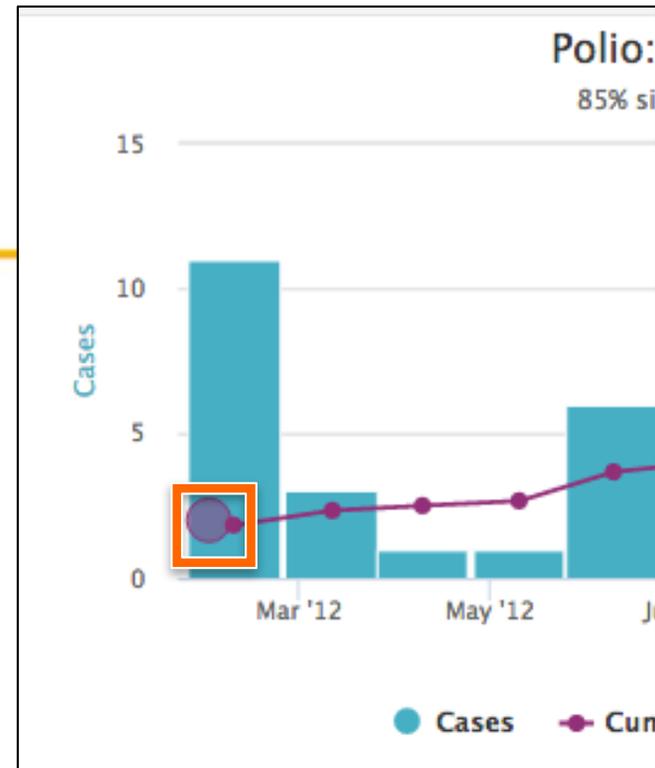
Laboratory records

Official reports

### Related BRD links

- USAID
- Disease Early Warning System

How was this outbreak scored?



Summary information included for every outbreak record in AIDO

R-17-24721

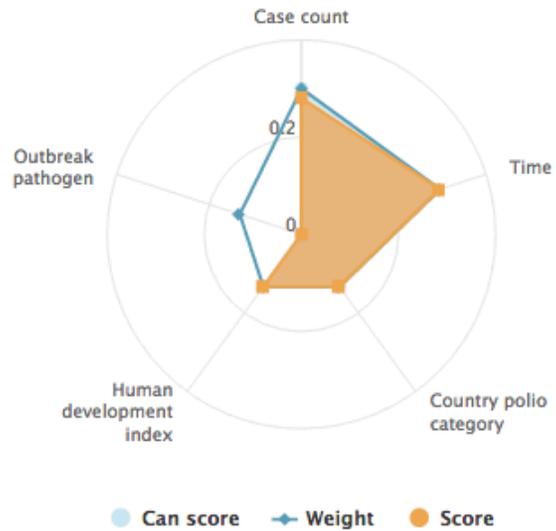
Slide 11



## How was this outbreak scored?

### Score breakdown

Export



Highcharts.com

Property	Outbreak value	Score	Weight	Weighted score
Case count	---	93.4%	0.300	28.0%
Time	---	100%	0.300	30%
Country polio category	Endemic country	100%	0.133	13.3%
Human development index	0.5	100%	0.133	13.3%
Outbreak pathogen	WPV	---	0.133	---
<b>Total</b>				<b>84.7%</b>
<b>Max possible score</b>				<b>86.7%</b>



Operated by Los Alamos National Security, LLC for NNSA

LA-UR-17-24

BRD Resources 124: Disease Early Warning System (DEWS) Content BSV Gateway

#### Identification

##### Basic Information

##### Disease and Geography

##### Datastreams

### Identification

<b>Name</b>	Disease Early Warning System
<b>Short name</b>	DEWS
<b>Status</b>	Active
<b>Category</b>	System
<b>Organizations</b>	(1) World Health Organization (WHO)
<b>Update frequency</b>	Weekly
<b>Created</b>	2012-10-05 03:59:55+00:00
<b>Modified</b>	2016-03-04 22:21:49.121965+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 measure 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** 2006

**URL** <http://www.emro.who.int/afg/programmes/communicable-disease-surveillance-response-dews.html>

**URL (alternate)** <http://www.emro.who.int/pak/information-resources/information-resources.html>

### Disease and Geography

**Locations** (1) Pakistan

**Geography** No

# Browsing the library

\* Disease

\* Sort by

\* Cases

\* First case report

\* Last case report

Location

Precipitation 
Data source

## 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* mosquitos. 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](#).

### Criteria for dengue ± warning signs

### Criteria for severe dengue

#### Probable dengue (DF)

#### Warning signs

- Live in/travel to dengue endemic area
- Fever and 2 of the following criteria:
  - Nausea, vomiting
  - Rash
  - Aches and pains
  - Leukopenia
  - Laboratory confirmation of dengue

- Abdominal pain or tenderness
- Persistent vomiting
- Clinical fluid accumulation
- Mucosal bleed
- Lethargy, restlessness
- Liver enlargement >2cm
- Increase in hematocrit concurrent with rapid decrease in platelet count

- Severe plasma leakage
  - Leading to dengue shock syndrome (DSS)
  - Fluid accumulation with respiratory distress
- Severe bleeding
- Severe organ involvement
  - Liver AST ≥1000
  - Heart and other organs function abnormally

Similarity score

Date

✓ Distance from a location

# Browsing the library

\* Disease

\* Sort by

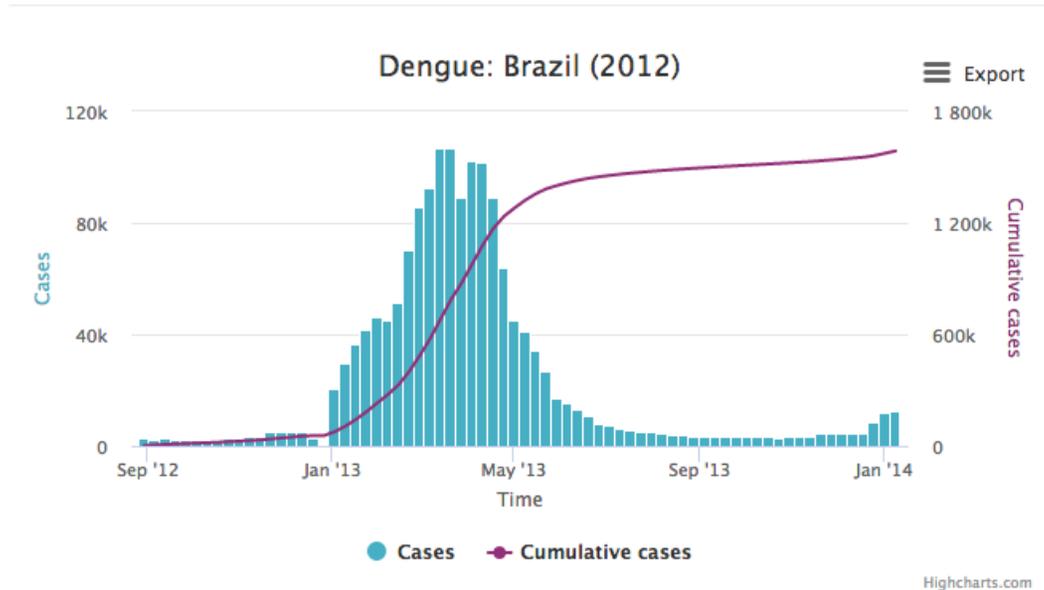
\* Location

**Restrict search**

Search

1 2 3 4 5 Next »

- Brazil (2012)
- Paraguay (2012)
- Brazil (2001)
- Peru (2012)
- Venezuela (2001)



Restrict search

Location

Precipitation

Data source

## 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

# RED Alert: About the tool

---

- 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

**Disease: ?**

-----

**Location: ?**

-----

**Historic case data source: ?**

-----

**Mode: ?**

Cumulative ?

Time Series ?

Historical ?

**Date: ?**

-----

**Population: ?**

-----

**Case count: ?**

-----

**Submit**

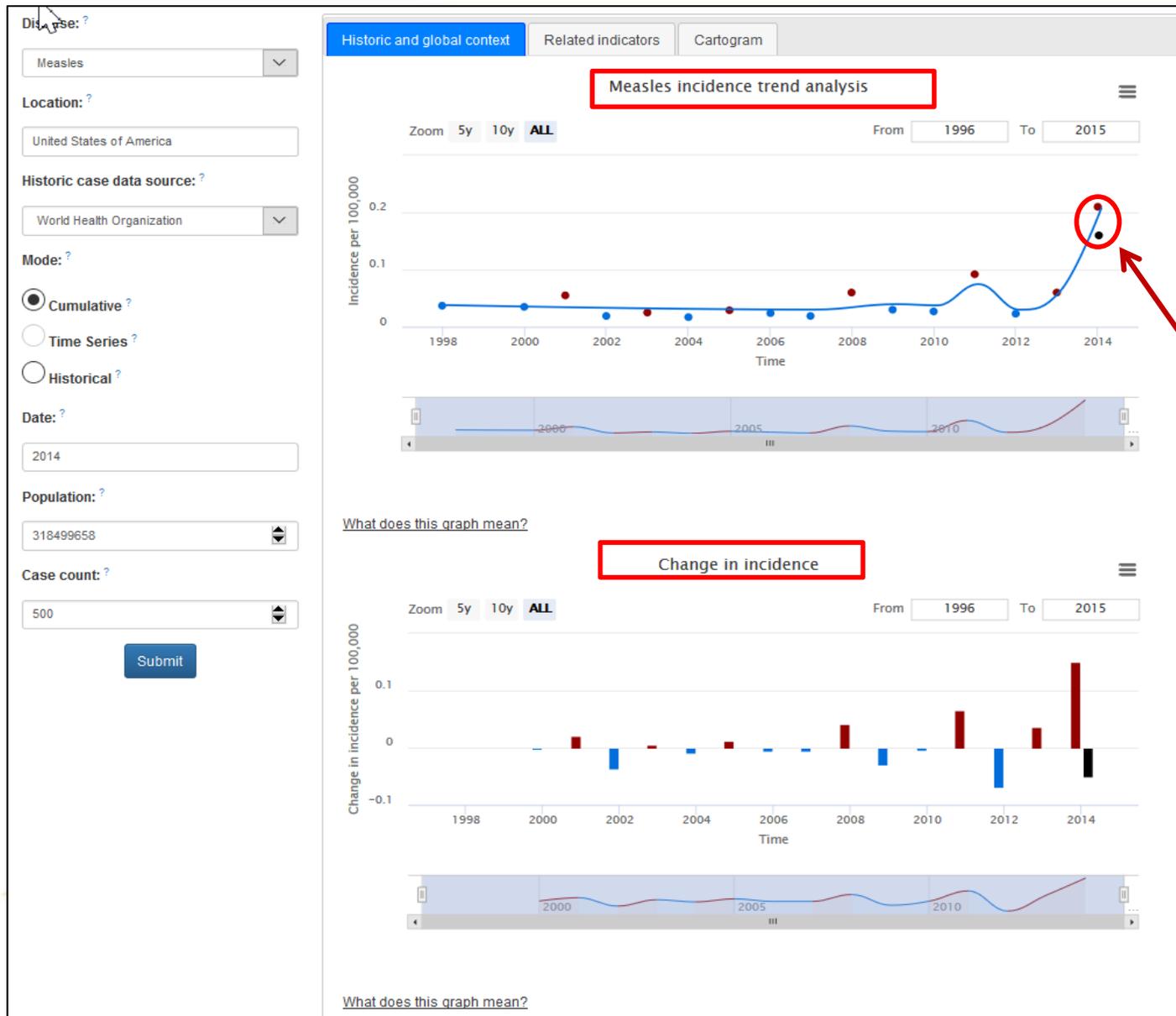
Historic and global context   Related indicators   Cartogram

**RED Alert**  
RE-EMERGING INFECTIOUS DISEASE ALERT

**Re-Emerging Infectious Disease Alert**

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.

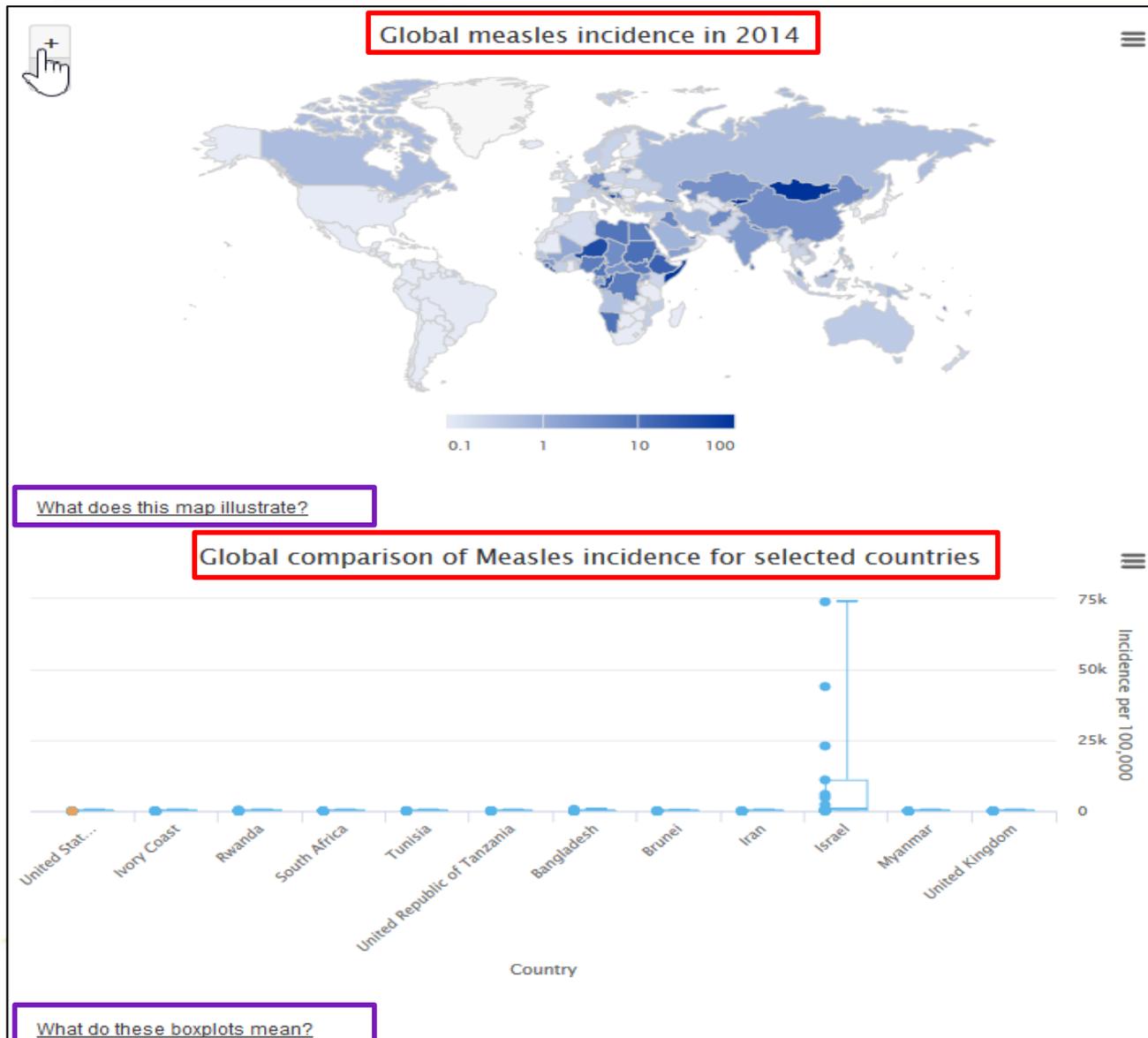
# Algorithm 1: Does my outbreak represent a re-emergence event?



**Example:  
Measles in USA  
2014, temporal  
incidence  
trends**

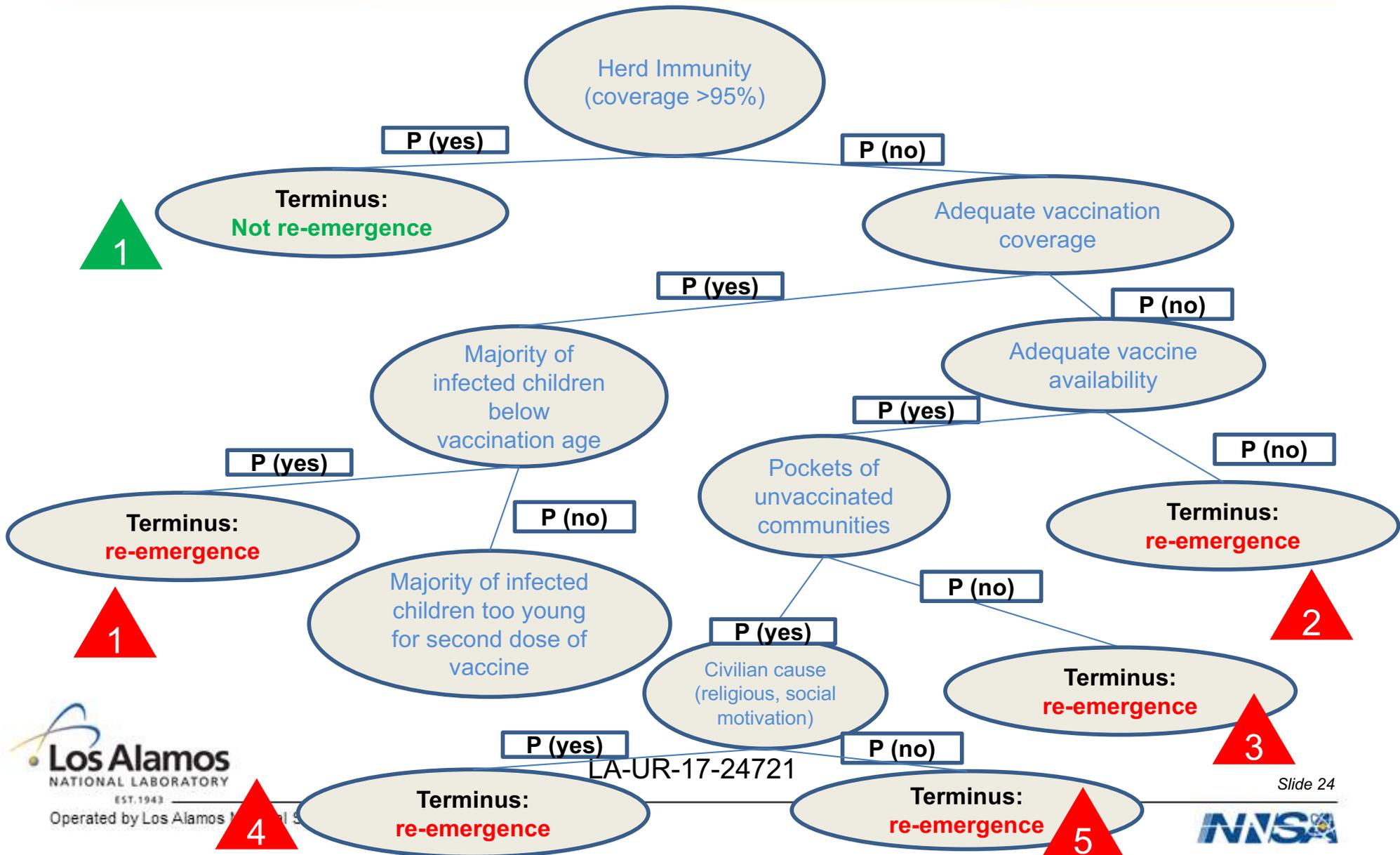
**User input  
transformed to  
disease  
incidence**

# 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?

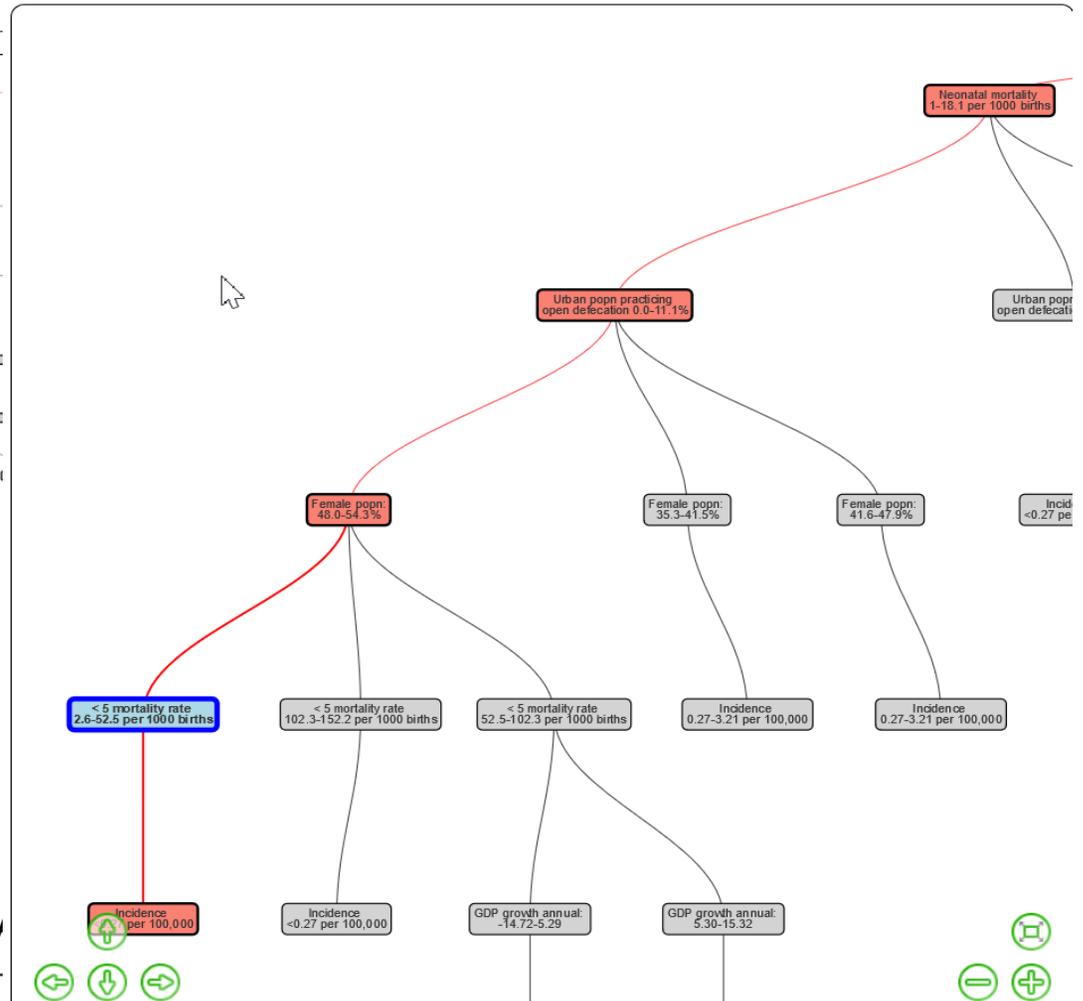
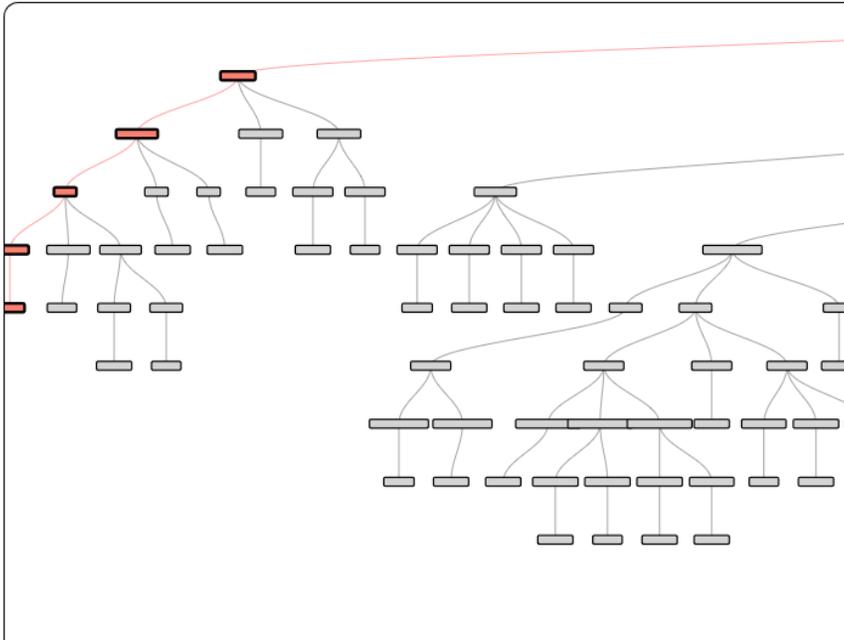


# Measles re-emergence component causes

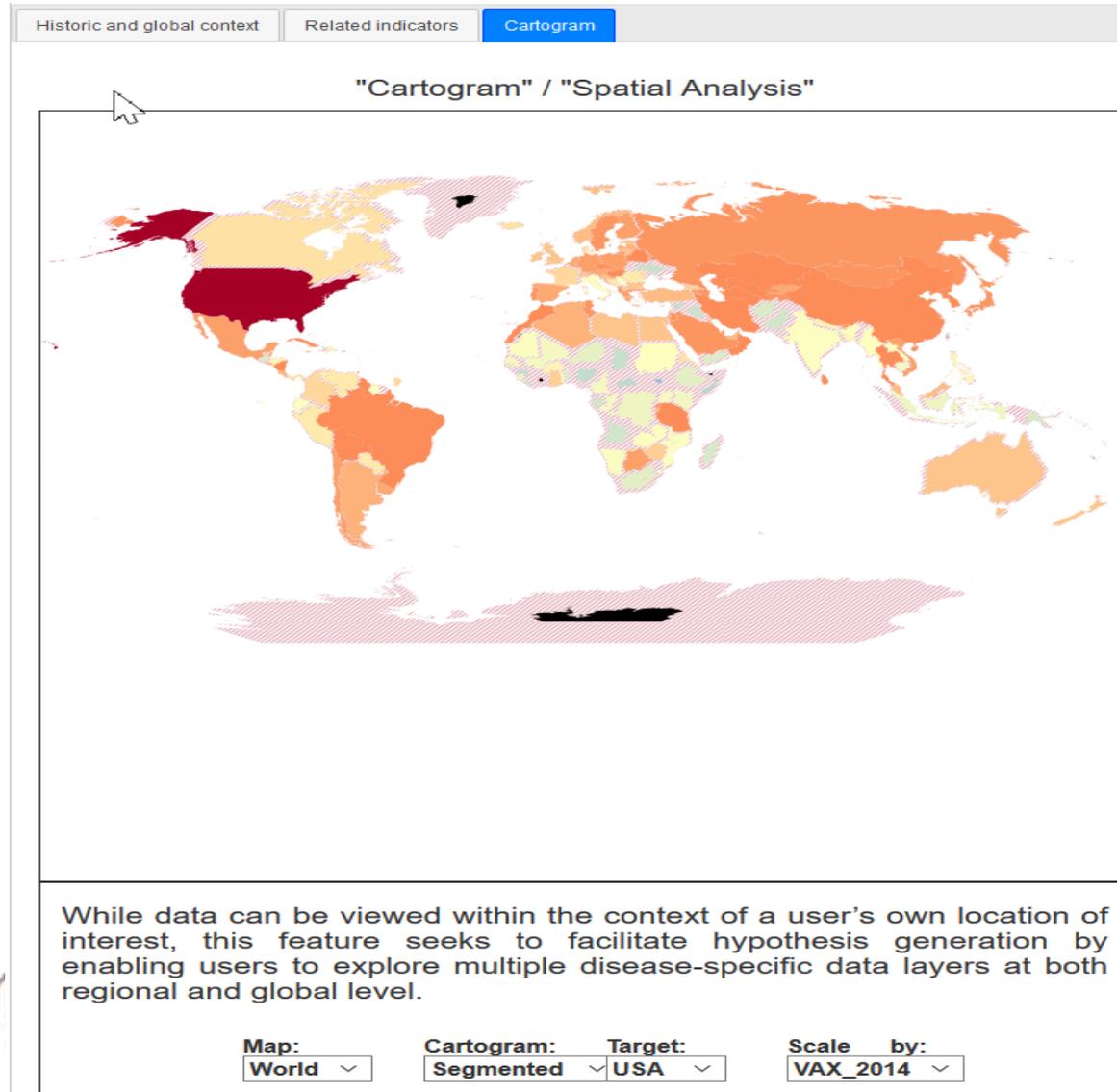
<b>Host</b>	Lack of herd immunity	Children below vaccination age
		People receiving only MCV1 not MCV2
		Low vaccination coverage (specific communities or nationally)
	Vaccine failure	Vaccine strategy (number of doses, age of vaccination)
Vaccine stability and immunogenicity		
Handling and administration factors (injection technique, cold chain issues)		
Vaccine failed to elicit immune response		
Weakened immunity	HIV positive infants too young to be vaccinated	
<b>Pathogen</b>	New serotype	Replacement of endemic strains with new strains
		Introduction of new strains to non endemic regions
<b>Environment</b>	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!

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