WHO AFIRM Strategy Roadmap Meeting

Outbreak Prediction Tools and Molecular Epidemiology

3/29/2022
Disclaimers
Outbreak Prediction: Preventing Outbreaks

Ultimate goal: To predict where and when an outbreak will occur to prevent loss of human life, animals, or crops (Prediction will allow preplacement of countermeasures or deployment of interventional strategies.)

Perhaps more realistic: To predict where and when an outbreak is likely to occur and to detect outbreaks early, allowing for the rapid containment, minimizing the loss of human life, animals, and crops.
Spring 2015: A workshop was organized by the RAPIDD to “take stock of the different models used throughout the outbreak and discuss improvement in forecasting accuracy for recent and future outbreaks”.

September-December 2015: RAPIDD Ebola forecasting challenge was launched. It convened 16 independent international academic groups and U.S. government agencies.

- Self-organized in eight teams, each used a different statistical or mathematical model.
- Four models had been used previously during the West African Ebola outbreak in similar versions (CDC-NIH, TOR, ASU, LSHTM).

Modeling Once an Outbreak Has Started
Strategy

- To use artificial intelligence, “big data”, and eventually machine learning to synthesize very large, complex, and diverse bodies of information/data to create models
- To rapidly update models to account for changes in variables to ensure accuracy of models

Challenges

- Models will only be as good as the data that is input or used to construct the model.
- Time and money
- Knowledge gaps
A Complex Problem

- Multiple factors that have to align depending on the scenario
  An oversimplified example using a zoonosis
  The likelihood that an outbreak will occur is the function of the following events:
  - exposure to an animal carrying the pathogen occurs,
  - exposure results in infection,
  - the pathogen establishes a productive infection that results in disease, and
  - the index case pass the infection to another host.

- Multiple variables and sub variables related to the pathogen, the host, the environment will come into play and may be dynamic (meaning they change year by year, season by season or even day by day
Buckets of Data

- The distribution of animals that carry or are likely to carry diseases
  - Examples: bats or migratory birds
- The distribution animals that amplify disease.
  - Examples: pigs or civet cats
- The size and density of the susceptible population
- The presence or distribution of populations that may be “at greatest” risk
  - Examples: hunters, health care workers, elderly, immunocompromised
- The environmental factors that might affect the size of the animal population or the interactions between or within a population
  - Examples: rain fall, deforestation, natural disasters
- The social and/or economical factors that could impact populations or behaviors
  - Examples: fuel shortages, shipping delays, vaccination avoidance
Identifying combinations of species, pathogens, susceptible groups, and environmental conditions that provide environments or conditions for new diseases to emerge and or spread

Refinement of Models

- Need for case studies
- Management of expectations:
  - Models won’t be perfect.
  - Continued investment will be needed.
- Failures in prediction will occur and will aid in refinement.
Review of Tools

- Review of papers/tools for predicting outbreaks of Ebola virus, Marburg virus, Zika virus, Lassa fever, Nipah virus, Henipaviral disease, Rift Valley fever, Crimean-Congo hemorrhagic fever, severe acute respiratory syndrome, Middle East respiratory syndrome, and “Disease X”.
- A total of 58 out of 3,959 articles met inclusion criteria.
- Five major prediction methods emerged:
  - Spatio-temporal risk maps predicted outbreak risk periods and locations through vector and climate data.
  - Stochastic models were predominant.
  - Rift Valley fever was the most predicted disease.
  - 10% of models were implemented by health authorities.
Developing a Tool for Filoviruses

- Have there been previous instances of the disease? Frequency?
- Is the reservoir located in the region?
- Evidence of the agent in the reservoir?
- Likelihood to have contact for with the reservoir?
- Likelihood to spread the disease within a community?
- Likelihood for the disease to spread beyond the community?
Some Examples

Local, national, and regional viral haemorrhagic fever pandemic potential in Africa: a multistage analysis

David M Pigott DPhil, Aniruddha Deshpande MPH, Ian Letourneau BA, Chloe Morozoff MPH, Robert C Reiner Jr PhD, Moritz U G Kraemer DPhil, B, H, Shannon E Brent MPH, Isaac I Bogoch MD, Kamran Khan MD, Molly H Biehl MPH, Roy Burstein BA, Lucas Earl MSc, Nancy Fullman MPH, Jane P Messina PhD, C, D, Adrian Q N Mylne MSc, Catherine L Moyes PhD, Freya M Shearer BSc, Samir Bhatt DPhil, M, Oliver J Brady DPhil, N, Peter W Gething PhD, Daniel J Weiss PhD, Andrew J Tatem PhD, N, Luke Caley MSc, Tom De Groeve PhD, Luca Vernaccini MSc, Nick Golding DPhil, Prof Peter Horby PhD, Jens H Kuhn MD, Sandra J Laney PhD, Edmond Ng MSc, Prof Peter Piot PhD, Prof Osman Sankoh DSc, Prof Christopher J L Murray PhD, Prof Simon I Hay DSc, M, A,
What can we do today to identify at-risk environments?

**In known areas of disease activity**
- Increased surveillance
  - Continued monitoring of dead bodies
  - Decentralized testing
  - Availability of sequencing
  - Enabling monitoring and health care of survivors and contacts

**What about in areas we have not observed the disease?**
- What is the distribution of the reservoir?
- Have serologic studies been performed?
- Are there behavioral, environmental or other factors that could alter host / pathogen dynamics
Novel tools use Web-based methods and Internet data.
  • Web queries
  • Google Trends
  • Google Flu Trends
  • Event-based surveillance
  • Remote sensing technology
  • Social media communications
  • Mobile phones
Summary

- Tools will come, but the utility will be based on quality of the data that is entered into them.
- We still have a number of unanswered questions that can and will impact prediction of future outbreaks:
  - Vaccine breakthroughs / durability
  - Viral persistence
  - Agent and reservoir distributions
  - Changing social and environmental conditions
- As the landscape changes, so does the complexity of our attempts to models.
- In the short term we can and should identify high-risk areas and implement active surveillance programs to reduce the size of future outbreaks.