

Stochastic Modeling of Infectious Diseases

The 34th Quality and Productivity Research Conference - 2017

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Agenda

- **Historical Example**
- Metabiota Overview
- Disease Spread Modeling
- Preparedness Index and Coronavirus Risk Model



Outbreak Starts...



- On February 21st (2003), 64-year-old doctor who was treating “atypical pneumonia” in Guangdong province (China) arrived in Hong Kong to attend a wedding and stayed in **Hotel Metropole**

- **Next day** he felt ill and was admitted to the intensive care unit
- On March 4 he died from a mysterious respiratory disease of **unknown origin**

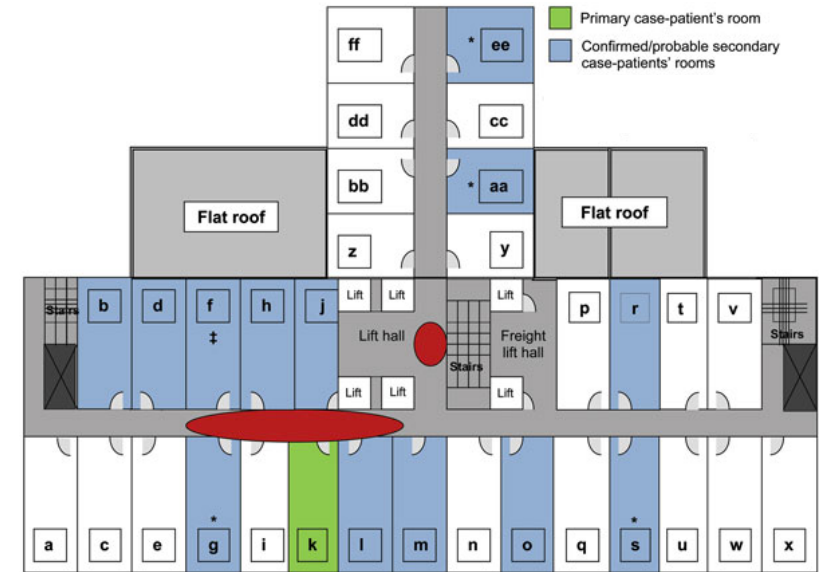


Outbreak Spreads...

- **20 cases** were associated with the transmission on 9th floor started from the index patient who spent only **one** night in the hotel



- 7 out of 20 cases were responsible for consequent large outbreaks in **Canada, Vietnam, Singapore, and Hong Kong** itself



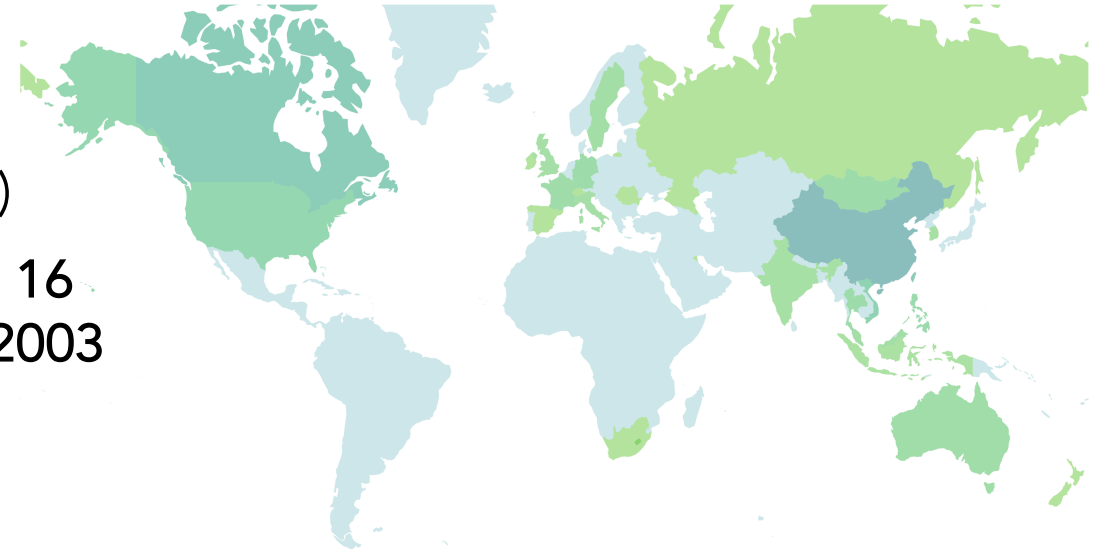
9th floor layout of the **Hotel Metropole** in Hong Kong

Source: Christopher R. Braden, Scott F. Dowell, Daniel B. Jernigan, and James M. Hughes - Emerging Infectious Diseases Journal, Volume 19, Number 6—June 2013

- In Vietnam, **Dr. Carlo Urbani**, a WHO physician, recognized a new and highly contagious disease. He later became infected and died, but his **early warning** started a massive response worldwide

Outbreak Aftermath...

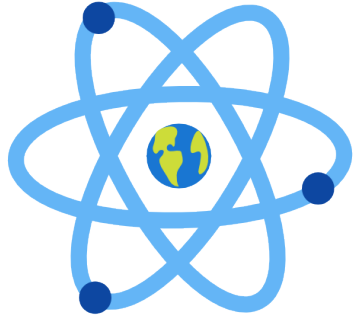
- Mysterious disease was eventually named as **Severe acute respiratory syndrome** (SARS)
- SARS outbreak started in Guangdong, China, on **16 November 2002** and ended in Taiwan on **5 July 2003** (spreading to **27 countries**)



Country	Cases	Fatal
China	5327	349
Hong Kong	1755	299
Taiwan	346	73
Canada	251	43
Singapore	238	33
Vietnam	63	5
USA	27	0
Philippines	14	2
Other	75	6
TOTAL	8096	810

- Numerous **Super-Spreading Events**, like one in Metropolitan Hotel, had been recorded
- **SARS-CoV** spread to humans from wild **palm civet cats** that are valued for their meat and are sold in Chinese markets.
- It is also believed that **bats** are the **natural reservoirs** of SARS-like coronaviruses.

Lessons learned for modeling...



- We must be **flexible** to consider different **disease specific characteristics** like Super-Spreading Events, availability of vaccines, vaccination strategies (mass or ring), etc.

- **Global connectivity** and **travel** patterns play a crucial role in the spread and magnitude of the disease epidemic



- We must be prepared for **newly emerging** infectious diseases



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Metabiota Mission

In the last decade, there have been over **470** human disease outbreaks

\$900M
Dengue Fever
(Brazil, 2013)

\$2B
Ebola
(W. Africa, 2015)

\$3.3B
Avian Flu
(US Midwest, 2015)

\$11B
Foot & Mouth
(UK, 2001)

\$23B
MERS
(Korea, 2015)

\$54B
SARS
(Global, 2003)



WE ARE BUILDING
A **GLOBAL**
IMMUNE SYSTEM
BY PROVIDING
PIONEERING
EPIDEMIC RISK
SOLUTIONS



Where is Metabiota?

- Founded in 2008 with offices in San Francisco, Canada, Ukraine, Democratic Republic of Congo, and Cameroon and operations in 20 countries



Metabiota Team

- Multidisciplinary team
- Collaboration with academic partners
- Perform epidemiological, statistical, and actuarial modeling



Cathine Lam
ACTUARIAL ASSOCIATE



Mike Gahan
ACTUARIAL ASSOCIATE



Mark Gallivan
MODELER



Ben Oppenheim
SENIOR SCIENTIFIC CONSU...



Kierste Miller
MODELER



Volodymyr Serhiyenko
DATA SCIENTIST/STATISTIC...



Nita Madhav
DIRECTOR, INFECTIOUS DL...



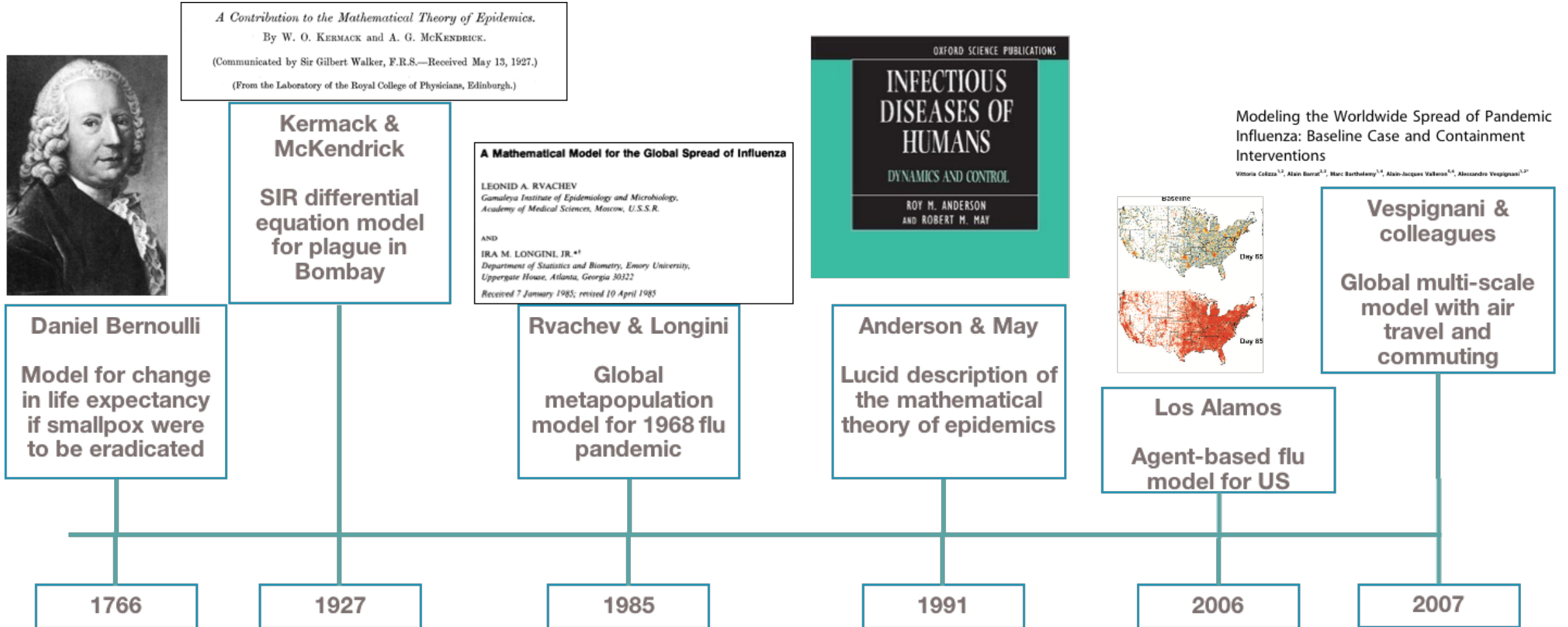
Nicole Stephenson
MODELER

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Milestones in Epidemic Modeling



Modeling Cooperation



- Metabiota closely cooperates with **Alessandro Vespignani** and his colleagues from Northeastern University's Laboratory for the **Modeling of Biological and Socio-technical Systems**

- Together we are developing disease spread models to realistically simulate disease spark, spread, and duration of epidemics

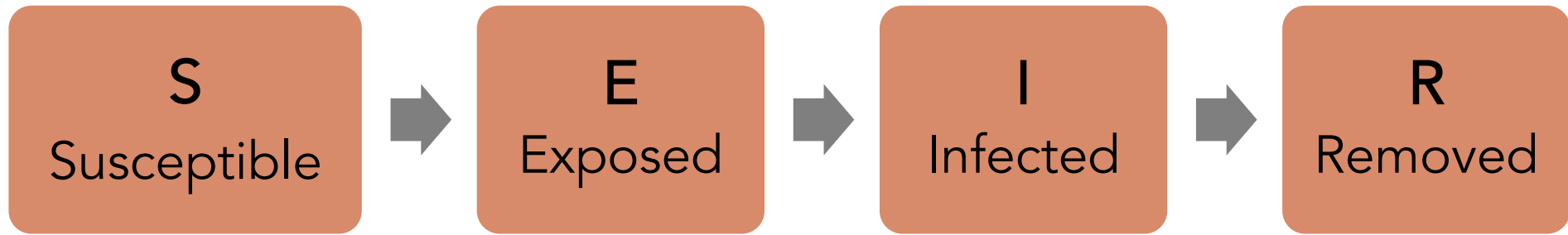


Laboratory for the
Modeling of Biological +
Socio-technical Systems

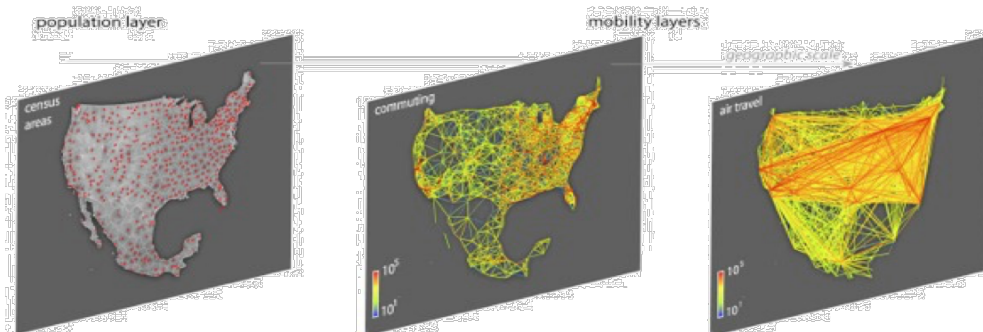


- Our main framework is **Global Epidemic and Mobility model (GLEaM)** that stochastically simulates the spread of epidemics at the worldwide scale

GLEaM framework



Underlying Compartmental Model



- Global population is divided into basins around transportation hubs (i.e. airports). The resulting network consists of **3,362** geographic subpopulations + Full **airline** transportation data + **Short-range** mobility network

Individual based model



- Model probabilistically progresses **individuals** through each compartment by **stochastically simulating** values from binomial and multinomial distributions

$$\text{Multinomial} \left(E_j(t), p_{E_j \rightarrow I_j^a}, p_{E_j \rightarrow I_j^t}, p_{E_j \rightarrow I_j^{nt}} \right)$$

$$\text{Binomial} \left(S_j(t), p_{S_j \rightarrow E_j} \right)$$

- More details can be found in:
Balcan, D., Gonçalves, B., Hu, H., Ramasco, J. J., Colizza, V., & Vespignani, A. (2010). Modeling the spatial spread of infectious diseases: The GLocal Epidemic and Mobility computational model. *Journal of computational science*, 1(3), 132-145.

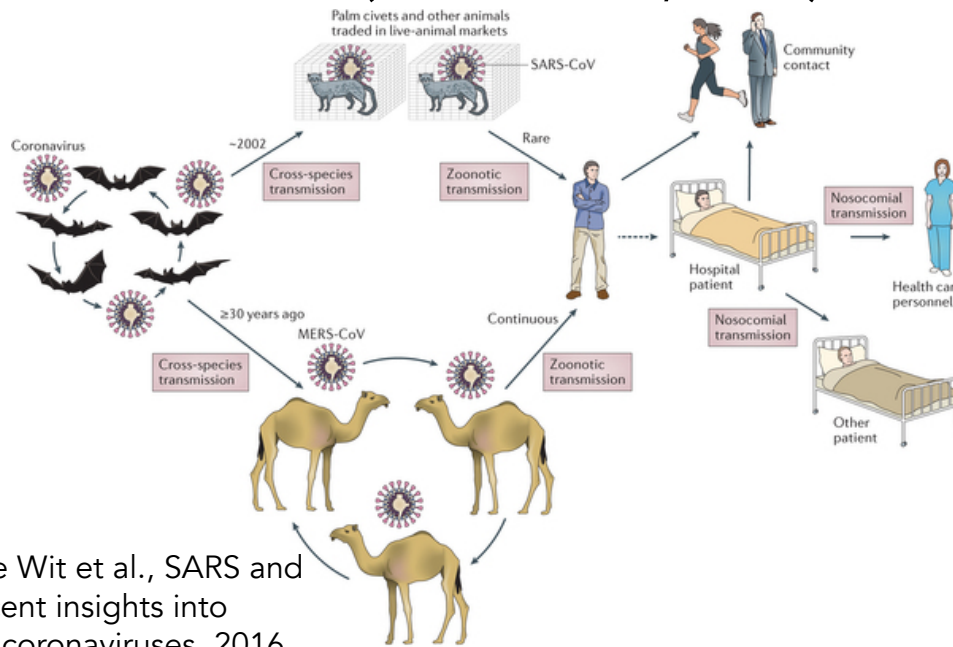
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Coronavirus Outbreaks

- SARS 2003 outbreak: **8096** cases, **810** deaths, **27** countries effected
- Middle East Respiratory Syndrome (MERS) 2013 outbreak: **1980** cases, **699** deaths, **15** countries effected (as of June 6, 2017) – caused by novel MERS-CoV

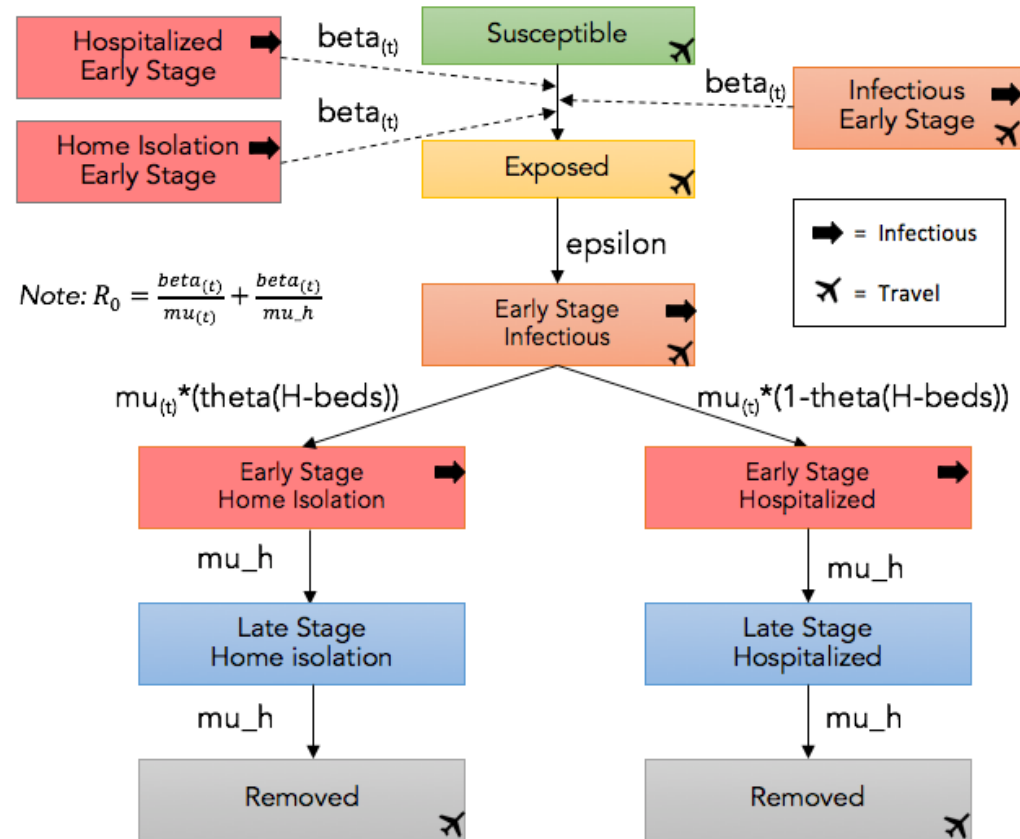


Source: de Wit et al., SARS and MERS: recent insights into emerging coronaviruses, 2016

Nature Reviews | Microbiology

- First case reported in Saudi Arabia April 2012, still **on-going**
- Saudi Arabia is the most affected country (80% of total cases)
- Notable event:
South Korea 2015 MERS outbreak
Caused by **one** index patient
182 cases with **37** deaths

Model Design – Compartments



- Main model parameters:

R_0 - basic reproductive number (number of secondary infections)

ϵ^{-1} - incubation period

μ^{-1} - infectious period

Travel Reduction (%)

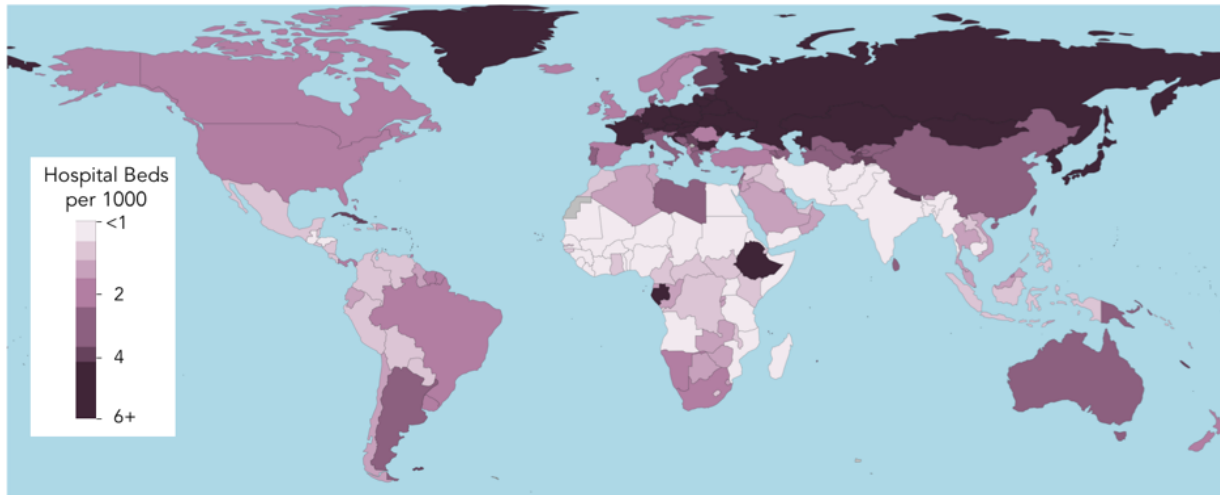
Transmissibility reduction time, etc.

- Super-Spreading Events:

Number of secondary cases $\sim \text{NegBinomial}(R_0, k)$

Differences among countries

Hospital beds per capita



Source: World Bank

If outbreak starts in **USA**, is it going to be different from **China** or **Sierra Leone** outbreak of the same disease?

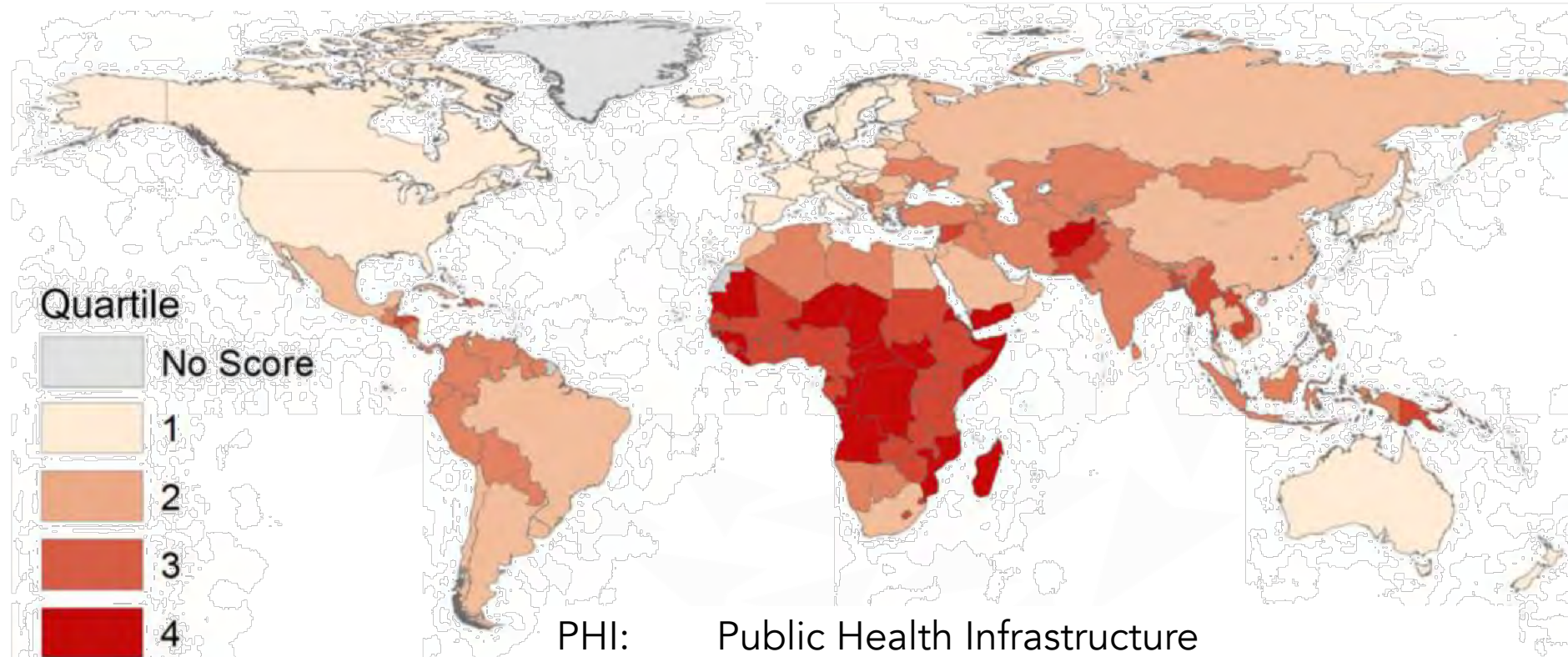
Country-level differences in

- Outbreak surveillance
- Outbreak reporting time
- Timing of intervention measures
- ...

How do we capture these differences?

Epidemic Preparedness Index

(1=most prepared, 4=least prepared)

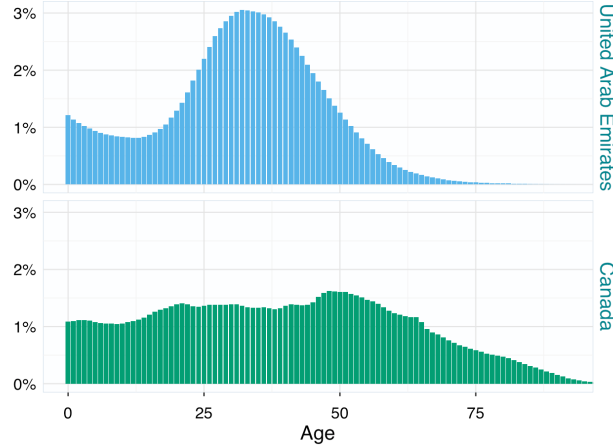


Source: Metabiota

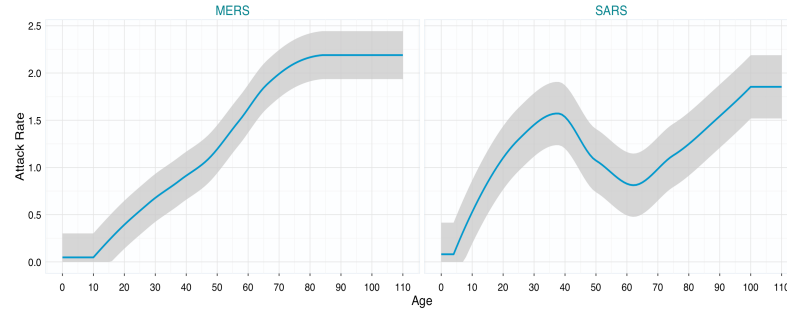
PHI: Public Health Infrastructure
PI: Physical and Communications Infrastructure
IC: Institutional Capacity
EF: Economic Factors
PHC: Public Health Communications

EPI influence on CFR

Age Structure

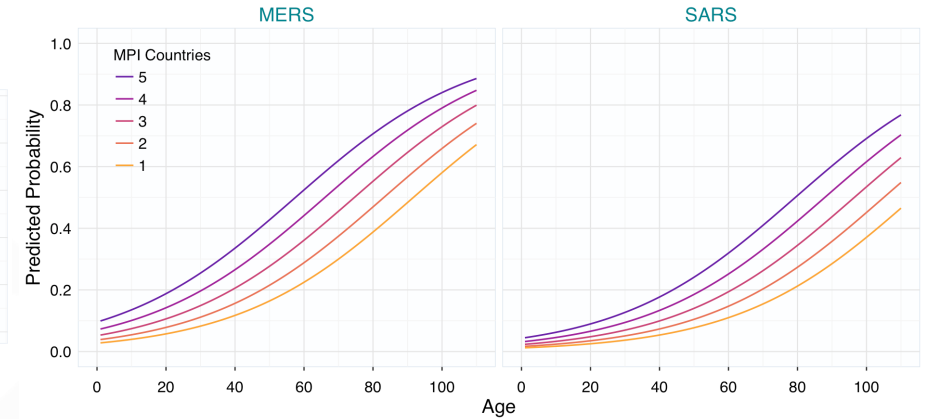


Modeled Attack Rates



Case Fatality Ratio Model

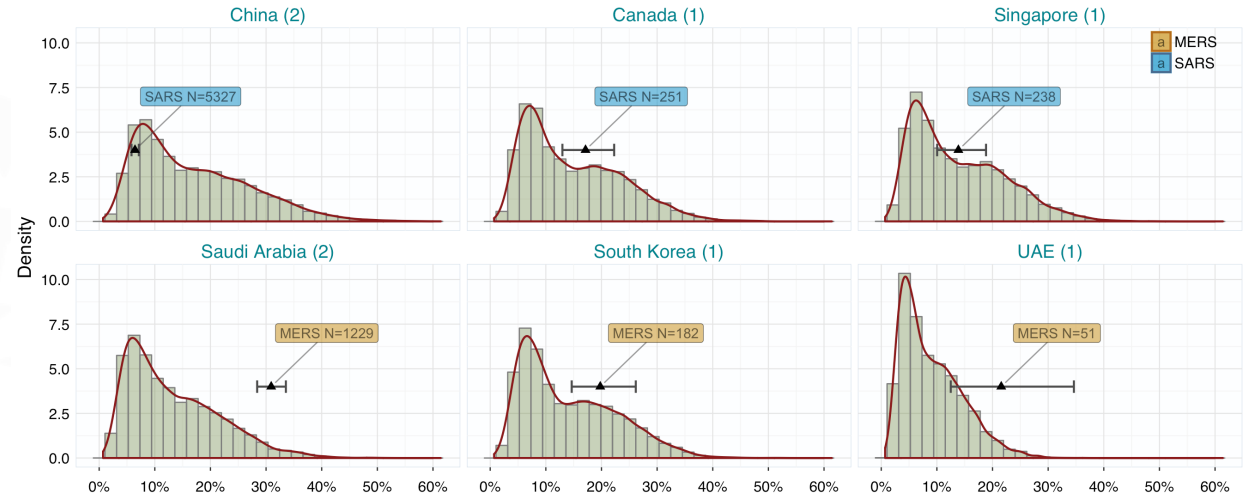
Probability of Fatal Outcome versus Age, Disease, and MPI



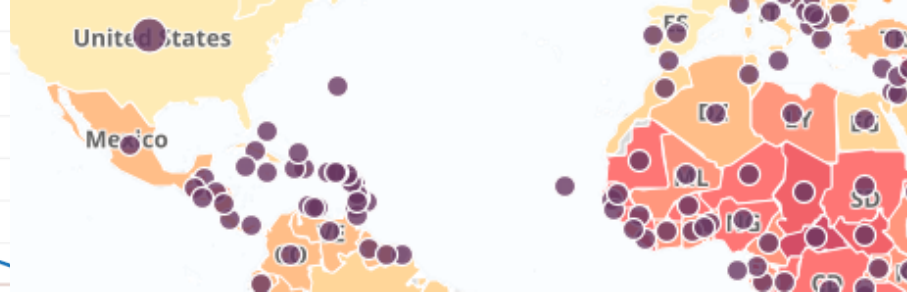
On average, improving country's Epidemic Preparedness by one unit is decreasing odds of dying by **28%**

Case Fatality Ratio: Modeled with Observed

1,000 cases; 10,000 Monte Carlo simulations; Observed CFR with Wilson 95%CI; MPI values in (.)



Be the Trusted Source for Best in Class Models

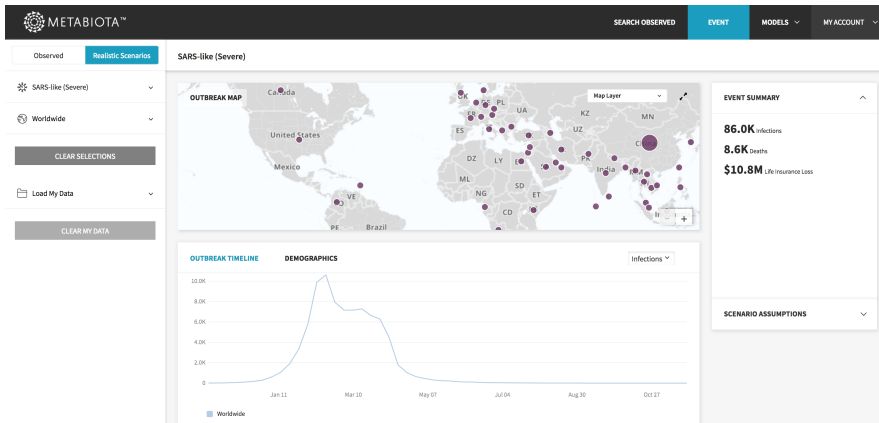


Proprietary Data Set

- 1,200+ Outbreaks
- 150+ Pathogens
- 240+ Data Sources
- 230+ Countries / Territories
- Over 48M Cases
- Over 6M Deaths
- Curated, cleansed, continuously updated

Disease Model Library

- 1M year stochastic event catalog
- 18M stochastic realizations with weekly resolution informed the event catalog
- 180K simulations evaluated
- 117K distinct demographic subpopulations
- 88K+ AWS Compute optimized hours to date
- 100+TB of data
- Largest in the industry



Thank you!

Questions?

Model Design – Spark Map

Data Layers
Bioclimatic Data
Number of shared human-bat viruses
Zoonotic mammal species
Proximity to large cities
Human Density
Bat (Taphozous sp.)
Dromedary Camel abundance
PREDICT (Metabiota) data

