

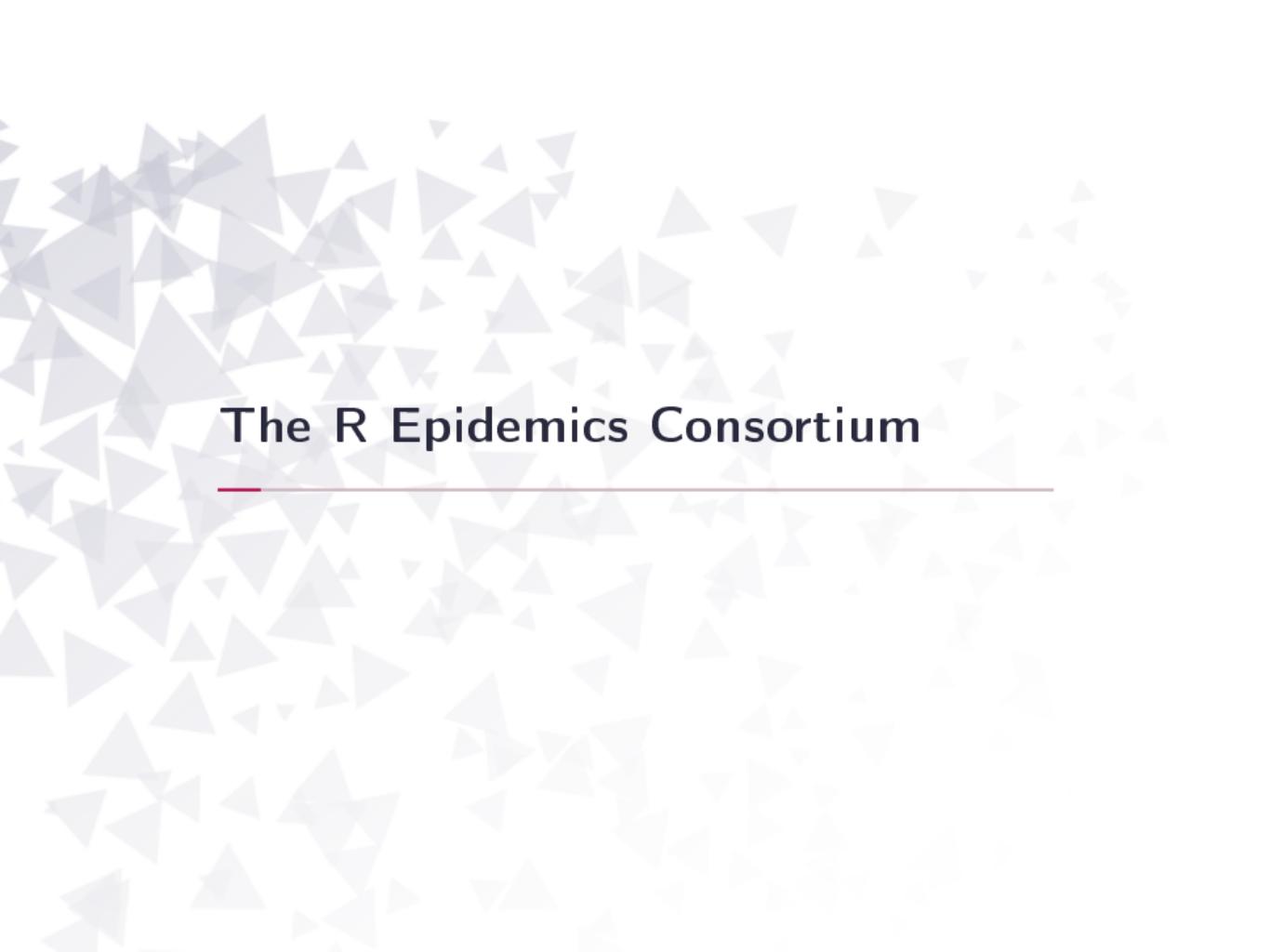
RECON

Operational modelling for outbreak response

Thibaut Jombart

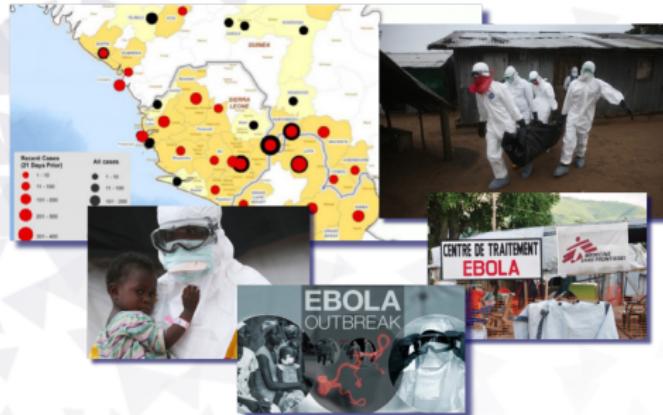
17th January 2018

Imperial College London
MRC Centre for Outbreak Analysis and Modelling



The R Epidemics Consortium

Lessons learnt from the Ebola response



Lessons learnt from the Ebola response



Lessons learnt from the Ebola response

WHO Ebola response team

Help improving situation awareness

Imperial College Ebola team

Timeline:

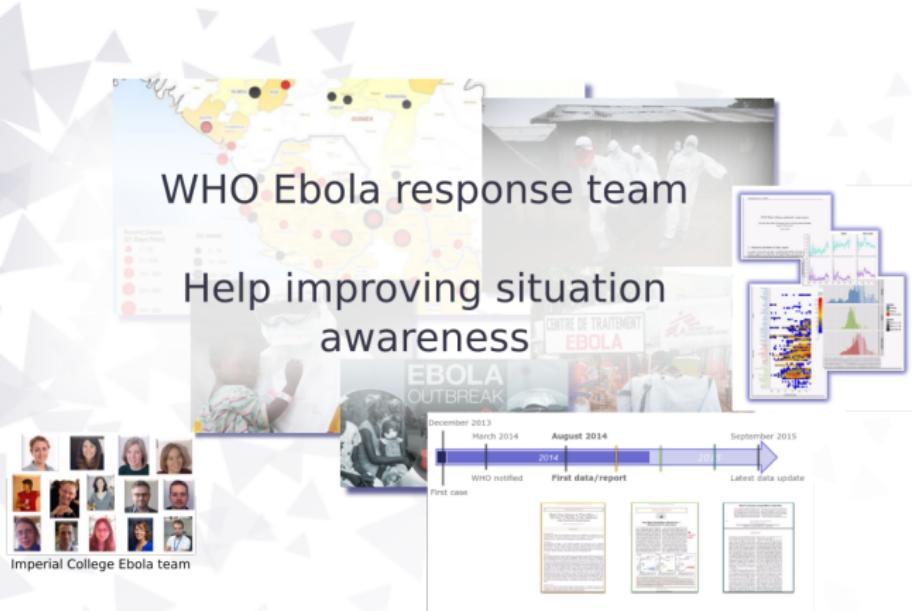
- December 2013: First case
- March 2014: WHO notified
- August 2014: First data/report
- September 2015: Latest data update

Centre de Traitement EBOLA

EBOLA OUTBREAK

WHO Ebola response team dashboard

Lessons learnt from the Ebola response



Most statistical/modelling tools for situation awareness were missing.

Who do we need to develop these tools?



Who do we need to develop these tools?

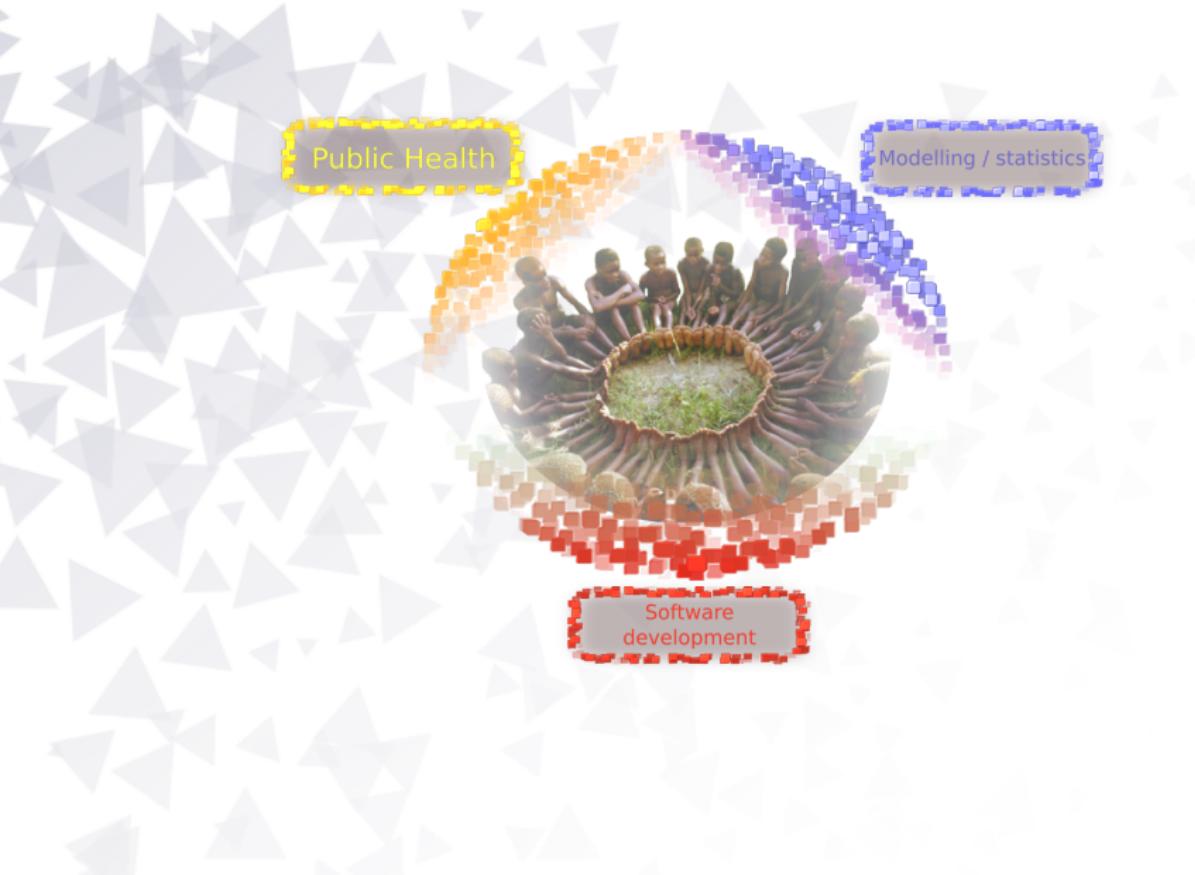
Public Health



Who do we need to develop these tools?



Who do we need to develop these tools?



From a hack to a pack



Hackout 3, summer 2016, Berkeley

From a hack to a pack



Hackout 3, summer 2016, Berkeley



From a hack to a pack



Hackout 3, summer 2016, Berkeley

functional
incubation
userfriendly secure dictionary
systems testing automated continuous
collection series repository
rpp efficiency number fast
secured bias outbreaks
parsing code integration
reporting gui
unit data delay
epidemiology security peak
situation anonymised
opensource contact
epiinfo delay
clean compiled
outbreaker interface tree
symptoms interface
lineelist fellow
tracing shiny
automation cdc
epicontacts edc
ggplot cleaning
dashboard clusters rates
parallel reliable
parameters contacttracing
epidemics genomics
distribution

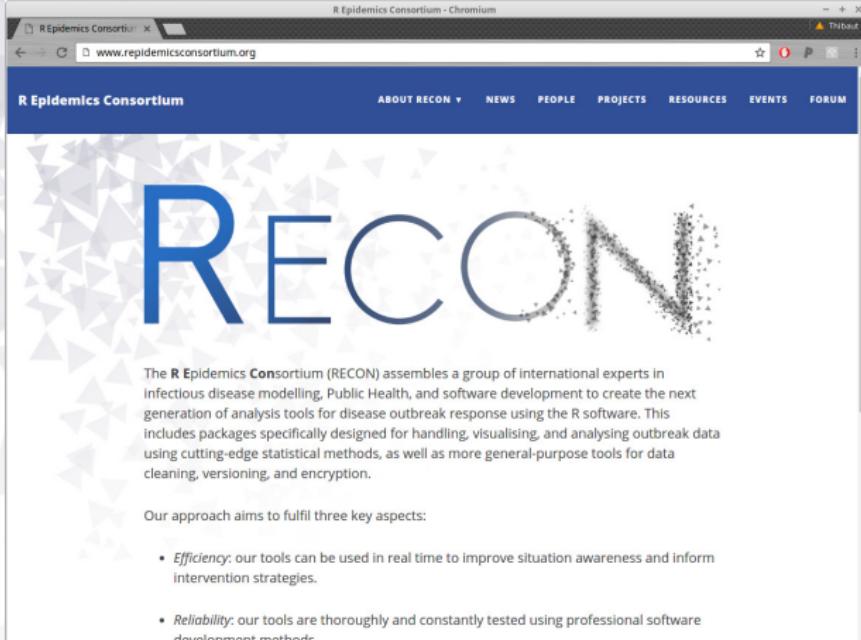
RECON
[The R Epidemics Consortium]

From a hack to a pack



RECON: the R Epidemics Consortium

A taskforce to build a new generation of outbreak response tools in .



The screenshot shows a web browser window for the "R Epidemics Consortium - Chromium" tab, displaying the homepage at www.repidemicsconsortium.org. The page features a dark blue header with the "R Epidemics Consortium" logo and navigation links for ABOUT RECON, NEWS, PEOPLE, PROJECTS, RESOURCES, EVENTS, and FORUM. The main content area has a light gray background with a large, stylized blue "RECON" logo where the letters are composed of small, scattered dots. Below the logo is a paragraph of text about the consortium's mission, followed by a section titled "Our approach aims to fulfil three key aspects:" with two bullet points.

The R Epidemics Consortium (RECON) assembles a group of international experts in infectious disease modelling, Public Health, and software development to create the next generation of analysis tools for disease outbreak response using the R software. This includes packages specifically designed for handling, visualising, and analysing outbreak data using cutting-edge statistical methods, as well as more general-purpose tools for data cleaning, versioning, and encryption.

Our approach aims to fulfil three key aspects:

- *Efficiency*: our tools can be used in real time to improve situation awareness and inform intervention strategies.
- *Reliability*: our tools are thoroughly and constantly tested using professional software development methods.

www.repidemicsconsortium.org

RECON

www.repidemicsconsortium.org

- started 6th September 2016
- ~70 members
- 20 countries, > 40 institutions
- ~ 9 packages released, 15 under development
- public forum, blog, online resources

RECON: activities

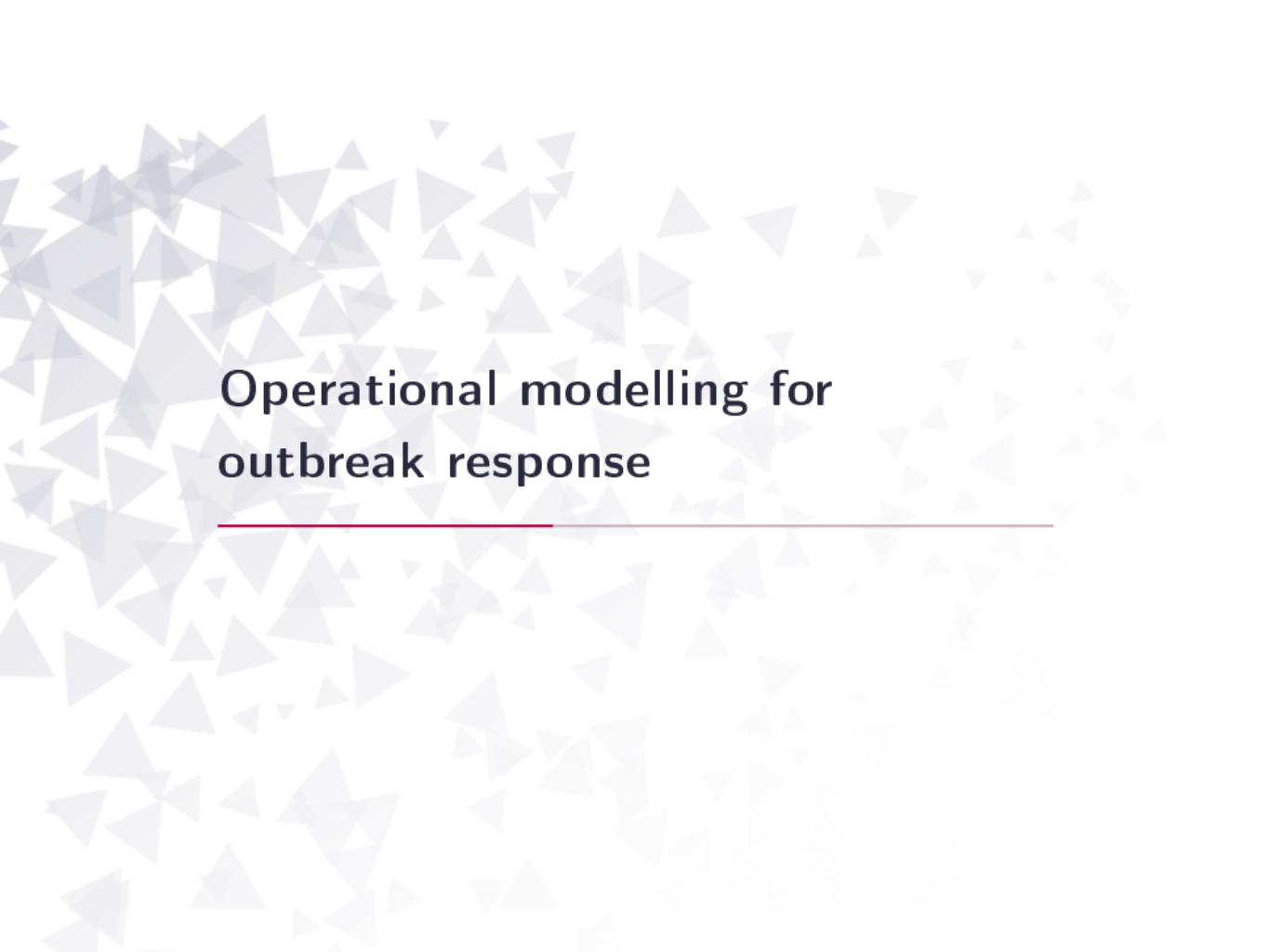
- **software development**: tools for real-time outbreak analytics (from data cleaning to modelling)
- **community support**: best practices, forums, hackathons, meetings
- **outbreak response**: deployment to the field
- **training**: RECON learn

RECON learn: training resources for epidemics analysis



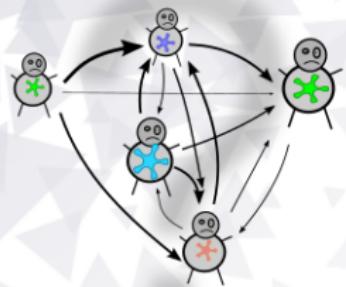
- repository for free, **open** training material
- lectures, practicals, case studies, code gists
- emphasis on **community contributions**
- **workshops** in 2018:
CDC, MSF, WHO, EPIET Alumni Network, ...

<https://reconlearn.netlify.com>

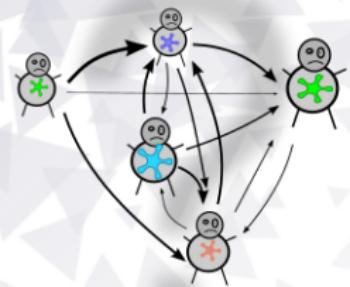


Operational modelling for outbreak response

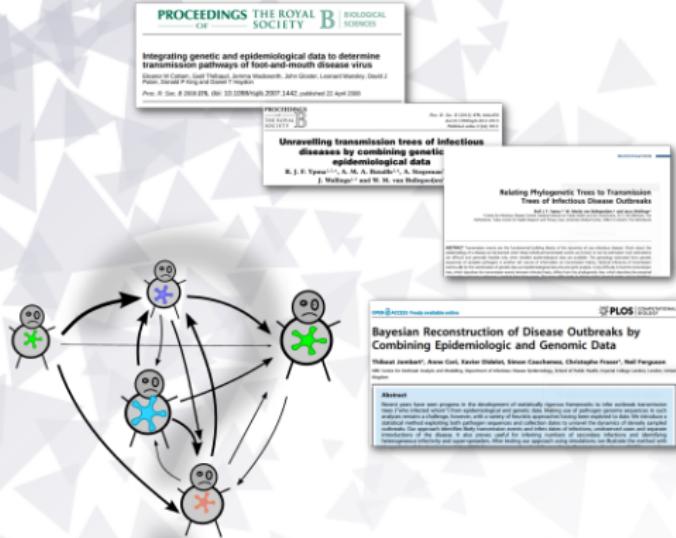
Who infects whom? Many answers for a single question



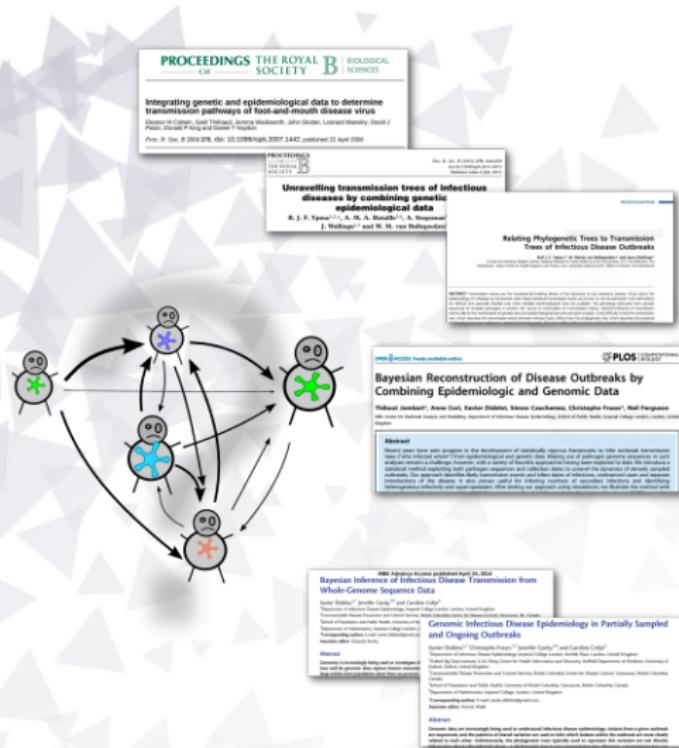
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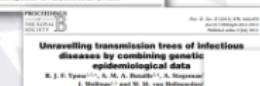
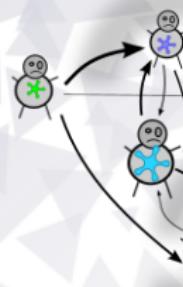
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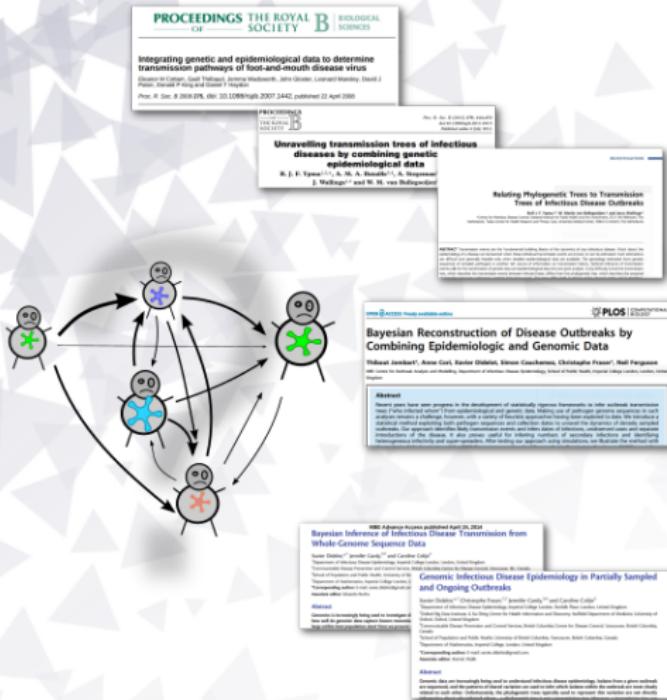
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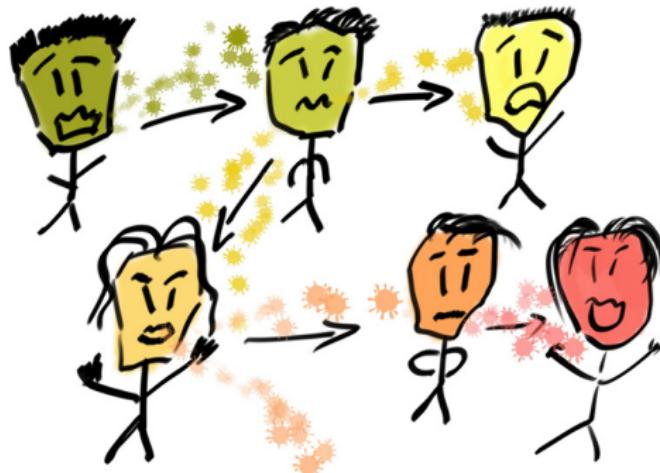
Who infects whom? Many answers for a single question



Methods heavily
rely on whole genome
sequence data

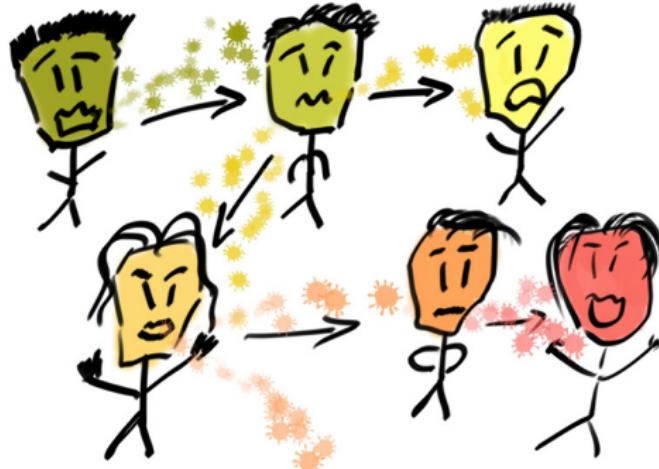


Using WGS to infer who infected whom



Mutations accumulate along transmission chains.

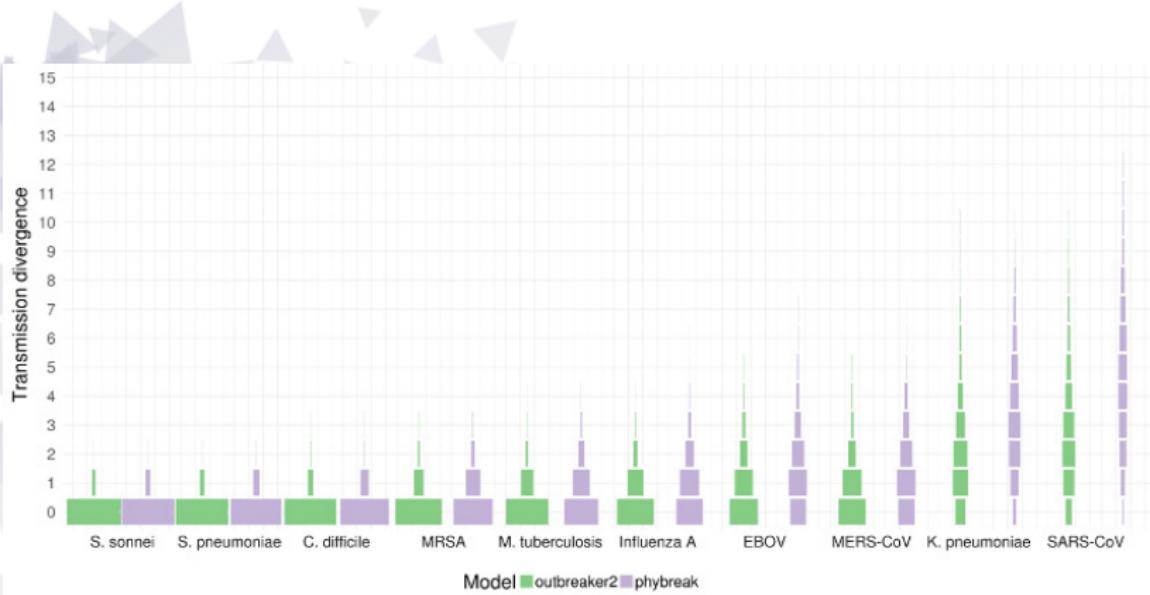
Using WGS to infer who infected whom



Mutations accumulate along transmission chains.

Can be used to reconstruct transmission trees.

How informative are whole genome sequences?



source: Finlay Campbell

Insufficient diversity for most diseases.

Evidence synthesis approach to outbreak reconstruction



Combine different data to shrink the set of plausible trees.

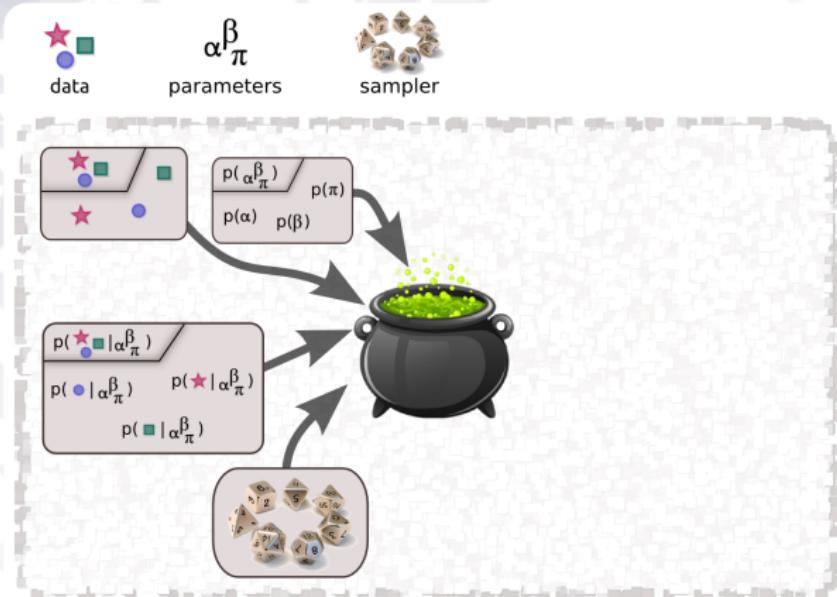
outbreaker2: evidence synthesis framework for outbreak reconstruction

Modularity: customise data, prior, likelihood, MCMC.



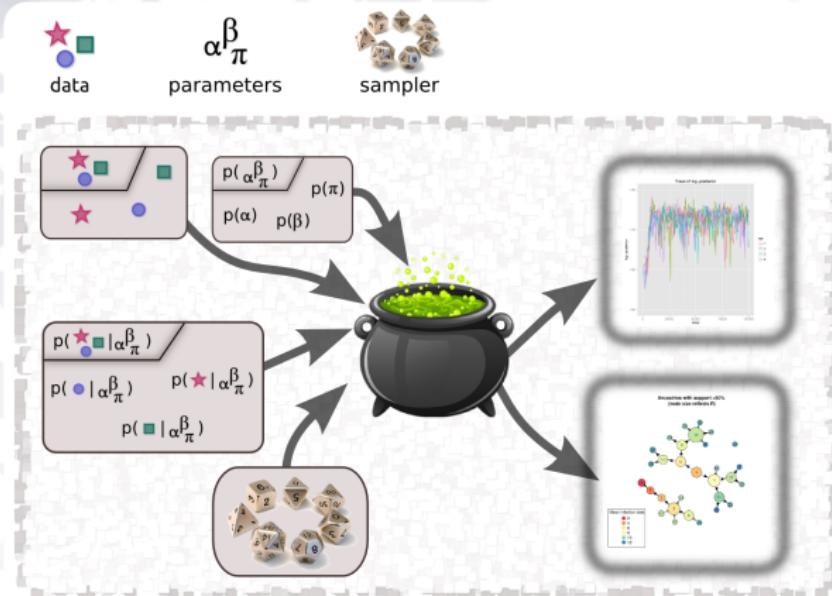
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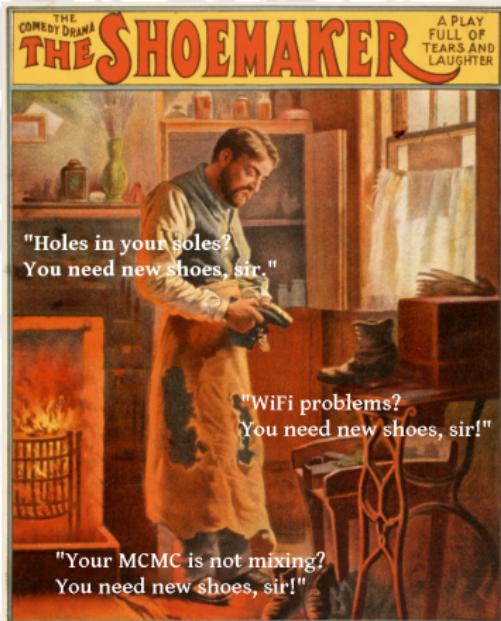


outbreaker2: evidence synthesis framework for outbreak reconstruction

Modularity: customise data, prior, likelihood, MCMC.



Do we even need this to respond to outbreaks?



- in general, **not needed for forecasting or control**

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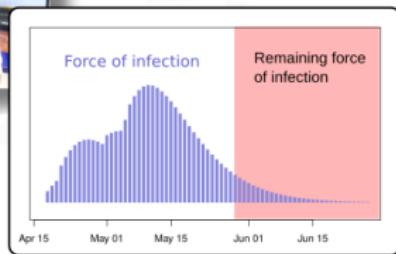


- in general, **not needed** for forecasting or control
- useful to detect **multiple introductions** or **superspreading**
- complement **contact tracing** data
- WGS are costly: **is it worth it?**

Ebola outbreak, Likati (DRC) 2017

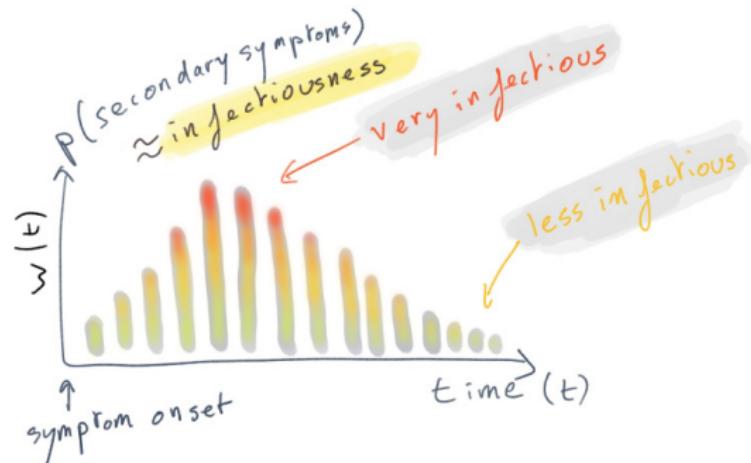


- EVD outbreak May 2017
- contact data visualisation tools used in contact tracing
- simple model informed response (scaling)
- end: 2nd July 2017



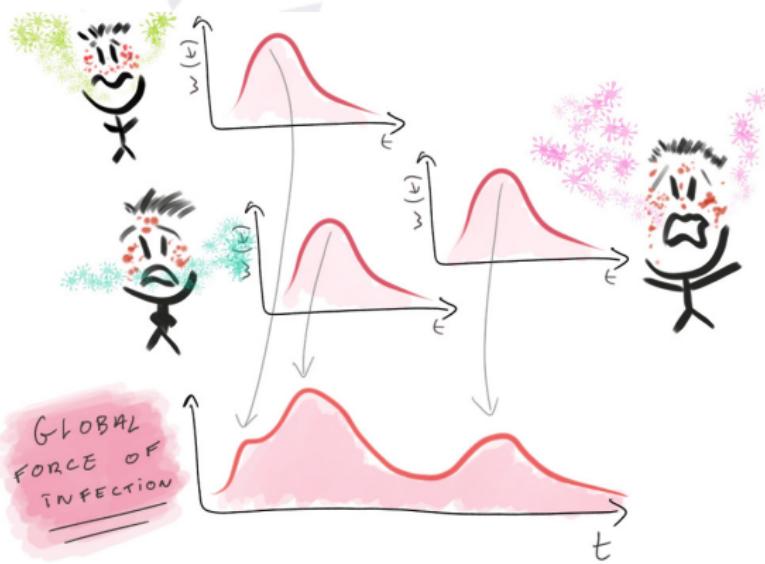
Individual infectiousness over time

Serial interval: delay between symptom onset in infector and infectees



Indicates when we expect new cases, if there are any.

A “simple” branching process model

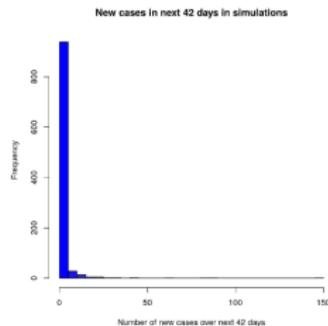
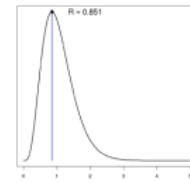
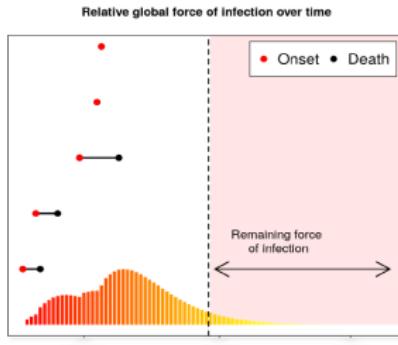


$$y_t \sim \mathcal{P}(\lambda_t) \quad ; \quad \lambda_t = R_0 \times \sum_i w(t - t_i)$$

y_t : incidence at time t ; $\mathcal{P}()$: Poisson distribution; λ_t : **global force of infection**; $w()$: serial interval distribution; t_i : date of symptom onset

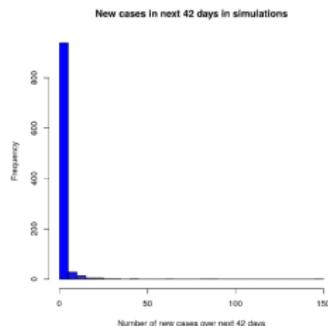
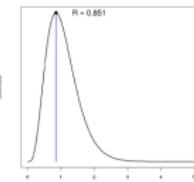
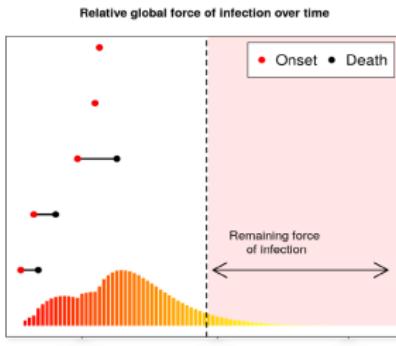
Scaling the response in real-time

Estimating remaining force of infection,
transmissibility (R), predicting new cases



Scaling the response in real-time

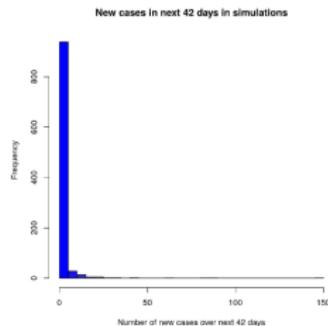
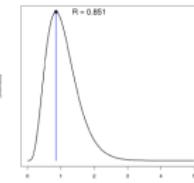
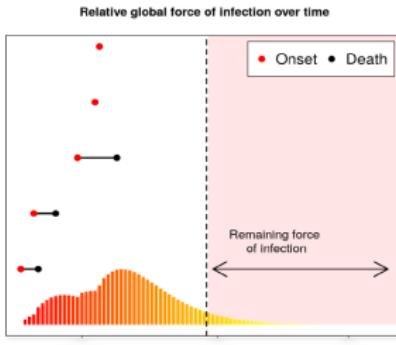
Estimating remaining force of infection,
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Despite uncertainty in R_0 , new cases were unlikely.

Scaling the response in real-time

Estimating remaining force of infection,
transmissibility (R), predicting new cases



Despite uncertainty in R_0 , new cases were unlikely.

Discouraged scaling up in resource-limited context.

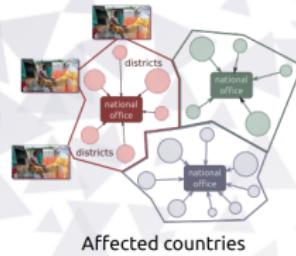
Challenges of a timely response



Challenges of a timely response

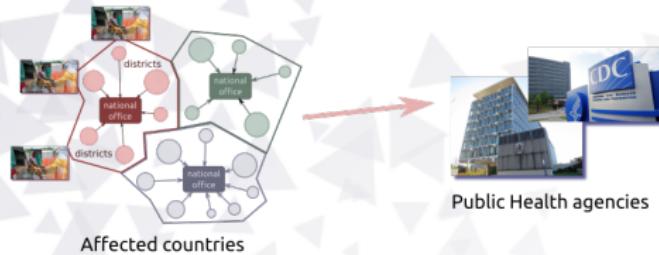


Challenges of a timely response

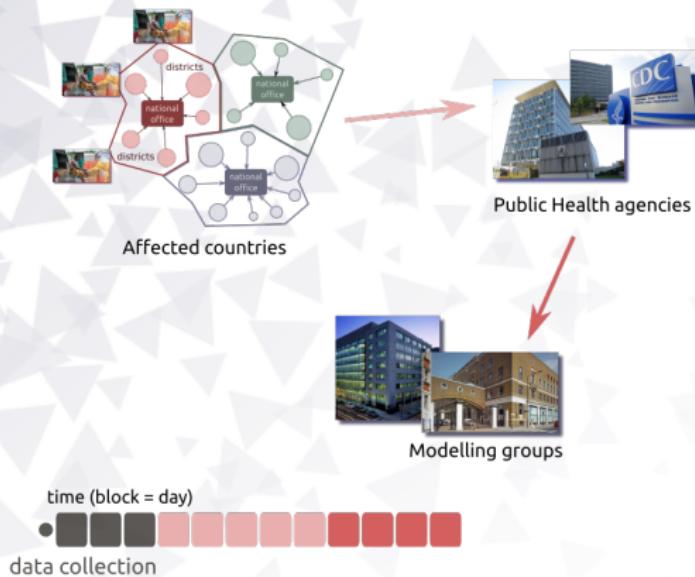


time (block = day)
• data collection

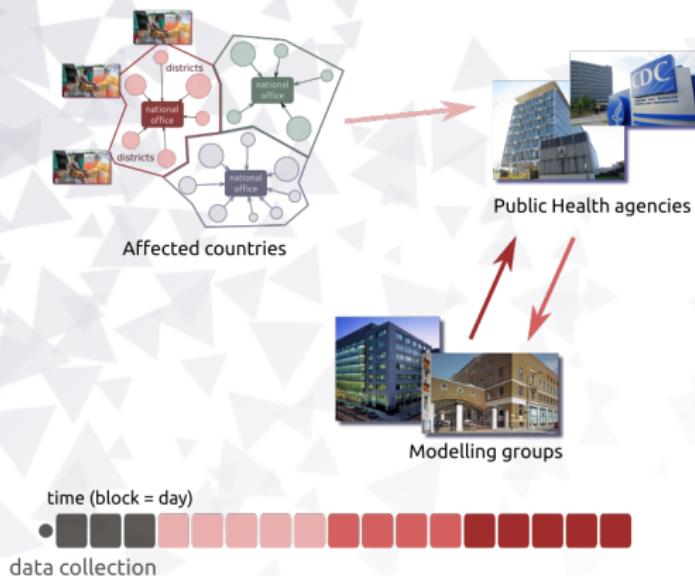
Challenges of a timely response



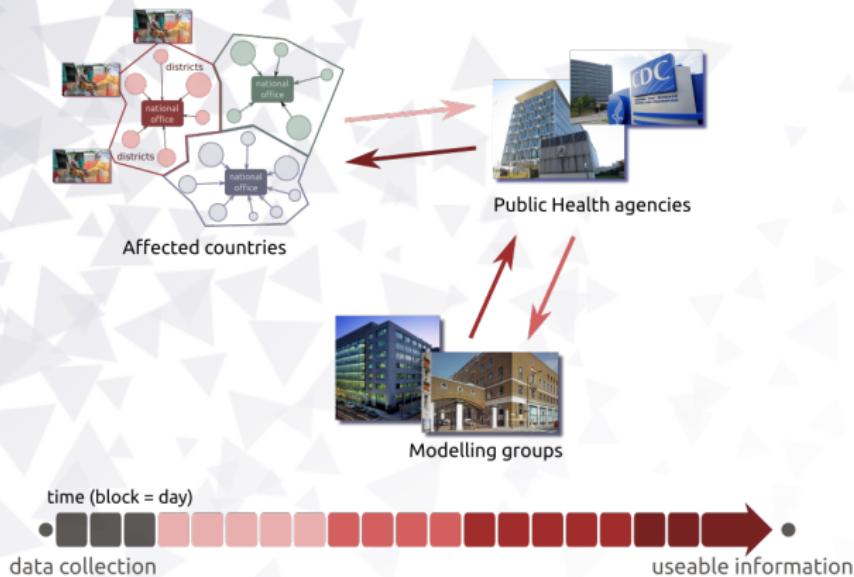
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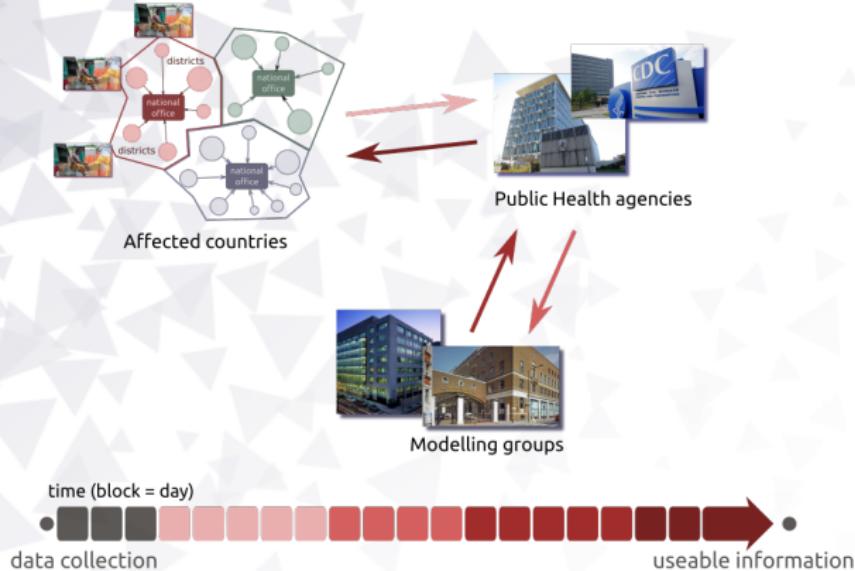
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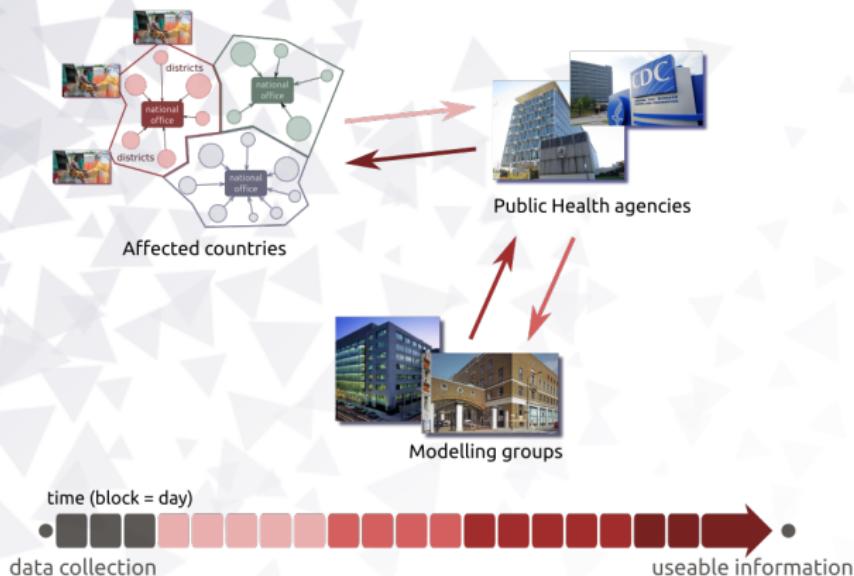


Challenges of a timely response



- efficient **tools** can shorten delays

Challenges of a timely response



- efficient **tools** can shorten delays
- embed **methodologists** in outbreak response teams

Thanks to:

- **Jimmy Whitworth, John Edmunds**
- **Colleagues:** Finlay Campbell, Amrish Baidjoe, Anne Cori, James Hayward, Rich Fitzjohn, Neil Ferguson
- **Groups:** WHO Ebola Response Team, Ebola Likati team, RECON members, GOARN
- **funding:** HPRU-NIHR, MRC

RECON

www.repidemicsconsortium.org

RECON Learn

A free and open collection of training resources
for epidemics analysis and outbreak response.

reconlearn.netlify.com/

Upcoming event!

https://recon-gathering-march2018.netlify.com/