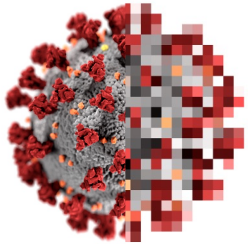
The **Epiverse** initiative



Adam Kucharski

Co-director, Centre for Epidemic Preparedness and Response

Epiverse/Harmonize workshop

July 2023

LONDON SCHOOL of HYGIENE &TROPICAL MEDICINE

Epidemic Preparedness & Response

What are we dealing with?

And what can we do about it?

Need to understand disease dynamics: COVID-19

Daily chart

How deadly is the new coronavirus?

Economist, 12th March 2020
Russell et al, Eurosurveillance, 2020

Coronavirus: What is the k number and can superspreading be stopped?

BBC News, 6th June 2020
Endo et al. Wellcome Open Res, 2020

Alpha

Coronavirus Variant Is Indeed More Transmissible, New Study Suggests

New York Times, 23rd Dec 2020
Davies et al. Science, 2021

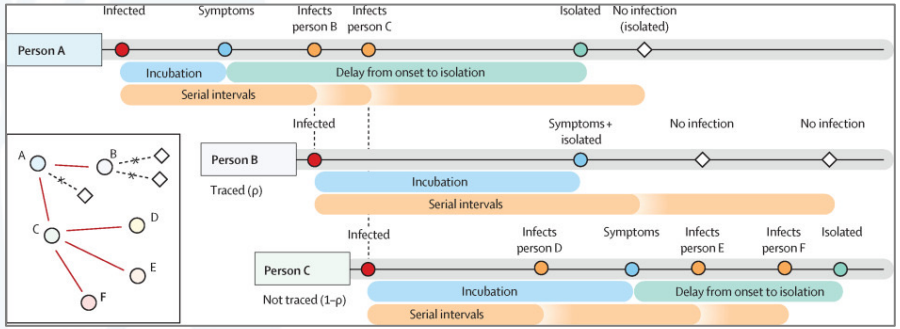
Delta

Is The Variant From India The Most Contagious Coronavirus Mutant On The Planet?

NPR, 14th May 2021
Kucharski et al. SPI-M/SAGE report, 12th May 2021

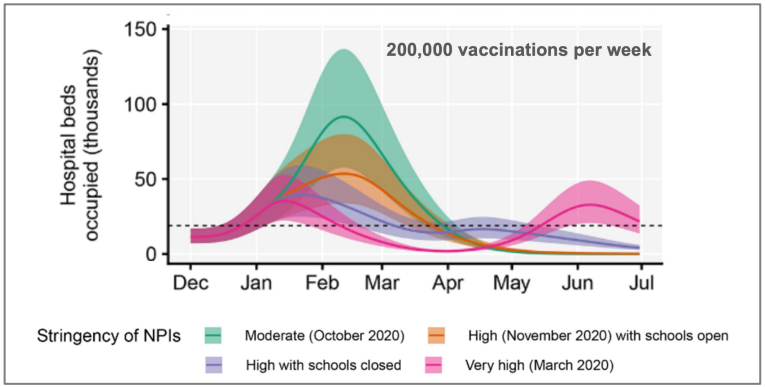
Need to understand control options: COVID-19

Early isolation/contact tracing modelling



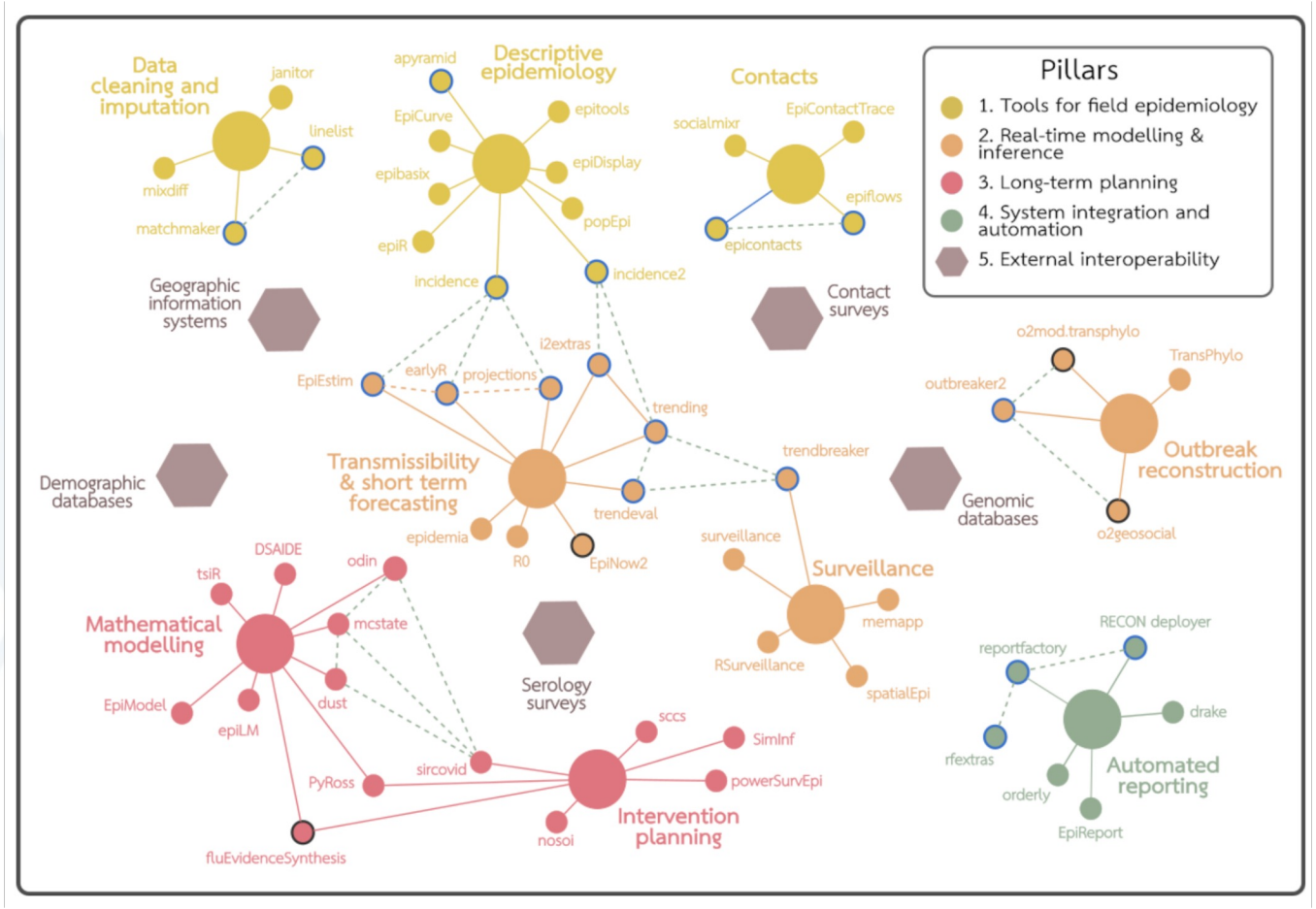
Hellewell et al, *Lancet Global Health*, 2020

Alpha variant scenario modelling



Davies et al. Science, 2021

Some important tools and methods, but a fragmented ecosystem



The **Epiverse** initiative

Aim: change how analytics are used in the global infectious disease response, moving from inflexible analytical tools and ad-hoc collaboration to integrated, generalisable and scalable community-driven software.

MRC Unit The Gambia

London School of Hygiene & Tropical Medicine

data.org

Pontificia Universidad Javeriana Colombia

Universidad de los Andes

github.com/epiverse-trace

The **Epiverse** initiative

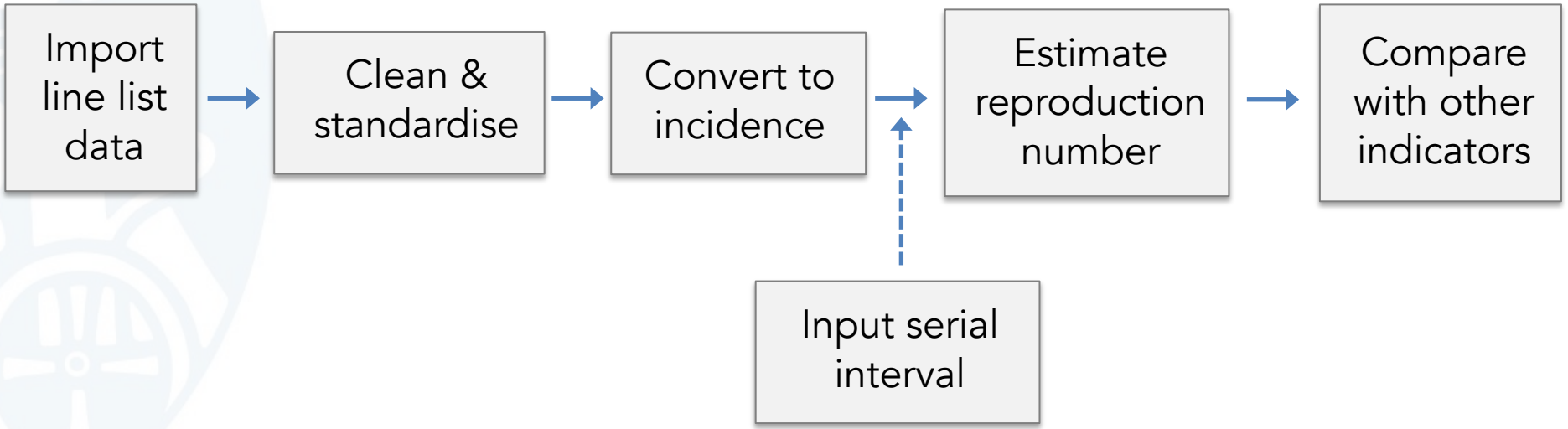
Aim: change how analytics are used in the global infectious disease response, moving from inflexible analytical tools and ad-hoc collaboration to integrated, generalisable and scalable community-driven software.

github.com/epiverse-trace

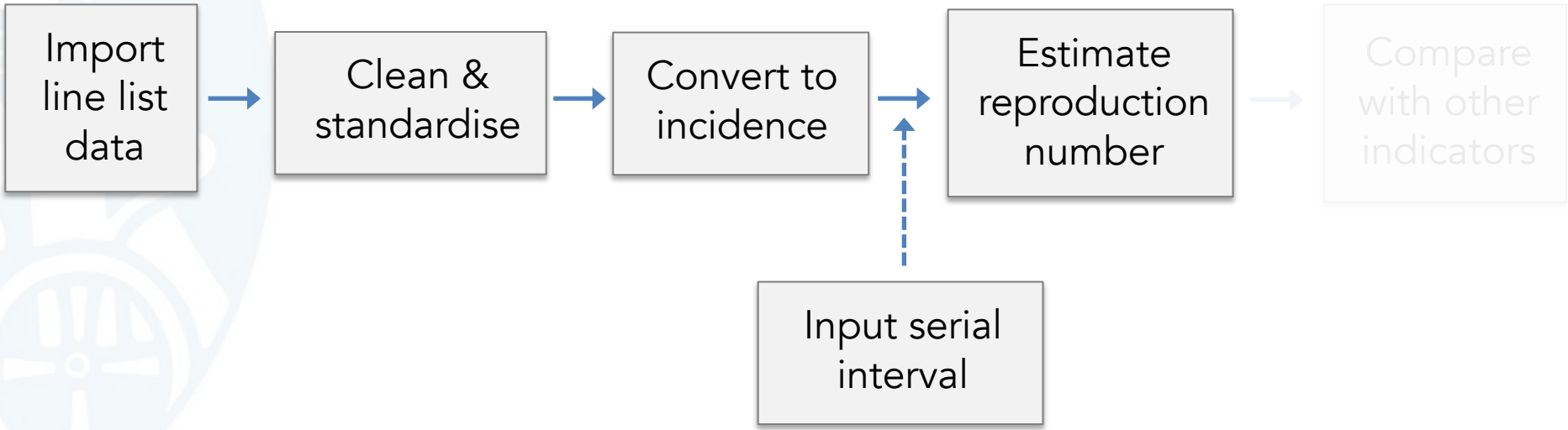
How does transmission vary over time?

And what drives this?

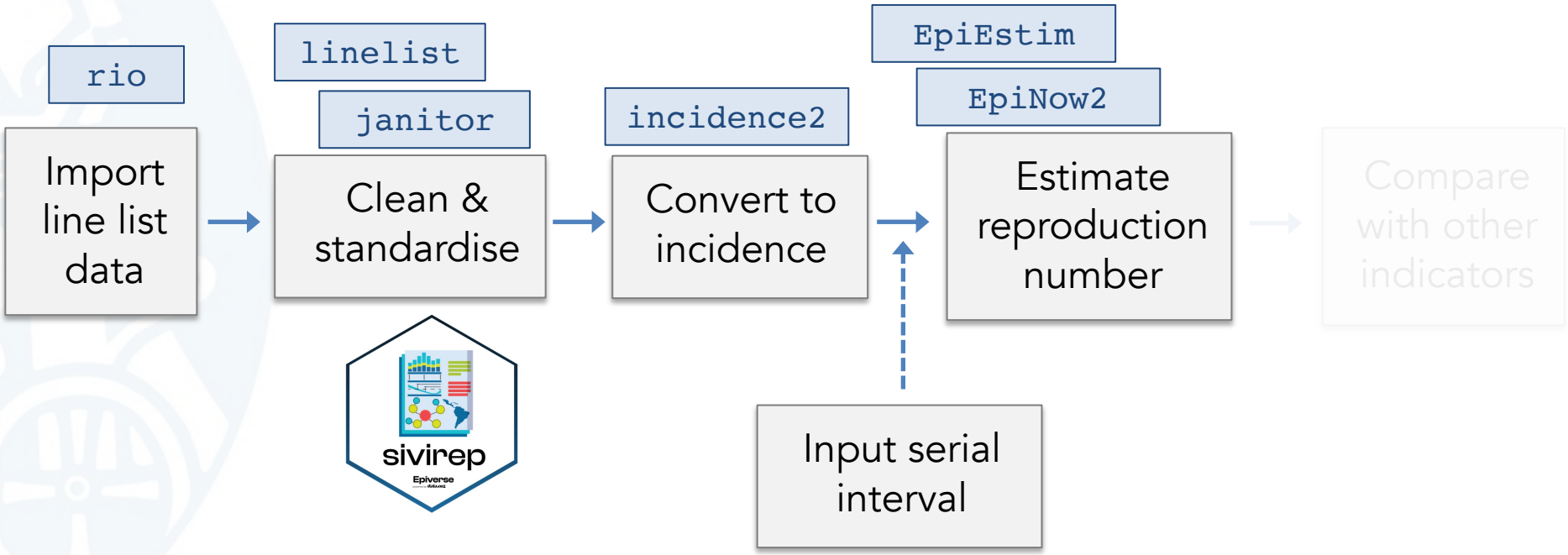
Steps to estimate transmission and compare to other indicators



Estimating reproduction number



Estimating reproduction number



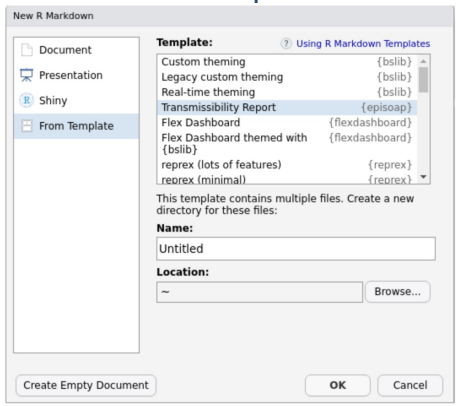
Outbreak analytics pipelines

episoap

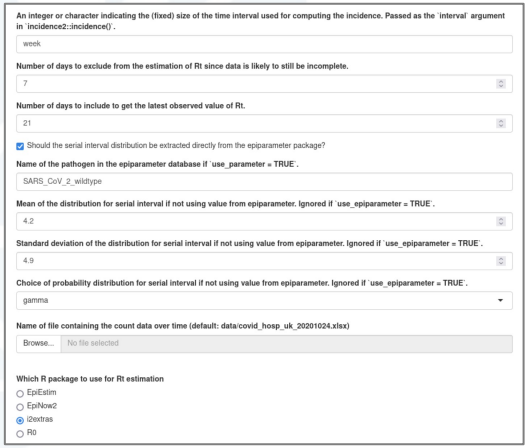
Epiverse powered by data.org

Work by Hugo Gruson et al

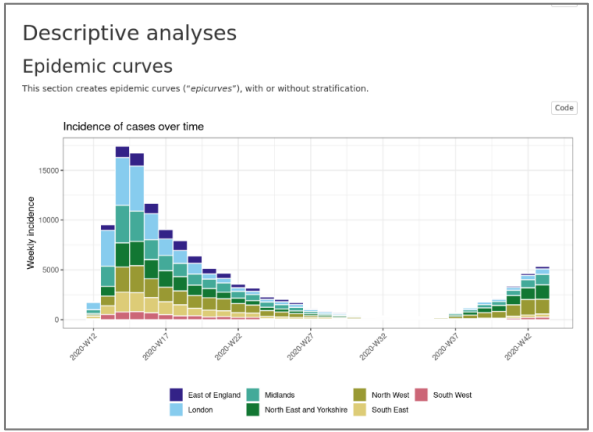
Choose template:



Select options:



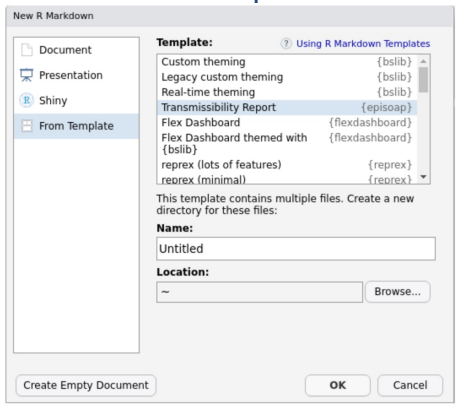
Descriptive curves:



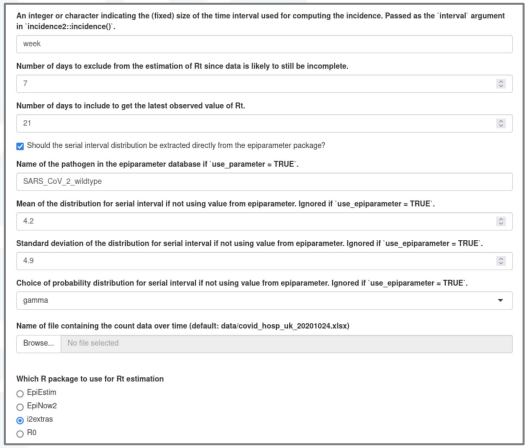
github.com/epiverse-trace/episoap

Outbreak analytics pipelines

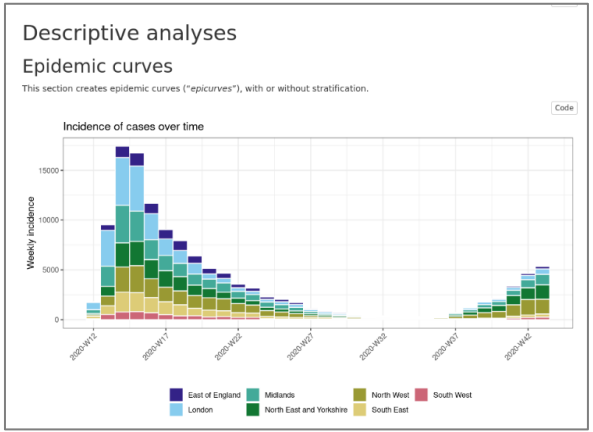
Choose template:



Select options:

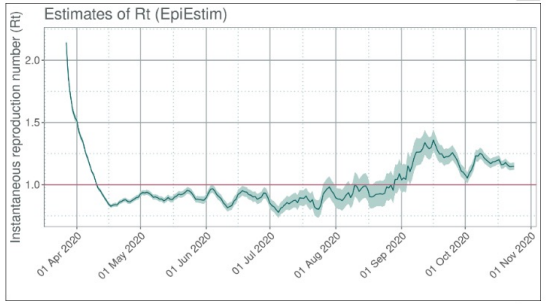


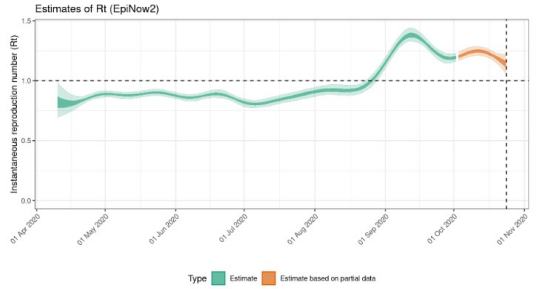
Descriptive curves:



Work by Hugo Gruson et al

R estimation:





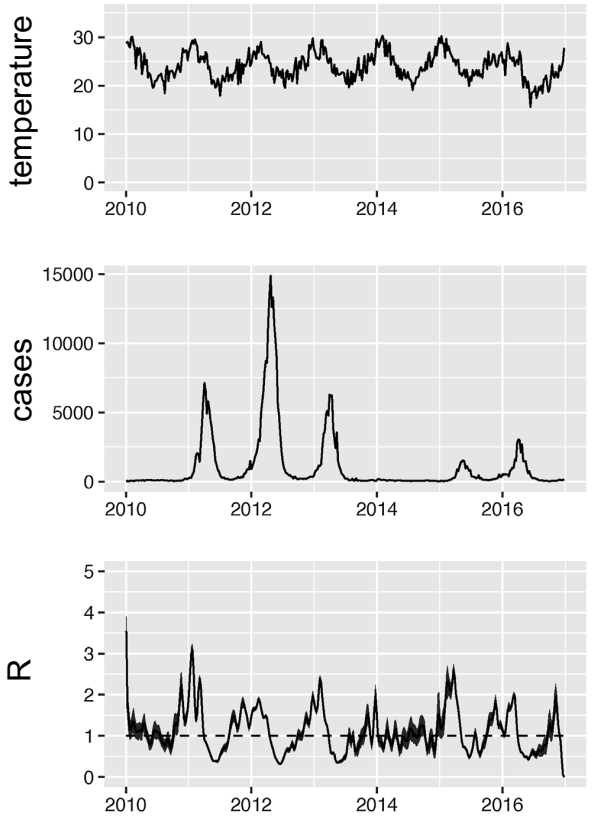
region	mean	median	95% ci
Midlands	1.3	1.3	[1.20 ; 1.40]
East of England	1.2	1.2	[1.10 ; 1.30]
London	1.2	1.2	[0.99 ; 1.30]
North East and Yorkshire	1.2	1.2	[1.10 ; 1.30]
South East	1.2	1.2	[1.10 ; 1.30]
South West	1.1	1.1	[0.95 ; 1.30]
North West	1.0	1.0	[0.90 ; 1.10]

episoap
Epiverse
powered by data.org

github.com/epiverse-trace/episoap

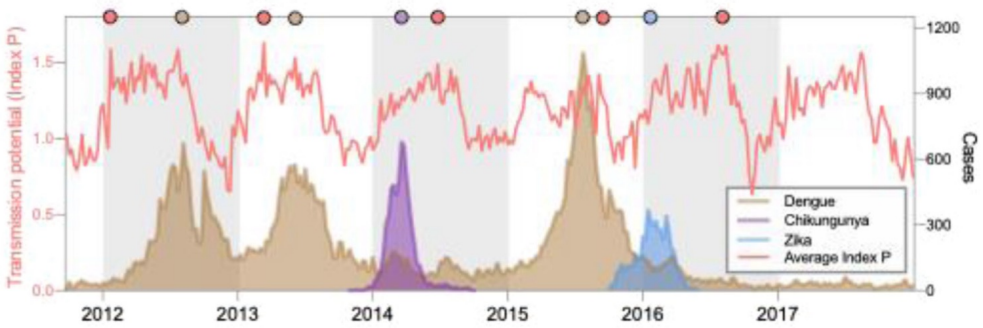
Climate data link: comparison of transmission & other indicators

Reproduction number in Rio de Janeiro



Codeço et al. (2018) *Epidemics*

Vector transmission potential vs cases in Dominican Republic



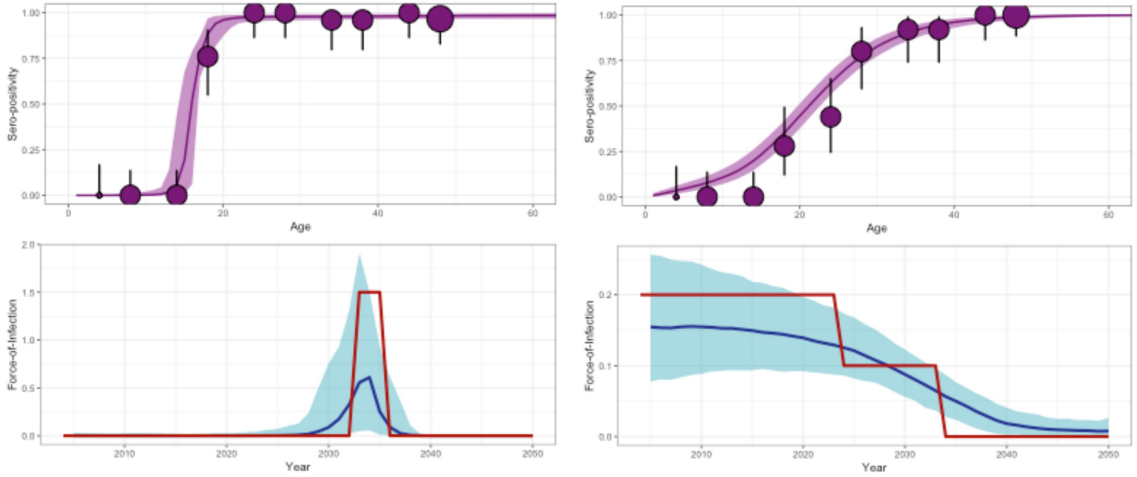
Petrone et al. (2021) *Nature Comms*

Climate data link: compare with estimates from serological data

- Can also use age-stratified serological data to estimate infection risk over longer period

- Complemenary method to using case surveillance data

Simulated antibody positivity by age vs estimated infection risk over time:



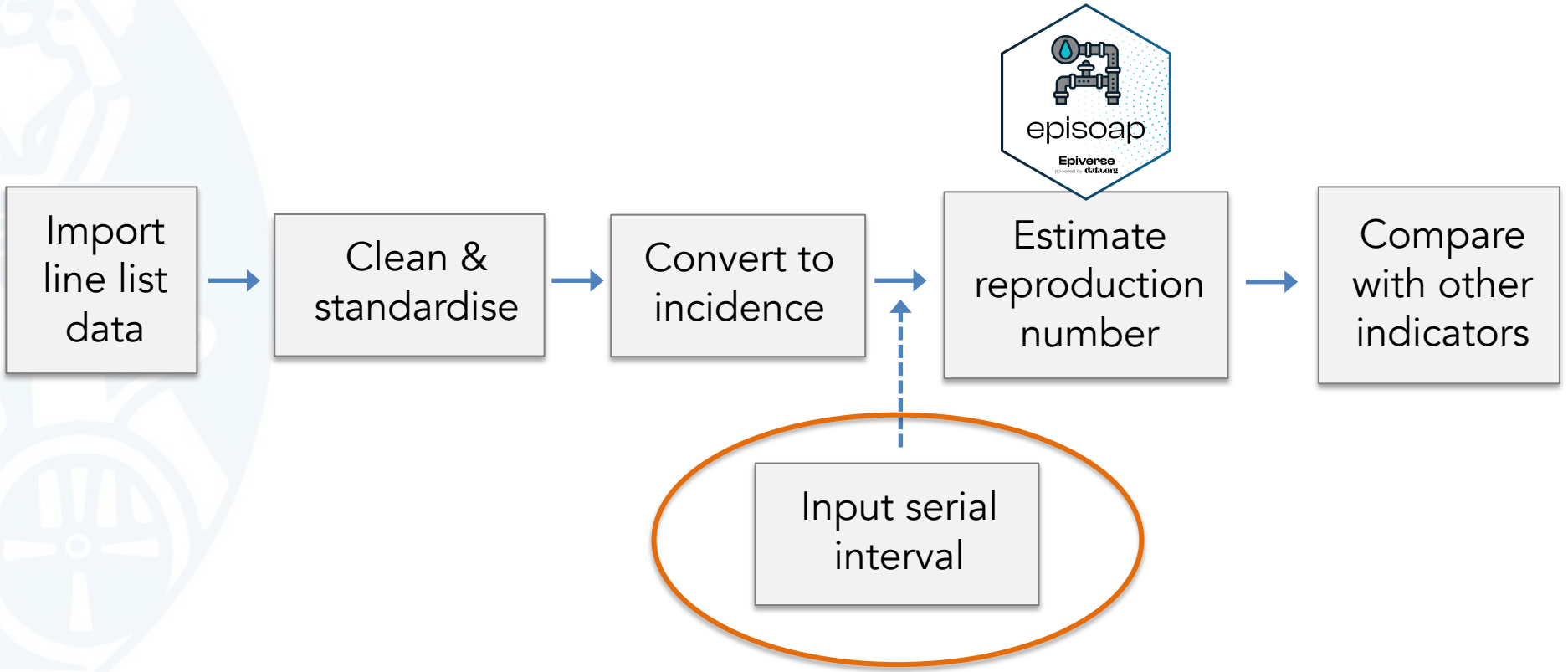
serofoi

Epiverse

Work by Zulma Cucunubá, Nicolás Domínguez et al

github.com/epiverse-trace/serofoi

Importing parameters



“Fitting a log-normal distribution to the data, we estimated the mean serial interval of COVID-19 to be 4.9 days (95% CI: 4.4–5.7 days)”

Extract, store and reuse epidemiological parameters

Extract distributions from summary statistics:

```
convert_gamma_summary_stats(mean = 2, sd = 2)
#> $shape
#> [1] 1
#>
#> $scale
#> [1] 2
```

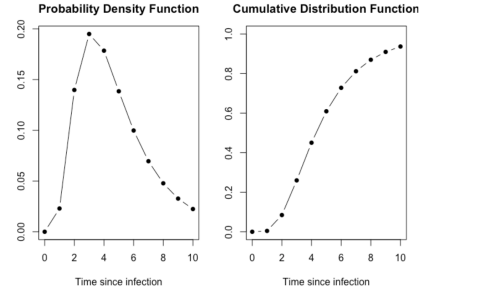
```
extract_param(
  type = "range",
  values = c(10, 5, 15),
  distribution = "lnorm",
  samples = 25
)
```

Load parameters from library:

```
epidist_db(
  disease = "COVID-19",
  epi_dist = "incubation_period",
  author = "Bui_etal"
)
#> Using Bui et al. (2020) <10.1371/journal.pone.0243889> PMID: 33362233.
#> To retrieve the short citation use the 'get_citation' function
#> Numerical approximation used, results may be unreliable.
#> Disease: COVID-19
#> Pathogen: SARS-CoV-2
#> Epi Distribution: incubation period
#> Study: Bui et al. (2020) <10.1371/journal.pone.0243889> PMID: 33362233
#> Distribution: weibull
#> Parameters:
#>   shape: 2.217
#>   scale: 7.226
```

Plot, process and reuse parameters:

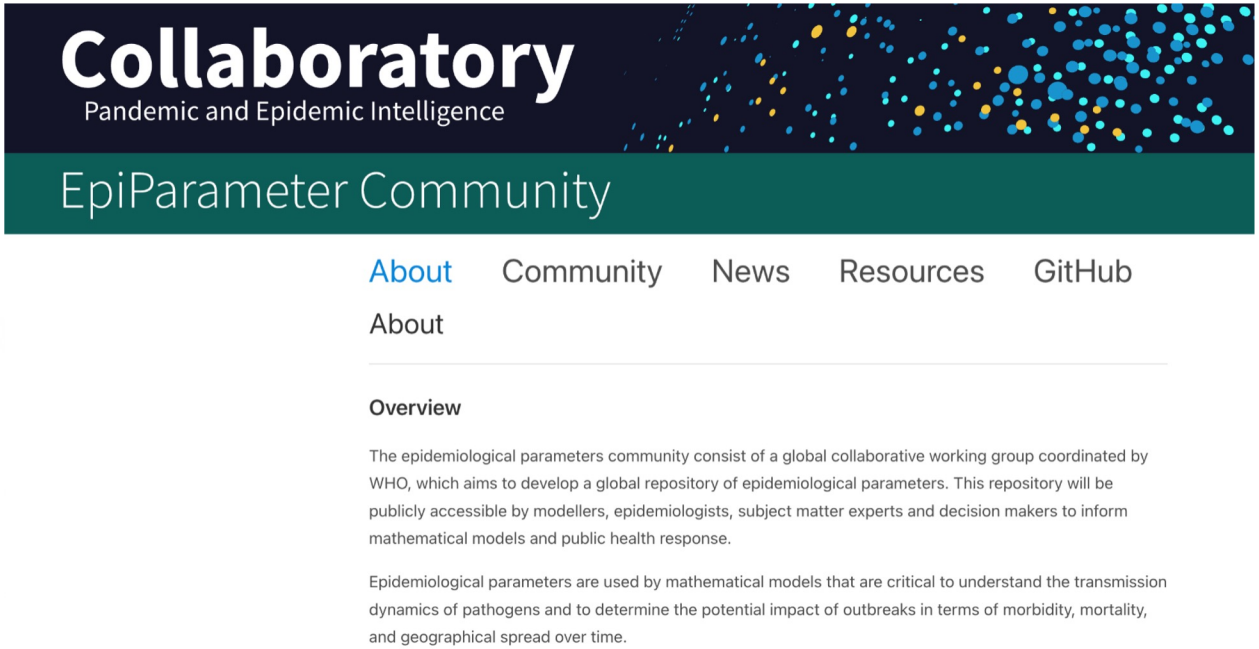
```
plot(influenza_incubation)
```



Work with Josh Lambert, Carmen Tamayo Cuartero et al

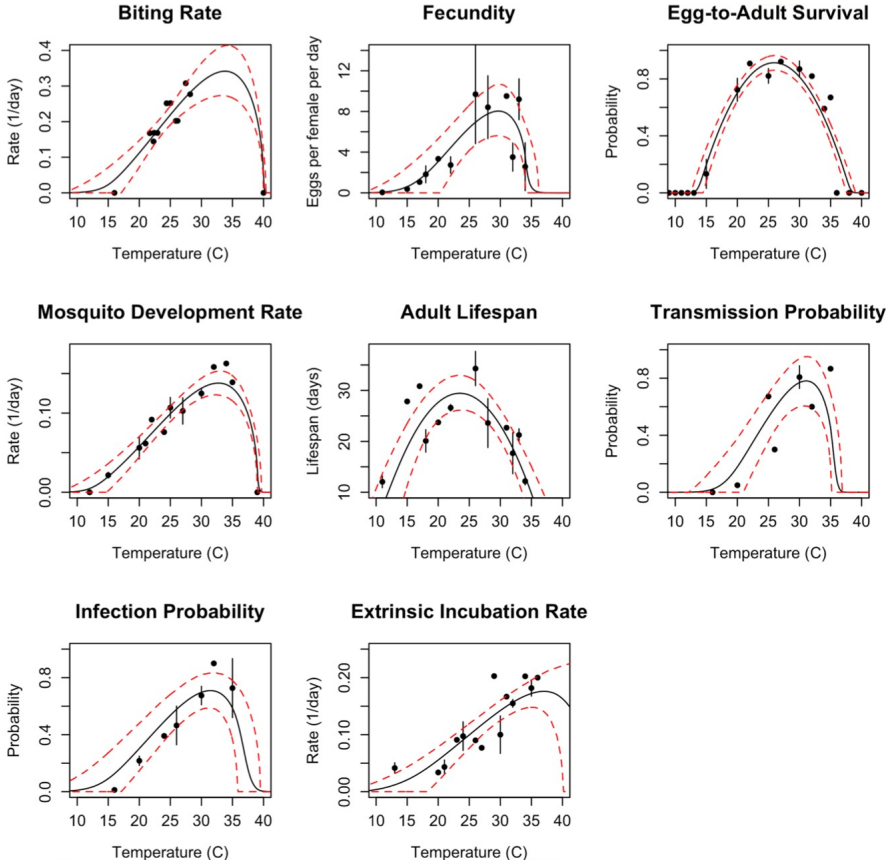
github.com/epiverse-trace/epiparameter

WHO collaboratory community to generate standardized library



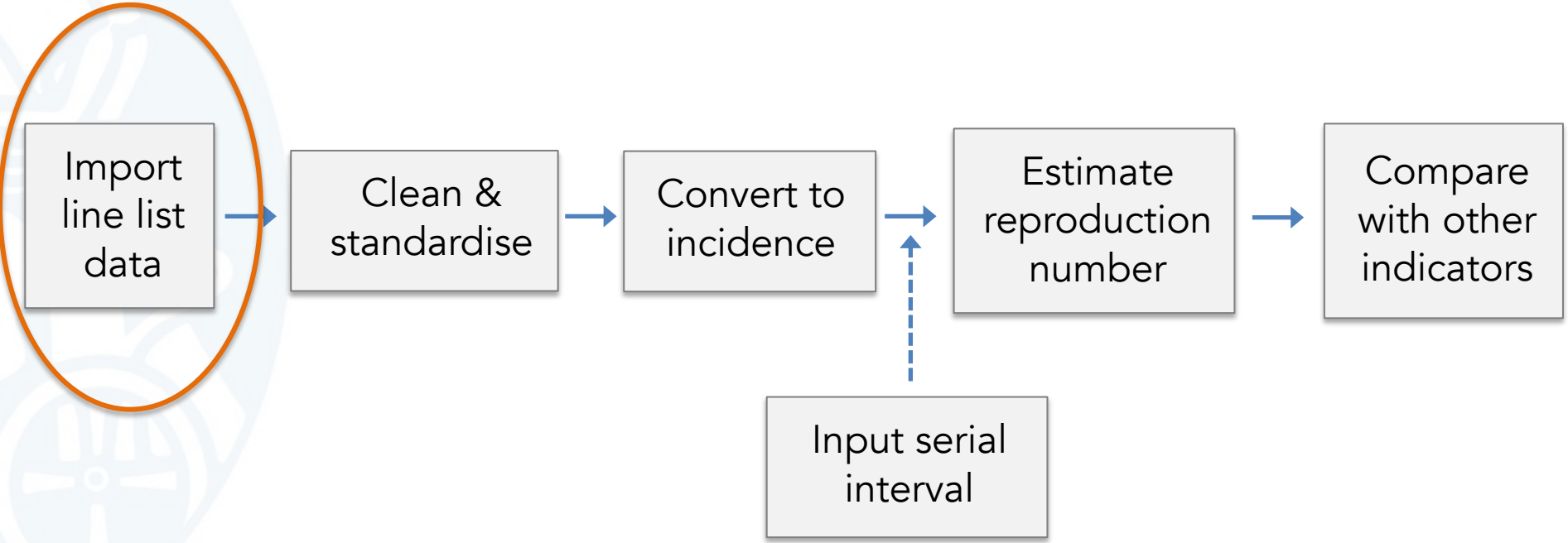
github.com/WorldHealthOrganization/collaboratory-epiparameter-community

Climate data link: vector-specific parameters

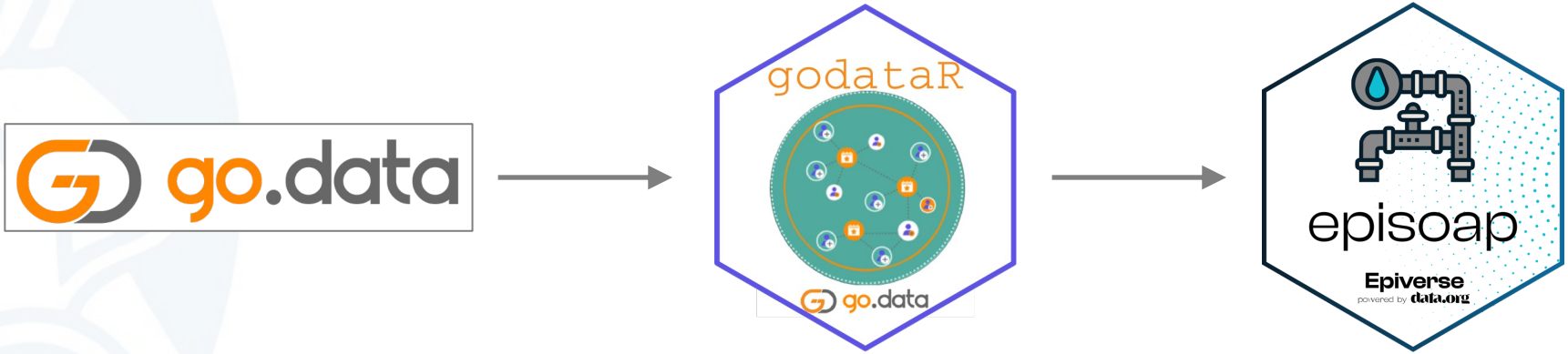


Mordecai et al. (2017) *PLOS NTD*

Processing epidemiological data



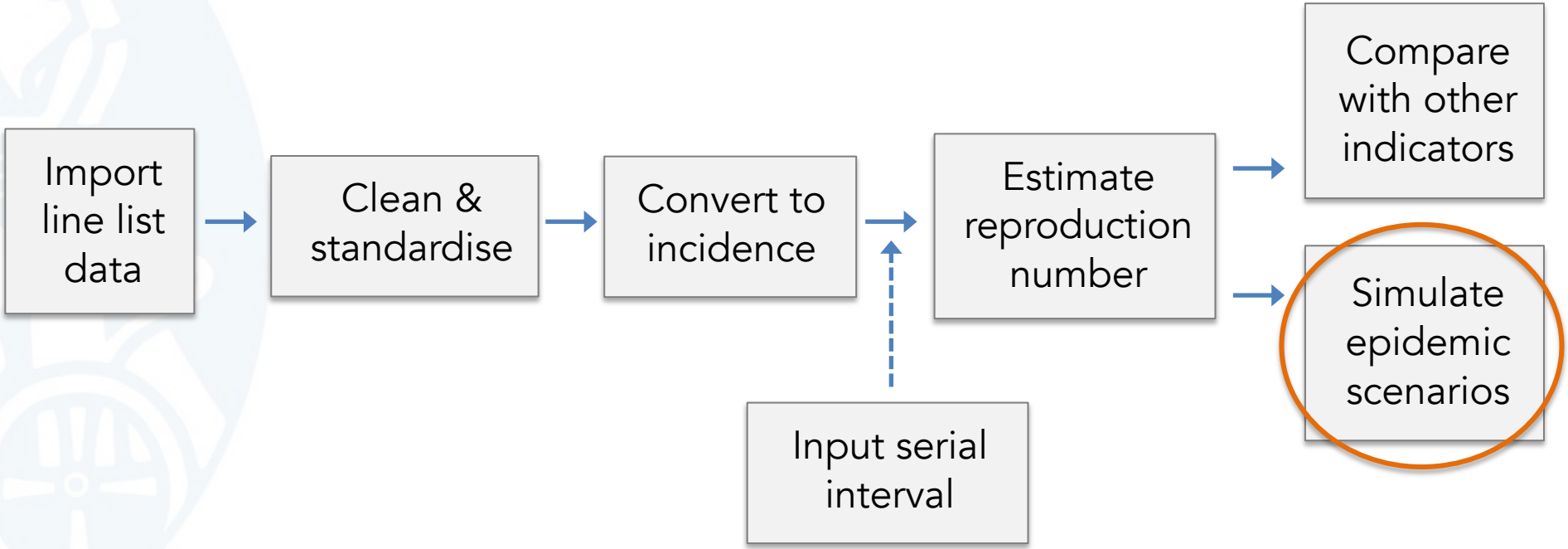
Importing, cleaning and analysing field data



Work with Sara Hollis, James Fuller, Josh Lambert et al

github.com/WorldHealthOrganization/godataR

Processing epidemiological data



Simulate epidemic scenarios

Define model options:

```
# Prepare epidemiological parameters as an infection object
pandemic <- infection(
  r0 = 1.5,
  preinfectious_period = 3,
  infectious_period = 7
)
```

```
# prepare an intervention with a differential effect on age groups
close_schools <- intervention(
  name = "School closure",
  time_begin = 200,
  time_end = 300,
  contact_reduction = matrix(c(0.5, 0.001, 0.001))
)
```

Run model

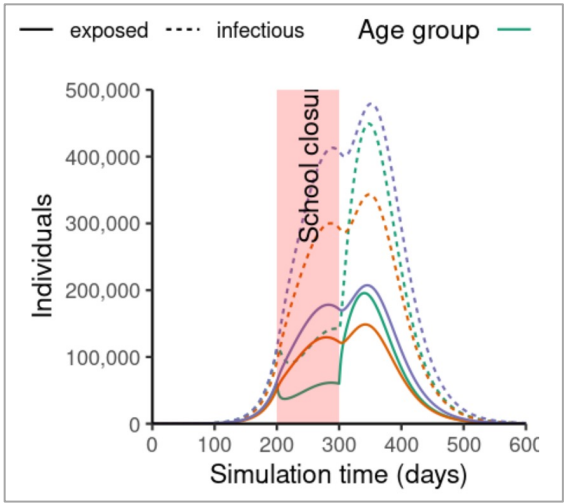
```
# run an epidemic model using `epidemic`
output <- epidemic(
  population = uk_population,
  infection = pandemic,
  intervention = close_schools,
  time_end = 600, increment = 1.0
)
```

Work with Pratik Gupte, Roz Eggo et al

epidemics

Epiverse

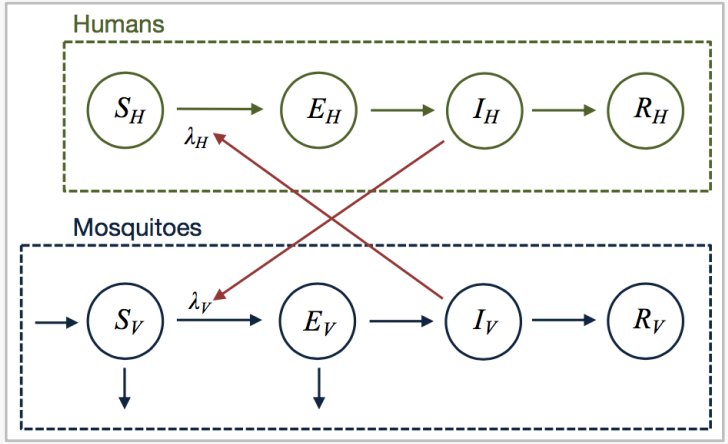
Show outputs



github.com/epiverse-trace/epidemics

Climate data link: inform transmission rate in models

Vector-borne transmission model

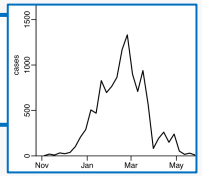


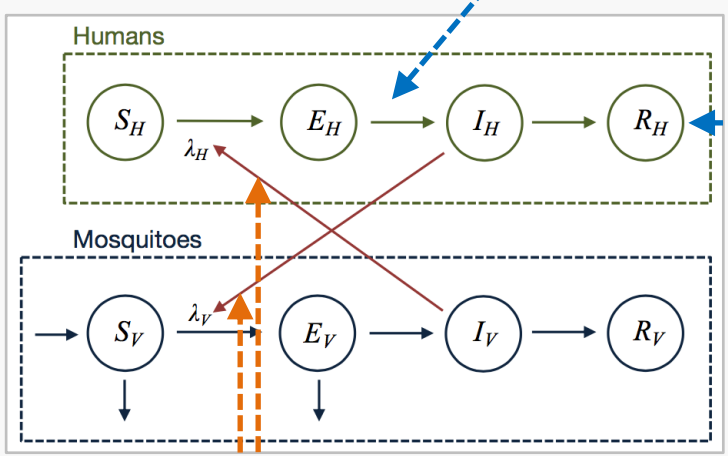
Kucharski et al. (2018) *eLife*

Climate data link: inform transmission rate in models

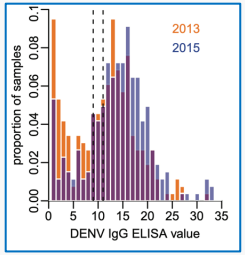
Vector-borne transmission model

Surveillance data to compare with disease incidence

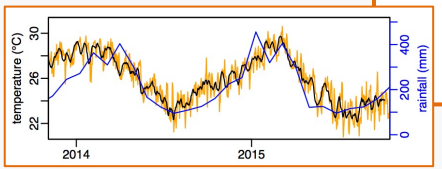




Serological data to compare with immunity

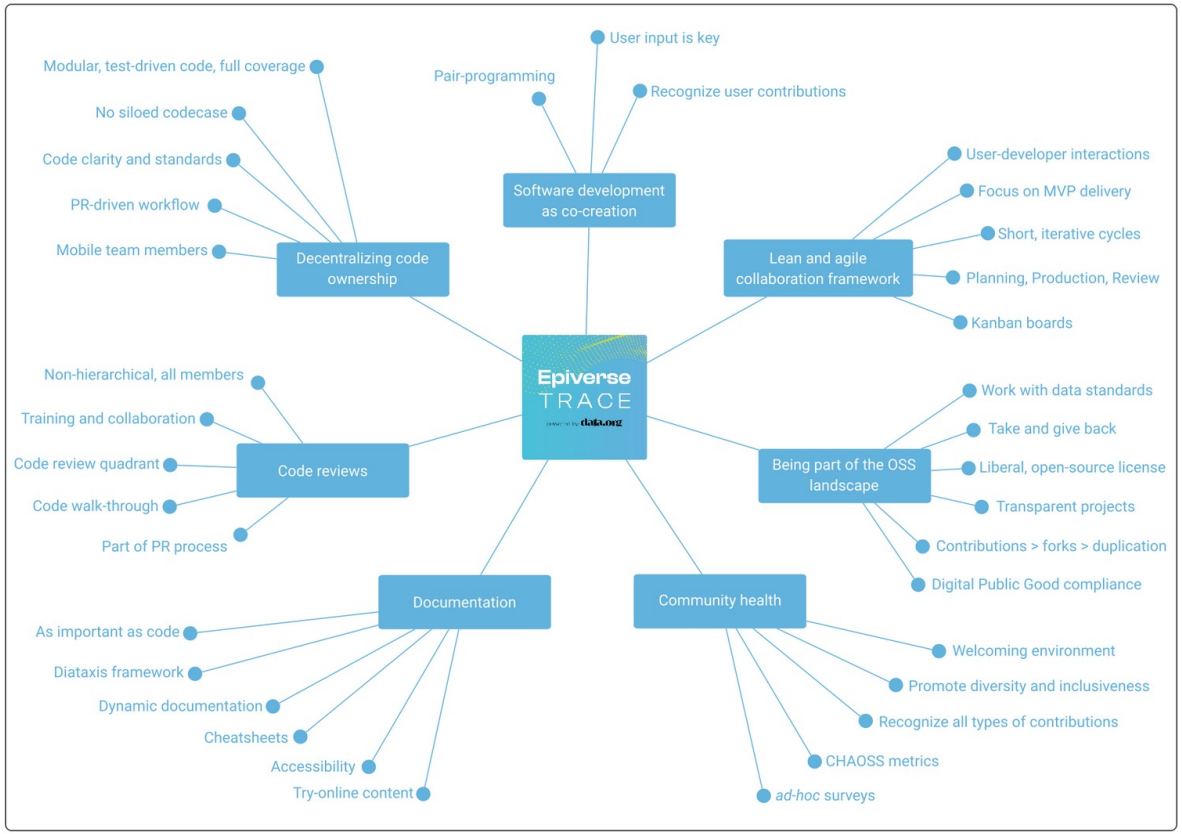


Climate data to inform temporal variation in transmission



Kucharski et al. (2018) *eLife*

Wider activites: community blueprints for best practice



epiverse-trace.github.io/blueprints

Wider activites: tool showcases and developer blog

Epiverse TRACE: January 2023 showcase

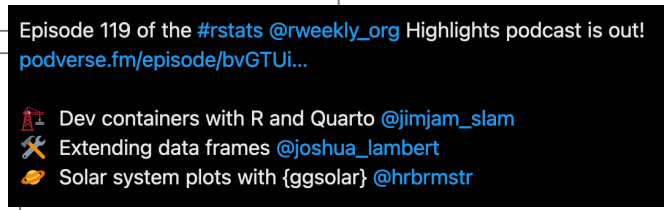
Epiverse TRACE: Spring 2023 showcase

What Should the First 100 Lines of Code Written During an Epidemic Look Like?

Ensuring & Showcasing the Statistical Correctness of your R Package

Convert Your R Function to an S3 Generic: Benefits, Pitfalls & Design Considerations

Improving the C++ Code Quality of an Rcpp Package



epiverse-trace.github.io/blog.html

Summary

- Huge potential to improve the ecosystem for epidemic analytics, from understanding dynamics to exploring control options .

- Several areas where climate data could be integrated into this ecosystem, including comparing transmission estimates to common indicators and incorporating climate-sensitive parameters into analysis.

Acknowledgements

Colleagues and collaborators at: the London School of Hygiene & Tropical Medicine, MRC Gambia, data.org, GOARN, WHO Pandemic Hub, Uniandes, Pontificia Universidad Javeriana

data.org

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