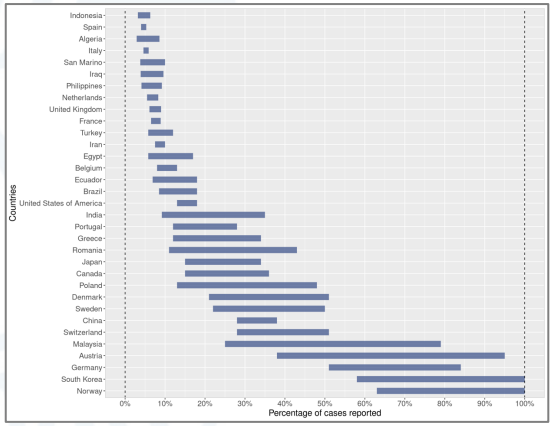
Improving code/software

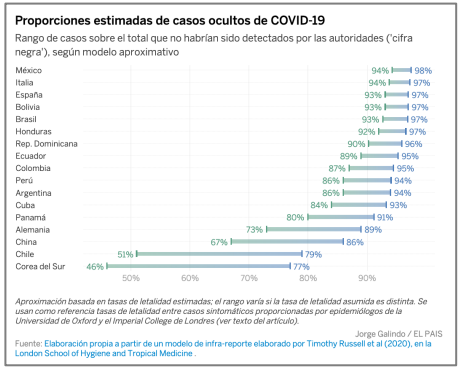
How many COVID-19 cases were being missed in early 2020?

LSHTM method to estimate
% cases reported:



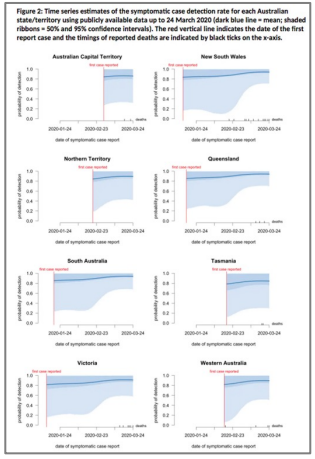
CMMID COVID-19 repository

Code reused

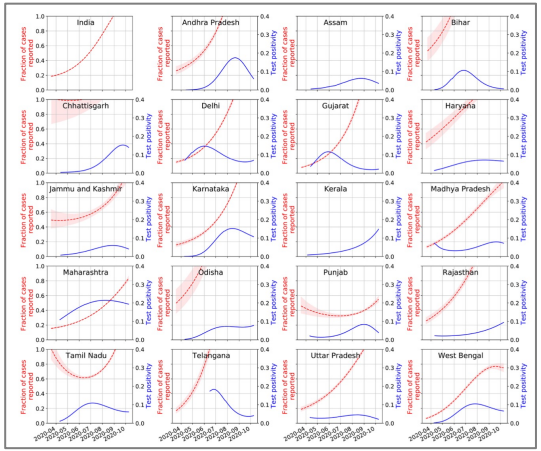


Spain (El Pais)

Switzerland (TA)



Australia (Doherty Institute)



India (Unnikrishnan et al, BMJ Open)

Work with Tim Russell et al

PCR estimates subsequently reused in range of studies…

The differential importation risks of COVID-19 from inbound travellers and the feasibility of targeted travel controls: A case study in Hong Kong

Bingyi Yang[a], Tim K. Tsang[a], Jessica Y. Wong[a], Yinan He[a], Huizhi Gao[a], Faith Ho[a], Eric H.Y. Lau[a,b], Peng Wu[a], Sheena G. Sullivan[c], Benjamin J. Cowling[a,b,*]

inc2prev

Estimate incidence from ONS prevalence estimates

Quarantine and testing strategies to ameliorate transmission due to travel during the COVID-19 pandemic: a modelling study

Chad R. Wells,[a,#] Abhishek Pandey,[a,#] Meagan C. Fitzpatrick,[a,b] William S. Crystal,[a] Burton H. Singer,[c] Seyed M. Moghadas,[d] Alison P. Galvani,[a,e] and Jeffrey P. Townsend,[e,f,g,h,]*

Research and analysis

Rapid testing strategies for traced contacts: comparing quarantine, quarantine and testing, and daily testing, 16 November 2020

Paper prepared by academics on behalf of the Centre for Mathematical Modelling of Infectious Diseases (CMMID) COVID-19 working group.

Quantifying SARS-CoV-2 Infection Risk Within the Google/Apple Exposure Notification Framework to Inform Quarantine Recommendations

Amanda M. Wilson, Nathan Aviles, James I. Petrie, Paloma I. Beamer, Zsombor Szabo, Michelle Xie, Janet McIllece, Yijie Chen, Young-Jun Son, Sameer Halai, Tina White, Kacey C. Ernst, Joanna Masel

SARS-CoV-2 infection in UK university students: lessons from September–December 2020 and modelling insights for future student return

Jessica Enright† ✉, Edward M. Hill† ✉, Helena B. Stage, Kirsty J. Bolton, Emily J. Nixon, Emma L. Fairbanks, Maria L. Tang, Ellen Brooks-Pollock, Louise Dyson, Chris J. Budd, Rebecca B. Hoyle, Lars Schewe, Julia R. Gog ✉ and Michael J. Tildesley ✉

COVID-19 in low-tolerance border quarantine systems: impact of the Delta variant of SARS-CoV-2

Cameron Zachreson,[1] Freya M. Shearer,[2] David J. Price,[2,3] Michael J. Lydeamore,[4] Jodie McVernon,[2,3] James McCaw,[2,3,5] and Nicholas Geard[1,3]

PERSPECTIVE

The COVID-19 response illustrates that traditional academic reward structures and metrics do not reflect crucial contributions to modern science

Adam J. Kucharski*, Sebastian Funk, Rosalind M. Eggo

PLOS Biology, 2020

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

What could the final size of an epidemic be?

What could the final size of an epidemic be?

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

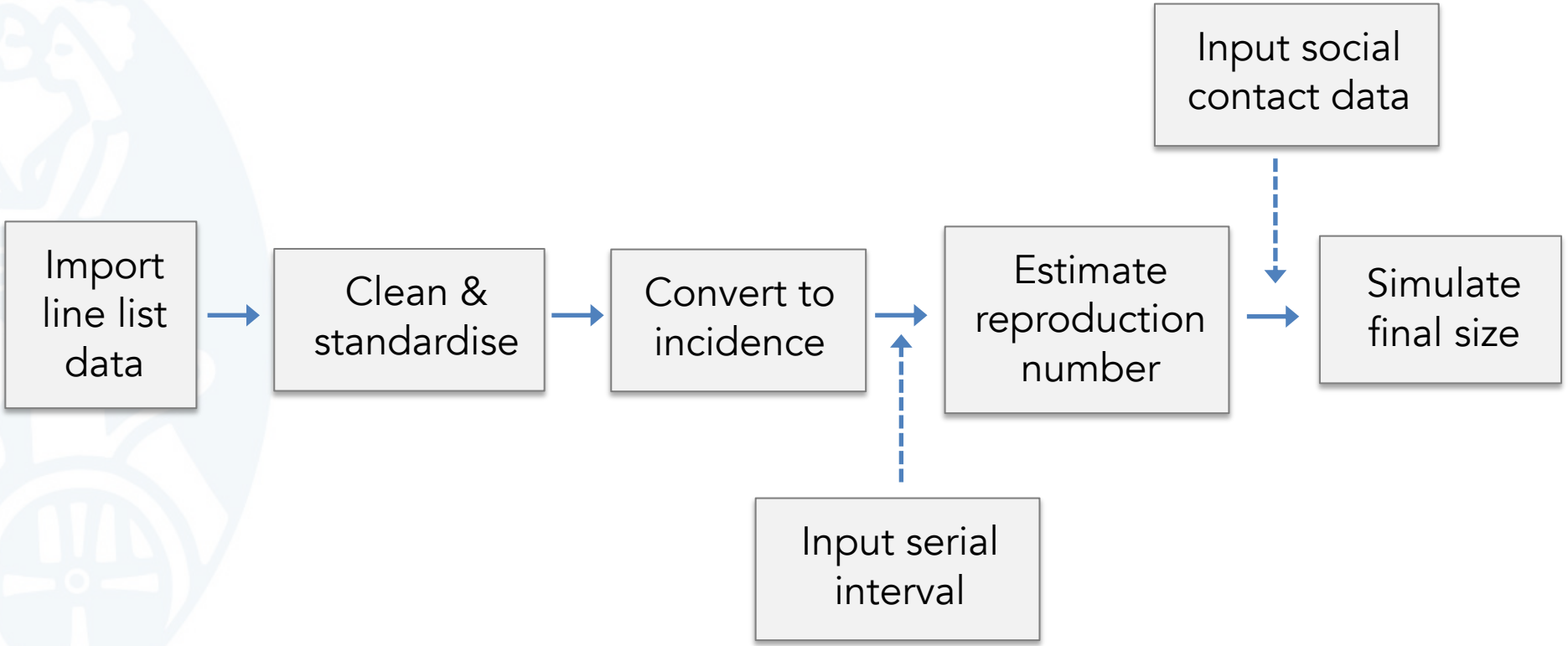
$$\frac{dR}{dt} = \gamma I$$

Bit of algebra and integration

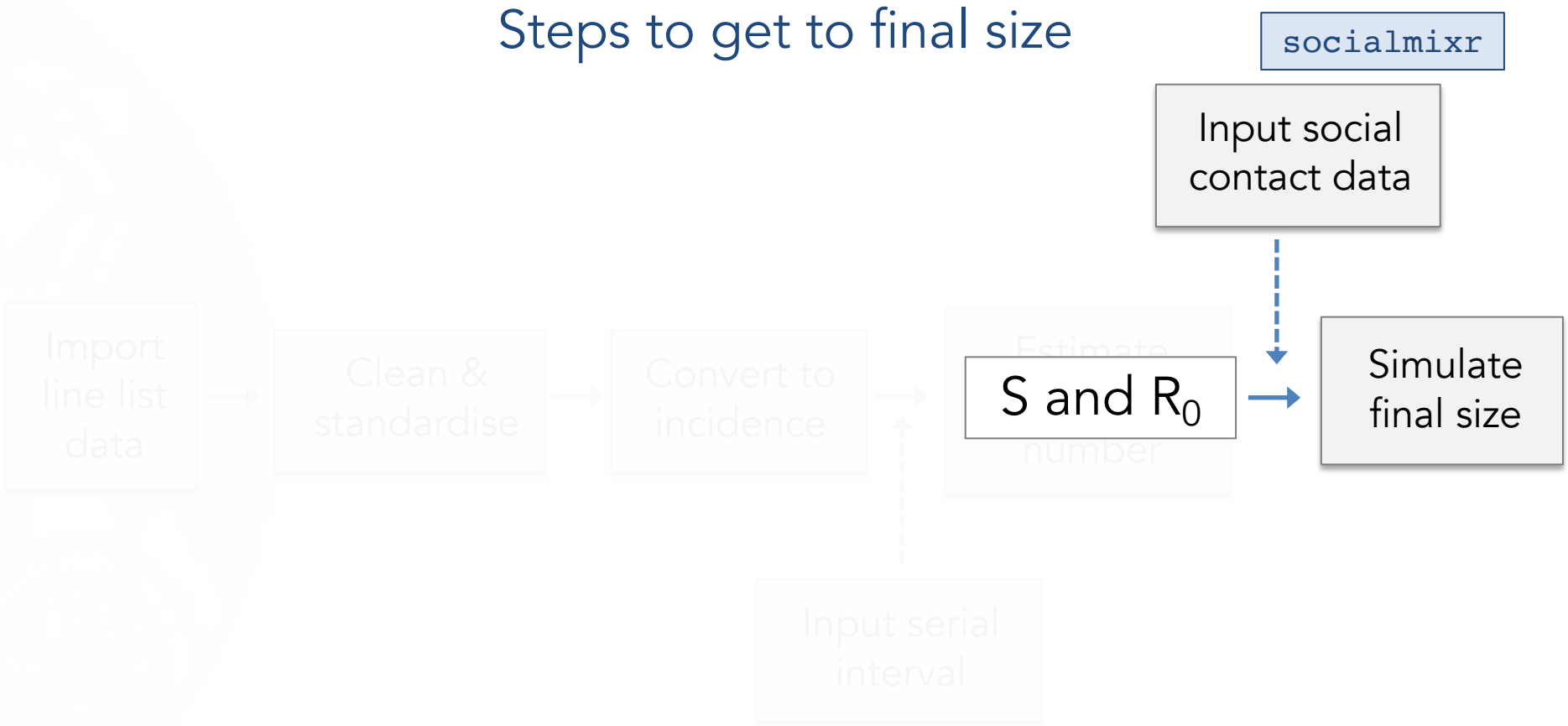
Final size equation:

$$Z = 1 - e^{-R_0 Z}$$

Steps to get to final size



Steps to get to final size



Calculating final size

Follow best practice:

- Modularisation
- Automated tests
- Documentation

Work with Pratik Gupte, Roz Eggo et al

github.com/epiverse-trace/finalsize

Calculating final size

Follow best practice:

- Modularisation
- Automated tests
- Documentation

Work with Pratik Gupte, Roz Eggo et al

finalsize

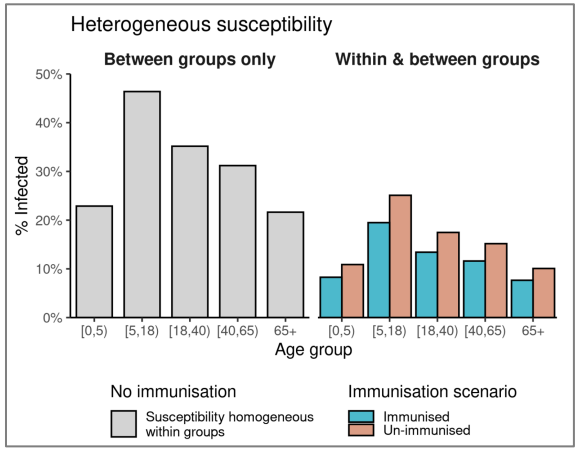
Epiverse

Load data and define model options:

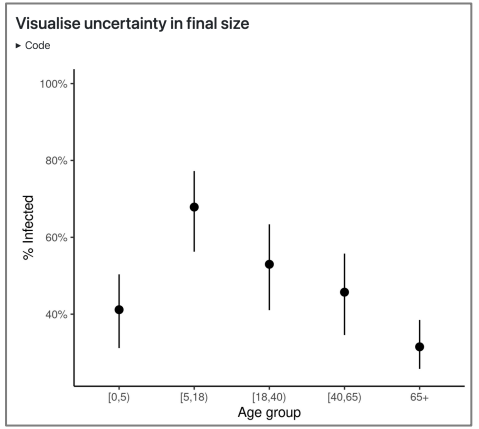
```
# get UK polymod data
polymod <- socialmixr::polymod
contact_data <- socialmixr::contact_matrix(
  polymod,
  countries = "United Kingdom",
  age.limits = c(0, 5, 18, 40, 65),
  symmetric = TRUE
)
```

```
# calculate final size
final_size_data <- final_size(
  r0 = r0,
  contact_matrix = contact_matrix,
  demography_vector = demography_vector,
  susceptibility = susc_uniform,
  p_susceptibility = p_susc_uniform
)
```

Calculate final size:

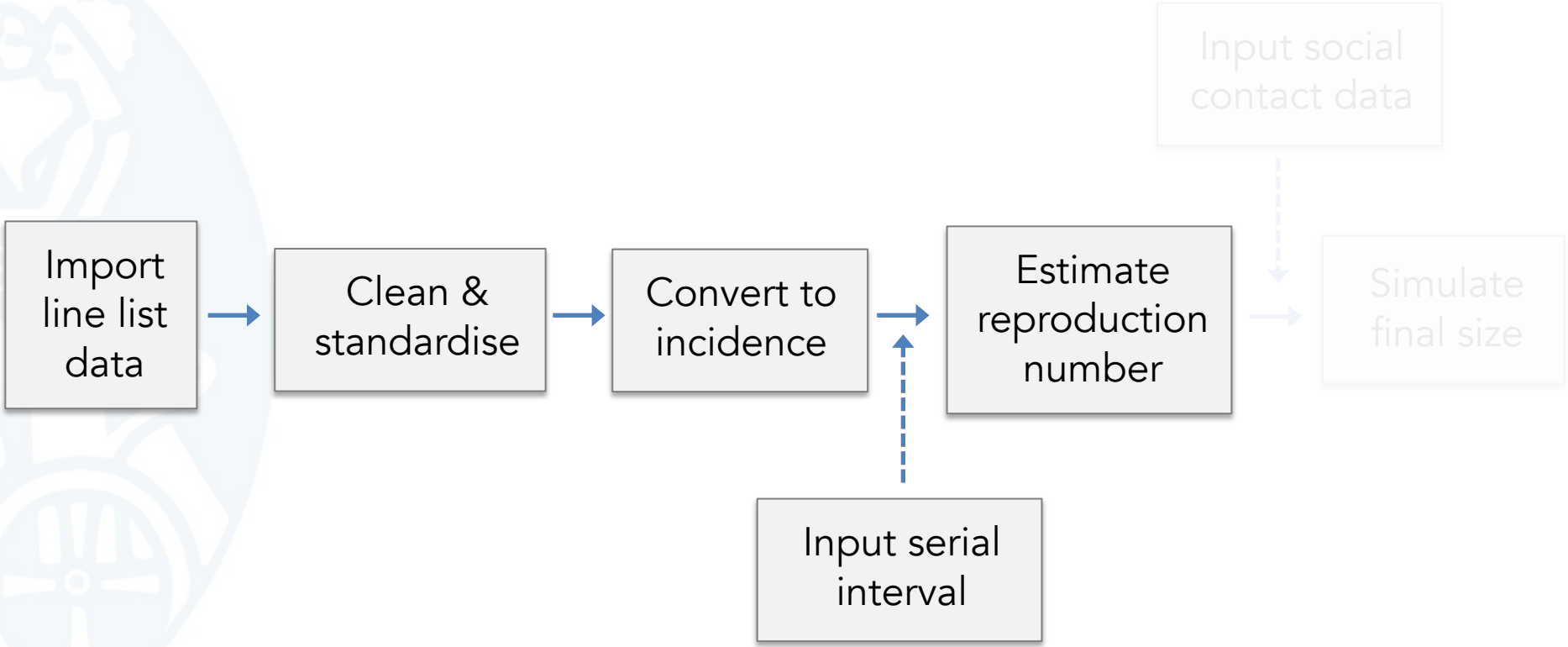


Propagate uncertainty:

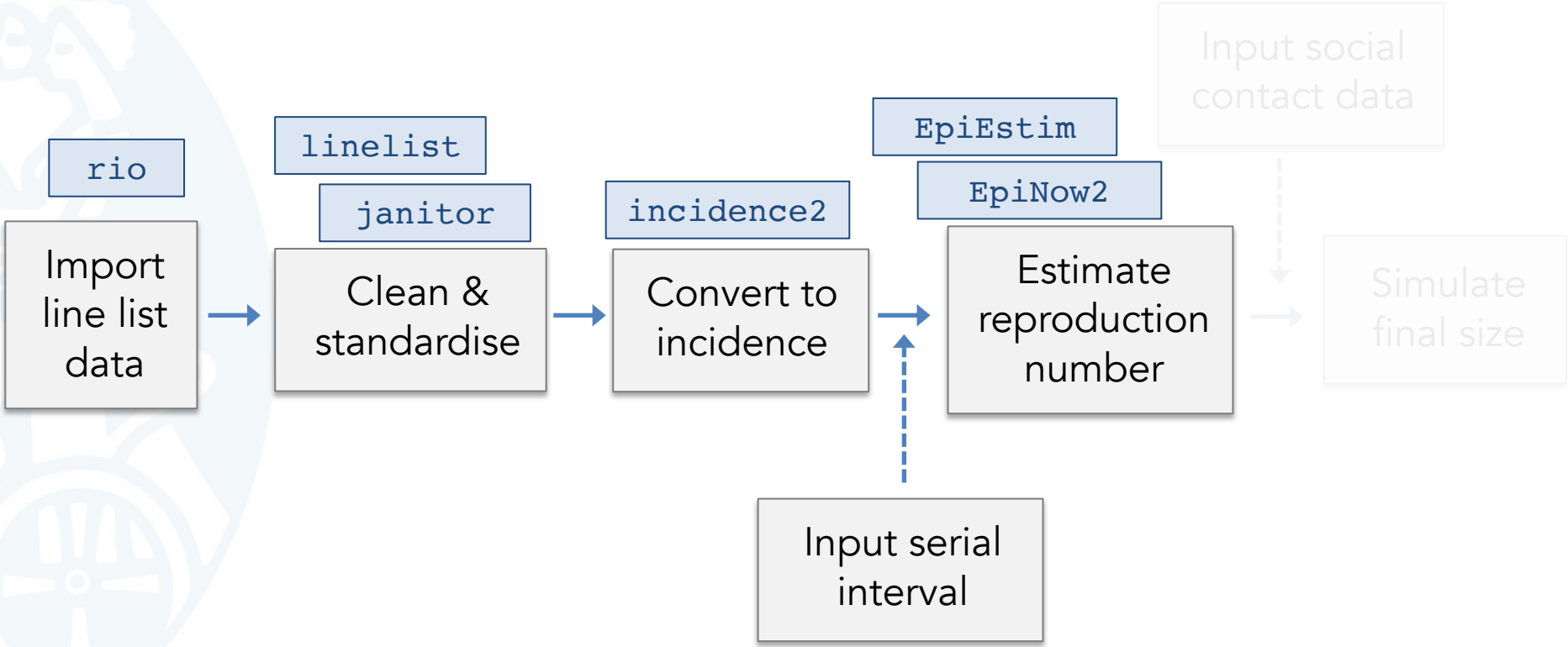


github.com/epiverse-trace/finalsize

Estimating R or R_0



Estimating R or R_0



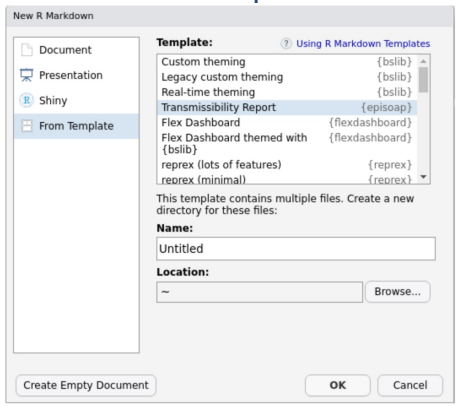
Outbreak analytics pipelines

episoap

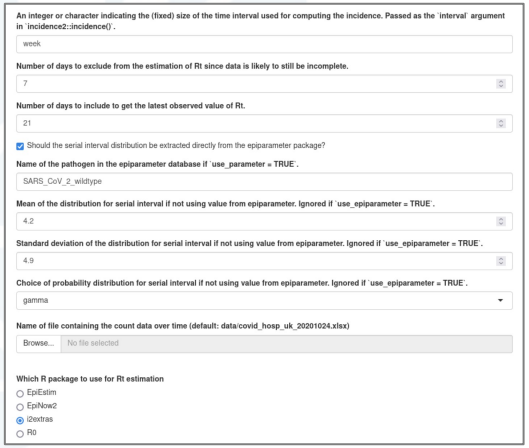
Epiverse powered by data.org

Work by Hugo Gruson et al

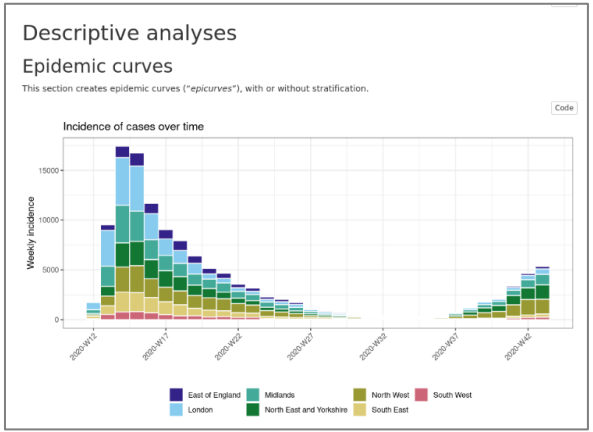
Choose template:



Select options:



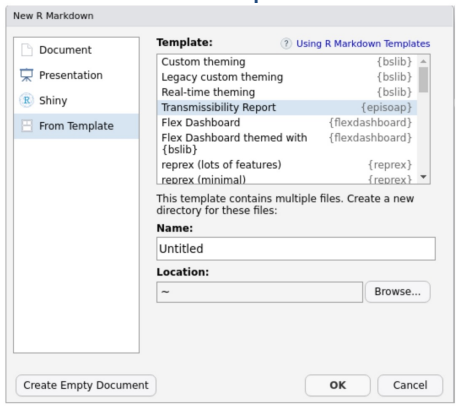
Descriptive curves:



github.com/epiverse-trace/episoap

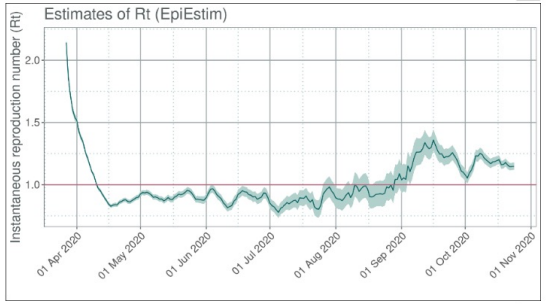
Outbreak analytics pipelines

Choose template:



Work by Hugo Gruson et al

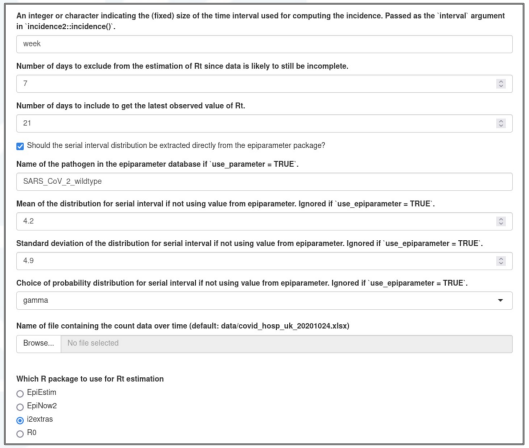
R estimation:



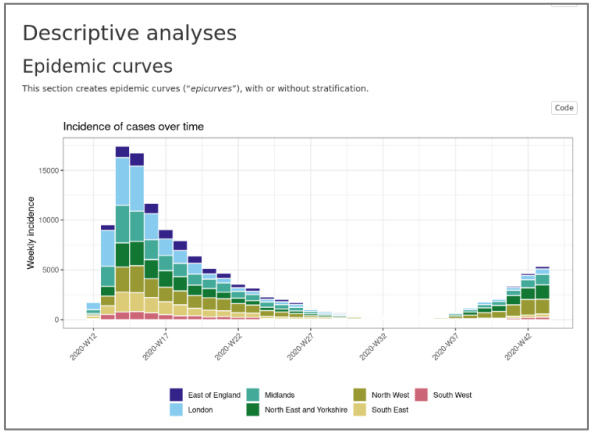
episoap

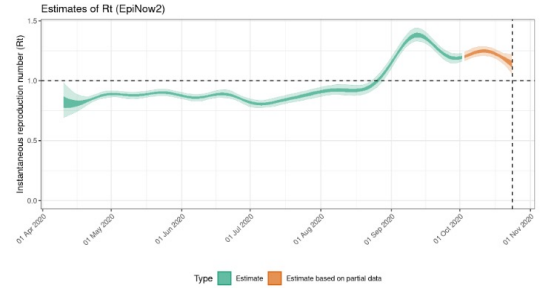
Epiverse powered by data.org

Select options:



Descriptive curves:

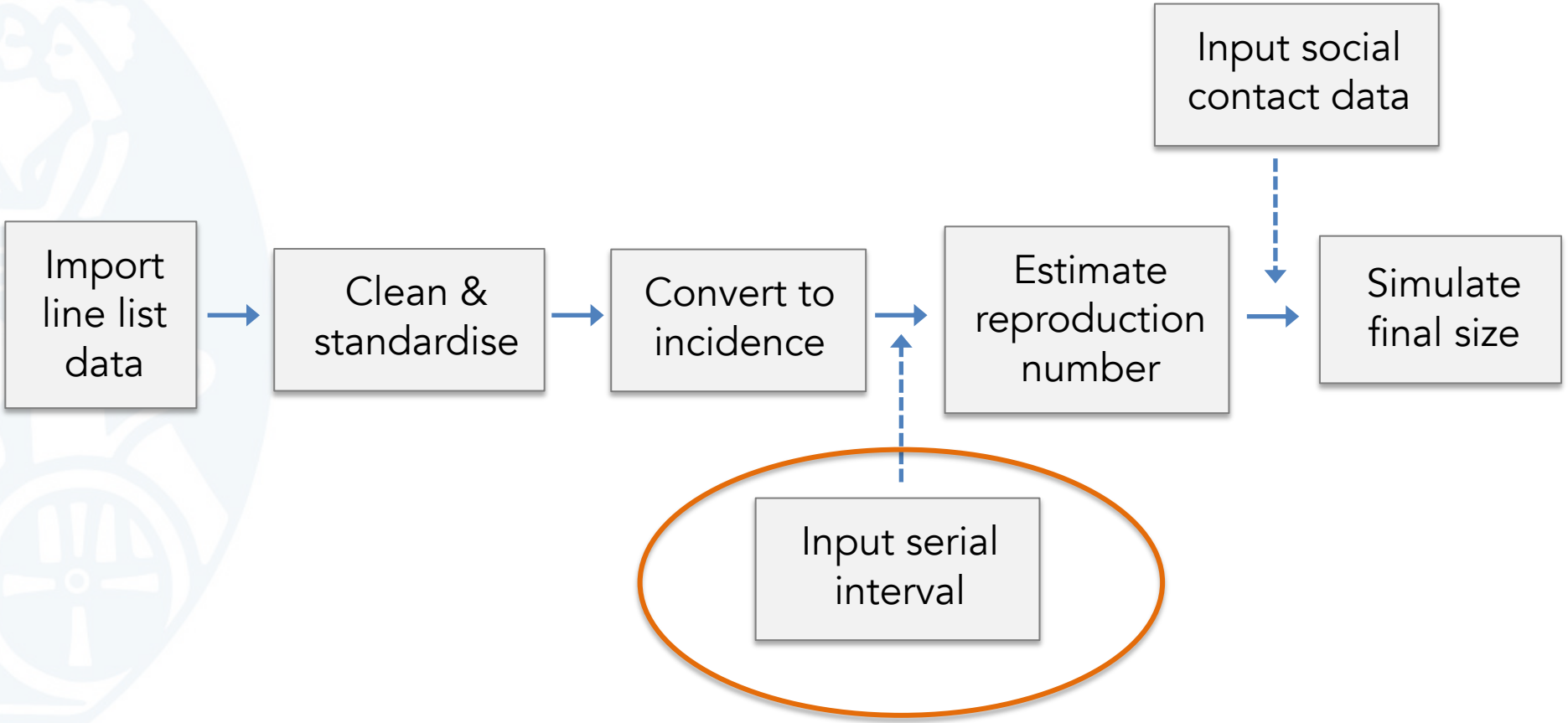




region	mean	median	95% ci
Midlands	1.3	1.3	[1.20 ; 1.40]
East of England	1.2	1.2	[1.10 ; 1.30]
London	1.2	1.2	[0.99 ; 1.30]
North East and Yorkshire	1.2	1.2	[1.10 ; 1.30]
South East	1.2	1.2	[1.10 ; 1.30]
South West	1.1	1.1	[0.95 ; 1.30]
North West	1.0	1.0	[0.90 ; 1.10]

github.com/epiverse-trace/episoap

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
```

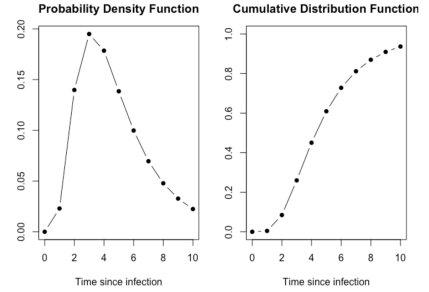
```
extract_param(
  type = "range",
  values = c(10, 5, 15),
  distribution = "lnorm",
  samples = 25
)
```

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:

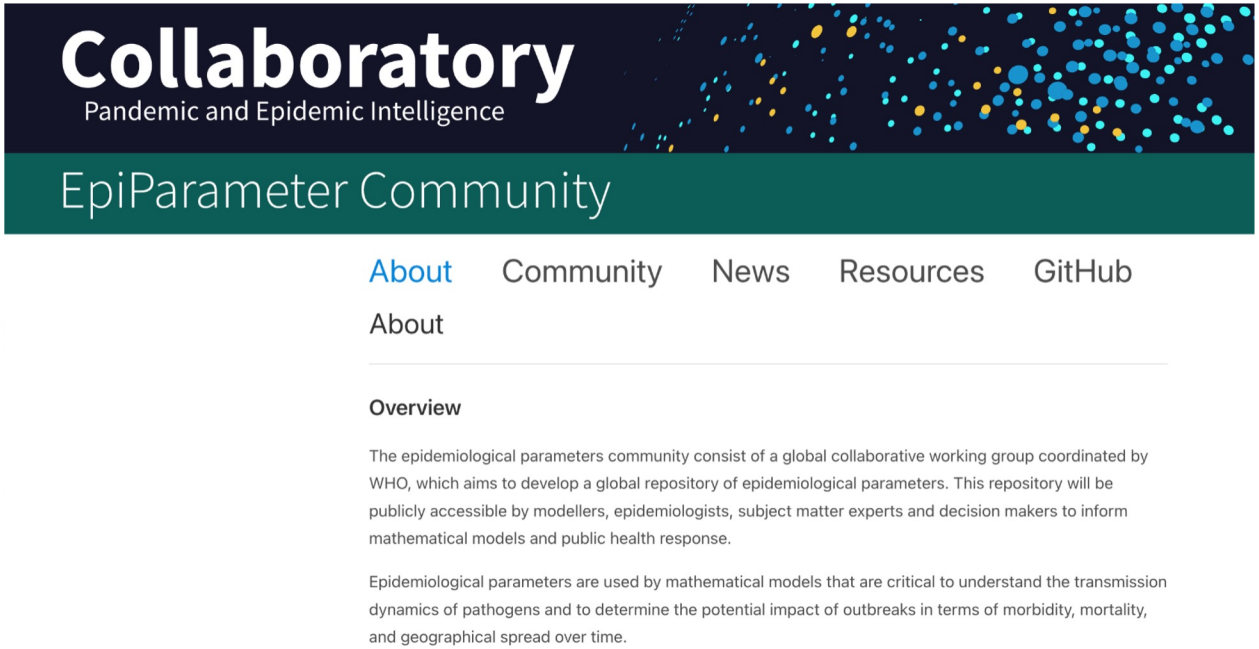
```
plot(influenza_incubation)
```



Work with Josh Lambert, Carmen Tamayo Cuartero et al

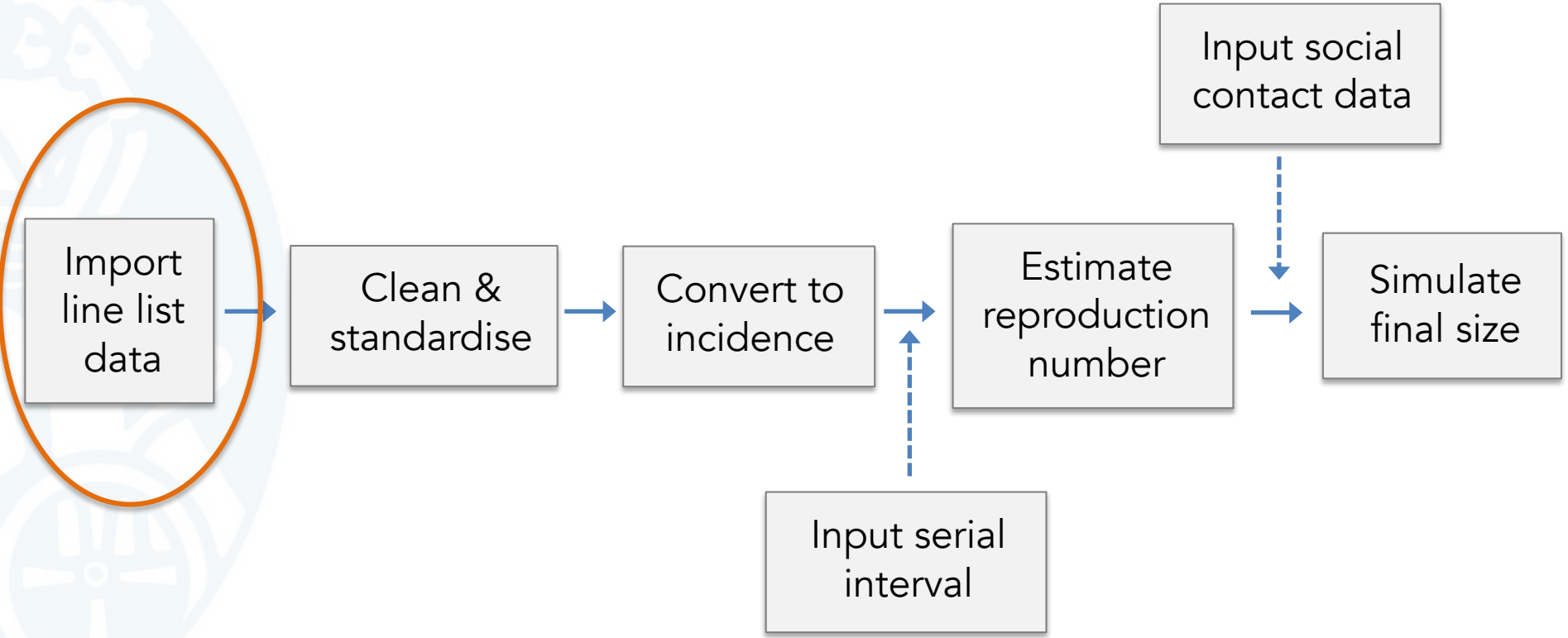
github.com/epiverse-trace/epiparameter

WHO collaboratory community to generate standardized library

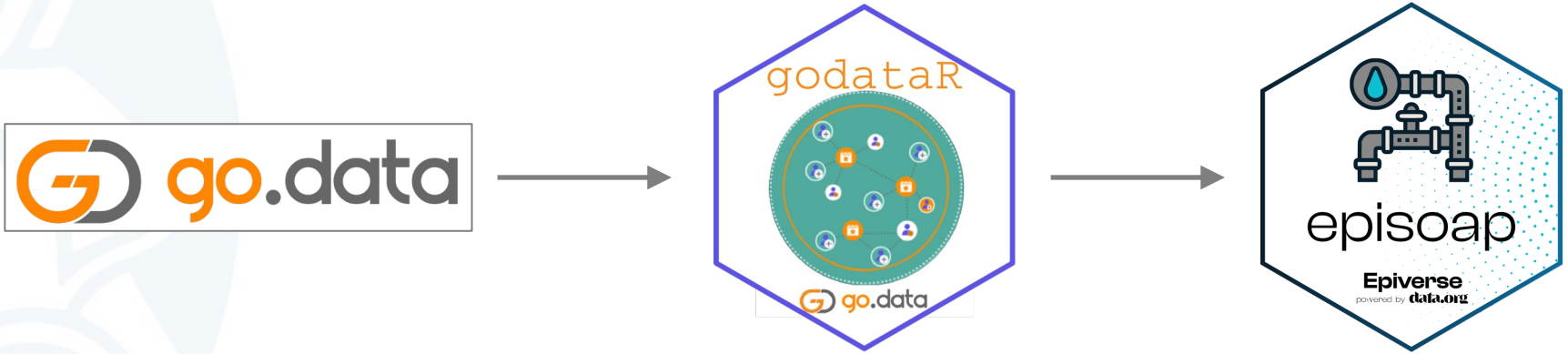


github.com/WorldHealthOrganization/collaboratory-epiparameter-community

Processing epidemiological data



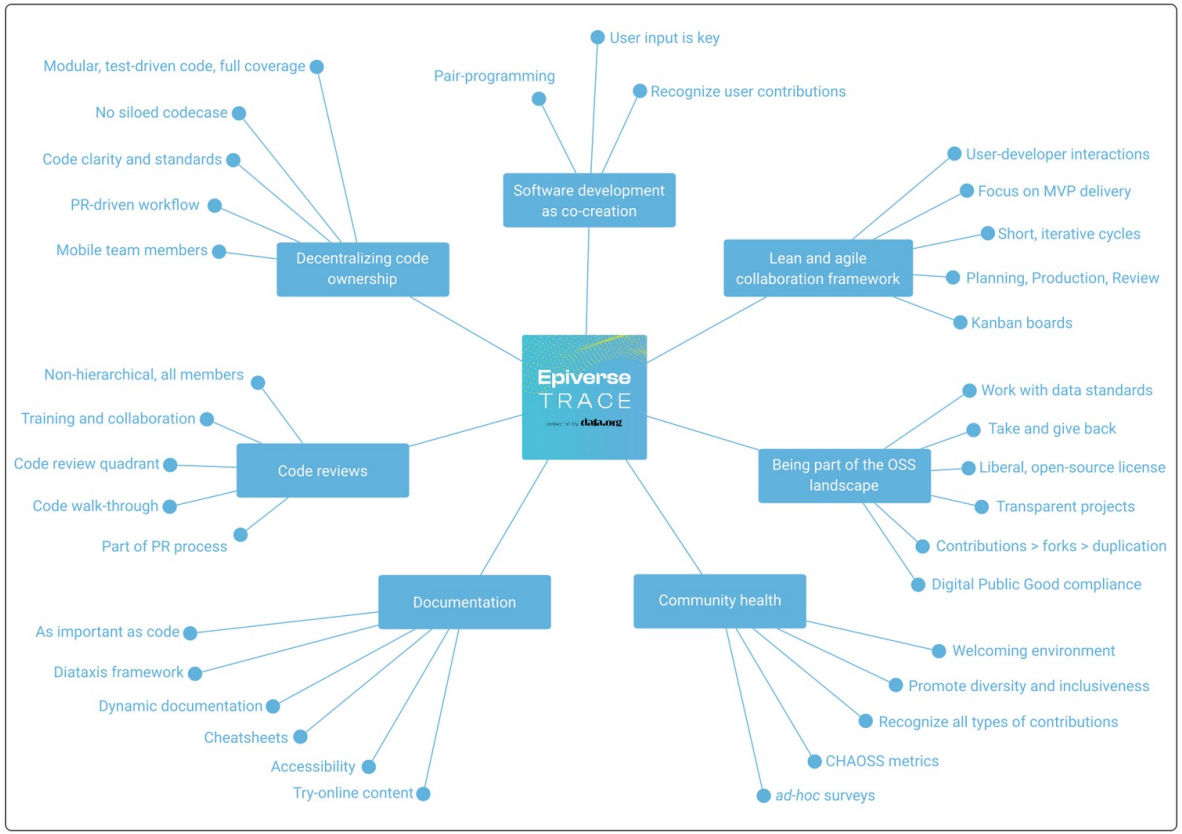
Importing, cleaning and analysing field data



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

github.com/WorldHealthOrganization/godataR

Wider community blueprints for best practice



epiverse-trace.github.io/blueprints

Tool showcases and developer blog

Epiverse TRACE: January 2023 showcase

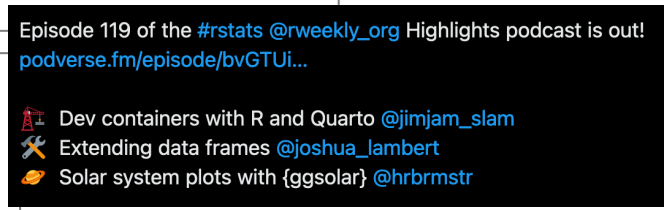
Epiverse TRACE: Spring 2023 showcase

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

How to get involved?

- Co-create in wider collaborations (e.g. WHO collaboratory)
- Suggest contributions to existing packages (e.g. godataR)
- Highlight methods to include in our pipelines (e.g. episoap)
- Showcase your packages/tools at an upcoming event
- Develop new tools that are interoperable with same standards
- Contribute to projects hosted on our GitHub (e.g. finalsize)