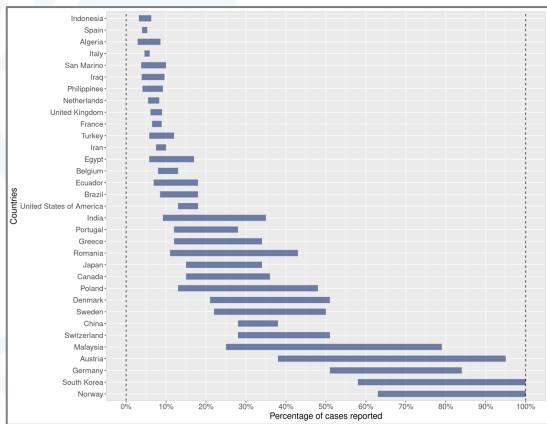


Improving code/software

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

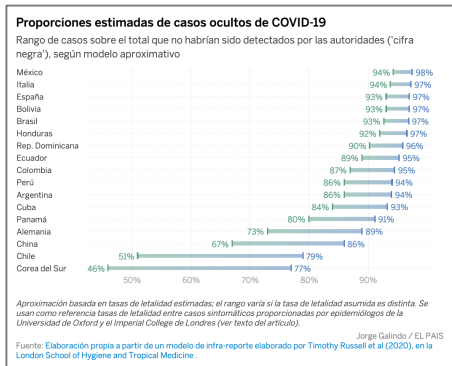
LSHTM method to estimate % cases reported:



CMMID COVID-19 repository

Work with Tim Russell et al

Code reused →



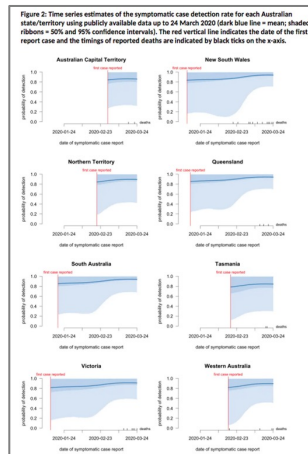
Spain (El País)

Nachgewiesen ist nur eine von fünf Infektionen

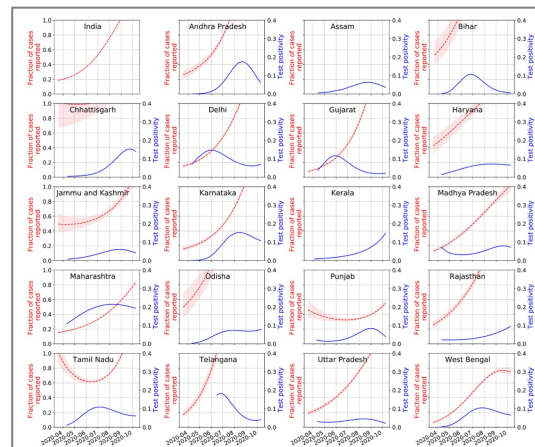
Eine Studie gibt erstmals Hinweise auf die Dunkelziffer der Corona-Infizierten in der Schweiz: In manchen Kantonen ist diese sehr groß



Switzerland (TA)



Australia (Doherty Institute)



India (Unnikrishnan et al, BMJ Open)

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, Yanan 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

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.




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,}*

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 McIllice, 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.**



data.org



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.**



What could the final size of an epidemic be?



What could the final size of an epidemic be?

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

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

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

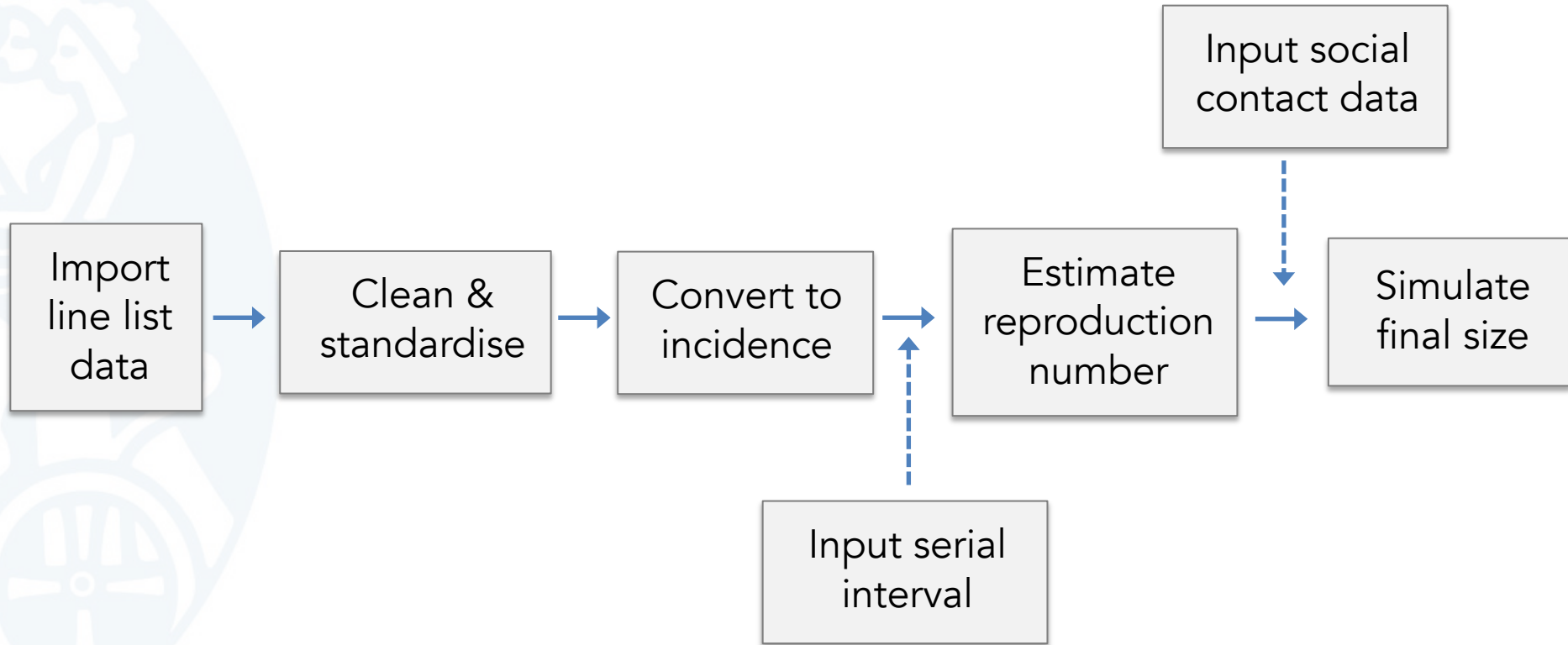


Bit of
algebra and
integration

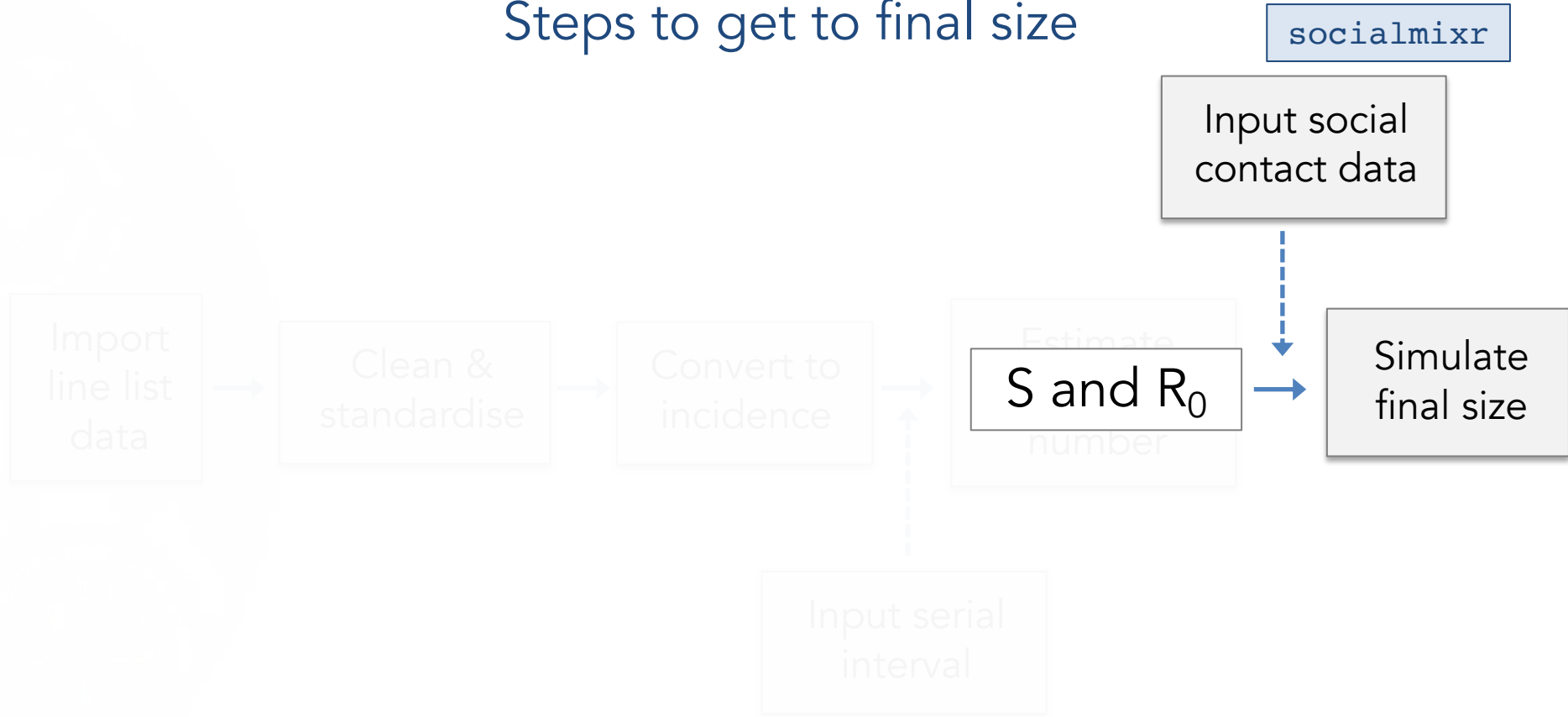
Final size equation:

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

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



Calculating final size

Follow best practice:

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Work with Pratik
Gupte, Roz Eggo et al

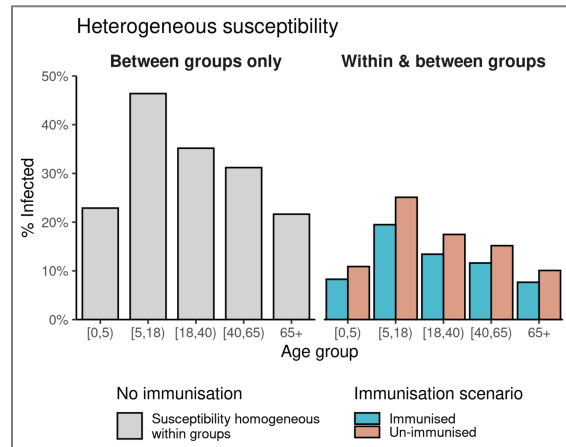


Load data and define
model options:

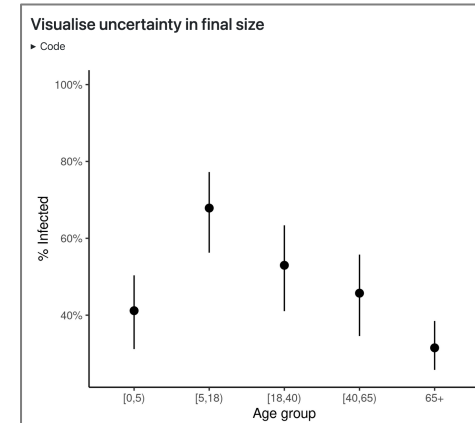
```
# get UK polymod data
polymod <- socialmixr::polymod
contact_data <- socialmixr::contact_matrix(
  polymod,
  countries = "United Kingdom",
  age.limits = c(0, 5, 18, 40, 65),
  symmetric = TRUE
)
```

```
# 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
)
```

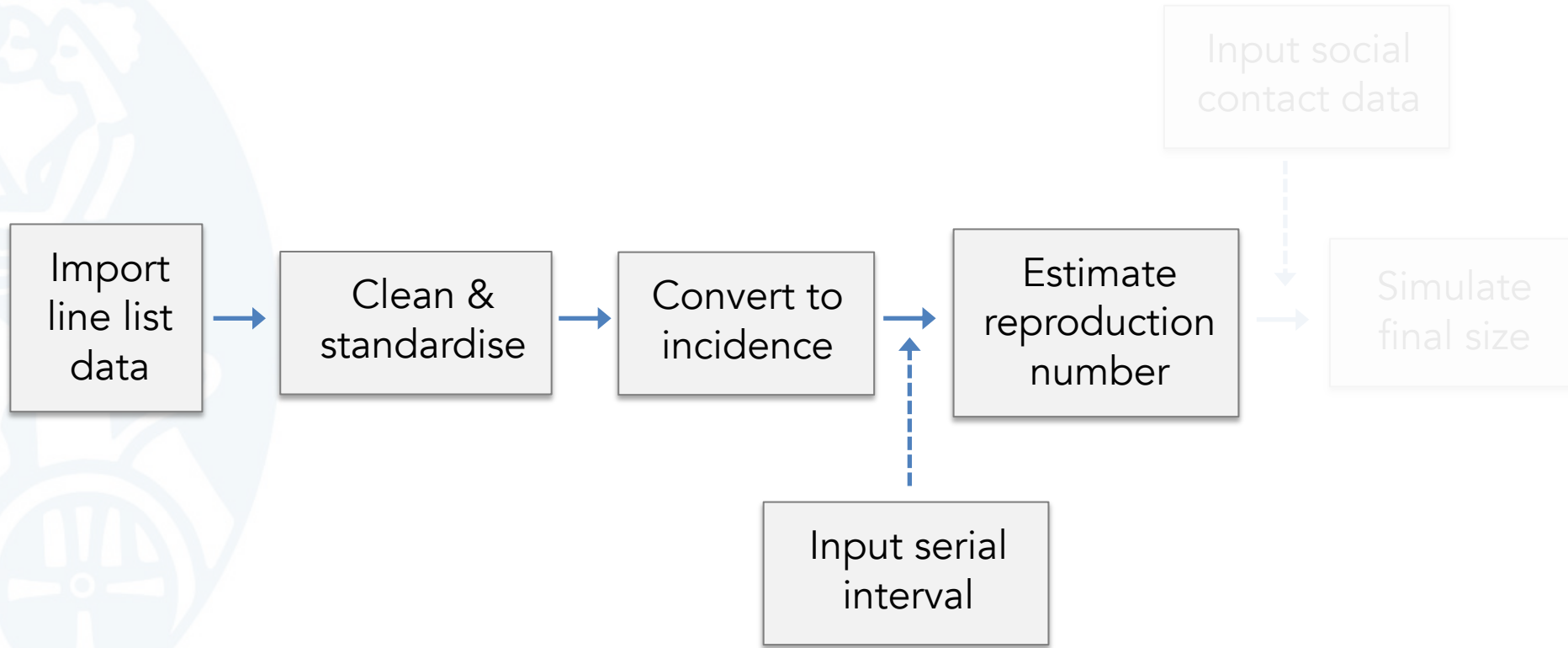
Calculate final size:



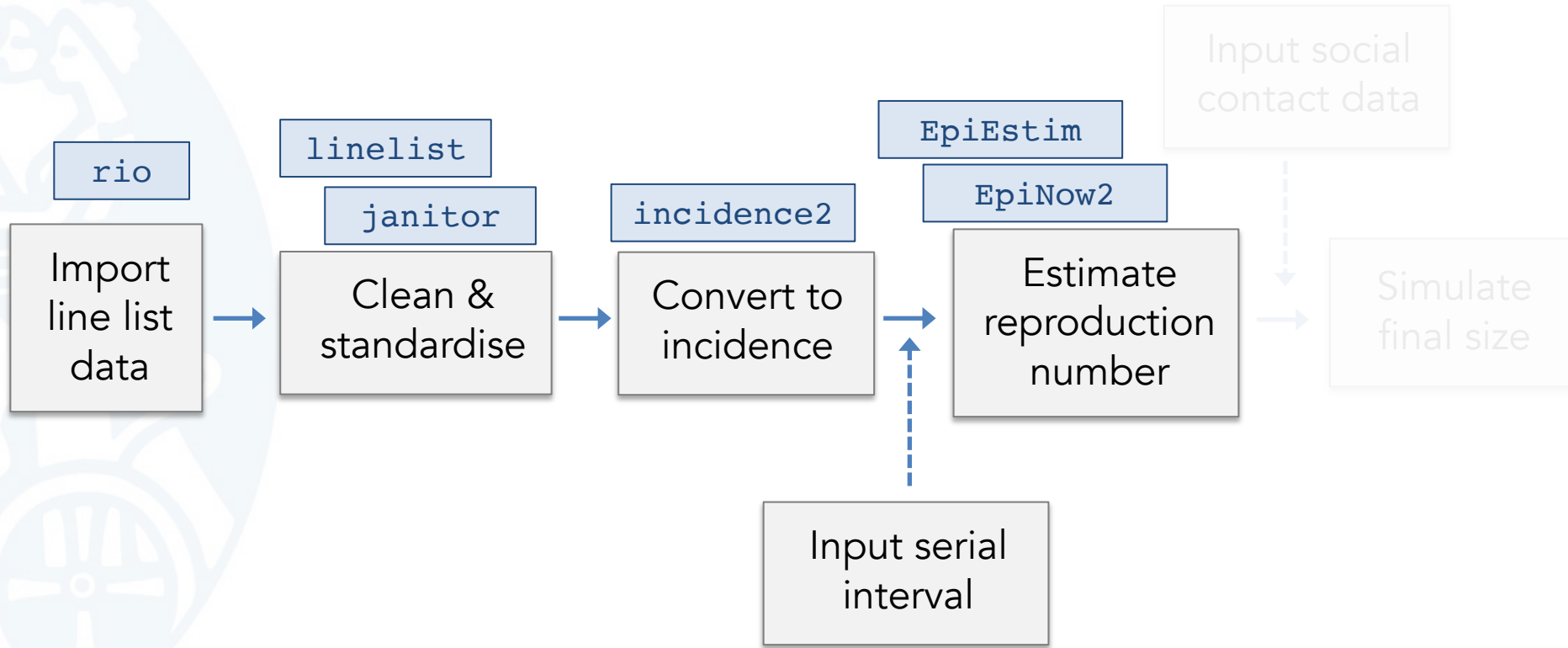
Propagate uncertainty:



Estimating R or R_0



Estimating R or R_0



Choose template:

New R Markdown

Document

Presentation

Shiny

From Template

Template: Using R Markdown Templates

- Custom theming {bslib}
- Legacy custom theming {bslib}
- Real-time theming {bslib}
- Transmissibility Report {episoap}
- Flex Dashboard {flexdashboard}
- Flex Dashboard themed with {bslib}
- reprex (lots of features) {reprex}
- reprex (minimal) {reprex}

This template contains multiple files. Create a new directory for these files:

Name: Untitled

Location: ~ Browse...

Create Empty Document

OK Cancel

Outbreak analytics pipelines

Work by Hugo Gruson et al



Select options:

An integer or character indicating the (fixed) size of the time interval used for computing the incidence. Passed as the 'interval' argument in 'incidence2:incidence()'.

week

Number of days to exclude from the estimation of Rt since data is likely to still be incomplete.

7

Number of days to include to get the latest observed value of Rt.

21

Should the serial interval distribution be extracted directly from the epiparameter package?

Name of the pathogen in the epiparameter database if 'use_parameter = TRUE'.

SARS_CoV_2_wildtype

Mean of the distribution for serial interval if not using value from epiparameter. Ignored if 'use_epiparameter = TRUE'.

4.2

Standard deviation of the distribution for serial interval if not using value from epiparameter. Ignored if 'use_epiparameter = TRUE'.

4.9

Choice of probability distribution for serial interval if not using value from epiparameter. Ignored if 'use_epiparameter = TRUE'.

gamma

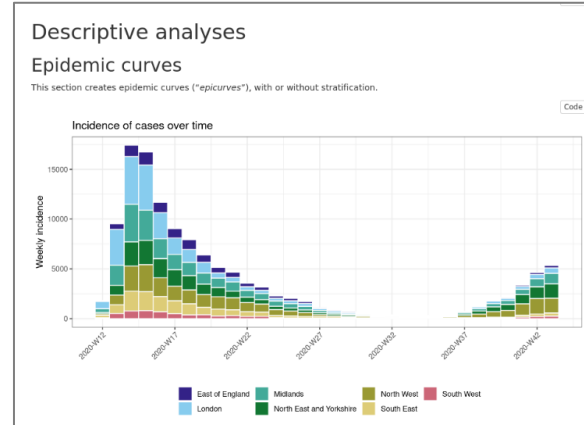
Name of file containing the count data over time (default: data/covid_hosp_uk_20201024.xlsx)

Browse... No file selected

Which R package to use for Rt estimation

- EpiEstim
- EpiNow2
- @centras
- Rt

Descriptive curves:



Choose template:

New R Markdown

Document

Presentation

Shiny

From Template

Template: Using R Markdown Templates

- Custom theming {bslib}
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- Real-time theming {bslib}
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- reprex (minimal) {reprex}

This template contains multiple files. Create a new directory for these files:

Name:

Location: Browse...

Create Empty Document

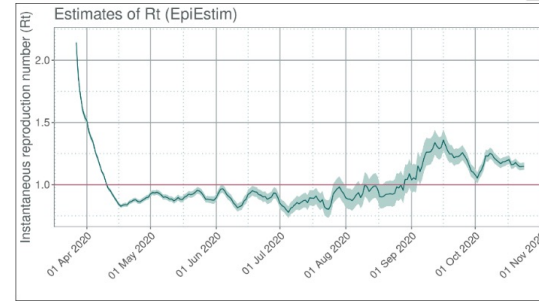
OK Cancel

Outbreak analytics pipelines

Work by Hugo Gruson et al



R estimation:



Select options:

An integer or character indicating the (fixed) size of the time interval used for computing the incidence. Passed as the 'interval' argument in 'incidence2::incidence()'.

week

Number of days to exclude from the estimation of Rt since data is likely to still be incomplete.

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gamma

Name of file containing the count data over time (default: data/covid_hosp_uk_20201024.xlsx)

Browse... No file selected

Which R package to use for Rt estimation

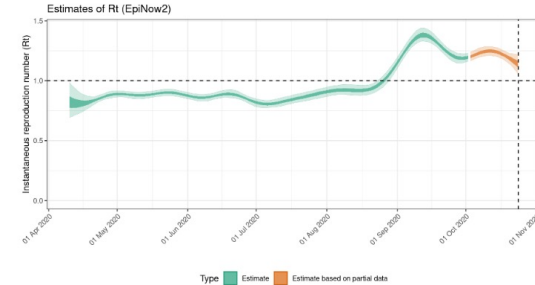
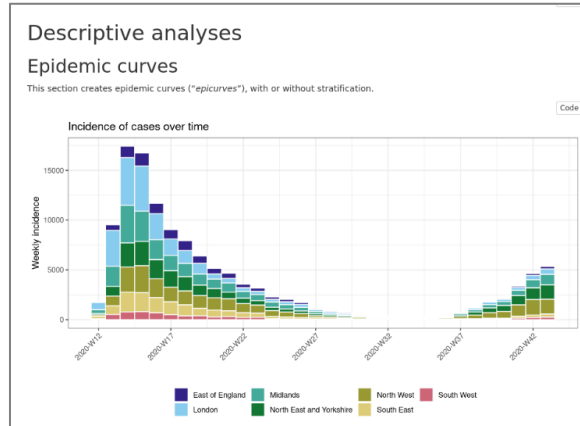
EpiEstim

EpiNow2

@centras

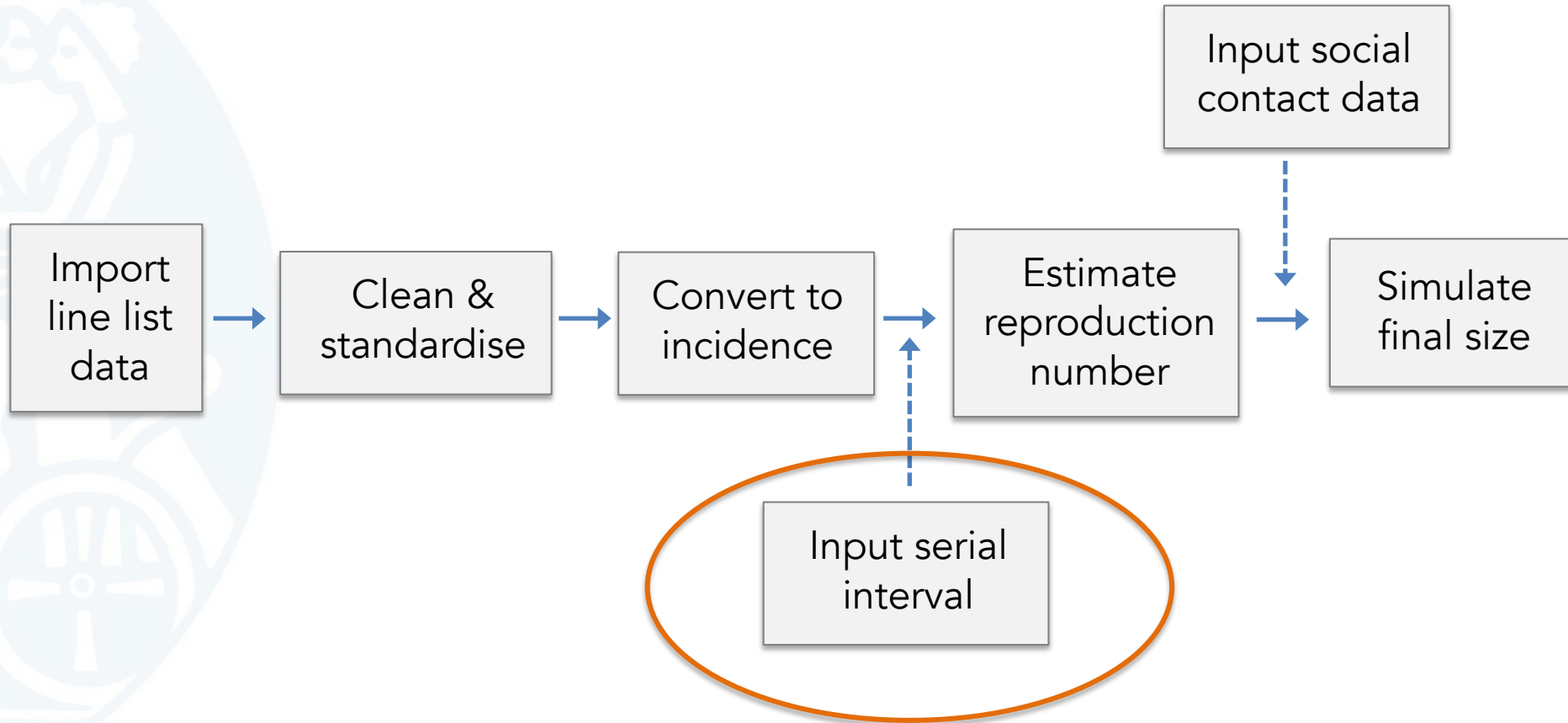
Ri


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]

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:

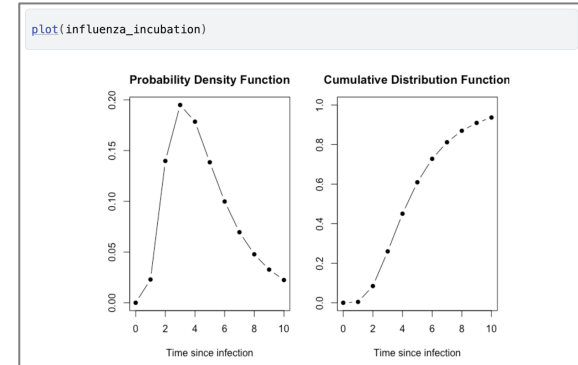
```
convert_gamma_summary_stats(mean = 2, sd = 2)
#> $shape
#> [1] 1
#>
#> $scale
#> [1] 2
```

```
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:



Work with Josh Lambert,
Carmen Tamayo Cuartero et al

WHO collaboratory community to generate standardized library

Collaboratory

Pandemic and Epidemic Intelligence

EpiParameter Community

[About](#) [Community](#) [News](#) [Resources](#) [GitHub](#)

About

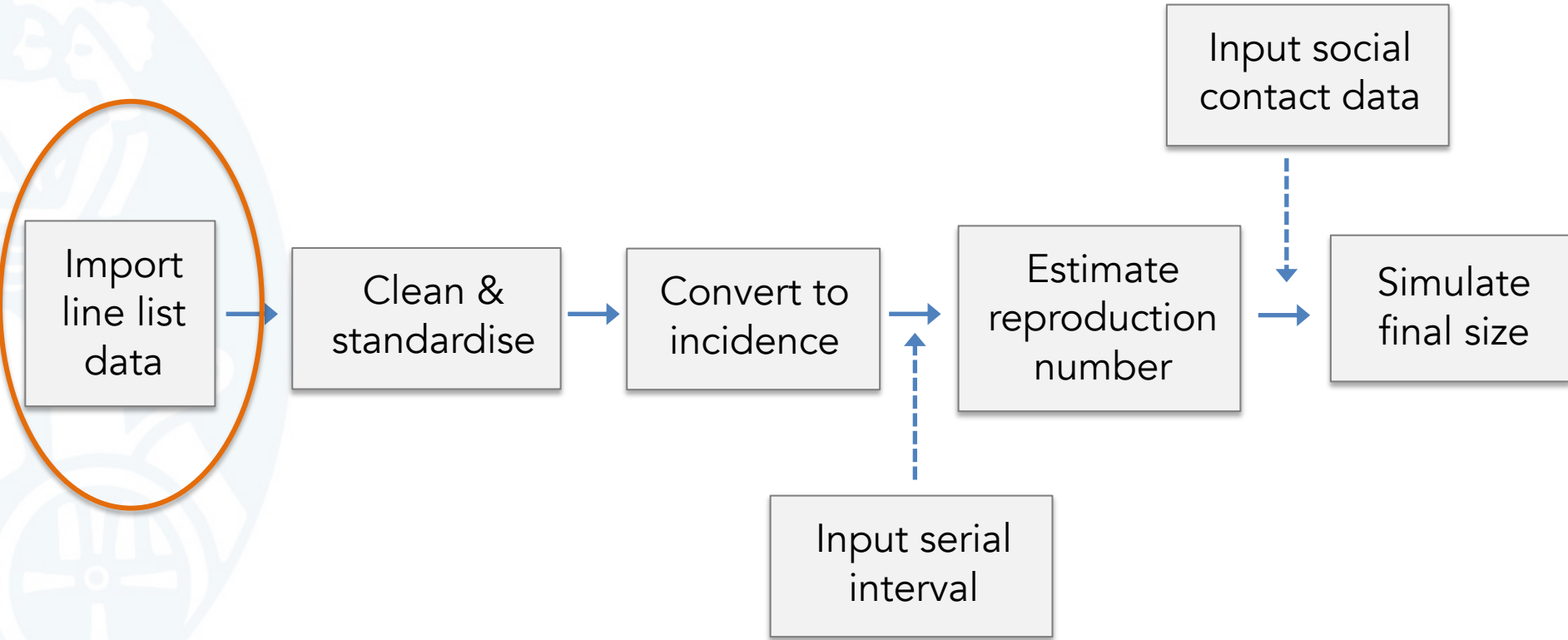
Overview

The epidemiological parameters community consist of a global collaborative working group coordinated by WHO, which aims to develop a global repository of epidemiological parameters. This repository will be publicly accessible by modellers, epidemiologists, subject matter experts and decision makers to inform mathematical models and public health response.

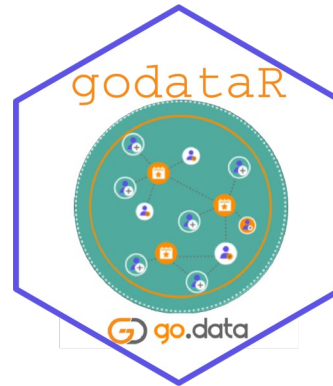
Epidemiological parameters are used by mathematical models that are critical to understand the transmission dynamics of pathogens and to determine the potential impact of outbreaks in terms of morbidity, mortality, and geographical spread over time.

github.com/WorldHealthOrganization/collaboratory-epiparameter-community

Processing epidemiological data

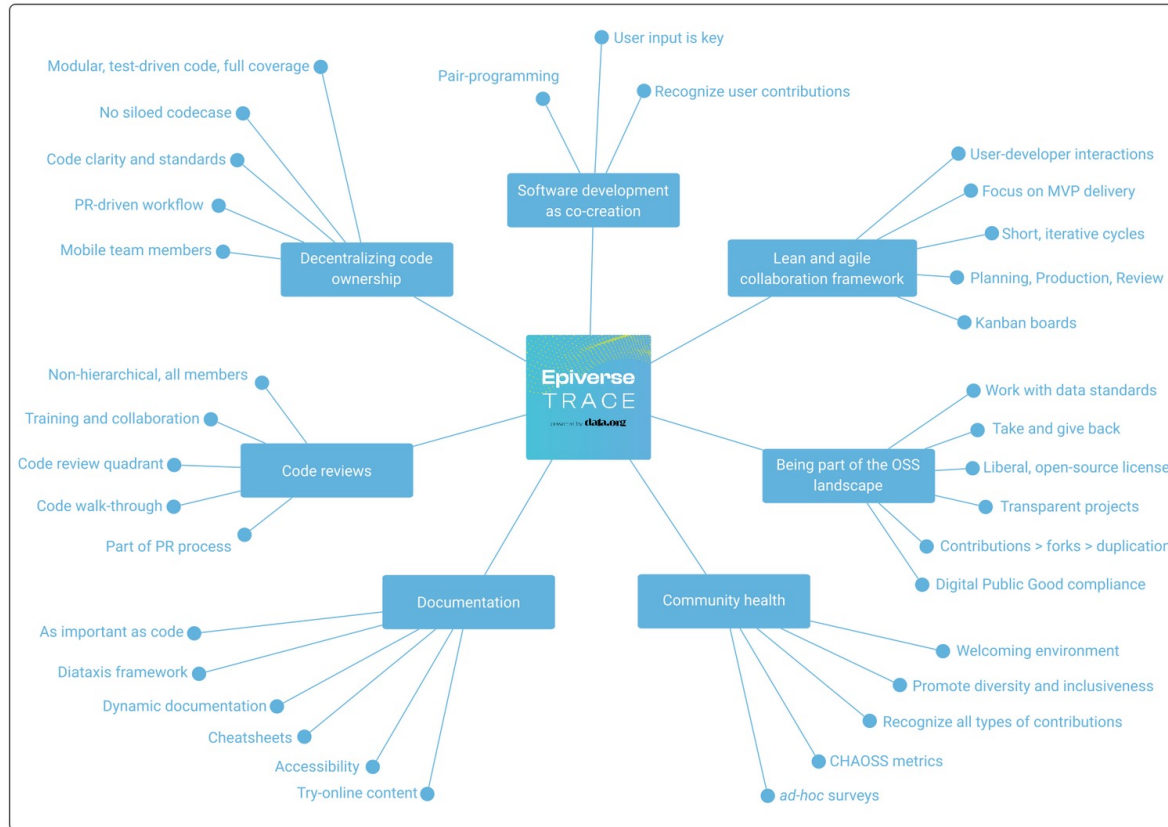


Importing, cleaning and analysing field data



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

Wider community blueprints for best practice



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

Episode 119 of the [#rstats @rweekly_org](#) Highlights podcast is out! [podverse.fm/episode/bvGTU...](#)

-  Dev containers with R and Quarto [@jimjam_slam](#)
-  Extending data frames [@joshua_lambert](#)
-  Solar system plots with {ggsolar} [@hrbmstr](#)

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)