

{epiparameter}



LONDON
SCHOOL of
HYGIENE
& TROPICAL
MEDICINE




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Project Aims

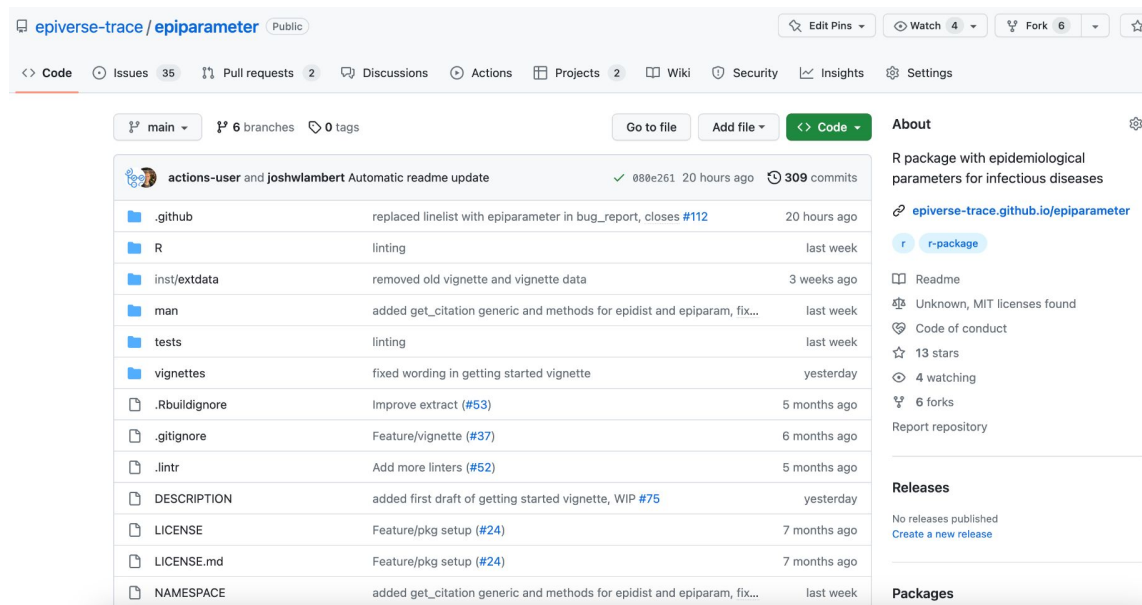
The Epiverse epiparameter project aims to facilitate outbreak analysis by providing a modular and interoperable software tool and database to integrate into epidemiological pipelines.

It has two central components:

1. Build a, hitherto lacking, library of epidemiological parameters
2. Develop an  package for working with epidemiological parameters

Structure of project

- Everything is housed in a single R package: {epiparameter}
- The project is open-source and developed on Github 



epiverse-trace / epiparameter Public

<> Code Issues 35 Pull requests 2 Discussions Actions Projects 2 Wiki Security Insights Settings

main 6 branches 0 tags

Go to file Add file <> Code

actions-user and joshwlambert Automatic readme update ✓ 088e261 20 hours ago 309 commits

File	Commit Message	Time
.github	replaced linelist with epiparameter in bug_report, closes #112	20 hours ago
R	linting	last week
inst/extdata	removed old vignette and vignette data	3 weeks ago
man	added get_citation generic and methods for epidist and epiparam, fix...	last week
tests	linting	last week
vignettes	fixed wording in getting started vignette	yesterday
.Rbuildignore	Improve extract (#53)	5 months ago
.gitignore	Feature/vignette (#37)	6 months ago
.lintr	Add more linters (#52)	5 months ago
DESCRIPTION	added first draft of getting started vignette, WIP #75	yesterday
LICENSE	Feature/pkg setup (#24)	7 months ago
LICENSE.md	Feature/pkg setup (#24)	7 months ago
NAMESPACE	added get_citation generic and methods for epidist and epiparam, fix...	last week

About

R package with epidemiological parameters for infectious diseases

[epiverse-trace.github.io/epiparameter](https://github.com/epiverse-trace/epiparameter)

r r-package

Readme

Unknown, MIT licenses found

Code of conduct

13 stars

4 watching

6 forks

Report repository

Releases

No releases published

[Create a new release](#)

Packages

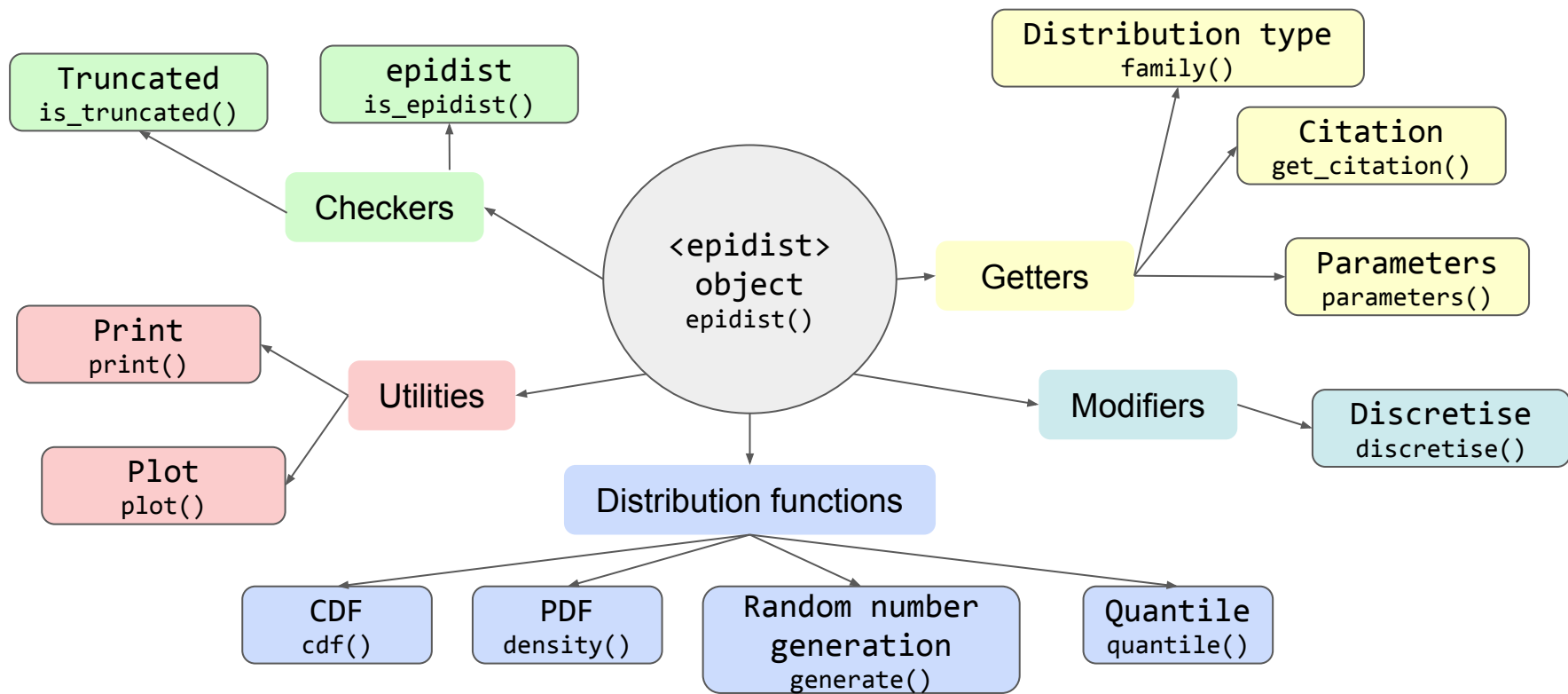
<https://github.com/epiverse-trace/epiparameter>

Technical details

- {epiparameter} adds three (S3) classes for working with epidemiological parameters
 - <epidist>
 - <epiparam>
 - <vb_epidist>
- Continuous integration (using Github Actions)
 - Checks package is working and passes testing suite
 - Parameter database validation

Technical details

Data objects/classes as interoperable units



Documentation

epiparameter 0.0.0.9000 Get started Reference Articles ▾

Getting Started with {epiparameter}

Source: [vignettes/epiparameter.Rmd](#)

It is often the case that in an infectious disease outbreak epidemiological parameters are required in order to characterise and model the dynamics of disease transmission and evaluate control strategies. In those scenarios, epidemiological parameters are commonly retrieved from the literature, and there is currently no library of parameters in order to contrast and compare different reported parameters for a range of infectious diseases and pathogens, from different published studies over time, of which some may be meta-analyses.

The {epiparameter} R package is a library of epidemiological parameters, with classes to handle this data and a set of functions to manipulate and use epidemiological parameters and distributions. The package also contains functionality for converting and extracting distribution parameters from summary statistics.

Use case

An outbreak of a known or potentially novel pathogen is detected and the parameters and a delay distribution (e.g. incubation period or serial interval) is required.

{epiparameter} can provide these distributions from a selection of published sources in order to provide reliable epidemiological parameters.



epiparameter 0.0.0.9000 Get started Reference Articles ▾

Search for



Data Collation and Synthesis Protocol

Source: [vignettes/data_protocol.Rmd](#)

About the package

The [epiparameter R package](#) contains a library of epidemiological distribution data and functions that read and handle this data. The delay distributions describe the time between two events in epidemiology, for example incubation periods, serial interval and onset-to-death; while the offspring distributions describe the number of secondary infections from a primary infection in disease transmission. The library is compiled by a process of collecting, reviewing and extracting data from peer-reviewed literature¹, including research articles, systematic reviews and meta-analyses.

To prevent bias in the collection or assessment of the data, a well-defined methodology of searching and refining, just as with other systematic reviews and meta-analyses, is required. This document aims to provide transparency on the methodology used by the [epiparameter](#) maintainers by outlining the steps taken at each stage of the data handling. This document should also facilitate reproducibility in the searches, results and appraisal steps.

There is a large body of work on the methods to best conduct literature searches and data collection as part of systematic reviews and meta-analyses², which we use as the basis for our protocol. These sources are:

- [Cochrane Handbook](#)
- [PRISMA](#)



On this page

About the package

Objective of epiparameter

Scope of package

Guide to identifying distributions in the literature

Guide to data refinement once sources identified

Guide to extracting parameters

Data quality assessment in epiparameter

Guide to the epiparameter review process

Updating parameters in the database

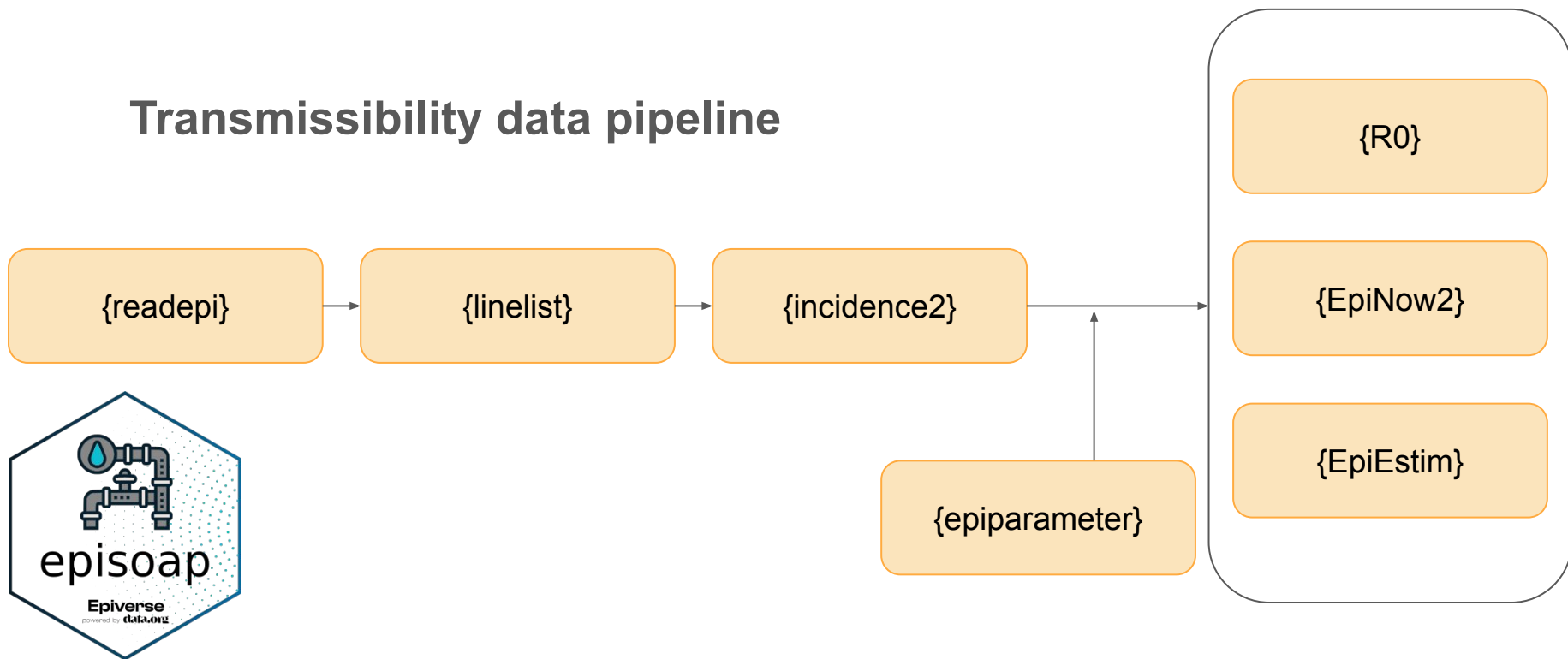
Database of excluded papers

<https://epiverse-trace.github.io/epiparameter/>

Applications

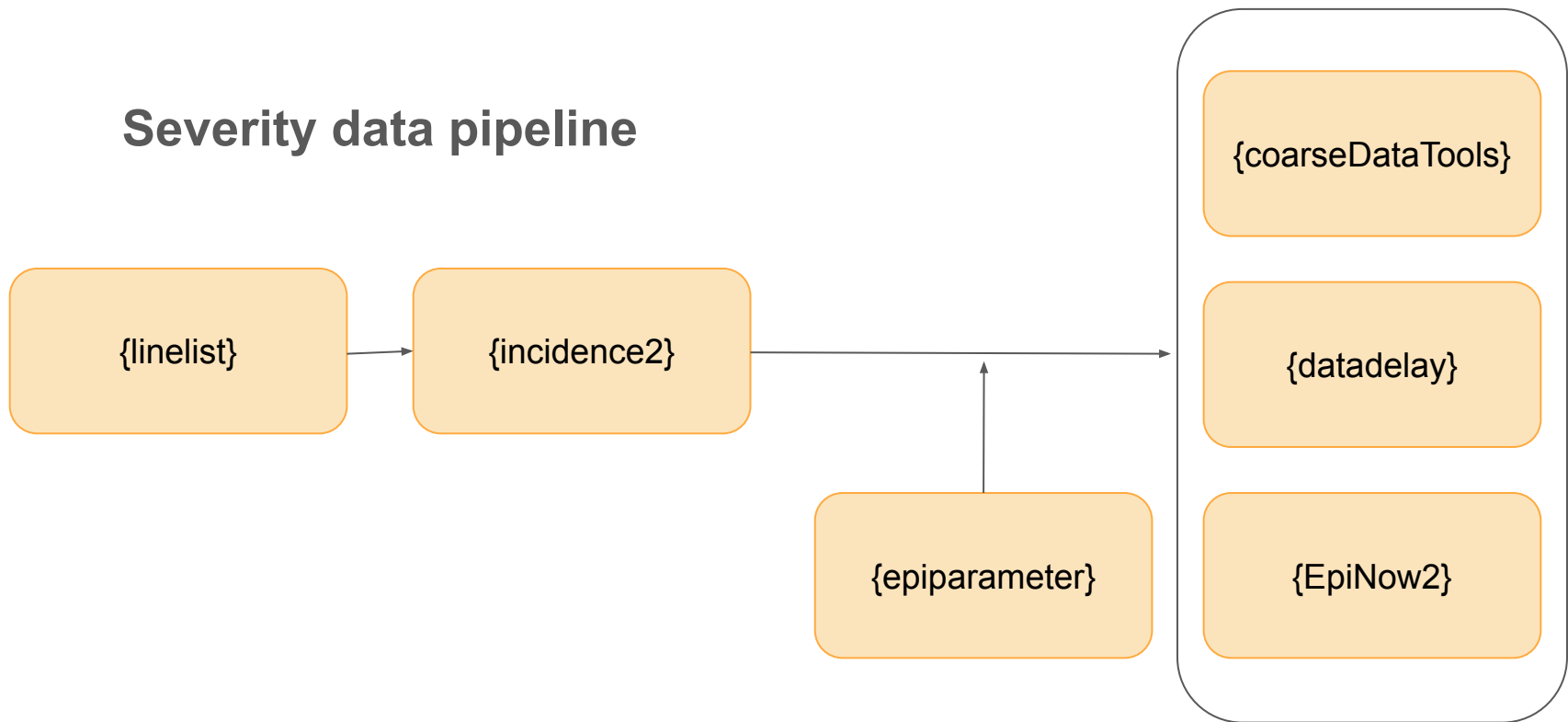
Reproduction number estimation

Transmissibility data pipeline



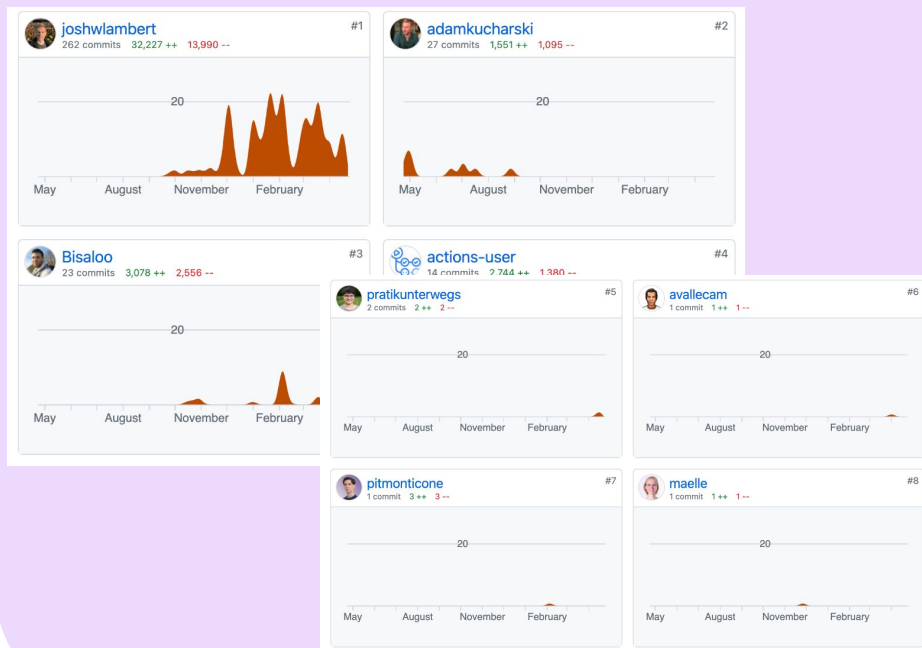
Applications

Severity data pipeline



Contributors and community

GitHub engagement



Direct community engagement

Epiverse-TRACE Winter 2023 showcase

EPIPARAMETER FINALSIZE EPISOAP SHOWCASE

AUTHORS
Anna Carnegie
Pratik Gupte
Joshua Lambert
Hugo Gruson

PUBLISHED
January 25, 2023

This showcase is part of a regular cycle of online meetings to present tools for epidemiology.

Time	Item	Presenter
16:00 - 16:05	Welcome	Anna
	<ul style="list-style-type: none">Intro to Epiverse-TRACEPurpose of the session	
	<ul style="list-style-type: none">Housekeeping - 10 mins per PKG, 5 min Q&A after each. Room at the end for open discussion	

On this page
[finalsize slides](#)
[epiparameter slides](#)
[episoap slides](#)

Thank you for listening

Any questions?

