

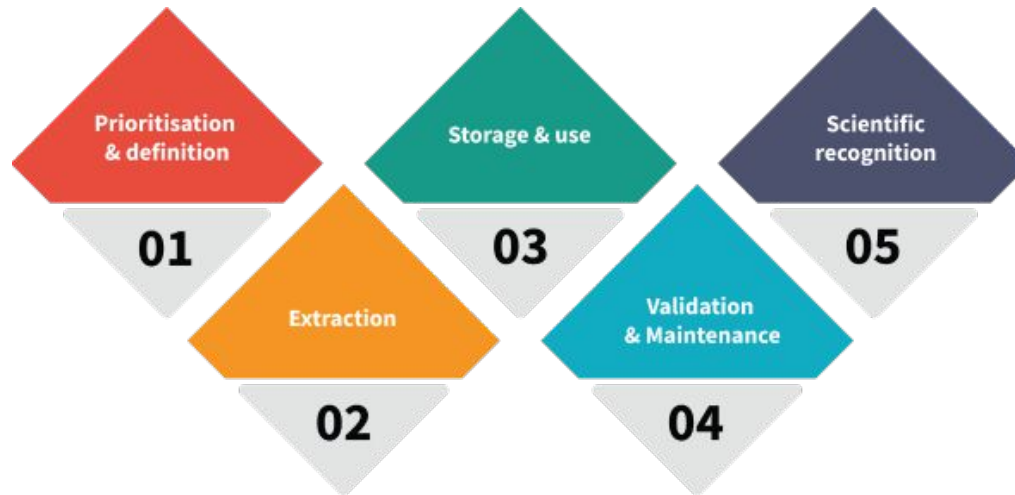
Epiparameter Collaboration Workstream 3: **Storage** & **Use**

Intro to the {epiparameter} R
package

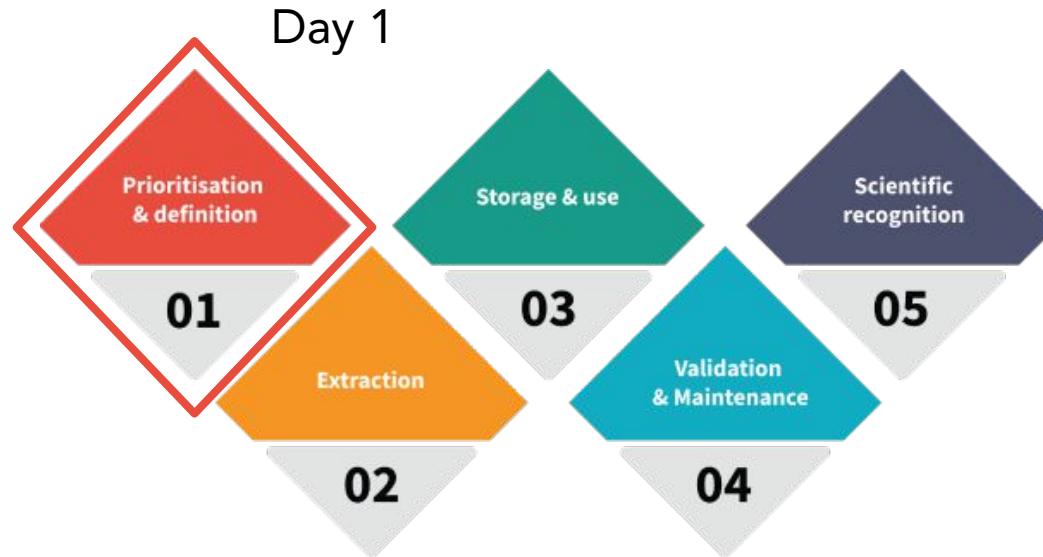
Pt. I

Epiparameter Collaboration Workstream 3: Storage & Use

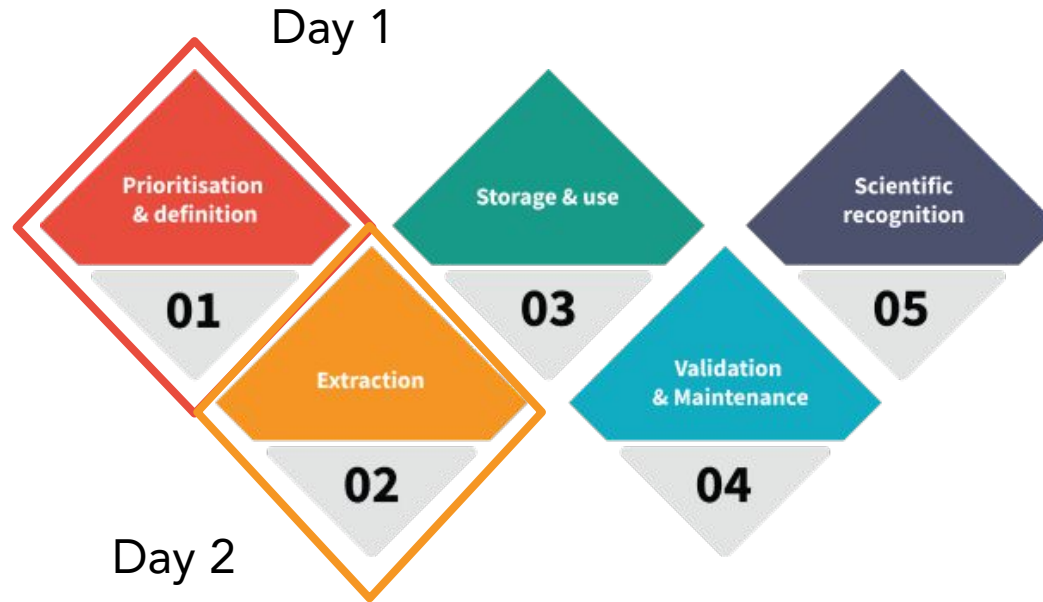
Collaboratory Epiparameter Community



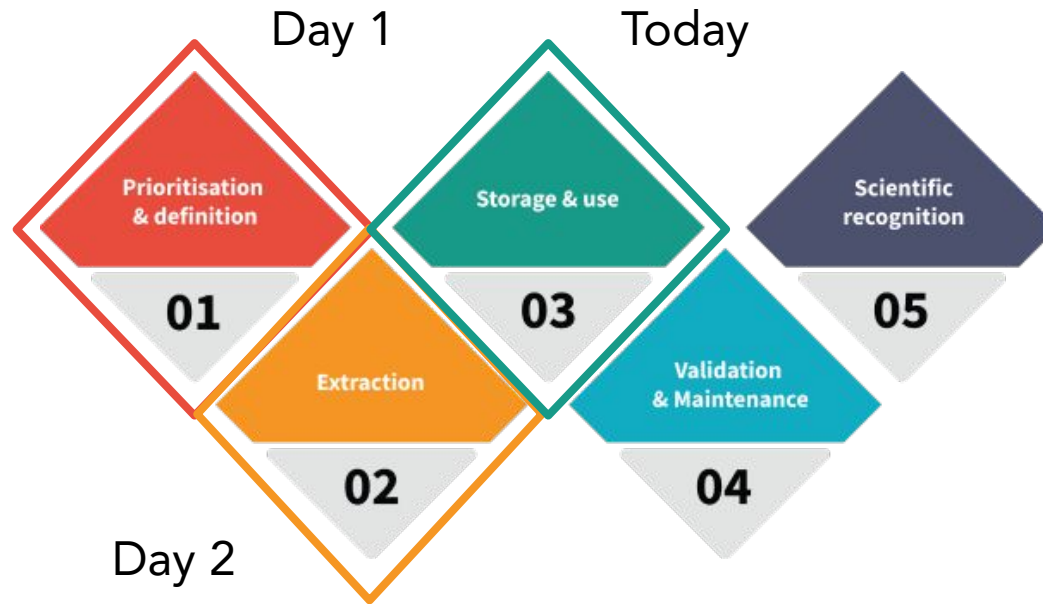
Collaboratory Epiparameter Community



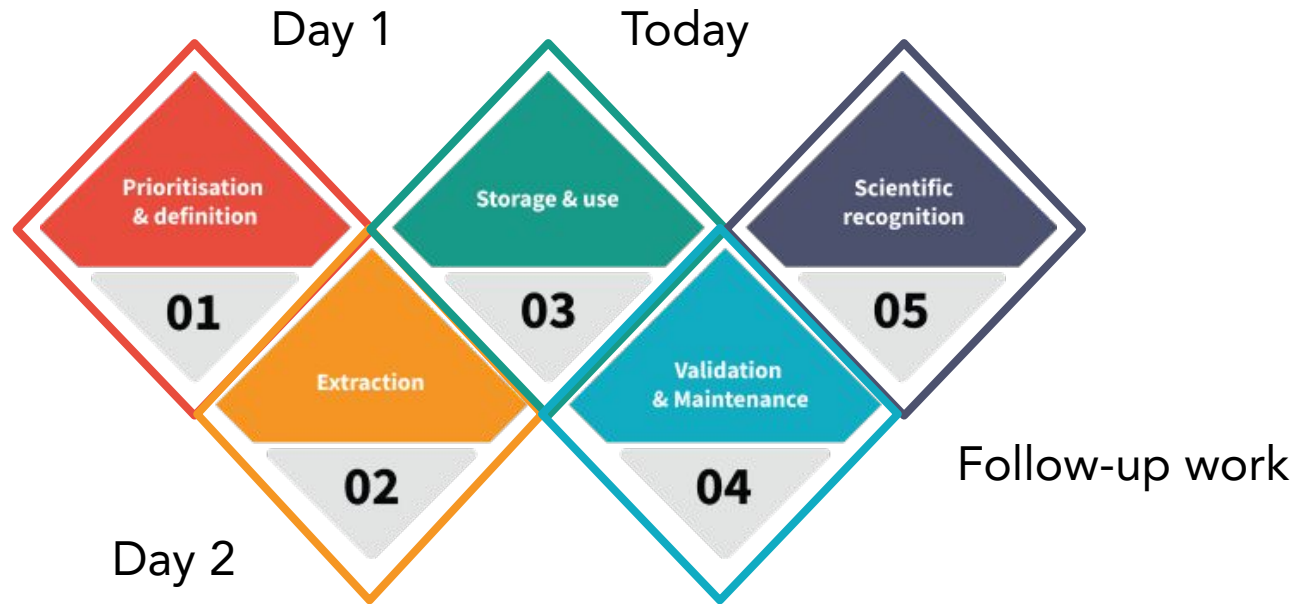
Collaboratory Epiparameter Community



Collaboratory Epiparameter Community

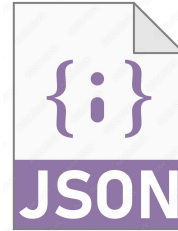
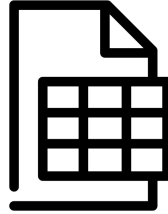
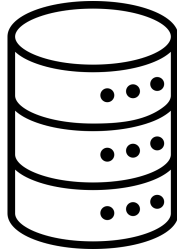


Collaboratory Epiparameter Community

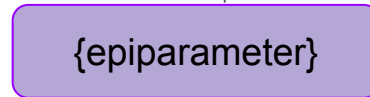
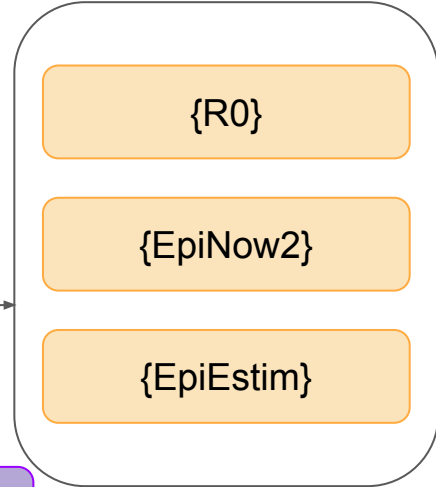
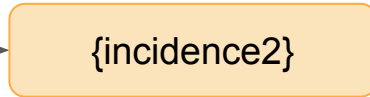


Workstream 3

Storage



Use



Pt. II

A brief intro to the {epiparameter} R package



Project Aims

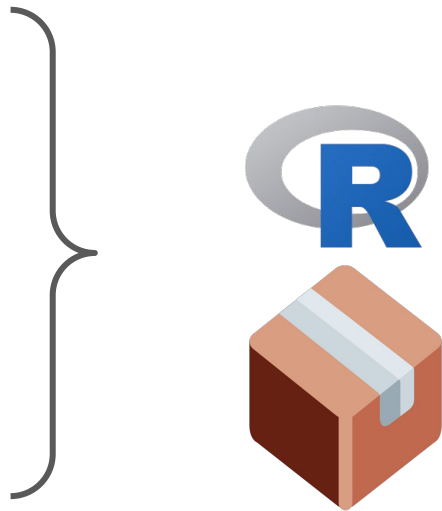
Objective of the `{epiparameter}` project is to facilitate outbreak analysis by providing:

- A library of epidemiological parameters
- Modular and interoperable tool to integrate into epidemiological pipelines.

Project Aims

Objective of the {epiparameter} project is to facilitate outbreak analysis by providing:

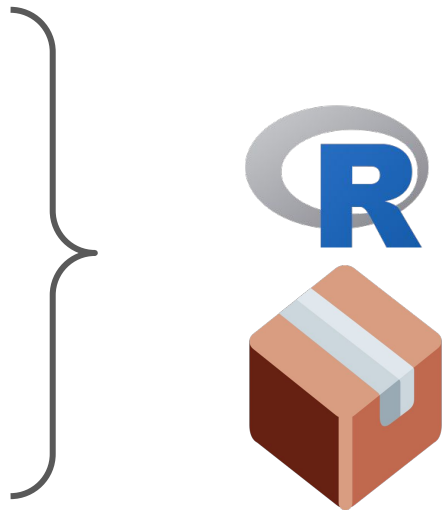
- A library of epidemiological parameters
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Project Aims

Objective of the {epiparameter} project is to facilitate outbreak analysis by providing:

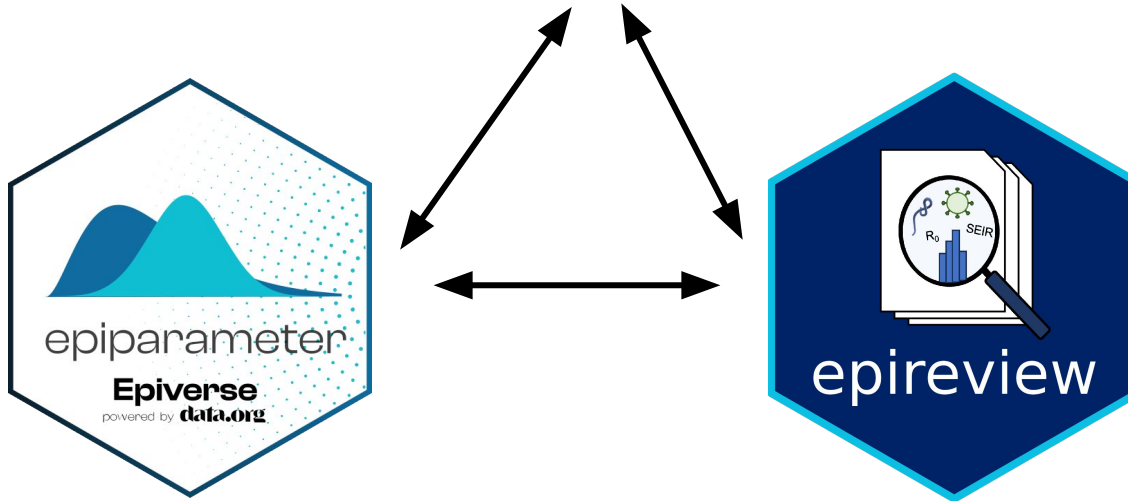
- A library of epidemiological parameters
- Modular and interoperable tool to integrate into epidemiological pipelines.



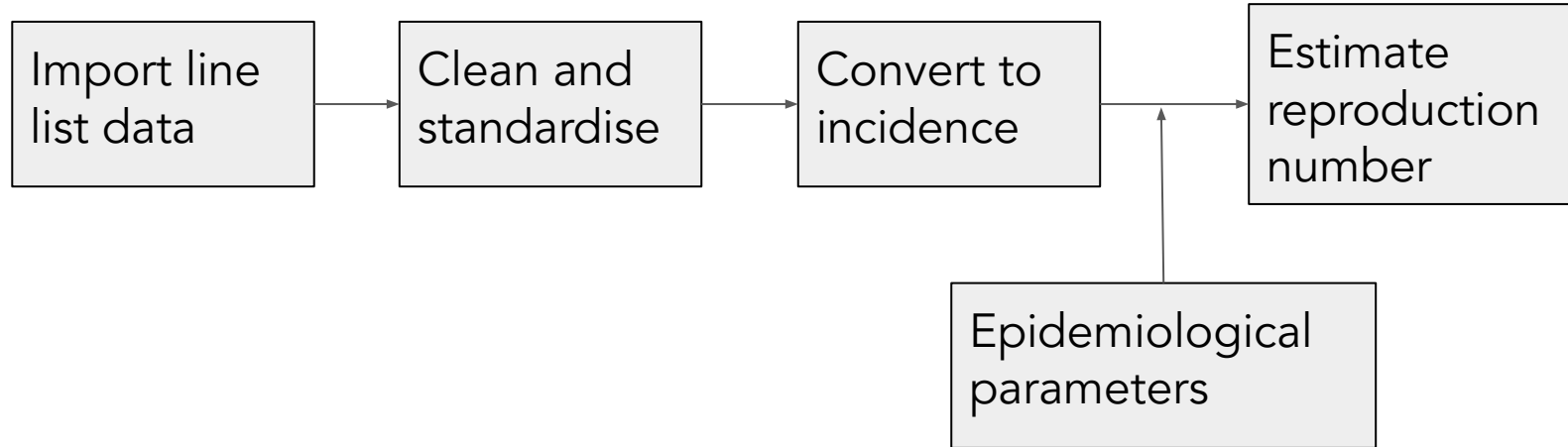
Fully open-source development of code and parameter library on GitHub

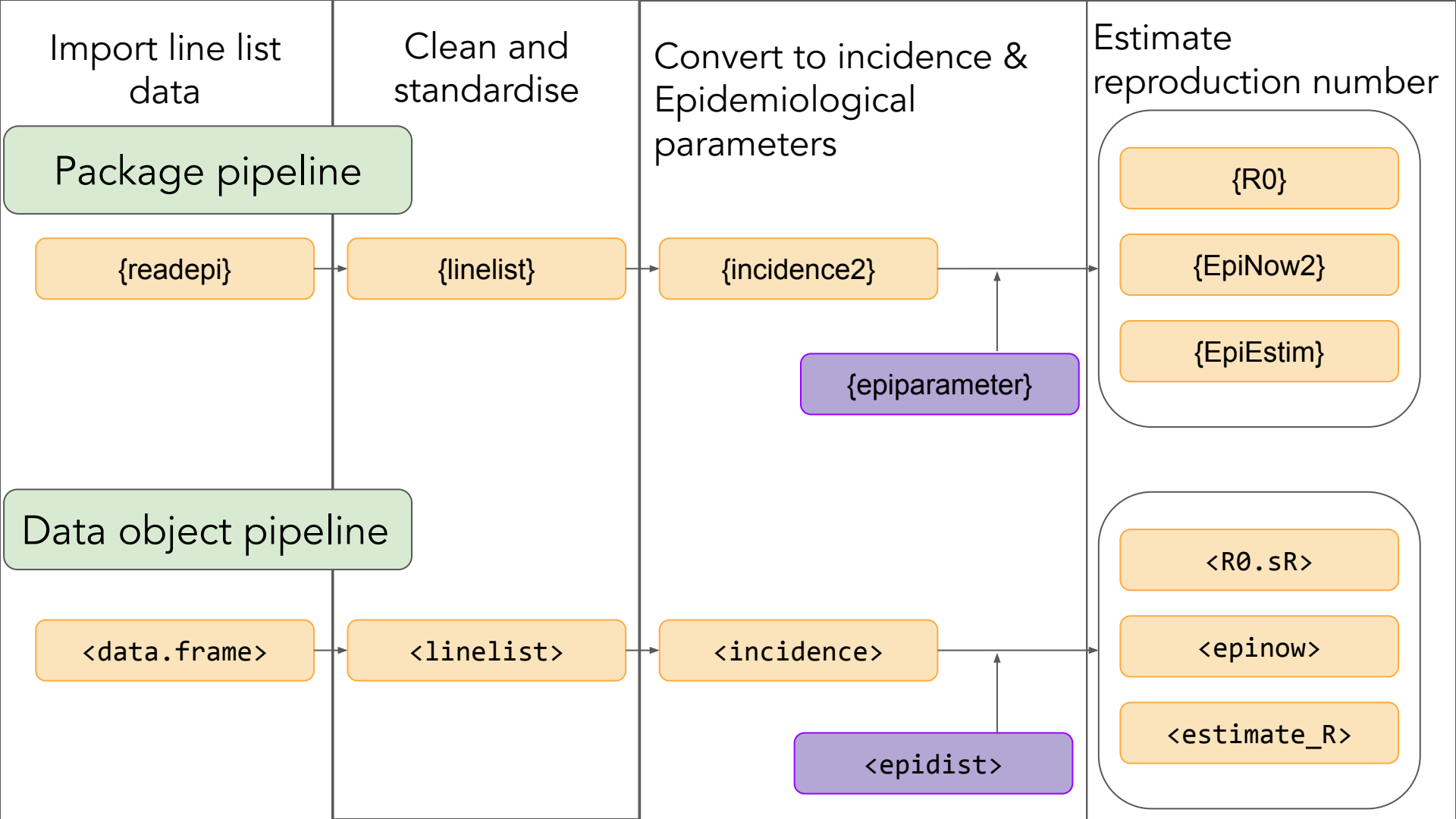


Redefining the project scope

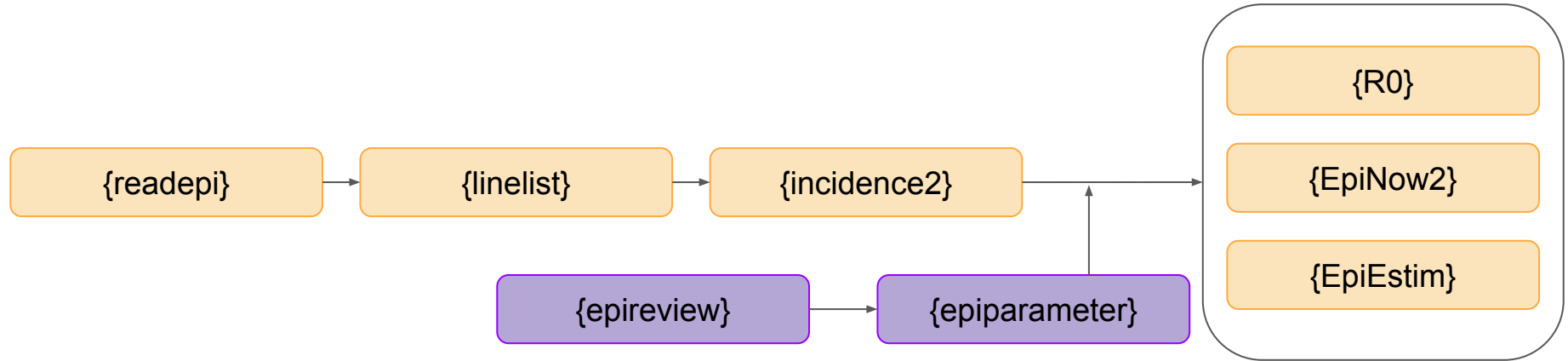


Epidemiological task workflow

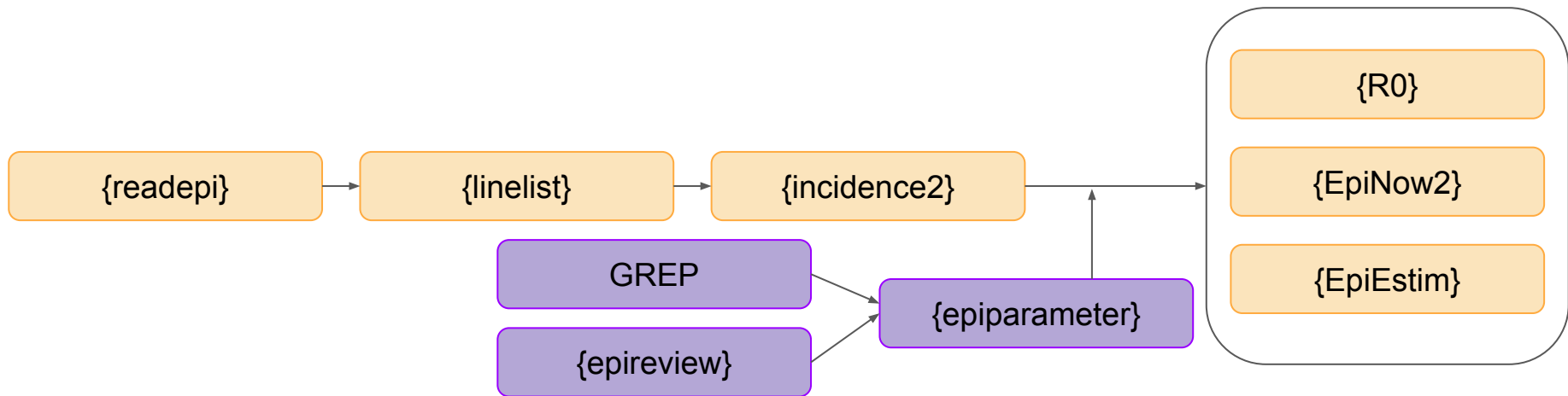




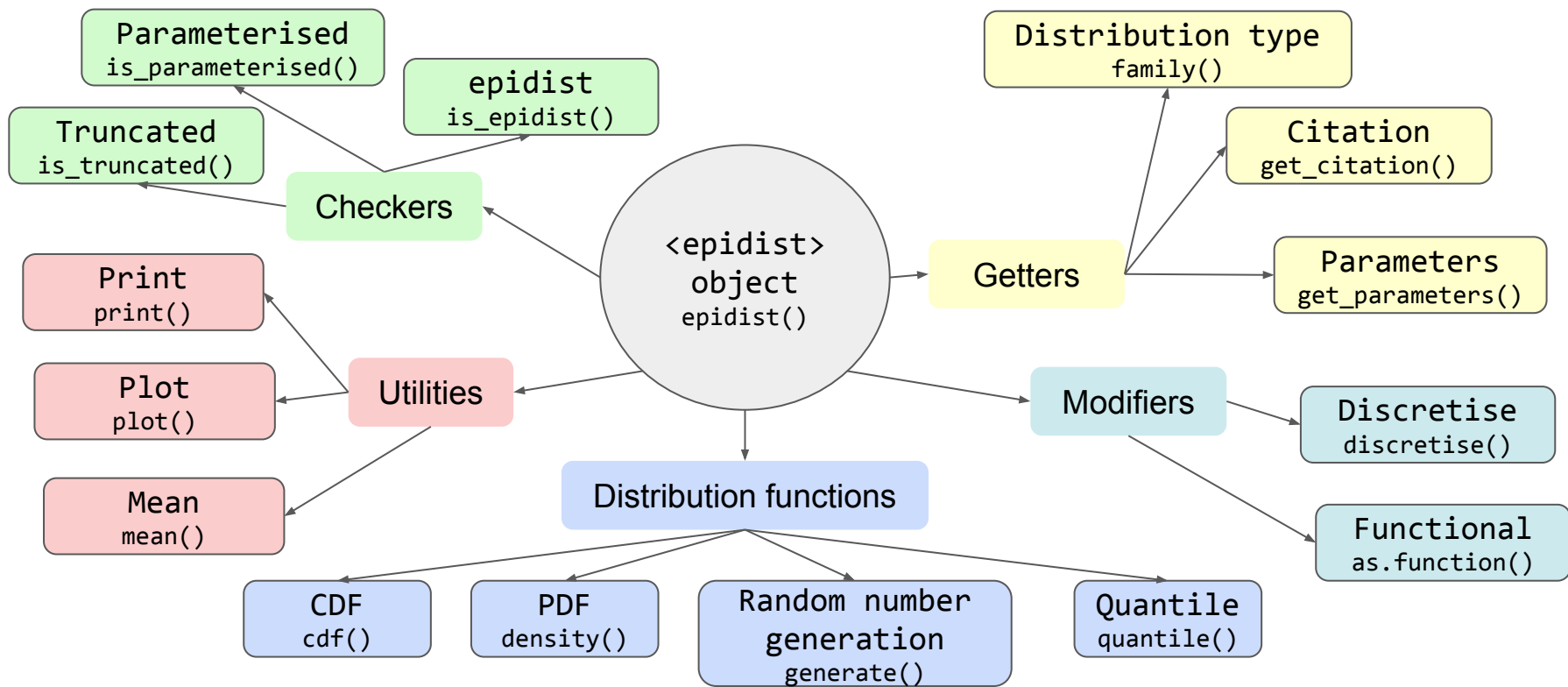
Epidemiological task workflow



Epidemiological task workflow



Benefits and shortcuts of data objects



Epidemiological parameters from {epiparameter} & {epireview}

- ❑ Access parameter library: `epidist_db()`
- ❑ Manually create parameter object: `epidist()`
- ❑ Convert {epireview} data to parameter object: `as_epidist()`

Other functionality from {epiparameter}

- ❑ Parameter conversion to and from summary statistics:

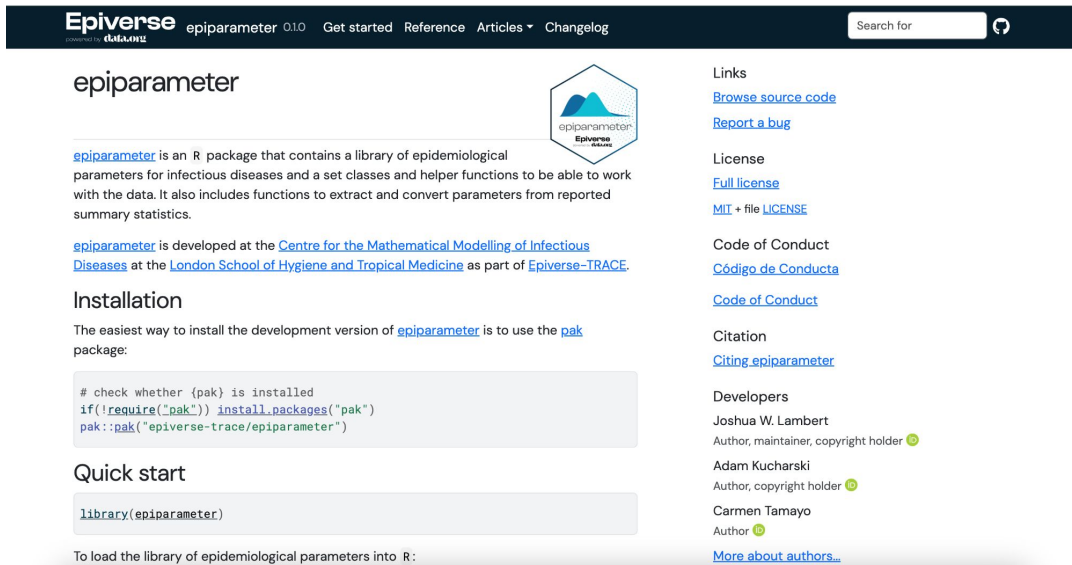
`convert_params_to_summary_stats()` &
`convert_summary_stats_to_params()`

- ❑ Parameter extraction from quantiles or range:


`extract_param()`

Documentation


- ❏ Get Started
- ❏ Extraction & Conversion
- ❏ Data Collation Protocol
- ❏ Extraction Bias
- ❏ Design Principles



The screenshot shows the documentation page for the `epiparameter` R package. The header includes the EpiVerse logo, the package name `epiparameter 0.1.0`, and navigation links: [Get started](#), [Reference](#), [Articles](#), and [Changelog](#). A search bar is on the right. The main content area has a title `epiparameter` and a hexagonal logo. The text describes the package as an R library for epidemiological parameters. It mentions development at the Centre for the Mathematical Modelling of Infectious Diseases at the London School of Hygiene and Tropical Medicine. The **Installation** section provides the easiest way to install the development version using the `pak` package, with a code block showing the installation and checking process. The **Quick start** section shows the command to load the library. On the right, there are links for **Links** (source code, bug report), **License** (full license, MIT, LICENSE), **Code of Conduct** (conduct code, code of conduct), **Citation** (citing package), and **Developers** (Joshua W. Lambert, Adam Kucharski, Carmen Tamayo).

EpiVerse epiparameter 0.1.0 [Get started](#) [Reference](#) [Articles](#) [Changelog](#) 

epiparameter



`epiparameter` is an R package that contains a library of epidemiological parameters for infectious diseases and a set classes and helper functions to be able to work with the data. It also includes functions to extract and convert parameters from reported summary statistics.

`epiparameter` is developed at the [Centre for the Mathematical Modelling of Infectious Diseases](#) at the [London School of Hygiene and Tropical Medicine](#) as part of [EpiVerse-TRACE](#).

Installation

The easiest way to install the development version of `epiparameter` is to use the `pak` package:

```
# check whether {pak} is installed
if(!require("pak")) install.packages("pak")
pak::pak("epiverse-trace/epiparameter")
```

Quick start

```
library(epiparameter)
```

To load the library of epidemiological parameters into R:

Links

- [Browse source code](#)
- [Report a bug](#)

License

- [Full license](#)
- [MIT](#) + file [LICENSE](#)




Code of Conduct

- [Código de Conducta](#)
- [Code of Conduct](#)

Citation

- [Citing epiparameter](#)

Developers

- Joshua W. Lambert
Author, maintainer, copyright holder 
- Adam Kucharski
Author, copyright holder 
- Carmen Tamayo
Author 

[More about authors...](#)

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

Pt. III

Overview of Day 3

Rationale for today's exercises

Day 1

Idea for EpiParameter workshop: explore range of tasks for which users will access the GREP database and assess this database's adequacy when applied to these tasks



Day 3

Apply existing EpiParameter databases and tooling to answer use cases and assess the their adequacy when applied to these tasks

Day 3: Assessing tooling for **storage** and **use**

Morning session		
9:00 – 9:10	Introduction to the Epiverse {epiparameter} project	Plenary session
9:10 – 9:30	Introduction to the {epiparameter} R package	Plenary session
9:30 – 11:00	Testing use cases to evaluate existing tools	Working groups
11:00 – 11:30	<i>Coffee break</i>	
11:30 – 13:00	Continue testing use cases, adding feedback to google document or on GitHub	Working groups
Afternoon session		
14:00 – 15:30	Working groups finalise reviewing and prepare something (slides and/or oral presentation) to share with the wider group.	Working groups
15:30 – 15:45	<i>Coffee break</i>	
15:45 – 16:30	Working group presents to the wider group to share their findings. Discussion time in this session can help outline high priority requirements for the GREP or R packages.	Working groups
16:30 – 16:45	Closing remarks by project leads: Julia, Lisa, Adam, Anne	Plenary session
16:45 – 17:00	Farewell	Plenary session

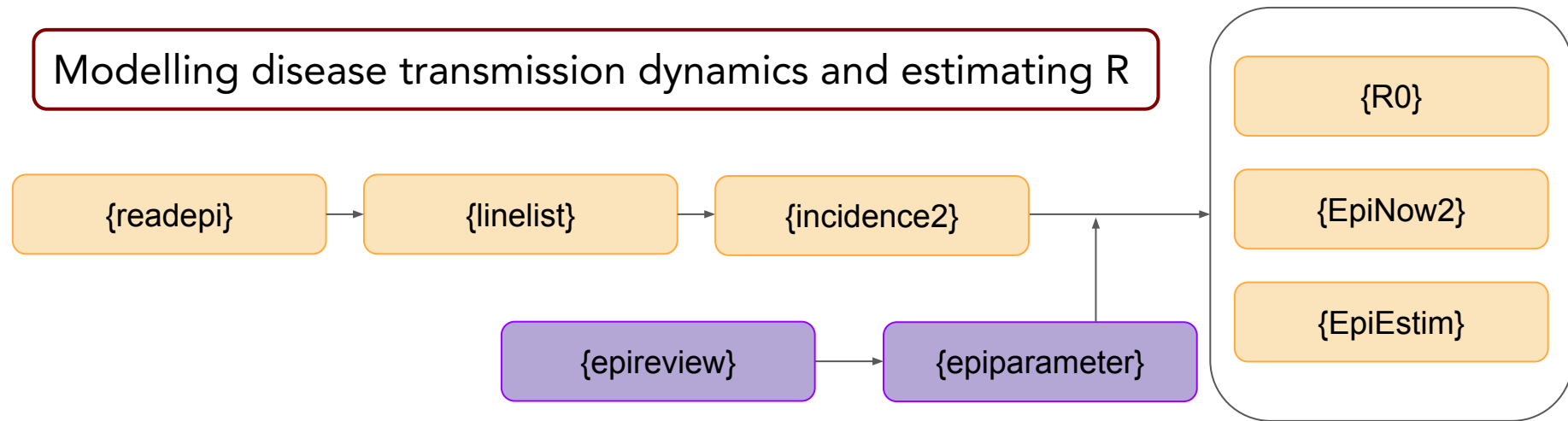
9:30 – 11:30

Testing use cases to evaluate existing tools

Working groups

Analytics pipeline

Modelling disease transmission dynamics and estimating R



11:30 – 12:00

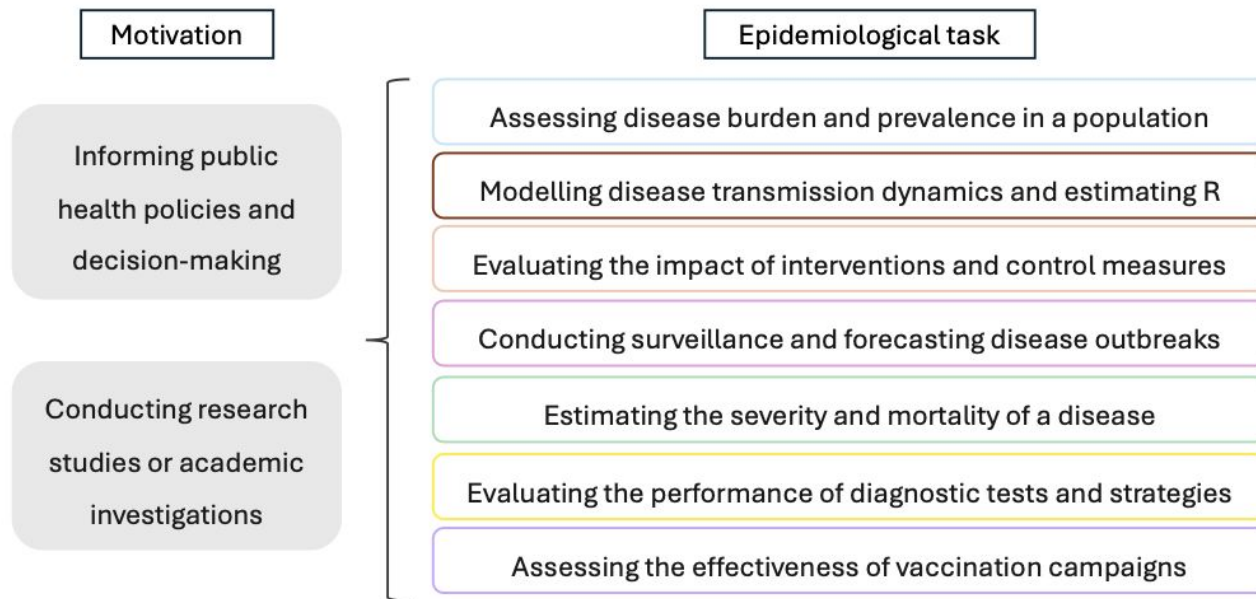
Coffee break

9:30 – 11:30

Testing use cases to evaluate existing tools

Working groups

Analytics pipeline



11:30 – 12:00

Coffee break

11:30 – 13:00

Continue testing use cases, adding feedback to google document or on GitHub

Working groups



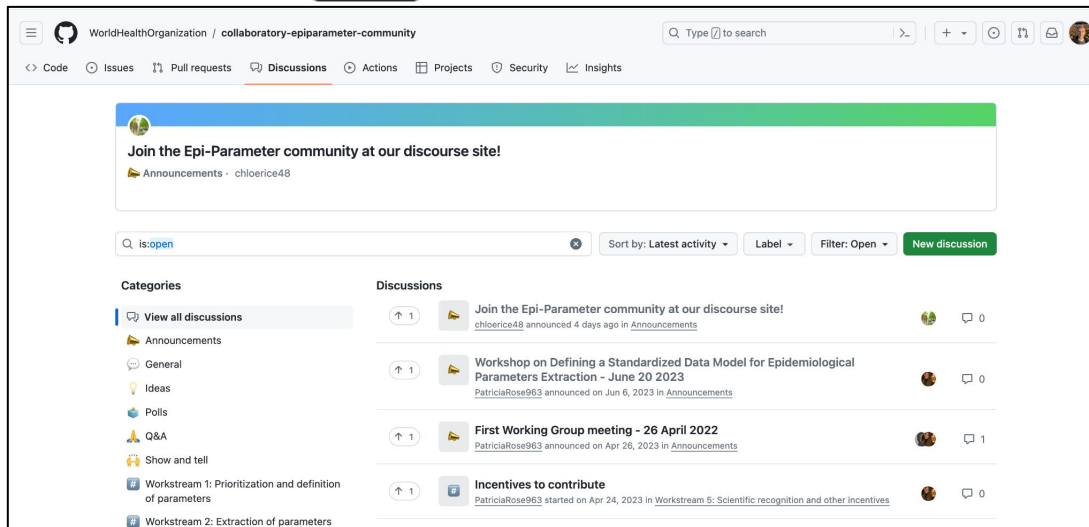
Issues



Pull requests



Discussion board



<https://github.com/WorldHealthOrganization/collaboratory-epiparameter-community/discussions>

14:00 – 15:30

Working groups finalise reviewing and prepare something (slides and/or oral presentation) to share with the wider group.

Working groups

Add slide(s) to slide desk

Name ↑



Day3ParticipantSlides



WG1_Tooling_assessment



WG2_Tooling_assessment



WG3_Tooling_assessment



WG4_Tooling_assessment



11:30 – 12:00

Coffee break

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Thanks for listening

Any Questions?



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