



MRC Centre for
Global Infectious
Disease Analysis

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epireview and the Pathogen Epidemiology Review Group (PERG)

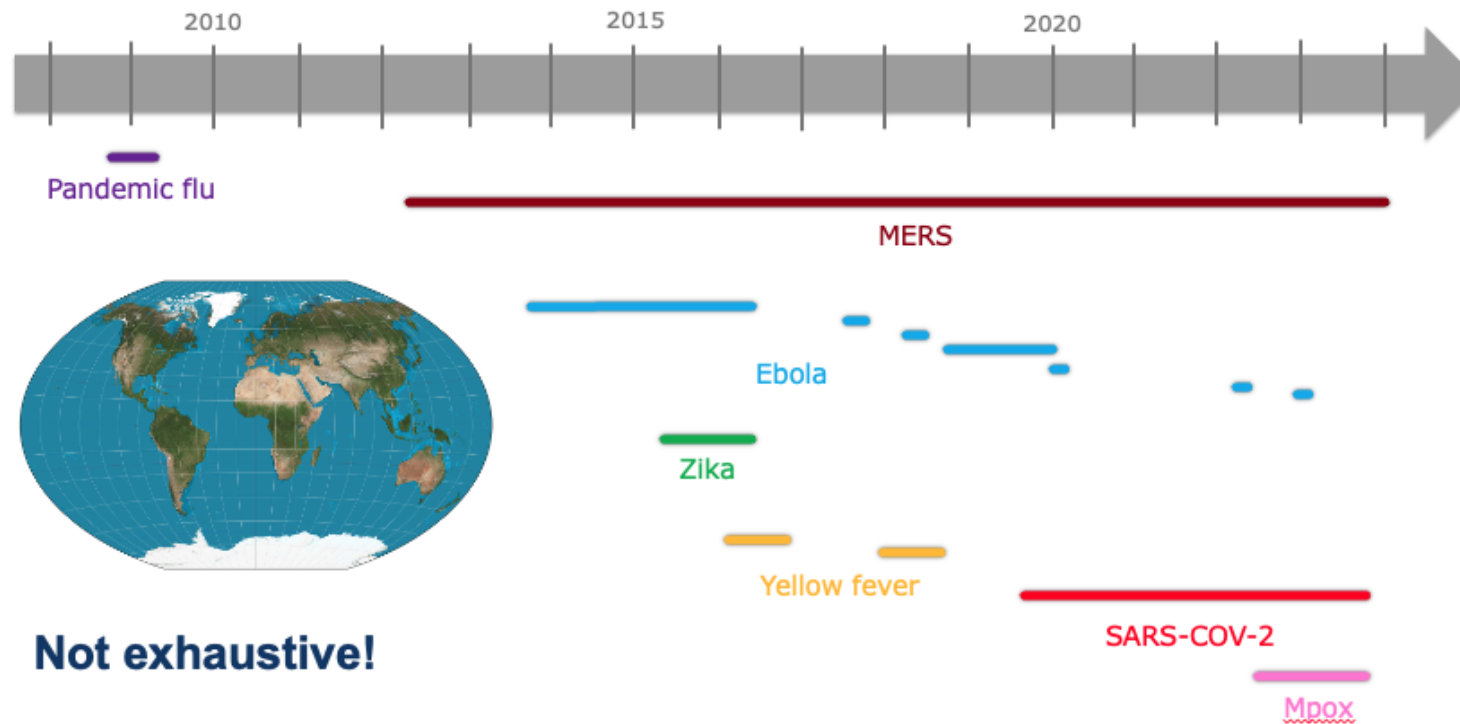
Anne Cori

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WHO Collaborating Centre for Infectious Disease modelling

*School of Public Health
Imperial College London*

- MRC Centre for Global Infectious Disease Analysis
- WHO collaborating centre for modelling ☐ rapid analysis of urgent infectious disease threats



- Recurring need:** rapidly design transmission models early in epidemics of emerging infections
- ☐ **Idea:** Proactively compile latest estimates/ranges for relevant epidemiological parameters

Systematic review of peer-reviewed literature on outbreaks, models & parameters

	Title & Abstracts	Full Text	Data extraction
CCHF	1967	656	247
Ebola	14690	1674	522
Lassa	2685	470	157
Marburg	3154	221	42
MERS	10382	623	179
Nipah	959	148	58
RVF	3341	418	149
SARS	14732	877	293
Zika	7315	238	143
Total	59225	5325	1790

Marburg: Cuomo-Dannenburg et al. Lancet ID 2023
Lassa: Doohan et al. medRxiv 2024
Ebola: Nash et al. medRxiv 2024
Prospero:
https://www.crd.york.ac.uk/prospero/display_record.php?RecordID=393345

R package – epireview

To store the information in a “live” database



<https://github.com/mrc-ide/epireview>

Epireview examples: information stored



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```
remotes::install_github('mrc-ide/epireview')
lassa <- epireview::load_epidata("lassa")
params <- lassa[["params"]]
```

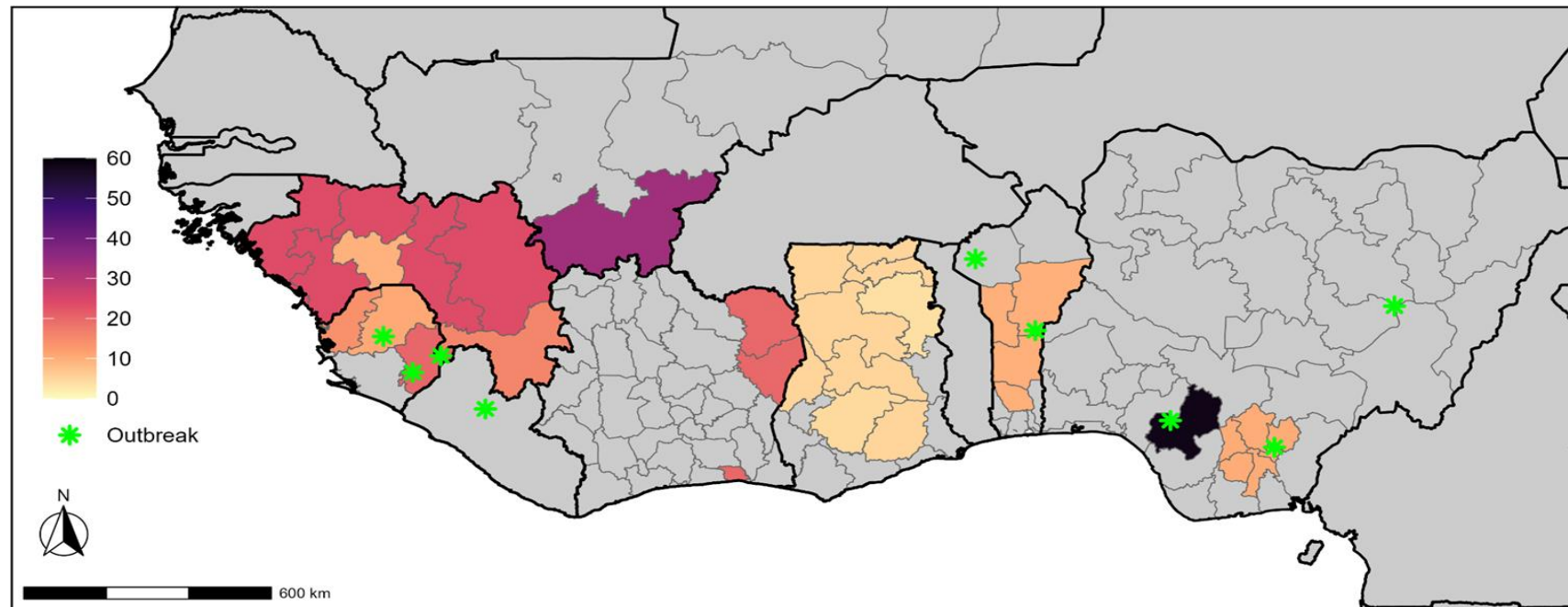
lassa	list [4]	List of length 4
articles	list [157 x 4] (S3: tbl_df, tbl, c	A tibble with 157 rows and 4 columns
params	list [374 x 63] (S3: tbl_df, tbl, c	A tibble with 374 rows and 63 columns
models	list [33 x 15] (S3: tbl_df, tbl, c	A tibble with 33 rows and 15 columns
outbreaks	list [28 x 25] (S3: tbl_df, tbl, c	A tibble with 28 rows and 25 columns

Complexity varies across pathogens

e.g. # parameters entries:

- 70 for Marburg
- 374 for Lassa
- 1224 for Ebola

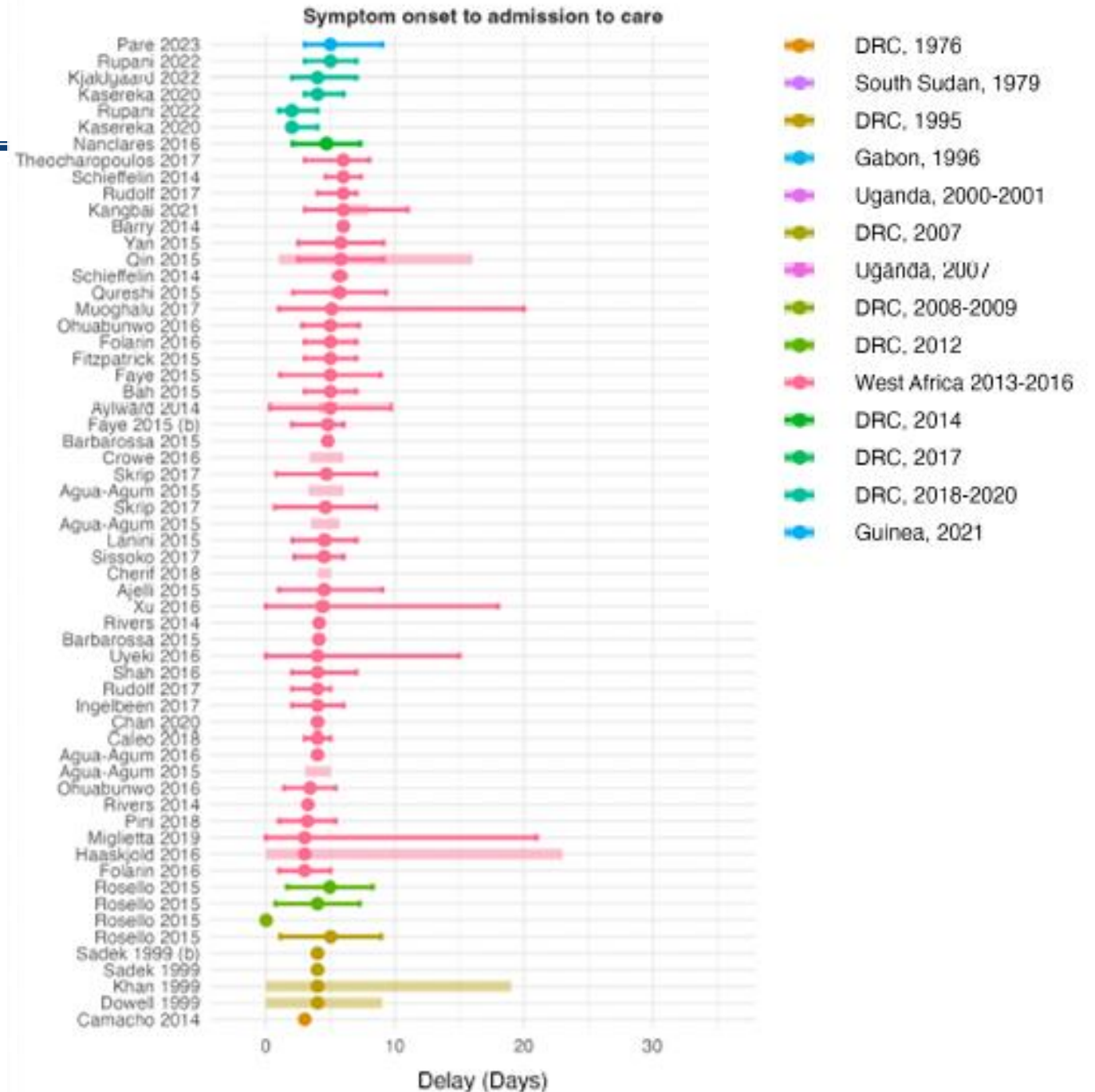
```
> unique(params[, "parameter_type"])
# A tibble: 20 x 1
  parameter_type
  <chr>
1 Human delay - time symptom to careseeking
2 Human delay - incubation period
3 Human delay - time symptom to outcome
4 Seroprevalence - IFA
5 Attack rate
6 Severity - case fatality rate (CFR)
7 Seroprevalence - HAI/HI
8 Seroprevalence - IgG
9 Reproduction number (Effective, Re)
10 Human delay - generation time
11 Mutations - evolutionary rate
12 Growth rate (r)
13 Doubling time
14 Mutations - substitution rate
15 Reproduction number (Basic R0)
16 Risk factors
17 Seroprevalence - IgM
18 Seroprevalence - Unspecified
19 Human delay - time in care
20 Mutations - mutation rate
```



Lassa seroprevalence
(function not yet in epireview)

Epireview examples: visualisation tools (cont.)

Delay from symptom onset to
hospitalisation for Ebola



Epireview examples: visualisation tools... and then???



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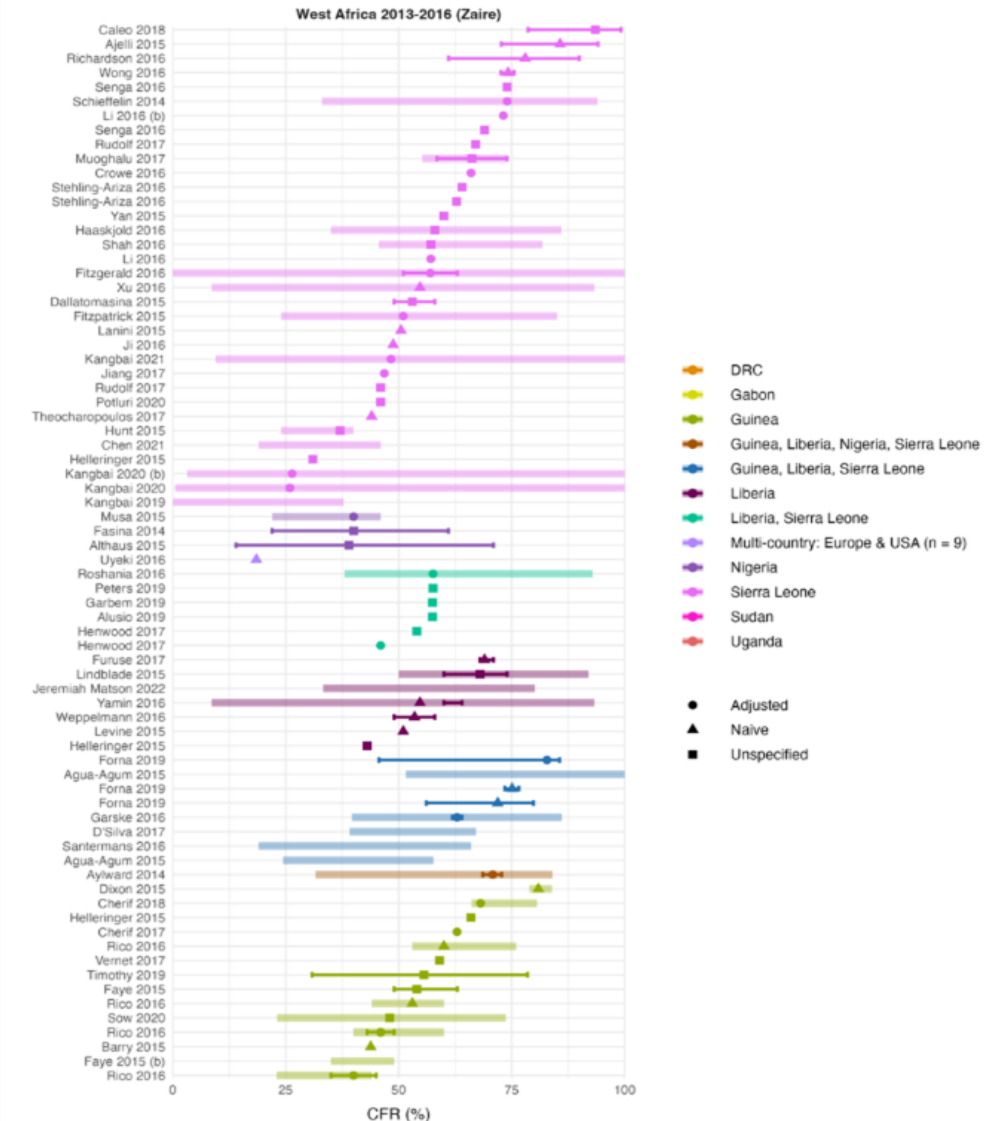
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West African Ebola CFR

How do we summarise this???

Importance of:

- Identifying redundancies
- Contextual info (e.g. age)
- Denominators
- Reporting format
- Quality of studies



Epireview examples: Summarising the information

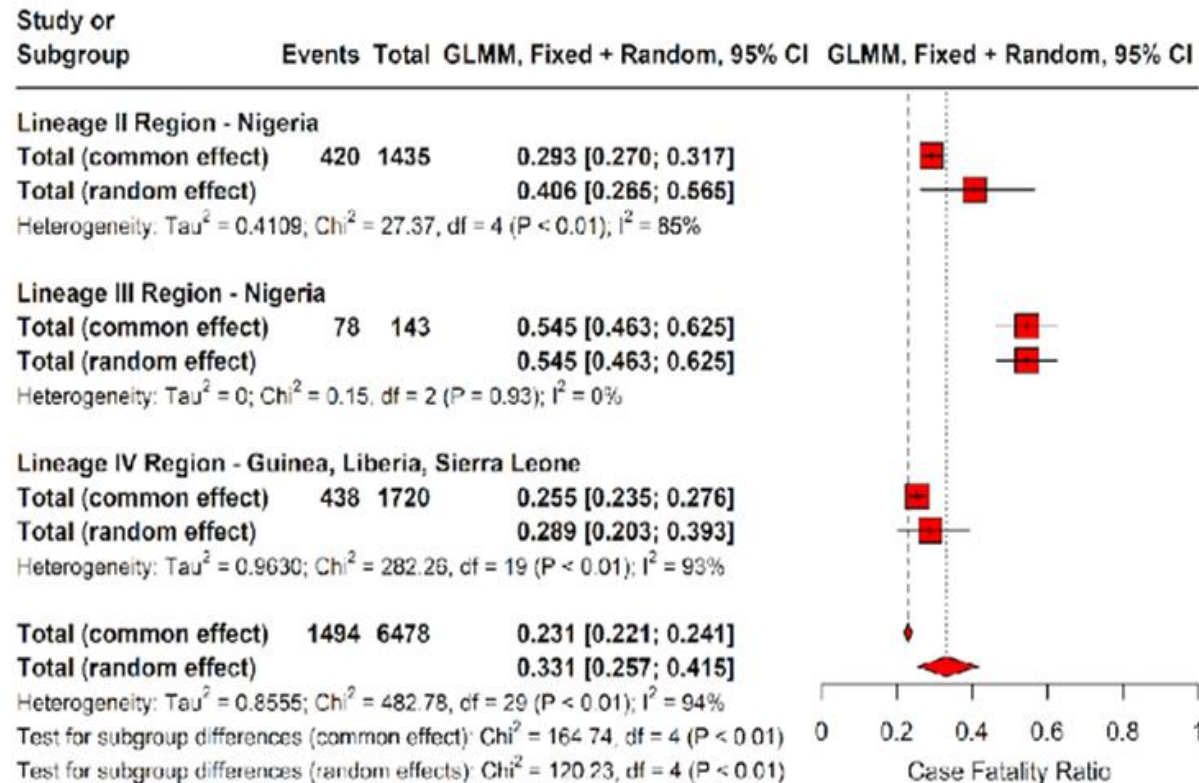


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For a subset of estimates ☐ meta-analyses, stratified by covariates

Functions to prepare data for analyses in 'meta' package (in development)



Do we even want a “consensus-estimate”?

e.g. for R_t estimates

Can we generate “reasonable ranges”?

- *Inconsistent reporting across papers*

Missing/ambiguous information (e.g. on context, denominators, method, and what exactly is reported)

How many different ways can you find to report the same information??? More than you think 😞

- *Variability vs uncertainty*

Inconsistencies in reporting **variability in a population** (e.g. SD of observed incubation periods) and **uncertainty of a parameter estimate** (e.g. SE / SD of posterior mean of incubation period)

- Particularly problematic for delay distributions

- *Changes in database structure between pathogens*

Due to each pathogen's specificity

Larger changes for vector borne diseases (adding new parameter types, dropdown options, etc.)

- *Tensions between rapidly compiling evidence for each pathogen / developing generic features*

Refactoring of epireview code ongoing to make it more generic

Epireview extraction template snapshot



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How we currently extract central + variability parameters - and uncertainty on both

Parameter data - Table

Add parameter data

OPEN A NEW RECORD AND SAVE!!!

Parameter ID

1

Article ID

1

Zambrana

2018

Pathogen

Zika virus

Extractor

Patrick

Add parameter data

Parameter type

Seroprevalence - Unspecified

Parameter only in figure/language-specific database

☐

Parameter 1 (e.g. mean or shape)

Parameter value

36.1

Exponent

0

Parameter range

Lower value

22

Upper value

58

Parameter value reported as inverse

☐

Unit

Percentage (%)

Parameter value type

Unspecified

Parameter taken from supplement

☐

Statistical approach

Unspecified

Parameter uncertainty

Parameter uncertainty - single type

Parameter uncertainty - single value

Parameter uncertainty - paired type

CI95%

Parameter uncertainty - paired values

Lower value

34.5

Upper value

37.8

Distribution type

Distribution parameter 1 - type

Distribution parameter 1 - value

Uncertainty?

☐

Distribution parameter 2 - type

Distribution parameter 2 - value

Uncertainty?

☐

Parameter 2 (e.g. SD or scale)

Parameter 2 value

Exponent

0

Parameter 2 range

Lower value

Upper value

Parameter 2 value reported as inverse

☐

Unit

Parameter 2 value type - single or paired

Parameter 2 paired values

Lower value

0

Upper value

0

Parameter 2 taken from supplement

☐

Statistical approach

Parameter 2 uncertainty

Parameter 2 uncertainty - single type

Parameter 2 uncertainty - single value

Parameter 2 uncertainty - paired type

Parameter 2 uncertainty - paired values

Lower value

Upper value

Distribution 2 type

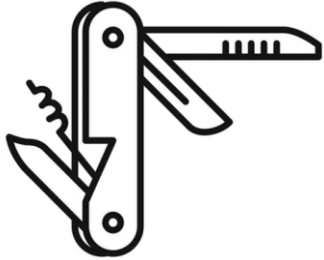
Distribution 2 parameter 1 - type

Distribution 2 parameter 1 - value

Uncertainty?

☐

Distribution 2 parameter 2 - type



Enhancing practical usability

- Improving internal functionalities
- Use case of new pathogens
- Interfacing with other tools e.g. epiparameters but also meta etc.



Moving towards a live resource

- Managing additions to the database for current pathogens
- Real-time “vignettes” – currently in <https://github.com/mrc-ide/priority-pathogens>
- Expansion to other pathogens / links with GREP

Sustainability issues

All unfunded at the moment

- how do we sustain the effort going forward? (database & software)
- how do we recognise and value contributions?
- who would support this sort of work?



Aaron Morris	Dariya Nikitin	Keith Fraser	Richard Sheppard
Alpha Forna	David Jorgensen	Kelly Charniga	Rob Johnson
Amy Dighe	Dominic Dee	Kelly McCain	Ruth McCabe
Anna Vicco	Ed Knock	Kieran Drake	Sabine van Elstrand
Anna-Maria Hartner	Ettie Unwin	Lily Geidelberg	Sangeeta Bhatia
Anne Cori	Gina Cuomo-Dannenburg	Lorenzo Cattarino	Sequoia Leuba
Arran Hamlet	Hayley Thompson	Mara Kont	Shazia Ruybal-Pesántez
Ben Lambert	Ilaria Dorigatti	Marc Baguelin	Sreejith Radhakrishnan
Bethan Cracknell Daniels	Isobel Routledge	Natsuko Imai-Eaton	Thomas Rawson
Charlie Whittaker	Jack Wardle	Pablo Perez Guzman	Tristan Naidoo
Christian Morgenstern	Janetta Skaap	Patrick Doohan	Zulma Cucunuba Perez
Cosmo Santoni	Joseph Hicks	Paula Christen	
Cyril Geismar	Kanchan Parchani	Rebecca Nash	