

# Package ‘serofoi’

May 9, 2026

**Title** Bayesian Estimation of the Force of Infection from Serological Data

**Type** Package

**Version** 1.0.3

**Description** Estimating the force of infection from time varying, age varying, or constant serocatalytic models from population based seroprevalence studies using a Bayesian framework, including data simulation functions enabling the generation of serological surveys based on this models. This tool also provides a flexible prior specification syntax for the force of infection and the seroreversion rate, as well as methods to assess model convergence and comparison criteria along with useful visualisation functions.

**License** MIT + file LICENSE

**URL** <https://github.com/epiverse-trace/serofoi>,  
<https://epiverse-trace.github.io/serofoi/>

**BugReports** <https://github.com/epiverse-trace/serofoi/issues>

**Depends** R (>= 4.1.0)

**Imports** bayesplot, checkmate, config, cowplot, dplyr, ggplot2, glue, graphics, loo, expm, methods, purrr, Rcpp (>= 0.12.0), rstan (>= 2.18.1), rstantools (>= 2.3.1), stats, tibble, tidy

**Suggests** knitr, rlang, rmarkdown, scales, spelling, testthat (>= 3.0.0)

**LinkingTo** BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**VignetteBuilder** knitr

**Biarch** true

**Config/Needs/website** epiverse-trace/epiversetheme

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-GB

**LazyData** true

**NeedsCompilation** yes

**RoxygenNote** 7.3.2

**SystemRequirements** GNU make

**Author** Zulma M. Cucunubá [aut, cre] (ORCID:

<<https://orcid.org/0000-0002-8165-3198>>),

Nicolás T. Domínguez [aut] (ORCID:

<<https://orcid.org/0009-0002-8484-1298>>),

Ben Lambert [aut],

Pierre Nouvellet [aut],

Geraldine Gómez [ctb] (ORCID: <<https://orcid.org/0009-0007-8701-0568>>),

Jaime A. Pavlich-Mariscal [ctb] (ORCID:

<<https://orcid.org/0000-0002-3892-6680>>),

Hugo Gruson [ctb] (ORCID: <<https://orcid.org/0000-0002-4094-1476>>),

David Santiago Quevedo [ctb] (ORCID:

<<https://orcid.org/0000-0003-1583-4262>>),

Miguel Gámez [ctb],

Sumali Bajaj [ctb],

Everlyn Kamau [ctb],

Richard Creswell [ctb],

International Development Research Center (IDRC) [fnd],

Pontificia Universidad Javeriana [cph]

**Maintainer** Zulma M. Cucunubá <[zulma.cucunuba@javeriana.edu.co](mailto:zulma.cucunuba@javeriana.edu.co)>

**Repository** CRAN

**Date/Publication** 2025-03-31 10:00:02 UTC

## Contents

serofoi-package . . . . .	3
add_age_group_to_serosurvey . . . . .	4
build_stan_data . . . . .	5
chagas2012 . . . . .	6
chik2015 . . . . .	7
extract_central_estimates . . . . .	7
fit_seromodel . . . . .	8
get_foi_index . . . . .	10
plot_foi_estimates . . . . .	11
plot_rhats . . . . .	12
plot_seromodel . . . . .	13
plot_seroprev_estimates . . . . .	15
plot_serosurvey . . . . .	16
plot_summary . . . . .	17
prepare_serosurvey_for_plot . . . . .	18
probability_exact_age_varying . . . . .	19
probability_exact_time_varying . . . . .	19
prob_seroprev_age_by_age . . . . .	20
prob_seroprev_age_time_by_age . . . . .	20

prob_seroprev_by_age . . . . .	21
prob_seroprev_gen_by_age . . . . .	22
prob_seroprev_time_by_age . . . . .	24
set_foi_init . . . . .	24
set_stan_data_defaults . . . . .	25
sf_cauchy . . . . .	26
sf_none . . . . .	26
sf_normal . . . . .	27
sf_uniform . . . . .	27
simulate_serosurvey . . . . .	28
simulate_serosurvey_age . . . . .	30
simulate_serosurvey_age_time . . . . .	31
simulate_serosurvey_general . . . . .	32
simulate_serosurvey_time . . . . .	34
summarise_central_estimate . . . . .	35
summarise_loo_estimate . . . . .	36
summarise_seromodel . . . . .	37
veev2012 . . . . .	39
<b>Index</b>	<b>40</b>

---

serofoi-package      *The 'serofoi' package.*

---

## Description

A DESCRIPTION OF THE PACKAGE

## Author(s)

**Maintainer:** Zulma M. Cucunubá <zulma.cucunuba@javeriana.edu.co> ([ORCID](#))

Authors:

- Nicolás T. Domínguez <ex-ntorres@javeriana.edu.co> ([ORCID](#))
- Ben Lambert
- Pierre Nouvellet

Other contributors:

- Geraldine Gómez ([ORCID](#)) [contributor]
- Jaime A. Pavlich-Mariscal ([ORCID](#)) [contributor]
- Hugo Gruson ([ORCID](#)) [contributor]
- David Santiago Quevedo ([ORCID](#)) [contributor]
- Miguel Gámez [contributor]
- Sumali Bajaj [contributor]
- Everlyn Kamau [contributor]

- Richard Creswell [contributor]
- International Development Research Center (IDRC) [funder]
- Pontificia Universidad Javeriana [copyright holder]

## References

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.26.22. <https://mc-stan.org>

#' @keywords internal

## See Also

Useful links:

- <https://github.com/epiverse-trace/serofoi>
- <https://epiverse-trace.github.io/serofoi/>
- Report bugs at <https://github.com/epiverse-trace/serofoi/issues>

---

add\_age\_group\_to\_ser survey

*Adds age group marker to ser survey*

---

## Description

Adds age group marker to ser survey

## Usage

```
add_age_group_to_ser survey(ser survey)
```

## Arguments

ser survey	survey_year	Year in which the survey took place (only needed to plot time models)
	age_min	Floor value of the average between age_min and age_max
	age_max	The size of the sample
	n_sample	Number of samples for each age group
	n_seropositive	Number of positive samples for each age group

## Value

ser survey with additional column specifying age group marker defined as the mean floor between age\_min and age\_max

---

build_stan_data	<i>Builds stan data for sampling depending on the selected model</i>
-----------------	--

---

### Description

Builds stan data for sampling depending on the selected model

### Usage

```
build_stan_data(
  serosurvey,
  model_type = "constant",
  foi_prior = sf_uniform(),
  foi_index = NULL,
  is_log_foi = FALSE,
  foi_sigma_rw = sf_none(),
  is_seroreversion = FALSE,
  seroreversion_prior = sf_none()
)
```

### Arguments

serosurvey	survey_year Year in which the survey took place (only needed to plot time models)
	age_min Floor value of the average between age_min and age_max
	age_max The size of the sample
	n_sample Number of samples for each age group
	n_seropositive Number of positive samples for each age group
model_type	Type of the model. Either "constant", "age" or "time"
foi_prior	Force-of-infection distribution specified by means of the helper functions. Currently available options are: <b>sf_normal</b> Function to set normal distribution priors <b>sf_uniform</b> Function to set uniform distribution priors
foi_index	Integer vector specifying the age-groups for which Force-of-Infection values will be estimated. It can be specified by means of <a href="#">get_foi_index</a>
is_log_foi	Boolean to set logarithmic scale in the FoI
foi_sigma_rw	Prior distribution for the standard deviation of the Force-of-Infection. Currently available options are: <b>sf_normal</b> Function to set normal distribution prior. Available for time models in the log-scale <b>sf_cauchy</b> Function to set Cauchy distribution prior. Available for time models in regular scale.
is_seroreversion	Boolean specifying whether to include seroreversion rate estimation in the model

seroreversion\_prior

seroreversion distribution specified by means of the helper functions. Currently available options are:

**sf\_normal** Function to set normal distribution priors

**sf\_uniform** Function to set uniform distribution priors

**sf\_none** Function to set no prior distribution

## Value

List with necessary data for sampling the specified model

---

chagas2012

*Chagas seroprevalence data in serfoi*

---

## Description

Datasets that measure the seroprevalence of IgG antibodies against *Trypanosoma cruzi* infection in rural areas of Colombia corresponding to a serosurvey conducted in 2012 for a rural indigenous community known to have long-term endemic transmission, where some control interventions have taken place over the years.

## Usage

```
data(chagas2012)
```

## Format

chagas2012:

A `<data.frame>` with 4 rows and 5 columns:

**survey\_year** Year in which the serosurvey was conducted

**n\_sample** Number of collected samples per age group

**n\_seropositive** Number of positive samples per age group

**age\_min** Age group minimal age

**age\_max** Age group maximal age

## Examples

```
data(chagas2012)
```

---

`chik2015`*Chikungunya seroprevalence data in serofoi*

---

**Description**

Datasets that measure the seroprevalence of IgG antibodies against the Chikungunya virus conducted in Bahia, Brazil in October-December 2015 by Dias et al. (2018). The survey was conducted immediately after a large Chikungunya epidemic in the area.

**Usage**

```
data(chik2015)
```

**Format**

`chik2015`:

A `<data.frame>` with 4 rows and 5 columns:

**survey\_year** Year in which the serosurvey was conducted

**n\_sample** Number of collected samples per age group

**n\_seropositive** Number of positive samples per age group

**age\_min** Age group minimal age

**age\_max** Age group maximal age

**Examples**

```
data(chik2015)
```

---

`extract_central_estimates`*Extracts central estimates from stan\_fit object for specified parameter*

---

**Description**

Extracts central estimates from `stan_fit` object for specified parameter

**Usage**

```
extract_central_estimates(  
  seromodel,  
  serosurvey,  
  alpha = 0.05,  
  par_name = "foi_vector"  
)
```

**Arguments**

seromodel	stan_fit object obtained from sampling a model with <code>fit_seromodel</code>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models)
	age_min Floor value of the average between age_min and age_max
	age_max The size of the sample
	n_sample Number of samples for each age group
	n_seropositive Number of positive samples for each age group
alpha	1 - alpha indicates the credibility level to be used
par_name	String specifying the parameter to be extracted from seromodel

**Value**

A dataframe with the following columns

median	Median of the samples computed as the 0.5 quantile
lower	Lower quantile alpha
upper	Upper quantile 1 - alpha

**Examples**

```
data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
central_estimates <- extract_central_estimates(
  seromodel,
  veev2012,
  par_name = "foi"
)
```

---

fit_seromodel	<i>Runs specified stan model for the Force-of-Infection (FoI)</i>
---------------	---

---

**Description**

Runs specified stan model for the Force-of-Infection (FoI)

**Usage**

```
fit_seromodel(
  serosurvey,
  model_type = "constant",
  is_log_foi = FALSE,
  foi_prior = sf_normal(),
  foi_sigma_rw = sf_none(),
  foi_index = NULL,
  foi_init = NULL,
```

```

    is_seroreversion = FALSE,
    seroreversion_prior = sf_normal(),
    ...
  )

```

### Arguments

serosurvey	survey_year	Year in which the survey took place (only needed to plot time models)
	age_min	Floor value of the average between age_min and age_max
	age_max	The size of the sample
	n_sample	Number of samples for each age group
	n_seropositive	Number of positive samples for each age group
model_type		Type of the model. Either "constant", "age" or "time"
is_log_foi		Boolean to set logarithmic scale in the FoI
foi_prior		Force-of-infection distribution specified by means of the helper functions. Currently available options are: <b>sf_normal</b> Function to set normal distribution priors <b>sf_uniform</b> Function to set uniform distribution priors
foi_sigma_rw		Prior distribution for the standard deviation of the Force-of-Infection. Currently available options are: <b>sf_normal</b> Function to set normal distribution prior. Available for time models in the log-scale <b>sf_cauchy</b> Function to set Cauchy distribution prior. Available for time models in regular scale.
foi_index		Integer vector specifying the age-groups for which Force-of-Infection values will be estimated. It can be specified by means of <a href="#">get_foi_index</a>
foi_init		Initialization function for sampling. If null, default is chosen depending on the foi-scale of the model
is_seroreversion		Boolean specifying whether to include seroreversion rate estimation in the model
seroreversion_prior		seroreversion distribution specified by means of the helper functions. Currently available options are: <b>sf_normal</b> Function to set normal distribution priors <b>sf_uniform</b> Function to set uniform distribution priors <b>sf_none</b> Function to set no prior distribution
...		Additional parameters for <a href="#">rstan</a>

### Value

stan\_fit object with Force-of-Infection and seroreversion (when applicable) samples

**Examples**

```

data(chagas2012)
seromodel <- fit_seromodel(
  serosurvey = chagas2012,
  model_type = "time",
  foi_index = data.frame(
    year = 1935:2011,
    foi_index = c(rep(1, 46), rep(2, 31))
  ),
  iter = 100
)

```

---

get\_foi\_index

*Generates Force-of-Infection indexes for heterogeneous age groups*


---

**Description**

Generates a list of integers indexing together the time/age intervals for which FoI values will be estimated in `fit_seromodel`. The max value in `foi_index` corresponds to the number of FoI values to be estimated when sampling. The serofoi approach to fitting serological data currently supposes that FoI is piecewise-constant across either groups of years or ages, and this function creates a Data Frame that communicates this grouping to the Stan model

**Usage**

```
get_foi_index(serosurvey, group_size, model_type)
```

**Arguments**

serosurvey	survey_year	Year in which the survey took place (only needed to plot time models)
	age_min	Floor value of the average between age_min and age_max
	age_max	The size of the sample
	n_sample	Number of samples for each age group
	n_seropositive	Number of positive samples for each age group
group_size		Age groups size
model_type		Type of the model. Either "age" or "time"

**Value**

A Data Frame which describes the grouping of years or ages (dependent on model) into pieces within which the FoI is assumed constant when performing model fitting. A single FoI value will be estimated for ages/years assigned with the same index

**Examples**

```
data(chagas2012)
foi_index <- get_foi_index(chagas2012, group_size = 25, model_type = "time")
```

---

plot\_foi\_estimates      *Plots Force-of-Infection central estimates*

---

**Description**

Plots Force-of-Infection central estimates

**Usage**

```
plot_foi_estimates(
  seromodel,
  serosurvey,
  alpha = 0.05,
  foi_df = NULL,
  foi_max = NULL,
  size_text = 11,
  plot_constant = FALSE,
  x_axis = NA
)
```

**Arguments**

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models) age_min Floor value of the average between age_min and age_max age_max The size of the sample n_sample Number of samples for each age group n_seropositive Number of positive samples for each age group
alpha	1 - alpha indicates the credibility level to be used
foi_df	Dataframe with columns year/age Year/Age (depending on the model) foi Force-of-infection values by year/age
foi_max	Max FoI value for plotting
size_text	Size of text for plotting (base_size in <a href="#">ggplot2</a> )
plot_constant	boolean specifying whether to plot single Force-of-Infection estimate and its corresponding rhat value instead of showing this information in the summary. Only relevant when seromodel@model_name == "constant")
x_axis	either "time" or "age". Specifies time axis values label for constant model additional plots. Only relevant when and seromodel@model_name == "constant"

**Value**

ggplot object with estimated FoI

**Examples**

```
data(chagas2012)
seromodel <- fit_seromodel(
  serosurvey = chagas2012,
  model_type = "time",
  foi_index = data.frame(
    year = 1935:2011,
    foi_index = c(rep(1, 46), rep(2, 31))
  ),
  iter = 100,
  chains = 2
)
plot_foi_estimates(seromodel, chagas2012)
```

---

plot\_rhats

*Plot r-hats convergence criteria for the specified model*

---

**Description**

Plot r-hats convergence criteria for the specified model

**Usage**

```
plot_rhats(
  seromodel,
  serosurvey,
  size_text = 11,
  plot_constant = FALSE,
  x_axis = NA
)
```

**Arguments**

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models)
age_min	Floor value of the average between age_min and age_max
age_max	The size of the sample
n_sample	Number of samples for each age group
n_seropositive	Number of positive samples for each age group
size_text	Size of text for plotting (base_size in <a href="#">ggplot2</a> )

`plot_constant` boolean specifying whether to plot single Force-of-Infection estimate and its corresponding  $r_{hat}$  value instead of showing this information in the summary. Only relevant when `seromodel@model_name == "constant"`)

`x_axis` either "time" or "age". Specifies time axis values label for constant model additional plots. Only relevant when and `seromodel@model_name == "constant"`

### Value

ggplot object showing the  $r$ -hats of the model to be compared with the convergence criteria (horizontal dashed line)

### Examples

```
data(chagas2012)
seromodel <- fit_seromodel(
  serosurvey = chagas2012,
  model_type = "time",
  foi_index = data.frame(
    year = 1935:2011,
    foi_index = c(rep(1, 46), rep(2, 31))
  ),
  iter = 100,
  chains = 2
)
plot_rhats(seromodel, chagas2012)
```

---

<code>plot_seromodel</code>	<i>Visualise results of the provided model</i>
-----------------------------	--

---

### Description

Visualise results of the provided model

### Usage

```
plot_seromodel(
  seromodel,
  serosurvey,
  alpha = 0.05,
  bin_serosurvey = FALSE,
  bin_step = 5,
  foi_df = NULL,
  foi_max = NULL,
  loo_estimate_digits = 1,
  central_estimate_digits = 2,
  seroreversion_digits = 2,
  rhat_digits = 2,
```

```

    size_text = 11,
    plot_constant = FALSE,
    x_axis = NA
  )

```

### Arguments

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models) age_min Floor value of the average between age_min and age_max age_max The size of the sample n_sample Number of samples for each age group n_seropositive Number of positive samples for each age group
alpha	1 - alpha indicates the credibility level to be used
bin_serosurvey	If TRUE, serodata is binned by means of prepare_bin_serosurvey. Otherwise, age groups are kept as originally input.
bin_step	Integer specifying the age groups bin size to be used when bin_serosurvey is set to TRUE.
foi_df	Dataframe with columns year/age Year/Age (depending on the model) foi Force-of-infection values by year/age
foi_max	Max FoI value for plotting
loo_estimate_digits	Number of loo estimate digits
central_estimate_digits	Number of central estimate digits
seroreversion_digits	Number of seroreversion rate digits
rhat_digits	Number of rhat estimate digits
size_text	Size of text for plotting (base_size in <a href="#">ggplot2</a> )
plot_constant	boolean specifying whether to plot single Force-of-Infection estimate and its corresponding rhat value instead of showing this information in the summary. Only relevant when seromodel@model_name == "constant")
x_axis	either "time" or "age". Specifies time axis values label for constant model additional plots. Only relevant when and seromodel@model_name == "constant"

### Value

seromodel summary plot

### Examples

```

data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
plot_seromodel(seromodel, veev2012)

```

---

`plot_seroprev_estimates`*Plot seroprevalence estimates on top of the serosurvey*

---

## Description

Plot seroprevalence estimates on top of the serosurvey

## Usage

```
plot_seroprev_estimates(  
  seromodel,  
  serosurvey,  
  alpha = 0.05,  
  size_text = 11,  
  bin_serosurvey = FALSE,  
  bin_step = 5  
)
```

## Arguments

<code>seromodel</code>	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
<code>serosurvey</code>	survey_year Year in which the survey took place (only needed to plot time models) age_min Floor value of the average between age_min and age_max age_max The size of the sample n_sample Number of samples for each age group n_seropositive Number of positive samples for each age group
<code>alpha</code>	1 - alpha indicates the credibility level to be used
<code>size_text</code>	Size of text for plotting (base_size in <a href="#">ggplot2</a> )
<code>bin_serosurvey</code>	If TRUE, serodata is binned by means of <code>prepare_bin_serosurvey</code> . Otherwise, age groups are kept as originally input.
<code>bin_step</code>	Integer specifying the age groups bin size to be used when <code>bin_serosurvey</code> is set to TRUE.

## Value

ggplot object with seroprevalence estimates and serosurveys plots

## Examples

```
data(veev2012)  
seromodel <- fit_seromodel(veev2012, iter = 100)  
plot_seroprev_estimates(seromodel, veev2012)
```

---

plot\_serosurvey      *Plots seroprevalence from the given serosurvey*

---

### Description

Plots seroprevalence from the given serosurvey

### Usage

```
plot_serosurvey(
  serosurvey,
  size_text = 11,
  bin_serosurvey = FALSE,
  bin_step = 5
)
```

### Arguments

serosurvey	survey_year	Year in which the survey took place (only needed to plot time models)
	age_min	Floor value of the average between age_min and age_max
	age_max	The size of the sample
	n_sample	Number of samples for each age group
	n_seropositive	Number of positive samples for each age group
size_text		Size of text for plotting (base_size in <a href="#">ggplot2</a> )
bin_serosurvey		If TRUE, serodata is binned by means of prepare_bin_serosurvey. Otherwise, age groups are kept as originally input.
bin_step		Integer specifying the age groups bin size to be used when bin_serosurvey is set to TRUE.

### Value

ggplot object with seroprevalence plot

### Examples

```
# Chikungunya example serosurvey
data(chik2015)
plot_serosurvey(chik2015)

# VEEV example serosurvey
data(veev2012)
plot_serosurvey(veev2012)
```

---

plot_summary	<i>Plots model summary</i>
--------------	----------------------------

---

## Description

Plots model summary

## Usage

```
plot_summary(
  seromodel,
  serosurvey,
  loo_estimate_digits = 1,
  central_estimate_digits = 2,
  rhat_digits = 2,
  size_text = 11,
  plot_constant = FALSE
)
```

## Arguments

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models) age_min Floor value of the average between age_min and age_max age_max The size of the sample n_sample Number of samples for each age group n_seropositive Number of positive samples for each age group
loo_estimate_digits	Number of loo estimate digits
central_estimate_digits	Number of central estimate digits
rhat_digits	Number of rhat estimate digits
size_text	Size of text for plotting (base_size in <a href="#">ggplot2</a> )
plot_constant	boolean specifying whether to plot single Force-of-Infection estimate and its corresponding rhat value instead of showing this information in the summary. Only relevant when seromodel@model_name == "constant")

## Value

ggplot object with a summary of the specified model

**Examples**

```
data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
plot_summary(seromodel, veev2012)
```

---

```
prepare_serosurvey_for_plot
      Prepares serosurvey for plotting
```

---

**Description**

Adds seroprevalence values with corresponding binomial confidence interval

**Usage**

```
prepare_serosurvey_for_plot(serosurvey, alpha = 0.05)
```

**Arguments**

serosurvey	survey_year	Year in which the survey took place (only needed to plot time models)
	age_min	Floor value of the average between age_min and age_max
	age_max	The size of the sample
	n_sample	Number of samples for each age group
	n_seropositive	Number of positive samples for each age group
alpha		1 - alpha indicates the confidence level to be used

**Value**

serosurvey with additional columns:

**seroprev** Seroprevalence computed as the proportion of positive cases n\_seropositive in the number of samples n\_sample for each age group

**seroprev\_lower** Lower limit of the binomial confidence interval of seroprev

**seroprev\_upper** Upper limit of the binomial confidence interval of seroprev

---

 probability\_exact\_age\_varying

*Computes the probability of being seropositive when Forces-of-Infection (FoIs) vary by age*

---

**Description**

Computes the probability of being seropositive when Forces-of-Infection (FoIs) vary by age

**Usage**

```
probability_exact_age_varying(ages, fois, seroreversion_rate = 0)
```

**Arguments**

ages	Integer indicating the ages of the exposed cohorts
fois	Numeric atomic vector corresponding to the age-varying Force-of-Infection to simulate from
seroreversion_rate	Non-negative seroreversion rate. Default is 0.

**Value**

vector of probabilities of being seropositive for age-varying FoI including seroreversion (ordered from youngest to oldest individuals)

---

probability\_exact\_time\_varying

*Computes the probability of being seropositive when Forces-of-Infection (FoIs) vary by time*

---

**Description**

Computes the probability of being seropositive when Forces-of-Infection (FoIs) vary by time

**Usage**

```
probability_exact_time_varying(years, fois, seroreversion_rate = 0)
```

**Arguments**

years	Integer indicating the years covering the birth ages of the sample
fois	Numeric atomic vector corresponding to the age-varying FoI to simulate from
seroreversion_rate	Non-negative seroreversion rate. Default is 0.

**Value**

vector of probabilities of being seropositive for age-varying FoI including seroreversion (ordered from youngest to oldest individuals)

---

prob\_seroprev\_age\_by\_age

*Generate probabilities of seropositivity by age based on an age-varying Force-of-Infection (FoI) model.*

---

**Description**

This function calculates the probabilities of seropositivity by age based on an age-varying FoI model. It takes into account the FoI and the rate of seroreversion.

**Usage**

```
prob_seroprev_age_by_age(foi, seroreversion_rate)
```

**Arguments**

**foi** A dataframe containing the FoI values for different ages. It should have two columns: 'age' and 'foi'.

**seroreversion\_rate** A non-negative numeric value representing the rate of seroreversion.

**Value**

A dataframe with columns 'age' and 'seropositivity'.

---

prob\_seroprev\_age\_time\_by\_age

*Generate probabilities of seropositivity by age based on an age-and-time varying Force-of-Infection (FoI) model.*

---

**Description**

This function calculates the probabilities of seropositivity by age based on an age-and-time-varying FoI model. It takes into account the FoI and the rate of seroreversion.

**Usage**

```
prob_seroprev_age_time_by_age(foi, seroreversion_rate)
```

**Arguments**

**foi** A dataframe containing the FoI values for different ages. It should have three columns: 'year', 'age' and 'foi'.

**seroreversion\_rate** A non-negative numeric value representing the rate of seroreversion.

**Value**

A dataframe with columns 'age' and 'seropositivity'.

---

prob\_seroprev\_by\_age *Generate probabilities of seropositivity by age based on model choice.*

---

**Description**

This function generates seropositivity probabilities based on either a time-varying Force-of-Infection (FoI) model, an age-varying FoI model, or an age-and-time-varying FoI model. In all cases, it is possible to optionally include seroreversion.

**Usage**

```
prob_seroprev_by_age(model, foi, seroreversion_rate = 0)
```

**Arguments**

**model** A string specifying the model type which can be either "age", "time", "age-time".

**foi** A dataframe containing the FoI values. For time-varying models the columns should be:

- year** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of the FoI by year

For age-varying models the columns should be:

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey
- foi** Corresponding values of the FoI by age

For age-and-time-varying models the columns should be:

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey
- time** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of FoI by age and year

**seroreversion\_rate** A non-negative value determining the rate of seroreversion (per year). Default is 0.

**Value**

A dataframe with columns 'age' and 'seropositivity'.

**Examples**

```
prob_seroprev_by_age(
  model = "age",
  foi = data.frame(
    age = 1:80,
    foi = rep(0.01, 80)
  )
)
```

---

prob\_seroprev\_gen\_by\_age

*Generate probabilities of seropositivity by age based on a general Force-of-Infection (FoI) model.*

---

**Description**

This function calculates the probabilities of seropositivity by age based on an abstract model of the serocatalytic system.

**Usage**

```
prob_seroprev_gen_by_age(
  construct_A_fun,
  calculate_seroprev_fun,
  initial_conditions,
  max_age,
  ...
)
```

**Arguments**

construct_A_fun	A function that constructs a matrix that defines the multiplier term in the linear ODE system.
calculate_seroprev_fun	A function which takes the state vector and returns the seropositive fraction.
initial_conditions	The initial state vector proportions for each birth cohort.
max_age	The maximum age to simulate seropositivity for.
...	Additional parameters for construct_A_fun

**Value**

A dataframe with columns 'age' and 'seropositivity'.

**Examples**

```
# define age- and time-specific multipliers
foi_df_time <- data.frame(
  year = seq(1946, 2025, 1),
  foi = c(rep(0, 40), rep(1, 40))
)

foi_df_age <- data.frame(
  age = 1:80,
  foi = 2 * dlnorm(1:80, meanlog = 3.5, sdlog = 0.5)
)

u <- foi_df_age$foi
v <- foi_df_time$foi

# function to construct A matrix for one piece
construct_A <- function(t, tau, u, v) {
  u_bar <- u[t - tau]
  v_bar <- v[t]

  A <- diag(-1, ncol = 12, nrow = 12)
  A[row(A) == (col(A) + 1)] <- 1
  A[1, 1] <- -u_bar * v_bar
  A[2, 1] <- u_bar * v_bar
  A[12, 12] <- 0

  A
}

# determines the sum of seropositive compartments of those still alive
calculate_seropositivity_fn <- function(Y) {
  sum(Y[2:11]) / (1 - Y[12])
}

# initial conditions in 12D state vector
initial_conditions <- rep(0, 12)
initial_conditions[1] <- 1

# calculate probability
seropositive_hiv <- prob_seroprev_gen_by_age(
  construct_A,
  calculate_seropositivity_fn,
  initial_conditions,
  max_age = 80,
  u,
  v
)
```

---

prob\_seroprev\_time\_by\_age

*Generate probabilities of seropositivity by age based on a time-varying Force-of-Infection (FoI) model.*

---

### Description

This function calculates the probabilities of seropositivity by age based on a time-varying FoI model. It takes into account the FoI and the rate of seroreversion.

### Usage

```
prob_seroprev_time_by_age(foi, seroreversion_rate)
```

### Arguments

**foi** A dataframe containing the FoI values for different years. It should have two columns: 'year' and 'foi'.

**seroreversion\_rate** A non-negative numeric value representing the rate of seroreversion.

### Value

A dataframe with columns 'age' and 'seropositivity'.

---

set\_foi\_init                      *Sets initialization function for sampling*

---

### Description

Sets initialization function for sampling

### Usage

```
set_foi_init(foi_init, is_log_foi, foi_index)
```

### Arguments

**foi\_init** Initialization function for sampling. If null, default is chosen depending on the foi-scale of the model

**is\_log\_foi** Boolean to set logarithmic scale in the FoI

**foi\_index** Integer vector specifying the age-groups for which Force-of-Infection values will be estimated. It can be specified by means of [get\\_foi\\_index](#)

**Value**

Function specifying initialization vector for the Force-of-Infection

**Examples**

```
data(chagas2012)
foi_index <- get_foi_index(chagas2012, group_size = 5, model_type = "age")
foi_init <- set_foi_init(
  foi_init = NULL,
  is_log_foi = FALSE,
  foi_index = foi_index
)
```

---

set\_stan\_data\_defaults

*Set stan data defaults for sampling*

---

**Description**

Set stan data defaults for sampling

**Usage**

```
set_stan_data_defaults(stan_data, is_log_foi = FALSE, is_seroreversion = FALSE)
```

**Arguments**

stan_data	List to be passed to <a href="#">rstan</a>
is_log_foi	Boolean to set logarithmic scale in the FoI
is_seroreversion	Boolean specifying whether to include seroreversion rate estimation in the model

**Value**

List with default values of stan data for sampling

---

sf_cauchy	<i>Sets Cauchy distribution parameters for sampling</i>
-----------	---

---

**Description**

Sets Cauchy distribution parameters for sampling

**Usage**

```
sf_cauchy(location = 0, scale = 1)
```

**Arguments**

location	Location of the Cauchy distribution
scale	Scale of the Cauchy distribution

**Value**

List with specified statistics and name of the distribution

**Examples**

```
my_prior <- sf_cauchy()
```

---

sf_none	<i>Sets empty prior distribution</i>
---------	--------------------------------------

---

**Description**

Sets empty prior distribution

**Usage**

```
sf_none()
```

**Value**

List with the name of the empty distribution

---

sf_normal	<i>Sets normal distribution parameters for sampling</i>
-----------	---

---

**Description**

Sets normal distribution parameters for sampling

**Usage**

```
sf_normal(mean = 0, sd = 1)
```

**Arguments**

mean	Mean of the normal distribution
sd	Standard deviation of the normal distribution

**Value**

List with specified statistics and name of the model

**Examples**

```
my_prior <- sf_normal()
```

---

sf_uniform	<i>Sets uniform distribution parameters for sampling</i>
------------	--

---

**Description**

Sets uniform distribution parameters for sampling

**Usage**

```
sf_uniform(min = 0, max = 10)
```

**Arguments**

min	Minimum value of the random variable of the uniform distribution
max	Maximum value of the random variable of the uniform distribution

**Value**

List with specified statistics and name of the model

**Examples**

```
my_prior <- sf_uniform()
```

---

simulate\_serosurvey     *Simulate serosurvey data based on various Force-of-Infection (FoI) models.*

---

### Description

This function generates binned serosurvey data based on either a time-varying FoI model, an age-varying FoI model, or an age-and-time-varying FoI model. In all cases, it is possible to optionally include seroreversion. This function allows construction of serosurveys with binned age groups, and it generates uncertainty in the distribution of a sample size within an age bin through multinomial sampling.

### Usage

```
simulate_serosurvey(model, foi, survey_features, seroreversion_rate = 0)
```

### Arguments

model	A string specifying the model type which can be either "age", "time", "age-time".
foi	A dataframe containing the FoI values. For time-varying models the columns should be: <b>year</b> Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey <b>foi</b> Corresponding values of the FoI by year For age-varying models the columns should be: <b>age</b> Ages starting at 1 and up to the age of the oldest person in the serosurvey <b>foi</b> Corresponding values of the FoI by age For age-and-time-varying models the columns should be: <b>age</b> Ages starting at 1 and up to the age of the oldest person in the serosurvey <b>time</b> Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey <b>foi</b> Corresponding values of FoI by age and year
survey_features	A dataframe containing information about the binned age groups and sample sizes for each. It should contain columns: <b>age_min</b> Left limits of the age groups to be considered in the serosurvey <b>age_max</b> Right limits of the age groups to be considered in the serosurvey <b>n_sample</b> Number of samples by age group The resulting age intervals are closed to the left [ and open to the right ).
seroreversion_rate	A non-negative value determining the rate of seroreversion (per year). Default is 0.

**Value**

A dataframe with simulated serosurvey data, including age group information, overall sample sizes, the number of seropositive individuals, and other survey features.

**Examples**

```
# time-varying model
foi_df <- data.frame(
  year = seq(1990, 2009, 1),
  foi = rnorm(20, 0.1, 0.01)
)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey(
  model = "time",
  foi = foi_df,
  survey_features = survey_features)

# age-varying model
foi_df <- data.frame(
  age = seq(1, 20, 1),
  foi = rnorm(20, 0.1, 0.01)
)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey(
  model = "age",
  foi = foi_df,
  survey_features = survey_features)

# age-and-time varying model
foi_df <- expand.grid(
  year = seq(1990, 2009, 1),
  age = seq(1, 20, 1)
)
foi_df$foi <- rnorm(20 * 20, 0.1, 0.01)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey(
  model = "age-time",
  foi = foi_df,
  survey_features = survey_features)
```

---

simulate\_serosurvey\_age

*Simulate serosurvey data based on an age-varying Force-of-Infection (FoI) model.*

---

## Description

This function generates binned serosurvey data based on an age-varying FoI model, optionally including seroreversion. This function allows construction of serosurveys with binned age groups, and it generates uncertainty in the distribution of a sample size within an age bin through multinomial sampling.

## Usage

```
simulate_serosurvey_age(foi, survey_features, seroreversion_rate = 0)
```

## Arguments

**foi** A dataframe containing the FoI values. For time-varying models the columns should be:

- year** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of the FoI by year

For age-varying models the columns should be:

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey
- foi** Corresponding values of the FoI by age

For age-and-time-varying models the columns should be:

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey
- time** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of FoI by age and year

**survey\_features** A dataframe containing information about the binned age groups and sample sizes for each. It should contain columns:

- age\_min** Left limits of the age groups to be considered in the serosurvey
- age\_max** Right limits of the age groups to be considered in the serosurvey
- n\_sample** Number of samples by age group

The resulting age intervals are closed to the left [ and open to the right ).

**seroreversion\_rate** A non-negative value determining the rate of seroreversion (per year). Default is 0.

**Value**

A dataframe with simulated serosurvey data, including age group information, overall sample sizes, the number of seropositive individuals, and other survey features.

**Examples**

```
# specify FOIs for each year
foi_df <- data.frame(
  age = seq(1, 20, 1),
  foi = rnorm(20, 0.1, 0.01)
)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey_age(
  foi_df, survey_features)
```

---

```
simulate_serosurvey_age_time
```

*Simulate serosurvey data based on an age-and-time-varying Force-of-Infection (FoI) model.*

---

**Description**

This function generates binned serosurvey data based on an age-and-time-varying FoI model, optionally including seroreversion. This function allows construction of serosurveys with binned age groups, and it generates uncertainty in the distribution of a sample size within an age bin through multinomial sampling.

**Usage**

```
simulate_serosurvey_age_time(foi, survey_features, seroreversion_rate = 0)
```

**Arguments**

**foi** A dataframe containing the FoI values. For time-varying models the columns should be:

- year** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of the FoI by year

For age-varying models the columns should be:.

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey
- foi** Corresponding values of the FoI by age

For age-and-time-varying models the columns should be:

- age** Ages starting at 1 and up to the age of the oldest person in the serosurvey

**time** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey

**foi** Corresponding values of FoI by age and year

survey\_features

A dataframe containing information about the binned age groups and sample sizes for each. It should contain columns:

**age\_min** Left limits of the age groups to be considered in the serosurvey

**age\_max** Right limits of the age groups to be considered in the serosurvey

**n\_sample** Number of samples by age group

The resulting age intervals are closed to the left [ and open to the right ).

seroreversion\_rate

A non-negative value determining the rate of seroreversion (per year). Default is 0.

## Value

A dataframe with simulated serosurvey data, including age group information, overall sample sizes, the number of seropositive individuals, and other survey features.

## Examples

```
# specify FOIs for each year
foi_df <- expand.grid(
  year = seq(1990, 2009, 1),
  age = seq(1, 20, 1)
)
foi_df$foi <- rnorm(20 * 20, 0.1, 0.01)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey_age_time(
  foi_df, survey_features)
```

---

simulate\_serosurvey\_general

*Simulate serosurvey data based on general serocatalytic model.*

---

## Description

This simulation method assumes only that the model system can be written as a piecewise-linear ordinary differential equation system.

**Usage**

```
simulate_serosurvey_general(
  construct_A_fun,
  calculate_seroprev_fun,
  initial_conditions,
  survey_features,
  ...
)
```

**Arguments**

**construct\_A\_fun**  
A function that constructs a matrix that defines the multiplier term in the linear ODE system.

**calculate\_seroprev\_fun**  
A function which takes the state vector and returns the seropositive fraction.

**initial\_conditions**  
The initial state vector proportions for each birth cohort.

**survey\_features**  
A dataframe containing information about the binned age groups and sample sizes for each. It should contain columns:  
**age\_min** Left limits of the age groups to be considered in the serosurvey  
**age\_max** Right limits of the age groups to be considered in the serosurvey  
**n\_sample** Number of samples by age group  
The resulting age intervals are closed to the left [ and open to the right ).

... Additional parameters for construct\_A\_fun

**Value**

A dataframe with simulated serosurvey data, including age group information, overall sample sizes, the number of seropositive individuals, and other survey features.

**Examples**

```
foi_df_time <- data.frame(
  year = seq(1946, 2025, 1),
  foi = c(rep(0, 40), rep(1, 40))
)

foi_df_age <- data.frame(
  age = 1:80,
  foi = 2 * dlnorm(1:80, meanlog = 3.5, sdlog = 0.5)
)

# generate age and time dependent FoI from multipliers
foi_age_time <- expand.grid(
  year = foi_df_time$year,
  age = foi_df_age$age
```

```

) |>
  dplyr::left_join(foi_df_age, by = "age") |>
  dplyr::rename(foi_age = foi) |>
  dplyr::left_join(foi_df_time, by = "year") |>
  dplyr::rename(foi_time = foi) |>
  dplyr::mutate(foi = foi_age * foi_time) |>
  dplyr::select(-c("foi_age", "foi_time"))

# create survey features for simulating
max_age <- 80
n_sample <- 50
survey_features <- data.frame(
  age_min = seq(1, max_age, 5),
  age_max = seq(5, max_age, 5)) |>
  dplyr::mutate(n_sample = rep(n_sample, length(age_min))
)

# simulate survey from age and time FoI
serosurvey <- simulate_serosurvey(
  model = "age-time",
  foi = foi_age_time,
  survey_features = survey_features
)

```

---

```
simulate_serosurvey_time
```

*Simulate serosurvey data based on a time-varying Force-of-Infection (FoI) model.*

---

## Description

This function generates binned serosurvey data based on a time-varying FoI model, optionally including seroreversion. This function allows construction of serosurveys with binned age groups, and it generates uncertainty in the distribution of a sample size within an age bin through multinomial sampling.

## Usage

```
simulate_serosurvey_time(foi, survey_features, seroreversion_rate = 0)
```

## Arguments

**foi** A dataframe containing the FoI values. For time-varying models the columns should be:

- year** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey
- foi** Corresponding values of the FoI by year

For age-varying models the columns should be:

**age** Ages starting at 1 and up to the age of the oldest person in the serosurvey

**foi** Corresponding values of the FoI by age

For age-and-time-varying models the columns should be:

**age** Ages starting at 1 and up to the age of the oldest person in the serosurvey

**time** Calendar years starting at the birth year of the oldest person and up to the time of the serosurvey

**foi** Corresponding values of FoI by age and year

**survey\_features**

A dataframe containing information about the binned age groups and sample sizes for each. It should contain columns:

**age\_min** Left limits of the age groups to be considered in the serosurvey

**age\_max** Right limits of the age groups to be considered in the serosurvey

**n\_sample** Number of samples by age group

The resulting age intervals are closed to the left [ and open to the right ).

**seroreversion\_rate**

A non-negative value determining the rate of seroreversion (per year). Default is 0.

## Value

A dataframe with simulated serosurvey data, including age group information, overall sample sizes, the number of seropositive individuals, and other survey features.

## Examples

```
# specify FOIs for each year
foi_df <- data.frame(
  year = seq(1990, 2009, 1),
  foi = rnorm(20, 0.1, 0.01)
)
survey_features <- data.frame(
  age_min = c(1, 3, 15),
  age_max = c(2, 14, 20),
  n_sample = c(1000, 2000, 1500))
serosurvey <- simulate_serosurvey_time(
  foi_df, survey_features)
```

---

summarise\_central\_estimate

*Summarise central estimate*

---

## Description

Summarise central estimate

**Usage**

```
summarise_central_estimate(
  seromodel,
  serosurvey,
  alpha,
  par_name = "seroreversion_rate",
  central_estimate_digits = 2
)
```

**Arguments**

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models)
	age_min Floor value of the average between age_min and age_max
	age_max The size of the sample
	n_sample Number of samples for each age group
	n_seropositive Number of positive samples for each age group
alpha	1 - alpha indicates the credibility level to be used
par_name	String specifying the parameter to be extracted from seromodel
central_estimate_digits	Number of central estimate digits

**Value**

Text summarising specified central estimate

**Examples**

```
data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
summarise_central_estimate(
  seromodel,
  veev2012,
  alpha = 0.05,
  par_name = "foi"
)
```

---

```
summarise_loo_estimate
```

*Extract specified loo estimate*

---

**Description**

Extract specified loo estimate

**Usage**

```
summarise_loo_estimate(
  seromodel,
  par_loo_estimate = "elpd_loo",
  loo_estimate_digits = 2
)
```

**Arguments**

`seromodel` `stan_fit` object obtained from sampling a model with [fit\\_seromodel](#)

`par_loo_estimate` Name of the loo estimate to be extracted. Available options are:  
 "elpd\_loo" Expected log pointwise predictive density  
 "p\_loo" Effective number of parameters  
 "looic" Leave-one-out cross-validation information criteria  
 For additional information refer to [loo](#).

`loo_estimate_digits` Number of loo estimate digits

**Value**

Text summarising specified loo estimate

**Examples**

```
data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
summarise_loo_estimate(seromodel)
```

---

`summarise_seromodel` *Summarise specified model*

---

**Description**

Summarise specified model

**Usage**

```
summarise_seromodel(
  seromodel,
  serosurvey,
  alpha = 0.05,
  par_loo_estimate = "elpd_loo",
  loo_estimate_digits = 1,
  central_estimate_digits = 2,
  rhat_digits = 2
)
```

**Arguments**

seromodel	stan_fit object obtained from sampling a model with <a href="#">fit_seromodel</a>
serosurvey	survey_year Year in which the survey took place (only needed to plot time models) age_min Floor value of the average between age_min and age_max age_max The size of the sample n_sample Number of samples for each age group n_seropositive Number of positive samples for each age group
alpha	1 - alpha indicates the credibility level to be used
par_loo_estimate	Name of the loo estimate to be extracted. Available options are: "elpd_loo" Expected log pointwise predictive density "p_loo" Effective number of parameters "looic" Leave-one-out cross-validation information criteria For additional information refer to <a href="#">loo</a> .
loo_estimate_digits	Number of loo estimate digits
central_estimate_digits	Number of central estimate digits
rhat_digits	Number of rhat estimate digits

**Value**

A list summarising the specified model

model_name	Name of the model
elpd	elpd and its standard deviation
foi	Estimated foi with credible interval (for 'constant' model)
foi_rhat	foi rhat value (for 'constant' model)
seroreversion_rate	Estimated seroreversion rate
seroreversion_rate_rhat	Seroreversion rate rhat value

**Examples**

```
data(veev2012)
seromodel <- fit_seromodel(veev2012, iter = 100)
summarise_seromodel(seromodel, veev2012)
```

---

veev2012	<i>Venezuelan Equine Encephalitis Virus (VEEV) seroprevalence data in serofoi</i>
----------	---

---

**Description**

Datasets that measure the seroprevalence of IgG antibodies against VEEV in a rural village in Panamá in 2012 [[Carrera2020](#)].

**Usage**

```
data(veev2012)
```

**Format**

veev2012:

A <data.frame> with 4 rows and 5 columns:

**survey\_year** Year in which the serosurvey was conducted

**n\_sample** Number of collected samples per age group

**n\_seropositive** Number of positive samples per age group

**age\_min** Age group minimal age

**age\_max** Age group maximal age

**Examples**

```
data(veev2012)
```

# Index

- \* **datasets**
  - chagas2012, [6](#)
  - chik2015, [7](#)
  - veev2012, [39](#)
- add\_age\_group\_to\_serosurvey, [4](#)
- build\_stan\_data, [5](#)
- chagas2012, [6](#)
- chik2015, [7](#)
- extract\_central\_estimates, [7](#)
- fit\_seromodel, [8](#), [8](#), [10–12](#), [14](#), [15](#), [17](#), [36–38](#)
- get\_foi\_index, [5](#), [9](#), [10](#), [24](#)
- ggplot2, [11](#), [12](#), [14–17](#)
- loo, [37](#), [38](#)
- plot\_foi\_estimates, [11](#)
- plot\_rhats, [12](#)
- plot\_seromodel, [13](#)
- plot\_seroprev\_estimates, [15](#)
- plot\_serosurvey, [16](#)
- plot\_summary, [17](#)
- prepare\_serosurvey\_for\_plot, [18](#)
- prob\_seroprev\_age\_by\_age, [20](#)
- prob\_seroprev\_age\_time\_by\_age, [20](#)
- prob\_seroprev\_by\_age, [21](#)
- prob\_seroprev\_gen\_by\_age, [22](#)
- prob\_seroprev\_time\_by\_age, [24](#)
- probability\_exact\_age\_varying, [19](#)
- probability\_exact\_time\_varying, [19](#)
- rstan, [9](#), [25](#)
- serofoi (serofoi-package), [3](#)
- serofoi-package, [3](#)
- set\_foi\_init, [24](#)
- set\_stan\_data\_defaults, [25](#)
- sf\_cauchy, [5](#), [9](#), [26](#)
- sf\_none, [6](#), [9](#), [26](#)
- sf\_normal, [5](#), [6](#), [9](#), [27](#)
- sf\_uniform, [5](#), [6](#), [9](#), [27](#)
- simulate\_serosurvey, [28](#)
- simulate\_serosurvey\_age, [30](#)
- simulate\_serosurvey\_age\_time, [31](#)
- simulate\_serosurvey\_general, [32](#)
- simulate\_serosurvey\_time, [34](#)
- summarise\_central\_estimate, [35](#)
- summarise\_loo\_estimate, [36](#)
- summarise\_seromodel, [37](#)
- veev2012, [39](#)