Package ‘seroreconstruct’

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Type Package

Title Reconstructing Antibody Dynamics to Estimate the Risk of Influenza Virus Infection

Version 1.1.5

Maintainer Tim Tsang <`timkltsang@gmail.com`>

Description A Bayesian framework for inferring influenza infection status from serial antibody measurements. Jointly estimates season-specific infection probabilities, antibody boosting and waning after infection, and baseline hemagglutination inhibition (HAI) titer distributions via Markov chain Monte Carlo (MCMC). Supports multi-season analysis and subgroup comparisons via a group_by interface. See Tsang et al. (2022) <doi:10.1038/s41467-022-29310-8> for methodological details.

License GPL (>= 2)

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LazyData TRUE

URL `https://github.com/timktsang/seroreconstruct`

BugReports `https://github.com/timktsang/seroreconstruct/issues`

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Author Tim Tsang [aut, cre] (ORCID: <`https://orcid.org/0000-0001-5037-6776`>)

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Contents

`flu_activity` *Example of flu activity data*

Description

This is an example of the flu activity data used in the `seroreconstruct` function. This data frame specifies the format of the flu activity data.

Usage

```
data(flu_activity)
```

Format

A data frame with 1 variable, where each row represents a date, and it should match the date in the input data:

h1.activity This is the influenza activity from surveillance data. It can be on a relative scale, as the model includes a scale parameter to estimate infection probability.

See Also

Other example_data: `para1`, `para2`

`inputdata` *Example of input data*

Description

This is an example of the input data used in the `seroreconstruct` function. This data frame illustrates the format of the input data.

Usage

```
data(inputdata)
```

Format

A data frame with 9 variables, where each row represents an individual:

age_group 0: children, 1: adults, 2: older adults

start_time start of follow-up

end_time end of follow-up

time1 date of first serum collection

time2 date of second serum collection

time3 date of third serum collection

HAI_titer_1 HAI titer for first serum collection

HAI_titer_2 HAI titer for second serum collection

HAI_titer3 HAI titer for third serum collection

`output_model_estimate` *Extract the model estimates from the fitted MCMC*

Description

`output_model_estimate` is deprecated; use `summary()` instead.

Usage

```
output_model_estimate(fitted_MCMC, period)
```

Arguments

`fitted_MCMC`	A `seroreconstruct_fit` object, or a list returned by an older version of `sero_reconstruct()`.
`period`	A vector indicating the start and the end of a season to compute the infection probabilities. If empty, the start and end of the season are inferred from the data.

Value

A data frame of model estimates (invisibly).

Examples

```
## Not run:
a1 <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
fitted_result <- output_model_estimate(a1)  # deprecated, use summary(a1)

## End(Not run)
```

`para1` *Example of parameter vector for the main model*

Description

This is an example of the parameter vector for the main model used in the `seroreconstruct` function. This data frame specifies the format of the parameter vector for the main model.

Usage

```
data(para1)
```

Format

A numeric vector with 10 elements (for a single-season model, `S = 1`). The general length is `6 + 4*S` where `S` is the number of seasons.

Elements 1–6 (shared) 1) random measurement error, 2) 2-fold error, 3) boosting for children (log2), 4) waning for children (log2), 5) boosting for adults (log2), 6) waning for adults (log2).

Elements 7–9 (per-season) infection risk scale parameters for children, adults, and older adults (3 per season).

Element 10 (per-season) log risk ratio of 2-fold increase in baseline HAI titer (1 per season).

See Also

Other example_data: `flu_activity`, `para2`

`para2` *Example of parameter vector for the baseline HAI titer for the main model*

Description

This is an example of the parameter vector for the baseline HAI titer for the main model used in the `seroreconstruct` function. This data frame specifies the format of the parameter vector for the baseline HAI titer for the main model.

Usage

```
data(para2)
```

Format

A numeric vector with 20 elements (for a single-season model, `S = 1`). The general length is `20 * S` where `S` is the number of seasons.

Elements 1–10 probability that the HAI titer is 0–9 for children

Elements 11–20 probability that the HAI titer is 0–9 for adults

For multi-season models, this pattern repeats for each season.

See Also

Other example_data: `flu_activity`, `para1`

`plot_boosting` *Plot posterior boosting distributions*

Description

Draws violin plots of the posterior fold-rise in antibody titer after infection, one violin per boosting parameter group. Matches the style of Figure 1C in Tsang et al. (2022).

Usage

```
plot_boosting(fit, cols = NULL, main = NULL, show_legend = TRUE, ...)
```

Arguments

`fit`	A `seroreconstruct_fit` or `seroreconstruct_joint` object. Only single-season fits are currently supported.
`cols`	Optional character vector of colors, one per group.
`main`	Optional plot title.
`show_legend`	Logical; whether to draw a legend. Default `TRUE`.
`...`	Additional graphical parameters passed to `plot()`.

Value

Invisible `NULL`. Called for its side effect of producing a plot.

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
plot_boosting(fit)
```

`plot_diagnostics` *MCMC diagnostic plots*

Description

Produces trace plots and posterior density plots for each model parameter. Trace plots show the MCMC chain with the posterior mean (red dashed line). Density plots show the marginal posterior with 95% credible interval bounds (blue dashed lines).

Usage

```
plot_diagnostics(fit, params = NULL)
```

Arguments

`fit`	A `seroreconstruct_fit`, `seroreconstruct_joint`, or `seroreconstruct_multi` object.
`params`	Optional character vector of parameter names to plot. If `NULL` (default), all parameters are plotted. Use `table_parameters(fit)$Parameter` to see available names.

Value

Invisible `NULL`. Called for its side effect of producing plots.

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
# Plot selected parameters (use params = NULL for all)
plot_diagnostics(fit, params = c("random_error", "twofold_error"))
```

`plot_infection_prob` *Plot infection probabilities (forest plot)*

Description

Forest plot showing posterior infection probabilities with 95% credible intervals. Supports single fits, multi-group fits, and combining results from multiple fits with section headers.

Usage

```
plot_infection_prob(
  fits,
  labels = NULL,
  main = NULL,
  file = NULL,
  width = 8,
  height = NULL,
  xlim = NULL,
  cex = 0.85,
  ...
)
```

Arguments

`fits`	A `seroreconstruct_fit`, `seroreconstruct_joint`, `seroreconstruct_multi` object, or a named list of fit objects. When a named list is provided, names are used as section headers.
`labels`	Optional character vector of custom labels for the strata within each fit. For a named list of fits, use a list of character vectors.
`main`	Optional plot title.
`file`	Optional file path for PDF output. Default: `NULL` (current device).
`width`	PDF width in inches. Default: 8.
`height`	PDF height in inches. Default: auto-calculated.
`xlim`	Numeric vector of length 2 for the x-axis range (probability scale, e.g. `c(0, 0.5)`). Default: auto-determined.
`cex`	Character expansion factor. Default: 0.85.
`...`	Additional graphical parameters passed to `plot()`.

Value

Invisible data frame of the plotted estimates (Stratum, Probability, Lower, Upper).

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
plot_infection_prob(fit)
```

`plot_trajectory` *Plot antibody trajectory with model fit*

Description

For a single individual, draws posterior-sampled antibody trajectories overlaid on observed HAI titers. Red lines show trajectories where infection occurred; blue lines show trajectories without infection. Matches the visualization style of Figure 1B in Tsang et al. (2022).

Usage

```
plot_trajectory(
  fit,
  id = 1,
  subjects = NULL,
  n_samples = 100,
  main = NULL,
  col_infected = NULL,
  col_uninfected = NULL,
  show_legend = TRUE,
  ...
)
```

Arguments

`fit`	A `seroreconstruct_fit` or `seroreconstruct_joint` object.
`id`	Row index (integer) or subject identifier to plot. Numeric values in the valid row range (1 to N) are treated as 1-based row indices. Numeric values outside that range are looked up in `subject_ids` or `subjects` if available. Non-numeric values are always looked up by subject identifier.
`subjects`	Optional vector of subject identifiers aligned with fit rows. Use this when `subject_ids` was not provided at fitting time. Example: `subjects = inputdata$subject_id`.
`n_samples`	Number of posterior samples to draw. Default 100.
`main`	Optional plot title. If `NULL`, a default title with the individual index and posterior infection probability is generated.
`col_infected`	Color for infected trajectories. Default semi-transparent red.
`col_uninfected`	Color for uninfected trajectories. Default semi-transparent blue.
`show_legend`	Logical; whether to draw a legend. Default `TRUE`.
`...`	Additional graphical parameters passed to `plot()`.

Value

Invisible `NULL`. Called for its side effect of producing a plot.

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
plot_trajectory(fit, id = 1)
```

`plot_waning` *Plot posterior waning curves*

Description

Shows the fraction of peak antibody remaining over time since infection, with posterior median and 95% credible band for each waning parameter group. Matches the style of Figure 1D in Tsang et al. (2022).

Usage

```
plot_waning(fit, days = 400, cols = NULL, main = NULL, show_legend = TRUE, ...)
```

Arguments

`fit`	A `seroreconstruct_fit` or `seroreconstruct_joint` object. Only single-season fits are currently supported.
`days`	Maximum number of days to plot on the x-axis. Default 400.
`cols`	Optional character vector of colors, one per group.
`main`	Optional plot title.
`show_legend`	Logical; whether to draw a legend. Default `TRUE`.
`...`	Additional graphical parameters passed to `plot()`.

Value

Invisible `NULL`. Called for its side effect of producing a plot.

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
plot_waning(fit)
```

`print.seroreconstruct_fit`

Print method for seroreconstruct_fit

Description

Print method for seroreconstruct_fit

Usage

```
## S3 method for class 'seroreconstruct_fit'
print(x, ...)
```

Arguments

`x`	A `seroreconstruct_fit` object.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`print.seroreconstruct_joint`

Print method for seroreconstruct_joint

Description

Print method for seroreconstruct_joint

Usage

```
## S3 method for class 'seroreconstruct_joint'
print(x, ...)
```

Arguments

`x`	A `seroreconstruct_joint` object.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`print.seroreconstruct_multi`
Print method for seroreconstruct_multi

Description

Print method for seroreconstruct_multi

Usage

```
## S3 method for class 'seroreconstruct_multi'
print(x, ...)
```

Arguments

`x`	A `seroreconstruct_multi` object.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`print.summary.seroreconstruct_fit`
Print method for summary.seroreconstruct_fit

Description

Print method for summary.seroreconstruct_fit

Usage

```
## S3 method for class 'summary.seroreconstruct_fit'
print(x, digits = 2, ...)
```

Arguments

`x`	A `summary.seroreconstruct_fit` object.
`digits`	Number of decimal places for rounding. Default 2.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`print.summary.seroreconstruct_joint`

Print method for summary.seroreconstruct_joint

Description

Print method for summary.seroreconstruct_joint

Usage

```
## S3 method for class 'summary.seroreconstruct_joint'
print(x, digits = 2, ...)
```

Arguments

`x`	A `summary.seroreconstruct_joint` object.
`digits`	Number of decimal places for rounding. Default 2.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`print.summary.seroreconstruct_multi`

Print method for summary.seroreconstruct_multi

Description

Print method for summary.seroreconstruct_multi

Usage

```
## S3 method for class 'summary.seroreconstruct_multi'
print(x, digits = 2, ...)
```

Arguments

`x`	A `summary.seroreconstruct_multi` object.
`digits`	Number of decimal places for rounding. Default 2.
`...`	Additional arguments (ignored).

Value

The input object `x`, invisibly.

`sero_reconstruct` *Run the MCMC for the Bayesian model*

Description

The main function to run the MCMC for the Bayesian model, to obtain individual dynamics, model parameters such as infection probability, boosting, waning, and measurement error.

Usage

```
sero_reconstruct(
  inputdata,
  inputILI,
  n_iteration = 2000,
  burnin = 1000,
  thinning = 1,
  group_by = NULL,
  shared = NULL,
  subject_ids = NULL
)
```

Arguments

`inputdata`	The data for running MCMC, in dataframe format. It should be in the same format as the data in the package. It includes: 1) age_group (0: children, 1: adults, 2: older adults), 2) start_time: start of follow-up, 3) end_time: end of follow-up, 4) time1: date for first serum collection, 5) time2: date for second serum collection, 6) time3: date for third serum collection, 7) HAI_titer_1: HAI titer for first serum collection, 8) HAI_titer_2: HAI titer for second serum collection, 9) HAI_titer_3: HAI titer for third serum collection.
`inputILI`	The data for influenza activity used in the inference. The row number should match with the date in the inputdata.
`n_iteration`	The number of iterations of the MCMC.
`burnin`	The iteration for burn-in for MCMC.
`thinning`	The number of thinning in MCMC.
`group_by`	Optional formula specifying grouping variables (e.g., `~age_group`). When provided, independent MCMCs are fit for each combination of the grouping variables. The formula uses interaction semantics: `~age + vac` means all age-by-vac combinations. Returns a `seroreconstruct_multi` object.
`shared`	Optional character vector specifying which parameters to share across groups when `group_by` is also provided. Measurement error parameters are always shared (they are a lab assay property, identical across groups). Valid values: `"error"` (measurement error only, the default when `shared` is non-NULL), `"boosting_waning"` (also share antibody boosting and waning across groups). When specified, a single joint MCMC is run with all groups pooled together,

	sharing the specified parameters while estimating group-specific infection probabilities. Returns a `seroreconstruct_joint` object.
`subject_ids`	Optional vector (character, numeric, or factor) of subject identifiers, one per row of `inputdata`. When provided, stored in the fit object and used by `plot_trajectory()` to look up individuals by ID rather than row index. Example: `subject_ids = inputdata$household_id`.

Details

Multi-season support: If `inputdata` contains an optional integer column named `season` (0-indexed, contiguous from 0 to `n_seasons - 1`), the model fits season-specific infection risk and HAI protection parameters. When no `season` column is present, all individuals are assigned to a single season (`n_seasons = 1`) and behavior is identical to previous versions. Validated with simulation recovery studies up to 7 seasons.

Shared parameters: When `shared` is provided together with `group_by`, a single joint MCMC chain is run with all individuals pooled. Measurement error and boosting/waning parameters are shared across groups (informed by all data), while infection risk and HAI protection parameters remain group-specific. This is more statistically efficient than independent chains when groups share biological or measurement properties.

Single-group design: When using `group_by` without `shared`, independent MCMCs are fit for each group. To compare children vs adults, fit each group separately using `group_by = ~age_group`.

Current limitation: `summary()` is not yet implemented for fits with `n_seasons > 1`. Multi-season posterior samples are accessible directly from the fit object (e.g., `fit$posterior_model_parameter`).

Value

A `seroreconstruct_fit` object (when `group_by` is `NULL`) or a `seroreconstruct_multi` object (when `group_by` is provided). Use `summary()` to extract model estimates.

Examples

```
a1 <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
summary(a1)
```

`simulate_data` *Simulation of the dataset of the Bayesian model*

Description

The function to simulate the dataset, for validation or other purpose.

Usage

```
simulate_data(inputdata, inputILI, para1, para2, n_groups = 3L)
```

Arguments

`inputdata`	The data with the same format that for running MCMC, in dataframe format.
`inputILI`	The data for influenza activity used in the inference. The row number should match with the date in the inputdata.
`para1`	Numeric vector of active model parameters. Length depends on the number of seasons `S` (determined by the `season` column in `inputdata`, default `S = 1`): • Elements 1–6 (shared): 1) random measurement error, 2) 2-fold error, 3) boosting for children (log2), 4) waning for children (log2), 5) boosting for adults (log2), 6) waning for adults (log2). • Elements 7 to `6 + 3*S` (per-season): infection risk scale parameters for children, adults, and older adults, repeated for each season. • Elements `6 + 3*S + 1` to `6 + 4*S` (per-season): log risk ratio of 2-fold increase in baseline HAI titer, one per season. Total length: `6 + (G + 1)*S` where `G` is `n_groups` (e.g., 10 for G=3 S=1, 34 for G=3 S=7). See `para1` for an example with `G = 3, S = 1`.
`para2`	Numeric vector for baseline HAI titer distributions. Length `20 * S`: for each season, 10 probabilities for children (HAI titer levels 0–9) followed by 10 probabilities for adults. See `para2` for an example with `S = 1`.
`n_groups`	Number of groups for infection risk parameters (default 3 for the standard 3-age-group model).

Value

A simulated data based on the input parameter vectors, with the format equal to the input data.

Examples

```
simulated <- simulate_data(inputdata, flu_activity, para1, para2)
```

`summary.seroreconstruct_fit`

Summary method for seroreconstruct_fit

Description

Computes estimates of infection probabilities, boosting, waning, and measurement error from a fitted MCMC object.

Usage

```
## S3 method for class 'seroreconstruct_fit'
summary(object, period, ...)
```

Arguments

`object`	A `seroreconstruct_fit` object.
`period`	Optional numeric vector of length 2 specifying the start and end of a season to compute infection probabilities. If omitted, the full follow-up period is used.
`...`	Additional arguments (ignored).

Value

A `summary.seroreconstruct_fit` object with element `$table`.

`summary.seroreconstruct_joint`

Summary method for seroreconstruct_joint

Description

Computes shared parameter estimates and per-group infection probabilities from a joint fit with shared parameters.

Usage

```
## S3 method for class 'seroreconstruct_joint'
summary(object, period, ...)
```

Arguments

`object`	A `seroreconstruct_joint` object.
`period`	Optional numeric vector of length 2 specifying the start and end of a season to compute infection probabilities.
`...`	Additional arguments (ignored).

Value

A `summary.seroreconstruct_joint` object with element `$table`.

`summary.seroreconstruct_multi` *Summary method for seroreconstruct_multi*

Description

Computes estimates for each group and combines into a single table.

Usage

```
## S3 method for class 'seroreconstruct_multi'
summary(object, period, ...)
```

Arguments

`object`	A `seroreconstruct_multi` object.
`period`	Optional numeric vector of length 2 specifying the start and end of a season to compute infection probabilities.
`...`	Additional arguments (ignored).

Value

A `summary.seroreconstruct_multi` object with element `$table`.

`table_infections` *Per-individual infection estimates*

Description

Summarizes posterior infection status, timing, and baseline titer for each individual in the dataset.

Usage

```
table_infections(fit)
```

Arguments

`fit`	A `seroreconstruct_fit` or `seroreconstruct_joint` object.

Value

A data frame with one row per individual and columns: `Individual` (row index), `Infection_prob` (posterior mean probability of infection), `Infection_time_mean` (mean infection time among infected samples), `Baseline_titer_mean` (mean imputed baseline HAI titer).

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
head(table_infections(fit))
```

`table_parameters` *Summary table of model parameters with credible intervals*

Description

Extracts posterior summaries (mean, median, credible intervals) for all active model parameters.

Usage

```
table_parameters(fit, probs = c(0.025, 0.975))
```

Arguments

`fit`	A `seroreconstruct_fit`, `seroreconstruct_joint`, or `seroreconstruct_multi` object.
`probs`	Numeric vector of length 2 giving the lower and upper quantile probabilities for the credible interval. Default `c(0.025, 0.975)` for a 95% interval.

Value

A data frame with columns: Parameter, Mean, Median, Lower, Upper.

Examples

```
fit <- sero_reconstruct(inputdata, flu_activity,
                        n_iteration = 2000, burnin = 1000, thinning = 1)
table_parameters(fit)
```

`[[.seroreconstruct_multi` *Subset a seroreconstruct_multi object*

Description

Access an individual group fit by name or index.

Usage

```
## S3 method for class 'seroreconstruct_multi'
x[[i, ...]]
```

Arguments

`x`	A `seroreconstruct_multi` object.
`i`	Group name (character) or index (integer).
`...`	Additional arguments (ignored).

Value

A `seroreconstruct_fit` object for the requested group.

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