

Package ‘Household.Transmission.Chain.Data.Analysis’

February 2, 2026

Title Household Transmission Chain Simulation and Estimation

Version 0.0.0.9000

Description Simulates and analyzes household transmission chains incorporating explicit viral load dynamics. The package provides three main capabilities. (1) Synthetic data generation with role-specific susceptibility and infectivity, community acquisition, within-household transmission driven by time-varying viral loads, and configurable surveillance testing; (2) Data preprocessing that constructs person-day panels and test-time matrices suitable for Bayesian inference, including time-since-infection tracking for latent period modeling; (3) Parameter estimation via Stan-based Markov chain Monte Carlo for community and household transmission rates, with support for estimating latent period duration. Includes diagnostic plots for infection timelines, secondary attack rates stratified by index case viral load, and aggregated incidence summaries. Designed for respiratory pathogens where transmission probability depends on the infector's viral shedding trajectory.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Imports data.table,
dplyr,
ggplot2,
tibble,
tidyr,
utils,
rstan,
stats

Suggests testthat (>= 3.0.0),
knitr,
rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

Contents

build_stan_household_arrays 2

GenSyn	3
main_parameter_estimation_pipeline	5
postprocess_stan_fit	8
prepare_stan_data	8
prepare_stan_households_from_user_data	9
print.GenSynResult	10
print.TransmissionChainResult	11
run_household_stan	12
simulate_households	12
TransmissionChainAnalysis	14

Index	17
--------------	-----------

build_stan_household_arrays

Build Stan data arrays from household list

Description

Converts a list of per-household data frames into Stan-ready arrays.

Usage

```
build_stan_household_arrays(
  households,
  T_max = 365L,
  seasonal_forcing_list = NULL,
  alpha_comm_by_role = 0.005,
  beta1 = 0.2,
  beta2 = 0.6,
  V_ref = 1000,
  reference_phi = 1,
  reference_kappa = 1,
  g_peak_day = 2,
  g_width = 4
)
```

Arguments

households	List of per-household data frames.
T_max	Integer; maximum time horizon.
seasonal_forcing_list	Named list of seasonal forcing vectors.
alpha_comm_by_role, beta1, beta2, V_ref	Numeric; model parameters.
reference_phi, reference_kappa	Numeric; reference parameters.
g_peak_day, g_width	Numeric; infectivity profile parameters.

Value

Named list for Stan.

GenSyn	<i>GenSyn: household simulation & estimation wrapper</i>
--------	--

Description

Runs `main_parameter_estimation_pipeline()` to simulate household data, fit via Bayesian Stan, and assemble a "GenSynResult".

Usage

```
GenSyn(
  n_households = 50,
  plots = c("daily", "weekly", "timeline", "sar"),
  print_plots = FALSE,
  index_vl_column = "vl_test",
  start_date = as.Date("2024-01-01"),
  end_date = as.Date("2024-12-31"),
  seasonal_forcing_list = NULL,
  max_days = 365,
  alpha_comm_by_role = 0.005,
  beta1 = 0.3,
  beta2 = 0.05,
  delta = 0,
  phi_by_role = c(adult = 1, child = 7, toddler = 7, elderly = 4),
  kappa_by_role = c(adult = 1, child = 1.5, toddler = 1.5, elderly = 1),
  latent_shape = 3,
  latent_scale = 0.5,
  infectious_shape = 3,
  infectious_scale = 1,
  resolve_shape = 1.5,
  resolve_scale = 0.5,
  peak_day = 1,
  width = 4,
  ptrans_threshold = 0.5,
  detect_threshold_log10 = 1,
  detect_threshold_Ct = 40,
  surveillance_interval = 7,
  test_daily = FALSE,
  viral_testing = "viral load",
  V_ref = 3,
  V_rho = 2.5,
  Ct_50 = 40,
  Ct_delta = 2,
  VL_params_list = default_VL_params,
  Ct_params_list = default_Ct_params,
  household_profile_list = default_household_profile,
  stan_file = "model.stan",
```

```

    stan_chains = 4,
    stan_iter = 2000,
    stan_warmup = 1000,
    stan_control = list(adapt_delta = 0.99, max_treedepth = 20),
    stan_init = "random",
    stan_refresh = 50,
    stan_cores = 4
)

```

Arguments

<code>n_households</code>	Integer; number of households to simulate.
<code>plots</code>	Character vector of plot names ("daily", "weekly", "sar", "timeline") or "all".
<code>print_plots</code>	Logical; print plots if TRUE.
<code>index_vl_column</code>	Character; viral-load (VL) column name for plotting (default "vl_test").
<code>start_date, end_date</code>	Date; study window.
<code>seasonal_forcing_list</code>	Optional named list of role vectors; seasonal forcing.
<code>max_days</code>	Integer; maximum simulated days.
<code>alpha_comm_by_role</code>	Numeric; baseline community acquisition rate.
<code>beta1, beta2</code>	Numeric; transmission coefficients.
<code>delta</code>	Numeric; household size scaling exponent.
<code>phi_by_role</code>	Named numeric vector; susceptibility multipliers by role.
<code>kappa_by_role</code>	Named numeric vector; infectivity multipliers by role.
<code>latent_shape, latent_scale</code>	Numeric; gamma parameters for latent period.
<code>infectious_shape, infectious_scale</code>	Numeric; gamma parameters for infectious period.
<code>resolve_shape, resolve_scale</code>	Numeric; gamma parameters for resolution period.
<code>peak_day, width</code>	Numeric; infectivity profile parameters.
<code>ptrans_threshold</code>	Numeric; transmission potential threshold.
<code>detect_threshold_log10</code>	Numeric; VL detection threshold in log10.
<code>detect_threshold_Ct</code>	Numeric; Ct detection threshold.
<code>surveillance_interval</code>	Integer; days between scheduled tests.
<code>test_daily</code>	Logical; switch to daily testing after first detection.
<code>viral_testing</code>	Character; "viral load" or "Ct".
<code>V_ref, V_rho</code>	Numeric; viral load reference and power.
<code>Ct_50, Ct_delta</code>	Numeric; Ct-based infectivity parameters.

VL_params_list Named list; role-specific VL trajectory parameters.

Ct_params_list Named list; role-specific Ct trajectory parameters.

household_profile_list
Named list; household composition probabilities.

stan_file Path to a Stan model file.

stan_chains, stan_iter, stan_warmup
Integers; Stan sampling controls.

stan_control List; Stan control list.

stan_init Character or function; Stan initialization.

stan_refresh Integer; Stan refresh rate.

stan_cores Integer; CPU cores for Stan.

Value

A "GenSynResult" list with elements: \$call, \$n_households, \$results, \$postprocessing, \$plot_list.

See Also

[main_parameter_estimation_pipeline](#), [TransmissionChainAnalysis](#)

Examples

```
## Not run:
# Simulate and estimate
seasonal_forcing_list <- list(
  adult=rep(0.1,365), child=rep(0.1,365), elderly=rep(0.1,365), toddler=rep(0.1,365)
)
fit <- GenSyn(
  n_households=50,
  seasonal_forcing_list=seasonal_forcing_list, max_days=365,
  stan_chains=4, stan_iter=2000, stan_warmup=1000, stan_cores=4
)

## End(Not run)
```

main_parameter_estimation_pipeline

Main parameter estimation pipeline

Description

End-to-end workflow for household transmission estimation via Bayesian Stan. Works with simulated or user-provided data.

Usage

```

main_parameter_estimation_pipeline(
  user_data = NULL,
  synthetic_data = TRUE,
  n_households = 10,
  start_date = as.Date("2024-01-01"),
  end_date = as.Date("2024-12-31"),
  seasonal_forcing_list = NULL,
  max_days = 365,
  alpha_comm_by_role = 0.005,
  beta1 = 0.3,
  beta2 = 0.05,
  delta = 0,
  phi_by_role = c(adult = 1, child = 7, toddler = 7, elderly = 4),
  kappa_by_role = c(adult = 1, child = 1.5, toddler = 1.5, elderly = 1),
  latent_shape = 3,
  latent_scale = 0.5,
  infectious_shape = 3,
  infectious_scale = 1,
  resolve_shape = 1.5,
  resolve_scale = 0.5,
  peak_day = 1,
  width = 4,
  ptrans_threshold = 0.5,
  detect_threshold_log10 = 1,
  detect_threshold_Ct = 40,
  surveillance_interval = 7,
  test_daily = FALSE,
  viral_testing = "viral load",
  V_ref = 3,
  V_rho = 2.5,
  Ct_50 = 40,
  Ct_delta = 2,
  VL_params_list = default_VL_params,
  Ct_params_list = default_Ct_params,
  household_profile_list = default_household_profile,
  stan_file = "model.stan",
  stan_chains = 4,
  stan_iter = 2000,
  stan_warmup = 1000,
  stan_control = list(adapt_delta = 0.99, max_treedepth = 20),
  stan_init = "random",
  stan_refresh = 50,
  stan_cores = 4
)

```

Arguments

<code>user_data</code>	Optional; data.frame or list of data.frames.
<code>synthetic_data</code>	Logical; if TRUE, simulate data internally.
<code>n_households</code>	Integer; number of households to simulate.

start_date, end_date	Date; analysis window.
seasonal_forcing_list	Optional named list for seasonality.
max_days	Integer; maximum days.
alpha_comm_by_role	Numeric; community acquisition rate.
beta1, beta2	Numeric; transmission coefficients.
delta	Numeric; household size scaling.
phi_by_role, kappa_by_role	Named numeric vectors.
latent_shape, latent_scale	Numeric; latent period parameters.
infectious_shape, infectious_scale	Numeric; infectious period parameters.
resolve_shape, resolve_scale	Numeric; resolution period parameters.
peak_day, width	Numeric; infectivity profile.
ptrans_threshold, detect_threshold_log10, detect_threshold_Ct	Numeric; testing thresholds.
surveillance_interval	Integer; days between tests.
test_daily	Logical; daily testing after detection.
viral_testing	Character; "viral load" or "Ct".
V_ref, V_rho	Numeric; viral load parameters.
Ct_50, Ct_delta	Numeric; Ct parameters.
VL_params_list, Ct_params_list, household_profile_list	Named lists.
stan_file	Path to Stan model file.
stan_chains, stan_iter, stan_warmup	Integers; Stan sampling controls.
stan_control	List; Stan control list.
stan_init	Character or function; Stan initialization.
stan_refresh	Integer; Stan refresh.
stan_cores	Integer; CPU cores for Stan.

Value

A list with raw_simulation, stan_data, fit, posterior_summary, and diagnostic_df.

See Also

[GenSyn](#)

postprocess_stan_fit	<i>Tidy posterior summary for role multipliers</i>
----------------------	--

Description

Extracts posterior summaries from a stanfit.

Usage

```
postprocess_stan_fit(fit)
```

Arguments

fit	A stanfit object.
-----	-------------------

Value

A data frame with posterior summaries.

prepare_stan_data	<i>Prepare Stan data from diagnostic testing records</i>
-------------------	--

Description

Converts raw diagnostic testing data into Stan-ready format with the time_since_infection matrix for soft-gate latent period modeling.

Usage

```
prepare_stan_data(
  raw_data,
  seasonal_forcing_list = NULL,
  viral_testing_mode = "viral load",
  T_max = 365,
  V_ref = 3,
  V_rho = 2.5,
  peak_day = 2,
  width = 4,
  alpha_comm_by_role = 0.005,
  reference_phi = 1,
  reference_kappa = 1
)
```


Arguments

raw_data	Data frame with columns hh_id, person_id, role, day_index, test_result, and optionally pcr_sample.
seasonal_forcing_list	Named list with seasonal forcing vectors by role.
viral_testing_mode	Character; "viral load" or "Ct".
T_max	Integer; maximum time horizon (days).
V_ref, V_rho	Numeric; viral load transmission parameters.
peak_day, width	Numeric; infectivity profile parameters.
alpha_comm_by_role	Numeric; community acquisition rate.
reference_phi, reference_kappa	Numeric; reference parameters.

Value

Named list suitable for Stan.

```
prepare_stan_households_from_user_data
```

Prepare per-household inputs for the Stan RSV/VL model

Description

Converts user data to a list of per-household data frames required by the Stan RSV/VL pipeline. Accepts either a long test-day table or a per-person episodes table.

Usage

```
prepare_stan_households_from_user_data(
  user_data,
  role_levels = c("adult", "child", "elderly", "toddler"),
  vl_mode = c("from_long", "auto"),
  vl_source = c("none", "column", "simulate"),
  vl_column = NULL,
  start_date = NULL,
  end_date = NULL
)
```

Arguments

user_data	Either: <ul style="list-style-type: none"> <i>Long format:</i> columns HH, individual_ID, role, test_date, infection_status (optionally a VL column); or <i>Per-person format:</i> columns hh_id, person_id, role, infection_time, infectious_start, infectious_end (optionally vl_full_trajectory).
role_levels	Character vector of allowed roles after normalization.

vl_mode Character; currently used only to trigger trajectory building.
 vl_source Character; one of "none", "column", "simulate".
 vl_column Optional name of the VL column when vl_source = "column".
 start_date, end_date Optional Date bounds.

Value

A named list of data frames (one per household).

<code>print.GenSynResult</code>	<i>Print method for GenSynResult</i>
---------------------------------	--------------------------------------

Description

Print method for GenSynResult

Usage

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

Arguments

x A GenSynResult object.
 ... Unused.

Value

x, invisibly.

Examples

```
## Not run:
# Simulate and estimate
seasonal_forcing_list <- list(
  adult=rep(0.1,365), child=rep(0.1,365), elderly=rep(0.1,365), toddler=rep(0.1,365)
)
fit <- GenSyn(
  n_households=50,
  seasonal_forcing_list=seasonal_forcing_list, max_days=365,
  stan_chains=4, stan_iter=2000, stan_warmup=1000, stan_cores=4
)
print(fit)

## End(Not run)
```

```
print.TransmissionChainResult
```

Print a TransmissionChainResult

Description

Nicely prints sections available in a `TransmissionChainResult` returned by [TransmissionChainAnalysis](#).

Usage

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

Arguments

<code>x</code>	A <code>TransmissionChainResult</code> object.
<code>...</code>	Passed to or from other methods (unused).

Value

`x`, returned invisibly.

See Also

[TransmissionChainAnalysis](#)

Examples

```
## Not run:
T_max <- 12
df_person <- data.frame(
  hh_id = c("HH1", "HH1", "HH1", "HH2", "HH2", "HH2"),
  person_id = c(1, 2, 3, 1, 2, 3),
  role = c("adult", "child", "elderly", "adult", "child", "elderly"),
  infection_time = c(2, 4, NA, 1, 3, NA),
  infectious_start = c(3, 6, NA, 2, 5, NA),
  infectious_end = c(8, 9, NA, 7, 9, NA),
  infection_resolved = c(9, 10, NA, 8, 10, NA)
)
seasonal_forcing_list <- list(
  adult = rep(1, T_max), child = rep(1, T_max),
  elderly = rep(1, T_max), toddler = rep(1, T_max)
)
result <- TransmissionChainAnalysis(
  user_data = df_person,
  seasonal_forcing_list = seasonal_forcing_list,
  max_days = T_max,
  stan_chains = 1, stan_iter = 300, stan_warmup = 150
)
print(result)

## End(Not run)
```

run_household_stan	<i>Run the Stan household model</i>
--------------------	-------------------------------------

Description

Wrapper around `rstan::sampling()` with reasonable defaults.

Usage

```
run_household_stan(
  stan_data,
  stan_file = "model.stan",
  chains = 4,
  iter = 2000,
  warmup = 1000,
  control = list(adapt_delta = 0.99, max_treedepth = 20),
  init = "random",
  refresh = 50,
  cores = 4,
  stan_code = NULL,
  package_name = NULL
)
```

Arguments

stan_data	Named list from <code>build_stan_household_arrays</code> or <code>prepare_stan_data</code> .
stan_file	Path to Stan model file.
chains, iter, warmup	Stan MCMC settings.
control	List passed to <code>rstan::sampling()</code> .
init, refresh, cores	Stan parameters.
stan_code	Optional character string with Stan program code.
package_name	Optional package name for <code>system.file</code> lookup.

Value

A stanfit object.

simulate_households	<i>Simulate households (RSV/VL engine)</i>
---------------------	--

Description

Generates synthetic household data for the RSV/VL–Stan pipeline. Returns a list with stacked data frame, per-household list, and long testing records (`diagnostic_df`).

Usage

```

simulate_households(
  n_households,
  start_date = as.Date("2024-01-01"),
  end_date = as.Date("2024-12-31"),
  max_days = 365,
  seasonal_forcing_list = NULL,
  alpha_comm_by_role = 0.005,
  beta1 = 0.3,
  beta2 = 0.05,
  delta = 0,
  phi_by_role = c(adult = 1, child = 7, toddler = 7, elderly = 4),
  kappa_by_role = c(adult = 1, child = 1.5, toddler = 1.5, elderly = 1),
  latent_shape = 3,
  latent_scale = 0.5,
  infectious_shape = 3,
  infectious_scale = 1,
  resolve_shape = 1.5,
  resolve_scale = 0.5,
  peak_day = 1,
  width = 4,
  ptrans_threshold = 0.5,
  detect_threshold_log10 = 1,
  detect_threshold_Ct = 40,
  surveillance_interval = 7,
  test_daily = FALSE,
  viral_testing = "viral load",
  V_ref = 3,
  V_rho = 2.5,
  Ct_50 = 40,
  Ct_delta = 2,
  VL_params_list = default_VL_params,
  Ct_params_list = default_Ct_params,
  household_profile_list = default_household_profile,
  verbose = FALSE
)

```

Arguments

<code>n_households</code>	Integer; number of households.
<code>start_date, end_date</code>	Date study window.
<code>max_days</code>	Integer; simulation horizon (days).
<code>seasonal_forcing_list</code>	Optional named list (adult, child, elderly, toddler) for seasonal forcing.
<code>alpha_comm_by_role</code>	Numeric; baseline community acquisition rate.
<code>beta1, beta2</code>	Numeric; transmission coefficients.
<code>delta</code>	Numeric; household size scaling exponent.
<code>phi_by_role</code>	Named numeric vector; susceptibility multipliers by role.

kappa_by_role Named numeric vector; infectivity multipliers by role.
 latent_shape, latent_scale
 Numeric; gamma parameters for latent period.
 infectious_shape, infectious_scale
 Numeric; gamma parameters for infectious period.
 resolve_shape, resolve_scale
 Numeric; gamma parameters for resolution period.
 peak_day, width Numeric; infectivity profile parameters.
 ptrans_threshold
 Numeric; transmission potential threshold.
 detect_threshold_log10
 Numeric; viral load detection threshold in log10.
 detect_threshold_Ct
 Numeric; Ct value detection threshold.
 surveillance_interval
 Integer; days between scheduled tests.
 test_daily Logical; switch to daily testing after first detection.
 viral_testing Character; one of "viral load" or "Ct".
 V_ref, V_rho Numeric; viral load reference and power for transmission.
 Ct_50, Ct_delta Numeric; Ct-based infectivity parameters.
 VL_params_list Named list; role-specific VL trajectory parameters.
 Ct_params_list Named list; role-specific Ct trajectory parameters.
 household_profile_list
 Named list; household composition probabilities.
 verbose Logical; print progress information.

Value

A list with `hh_df` (stacked data frame), `households` (per-household list), and `diagnostic_df` (long testing records).

TransmissionChainAnalysis

TransmissionChainAnalysis: analyze user-supplied household data

Description

Runs the end-to-end workflow on *user-provided* data using Bayesian Stan estimation. This function does not simulate data; it expects input in tabular form (see Details).

Usage

```

TransmissionChainAnalysis(
  user_data,
  index_vl_column = "vl_test",
  start_date = as.Date("2024-01-01"),
  end_date = as.Date("2024-12-31"),
  seasonal_forcing_list = NULL,
  max_days = 365,
  stan_file = "model.stan",
  stan_chains = 4,
  stan_iter = 2000,
  stan_warmup = 1000,
  stan_control = list(adapt_delta = 0.99, max_treedepth = 20),
  stan_init = "random",
  stan_refresh = 50,
  stan_cores = 4,
  vl_mode = c("auto", "from_long"),
  vl_source = c("column", "simulate", "none"),
  vl_column = NULL,
  role_levels = c("adult", "child", "elderly", "toddler")
)

```

Arguments

<code>user_data</code>	A data.frame or a list of data.frames describing household testing or episode data (see Details for accepted shapes). Lists are row-bound internally.
<code>index_vl_column</code>	Optional character; name of the viral-load (VL) column used by SAR-by-VL plotting. Defaults to "vl_test" when present.
<code>start_date, end_date</code>	Date study window.
<code>seasonal_forcing_list</code>	Optional named list of role vectors for forcing.
<code>max_days</code>	Integer; maximum modeled days.
<code>stan_file</code>	Path to a Stan model file.
<code>stan_chains, stan_iter, stan_warmup</code>	Integers; Stan sampling controls.
<code>stan_control</code>	List; passed to <code>rstan::sampling(..., control = ...)</code> .
<code>stan_init</code>	Character or function; Stan initialization.
<code>stan_refresh</code>	Integer; Stan refresh rate.
<code>stan_cores</code>	Integer; CPU cores for Stan.
<code>vl_mode</code>	One of <code>c("auto", "from_long")</code> indicating how to derive VL.
<code>vl_source</code>	One of <code>c("column", "simulate", "none")</code> indicating the VL source.
<code>vl_column</code>	Optional character; the VL column when <code>vl_source="column"</code> .
<code>role_levels</code>	Character vector; canonical role levels for normalization.

Details

Accepted input shapes:

- Long testing table with columns like HH, individual_ID, role, test_date, infection_status, and optionally a VL column.
- Per-person episode table with hh_id, person_id, role, infection_time, infectious_start, infectious_end, and optionally a viral-load trajectory.

Value

An object of class "TransmissionChainResult" containing:

- \$results: Contains fit (the Stan object) and posterior_summary.
- \$postprocessing: Stan posterior summary.
- \$plot_list: named list of ggplot objects when built.

See Also

[main_parameter_estimation_pipeline](#), [GenSyn](#)

Examples

```
## Not run:
T_max <- 12
df_person <- data.frame(
  hh_id = c("HH1", "HH1", "HH1", "HH2", "HH2", "HH2"),
  person_id = c(1, 2, 3, 1, 2, 3),
  role = c("adult", "child", "elderly", "adult", "child", "elderly"),
  infection_time = c(2, 4, NA, 1, 3, NA),
  infectious_start = c(3, 6, NA, 2, 5, NA),
  infectious_end = c(8, 9, NA, 7, 9, NA),
  infection_resolved = c(9, 10, NA, 8, 10, NA)
)
seasonal_forcing_list <- list(
  adult = rep(1, T_max), child = rep(1, T_max),
  elderly = rep(1, T_max), toddler = rep(1, T_max)
)
result <- TransmissionChainAnalysis(
  user_data = df_person,
  seasonal_forcing_list = seasonal_forcing_list,
  max_days = T_max,
  stan_chains = 1, stan_iter = 300, stan_warmup = 150
)

## End(Not run)
```


Index

`build_stan_household_arrays`, [2](#)

`GenSyn`, [3](#), [7](#), [16](#)

`main_parameter_estimation_pipeline`, [3](#),
[5](#), [5](#), [16](#)

`postprocess_stan_fit`, [8](#)

`prepare_stan_data`, [8](#)

`prepare_stan_households_from_user_data`,
[9](#)

`print.GenSynResult`, [10](#)

`print.TransmissionChainResult`, [11](#)

`run_household_stan`, [12](#)

`simulate_households`, [12](#)

`TransmissionChainAnalysis`, [5](#), [11](#), [14](#)