

Package ‘HHBayes’

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Title Bayesian Household Transmission Chain Analysis with Viral Load Dynamics

Version 0.0.9

Description Provides a streamlined pipeline to simulate household infection dynamics, estimate transmission parameters, and visualize epidemic timelines. Uses a Bayesian approach with Stan that models transmission probability as a Function of viral load, seasonality and infectivity, multiple infection episodes (reinfections), and waning immunity modeling.

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fit_household_model *Fit Household Transmission Model*

Description

Fits the compiled Stan model to the prepared household data.

Usage

```
fit_household_model(
  stan_data,
  iter = 2000,
  chains = 4,
  warmup = 1000,
  init_fun = NULL,
  control = list(adapt_delta = 0.95, max_treedepth = 15),
  cores = 4,
  refresh = 50,
  ...
)
```

Arguments

stan_data	A list of data formatted by <code>prepare_stan_data</code> .
iter	Integer; number of iterations per chain (including warmup).
chains	Integer; number of Markov chains.
warmup	Integer; number of warmup iterations.
init_fun	Function or List; initial values for the sampler.
control	List; Stan control parameters.
cores	Integer; number of CPU cores.
refresh	Integer; refresh rate for output.
...	Additional arguments passed to <code>rstan::sampling</code> .

Value

A `stanfit` object containing the posterior samples.

Examples

```
## Not run:
household_profile <- list(
  prob_adults = c(0, 0, 1),
  prob_infant = 1.0,
  prob_siblings = c(0, .8, .2),
  prob_elderly = c(0.7, 0.1, 0.2)
)

sim_res <- simulate_multiple_households_com(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,
  waning_shape = 6,
  waning_scale = 10,
  surveillance_interval = 4,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = surveillance_data,
  seed = 123,
  household_profile_list = household_profile
)
person_covariates <- sim_res$hh_df %>%
  dplyr::select(hh_id, person_id, vacc_status) %>%  dplyr::distinct()

df_for_stan <- sim_res$diagnostic_df %>%
  dplyr::left_join(person_covariates, by = c("hh_id", "person_id"))

stan_input <- prepare_stan_data(
  df_clean = df_for_stan,
  use_vl_data = 1,
  study_start_date = as.Date(study_start),
  study_end_date = as.Date(study_end),
  surveillance_df = surveillance_data,
  study_start_date = as.Date(study_start),
  study_end_date = as.Date(study_end),
```

```
imputation_params = VL_params_list)
fit <- fit_household_model(stan_input)

## End(Not run)
```

GenSyn

*Simulate Household Transmission and Estimate Parameters***Description**

Simulates household infection dynamics with viral load trajectories, reinfections, and covariate effects, then estimates transmission parameters using Bayesian inference via Stan.

Usage

```
GenSyn(
  n_households = 50,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = NULL,
  seasonal_forcing_list = NULL,
  covariates_config = NULL,
  alpha_comm_by_role = 5e-04,
  beta1 = 0.008,
  beta2 = 0.008,
  delta = 0,
  phi_by_role = c(adult = 1, infant = 4, toddler = 5, elderly = 1),
  kappa_by_role = c(adult = 1, infant = 1, toddler = 1.2, elderly = 1),
  infectious_shape = 3,
  infectious_scale = 1,
  waning_shape = 16,
  waning_scale = 10,
  peak_day = 1,
  width = 4,
  detect_threshold_log10 = 1e-06,
  detect_threshold_Ct = 99,
  surveillance_interval = 1,
  test_daily = FALSE,
  viral_testing = "viral load",
  V_ref = 3,
  V_rho = 2.5,
  Ct_50 = 40,
  Ct_delta = 2,
  VL_params_list = NULL,
  Ct_params_list = NULL,
  household_profile_list = NULL,
  max_infections = Inf,
  use_vl_data = TRUE,
  priors = NULL,
  covariates_susceptibility = NULL,
  covariates_infectivity = NULL,
```

```

recovery_params = NULL,
imputation_params = NULL,
stan_chains = 4,
stan_iter = 2000,
stan_warmup = 1000,
stan_control = list(adapt_delta = 0.95, max_treedepth = 15),
stan_cores = 4,
stan_refresh = 50,
seed = NULL
)

```

Arguments

n_households Integer; number of households to simulate.

start_date, end_date Character or Date; study period bounds.

surveillance_df Optional data frame with 'date' and 'cases' columns for seasonal forcing. If provided, overrides **seasonal_forcing_list**.

seasonal_forcing_list Optional named list with seasonal forcing vectors for each role (adult, infant, toddler, elderly).

covariates_config Optional list of covariate configurations for simulation. Each element should be a list with: name (column name), efficacy (effect size, 0-1), effect_on ("susceptibility", "infectivity", or "both"), and coverage (list of probabilities by role).

alpha_comm_by_role Numeric; baseline community acquisition rate.

beta1, beta2 Numeric; transmission coefficients.

delta Numeric; household size scaling exponent.

phi_by_role Named numeric vector; susceptibility multipliers by role.

kappa_by_role Named numeric vector; infectivity multipliers by role.

infectious_shape, infectious_scale Numeric; gamma parameters for infectious period.

waning_shape, waning_scale Numeric; gamma parameters for immunity waning period.

peak_day, width Numeric; infectivity profile parameters.

detect_threshold_log10 Numeric; viral load detection threshold (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; "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 viral load trajectory parameters.
Ct_params_list Named list; role-specific Ct trajectory parameters.
household_profile_list
 Named list; household composition probabilities.
max_infections Integer; maximum infections per person (for reinfection modeling).
use_vl_data Logical; whether to use viral load data in estimation.
priors Named list; prior specifications for Stan model. Each element should be a list with `dist` ("normal", "uniform", "lognormal") and `params` (parameter vector). Available priors: `beta1`, `beta2`, `alpha`, `covariates`, `gen_shape`, `gen_rate`, `ct50`, `slope`.
covariates_susceptibility
 Character vector; names of susceptibility covariates.
covariates_infectivity
 Character vector; names of infectivity covariates.
recovery_params
 Named list; Gamma parameters (shape, scale) for immunity tail duration by role.
imputation_params
 Named list; parameters for viral curve imputation by role.
stan_chains, **stan_iter**, **stan_warmup**
 Integers; Stan sampling controls.
stan_control List; Stan control parameters.
stan_cores Integer; number of CPU cores for Stan.
stan_refresh Integer; refresh rate for Stan output.
seed Integer; random seed for reproducibility.

Value

An object of class "GenSynResult" containing:

- \$call** The matched call
- \$n_households** Number of households simulated
- \$simulation** Raw simulation output with `hh_df` and `diagnostic_df`
- \$stan_data** Data prepared for Stan
- \$fit** The `stanfit` object
- \$postprocessing** Tidy posterior summary
- \$attack_rates** Attack rate and reinfection summaries
- \$transmission_chains** Reconstructed transmission links

See Also

[TransmissionChainAnalysis](#), [plot.GenSynResult](#)

Examples

```
## Not run:
# Basic simulation
result <- GenSyn(
  n_households = 50,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  stan_chains = 2,
  stan_iter = 1000,
  stan_warmup = 500,
  seed = 123
)

# View results
print(result)
plot(result, which = "posterior")

## End(Not run)
```

plot.GenSynResult *Plot method for GenSynResult*

Description

Plot method for GenSynResult

Usage

```
## S3 method for class 'GenSynResult'
plot(x, which = "posterior", print = TRUE, hh_id = 1, prob_cutoff = 0, ...)
```

Arguments

<code>x</code>	A GenSynResult object.
<code>which</code>	Character vector specifying which plots to generate. Options: "posterior", "covariate_effects", "epidemic_curve", "transmission_chains", or "all".
<code>print</code>	Logical; whether to print plots immediately.
<code>hh_id</code>	Integer; household ID for transmission chain plot (default: 1).
<code>prob_cutoff</code>	Numeric; minimum probability threshold for chain links (default: 0).
<code>...</code>	Additional arguments (unused).

Value

A named list of ggplot objects (invisibly if `print = TRUE`).

Examples

```
## Not run:
# Basic simulation
result <- GenSyn(
  n_households = 50,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  stan_chains = 2,
  stan_iter = 1000,
  stan_warmup = 500,
  seed = 123
)

# View results
plot(result, which = "posterior")

## End(Not run)
```

plot.TransmissionChainResult

Plot method for TransmissionChainResult

Description

Plot method for TransmissionChainResult

Usage

```
## S3 method for class 'TransmissionChainResult'
plot(
  x,
  which = "posterior",
  print = TRUE,
  hh_id = 1,
  prob_cutoff = 0,
  bin_width = 7,
  ...
)
```

Arguments

<code>x</code>	A TransmissionChainResult object.
<code>which</code>	Character vector specifying which plots to generate. Options: "posterior", "transmission_chains", "covariate_effects", "epidemic_curve", or "all".
<code>print</code>	Logical; whether to print plots immediately.
<code>hh_id</code>	Integer; household ID for transmission chain plot (default: 1).
<code>prob_cutoff</code>	Numeric; minimum probability threshold for chain links (default: 0).
<code>bin_width</code>	Integer; number of days per bin for epidemic curve (default: 7).
<code>...</code>	Additional arguments (unused).

Value

A named list of ggplot objects (invisibly if `print = TRUE`).

Examples

```
## Not run:
# Per-person episode format
T_max <- 30
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","infant","elderly","adult","infant","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)
)

result <- TransmissionChainAnalysis(
  user_data = df_person,
  max_days = T_max,
  stan_chains = 2,
  stan_iter = 1000,
  stan_warmup = 500
)

plot(result, which = "posterior")

## End(Not run)
```

plot_covariate_effects

Plot Covariate Coefficients (Forest Plot)

Description

Creates a forest plot showing the effects of covariates on susceptibility and infectivity.

Usage

```
plot_covariate_effects(fit, stan_data)
```

Arguments

- | | |
|------------------------|--------------------------------|
| <code>fit</code> | A <code>stanfit</code> object. |
| <code>stan_data</code> | The list data passed to Stan. |

Value

A ggplot object.

Examples

```
## Not run:
# fit <- run_household_stan(stan_data = stan_input, ...)
# stan_input should include K_susc / K_inf and match the fitted model
p_beta <- plot_covariate_effects(fit, stan_input)
print(p_beta)

## End(Not run)
```

plot_epidemic_curve *Plot Dual-Axis Epidemic Curve (Binned)*

Description

Overlays a stacked bar chart of simulated infections with a line chart of surveillance data. Both datasets are aggregated by 'bin_width' days.

Usage

```
plot_epidemic_curve(
  sim_result,
  surveillance_df,
  start_date_str = "2024-07-01",
  bin_width = 7
)
```

Arguments

<code>sim_result</code>	Output object from <code>simulate_multiple_households_comm</code> .
<code>surveillance_df</code>	Dataframe with date and cases columns.
<code>start_date_str</code>	Character; start date of the simulation.
<code>bin_width</code>	Integer; aggregation window in days (default 7).

Value

A ggplot object.

Examples

```
## Not run:
# sim_result should be a simulation output containing sim_result$hh_df
# with at least: infection_time, role
# surveillance_df must include: date, cases

p.epi <- plot_epidemic_curve(
  sim_result,
  surveillance_df,
  start_date_str = "2024-07-01",
  bin_width = 7
)
print(p.epi)
```

```
## End(Not run)
```

plot_household_timeline*Plot Household Timeline with Transmission Chains***Description**

Creates a timeline visualization of infections within a household, showing transmission links with probabilities.

Usage

```
plot_household_timeline(
  trans_df,
  stan_data,
  target_hh_id,
  start_date_str = "2024-10-08",
  prob_cutoff = 0,
  plot_width = 11,
  plot_height = 7
)
```

Arguments

<code>trans_df</code>	Data frame from <code>reconstruct_transmission_chains</code> .
<code>stan_data</code>	The list data passed to Stan.
<code>target_hh_id</code>	Integer; household ID to plot.
<code>start_date_str</code>	Character; start date string.
<code>prob_cutoff</code>	Numeric; minimum probability for displaying links.
<code>plot_width, plot_height</code>	Numeric; plot dimensions.

Value

A ggplot object.

Examples

```
## Not run:
# After fitting the Stan model and post-processing (object names may vary):
# fit      <- run_household_stan(stan_data = stan_input, ...)
# chains   <- postprocess_stan_fit(fit, stan_input)
# trans_df <- chains$trans_df  # must include: hh_id, source, target, prob

# Plot a specific household (e.g., HH #2)
p_hh <- plot_household_timeline(
  trans_df,
  stan_input,
  target_hh_id = 2,
```

```

    start_date_str = "2024-10-08",
    prob_cutoff = 0.10
)
print(p_hh)

## End(Not run)

```

plot_posterior_distributions*Plot Posterior Distributions (Phi and Kappa)***Description**

Creates violin plots of posterior distributions for susceptibility and infectivity parameters by role.

Usage

```
plot_posterior_distributions(fit)
```

Arguments

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

Value

A combined ggplot object.

Examples

```

## Not run:
# fit <- run_household_stan(stan_data = stan_input, ...)
p_post <- plot_posterior_distributions(fit)
print(p_post)

## End(Not run)

```

plot_user_epidemic_curve*Plot Epidemic Curve for User Data***Description**

Creates an epidemic curve from user-provided data, optionally overlaying surveillance data if available.

Usage

```
plot_user_epidemic_curve(
  user_data,
  start_date,
  surveillance_df = NULL,
  bin_width = 7
)
```

Arguments

user_data	Dataframe with user's infection data.
start_date	Date; study start date.
surveillance_df	Optional dataframe with date and cases columns.
bin_width	Integer; aggregation window in days (default 7).

Value

A ggplot object.

Examples

```
## Not run:
# user_data can be in per-person format (recommended for this example),
# with at least: infection_time, role (and optionally HH, individual_ID, etc.)

p_user <- plot_user_epidemic_curve(
  user_data,
  start_date = "2024-10-08",
  bin_width = 7
)
print(p_user)

# Optional: overlay surveillance (must include: date, cases)
p_user2 <- plot_user_epidemic_curve(
  user_data,
  start_date = "2024-10-08",
  surveillance_df = surveillance_df,
  bin_width = 7
)
print(p_user2)

## End(Not run)
```

`postprocess_stan_fit` *Postprocess Stan Fit*

Description

Extracts and summarizes posterior distributions from a stanfit object.

Usage

```
postprocess_stan_fit(fit)
```

Arguments

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

Value

A data frame with parameter summaries.

Examples

```

## Not run:
household_profile <- list(
  prob_adults    = c(0, 0, 1),
  prob_infant    = 1.0,
  prob_siblings  = c(0, .8, .2),
  prob_elderly   = c(0.7, 0.1, 0.2)
)

sim_res <- simulate_multiple_households_comm(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,
  waning_shape = 6,
  waning_scale = 10,
  surveillance_interval = 4,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = surveillance_data,
  seed = 123,
  household_profile_list = household_profile
)
person_covariates <- sim_res$hh_df %>%
  dplyr::select(hh_id, person_id, vacc_status) %>%  dplyr::distinct()

df_for_stan <- sim_res$diagnostic_df %>%
  dplyr::left_join(person_covariates, by = c("hh_id", "person_id"))

stan_input <- prepare_stan_data(
  df_clean = df_for_stan,
  use_vl_data      = 1,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  surveillance_df = surveillance_data,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  imputation_params = VL_params_list)
fit <- fit_household_model(stan_input)
posterior_summary <- postprocess_stan_fit(fit)
print(posterior_summary)

## End(Not run)

```

Description

Prepares household observation data for Stan model fitting, including imputation of episode timing, covariate matrices, and viral load data.

Usage

```
prepare_stan_data(
  df_clean,
  surveillance_df = NULL,
  role_levels = c("adult", "infant", "toddler", "elderly"),
  study_start_date = as.Date("2024-07-01"),
  study_end_date = as.Date("2025-07-01"),
  seasonal_forcing_list = NULL,
  use_vl_data = TRUE,
  covariates_susceptibility = NULL,
  covariates_infectivity = NULL,
  recovery_params = NULL,
  imputation_params = NULL,
  priors = list(),
  seed = 123
)
```

Arguments

`df_clean` Dataframe with observation data (must contain 'episode_id').
`surveillance_df` Dataframe with columns 'date' and 'cases'.
`role_levels` Character vector; canonical role levels.
`study_start_date, study_end_date` Date objects; study period.
`seasonal_forcing_list` Named list of forcing vectors.
`use_vl_data` Logical; whether to use viral load data.
`covariates_susceptibility` Character vector; susceptibility covariate names.
`covariates_infectivity` Character vector; infectivity covariate names.
`recovery_params` List of Gamma parameters (shape, scale) by role.
`imputation_params` List of viral curve parameters by role.
`priors` List of flexible priors (dist, params).
`seed` Integer; random seed.

Value

A list of data formatted for Stan.

Examples

```
## Not run:
household_profile <- list(
  prob_adults  = c(0, 0, 1),
  prob_infant  = 1.0,
  prob_siblings = c(0, .8, .2),
  prob_elderly = c(0.7, 0.1, 0.2)
```

```

)
sim_res <- simulate_multiple_households_comm(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,
  waning_shape = 6,
  waning_scale = 10,
  surveillance_interval = 4,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = surveillance_data,
  seed = 123,
  household_profile_list = household_profile
)
person_covariates <- sim_res$hh_df %>%
  dplyr::select(hh_id, person_id, vacc_status) %>%  dplyr::distinct()

df_for_stan <- sim_res$diagnostic_df %>%
  dplyr::left_join(person_covariates, by = c("hh_id", "person_id"))

stan_input <- prepare_stan_data(
  df_clean = df_for_stan,
  use_vl_data      = 1,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  surveillance_df  = surveillance_data,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  imputation_params = VL_params_list)

## End(Not run)

```

print.GenSynResult *Print method for GenSynResult*

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:
# Basic simulation
result <- GenSyn(
  n_households = 50,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  stan_chains = 2,
  stan_iter = 1000,
  stan_warmup = 500,
  seed = 123
)

# View results
print(result)

## End(Not run)
```

`print.TransmissionChainResult`

Print method for TransmissionChainResult

Description

Print method for TransmissionChainResult

Usage

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

Arguments

<code>x</code>	A <code>TransmissionChainResult</code> object.
...	Unused.

Value

`x`, invisibly.

Examples

```
## Not run:
# Per-person episode format
T_max <- 30
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", "infant", "elderly", "adult", "infant", "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)
```

```

)
result <- TransmissionChainAnalysis(
  user_data = df_person,
  max_days = T_max,
  stan_chains = 2,
  stan_iter = 1000,
  stan_warmup = 500
)
print(result)

## End(Not run)

```

reconstruct_transmission_chains*Reconstruct Transmission Chains (Covariate-Aware)***Description**

Identifies potential infectors for each infection event based on posterior estimates, accounting for covariates if present.

Usage

```
reconstruct_transmission_chains(fit, stan_data, min_prob_threshold = 0.01)
```

Arguments

- fit** A stanfit object.
- stan_data** The list data passed to Stan.
- min_prob_threshold** Minimum probability threshold for links.

Value

A data frame of transmission links with probabilities.

Examples

```

## Not run:
household_profile <- list(
  prob_adults  = c(0, 0, 1),
  prob_infant   = 1.0,
  prob_siblings = c(0, .8, .2),
  prob_elderly  = c(0.7, 0.1, 0.2)
)

sim_res <- simulate_multiple_households_comm(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,

```

```
waning_shape = 6,
waning_scale = 10,
surveillance_interval = 4,
start_date = "2024-07-01",
end_date = "2025-06-30",
surveillance_df = surveillance_data,
seed = 123,
household_profile_list = household_profile
)
person_covariates <- sim_res$hh_df %>%
  dplyr::select(hh_id, person_id, vacc_status) %>%  dplyr::distinct()

df_for_stan <- sim_res$diagnostic_df %>%
  dplyr::left_join(person_covariates, by = c("hh_id", "person_id"))

stan_input <- prepare_stan_data(
  df_clean = df_for_stan,
  use_vl_data      = 1,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  surveillance_df  = surveillance_data,
  study_start_date = as.Date(study_start),
  study_end_date   = as.Date(study_end),
  imputation_params = VL_params_list)
fit <- fit_household_model(stan_input)
chains <- reconstruct_transmission_chains(fit, stan_input, min_prob_threshold = 0.001)

## End(Not run)
```

simulate_multiple_households_comm*Simulate Multiple Households with Community Transmission***Description**

Simulates household infection dynamics across multiple households with support for generic covariates, reinfections, and viral load trajectories.

Usage

```
simulate_multiple_households_comm(
  n_households = 50,
  surveillance_df = NULL,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  alpha_comm_by_role = 5e-04,
  beta1 = 0.008,
  beta2 = 0.008,
  delta = 0,
  phi_by_role = c(adult = 1, infant = 4, toddler = 5, elderly = 1),
  kappa_by_role = c(adult = 1, infant = 1, toddler = 1.2, elderly = 1),
  infectious_shape = 3,
  infectious_scale = 1,
```

```

waning_shape = 16,
waning_scale = 10,
peak_day = 1,
width = 4,
verbose = FALSE,
seasonal_forcing_list = NULL,
detect_threshold_log10 = 1e-06,
detect_threshold_Ct = 99,
surveillance_interval = 1,
test_daily = FALSE,
viral_testing = "viral load",
V_ref = 3,
V_rho = 2.5,
Ct_50 = 40,
Ct_delta = 2,
VL_params_list = NULL,
Ct_params_list = NULL,
household_profile_list = NULL,
perfect_detection = TRUE,
contact_mat = NULL,
covariates_config = NULL,
seed = NULL,
max_infections = Inf
)

```

Arguments

n_households	Integer; number of households to simulate.
surveillance_df	Optional data frame with 'date' and 'cases' columns.
start_date, end_date	Character or Date; study period bounds.
alpha_comm_by_role	Numeric; community acquisition rate.
beta1, beta2	Numeric; transmission coefficients.
delta	Numeric; household size scaling exponent.
phi_by_role, kappa_by_role	Named numeric vectors.
infectious_shape, infectious_scale	Numeric; Gamma parameters.
waning_shape, waning_scale	Numeric; Gamma parameters.
peak_day, width	Numeric; infectivity profile.
verbose	Logical; print progress.
seasonal_forcing_list	Named list of forcing vectors.
detect_threshold_log10	Numeric; detection threshold (log10 VL).
detect_threshold_Ct	Numeric; detection threshold (Ct).

```

surveillance_interval
    Integer; days between tests.

test_daily      Logical; test daily after detection.

viral_testing   Character; "viral load" or "Ct".

V_ref, V_rho    Numeric; VL parameters.

Ct_50, Ct_delta Numeric; Ct parameters.

VL_params_list, Ct_params_list
    Named lists of trajectory parameters.

household_profile_list
    Named list for household composition.

perfect_detection
    Logical.

contact_mat     Optional contact matrix.

covariates_config
    List of covariate configurations.

seed            Integer; random seed.

max_infections Integer; max infections per person.

```

Value

List with hh_df and diagnostic_df.

Examples

```

## Not run:
household_profile <- list(
  prob_adults  = c(0, 0, 1),
  prob_infant   = 1.0,
  prob_siblings = c(0, .8, .2),
  prob_elderly  = c(0.7, 0.1, 0.2)
)

sim_res <- simulate_multiple_households_comm(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,
  waning_shape = 6,
  waning_scale = 10,
  surveillance_interval = 4,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = surveillance_data,
  seed = 123,
  household_profile_list = household_profile
)

## End(Not run)

```

summarize_attack_rates*Summarize Attack Rates and Reinfections*

Description

Calculates the Primary Attack Rate (proportion of people infected at least once) and a separate summary of Reinfections (secondary episodes).

Usage

```
summarize_attack_rates(sim_result)
```

Arguments

`sim_result` A list object returned by `simulate_multiple_households_comm`.

Value

A list containing four dataframes:

`primary_overall` Overall primary attack rate statistics.

`primary_by_role` Primary attack rate stratified by age group.

`reinf_overall` Overall summary of reinfection counts and rates.

`reinf_by_role` Reinfection counts stratified by age group.

Examples

```
## Not run:
household_profile <- list(
  prob_adults    = c(0, 0, 1),
  prob_infant    = 1.0,
  prob_siblings  = c(0, .8, .2),
  prob_elderly   = c(0.7, 0.1, 0.2)
)

sim_res <- simulate_multiple_households_comm(
  n_households = 100,
  viral_testing = "viral load",
  infectious_shape = 10,
  infectious_scale = 1,
  waning_shape = 6,
  waning_scale = 10,
  surveillance_interval = 4,
  start_date = "2024-07-01",
  end_date = "2025-06-30",
  surveillance_df = surveillance_data,
  seed = 123,
  household_profile_list = household_profile
)
rates <- summarize_attack_rates(sim_res)

## End(Not run)
```

TransmissionChainAnalysis*Analyze User-Supplied Household Transmission Data*

Description

Runs Bayesian estimation on user-provided household testing or episode data. This function does not simulate data; it expects input in tabular form.

Usage

```
TransmissionChainAnalysis(
  user_data,
  start_date = as.Date("2024-01-01"),
  end_date = as.Date("2024-12-31"),
  surveillance_df = NULL,
  seasonal_forcing_list = NULL,
  max_days = NULL,
  use_vl_data = TRUE,
  priors = NULL,
  covariates_susceptibility = NULL,
  covariates_infectivity = NULL,
  recovery_params = NULL,
  imputation_params = NULL,
  role_levels = c("adult", "infant", "toddler", "elderly"),
  stan_chains = 4,
  stan_iter = 2000,
  stan_warmup = 1000,
  stan_control = list(adapt_delta = 0.95, max_treedepth = 15),
  stan_cores = 4,
  stan_refresh = 50,
  seed = NULL
)
```

Arguments

user_data	A data.frame or list of data.frames with household data. Accepts two formats:
	<ul style="list-style-type: none"> • Long testing table: columns HH, individual_ID, role, test_date, infection_status (and optionally a viral load column) • Per-person episode table: columns hh_id, person_id, role, infection_time, infectious_start, infectious_end, infection_resolved
start_date, end_date	Date objects or character; study period bounds.
surveillance_df	Optional data frame with 'date' and 'cases' columns for seasonal forcing.
seasonal_forcing_list	Optional named list with seasonal forcing vectors for each role.
max_days	Integer; maximum time horizon (days).
use_vl_data	Logical; whether to use viral load data in estimation.

priors	Named list; prior specifications for Stan model. Each element should be a list with <code>dist</code> ("normal", "uniform", "lognormal") and <code>params</code> (parameter vector).
covariates_susceptibility	Character vector; column names for susceptibility covariates in the data.
covariates_infectivity	Character vector; column names for infectivity covariates in the data.
recovery_params	Named list; Gamma parameters (shape, scale) for immunity tail duration by role.
imputation_params	Named list; parameters for viral curve imputation by role.
role_levels	Character vector; canonical role levels for normalization.
stan_chains, stan_iter, stan_warmup	Integers; Stan sampling controls.
stan_control	List; Stan control parameters.
stan_cores	Integer; number of CPU cores for Stan.
stan_refresh	Integer; refresh rate for Stan output.
seed	Integer; random seed for reproducibility.

Value

An object of class "TransmissionChainResult" containing:

\$call The matched call
\$user_data The processed user data
\$stan_data Data prepared for Stan
\$fit The stanfit object
\$postprocessing Tidy posterior summary
\$transmission_chains Reconstructed transmission links

See Also

[GenSyn](#), [plot.TransmissionChainResult](#)

Examples

```

## Not run:
# Per-person episode format
T_max <- 30
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","infant","elderly","adult","infant","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)
)

result <- TransmissionChainAnalysis(
  user_data = df_person,
  max_days = T_max,

```

```
stan_chains = 2,  
stan_iter = 1000,  
stan_warmup = 500  
)  
  
print(result)  
plot(result, which = "posterior")  
  
## End(Not run)
```

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