Package: seairmobility (via r-universe)

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Type Package

Title Mobility-Based SEAIR Epidemic Models

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Description Tools for simulating, analysing, and fitting mobility-based SEAIR (Susceptible-Exposed-Asymptomatic-Infectious-Recovered) compartmental epidemic models with heterogeneous individual mobility. Each individual carries a fixed mobility trait that scales susceptibility and infectiousness through a rank-one kernel, extending the mobility-based compartmental framework of Jiang et al. (2025) <doi:10.1137/24M1691557> by adding a latent stage and a behavioural split between asymptomatic and symptomatic infectiousness. Provides a numerical solver for the underlying partial differential equation system, closed-form computation of the basic reproduction number R0 and the final epidemic size, and a parametric least-squares routine for recovering the mobility distribution from an observed aggregate symptomatic time series.

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Contents

`seairmobility-package` *seairmobility: Mobility-Based SEAIR Epidemic Models*

Description

The **seairmobility** package provides tools for simulating and analysing mobility-based SEAIR compartmental epidemic models. Each individual in the population carries a fixed mobility trait $m \in (0, 1)$ that scales both their susceptibility and their infectiousness through a rank-one transmission kernel. The infectious period is split into an asymptomatic stage with relative infectiousness α and a symptomatic stage with mobility-reduction factor δ.

Details

The main functions are

`seair_params` Build a parameter list.

`seair_init` Build initial conditions.

`seair_solve` Solve the SEAIR system.

`seair_aggregate` Aggregate solution over mobility.

`R0_seair` Basic reproduction number.

`final_size` Final epidemic size under vanishing seed.

`fit_mobility` Parametric least-squares fit of the mobility distribution from an observed symptomatic time series.

Author(s)

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References

Jiang, N., Chu, W., and Li, Y. (2025). Modeling, inference, and prediction in mobility-based compartmental models for epidemiology. *SIAM Journal on Applied Mathematics*, 85(5), 2355–2375. doi:10.1137/24M1691557.

`beta_mixture_density` *Beta-mixture density on [0, 1]*

Description

Evaluates a weighted mixture of Beta densities

$$f(m) \;=\; \sum_{k=1}^{K} w_k \,\mathrm{Beta}(m; a_k, b_k),$$

renormalised on $[0, 1]$. Weights are coerced to be nonnegative and to sum to one.

Usage

```
beta_mixture_density(m, weights, shape1, shape2)
```

Arguments

`m`	Numeric vector of finite evaluation points in $[0, 1]$.
`weights`	Numeric vector of mixture weights (length K).
`shape1`	Numeric vector of Beta a_k parameters.
`shape2`	Numeric vector of Beta b_k parameters.

Value

Numeric vector of densities at `m`.

Examples

```
m <- seq(0, 1, length.out = 101)
beta_mixture_density(m,
                     weights = c(0.5, 0.3, 0.2),
                     shape1  = c(2, 5, 9),
                     shape2  = c(8, 3, 2))
```

`c_effective` *Effective infectiousness duration of the SEAIR chain*

Description

Computes the scalar

$$c \;=\; \frac{\alpha}{\kappa + \gamma_A} \;+\; \frac{\delta\,\kappa}{(\kappa + \gamma_A)\,\gamma_I},$$

the integrated contribution of a unit of newly infected mass to the force of infection, collapsing the $E \to A \to I$ stage chain into a single number. The latency rate σ does not appear in c.

Usage

```
c_effective(params)
```

Arguments

`params`	A "`seair_params`" object.

Value

A positive scalar.

Examples

```
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
c_effective(pars)
```

`final_size` *Final epidemic size under the vanishing-seed regime*

Description

Solves the scalar fixed-point equation

$$M_R^\infty \;=\; \int_0^1 m f(m)\,(1 - e^{-\beta c M_R^\infty m})\,dm$$

for the first mobility moment of the recovered compartment at the end of the epidemic (with $I_0 \equiv 0$, $R_0 \equiv 0$, $S_0 = f$), and returns the total final epidemic size

$$R_\infty \;=\; 1 - \int_0^1 f(m)\,e^{-\beta c M_R^\infty m}\,dm.$$

When the basic reproduction number is less than or equal to one, the function returns $R_\infty = 0$.

Usage

```
final_size(params, f, m_grid = NULL, tol = 1e-10)
```

Arguments

`params`	A `"seair_params"` object.
`f`	A mobility density, either a function on $[0, 1]$ or a numeric vector of values on `m_grid`.
`m_grid`	Optional mobility grid used when `f` is numeric, or to evaluate the integrals (default: uniform grid of 201 points).
`tol`	Tolerance for `uniroot`.

Value

A list with `R_inf` (total final size), `MR_inf` (first moment), `R0` (basic reproduction number), and `converged` (logical).

Examples

```
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
f <- function(m) 6 * m * (1 - m)
final_size(pars, f)
```

`final_size_general` *Final epidemic size under general proportional initial conditions*

Description

Solves the scalar equation of Theorem 4.3 (final-size relation),

$$M_R^\infty + \int_0^1 mS_0(m)\,\exp\!\big(-\beta m[c\,(M_R^\infty - M_R^0) + (\delta/\gamma_I - c)\,M_I^0]\big)dm \;=\; \int_0^1 mf(m)\,dm,$$

allowing a nonzero initial symptomatic fraction $I_0 = I_{\text{seed}} f$, with $E_0 = A_0 = R_0 = 0$.

Usage

```
final_size_general(params, f, m_grid = NULL, I_seed = 1e-04, tol = 1e-10)
```

Arguments

`params`	A `"seair_params"` object.
`f`	A mobility density, either a function on $[0,1]$ or a numeric vector of values on `m_grid`.
`m_grid`	Optional mobility grid used when `f` is numeric, or to evaluate the integrals (default: uniform grid of 201 points).
`I_seed`	Initial symptomatic fraction.
`tol`	Tolerance for `uniroot`.

Value

A list with `R_inf`, `MR_inf`, `R0`, and `converged`.

Examples

```
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
f <- function(m) 6 * m * (1 - m)
final_size_general(pars, f, I_seed = 0.001)
```

`fit_mobility` *Fit a mobility distribution to an observed symptomatic time series*

Description

Fits a Beta-mixture mobility distribution f by minimising the sum of squared errors between an observed aggregate symptomatic time series $\langle I\rangle(t)$ and the simulated output of the mobility-based SEAIR model at the same times. All transmission and stage parameters are held fixed.

Usage

```
fit_mobility(
  times,
  I_obs,
  params,
  K = 3,
  m_grid = seq(0, 1, length.out = 51),
  I_seed = 1e-04,
  start = NULL,
  n_restarts = 5,
  control = list(maxit = 500),
  verbose = FALSE
)
```

Arguments

`times`	Numeric vector of observation times (starting at 0).
`I_obs`	Observed aggregate symptomatic fraction at each time.
`params`	A `"seair_params"` object holding fixed transmission and stage parameters.
`K`	Number of Beta-mixture components (default 3).
`m_grid`	Mobility grid for the solver.
`I_seed`	Initial symptomatic fraction in $[0, 1)$.
`start`	Optional finite user-supplied starting parameter vector of length $3K - 1$.
`n_restarts`	Number of random restarts (default 5).
`control`	List of `optim` control options.
`verbose`	Logical; if `TRUE`, print progress.

Details

The unconstrained optimisation parameter is, for each component $k = 1, \ldots, K$, a triple $(\log a_k, \log b_k, \log \tilde{w}_k)$ with mixture weights recovered as $w_k = \tilde{w}_k / \sum_j \tilde{w}_j$. The first weight's log is fixed to 0 to remove the scale ambiguity, so the parameter vector has length $3K - 1$.

Value

A list with `weights`, `shape1`, `shape2` (the fitted Beta-mixture parameters), `f_hat` (density on `m_grid`), `m_grid`, `loss` (final SSE), `I_fit` (simulated aggregate symptomatic time series at `times`), and `optim_result`.

Examples

```
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
m <- seq(0, 1, length.out = 21)
f_true <- dbeta(m, 3, 3)
init <- seair_init(m, f_true, I_seed = 1e-4)
times <- seq(0, 20, by = 5)
sol <- seair_solve(init, pars, times)
I_obs <- seair_aggregate(sol)$I

fit <- fit_mobility(times, I_obs, pars,
                    K = 1, m_grid = m,
                    start = log(c(3, 3)),
                    n_restarts = 0,
                    control = list(maxit = 20))
fit$loss
```

`plot_seair` *Plot aggregate compartment trajectories*

Description

Convenience plot of the five aggregate compartment trajectories produced by a SEAIR solution.

Usage

```
plot_seair(sol, which = c("S", "E", "A", "I", "R"), ...)
```

Arguments

`sol`	A `"seair_solution"` object.
`which`	Character vector of compartments to plot; any subset of `c("S","E","A","I","R")`.
`...`	Additional graphical parameters passed to `matplot`.

Value

Invisibly returns the aggregate data frame.

Examples

```
m <- seq(0, 1, length.out = 31)
f <- dbeta(m, 2, 2)
init <- seair_init(m, f, I_seed = 1e-4)
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
sol <- seair_solve(init, pars, times = seq(0, 30, by = 2))
plot_seair(sol, which = c("S","I","R"))
```

`R0_seair` *Basic reproduction number of the mobility-based SEAIR model*

Description

For a mobility distribution f on $(0, 1)$, the basic reproduction number at the disease-free equilibrium is

$$\mathcal{R}_0 \;=\; \beta\, c\, \langle m^2 f \rangle,$$

where c is as in `c_effective` and $\langle m^2 f \rangle = \int_0^1 m^2 f(m)\, dm$.

Usage

```
R0_seair(params, f, m_grid = NULL)
```

Arguments

`params`	A `"seair_params"` object.
`f`	A function returning the density $f(m)$ on $[0, 1]$, or a numeric vector of f values evaluated on `m_grid`.
`m_grid`	Mobility grid (used only if `f` is numeric).

Value

The basic reproduction number $\mathcal{R}_0$.

Examples

```
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)

## f given as a function (normalised automatically by the caller).
f <- function(m) 6 * m * (1 - m)    # Beta(2, 2) density on [0, 1]
R0_seair(pars, f)

## f given as values on a grid.
m <- seq(0, 1, length.out = 101)
R0_seair(pars, f(m), m_grid = m)
```

`seair_aggregate` *Aggregate a SEAIR solution over mobility*

Description

Computes the aggregate time series $\int_0^1 S(m,t)\,dm$, $\int_0^1 E(m,t)\,dm$, etc., using the trapezoidal rule on the solver's mobility grid.

Usage

```
seair_aggregate(sol)
```

Arguments

`sol`	A `"seair_solution"` object returned by `seair_solve`.

Value

A data frame with columns `time`, `S`, `E`, `A`, `I`, `R` (aggregate ratios).

Examples

```
m <- seq(0, 1, length.out = 31)
f <- dbeta(m, 2, 2)
init <- seair_init(m, f, I_seed = 1e-4)
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
sol <- seair_solve(init, pars, times = seq(0, 30, by = 2))
agg <- seair_aggregate(sol)
head(agg)
```

`seair_init` *Build initial conditions for the SEAIR system*

Description

Constructs initial profiles $(S_0, E_0, A_0, I_0, R_0)$ on the mobility grid from a user-supplied mobility density $f(m)$ and a seed fraction I_{seed} placed in the symptomatic compartment. The initial condition is "proportional": $S_0 = (1 - I_{\text{seed}})f$, $I_0 = I_{\text{seed}}f$, $E_0 = A_0 = R_0 = 0$.

Usage

```
seair_init(m_grid, f_vals, I_seed = 1e-04)
```

Arguments

`m_grid`	Numeric vector of mobility grid points in $[0, 1]$.
`f_vals`	Numeric vector of densities $f(m)$ evaluated at `m_grid`. It is renormalised internally so that the trapezoidal integral over `m_grid` equals 1.
`I_seed`	Non-negative fraction of the population seeded in the symptomatic compartment (default `1e-4`).

Value

A list of class `"seair_init"` with entries `m_grid`, `f`, `S`, `E`, `A`, `I`, `R`, and `I_seed`.

Examples

```
m <- seq(0, 1, length.out = 101)
f <- dbeta(m, 2, 2)
seair_init(m, f, I_seed = 1e-4)
```

`seair_params` *Build a parameter list for the mobility-based SEAIR model*

Description

Constructs and validates the list of transmission and stage-progression parameters used by the mobility-based SEAIR model $\partial_t S = -\beta m S \mathcal{K}$, $\partial_t E = \beta m S \mathcal{K} - \sigma E$, $\partial_t A = \sigma E - (\kappa + \gamma_A) A$, $\partial_t I = \kappa A - \gamma_I I$, $\partial_t R = \gamma_A A + \gamma_I I$, where $\mathcal{K}(A, I) = \int_0^1 \bar{m} \, (\alpha A(\bar{m}) + \delta I(\bar{m})) \, d\bar{m}$.

Usage

```
seair_params(beta, sigma, kappa, gamma_A, gamma_I, alpha = 1, delta = 1)
```

Arguments

`beta`	Transmission rate $\beta > 0$.
`sigma`	Rate $\sigma > 0$ of progression from latent (E) to asymptomatic (A).
`kappa`	Symptom-onset rate $\kappa > 0$ (A to I).
`gamma_A`	Recovery rate $\gamma_A > 0$ from the asymptomatic compartment.
`gamma_I`	Recovery rate $\gamma_I > 0$ from the symptomatic compartment.
`alpha`	Relative infectiousness $\alpha \in [0, 1]$ of the asymptomatic stage.
`delta`	Mobility-reduction factor $\delta \in (0, 1]$ for the symptomatic stage.

Value

A list of class `"seair_params"` containing the checked parameters.

Examples

```
seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
             gamma_A = 0.1, gamma_I = 0.13,
             alpha = 0.5, delta = 0.3)
```

`seair_solve` *Solve the mobility-based SEAIR system*

Description

Discretises the mobility-based SEAIR system on the user-supplied mobility grid (using the trapezoidal rule for the non-local integral $\mathcal{K}$) and integrates the resulting coupled ODE system over `times` with **deSolve**.

Usage

```
seair_solve(init, params, times, method = "lsoda", ...)
```

Arguments

`init`	A `"seair_init"` object from `seair_init`.
`params`	A `"seair_params"` object from `seair_params`.
`times`	Numeric vector of times at which the solution is reported (must be increasing and include `0`).
`method`	Integration method passed to `ode` (default `"lsoda"`).
`...`	Additional arguments passed to `ode`.

Value

A list of class `"seair_solution"` with entries `times`, `m_grid`, `S`, `E`, `A`, `I`, `R` (each a matrix of dimension `length(times)` by `length(m_grid)`), together with the input `params` and `init`.

Examples

```
m <- seq(0, 1, length.out = 31)
f <- dbeta(m, 2, 2)
init <- seair_init(m, f, I_seed = 1e-4)
pars <- seair_params(beta = 1.5, sigma = 0.3, kappa = 0.2,
                     gamma_A = 0.1, gamma_I = 0.13,
                     alpha = 0.5, delta = 0.3)
sol <- seair_solve(init, pars, times = seq(0, 30, by = 2))
```

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