

# Package ‘fastbeta’

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**Title** Fast Approximation of Time-Varying Infectious Disease  
Transmission Rates

**Description** A fast method for approximating time-varying infectious disease  
transmission rates from disease incidence time series and other  
data, based on a discrete time approximation of an SEIR model, as  
analyzed in Jagan et al. (2020) <[doi:10.1371/journal.pcbi.1008124](https://doi.org/10.1371/journal.pcbi.1008124)>.

**License** GPL (>= 2)

**URL** <https://github.com/davidearn/fastbeta>

**BugReports** <https://github.com/davidearn/fastbeta/issues>

**Depends** R (>= 4.3)

**Imports** grDevices, graphics, stats

**Suggests** adaptivetau, deSolve, tools, utils

**BuildResaveData** no

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fastbeta-package	R Package <b>fastbeta</b>
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**Description**

An R package for approximating time-varying infectious disease transmission rates from disease incidence time series and other data.

**Details**

The “main” function is [fastbeta](#).  
To render a list of available help topics, use [help](#)(package = "fastbeta").  
To report a bug or request a change, use [bug.report](#)(package = "fastbeta").

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deconvolve	<i>Richardson-Lucy Deconvolution</i>
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**Description**

Performs a modified Richardson-Lucy iteration for the purpose of estimating incidence from reported incidence or mortality, conditional on a reporting probability and on a distribution of the time to reporting.

**Usage**

```
deconvolve(x, prob = 1, delay = 1,  
           start, tol = 1, iter.max = 32L, complete = FALSE)
```

**Arguments**

<code>x</code>	a numeric vector of length <code>n</code> giving the number of infections or deaths reported during <code>n</code> observation intervals of equal duration.
<code>prob</code>	a numeric vector of length <code>d+n</code> such that <code>prob[d+i]</code> is the probability that an infection during interval <code>i</code> is eventually reported. <code>prob</code> of length 1 is recycled.
<code>delay</code>	a numeric vector of length <code>d+1</code> such that <code>delay[j]</code> is the probability that an infection during interval <code>i</code> is reported during interval <code>i+j-1</code> , given that it is eventually reported. <code>delay</code> need not sum to 1 but must not sum to 0.
<code>start</code>	a numeric vector of length <code>d+n</code> giving a starting value for the iteration. <code>start[d+i]</code> estimates the expected number of infections during interval <code>i</code> that are eventually reported. If missing, then a starting value is generated by padding <code>x</code> on the left and right with <code>d-d0</code> and <code>d0</code> zeros, choosing <code>d0 = which.max(delay)-1</code> .
<code>tol</code>	a tolerance indicating a stopping condition; see the reference.
<code>iter.max</code>	the maximum number of iterations.
<code>complete</code>	a logical flag indicating if the result should preserve successive updates to <code>start</code> .

**Value**

A list with elements:

<code>value</code>	the result of updating <code>start</code> <code>iter</code> times then dividing by <code>prob</code> . If <code>complete = TRUE</code> , then <code>value</code> is a $(d+n)$ -by- $(1+iter)$ matrix containing <code>start</code> and the <code>iter</code> successive updates, each divided by <code>prob</code> .
<code>chisq</code>	the chi-squared statistics corresponding to <code>value</code> .
<code>iter</code>	the number of iterations performed.

**References**

Goldstein, E., Dushoff, J., Ma, J., Plotkin, J. B., Earn, D. J. D., & Lipsitch, M. (2020). Reconstructing influenza incidence by deconvolution of daily mortality time series. *Proceedings of the National Academy of Sciences U. S. A.*, 106(51), 21825-21829. doi:10.1073/pnas.0902958106

**Examples**

```
set.seed(2L)
n <- 200L
d <- 50L
p <- 0.1
prob <- plogis(rlogis(d + n, location = qlogis(p), scale = 0.1))
delay <- diff(pgamma(0L:(d + 1L), 12, 0.4))

h <- function(x, a = 1, b = 1, c = 0) a * exp(-b * (x - c)^2)
ans <- floor(h(seq(-60, 60, length.out = d + n), a = 1000, b = 0.001))

x0 <- rbinom(d + n, ans, prob)
x <- tabulate(rep(1L:(d + n), x0) +
              sample(0L:d, size = sum(x0), replace = TRUE, prob = delay),
              d + n)[-1L:d]
```

```

str(D0 <- deconvolve(x, prob, delay, complete = FALSE))
str(D1 <- deconvolve(x, prob, delay, complete = TRUE))

matplot(-(d - 1L):n,
        cbind(x0, c(rep(NA, d), x), prob * D0[["value"]], p * ans),
        type = c("p", "p", "p", "l"),
        col = c(1L, 1L, 2L, 4L), pch = c(16L, 1L, 16L, NA),
        lty = c(0L, 0L, 0L, 1L), lwd = c(NA, NA, NA, 3L),
        xlab = "Time", ylab = "Count")
legend("topleft", NULL,
       c("actual", "actual+delay", "actual+delay+deconvolution", "p*h"),
       col = c(1L, 1L, 2L, 4L), pch = c(16L, 1L, 16L, NA),
       lty = c(0L, 0L, 0L, 1L), lwd = c(NA, NA, NA, 3L),
       bty = "n")

plot(0L:D1[["iter"]], D1[["chisq"]], xlab = "Iterations", ylab = quote(chi^2))
abline(h = 1, lty = 2L)

```

fastbeta

*Estimate a Time-Varying Infectious Disease Transmission Rate*

## Description

Generates a discrete approximation of a time-varying infectious disease transmission rate from an equally spaced disease incidence time series and other data.

## Usage

```
fastbeta(series, sigma = 1, gamma = 1, delta = 0,
         m = 1L, n = 1L, init, ...)
```

## Arguments

<code>series</code>	a “multiple time series” object, inheriting from class <code>mts</code> , with three columns storing (“parallel”, equally spaced) time series of incidence, births, and the per capita natural mortality rate, in that order.
<code>sigma, gamma, delta</code>	non-negative numbers. $m \times \text{sigma}$ , $n \times \text{gamma}$ , and <code>delta</code> are the rates of removal from each latent, infectious, and recovered compartment.
<code>m</code>	a non-negative integer indicating a number of latent stages.
<code>n</code>	a positive integer indicating a number of infectious stages.
<code>init</code>	a numeric vector of length $1+m+n+1$ giving an initial state with compartments ordered as $(S, E, I, R)$ .
<code>...</code>	optional arguments passed to <code>deconvolve</code> , if the first column of <code>series</code> represents <i>observed</i> incidence rather than actual or estimated incidence.

## Details

The algorithm implemented by fastbeta is based on an SEIR model with

- $m$  latent stages ( $E^i, i = 1, \dots, m$ );
- $n$  infectious stages ( $I^j, j = 1, \dots, n$ );
- time-varying rates  $\beta, \nu$ , and  $\mu$  of transmission, birth, and natural death; and
- constant rates  $m\sigma, n\gamma$ , and  $\delta$  of removal from each latent, infectious, and recovered compartment, where removal from the recovered compartment implies return to the susceptible compartment (loss of immunity).

It is derived by linearizing of the system of ordinary differential equations

$$\begin{aligned}
 dS/dt &= \delta R - (\lambda(t) + \mu(t))S + \nu(t) \\
 dE^1/dt &= \lambda(t)S - (m\sigma + \mu(t))E^1 \\
 dE^{i+1}/dt &= m\sigma E^i - (m\sigma + \mu(t))E^{i+1} \\
 dI^1/dt &= m\sigma E^m - (n\gamma + \mu(t))I^1 \\
 dI^{j+1}/dt &= n\gamma I^j - (n\gamma + \mu(t))I^{j+1} \\
 dR/dt &= n\gamma I^n - (\delta + \mu(t))R
 \end{aligned}
 \quad \lambda(t) = \beta(t) \sum_j I^j$$

and substituting actual or estimated incidence and births for definite integrals of  $\lambda S$  and  $\nu$ . This procedure yields a system of linear difference equations from which one recovers a discrete approximation of  $\beta$ :

$$\begin{aligned}
 E_{t+1}^1 &= [(1 - \frac{1}{2}(m\sigma + \mu_t))E_t^1 + Z_{t+1}] / [1 + \frac{1}{2}(m\sigma + \mu_{t+1})] \\
 E_{t+1}^{i+1} &= [(1 - \frac{1}{2}(m\sigma + \mu_t))E_t^{i+1} + \frac{1}{2}m\sigma(E_t^i + E_{t+1}^i)] / [1 + \frac{1}{2}(m\sigma + \mu_{t+1})] \\
 I_{t+1}^1 &= [(1 - \frac{1}{2}(n\gamma + \mu_t))I_t^1 + \frac{1}{2}m\sigma(E_t^m + E_{t+1}^m)] / [1 + \frac{1}{2}(n\gamma + \mu_{t+1})] \\
 I_{t+1}^{j+1} &= [(1 - \frac{1}{2}(n\gamma + \mu_t))I_t^{j+1} + \frac{1}{2}n\gamma(I_t^j + I_{t+1}^j)] / [1 + \frac{1}{2}(n\gamma + \mu_{t+1})] \\
 R_{t+1} &= [(1 - \frac{1}{2}(\delta + \mu_t))R_t + \frac{1}{2}n\gamma(I_t^n + I_{t+1}^n)] / [1 + \frac{1}{2}(\delta + \mu_{t+1})] \\
 S_{t+1} &= [(1 - \frac{1}{2}(\mu_t))S_t + \frac{1}{2}\delta(R_t + R_{t+1}) - Z_{t+1} + B_{t+1}] / [1 + \frac{1}{2}(\mu_{t+1})]
 \end{aligned}
 \quad \beta_t = (Z_t + Z_{t+1}) / (2S_t \sum_j I_{t+1}^j)$$

where we use the notation

$$\begin{aligned}
 Z(t) &= \int_{t-1}^t \lambda(s)S(s) ds \\
 B(t) &= \int_{t-1}^t \nu(s) ds
 \end{aligned}
 \quad X_t \sim X(t) : X = S, E^i, I^j, R, Z, B, \mu, \beta$$

and it is understood that the independent variable  $t$  is a unitless measure of time relative to the spacing of the substituted time series of incidence and births.

## Value

A “multiple time series” object, inheriting from class `mts`, with  $1+m+n+1+1$  columns (named S, E, I, R, and beta) storing the result of the iteration described in ‘Details’. It is completely parallel to argument series, having the same `tsp` attribute.

## References

Jagan, M., deJonge, M. S., Krylova, O., & Earn, D. J. D. (2020). Fast estimation of time-varying infectious disease transmission rates. *PLOS Computational Biology*, 16(9), Article e1008124, 1-39. [doi:10.1371/journal.pcbi.1008124](https://doi.org/10.1371/journal.pcbi.1008124)

## Examples

```
if (requireNamespace("adaptivetau")) withAutoprint({

  data(seir.ts02, package = "fastbeta")
  a <- attributes(seir.ts02)
  str(seir.ts02)
  plot(seir.ts02)

  ## We suppose that we have perfect knowledge of incidence,
  ## births, and the data-generating parameters
  series <- cbind(seir.ts02[, c("Z", "B")], mu = a[["mu"]](0))
  colnames(series) <- c("Z", "B", "mu") # FIXME: stats::cbind.ts mangles dimnames

  args <- c(list(series = series),
            a[c("sigma", "gamma", "delta", "m", "n", "init")])
  str(args)

  X <- do.call(fastbeta, args)
  str(X)
  plot(X)

  plot(X[, "beta"], ylab = "Transmission rate")
  lines(a[["beta"]](time(X)), col = "red") # the "truth"

})
```

---

fastbeta.bootstrap      *Parametric Bootstrapping*

---

## Description

A simple wrapper around [fastbeta](#) using it to generate a “primary” estimate of a time-varying transmission rate and  $r$  bootstrap estimates. Bootstrap estimates are computed for incidence time series simulated using [seir](#), with transmission rate defined as the linear interpolant of the primary estimate.

## Usage

```
fastbeta.bootstrap(r,
                  series, sigma = 1, gamma = 1, delta = 0,
                  m = 1L, n = 1L, init, ...)
```

## Arguments

<code>r</code>	a non-negative integer indicating a number of replications.
<code>series</code>	a “multiple time series” object, inheriting from class <code>mts</code> , with three columns storing (“parallel”, equally spaced) time series of incidence, births, and the per capita natural mortality rate, in that order.
<code>sigma, gamma, delta</code>	non-negative numbers. $m \times \text{sigma}$ , $n \times \text{gamma}$ , and <code>delta</code> are the rates of removal from each latent, infectious, and recovered compartment.
<code>m</code>	a non-negative integer indicating a number of latent stages.
<code>n</code>	a positive integer indicating a number of infectious stages.
<code>init</code>	a numeric vector of length $1+m+n+1$ giving an initial state with compartments ordered as $(S, E, I, R)$ .
<code>...</code>	optional arguments passed to <code>seir</code> and/or <code>deconvolve</code> . Both take optional arguments <code>prob</code> and <code>delay</code> . When <code>prob</code> is supplied but not <code>delay</code> , <code>seir</code> and <code>deconvolve</code> receive <code>prob</code> as is. When both are supplied, <code>seir</code> receives <code>prob</code> as is, whereas <code>deconvolve</code> receives <code>prob</code> augmented with <code>length(delay)-1</code> ones.

## Value

A “multiple time series” object, inheriting from class `mts`, with  $1+r$  columns storing the one primary and `r` bootstrap estimates. It is completely parallel to argument `series`, having the same `tsp` attribute.

## Examples

```
if (requireNamespace("adaptivetau")) withAutoprint({

  data(seir.ts02, package = "fastbeta")
  a <- attributes(seir.ts02)
  str(seir.ts02)
  plot(seir.ts02)

  ## We suppose that we have perfect knowledge of incidence,
  ## births, and the data-generating parameters
  series <- cbind(seir.ts02[, c("Z", "B")], mu = a[["mu"]](0))
  colnames(series) <- c("Z", "B", "mu") # FIXME: stats::cbind.ts mangles dimnames

  args <- c(list(r = 100L, series = series),
            a[c("sigma", "gamma", "delta", "m", "n", "init")])
  str(args)

  R <- do.call(fastbeta.bootstrap, args)
  str(R)
  plot(R)
  plot(R, level = 0.95)

})
```

---

fastbeta.matrix	<i>Calculate Coefficient Matrix for Iteration Step</i>
-----------------	--

---

### Description

Calculates the coefficient matrix corresponding to one step of the iteration carried out by [fastbeta](#):

```
y <- c(1, E, I, R, S)
for (pos in seq_len(nrow(series) - 1L)) {
  L <- fastbeta.matrix(pos, series, ...)
  y <- L %*% y
}
```

### Usage

```
fastbeta.matrix(pos,
                series, sigma = 1, gamma = 1, delta = 0,
                m = 1L, n = 1L)
```

### Arguments

pos	an integer indexing a row (but not the last row) of series.
series	a “multiple time series” object, inheriting from class <a href="#">mts</a> , with three columns storing (“parallel”, equally spaced) time series of incidence, births, and the per capita natural mortality rate, in that order.
sigma, gamma, delta	non-negative numbers. $m \times \text{sigma}$ , $n \times \text{gamma}$ , and delta are the rates of removal from each latent, infectious, and recovered compartment.
m	a non-negative integer indicating a number of latent stages.
n	a positive integer indicating a number of infectious stages.

### Value

A lower triangular matrix of size  $1+m+n+1+1$ .

### Examples

```
if (requireNamespace("adaptivetau")) withAutoprint({

  data(seir.ts02, package = "fastbeta")
  a <- attributes(seir.ts02); p <- length(a[["init"]])
  str(seir.ts02)
  plot(seir.ts02)

  ## We suppose that we have perfect knowledge of incidence,
  ## births, and the data-generating parameters
  series <- cbind(seir.ts02[, c("Z", "B")], mu = a[["mu"]](0))
```



```

colnames(series) <- c("Z", "B", "mu") # FIXME: stats::cbind.ts mangles dimnames

args <- c(list(series = series),
          a[c("sigma", "gamma", "delta", "init", "m", "n")])
str(args)

X <- unclass(do.call(fastbeta, args))[, seq_len(p)]
colnames(X)
Y <- Y. <- cbind(1, X[, c(2L:p, 1L)], deparse.level = 2L)
colnames(Y)

args <- c(list(pos = 1L, series = series),
          a[c("sigma", "gamma", "delta", "m", "n")])
str(args)

L <- do.call(fastbeta.matrix, args)
str(L)
symnum(L != 0)

for (pos in seq_len(nrow(series) - 1L)) {
  args[["pos"]] <- pos
  L. <- do.call(fastbeta.matrix, args)
  Y.[pos + 1L, ] <- L. %*% Y.[pos, ]
}
stopifnot(all.equal(Y, Y.))
})

```

---

ptpi

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*Peak to Peak Iteration*


---

## Description

Approximates the state of an SEIR model at a reference time from an equally spaced,  $T$ -periodic incidence time series and other data. The algorithm relies on a strong assumption: that the incidence time series was generated by the asymptotic dynamics of an SEIR model admitting a locally stable,  $T$ -periodic attractor. Hence do interpret with care.

## Usage

```

ptpi(series, sigma = 1, gamma = 1, delta = 0,
      m = 1L, n = 1L, init,
      start = tsp(series)[1L], end = tsp(series)[2L],
      tol = 1e-03, iter.max = 32L,
      backcalc = FALSE, complete = FALSE, ...)

```

## Arguments

<code>series</code>	a “multiple time series” object, inheriting from class <code>mts</code> , with three columns storing (“parallel”, equally spaced) time series of incidence, births, and the per capita natural mortality rate, in that order.
<code>sigma, gamma, delta</code>	non-negative numbers. $m \times \text{sigma}$ , $n \times \text{gamma}$ , and <code>delta</code> are the rates of removal from each latent, infectious, and recovered compartment.
<code>m</code>	a non-negative integer indicating a number of latent stages.
<code>n</code>	a positive integer indicating a number of infectious stages.
<code>init</code>	a numeric vector of length $1+m+n+1$ giving an initial guess for the state at time start.
<code>start, end</code>	start and end times for the iteration, whose difference should be approximately equal to an integer number of periods. One often chooses the time of the first peak in the incidence time series and the time of the last peak in phase with the first.
<code>tol</code>	a tolerance indicating a stopping condition; see ‘Details’.
<code>iter.max</code>	the maximum number of iterations.
<code>backcalc</code>	a logical indicating if the state at time <code>tsp(series)[1]</code> should be back-calculated from the state at time <code>start</code> if that is later.
<code>complete</code>	a logical indicating if intermediate states should be recorded in an array. Useful mainly for didactic or diagnostic purposes.
<code>...</code>	optional arguments passed to <code>deconvolve</code> , if the first column of <code>series</code> represents <i>observed</i> incidence rather than actual or estimated incidence.

## Details

`ptpi` can be understood as an iterative application of `fastbeta` to a subset of `series`. The basic algorithm can be expressed in R code as:

```
w <- window(series, start, end); i <- nrow(s); j <- seq_along(init)
diff <- Inf; iter <- 0L
while (diff > tol && iter < iter.max) {
  init. <- init
  init <- fastbeta(w, sigma, gamma, delta, m, n, init)[i, j]
  diff <- sqrt(sum((init - init.)^2) / sum(init.^2))
  iter <- iter + 1L
}
value <- init
```

Back-calculation involves solving a linear system of equations; the back-calculated result can mislead if the system is ill-conditioned.

## Value

A list with elements:

value	an approximation of the state at time <code>start</code> or at time <code>tsp(series)[1L]</code> , depending on <code>backcalc</code> .
diff	the relative difference between the last two approximations.
iter	the number of iterations performed.
x	if <code>complete = TRUE</code> , then a “multiple time series” object, inheriting from class <code>mts</code> , with dimensions <code>c(nrow(w), length(value), iter)</code> , where <code>w = window(series, start, end)</code> . <code>x[, , k]</code> contains the state at each time( <code>w</code> ) in iteration <code>k</code> .

## References

Jagan, M., deJonge, M. S., Krylova, O., & Earn, D. J. D. (2020). Fast estimation of time-varying infectious disease transmission rates. *PLOS Computational Biology*, 16(9), Article e1008124, 1-39.  
[doi:10.1371/journal.pcbi.1008124](https://doi.org/10.1371/journal.pcbi.1008124)

## Examples

```
if (requireNamespace("deSolve")) withAutoprint({

data(seir.ts01, package = "fastbeta")
a <- attributes(seir.ts01); p <- length(a[["init"]])
str(seir.ts01)
plot(seir.ts01)

## We suppose that we have perfect knowledge of incidence,
## births, and the data-generating parameters, except for
## the initial state, which we "guess"
series <- cbind(seir.ts01[, c("Z", "B")], mu = a[["mu"]](0))
colnames(series) <- c("Z", "B", "mu") # FIXME: stats::cbind.ts mangles dimnames

plot(series[, "Z"])
start <- 23; end <- 231
abline(v = c(start, end), lty = 2)

set.seed(0L)
args <- c(list(series = series),
          a[c("sigma", "gamma", "delta", "m", "n", "init")],
          list(start = start, end = end, complete = TRUE))
init <- seir.ts01[which.min(abs(time(seir.ts01) - start)), seq_len(p)]
args[["init"]] <- init * rlnorm(p, 0, 0.1)
str(args)

L <- do.call(ptpi, args)
str(L)

S <- L[["x"]][, "S", ]
plot(S, plot.type = "single")
lines(seir.ts01[, "S"], col = "red", lwd = 4) # the "truth"
abline(h = L[["value"]][["S"], v = start, col = "blue", lwd = 4, lty = 2)

## Relative error
L[["value"]] / init - 1
```

```
})
```

---

seir

---

*Simulate Infectious Disease Time Series*


---

## Description

Simulates incidence time series based on an SEIR model with user-defined forcing and a simple model for observation error.

Note that simulation code depends on availability of suggested packages **adaptivetau** and **deSolve**. If the dependency cannot be loaded then an error is signaled.

## Usage

```
seir(length.out = 1L,
      beta, nu = function (t) 0, mu = function (t) 0,
      sigma = 1, gamma = 1, delta = 0,
      m = 1L, n = 1L, init,
      stochastic = TRUE, prob = 1, delay = 1,
      aggregate = FALSE, useCompiled = TRUE, ...)
```

## A basic wrapper for the m=0L case:

```
sir(length.out = 1L,
     beta, nu = function (t) 0, mu = function (t) 0,
     gamma = 1, delta = 0,
     n = 1L, init,
     stochastic = TRUE, prob = 1, delay = 1,
     aggregate = FALSE, useCompiled = TRUE, ...)
```

## Arguments

length.out	a non-negative integer indicating the time series length.
beta, nu, mu	functions of one or more arguments returning transmission, birth, and natural death rates at the time point indicated by the first argument. Arguments after the first must be strictly optional. The functions need not be vectorized.
sigma, gamma, delta	non-negative numbers. $m \times \text{sigma}$ , $n \times \text{gamma}$ , and $\text{delta}$ are the rates of removal from each latent, infectious, and recovered compartment.
m	a non-negative integer indicating a number of latent stages.
n	a positive integer indicating a number of infectious stages.
init	a numeric vector of length $1+m+n+1$ giving an initial state with compartments ordered as $(S, E, I, R)$ .
stochastic	a logical indicating if the simulation should be stochastic; see ‘Details’.

prob	a numeric vector of length $n$ such that $\text{prob}[i]$ is the probability that an infection during interval $i$ is eventually observed. $\text{prob}$ of length 1 is recycled.
delay	a numeric vector of positive length such that $\text{delay}[i]$ is the probability that an infection during interval $j$ is observed during interval $j+i-1$ , given that it is eventually observed. $\text{delay}$ need not sum to 1 but must not sum to 0.
aggregate	a logical indicating if latent and infectious compartments should be aggregated.
useCompiled	a logical indicating if derivatives should be computed by compiled C functions rather than by R functions (which <i>may</i> be <i>byte-compiled</i> ). Set to FALSE only if TRUE seems to cause problems, and in that case please report the problems with <a href="#">bug.report</a> (package = "fastbeta").
...	optional arguments passed to <a href="#">lsoda</a> (directly) or <a href="#">ssa.adaptivetau</a> (via its list argument <code>tl.params</code> ), depending on <code>stochastic</code> .

## Details

Simulations are based on an SEIR model with

- $m$  latent stages ( $E^i, i = 1, \dots, m$ );
- $n$  infectious stages ( $I^j, j = 1, \dots, n$ );
- time-varying rates  $\beta, \nu$ , and  $\mu$  of transmission, birth, and natural death; and
- constant rates  $m\sigma, n\gamma$ , and  $\delta$  of removal from each latent, infectious, and recovered compartment, where removal from the recovered compartment implies return to the susceptible compartment (loss of immunity).

`seir(stochastic = FALSE)` works by numerically integrating the system of ordinary differential equations

$$\begin{aligned}
 dS/dt &= \delta R - (\lambda(t) + \mu(t))S + \nu(t) \\
 dE^1/dt &= \lambda(t)S - (m\sigma + \mu(t))E^1 \\
 dE^{i+1}/dt &= m\sigma E^i - (m\sigma + \mu(t))E^{i+1} \\
 dI^1/dt &= m\sigma E^m - (n\gamma + \mu(t))I^1 \\
 dI^{j+1}/dt &= n\gamma I^j - (n\gamma + \mu(t))I^{j+1} \\
 dR/dt &= n\gamma I^n - (\delta + \mu(t))R
 \end{aligned}
 \quad \lambda(t) = \beta(t) \sum_j I^j$$

where it is understood that the independent variable  $t$  is a unitless measure of time relative to an observation interval. To get time series of incidence and births, the system is augmented with two equations describing *cumulative* incidence and births

$$\begin{aligned}
 dZ/dt &= \lambda(t)S \\
 dB/dt &= \nu(t)
 \end{aligned}$$

and the *augmented* system is numerically integrated. Observed incidence is simulated from incidence by scaling the latter by `prob` and convolving the result with `delay`.

`seir(stochastic = TRUE)` works by simulating a Markov process corresponding to the augmented system, as described in the reference. Observed incidence is simulated from incidence by binning binomial samples taken with probabilities `prob` over future observation intervals according to multinomial samples taken with probabilities `delay`.

## Value

A “multiple time series” object, inheriting from class `mts`. Beneath the class, it is a `length.out-by-(1+m+n+1+2)` numeric matrix with columns S, E, I, R, Z, and B, where Z and B specify incidence and births as the number of infections and births since the previous time point.

If `prob` or `delay` is not missing, then there is an additional column `Z.obs` specifying *observed* incidence as the number of infections observed since the previous time point. The first `length(delay)` elements of this column contain partial counts.

## References

Cao, Y., Gillespie, D. T., & Petzold, L. R. (2007). Adaptive explicit-implicit tau-leaping method with automatic tau selection. *Journal of Chemical Physics*, 126(22), Article 224101, 1-9. doi:10.1063/1.2745299

## See Also

[seir.auxiliary](#), [seir.library](#).

## Examples

```
if (requireNamespace("adaptivetau")) withAutoprint({

  beta <- function (t, a = 1e-01, b = 1e-05) b * (1 + a * sinpi(t / 26))
  nu   <- function (t) 1e+03
  mu   <- function (t) 1e-03

  sigma <- 0.5
  gamma <- 0.5
  delta <- 0

  init <- c(S = 50200, E = 1895, I = 1892, R = 946011)

  length.out <- 250L
  prob <- 0.1
  delay <- diff(pgamma(0:8, 2.5))

  set.seed(0L)
  X <- seir(length.out, beta, nu, mu, sigma, gamma, delta, init = init,
            prob = prob, delay = delay, epsilon = 0.002)
  ##                                     ^^^^^
  ## default epsilon = 0.05 allows too big leaps => spurious noise
  ##
  str(X)
  plot(X)

  r <- 10L
  Y <- do.call(cbind, replicate(r, simplify = FALSE,
    seir(length.out, beta, nu, mu, sigma, gamma, delta, init = init,
      prob = prob, delay = delay, epsilon = 0.002)[, "Z.obs"])))
  str(Y) # FIXME: stats::cbind.ts mangles dimnames
  plot(window(Y, start = tsp(Y)[1L] + length(delay) / tsp(Y)[3L]),
```

```

##          ^^^^^
## discards points showing edge effects due to 'delay'
##
plot.type = "single", col = seq_len(r), ylab = "Case reports")

})

```

seir.auxiliary

*Auxiliary Functions for the SEIR Model without Forcing***Description**

Calculate the basic reproduction number, endemic equilibrium, and Jacobian matrix of the SEIR model without forcing.

**Usage**

```

seir.R0      (beta, nu = 0, mu = 0, sigma = 1, gamma = 1, delta = 0,
              m = 1L, n = 1L, N = 1)
seir.ee      (beta, nu = 0, mu = 0, sigma = 1, gamma = 1, delta = 0,
              m = 1L, n = 1L, N = 1)
seir.jacobian(beta, nu = 0, mu = 0, sigma = 1, gamma = 1, delta = 0,
              m = 1L, n = 1L)

```

**Arguments**

**beta, nu, mu, sigma, gamma, delta**  
non-negative numbers. beta, nu, and mu are the rates of transmission, birth, and natural death. m\*sigma, n\*gamma, and delta are the rates of removal from each latent, infectious, and recovered compartment.

**m**  
a non-negative integer indicating a number of latent stages.

**n**  
a positive integer indicating a number of infectious stages.

**N**  
a non-negative number indicating a population size for the (nu == 0 && mu == 0) case.

**Details**

If  $\mu, \nu = 0$ , then the basic reproduction number is computed as

$$\mathcal{R}_0 = N\beta/\gamma$$

and the endemic equilibrium is computed as

$$\begin{bmatrix} S \\ E^i \\ I^j \\ R \end{bmatrix} = \begin{bmatrix} \gamma/\beta \\ w\delta/(m\sigma) \\ w\delta/(n\gamma) \\ w \end{bmatrix}$$

where  $w$  is chosen so that the sum is  $N$ .

If  $\mu, \nu > 0$ , then the basic reproduction number is computed as

$$\mathcal{R}_0 = \nu \beta a^{-m} (1 - b^{-n}) / \mu^2$$

and the endemic equilibrium is computed as

$$\begin{bmatrix} S \\ E^i \\ I^j \\ R \end{bmatrix} = \begin{bmatrix} \mu a^m / (\beta(1 - b^{-n})) \\ w a^{m-i} b^n (\delta + \mu) / (m\sigma) \\ w b^{n-j} (\delta + \mu) / (n\gamma) \\ w \end{bmatrix}$$

where  $w$  is chosen so that the sum is  $\nu/\mu$ , the population size at equilibrium, and  $a = 1 + \mu/(m\sigma)$  and  $b = 1 + \mu/(n\gamma)$ .

Currently, none of the functions documented here are vectorized. Arguments must have length 1.

### Value

`seir.R0` returns a numeric vector of length 1. `seir.ee` returns a numeric vector of length  $1+m+n+1$ . `seir.jacobian` returns a function of one argument  $x$  (which must be a numeric vector of length  $1+m+n+1$ ) whose return value is a square numeric matrix of size `length(x)`.

### See Also

[seir](#), for the system of ordinary differential equations on which these computations are predicated.

---

seir.library

*Often Used Simulations*

---

### Description

Infectious disease time series simulated using [seir](#), for use primarily in examples, tests, and vignettes. Users should not rely on simulation details, which may change between package versions.

Note that simulation code depends on availability of suggested packages **adaptivetau** and **deSolve**. If the dependency cannot be loaded then the value of the data set is `NULL`.

### Usage

```
## if (requireNamespace("deSolve"))
data(seir.ts01, package = "fastbeta")
## else ...

## if (requireNamespace("adaptivetau"))
data(seir.ts02, package = "fastbeta")
## else ...
```



**Format**

A “multiple time series” object, inheriting from class `mts`, always a subset of the result of a call to `seir`, discarding transient behaviour. Simulation parameters may be preserved as attributes.

**Source**

Scripts sourced by `data` to reproduce the simulations are located in subdirectory ‘data’ of the **fastbeta** installation; see, e.g. `system.file("data", "seir.ts01.R", package = "fastbeta")`.

**See Also**

`seir`.

**Examples**

```
if (requireNamespace("deSolve")) withAutoprint({

  data(seir.ts01, package = "fastbeta")
  str(seir.ts01)
  plot(seir.ts01)

})

if (requireNamespace("adaptivetau")) withAutoprint({

  data(seir.ts02, package = "fastbeta")
  str(seir.ts02)
  plot(seir.ts02)

})
```

---

sir.aoi

---

*Solve the SIR Equations Structured by Age of Infection*


---

**Description**

Numerically integrates the SIR equations with rates of transmission and recovery structured by age of infection.

**Usage**

```
sir.aoi(from = 0, to = from + 1, by = 1,
        R0, ell = 1, n = max(length(R0), length(ell)),
        init = c(1 - init.infected, init.infected),
        init.infected = .Machine[["double.neg.eps"]],
        weights = rep(c(1, 0), c(1L, n - 1L)),
        root = NULL, aggregate = FALSE, ...)

## S3 method for class 'sir.aoi'
summary(object, tol = 1e-6, ...)
```

## Arguments

from, to, by	passed to <code>seq.int</code> in order to generate an increasing, equally spaced vector of time points in units of the mean time spent infectious.
$R_0$	a numeric vector of length $n$ such that $\text{sum}(R_0)$ is the basic reproduction number and $R_0[j]$ is the contribution of infected compartment $j$ . Otherwise, a numeric vector of length 1, handled as equivalent to $\text{rep}(R_0/n, n)$ .
ell	a numeric vector of length $n$ such that $\text{ell}[j]$ is the ratio of the mean time spent in infected compartment $j$ and the mean time spent infectious; internally, $\text{ell}/\text{sum}(\text{ell}[R_0 > 0])$ is used, hence ell is determined only up to a positive factor. Otherwise (and by default), a numeric vector of length 1, handled as equivalent to $\text{rep}(1, n)$ .
$n$	a positive integer giving the number of infected compartments. Setting $n$ and thus overriding the default expression is necessary only if the lengths of $R_0$ and ell are both 1.
init	a numeric vector of length 2 giving initial susceptible and infected proportions.
init.infected	a number in $(0, 1]$ used only to define the default expression for init; see ‘Usage’.
weights	a numeric vector of length $n$ containing non-negative weights, defining the initial distribution of infected individuals among the infected compartments. By default, all infected individuals occupy the first compartment.
root	a function returning a numeric vector of length 1, with formal arguments ( $\tau$ , $S$ , $I$ , $Y$ , $dS$ , $dI$ , $dY$ , $R_0$ , ell) (or a subset); otherwise, NULL.
aggregate	a logical indicating if infected compartments should be aggregated.
...	optional arguments passed to <code>lsoda</code> .
object	an R object inheriting from class <code>sir.aoi</code> , typically the value of a call to <code>sir.aoi</code> .
tol	a positive number giving an upper bound on the relative change (from one time point to the next) in the slope of log prevalence, defining time windows in which growth or decay of prevalence is considered to be exponential.

## Details

The standard SIR equations with rates of transmission and recovery structured by age of infection are

$$\begin{aligned}
 dS/dt &= -\sum_j (\beta_j/N) S I_j \\
 dI_1/dt &= \sum_j (\beta_j/N) S I_j - \gamma_1 I_1 \\
 dI_{j+1}/dt &= \gamma_j I_j - \gamma_{j+1} I_{j+1} \\
 dR/dt &= \gamma_n I_n
 \end{aligned}$$

where  $N = S + \sum_j I_j + R$  is the (constant, positive) population size. Nondimensionalization using parameters  $N = 1$ ,  $\mathcal{R}_{0,j} = \beta_j/\gamma_j$ , and  $\ell_j = (1/\gamma_j)/\sum_{j:\mathcal{R}_{0,j}>0} (1/\gamma_j)$  and time unit  $\tau =$

$t / \sum_{j: \mathcal{R}_{0,j} > 0} (1/\gamma_j)$ , gives

$$\begin{aligned} dS / d\tau &= - \sum_j (\mathcal{R}_{0,j} / \ell_j) S I_j \\ dI_1 / d\tau &= \sum_j (\mathcal{R}_{0,j} / \ell_j) S I_j - (1/\ell_1) I_1 \\ dI_{j+1} / d\tau &= (1/\ell_j) I_j - (1/\ell_{j+1}) I_{j+1} \\ dR / d\tau &= (1/\ell_n) I_n \end{aligned}$$

`sir.aoi` works with the nondimensional equations, dropping the last equation (which is redundant given  $R = 1 - S - \sum_j I_j$ ) and augments the resulting system of  $1 + n$  equations with a new equation

$$dY/d\tau = \left( \sum_j \mathcal{R}_{0,j} S - 1 \right) \sum_{j: \mathcal{R}_{0,j} > 0} I_j$$

due to the usefulness of the solution  $Y$  in applications.

### Value

`root = NULL` a “multiple time series” object, inheriting from class `sir.aoi` and transitively from class `mts`. Beneath the class, it is a `length(seq(from, to, by))`-by-`(1+n+1)` numeric matrix of the form `cbind(S, I, Y)`.

`root = function (tau, S, I, Y, dS, dI, dY, R0, ell)` a numeric vector of length  $1+1+n+1$  of the form `c(tau, S, I, Y)` storing the root of the function `root` in units of the mean time spent infectious and the state at that time. Attribute `curvature` stores the curvature of  $Y$  at the root. If a root is not found between times `from` and `to`, then the value is `NULL`.

If `aggregate = TRUE`, then infected compartments are aggregated so that the number of columns (elements, if `root` is a function) named `I` is 1 rather than `n`. This column or element stores prevalence, the proportion of the population that is infected. For convenience, there are 2 additional columns (elements) named `I.E` and `I.I`. These store the non-infectious and infectious components of prevalence, as indicated by `sign(R0)`, hence `I.E + I.I = I`.

The method for `summary` returns a numeric vector of length 2 containing the left and right “tail exponents”, defined as the asymptotic values of the slope of log prevalence. `NaN` elements indicate that a tail exponent cannot be approximated from the prevalence time series represented by object, because the time window does not cover enough of the tail, where the meaning of “enough” is set by `tol`.

### Note

`sir.aoi` is not a special case of `sir` nor a generalization. The two functions were developed independently and for different purposes: `sir.aoi` to validate analytical results concerning the SIR equations as formulated here, `sir` to simulate incidence time series suitable for testing `fastbeta`.

### Examples

```
if (requireNamespace("deSolve")) withAutoprint({
  to <- 100; by <- 0.01; R0 <- c(0, 16); ell <- c(0.5, 1)
  peak <- sir.aoi(to = to, by = by, R0 = R0, ell = ell,
```

```

      root = function (S, R0) sum(R0) * S - 1,
      aggregate = TRUE)
peak

to <- 4 * peak[["tau"]] # a more principled endpoint

soln <- sir.aoi(to = to, by = by, R0 = R0, ell = ell,
               aggregate = TRUE)
head(soln)

plot(soln) # dispatching stats::plot.ts

plot(soln[, "Y"], ylab = "Y")
abline(v = peak[["tau"]], h = peak[["Y"]],
       lty = 2, lwd = 2, col = "red")

xoff <- function (x, k) x - x[k]
lamb <- summary(soln)
k <- c(16L, nrow(soln)) # c(1L, nrow(soln)) suffers due to transient
plot(soln[, "I"], log = "y", ylab = "Prevalence")
for (i in 1:2)
  lines(soln[k[i], "I"] * exp(lamb[i] * xoff(time(soln), k[i])),
        lty = 2, lwd = 2, col = "red")

wrap <-
function (root)
  sir.aoi(to = to, by = by, R0 = R0, ell = ell,
          root = root, aggregate = TRUE)
Ymax <- peak[["Y"]]

## NB: want *simple* roots, not *multiple* roots
F <- list(function (Y) (Y - Ymax * 0.5) ,
          function (Y) (Y - Ymax * 0.5)^2,
          function (Y) (Y - Ymax      ) ,
          function (Y) (Y - Ymax      )^2)
lapply(F, wrap)

## NB: critical values can be attained twice
F <- list(function (Y, dY) if (dY > 0) Y - Ymax * 0.5 else 1,
          function (Y, dY) if (dY < 0) Y - Ymax * 0.5 else 1)
lapply(F, wrap)

})

```

---

smallpox

*Smallpox Mortality in London, England, 1661-1930*


---

## Description

Time series of deaths due to smallpox, deaths due to all causes, and births in London, England, from 1661 to 1930, as recorded in the London Bills of Mortality and the Registrar General's Weekly

Returns.

### Usage

```
data(smallpox, package = "fastbeta")
```

### Format

A data frame with 13923 observations of 5 variables:

**from** start date of the record.

**nday** length of the record, which is the number of days (typically 7) over which deaths and births were counted.

**smallpox** count of deaths due to smallpox.

**allcauses** count of deaths due to all causes.

**births** count of births.

### Source

A precise description of the data set and its correspondence to the original source documents is provided in the reference.

A script generating the smallpox data frame from a CSV file accompanying the reference is available as `system.file("scripts", "smallpox.R", package = "fastbeta")`.

### References

Krylova, O. & Earn, D. J. D. (2020). Patterns of smallpox mortality in London, England, over three centuries. *PLOS Biology*, 18(12), Article e3000506, 1-27. doi:[10.1371/journal.pbio.3000506](https://doi.org/10.1371/journal.pbio.3000506)

### Examples

```
data(smallpox, package = "fastbeta")
str(smallpox)
table(smallpox[["nday"]]) # not all 7 days, hence:
plot(7 * smallpox / as.double(nday) ~ from, smallpox, type = "l")
```

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