

# Package ‘EpiLPS’

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**Type** Package

**Title** A Bayesian Tool for Fast and Flexible Estimation of the  
Reproduction Number

**Version** 1.1.0

**Depends** R (>= 4.1.0)

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**BugReports** <https://github.com/oswaldogressani/EpiLPS/issues>

**Description** Estimation of the instantaneous reproduction number with  
Laplacian-P-splines following the methodology of Gressani et al. (2022)  
<[doi:10.1371/journal.pcbi.1010618](https://doi.org/10.1371/journal.pcbi.1010618)>. The negative binomial  
distribution is used to model the time series of incidence data. Two methods are  
available for inference : (1) a sampling-free approach based on a maximum a  
posteriori calibration of the hyperparameter vector and (2) a fully stochastic  
approach with a Metropolis-adjusted Langevin algorithm for  
efficient sampling of the posterior distribution.

**URL** <<https://github.com/oswaldogressani/EpiLPS>>

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**LinkingTo** RcppArmadillo, Rcpp

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ggplot2 (>= 3.3.5), gridExtra (>= 2.3)

**Suggests** rmarkdown, knitr

**VignetteBuilder** knitr

**NeedsCompilation** yes

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epicurve	<i>Plot the epidemic curve</i>
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### Description

This routine gives a graphical representation of the epidemic curve based on an incidence time series.

### Usage

```
epicurve(incidence, dates = NULL, datelab = "7d", col = "deepskyblue4", barwidth = 1,
         title = "Epidemic curve", xtickangle = 0, smooth = NULL, smoothcol = "orange")
```

### Arguments

incidence	A vector containing the incidence time series
dates	A vector of dates in format "YYYY-MM-DD".
datelab	The spacing for ticks on the x-axis. Default "7d".
col	The color of the epidemic curve.
barwidth	The width of the bars. Default is 1.
title	Title of the plot.
xtickangle	The angle of the x-ticks. Default is 0 (horizontal).
smooth	An object of class Rt obtained with the <code>estimR</code> or <code>estimRmcmc</code> routine. It is used to draw a smoothed estimate of the epidemic curve based on the Laplacian-P-splines model.
smoothcol	The color of the smoothed curve and associated credible interval.

**Value**

A plot of the epidemic curve.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**Examples**

```
si <- c(0.05, 0.05, 0.1, 0.1, 0.1, 0.1, 0.1, 0.05, 0.05, 0.1, 0.1, 0.1)
epidemic <- episim(si = si, Rpattern = 4)
epicurve(epidemic$y)
```

---

episim

*Simulation of an incidence time series*

---

**Description**

Based on a serial interval and a functional input for the reproduction number over  $T$  days, the routine generates an incidence time series following a Poisson or negative binomial model. The link between the reproduction number and the generated incidence data is governed by the renewal equation. The baseline (mean) number of cases at day 1 is fixed at 10. The mean number of cases for the remaining days of the epidemic are generated following equation (2) of Azmon et al. (2013).

**Usage**

```
episim(si, endepi = 50, Rpattern = 1, Rconst = 2.5,
       dist = c("poiss", "negbin"), overdisp = 1, verbose = FALSE, plotsim = FALSE)
```

**Arguments**

si	The serial interval distribution.
endepi	The total number of days of the epidemic.
Rpattern	Different scenarios for the true underlying curve of $R_t$ . Six scenarios are possible with 1,2,3,4,5,6.
Rconst	The constant value of $R$ (if scenario 1 is selected), default is 2.5.
dist	The distribution from which to sample the incidence counts. Either Poisson (default) or negative binomial.
overdisp	Overdispersion parameter for the negative binomial setting.
verbose	Should metadata of the simulated epidemic be printed?
plotsim	Create a plot of the incidence time series, the true reproduction number curve and the serial interval.

**Value**

An object of class `episim` consisting of a list with the generated incidence time series, the mean vector of the Poisson/negative binomial distribution, the true underlying R function for the data generating process and the chosen serial interval distribution.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**References**

Azmon, A., Faes, C., Hens, N. (2014). On the estimation of the reproduction number based on misreported epidemic data. *Statistics in medicine*, **33**(7):1176-1192.

**Examples**

```
si <- c(0.05, 0.05, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.05, 0.05, 0.1, 0.1, 0.1)
epidemic <- episim(si = si, Rpattern = 1)
```

---

estimR

*Estimation of the reproduction number with Laplacian-P-splines*

---

**Description**

This routine estimates the instantaneous reproduction number  $R_t$ ; the mean number of secondary infections generated by an infected individual at time  $t$  (White et al. 2020); by using Bayesian P-splines and Laplace approximations (Gressani et al. 2022). Estimation of  $R_t$  is based on a time series of incidence counts and (a discretized) serial interval distribution. The negative binomial distribution is used to model incidence count data and P-splines (Eilers and Marx, 1996) are used to smooth the epidemic curve. The link between the epidemic curve and the reproduction number is established via the renewal equation.

**Usage**

```
estimR(incidence, si, K = 30, dates = NULL, maxmethod = c("NelderMead", "HillClimb"),
CoriR = FALSE, WTR = FALSE, optimstep = 0.3, priors = Rmodelpriors())
```

**Arguments**

<code>incidence</code>	A vector containing the incidence time series. If <code>incidence</code> contains NA values at certain time points, these are replaced by the average of the left- and right neighbor counts. If the right neighbor is NA, the left neighbor is used as a replacement value.
<code>si</code>	The (discrete) serial interval distribution.
<code>K</code>	Number of B-splines in the basis.
<code>dates</code>	A vector of dates in format "YYYY-MM-DD" (optional).

maxmethod	The method to maximize the hyperparameter posterior distribution.
CoriR	Should the $R_t$ estimate of Cori (2013) be also computed?
WTR	Should the $R_t$ estimate of Wallinga-Teunis (2004) be also computed?
optimstep	Learning rate for the "HillClimb" method to maximize the posterior distribution of the hyperparameters.
priors	A list containing the prior specification of the model hyperparameters as set in Rmodelpriors. See ?Rmodelpriors.

## Details

The `estimR` routine estimates the reproduction number in a totally "sampling-free" fashion. The hyperparameter vector (containing the penalty parameter of the P-spline model and the overdispersion parameter of the negative binomial model for the incidence time series) is fixed at its maximum a posteriori (MAP). By default, the algorithm for maximization is the one of Nelder and Mead (1965). If `maxmethod` is set to "HillClimb", then a gradient ascent algorithm is used to maximize the hyperparameter posterior.

## Value

A list with the following components:

- `incidence`: The incidence time series.
- `si`: The serial interval distribution.
- `RLPS`: A data frame containing estimates of the reproduction number obtained with the Laplacian-P-splines methodology.
- `thetahat`: The estimated vector of B-spline coefficients.
- `Sigmat`: The estimated variance-covariance matrix of the Laplace approximation to the conditional posterior distribution of the B-spline coefficients.
- `RCori`: A data frame containing the estimates of the reproduction obtained with the method of Cori (2013).
- `RWT`: A data frame containing the estimates of the reproduction obtained with the method of Wallinga-Teunis (2004).
- `LPS_elapsed`: The routine real elapsed time (in seconds) when estimation of the reproduction number is carried out with Laplacian-P-splines.
- `Cori_elapsed`: The routine real elapsed time (in seconds) when estimation of the reproduction number is carried out with the method of Cori (2013).
- `penparam`: The estimated penalty parameter related to the P-spline model.
- `K`: The number of B-splines used in the basis.
- `NegBinoverdisp`: The estimated overdispersion parameter of the negative binomial distribution for the incidence time series.
- `optimconverged`: Indicates whether the algorithm to maximize the posterior distribution of the hyperparameters has converged.
- `method`: The method to estimate the reproduction number with Laplacian-P-splines.
- `optim_method`: The chosen method to to maximize the posterior distribution of the hyperparameters.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**References**

- Gressani, O., Wallinga, J., Althaus, C. L., Hens, N. and Faes, C. (2022). EpiLPS: A fast and flexible Bayesian tool for estimation of the time-varying reproduction number. *Plos Computational Biology*, **18**(10): e1010618.
- Cori, A., Ferguson, N.M., Fraser, C., Cauchemez, S. (2013). A new framework and software to estimate time-varying reproduction numbers during epidemics. *American Journal of Epidemiology*, **178**(9):1505–1512.
- Wallinga, J., & Teunis, P. (2004). Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. *American Journal of Epidemiology*, **160**(6), 509-516.
- White, L.F., Moser, C.B., Thompson, R.N., Pagano, M. (2021). Statistical estimation of the reproductive number from case notification data. *American Journal of Epidemiology*, **190**(4):611-620.
- Eilers, P.H.C. and Marx, B.D. (1996). Flexible smoothing with B-splines and penalties. *Statistical Science*, **11**(2):89-121.

**Examples**

```
# Illustration on simulated data
si<- Idist(mean = 5, sd = 3)$pvec
datasim <- episim(si = si, endepi = 60, Rpattern = 5, dist="negbin", overdisp = 50)
epifit_sim <- estimR(incidence = datasim$y, si = si, CoriR = TRUE)
plot(epifit_sim, addfit = "Cori")

# Illustration on the 2003 SARS epidemic in Hong Kong.
data(sars2003)
epifit_sars <- estimR(incidence = sars2003$incidence, si = sars2003$si, K = 40)
tail(epifit_sars$RLPS)
summary(epifit_sars)
plot(epifit_sars)
```

---

estimRmcmc

*Estimation of the reproduction number with Laplacian-P-splines via MCMC*

---

**Description**

This routine estimates the instantaneous reproduction number  $R_t$ ; the mean number of secondary infections generated by an infected individual at time  $t$  (White et al. 2020); by using Bayesian P-splines and Laplace approximations (Gressani et al. 2022). The inference approach is fully stochastic with a Metropolis-adjusted Langevin algorithm. The `estimRmcmc()` routine estimates  $R_t$  based on a time series of incidence counts and a (discretized) serial interval distribution. The negative binomial distribution is used to model incidence count data and P-splines (Eilers and Marx, 1996) are used to smooth the epidemic curve. The link between the epidemic curve and the reproduction number is established via the renewal equation.

**Usage**

```
estimRmcmc(incidence, si, K = 30, dates = NULL, niter = 5000, burnin = 2000,
           CoriR = FALSE, WTR = FALSE, priors = Rmodelpriors())
```

**Arguments**

incidence	A vector containing the incidence time series. If incidence contains NA values at certain time points, these are replaced by the average of the left- and right neighbor counts. If the right neighbor is NA, the left neighbor is used as a replacement value.
si	The (discrete) serial interval distribution.
K	Number of B-splines in the basis.
dates	A vector of dates in format "YYYY-MM-DD" (optional).
niter	The number of MCMC samples.
burnin	The burn-in size.
CoriR	Should the $R_t$ estimate of Cori (2013) be also computed?
WTR	Should the $R_t$ estimate of Wallinga-Teunis (2004) be also computed?
priors	A list containing the prior specification of the model hyperparameters as set in Rmodelpriors. See ?Rmodelpriors.

**Value**

A list with the following components:

- incidence: The incidence time series.
- si: The serial interval distribution.
- RLPS: A data frame containing estimates of the reproduction number obtained with the Laplacian-P-splines methodology.
- thetahat: The estimated vector of B-spline coefficients.
- Sighat: The estimated variance-covariance matrix of the Laplace approximation to the conditional posterior distribution of the B-spline coefficients.
- RCori: A data frame containing the estimates of the reproduction obtained with the method of Cori (2013).
- RWT: A data frame containing the estimates of the reproduction obtained with the method of Wallinga-Teunis (2004).
- LPS\_elapsed: The routine real elapsed time (in seconds) when estimation of the reproduction number is carried out with Laplacian-P-splines.
- penparam: The estimated penalty parameter related to the P-spline model.
- K: The number of B-splines used in the basis.
- NegBinoverdisp: The estimated overdispersion parameter of the negative binomial distribution for the incidence time series.
- optimconverged: Indicates whether the algorithm to maximize the posterior distribution of the hyperparameters has converged.

- method: The method to estimate the reproduction number with Laplacian-P-splines.
- optim\_method: The chosen method to to maximize the posterior distribution of the hyperparameters.
- HPD90\_Rt: The 90% HPD interval for Rt obtained with the LPS methodology.
- HPD95\_Rt: The 95% HPD interval for Rt obtained with the LPS methodology.

### Author(s)

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

### References

- Gressani, O., Wallinga, J., Althaus, C. L., Hens, N. and Faes, C. (2022). EpiLPS: A fast and flexible Bayesian tool for estimation of the time-varying reproduction number. *Plos Computational Biology*, **18(10)**: e1010618.
- Cori, A., Ferguson, N.M., Fraser, C., Cauchemez, S. (2013). A new framework and software to estimate time-varying reproduction numbers during epidemics. *American Journal of Epidemiology*, **178(9)**:1505–1512.
- Wallinga, J., & Teunis, P. (2004). Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. *American Journal of Epidemiology*, **160(6)**, 509-516.
- White, L.F., Moser, C.B., Thompson, R.N., Pagano, M. (2021). Statistical estimation of the reproductive number from case notification data. *American Journal of Epidemiology*, **190(4)**:611-620.
- Eilers, P.H.C. and Marx, B.D. (1996). Flexible smoothing with B-splines and penalties. *Statistical Science*, **11(2)**:89-121.

### Examples

```
# Illustration on the 2009 influenza pandemic in Pennsylvania.
data(influenza2009)
epifit_flu <- estimRmcmc(incidence = influenza2009$incidence, dates = influenza2009$dates,
                      si = influenza2009$si[-1], niter = 2500, burnin = 1500)

tail(epifit_flu$RLPS)
summary(epifit_flu)
plot(epifit_flu)
```

---

Idist

*Density function and discrete distribution for a disease interval*

---

### Description

This function computes the probability density function and probability mass function for a disease interval (e.g. the serial interval defined as the time elapsed between the symptom onset in an infector and the onset of symptoms in the secondary cases generated by that infector). It takes as input the mean and the standard deviation of the disease interval (expressed in days) and gives as an output the interval distribution based on a chosen parametric family.



**Usage**

```
Idist(mean, sd, dist = c("gamma", "weibull", "lognorm"), probs = NULL)
```

**Arguments**

mean	The mean of the disease interval (must be larger than 1).
sd	A positive and finite real number corresponding to the standard deviation of the disease interval.
dist	A choice among a Gamma, Weibull or Log-normal distribution for the disease interval.
probs	A vector of probabilities for the interval distribution.

**Details**

The discretization is based on the formula in Held et al. (2019).

**Value**

A list of class `Idist` containing a vector of probabilities corresponding to the discrete distribution of the disease interval, the name of the chosen parametric distribution and its parameters.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**References**

Held, L., Hens, N., D O'Neill, P., and Wallinga, J. (2019). Handbook of infectious disease data analysis. *CRC Press*.

**Examples**

```
Idist(mean = 2.6, sd = 1.5)
```

---

influenza2009

*Data on the 2009 pandemic influenza in Pennsylvania*

---

**Description**

A list with the daily incidence of onset of symptoms among children in a school in Pennsylvania (2009), a vector of dates and a discrete serial interval distribution.

**Usage**

```
data(influenza2009)
```

**Format**

A list with three components:

incidence An incidence time series of length 32.

dates A vector of dates in "YYYY-MM-DD" format.

si A vector of probabilities corresponding to the serial interval distribution.

**Source**

<https://cran.r-project.org/package=EpiEstim>

**References**

Ferguson N.M. et al. (2005) Strategies for containing an emerging influenza pandemic in Southeast Asia. *Nature* **437**(7056), 209-214.

Cauchemez S. et al. (2011) Role of social networks in shaping disease transmission during a community outbreak of 2009 H1N1 pandemic influenza. *Proc Natl Acad Sci USA* **108**(7), 2825-2830.

---

perfRestim

*Routine to measure the performance of estimR and estimRmcmc*

---

**Description**

This routine can be used to check the 'statistical performance' of the `estimR()` and `estimRmcmc()` routines to estimate the reproduction number  $R_t$ . It simulates epidemics using the `episim()` function and computes the Bias, MSE, coverage probability (CP) and width of 90% and 95% credible intervals for  $R_t$  averaged over days  $t = 8, \dots, T$ , where  $T$  is the total number of days of the simulated epidemics. As such, it can be used to reproduce part of the results in Gressani et al. (2022) Table 1 and Table 2, respectively. Small differences in results are due to a restructuring of the code since version 1.0.6. If strict reproducible results are required, please refer to version 1.0.6 of the EpiLPS package or visit the GitHub repository <https://github.com/oswaldogressani/EpiLPS-ArticleCode>.

**Usage**

```
perfRestim(nsim = 100, scenario = 1, days = 40, K = 40,
  method = c("LPSMAP", "LPSMALA"), mcmciter = 3000, burnin = 1000,
  si = c("flu", "sars", "mers"), seed = 1325, overdisp = 1000)
```

**Arguments**

nsim	Total number of simulated epidemics.
scenario	The scenario to be used in <code>episim()</code> .
days	Number of days for the simulated epidemics.
K	Number of B-splines basis function in the P-spline model.

method	The method for LPS, either LPSMAP or LPSMALA.
mcmciter	Number of MCMC samples for method LPSMALA.
burnin	Burn-in for method LPSMALA.
si	The discrete serial interval distribution. Possible specifications are "flu", "sars" or "mers".
seed	A seed for reproducibility.
overdisp	The value of the overdispersion parameter for the negative binomial model in the episim() routine.

### Value

A list with the following components:

- LPS: Results for the LPS approach.
- EpiEstim: Results for the EpiEstim approach with weekly sliding windows.
- inciplot: The simulated incidence time series.
- Rlpsplot: Estimated  $R_t$  trajectories with LPS.
- Repestimplot: Estimated  $R_t$  trajectories with EpiEstim.

### Author(s)

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

### References

Gressani, O., Wallinga, J., Althaus, C. L., Hens, N. and Faes, C. (2022). EpiLPS: A fast and flexible Bayesian tool for estimation of the time-varying reproduction number. *Plos Computational Biology*, **18**(10): e1010618.

### Examples

```
## # FLU serial interval (Scenarios 1-4)
# S1 <- perfRestim(si = "flu", scenario = 1, seed = 1325)
# S1mcmc <- perfRestim(si = "flu", scenario = 1, seed = 1325, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S1$inciplot, S1$Rlpsplot, S1$Repestimplot, nrow = 1))
# S2 <- perfRestim(si = "flu", scenario = 2, seed = 1123)
# S2mcmc <- perfRestim(si = "flu", scenario = 2, seed = 1123, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S2$inciplot, S2$Rlpsplot, S2$Repestimplot, nrow = 1))
# S3 <- perfRestim(si = "flu", scenario = 3, seed = 1314)
# S3mcmc <- perfRestim(si = "flu", scenario = 3, seed = 1314, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S3$inciplot, S3$Rlpsplot, S3$Repestimplot, nrow = 1))
# S4 <- perfRestim(si = "flu", scenario = 4, seed = 1966)
# S4mcmc <- perfRestim(si = "flu", scenario = 4, seed = 1966, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S4$inciplot, S4$Rlpsplot, S4$Repestimplot, nrow = 1))
#
## # SARS serial interval (Scenarios 5-8)
# S5 <- perfRestim(si = "sars", scenario = 1, seed = 1998, overdisp = 5)
# S5mcmc <- perfRestim(si = "sars", scenario = 1, seed = 1998, overdisp = 5, method = "LPSMALA")
```

```

# suppressWarnings(gridExtra::grid.arrange(S5$inciplot, S5$Rlpsplot, S5$Repiestimplot, nrow = 1))
# S6 <- perfRestim(si = "sars", scenario = 2, seed = 1870, overdisp = 5)
# S6mcmc <- perfRestim(si = "sars", scenario = 2, seed = 1870, overdisp = 5, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S6$inciplot, S6$Rlpsplot, S6$Repiestimplot, nrow = 1))
# S7 <- perfRestim(si = "sars", scenario = 3, seed = 115, overdisp = 5)
# S7mcmc <- perfRestim(si = "sars", scenario = 3, seed = 115, overdisp = 5, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S7$inciplot, S7$Rlpsplot, S7$Repiestimplot, nrow = 1))
# S8 <- perfRestim(si = "sars", scenario = 4, seed = 1464, overdisp = 5)
# S8mcmc <- perfRestim(si = "sars", scenario = 4, seed = 1464, overdisp = 5, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S8$inciplot, S8$Rlpsplot, S8$Repiestimplot, nrow = 1))
#
# # MERS serial interval (Scenario 9)
# S9 <- perfRestim(si = "mers", scenario = 5, days = 60, seed = 1905, overdisp = 50)
# S9mcmc <- perfRestim(si = "mers", scenario = 5, days = 60,
# seed = 1905, overdisp = 50, method = "LPSMALA")
# suppressWarnings(gridExtra::grid.arrange(S9$inciplot, S9$Rlpsplot,
# S9$Repiestimplot, nrow = 1))
#
# #(Partially recovering Table 2 and Table 3 of Gressani et al. 2022)
# simsummary <- matrix(0, nrow = 36, ncol = 7)
# colnames(simsummary) <- c("Method", "Bias", "MSE", "CP90%", "CP95%",
# "CIwidth90%", "CIwidth95%")
# simsummary <- as.data.frame(simsummary)
#
# # Scenario 1
# simsummary[1,] <- c(rownames(S1$LPS), S1$LPS)
# simsummary[2,] <- c(rownames(S1mcmc$LPS), S1mcmc$LPS)
# simsummary[3,] <- c(rownames(S1$EpiEstim), S1$EpiEstim)
# simsummary[4,] <- rep("--", 7)
# # Scenario 2
# simsummary[5,] <- c(rownames(S2$LPS), S2$LPS)
# simsummary[6,] <- c(rownames(S2mcmc$LPS), S2mcmc$LPS)
# simsummary[7,] <- c(rownames(S2$EpiEstim), S2$EpiEstim)
# simsummary[8,] <- rep("--", 7)
# # Scenario 3
# simsummary[9,] <- c(rownames(S3$LPS), S3$LPS)
# simsummary[10,] <- c(rownames(S3mcmc$LPS), S3mcmc$LPS)
# simsummary[11,] <- c(rownames(S3$EpiEstim), S3$EpiEstim)
# simsummary[12,] <- rep("--", 7)
# # Scenario 4
# simsummary[13,] <- c(rownames(S4$LPS), S4$LPS)
# simsummary[14,] <- c(rownames(S4mcmc$LPS), S4mcmc$LPS)
# simsummary[15,] <- c(rownames(S4$EpiEstim), S4$EpiEstim)
# simsummary[16,] <- rep("--", 7)
# # Scenario 5
# simsummary[17,] <- c(rownames(S5$LPS), S5$LPS)
# simsummary[18,] <- c(rownames(S5mcmc$LPS), S5mcmc$LPS)
# simsummary[19,] <- c(rownames(S5$EpiEstim), S5$EpiEstim)
# simsummary[20,] <- rep("--", 7)
# # Scenario 6
# simsummary[21,] <- c(rownames(S6$LPS), S6$LPS)
# simsummary[22,] <- c(rownames(S6mcmc$LPS), S6mcmc$LPS)
# simsummary[23,] <- c(rownames(S6$EpiEstim), S6$EpiEstim)

```

```

# simsummary[24,] <- rep("--",7)
# # Scenario 7
# simsummary[25,] <- c(rownames(S7$LPS),S7$LPS)
# simsummary[26,] <- c(rownames(S7mcmc$LPS),S7mcmc$LPS)
# simsummary[27,] <- c(rownames(S7$EpiEstim),S7$EpiEstim)
# simsummary[28,] <- rep("--",7)
# # Scenario 8
# simsummary[29,] <- c(rownames(S8$LPS),S8$LPS)
# simsummary[30,] <- c(rownames(S8mcmc$LPS),S8mcmc$LPS)
# simsummary[31,] <- c(rownames(S8$EpiEstim),S8$EpiEstim)
# simsummary[32,] <- rep("--",7)
# # Scenario 9
# simsummary[33,] <- c(rownames(S9$LPS),S9$LPS)
# simsummary[34,] <- c(rownames(S9mcmc$LPS),S9mcmc$LPS)
# simsummary[35,] <- c(rownames(S9$EpiEstim),S9$EpiEstim)
# simsummary[36,] <- rep("--",7)
# simsummary

```

---

plot.Idist

*Plot the interval distribution from an Idist object*


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## Description

This routine plots the interval distribution based on an Idist object.

## Usage

```

## S3 method for class 'Idist'
plot(x, barcol = "firebrick", denscol = "pink", denstransparent = 0.5,
     barwidth = 0.30, title = NULL, themetype = c("gray","classic","light","dark"),
     titlesize = 15, xtitlesize = 13, ytitlesize = 13, ...)

```

## Arguments

x	An object of class Idist.
barcol	Color of the discretized interval distribution.
denscol	Color of the probability density function (pdf).
denstransparent	The transparency of the pdf.
barwidth	Width of the bars for the discrete distribution.
title	Title of the plot.
themetype	Theme of the plot.
titlesize	Size of the plot title. Default is 15.
xtitlesize	Size of title and text on x axis. Default is 13.
ytitlesize	Size of title and text on y axis. Default is 13.
...	Further arguments to be passed to plot.

**Value**

A plot of the interval distribution.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**Examples**

```
x <- Idist(mean = 3, sd = 1.6, dist = "weibull")
plot(x)
```

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plot.Rt

*Plot the estimated reproduction number*

---

**Description**

This routine can be used to plot the estimated reproduction number based on an object of class Rt.

**Usage**

```
## S3 method for class 'Rt'
plot(x, datelab = "7d", cilevel = 0.95, col = "black", cicol = "gray",
      xtickangle = 0, legendpos = "right", title = "Estimated R",
      addfit = c("none", "Cori", "WT"), theme = "gray", timecut = 0, ...)
```

**Arguments**

x	An object of class Rt.
datelab	Spacing for the ticks on the x-axis.
cilevel	Level of the credible interval.
col	Color of the fitted $R_t$ curve for LPS.
cicol	Color for shading the credible envelope.
xtickangle	Angle of the x-ticks. Default is 0 (horizontal).
legendpos	Position of the legend.
title	Title of the plot.
addfit	Should an additional $R_t$ fit be added?
theme	Theme, either "gray", "classic", "light", "dark"
timecut	Cut time points on plot.
...	Further arguments to be passed to plot.

**Value**

A plot of the fitted time-varying reproduction number.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**Examples**

```
si <- c(0.05, 0.05, 0.1, 0.1, 0.1, 0.1, 0.1, 0.05, 0.05, 0.1, 0.1, 0.1)
epidemic <- episim(si = si, Rpattern = 2, endepi = 30)
epifit <- estimR(incidence = epidemic$y, K = 30, si = si)
plot(epifit)
```

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Rmodelpriors

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*Prior specification for model hyperparameters*


---

**Description**

Specification of the hyperparameters for the Gamma prior on the roughness penalty parameter associated to the P-spline model and the Gamma prior on the overdispersion parameter of the negative binomial model underlying the incidence data.

**Usage**

```
Rmodelpriors(
  listcontrol = list(a_delta = 10, b_delta = 10, phi = 2, a_rho = 1e-04, b_rho = 1e-04)
)
```

**Arguments**

**listcontrol** A list specifying the hyperparameters in the Gamma priors for the roughness penalty parameter of the P-spline model (named  $a_\delta$ ,  $b_\delta$  and  $\phi$ ) and the overdispersion parameter of the negative binomial model for the incidence data (named  $a_\rho$  and  $b_\rho$ ).

**Value**

A list with the specified hyperparameter components. By default,  $a_\delta = b_\delta = 10$ ,  $\phi = 2$  and  $a_\rho = b_\rho = 10^{-4}$ .

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

**References**

Gressani, O., Wallinga, J., Althaus, C. L., Hens, N. and Faes, C. (2022). EpiLPS: A fast and flexible Bayesian tool for estimation of the time-varying reproduction number. *Plos Computational Biology*, **18**(10): e1010618.

sars2003

*Daily incidence of the 2003 SARS epidemic in Hong Kong*

---

**Description**

A list with the daily incidence of onset of symptoms for the 2003 SARS outbreak in Hong Kong and a discretized serial interval distribution.

**Usage**

```
data(sars2003)
```

**Format**

A list with two components:

incidence A vector with 107 observations.

si A vector of probabilities corresponding to the serial interval distribution.

**Source**

<https://cran.r-project.org/package=EpiEstim>

**References**

Cori A. et al. (2009). Temporal variability and social heterogeneity in disease transmission: the case of SARS in Hong Kong. *Plos Computational Biology* 5(8) : e1000471.

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summary.Rt

*Summarize the estimated reproduction number*

---

**Description**

This routine can be used to summarize estimation results for related to the reproduction number.

**Usage**

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

**Arguments**

object An object of class Rt.

... Further arguments to be passed.



**Value**

A summary output.

**Author(s)**

Oswaldo Gressani <oswaldo\_gressani@hotmail.fr>

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zika2015

*Data on the 2015 Zika virus disease in Colombia*

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**Description**

A list containing incidence data for the 2015 Zika disease in Girardot (Colombia) from October 2015 to January 2016, a vector of dates and a discrete serial interval distribution.

**Usage**

```
data(zika2015)
```

**Format**

A list with three components:

`incidence` An incidence time series of length 93.

`dates` A vector of dates in "YYYY-MM-DD" format.

`si` A vector of probabilities corresponding to the serial interval distribution with a mean of 7 days and standard deviation of 1.5 days.

**Source**

<https://cran.r-project.org/package=outbreaks>

**References**

Rojas, D. P. et al. (2016). The epidemiology and transmissibility of Zika virus in Girardot and San Andres island, Colombia, September 2015 to January 2016. *Eurosurveillance*, **21**(28), 30283.

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