Package 'EpiLPS'

Type Package

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

Version 1.0.6

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.(2021)
<doi:10.1101/2021.12.02.21267189>. The negative Binomial
distribution is used to model the time series of case counts. 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-within-Gibbs algorithm and Langevin diffusions for
efficient sampling of the posterior distribution.

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

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.1

LinkingTo RcppArmadillo, Rcpp

Imports Rcpp (>= 1.0.7), coda (>= 0.19-4), progress (>= 1.2.2), crayon
(>= 1.4.1), MASS (>= 7.3-54), EpiEstim (>= 2.2-4), ggplot2 (>=
3.3.5), grDevices (>= 4.1.0), gridExtra (>= 2.3)

Suggests rmarkdown, knitr

VignetteBuilder knitr

NeedsCompilation yes

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R topics documented:

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epilps	*Estimation of the time-varying reproduction number with Laplacian-P-splines*

Description

This routine estimates the instantaneous reproduction number Rt (the mean number of secondary cases generated by an infectious individual at time t, White et al. 2020) using Bayesian P-splines and Laplace approximations. Two methods are possible for inference. LPSMAP is a fully sampling-free approach based on Laplace approximations to the conditional posterior distribution of the spline vector. LPSMALA is an MCMC-based approach based on Langevin diffusions to sample the joint posterior of the model parameters. The epilps() routine estimates Rt based on a time series of incidence conts and a given 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. 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.

Usage

```
epilps(incidence, K = 30, method = c("LPSMAP","LPSMALA"),
       serial_interval, penorder = 2, hyperprior = c(10,10),
       chain_length = 5000, burn = 2000, progmala = TRUE, ci_level = 0.95,
     etainit = c(1,5), cimethod = 1, verbose = TRUE, dates = NULL, tictoc = FALSE)
```

Arguments

incidence	A vector containing the case counts per unit of time.
K	Number of (cubic) B-splines in the basis.
method	Either LPSMAP (fully sampling-free) or LPSMALA (MCMC-based).
serial_interval	
	The discrete serial interval distribution.
penorder	The order of the penalty (Default is second-order).
hyperprior	Parameters for the Gamma prior on the dispersion parameter.
chain_length	The length of the MCMC chain for method "LPSMALA" (default 5,000).
burn	The warm up period for method "LPSMALA" (default 2,000).

progmala	Should the progress bar of LPSMALA be shown? (default TRUE).
ci_level	Level of the credible intervals to be computed.
etainit	Initial values for the hyperparameter vector (for the optimization) in log scale.
cimethod	The method used to construct credible intervals for Rt with method LPSMAP. Default is 1 (log-normal approx) with scaling correction on the covariance matrix. Setting it to 2 ignores the scaling correction.
verbose	Should metainformation be printed?
dates	A vector of date values (optional).
tictoc	Should routine timing (in seconds) be measured?

Value

An object of class epilps containing the pointwise and set estimates of the time-varying reproduction number and the epidemic curve respectively.

Author(s)

Oswaldo Gressani <oswaldo_gressani@hotmail.fr>

References

Gressani, O., Wallinga, J., Althaus, C., Hens, N. and Faes, C. (2021). EpiLPS: a fast and flexible Bayesian tool for near real-time estimation of the time-varying reproduction number. *MedRxiv preprint*.

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

```
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(serial_interval = si, Rpattern = 2, endepi = 30)
epifit <- epilps(incidence = epidemic$y, K = 30, serial_interval = si,)
# plot(epifit)
```

---

episim   *Simulation of incidence count data*

Description

Based on a serial interval and a functional input for the reproduction number over T days, the routine generates a set of incidence counts 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(serial_interval, endepi = 50, Rpattern = 1, Rconst = 2.5,
      dist = c("poiss", "negbin"), overdisp = 1, verbose = FALSE, plotsim = FALSE)
```

Arguments

serial_interval

        A vector of values for the discrete serial interval (must sum to 1).

endepi   The total number of days of the epidemic.

Rpattern   Different scenarios for the true underlying curve of Rt. 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 of cases. Either Poisson (default) or negative binomial.

overdisp   Overdispersion parameter for the negative binomial setting.

verbose   Should metadata on 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 time series of cases, 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, 0.05, 0.05, 0.1, 0.1, 0.1)
epidemic <- episim(serial_interval = si, Rpattern = 1)
```

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perfcheck   *Check the statistical performance of EpiLPS with simulations*

Description

The `perfcheck()` routine can be used to check the performance of EpiLPS in various epidemic scenarios. The user can choose between 6 scenarios, each scenario corresponding to a different data generating process for the incidence data with a specific target dynamics for the reproduction number. The aim of these simulations is to assess how close EpiLPS can reproduce the target reproduction number curve. Different performance measures are computed and comparisons with the `estimate_R()` routine of the EpiEstim package (Cori et al. 2013) is also shown.

Usage

```
perfcheck(S = 10, serial_interval, scenario = 3, epidays = 50,
          K = 30, method = "LPSMAP", midwindow = FALSE, penorder = 2,
          hyperprior = c(10,10), slidewindow = 6, ci_level = 0.95,
       cimethod = 1, chain_length = 5000, burn = 2000, dist = c("poiss", "negbin"),
       overdisp = 1, Rconst = 2.5, themetype = c("classic","gray","light","dark"),
          coltraj = 1, seed = 123)
```

Arguments

S	The total number of replications.
serial_interval	
	The (discrete) serial interval distribution.
scenario	The scenario (1,2,3 or 4).
epidays	The total number of days of the epidemic. Default is 50.
K	Number of (cubic) B-splines in the basis.
method	Either LPSMAP (fully sampling-free) or LPSMALA (MCMC-based).
midwindow	Should Rt be reported at the middle of the window for EpiEstim as recommended by Gostic et al. (2020)? Default is FALSE.
penorder	The order of the penalty (Default is second-order).
hyperprior	Parameters for the Gamma prior on the dispersion parameter.
slidewindow	The sliding window for EpiEstim (defaults to 1 week).
ci_level	Level of the credible intervals to be computed.
cimethod	The method used to construct credible intervals for R(t) with method LPSMAP. Default is 1 (log-normal approx with correction). Setting it to 2 ignores the correction.
chain_length	the length of the MCMC chain for method "LPSMALA" (default 5,000).
burn	The burn-in period for method "LPSMALA" (default 2,000).
dist	Distribution to sample incidence case data. Either "poiss" for the Poisson distribution or "negbin" for the negative binomial distribution.

overdisp	Overdispersion parameter for the negative binomial setting.
Rconst	The constant value of R (if scenario 1 is selected), default is 2.5.
themetype	What theme should be use for plotting the R curves?
coltraj	Either 1 (default) or 2 to color the esimated R trajectories. Number 1 results in blue (for EpiLPS) and green (for EpiEstim). Number 2 results in orange (for EpiLPS) and pink (for EpiEstim).
seed	A seed for reproducibility.

Value

An object of class `perfcheck` containing a table of summary statistics for the EpiLPS and EpiEstim routines.

Author(s)

Oswaldo Gressani `<oswaldo_gressani@hotmail.fr>`

References

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.

Examples

```
# simex <- perfcheck(S = 5, serial_interval = c(0.2, 0.4, 0.2, 0.1, 0.1),
#             scenario = 3, ci_level = 0.95,  seed = 1234, epidays = 30,
#             themetype = "gray")
```

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plot.epilps   *Plot the EpiLPS fitted epidemic curve and reproduction number*

Description

This routine can be used to plot the estimated epidemic curve and reproduction number with EpiLPS.

Usage

```
## S3 method for class 'epilps'
plot(x, plotout = c("rt", "epicurve"), dates = NULL,
     datelab = c("7d", "1m", "3m", "6m"), overlayEpiestim = FALSE, Rtitle = "",
     epititle = "", rtcol = "red", cicol = "gray", transparency = 0.5,
   epicol = "red", epiestimcol = "lightslateblue", incibars = FALSE, barwidth = 0.35,
   themetype = c("gray", "classic", "light", "dark"),  tcut = NULL, titlesize = 15,
     xtitlesize = 13, ytitlesize = 13, ...)
```

Arguments

x	An object of class `epilps`.
plotout	The type of plot, either "rt" for showing the reproduction number or "epicurve" for showing the epidemic curve.
dates	A vector of dates in format "YY-MM-DD".
datelab	The spacing for ticks on the x-axis. Either 7 days, 1 month, 3 months or 6 months.
overlayEpiestim	
	Should the EpiEstim fit be overlayed?
Rtitle	The title for the plot of R.
epititle	The title for the plot of the epidemic curve.
rtcol	Color for the reproduction number curve fit.
cicol	Color for shading the credible envelope.
transparency	Controls the transparency of the credible envelope.
epicol	The color for the epidemic curve.
epiestimcol	The color for the EpiEstim Rt estimate.
incibars	Should the bars of the incidence time series be shown?
barwidth	The bar width associated to the incidence time series.
themetype	Type of theme for the plot.
tcut	Remove early estimates (starting day 8 in plot).
titlesize	The size of the plot title. Default is 15.
xtitlesize	The size of title and text on x axis. Default is 13.
ytitlesize	The size of title and text on y axis. Default is 13.
...	Further arguments to be passed to plot.

Value

A plot of the fitted time-varying reproduction number (default) or 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(serial_interval = si, Rpattern = 2, endepi = 30)
epifit <- epilps(incidence = epidemic$y, K = 30, serial_interval = si)
# gridExtra::grid.arrange(plot(epifit, Rtitle = "Estimated R"),
#                          plot(epifit, plotout = "epicurve", epicol = "blue",
#                          epititle = "Epidemic curve"), nrow = 2)
```

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