Package ‘EpiLPS’

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Type Package

Title A Bayesian Tool for Near Real-Time Estimation of the Reproduction Number

Version 1.0.2

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 7.1.2

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

Description

This routine estimates the instantaneous reproduction number (the mean number of secondary cases generated by infectious individuals 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 R(t) based on a time series of case counts and a given serial/generation 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,
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 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).
episim

episim

progmala Should the progress bar of LPSMALA be shown? (default TRUE).
ci_level Level of the credible intervals to be computed.
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


Examples

si <- c(0.05, 0.05, 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)
epifit <- epilps(incidence = epidemic$y, K = 30, serial_interval = si)
plot(epifit)

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 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 15. 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, verbose = FALSE, plotsim = FALSE)
Arguments

serial_interval
A vector of values for the serial interval.

depend
The total number of days of the epidemic.

Rpattern
Different scenarios for the true underlying curve of Rt. Four scenarios are possible with 1,2,3,4.

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 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

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

Description
The perfcheck() routine can be used to check the performance of EpiLPS in various epidemic scenarios. The user can choose between 4 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 metrics are given as outputs 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, K = 30, method = "LPSMAP", slidewindow = 6, ci_level = 0.95, themetype = c("classic","gray","light","dark"), seed = 123)

Check the statistical performance of EpiLPS with simulations

perfcheck
Arguments

S: The total number of replications.
serial_interval: The serial interval distribution.
scenario: The scenario (1, 2, 3, or 4).
K: Number of (cubic) B-splines in the basis.
method: Either LPSMAP (fully sampling-free) or LPSMALA (MCMC-based).
slidewindow: The sliding window for EpiEstim (defaults to 1 week).
ci_level: Level of the credible intervals to be computed.
themetype: What theme should be used for plotting the R curves?
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


Examples

```r
simex <- perfcheck(S = 10, serial_interval = c(0.2, 0.4, 0.2, 0.1, 0.1),
                    scenario = 3, ci_level = 0.95, seed = 1234, 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"), 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.

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.

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)
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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