Package 'eSIR'

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Type Package

Title Extended state-space SIR models

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Description An inplementation of extended state-space SIR models developed by Song Lab at UM school of Public Health

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Depends rjags, scales, ggplot2, chron, gtools

RoxygenNote 6.1.1

R topics documented:

`qh.eSIR` *Extended state-space SIR with quarantine*

Description

Fit an extended state-space SIR model being reduced by in-home hospitalization.

Usage

```
qh.eSIR(Y, R, phi0 = NULL, change_time = NULL,
  begin_str = "01/13/2020", T_fin = 200, nchain = 4,
  nadapt = 10000, M = 500, thn = 10, nburnin = 200, dic = FALSE,
  death_in_R = 0.02, casename = "qh.eSIR", beta0 = 0.2586,
  gamma0 = 0.0821, R0 = beta0/gamma0, gamma0_sd = 0.1, R0_sd = 1,
  file_add = character(0), save_files = FALSE, save_mcmc = FALSE)
```

Arguments

Y	the time series of daily observed infected compartment proportions.
R	the time series of daily observed removed compartment proportions, including death and recovered.
phi0	a vector of values of the dirac delta function ϕ_t. Each entry denotes the proportion that will be qurantined at each change time point. Note that all the entries lie between 0 and 1, its default is NULL.
change_time	the change points over time corresponding to phi0, to formulate the dirac delta function ϕ_t; its defalt value is NULL.
begin_str	the character of starting time, the default is "01/13/2020".
T_fin	the end of follow-up time after the beginning date begin_str, the default is 200.
nchain	the number of MCMC chains generated by rjags, the default is 4.
nadapt	the iteration number of adaptation in the MCMC. We recommend using at least the default value 1e4 to obtained fully adapted chains.
M	the number of draws in each chain, with no thinning. The default is M=5e2 but suggest using 5e5.
thn	the thinning interval between mixing. The total number of draws thus would become round(M/thn)*nchain. The default is 10.
nburnin	the burn-in period. The default is 2e2 but suggest 2e5.
dic	logical, whether compute the DIC (deviance information criterion) for model selection.
death_in_R	the numeric value of average of cumulative deaths in the removed compartments. The default is 0.4 within Hubei and 0.02 outside Hubei.
casename	the string of the job's name. The default is "qh.eSIR".
beta0	the hyperparameter of average transmission rate, the default is the one estimated from the SARS first-month outbreak (0.2586).
gamma0	the hyperparameter of average removed rate, the default is the one estimated from the SARS first-month outbreak (0.0821).
R0	the hyperparameter of the mean reproduction number R0. The default is thus the ratio of beta0/gamma0, which can be specified directly.
gamma0_sd	the standard deviation for the prior distrbution of the removed rate γ, the default is 0.1.
R0_sd	the standard deviation for the prior disbution of R0, the default is 1.
file_add	the string to denote the location of saving output files and tables.
save_mcmc	logical, whether save (TRUE) all the MCMC outputs or not (FALSE).The output file will be an .RData file named by the *casename*. We include arrays of prevalence values of the three compartments with their matrices of posterior draws up to the last date of the collected data as theta_p[,,1] and afterwards as theta_pp[,,1] for θ_t^S, theta_p[,,2] and theta_pp[,,2] for θ_t^I, and theta_p[,,3] and theta_pp[,,3] for θ_t^R. The posterior draws of the prevalence process of the quarantine compartment can be obtained via thetaQ_p and thetaQ_pp. Moreover, the input and predicted proportions Y, Y_pp, R and R_pp can also be retrieved. The prevalence and prediceted proportion matrices have rows for MCMC replicates, and columns for days. The MCMC posterior draws of other parameters including beta, gamma, R0, and variance controllers k_p, lambdaY_p, lambdaR_p are also available.

Details

In this function we allow it to characterize time-varying proportions of susceptible due to government-enforced stringent in-home isolation. We expanded the SIR model by adding a quarantine compartment with a time-varying rate of quarantine ϕ_t, the chance of a susceptible person being willing to take in-home isolation at time t.

Value

`casename` the predefined `casename`.

`incidence_mean`
mean incidence.

`incidence_ci` 2.5%, 50%, and 97.5% quantiles of the incidences.

`out_table` summary tables including the posterior mean of the prevalance processes of the 3 states compartments ($\theta_t^S, \theta_t^I, \theta_t^R, \theta_t^H$) at last date of data collected ((t') decided by the lengths of your input data `Y` and `R`), and their respective credible inctervals (ci); the respective means and ci's of the reporduction number (R0), removed rate (γ), transmission rate (β).

`plot_infection`
plot of summarizing and forecasting for the infection compartment, in which the vertial blue line denotes the last date of data collected (t'), the vertial dark-gray line denotes the deacceleration point (first turning point) that the posterior mean first-derivative of infection prevalence $\dot{\theta}_t^I$ achieves the maximum, the vertical purple line denotes the second turning point that the posterior mean first-derivative infection proportion $\dot{\theta}_t^I$ equals zero, the darkgray line denotes the posterior mean of the infection prevalence θ_t^I and the red line denotes its posterior median.

`plot_removed` plot of summarizing and forecasting for the removed compartment with lines similar to those in the `plot_infection`. The vertical lines are identical, but the horizontal mean and median correspond to the posterior mean and median of the removed process θ_t^R. An additional line indicates the estimated death prevalence from the input `death_in_R`.

`first_tp_mean`
the date t at which $\ddot{\theta}_t^I = 0$, calculated as the average of the time points with maximum posterior first-order derivatives $\dot{\theta}_t^I$; this value may be slightly different from the one labeled by the "darkgreen" lines in the two plots `plot_infection` and `plot_removed`, which indicate the stationary point such that the first-order derivative of the averaged posterior of θ_t^I reaches its maximum.

`first_tp_mean`
the date t at which $\ddot{\theta}_t^I = 0$, calculated as the average of the time points with maximum posterior first-order derivatives $\dot{\theta}_t^I$; this value may be slightly different from the one labeled by the "darkgreen" lines in the two plots `plot_infection` and `plot_removed`, which indicate the stationary point such that the first-order derivative of the averaged posterior of θ_t^I reaches its maximum.

`first_tp_ci` fwith `first_tp_mean`, it reports the corresponding credible interval and median.

`second_tp_mean`
the date t at which $\theta_t^I = 0$, calculated as the average of the stationary points of all of posterior first-order derivatives $\dot{\theta}_t^I$; this value may be slightly different from the one labeled by the "pruple" lines in the plots of `plot_infection` and `plot_removed`. The latter indicate stationary t at which the first-order derivative of the averaged posterior of θ_t^I equals zero.

second_tp_ci with second_tp_mean, it reports the corresponding credible interval and median.

dic_val the output of dic.sample() in dic.sample, computing deviance information criterion for model comparison.

Examples

```
NI_complete <- c( 41,41,41,45,62,131,200,270,375,444,549, 729,
             1052,1423,2714,3554,4903,5806,7153,9074,11177,
             13522,16678,19665,22112,24953,27100,29631,31728,33366)
RI_complete <- c(1,1,7,10,14,20,25,31,34,45,55,71,94,121,152,213,
             252,345,417,561,650,811,1017,1261,1485,1917,2260,
             2725,3284,3754)
N=58.5e6
R <- RI_complete/N
Y <- NI_complete/N- R #Jan13->Feb 11

change_time <- c("01/23/2020","02/04/2020","02/08/2020")
phi0 <- c(0.1,0.4,0.4)
res.q <- qh.eSIR (Y,R,begin_str="01/13/2020",death_in_R = 0.4,
                  phi0=phi0,change_time=change_time,
                 casename="Hubei_q",save_files = T,save_mcmc = F,
                  M=5e2,nburnin = 2e2)
res.q$plot_infection
#res.q$plot_removed

res.noq <- qh.eSIR (Y,R,begin_str="01/13/2020",death_in_R = 0.4,
                    T_fin=200,casename="Hubei_noq",
                    M=5e2,nburnin = 2e2)
res.noq$plot_infection
```

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tvt.eSIR *Fit extended state-space SIR model with time-varying transmission rates*

Description

Fit extended state-space SIR model with prespecified changes in the transmission rate, either stepwise or continuous, accomodating time-varying quaratine protocols.

Usage

```
tvt.eSIR(Y, R, pi0 = NULL, change_time = NULL, exponential = FALSE,
  lambda0 = NULL, begin_str = "01/13/2020", T_fin = 200,
  nchain = 4, nadapt = 10000, M = 500, thn = 10, nburnin = 200,
  dic = FALSE, death_in_R = 0.02, beta0 = 0.2586, gamma0 = 0.0821,
  R0 = beta0/gamma0, gamma0_sd = 0.1, R0_sd = 1,
  casename = "tvt.eSIR", file_add = character(0), save_files = FALSE,
  save_mcmc = FALSE)
```

Arguments

Y	the time series of daily observed infected compartment proportions.
R	the time series of daily observed removed compartment proportions, including death and recovered.
pi0	the time-dependent transission rate modifier $\pi(t)$ between 0 and 1.
change_time	the change points over time for step function pi, defalt value is NULL.
exponential	logical, whether $\pi(t)$ is exponential $\exp(-\lambda_0 t)$ or not; the default is FALSE.
lambda0	the rate of decline in the exponential survival function in $\exp(-\lambda_0 t)$.
begin_str	the character of starting time, the default is "01/13/2020".
T_fin	the end of follow-up time after the beginning date begin_str, the default is 200.
nchain	the number of MCMC chains generated by rjags, the default is 4.
nadapt	the iteration number of adaptation in the MCMC. We recommend using at least the default value 1e4 to obtained fully adapted chains.
M	the number of draws in each chain, with no thinning. The default is M=5e2 but suggest using 5e5.
thn	the thinning interval between mixing. The total number of draws thus would become round(M/thn)*nchain. The default is 10.
nburnin	the burn-in period. The default is 2e2 but suggest 2e5.
dic	logical, whether compute the DIC (deviance information criterion) for model selection.
death_in_R	the numeric value of average of cumulative deaths in the removed compartments. The default is 0.4 within Hubei and 0.02 outside Hubei.
beta0	the hyperparameter of average transmission rate, the default is the one estimated from the SARS first-month outbreak (0.2586).
gamma0	the hyperparameter of average removed rate, the default is the one estimated from the SARS first-month outbreak (0.0821).
R0	the hyperparameter of the mean reproduction number R0. The default is thus the ratio of beta0/gamma0, which can be specified directly.
gamma0_sd	the standard deviation for the prior distrbution of the removed rate γ, the default is 0.1.
R0_sd	the standard deviation for the prior disbution of R0, the default is 1.
casename	the string of the job's name. The default is "tvt.eSIR".
file_add	the string to denote the location of saving output files and tables.
save_files	logical, whether save (TRUE) results or not (FALSE). This enables to save summary tables, trace plots, and plots of the posterior means of the first-order derivatives of the infection prevalence process θ_t^I.
save_mcmc	logical, whether save (TRUE) all the MCMC outputs or not (FALSE).The output file will be an .RData file named by the $casename$. We include arrays of prevalence values of the three compartments with their matrices of posterior draws up to the last date of the collected data as theta_p[,,1] and afterwards as theta_pp[,,1] for θ_t^S, theta_p[,,2] and theta_pp[,,2] for θ_t^I, and theta_p[,,3] and theta_pp[,,3] for θ_t^R. Moreover, the input and predicted proportions Y, Y_pp, R and R_pp can also be retrieved. The prevalence and prediceted proportion matrices have rows for MCMC replicates, and columns for days. The MCMC posterior draws of other parameters including beta_p, gamma_p, R0_p, and variance controllers k_p, lambdaY_p, lambdaR_p are also available.

Details

We fit a state-space model with extended SIR, in which a time-varying transmission rate modifier $\pi(t)$ (between 0 and 1) is introcuded to model. This allows us to accommodate quarantine protocol changes and ignored resources of hospitalization. The form of reducing rate may be a step-function with jomps at times of big policy changes or a smooth exponential survival function $\exp(-\lambda_0 t)$. The parameters of the function and change points, if any, should be predefined.

Value

`casename` the predefined `casename`.

`incidence_mean`
mean incidence.

`incidence_ci` 2.5%, 50%, and 97.5% quantiles of the incidences.

`out_table` summary tables including the posterior mean of the prevalance processes of the 3 states compartments ($\theta_t^S, \theta_t^I, \theta_t^R$) at last date of data collected ((t') decided by the lengths of your input data `Y` and `R`), and their respective credible inctervals (ci); the respective means and ci's of the reporduction number (R0), removed rate (γ), transmission rate (β).

`plot_infection`
plot of summarizing and forecasting for the infection compartment, in which the vertial blue line denotes the last date of data collected (t'), the vertial dark-gray line denotes the deacceleration point (first turning point) that the posterior mean first-derivative of infection prevalence $\dot{\theta}_t^I$ achieves the maximum, the vertical purple line denotes the second turning point that the posterior mean first-derivative infection proportion $\dot{\theta}_t^I$ equals zero, the darkgray line denotes the posterior mean of the infection prevalence θ_t^I and the red line denotes its posterior median.

`plot_removed` plot of summarizing and forecasting for the removed compartment with lines similar to those in the `plot_infection`. The vertical lines are identical, but the horizontal mean and median correspond to the posterior mean and median of the removed process θ_t^R. An additional line indicates the estimated death prevalence from the input `death_in_R`.

`first_tp_mean`
the date t at which $\ddot{\theta}_t^I = 0$, calculated as the average of the time points with maximum posterior first-order derivatives $\dot{\theta}_t^I$; this value may be slightly different from the one labeled by the "darkgreen" lines in the two plots `plot_infection` and `plot_removed`, which indicate the stationary point such that the first-order derivative of the averaged posterior of θ_t^I reaches its maximum.

`first_tp_ci` fwith `first_tp_mean`, it reports the corresponding credible interval and median.

`second_tp_mean`
the date t at which $\theta_t^I = 0$, calculated as the average of the stationary points of all of posterior first-order derivatives $\dot{\theta}_t^I$; this value may be slightly different from the one labeled by the "pruple" lines in the plots of `plot_infection` and `plot_removed`. The latter indicate stationary t at which the first-order derivative of the averaged posterior of θ_t^I equals zero.

`second_tp_ci` with `second_tp_mean`, it reports the corresponding credible interval and median.

`dic_val` the output of `dic.sample()` in `dic.sample`, computing deviance information criterion for model comparison.

Examples

```
NI_complete <- c( 41,41,41,45,62,131,200,270,375,444,549, 729,
                  1052,1423,2714,3554,4903,5806,7153,9074,11177,
                13522,16678,19665,22112,24953,27100,29631,31728,33366)
RI_complete <- c(1,1,7,10,14,20,25,31,34,45,55,71,94,121,152,213,
                 252,345,417,561,650,811,1017,1261,1485,1917,2260,
                 2725,3284,3754)
N=58.5e6
R <- RI_complete/N
Y <- NI_complete/N- R #Jan13->Feb 11
### Step function of pi(t)
change_time <- c("01/23/2020","02/04/2020","02/08/2020")
pi0<- c(1.0,0.9,0.5,0.1)
res.step <-tvt.eSIR(Y,R,begin_str="01/13/2020",death_in_R = 0.4,
         T_fin=200,pi0=pi0,change_time=change_time,dic=T,
         casename="Hubei_step",save_files = T,
         save_mcmc=F,M=5e2,nburnin = 2e2)
res.step$plot_infection
res.step$plot_removed
res.step$dic_val

### continuous exponential function of pi(t)
res.exp <- tvt.eSIR(Y,R,begin_str="01/13/2020",death_in_R = 0.4,
           T_fin=200,exponential=TRUE,dic=F,lambda0=0.05,
           casename="Hubei_exp",save_files = F,save_mcmc=F,
           M=5e2,nburnin = 2e2)
res.exp$plot_infection
#res.exp$plot_removed

### without pi(t), the standard state-space SIR model without intervention
res.nopi <- tvt.eSIR(Y,R,begin_str="01/13/2020",death_in_R = 0.4,
                T_fin=200,casename="Hubei_nopi",save_files = F,
                M=5e2,nburnin = 2e2)
res.nopi$plot_infection
#res.nopi$plot_removed
```

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