Package ‘bliss’

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BIC_model_choice

Description

Model selection with BIC criterion.

Usage

BIC_model_choice(Ks, iter, data, verbose = T)

Arguments

- **Ks**
  - a numerical vector containing the K values.

- **iter**
  - an integer, the number of iteration for each run of fit_Bliss.

- **data**
  - a list containing:
    - **Q** an integer, the number of functional covariates.
**bliss**

- **y** a numerical vector, the outcomes.
- **x** a list of matrices, the qth matrix contains the observations of the qth functional covariate at time points given by **grids**.
- **grids** a list of numerical vectors, the qth vector is the grid of time points for the qth functional covariate.
- **verbose** write stuff if TRUE (optional).

**Value**

A numerical vector, the BIC values for the Bliss model for different K value.

**Examples**

```r
param_sim <- list(Q=1,n=100,p=c(50),grids_lim=list(c(0,1)))
data <- sim(param_sim,verbose=TRUE)
iter = 1e2
Ks <- 1:5

res_BIC <- BIC_model_choice(Ks,iter,data)
plot(res_BIC,xlab="K",ylab="BIC")
```

---

**bliss**

*bliss: Bayesian functional Linear regression with Sparse Step functions*

**Description**

A method for the Bayesian Functional Linear Regression model (functions-on-scalar), including two estimators of the coefficient function and an estimator of its support. A representation of the posterior distribution is also available.

**Bliss_Gibbs_Sampler**

**Bliss_Gibbs_Sampler**

**Description**

A Gibbs Sampler algorithm to sample the posterior distribution of the Bliss model.

**Usage**

```r
Bliss_Gibbs_Sampler(data, param, verbose = FALSE)
```
Arguments

data a list containing:

  Q an integer, the number of functional covariates.
  y a numerical vector, the outcome values $y_i$.
  x a list of matrices, the $q$th matrix contains the observations of the $q$th functional covariate at time points given by grids.
  grids a list of numerical vectors, the $q$th vector is the grid of time points for the $q$th functional covariate.

param a list containing:

  iter an integer, the number of iterations of the Gibbs sampler algorithm.
  K a vector of integers, corresponding to the numbers of intervals for each covariate.
  p an integer, the number of time points.
  basis a character vector (optional). The possible values are "uniform" (default), "epanechnikov", "gauss" and "triangular" which correspond to different basis functions to expand the coefficient function and the functional covariates
  verbose write stuff if TRUE (optional).

Value

a list containing:

  trace a matrix, the trace of the Gibbs Sampler.
  param a list containing parameters used to run the function.

Examples

# May take a while
param_sim <- list(Q=1,n=25,p=50,grids_lim=list(c(0,1)),iter=1e4,K=2)
data_sim <- sim(param_sim,verbose=FALSE)
res_Bliss_Gibbs_Sampler <- Bliss_Gibbs_Sampler(data_sim,param_sim)
theta_1 <- res_Bliss_Gibbs_Sampler$trace[,1]
theta_1
# Resultat for few iterations
param_sim <- list(Q=1,n=25,p=50,grids_lim=list(c(0,1)),iter=5e2,K=2)
data_sim <- sim(param_sim,verbose=FALSE)
res_Bliss_Gibbs_Sampler <- Bliss_Gibbs_Sampler(data_sim,param_sim)
theta_1 <- res_Bliss_Gibbs_Sampler$trace[,1]
theta_1
Description

A Simulated Annealing algorithm to compute the Bliss estimate.

Usage

Bliss_Simulated_Annealing(beta_sample, normalization_values, param, verbose = FALSE)

Arguments

- **beta_sample**: a matrix. Each row is a coefficient function computed from the posterior sample.
- **normalization_values**: a matrix given by the function Bliss_Gibbs_Sampler.
- **param**: a list containing:
  - **grid**: a numerical vector, the time points.
  - **K**: an integer, the number of intervals.
  - **basis**: a character vector (optional). The possible values are "uniform" (default), "epanechnikov", "gauss" and "triangular" which correspond to different basis functions to expand the coefficient function and the functional covariates.
  - **burnin**: an integer (optional), the number of iteration to drop from the posterior sample.
  - **iter_sann**: an integer (optional), the number of iteration of the Simulated Annealing algorithm.
  - **k_max**: an integer (optional), the maximal number of intervals for the Simulated Annealing algorithm.
  - **l_max**: an integer (optional), the maximal interval length for the Simulated Annealing algorithm.
  - **Temp_init**: a nonnegative value (optional), the initial temperature for the cooling function of the Simulated Annealing algorithm.
  - **verbose**: write stuff if TRUE (optional).

Value

- a list containing:
  - **Bliss_estimate**: a numerical vector, corresponding to the Bliss estimate of the coefficient function.
  - **Smooth_estimate**: a numerical vector, which is the posterior expectation of the coefficient function for each time points.
  - **trace**: a matrix, the trace of the algorithm.
argmin an integer, the index of the iteration minimizing the Bliss loss.
difference a numerical vector, the difference between the Bliss estimate and the smooth estimate.
sdifference a numerical vector, a smooth version of difference.

Examples

data(data1)
data(param1)
param1$grids<-data1$grids
# result of res_bliss1<-fit_Bliss(data=data1,param=param1)
data(res_bliss1)
beta_sample <- compute_beta_sample(posterior_sample=res_bliss1$posterior_sample,
                                 param=param1,Q=1)
param_test<-.list(grid=param1$grids[[1]],iter=1e3,K=2)
test<-Bliss_Simulated_Annealing(beta_sample[[1]],
                                 res_bliss1$posterior_sample$param$normalization_values[[1]],
                                 param=param_test)
ylim <- range(range(test$Bliss_estimate),range(test$Smooth_estimate))
plot(param_test$grid,test$Bliss_estimate,type="l",ylim=ylim)
lines(param_test$grid,test$Smooth_estimate,lty=2)

Description

Define a Fourier basis to simulate functional covariate observations.

Usage

build_Fourier_basis(grid, dim, per = 2 * pi)

Arguments

grid a numerical vector.
dim a numerical value. It corresponds to dim(basis)/2.
per a numerical value which corresponds to the period of the sine and cosine functions.

Details

See the sim_x function.

Value

a matrix. Each row is an functional observation evaluated on the grid time points.
change_grid

Examples

  # See the function \code{sim_x}.

Description

  Compute a function (evaluated on a grid) on a given (finer) grid.

Usage

  change_grid(fct, grid, new_grid)

Arguments

  fct       a numerical vector, the function to evaluate on the new grid.
  grid     a numerical vector, the initial grid.
  new_grid a numerical vector, the new grid.

Value

  a numerical vector, the approximation of the function on the new grid.

Examples

  grid <- seq(0,1,l=1e1)
  new_grid <- seq(0,1,l=1e2)
  fct <- 3*grid^2 + sin(grid*2*pi)
  plot(grid,fct,type="o",lwd=2,cex=1.5)
  lines(new_grid,change_grid(fct,grid,new_grid),type="o",col="red",cex=0.8)

choose_beta

Description

  Compute a coefficient function for the Function Linear Regression model.

Usage

  choose_beta(param)
Arguments

param a list containing:

grid a numerical vector, the time points.
p a numerical value, the length of the vector grid.
shape a character vector: "smooth", "random_smooth", "simple", "simple_bis",
"random_simple", "sinusoid", "flat_sinusoid" and "sharp"

Details

Several shapes are available.

Value

A numerical vector which corresponds to the coefficient function at given times points (grid).

Examples

### smooth

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="smooth")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="l")
```

### random_smooth

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="random_smooth")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="l")
```

### simple

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="simple")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="s")
```

### simple_bis

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="simple_bis")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="s")
```

### random_simple

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="random_simple")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="s")
```

### sinusoid

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="sinusoid")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="l")
```

### flat_sinusoid

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="flat_sinusoid")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="l")
```

### sharp

```r
param <- list(p=100, grid=seq(0,1,length=100), shape="sharp")
beta_function <- choose_beta(param)
plot(param$grid, beta_function, type="l")
```
compute_beta_posterior_density

compute_beta_posterior_density

Description

Compute the posterior density of the coefficient function.

Usage

compute_beta_posterior_density(beta_sample, param, verbose = FALSE)

Arguments

beta_sample a matrix. Each row is a coefficient function computed from the posterior sample.
param a list containing:
  grid a numerical vector, the time points.
  lims_estimate a numerical vector, the time points.
  burnin an integer (optional), the number of iteration to drop from the Gibbs sample.
  lims_kde an integer (optional), correspond to the lims option of the kde2d function.
  new_grid a numerical vector (optional) to compute beta sample on a different grid.
  thin an integer (optional) to thin the posterior sample.
verbose write stuff if TRUE (optional).

Details

The posterior densities correspond to approximations of the marginal posterior distributions (of beta(t) for each t). The sample is thinned in order to reduce the correlation and the computational time of the function kde2d.

Value

An approximation of the posterior density on a two-dimensional grid (corresponds to the result of the kde2d function).

Examples

library(RColorBrewer)
data(data1)
data(param1)
# result of res_bliss1<-fit_Bliss(data=data1,param=param1)
data(res_bliss1)
compute_beta_sample

```r
q <- 1
param_beta_density <- list(grid = data1["grids"][[q]],
iter = param1["iter"],
p = param1["p"][[q]],
n = length(data1["y"]),
thin = param1["thin"],
burnin = param1["burnin"],
lims_kde = param1["lims_kde"],
new_grid = param1["new_grids"],
lims_estimate = range(res_bliss1$Smooth_estimate[[q]]))
density_estimate <- compute_beta_posterior_density(res_bliss1$beta_sample[[q]], param_beta_density)
image(density_estimate$grid_t,
density_estimate$grid_beta_t,
density_estimate$density, col = rev(heat.colors(100)))
```

density_estimate <- compute_beta_posterior_density(res_bliss1$beta_sample[[q]], param_beta_density)

compute_beta_sample  compute_beta_sample

---

**Description**

Compute the posterior coefficient function from the posterior sample.

**Usage**

```r
compute_beta_sample(posterior_sample, param, Q, verbose = FALSE)
```

**Arguments**

- **posterior_sample**
  - a list provided by the function `Bliss_Gibbs_Sampler`.

- **param**
  - a list containing:
    - **K** a vector of integers, corresponding to the numbers of intervals for each covariate.
    - **grids** a numerical vector, the observation time points.
    - **basis** a vector of characters (optional) among: "uniform" (default), "epanechnikov", "gauss" and "triangular" which correspond to different basis functions to expand the coefficient function and the functional covariates.

- **Q** numeric

- **verbose** write stuff if TRUE (optional).

**Value**

return a matrix containing the coefficient function posterior sample.
Examples

```r
library(RColorBrewer)
data(data1)
data(param1)
param1$grids<-data1$grids
# result of res_bliss1<-fit_Bliss(data=data1,param=param1)
data(res_bliss1)
beta_sample <- compute_beta_sample(posterior_sample=res_bliss1$posterior_sample,
                                   param=param1,Q=1)
indexes <- sample(nrow(beta_sample[[1]]),1e2,replace=FALSE)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(1e2)
matplot(param1$grids[[1]],t(beta_sample[[1]][indexes,]),type="l",lty=1,col=cols,
xlab="grid",ylab="")
```

---

**compute_chains_info**

**compute_chains_info**

Description

Compute summaries of Gibbs Sampler chains.

Usage

```
compute_chains_info(chain, param)
```

Arguments

- `chain` a list given by the `Bliss_Gibbs_Sampler` function.
- `param` a list containing:
  - `K` a vector of integers, corresponding to the numbers of intervals for each covariate.
  - `grids` a numerical vector, the observation time points.
  - `basis` a vector of characters (optional) among: "uniform" (default), "epanechnikov", "gauss" and "triangular" which correspond to different basis functions to expand the coefficient function and the functional covariates.

Value

Return a list containing the estimates of `mu` and `sigma_sq`, the Smooth estimate and the chain autocorrelation for `mu`, `sigma_sq` and `beta`.

Examples

```r
param_sim <- list(Q=1,
n=100,
p=c(50),
```
grids_lim=list(c(0,1)))
data <- sim(param_sim,verbose=TRUE)

param <- list(iter=5e2,
K=c(3),
n_chains = 3)
res_bliss <- fit_Bliss(data,param,verbose=TRUE,compute_density=FALSE,sann=FALSE)

param$grids <- data$grids
chains_info1 <- compute_chains_info(res_bliss$chains[[1]],param)
chains_info2 <- compute_chains_info(res_bliss$chains[[2]],param)
chains_info3 <- compute_chains_info(res_bliss$chains[[3]],param)

# Smooth estimates
ylim <- range(range(chains_info1$estimates$Smooth_estimate),
range(chains_info2$estimates$Smooth_estimate),
range(chains_info3$estimates$Smooth_estimate))
plot(data$grids[[1]],chains_info1$estimates$Smooth_estimate,type="l",ylim=ylim,
xlab="grid",ylab="")
lines(data$grids[[1]],chains_info2$estimates$Smooth_estimate,col=2)
lines(data$grids[[1]],chains_info3$estimates$Smooth_estimate,col=3)

# Autocorrelation
plot(chains_info1$autocorr_lag[,1],type="h")

---

### compute_random_walk

#### Description

Compute a (Gaussian) random walk.

#### Usage

```r
compute_random_walk(n, p, mu, sigma, start = rep(0, n))
```

#### Arguments

- `n`  
an integer, the number of random walks.
- `p`  
an integer, the length of the random walks.
- `mu`  
a numerical vector, the mean of the random walks.
- `sigma`  
a numerical value which is the standard deviation of the gaussian distribution used to compute the random walks.
- `start`  
a numerical vector (optional) which is the initial value of the random walks.

#### Details

See the `sim_x` function.
compute_starting_point_sann

Value

a matrix where each row is a random walk.

Examples

# see the sim_x() function.

data(res_bliss1)
mystart<-compute_starting_point_sann(apply(res_bliss1$beta_sample[1],2,mean))

corr_matrix

Description

Compute an autocorrelation matrix.

Usage

corr_matrix(diagonal, ksi)
Arguments

diagonal  a numerical vector corresponding to the diagonal.
ksi  a numerical value, related to the correlation.

Value

a symmetric matrix.

Examples

### Test 1 : weak autocorrelation  
ksi <- 1  
diagVar <- abs(rnorm(100,50,5))  
Sigma <- corr_matrix(diagVar,ksi^2)  
persp(Sigma)

### Test 2 : strong autocorrelation  
ksi <- 0.2  
diagVar <- abs(rnorm(100,50,5))  
Sigma <- corr_matrix(diagVar,ksi^2)  
persp(Sigma)

---

data1  a list of data

Description

A data object for bliss model

Usage

data1

Format

a list of data

- **Q**  the number of functional covariates
- **y**  y coordinate
- **x**  x coordinate
- **betas**  the coefficient function used to generate the data
- **grids**  the grid of the observation times
**determine_intervals**

### Description

Determine for which intervals a function is nonnull.

### Usage

```r
determine_intervals(beta_fct)
```

### Arguments

- `beta_fct`: a numerical vector.

### Value

A matrix with 3 columns: "begin", "end" and "value". The two first columns define the begin and the end of the intervals and the third gives the mean values of each interval.

### Examples

```r
data(data1)
data(param1)
# result of res_bliss1<-fit_Bliss(data=data1,param=param1)
data(res_bliss1)
intervals <- determine_intervals(res_bliss1$Bliss_estimate[[1]])
plot(data1$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s")
for(k in 1:nrow(intervals)){
  segments(data1$grids[[1]][intervals[k,1]],intervals[k,3],
           data1$grids[[1]][intervals[k,2]],intervals[k,3],col=2,lwd=4)
}
```

---

**dposterior**

### Description

Compute (non-normalized) posterior densities for a given parameter set.

### Usage

```r
dposterior(posterior_sample, data, theta = NULL)
```
Arguments

* posterior_sample
  a list given by the Bliss_Gibbs_Sampler function.

* data
  a list containing
    * y a numerical vector, the outcomes.
    * x a list of matrices, the qth matrix contains the observations of the qth functional covariate at time points given by grids.

* theta
  a matrix or a vector which contains the parameter set.

Details

If the theta is NULL, the posterior density is computed from the MCMC sample given in the posterior_sample.

Value

Return the (log) posterior density, the (log) likelihood and the (log) prior density for the given parameter set.

Examples

```r
data(data1)
data(param1)
# result of res_bliss1 <- fit_Bliss(data=data1, param=param1)
data(res_bliss1)
# Compute the posterior density of the MCMC sample :
res_poste <- dposterior(res_bliss1$posterior_sample, data1)
```

Description

Fit the Bayesian Functional Linear Regression model (with Q functional covariates).

Usage

```r
fit_Bliss(data, param, compute_density = TRUE, sann = TRUE, verbose = FALSE)
```

Arguments

* data
  a list containing:
    * Q an integer, the number of functional covariates.
    * y a numerical vector, the outcomes.
fit_Bliss

x  a list of matrices, the qth matrix contains the observations of the qth functional
    covariate at time points given by grids.

grids  a list of numerical vectors, the qth vector is the grid of time points for the
    qth functional covariate.

param  a list containing:

iter  an integer, the number of iterations of the Gibbs sampler algorithm.
K  a vector of integers, corresponding to the numbers of intervals for each co-
    variate.

basis  a character vector (optional). The possible values are "uniform" (default),
    "epanechnikov", "gauss" and "triangular" which correspond to different ba-
    sis functions to expand the coefficient function and the functional covariates

burnin  an integer (optional), the number of iteration to drop from the posterior
    sample.

iter_sann  an integer (optional), the number of iteration of the Simulated An-
    nealing algorithm.

k_max  an integer (optional), the maximal number of intervals for the Simulated An-
    nealing algorithm.

l_max  an integer (optional), the maximal interval length for the Simulated An-
    nealing algorithm.

lims_kde  an integer (optional), correspond to the lims option of the kde2d
    function.

n_chains  an integer (optional) which corresponds to the number of Gibbs sam-
    pler runs.

new_grids  a list of Q vectors (optional) to compute beta samples on different
    grids.

Temp_init  a nonnegative value (optional), the initial temperature for the cool-
    ing function of the Simulated Annealing algorithm.

thin  an integer (optional) to thin the posterior sample.

times_sann  an integer (optional), the number of times the algorithm will be
    executed

compute_density  a logical value. If TRUE, the posterior density of the coef-
    ficient function is computed. (optional)

sann  a logical value. If TRUE, the Bliss estimate is computed with a Simulated An-
    nealing Algorithm. (optional)

verbose  write stuff if TRUE (optional).

Value

return a list containing:

alpha  a list of Q numerical vector. Each vector is the function alpha(t) associated to a functional
covariate. For each t, alpha(t) is the posterior probabilities of the event "the support covers t".

beta_posterior_density  a list of Q items. Each item contains a list containing information to plot
    the posterior density of the coefficient function with the image function.
grid_t a numerical vector: the x-axis.
grid_beta_t a numerical vector: the y-axis.
density a matrix: the z values.
new_beta_sample a matrix: beta sample used to compute the posterior densities.

beta_sample a list of Q matrices. The qth matrix is a posterior sample of the qth functional covariates.
Bliss_estimate a list of numerical vectors corresponding to the Bliss estimates of each functional covariate.
chains a list of posterior_sample. chains is NULL if n_chains=1.
chains_info a list for each chain providing: a mu estimate, a sigma_sq estimate, the Smooth estimate of the coefficient function and the autocorrelation of the Markov Chain.
data a list containing the data.
posterior_sample a list of information about the posterior sample: the trace matrix of the Gibbs sampler, a list of Gibbs sampler parameters and the posterior densities.
support_estimate a list of support estimates of each functional covariate.
support_estimate_fct another version of the support estimates.
trace_sann a list of Q matrices which are the trace of the Simulated Annealing algorithm.

Examples

# see the vignette BlissIntro.
### integrate_trapeze

**Examples**

```r
library(RColorBrewer)
data(data1)
data(param1)
data(res_bliss1)
param1$cols <- colorRampPalette(brewer.pal(9,“Reds”))(1e2)
image_Bliss(res_bliss1$beta_posterior_density,param1,q=1)
lines(res_bliss1$data$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s",lwd=2)
lines(res_bliss1$data$grids[[1]],res_bliss1$data$betas[[1]],col=3,lwd=2,type="s")

# ---- not run
param1$cols <- colorRampPalette(brewer.pal(9,“YlOrRd”))(1e2)
image_Bliss(res_bliss1$beta_posterior_density,param1,q=1)
lines(res_bliss1$data$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s",lwd=2)
lines(res_bliss1$data$grids[[1]],res_bliss1$data$betas[[1]],col=3,lwd=2,type="s")

param1$cols <- rev(heat.colors(12))
param1$col_scale <- "quantile"
image_Bliss(res_bliss1$beta_posterior_density,param1,q=1)
lines(res_bliss1$data$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s",lwd=2)
lines(res_bliss1$data$grids[[1]],res_bliss1$data$betas[[1]],col=3,lwd=2,type="s")

param1$cols <- rev(terrain.colors(12))
image_Bliss(res_bliss1$beta_posterior_density,param1,q=1)
lines(res_bliss1$data$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s",lwd=2)
lines(res_bliss1$data$grids[[1]],res_bliss1$data$betas[[1]],col=2,lwd=2,type="s")

param1$cols <- rev(topo.colors(12))
image_Bliss(res_bliss1$beta_posterior_density,param1,q=1)
lines(res_bliss1$data$grids[[1]],res_bliss1$Bliss_estimate[[1]],type="s",lwd=2)
lines(res_bliss1$data$grids[[1]],res_bliss1$data$betas[[1]],col=2,lwd=2,type="s")
```

**Description**

Trapezoidal rule to approximate an integral.

**Usage**

```r
integrate_trapeze(x, y)
```

**Arguments**

- `x` a numerical vector, the discretization of the domain.
- `y` a numerical value, the discretization of the function to integrate.
Value

a numerical value, the approximation.

Examples

x <- seq(0,1,le=1e2)
integrate_trapeze(x,x^2)

integrate_trapeze(data1$grids[[1]],t(data1$x[[1]]))

interpretation_plot

interpretation_plot

Description

Provide a graphical representation of the functional data with a focus on the detected periods with the Bliss method.

Usage

interpretation_plot(data, Bliss_estimate, q = 1, centered = FALSE, cols = NULL)

Arguments

data a list containing:
    y a numerical vector, the outcomes.
    x a list of matrices, the qth matrix contains the observations of the qth functional covariate at time points given by grids.
    grids a list of numerical vectors, the qth vector is the grid of time points for the qth functional covariate.
Bliss_estimate a numerical vector, the Bliss estimate.
q an integer (optional), the index of the functional covariate to plot.
centered a logical value (optional), If TRUE, the functional data are centered.
cols a numerical vector of colours (optional).

Examples

data(data1)
data(param1)
# result of res_bliss1 <- fit_Bliss(data=data1,param=param1,verbose=TRUE)
data(res_bliss1)
interpretation_plot(data=data1,Bliss_estimate=res_bliss1$Bliss_estimate,q=1)
interpretation_plot(data=data1,Bliss_estimate=res_bliss1$Bliss_estimate,q=1,centered=TRUE)
lines_bliss

Description
A suitable representation of the Bliss estimate.

Usage
\[
\text{lines\_bliss}(x, y, \text{connect} = \text{FALSE}, \ldots)
\]

Arguments
- \(x\) \quad \text{the coordinates of points in the plot.}
- \(y\) \quad \text{the y coordinates of points in the plot.}
- \text{connect} \quad \text{a logical value (optional), to handle discontinuous function. If connect is TRUE, the plot is one line. Otherwise, several lines are used.}
- \ldots \quad \text{Arguments to be passed to methods, such as graphical parameters (see par).}

Examples
### Plot the BLiss estimate on a suitable grid
```r
data(data1)
data(param1)
# res_bliss1 <- fit_Bliss(data=data1, param=param1, verbose=TRUE)
data(res_bliss1)
### Plot the BLiss estimate on a suitable grid
plot_bliss(res_bliss1$data$grids[[1]],
           res_bliss1$Bliss_estimate[[1]], lwd=2, bound=FALSE)
lines_bliss(res_bliss1$data$grids[[1]],
            res_bliss1$Smooth_estimate[[1]], lty=2)
```

param1

A list of param for bliss model

Description
A list of param for bliss model

Usage
\[
\text{param1}
\]
Format

a list of param for bliss model

Q   the number of functional covariates
n   the sample size
p   the number of observation times
beta_shapes  the shapes of the coefficient functions
grids_lim  the range of the observation times
grids   the grids of the observation times
K   the number of intervals for the coefficient function

Description

Probability function of a discretized Exponential distribution.

Usage

pdexp(a, l_values)

Arguments

a   a positive value, the mean of the Exponential prior.
l_values   a numerical value, the discrete support of the parameter l.

Value

a numerical vector, which is the probability function on l_values.

Examples

pdexp(10, seq(0,1,1))

x <- seq(0,10,le=10)
plot(x,dexp(x,0.5),lty=2,type="l")
lines(pdexp(0.5,1:10),type="p")
plot_bliss

Description
A suitable representation of the Bliss estimate.

Usage
plot_bliss(x, y, connect = FALSE, xlab = "", ylab = "", ylim = NULL, ...)

Arguments
- `x`: the coordinates of points in the plot.
- `y`: the y coordinates of points in the plot.
- `connect`: a logical value (optional), to handle discontinuous function. If `connect` is `TRUE`, the plot is one line. Otherwise, several lines are used.
- `xlab`: a title for the x axis.
- `ylab`: a title for the y axis.
- `ylim`: a numeric vectors of length 2, giving the y coordinate range.
- `...`: Arguments to be passed to methods, such as graphical parameters (see `par`).

Examples
```r
data(data1)
data(param1)
# res_bliss1 <- fit_Bliss(data=data1,param=param1,verbose=TRUE)
data(res_bliss1)
### Plot the BLiss estimate on a suitable grid
plot_bliss(res_bliss1$data$grids[[1]],
           res_bliss1$Bliss_estimate[[1]],lwd=2,bound=FALSE)
```

---

printbliss

Print a bliss Object

Description
Print a bliss Object

Usage
printbliss(x, ...)

Arguments

- **x**: input bliss Object
- **...**: further arguments passed to or from other methods

Examples

```r
# See fit_Bliss() function
```

```
res_bliss1

A result of the BliSS method
```

Description

A result of the BliSS method

Usage

```r
res_bliss1
```

Format

- A Bliss object (list)
  - **alpha**: a list of Q numerical vector. Each vector is the function \( \alpha(t) \) associated to a functional covariate. For each \( t \), \( \alpha(t) \) is the posterior probabilities of the event "the support covers \( t \)".
  - **beta_posterior_density**: a list of Q items. Each item contains a list containing information to plot the posterior density of the coefficient function with the `image` function.
    - **grid_t**: a numerical vector: the x-axis.
    - **grid_beta_t**: a numerical vector: the y-axis.
    - **density**: a matrix: the z values.
    - **new_beta_sample**: a matrix: beta sample used to compute the posterior densities.
  - **beta_sample**: a list of Q matrices. The qth matrix is a posterior sample of the qth functional covariates.
  - **Bliss_estimate**: a list of numerical vectors corresponding to the Bliss estimates of each functional covariates.
  - **chains_info**: a list containing (for each chain): a mu estimate, a sigma_sq estimate, the Smooth estimate of the coefficient function and the autocorrelation of the Markov Chain.
  - **data**: see the description of the object `data1`.
  - **posterior_sample**: a list containing (for each chain) the result of the `Bliss_Gibbs_Sampler` function.
  - **Smooth_estimate**: a list containing the Smooth estimates of the coefficient functions.
  - **support_estimate**: a list containing the estimations of the support.
  - **support_estimate_fct**: a list containing the estimation of the support.
  - **trace_sann**: a list containing (for each chain) the trace of the Simulated Annealing algorithm.
Description

Compute a sigmoid function.

Usage

sigmoid(x, asym = 1, v = 1)

Arguments

x  a numerical vector, time points.

asym  a numerical value (optional), the asymptote of the sigmoid function.

v  a numerical value (optional), related to the slope at the origin.

Details

see the function sim_x.

Value

a numerical vector.

Examples

## Test 1 :
x <- seq(-7,7,0.1)
y <- sigmoid(x)
plot(x,y,type="l",main="Sigmoid function")
## Test 2 :
x <- seq(-7,7,0.1)
y <- sigmoid(x)
y2 <- sigmoid(x,asym=0.5)
y3 <- sigmoid(x,v = 5)
plot(x,y,type="l",main="Other sigmoid functions")
lines(x,y2,col=2)
lines(x,y3,col=3)
Description

Compute a sharp sigmoid function.

Usage

sigmoid_sharp(x, loc = 0, ...)

Arguments

x  
a numerical vector, time points.

loc  
a numerical value (optional), the time of the sharp.

...  
Arguments (optional) for the function sigmoid.

Details

see the function sim_x.

Value

a numerical vector.

Examples

## Test 1 :
x <- seq(-7,7,0.1)
y <- sigmoid_sharp(x)
plot(x,y,type="l",main="Sharp sigmoid")
## Test 2 :
x <- seq(-7,7,0.1)
y <- sigmoid_sharp(x,loc=3)
y2 <- sigmoid_sharp(x,loc=3,asym=0.5)
y3 <- sigmoid_sharp(x,loc=3,v = 5)
plot(x,y,type="l",main="Other sharp sigmoids")
lines(x,y2,col=2)
lines(x,y3,col=3)
Description

Simulate a dataset for the Function Linear Regression model.

Usage

sim(param, verbose = FALSE)

Arguments

param a list containing:

beta_shapes a character vector. The qth item indicates the shape of the coefficient function associated to the qth functional covariate.

n an integer, the sample size.

p a vector of integers, the qth component is the number of times for the qth covariate.

Q an integer, the number of functional covariates.

autocorr_diag a list of numerical vectors (optional), the qth vector is the diagonal of the autocorrelation matrix of the qth functional covariate.

autocorr_spread a vector of numerical values (optional) which are related to the autocorrelation of the functional covariates.

grids a list of numerical vectors (optional), the qth vector is the grid of time points for the qth functional covariate.

grids_lim a list of numerical vectors (optional), the qth item is the lower and upper boundaries of the domain for the qth functional covariate.

link a function (optional) to simulate data from the Generalized Functional Linear Regression model.

mu a numerical value (optional), the 'true' intercept of the model.

r a nonnegative value (optional), the signal to noise ratio.

x_shapes a character vector (optional). The qth item indicates the shape of the functional covariate observations.

verbose write stuff if TRUE.

Value

a list containing:

Q an integer, the number of functional covariates.

y a numerical vector, the outcome observations.

x a list of matrices, the qth matrix contains the observations of the qth functional covariate at time points given by grids.
**grids** a list of numerical vectors, the qth vector is the grid of time points for the qth functional covariate.

**betas** a list of numerical vectors, the qth vector is the 'true' coefficient function associated to the qth covariate on a grid of time points given with grids.

**Examples**

```r
library(RColorBrewer)
param <- list(Q=2,n=25,p=c(50,50),grids_lim=list(c(0,1),c(-1,2)))
data <- sim(param)
data$y
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(10)
q=2
matplot(data$grids[[q]],t(data$x[[q]]),type="l",lty=1,col=cols)
plot(data$grids[[q]],data$betas[[q]],type="l")
abline(h=0,lty=2,col="gray")
```

**Description**

Simulate functional covariate observations.

**Usage**

```r
sim_x(param)
```

**Arguments**

- `param` a list containing :
  - `grid` a numerical vector, the observation times.
  - `n` an integer, the sample size.
  - `p` an integer, the number of observation times.
  - `diagVar` a numerical vector (optional), the diagonal of the autocorrelation matrix.
  - `dim` a numerical value (optional), the dimension of the Fourier basis, if "shape" is "Fourier" or "Fourier2".
  - `ksi` a numerical value (optional) related to the observations correlation.
  - `x_shape` a character vector (optional), the shape of the observations.

**Details**

Several shape are available for the observations: "Fourier", "Fourier2", "random_walk", "random_sharp", "uniform", "gaussian", "mvgauss", "mvgauss_different_scale", "mvgauss_different_scale2", "mvgauss_different_scale3" and "mvgauss_different_scale4".
Value

a matrix which contains the functional covariate observations at time points given by grid.

Examples

library(RColorBrewer)
### Fourier
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_shape="Fourier")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### Fourier2
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="Fourier2")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### random_walk
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="random_walk")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### random_sharp
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="random_sharp")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### uniform
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="uniform")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### gaussian
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="gaussian")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
### mvgauss
param <- list(n=15,p=100,grid=seq(0,1,length=100),x_type="mvgauss")
x <- sim_x(param)
cols <- colorRampPalette(brewer.pal(9,"YlOrRd"))(15)
matplot(param$grid,t(x),type="l",lty=1,col=cols)
Usage

\[
\text{support\_estimation}(\text{beta\_sample\_q}, \text{gamma} = 0.5)
\]

Arguments

- \text{beta\_sample\_q} \ a matrix. Each row is a coefficient function computed from the posterior sample.
- \text{gamma} \ a numeric value, the default value is 0.5.

Value

- a list containing:
  - \text{alpha} \ a numerical vector. The approximated posterior probabilities that the coefficient function support covers \( t \) for each time point \( t \).
  - \text{estimate} \ a numerical vector, the support estimate.
  - \text{estimate\_fct} \ a numerical vector, another version of the support estimate.

Examples

\begin{verbatim}
data(data1)
data(param1)
# result of res\_bliss1<-fit\_Bliss(data=data1,param=param1)
data(res\_bliss1)
res\_support <- support\_estimation(res\_bliss1$beta\_sample[[1]])

### The estimate
res\_support$estimate

### Plot the result
grid <- res\_bliss1$data$grids[[1]]
plot(grid,res\_support$alpha,ylim=c(0,1),type="l",xlab="",ylab="")
for(k in 1:nrow(res\_support$estimate)){
  segments(grid[res\_support$estimate[k,1]],0.5,
           grid[res\_support$estimate[k,2]],0.5,lwd=2,col=2)
  points(grid[res\_support$estimate[k,1]],0.5,pch="|",lwd=2,col=2)
  points(grid[res\_support$estimate[k,2]],0.5,pch="|",lwd=2,col=2)
}
abline(h=0.5,col=2,lty=2)
\end{verbatim}

Description

Check if a number belong to a given interval.

Usage

\[
value \ %\text{between}\% interval
\]
Arguments

- value: a numerical value.
- interval: a numerical vector: (lower,upper).

Value

- a logical value.

Examples

1. `%between% c(0,2)`
2. `%between% c(0,2)`
3. `%between% c(0,2)`
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