Package 'SISIR'

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Type Package

Title Select Intervals Suited for Functional Regression

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Description Interval fusion and selection procedures for regression with functional inputs. Methods include a semiparametric approach based on Sliced Inverse Regression (SIR), as described in <doi:10.1007/s11222-018-9806-6> (standard ridge and sparse SIR are also included in the package) and a random forest based approach, as described in <doi:10.1002/sam.11705>.

Depends R (>= 3.5.0), foreach, doParallel, graphics, stats

URL https://sfcb.pages-forge.inrae.fr/sisir, https://forge.inrae.fr/sfcb/sisir

BugReports https://forge.inrae.fr/sfcb/sisir/-/issues

Imports Matrix, expm, RSpectra, glmnet, dplyr, mixOmics, purrr, ranger, tidyr, tidyselect, adjclust, magrittr, rlang, ggplot2, aricode, dendextend, reshape2, RColorBrewer, utils, Boruta

Suggests testthat, CORElearn

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`project` *sparse SIR*

Description

`project` performs the projection on the sparse EDR space (as obtained by the `glmnet`)

Usage

```
## S3 method for class 'sparseRes'
project(object)

project(object)
```

Arguments

`object`	an object of class `sparseRes` as obtained from the function `sparseSIR`

Details

The projection is obtained by the function `predict.glmnet`.

Value

a matrix of dimension n x d with the projection of the observations on the d dimensions of the sparse EDR space

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References

Picheny, V., Servien, R. and Villa-Vialaneix, N. (2016) Interpretable sparse SIR for digitized functional data. *Statistics and Computing*, **29**(2), 255–267.

See Also

sparseSIR

Examples

```
set.seed(1140)
tsteps <- seq(0, 1, length = 200)
nsim <- 100
simulate_bm <- function() return(c(0, cumsum(rnorm(length(tsteps)-1, sd=1))))
x <- t(replicate(nsim, simulate_bm()))
beta <- cbind(sin(tsteps*3*pi/2), sin(tsteps*5*pi/2))
beta[((tsteps < 0.2) | (tsteps > 0.5)), 1] <- 0
beta[((tsteps < 0.6) | (tsteps > 0.75)), 2] <- 0
y <- log(abs(x %*% beta[ ,1]) + 1) + sqrt(abs(x %*% beta[ ,2]))
y <- y + rnorm(nsim, sd = 0.1)

res_ridge <- ridgeSIR(x, y, H = 10, d = 2)
res_sparse <- sparseSIR(res_ridge, rep(1, ncol(x)))
proj_data <- project(res_sparse)
```

---

ridgeRes *Print ridgeRes object*

Description

Print a summary of the result of ridgeSIR (ridgeRes object)

Usage

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

## S3 method for class 'ridgeRes'
print(x, ...)
```

Arguments

object	a ridgeRes object
...	not used
x	a ridgeRes object

Author(s)

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See Also

ridgeSIR

`ridgeSIR` *ridge SIR*

Description

`ridgeSIR` performs the first step of the method (ridge regularization of SIR)

Usage

```
ridgeSIR(x, y, H, d, mu2 = NULL)
```

Arguments

`x`	explanatory variables (numeric matrix or data frame)
`y`	target variable (numeric vector)
`H`	number of slices (integer)
`d`	number of dimensions to be kept
`mu2`	ridge regularization parameter (numeric, positive)

Details

SI-SIR

Value

S3 object of class `ridgeRes`: a list consisting of

`EDR` the estimated EDR space (a p x d matrix)

`condC` the estimated slice projection on EDR (a d x H matrix)

`eigenvalues` the eigenvalues obtained during the generalized eigendecomposition performed by SIR

`parameters` a list of hyper-parameters for the method:

- `H` number of slices
- `d` dimension of the EDR space
- `mu2` regularization parameter for the ridge penalty

`utils` useful outputs for further computations:

`Sigma` covariance matrix for x

`slices` slice number for all observations

`invsqrtS` value of the inverse square root of the regularized covariance matrix for x

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References

Picheny, V., Servien, R. and Villa-Vialaneix, N. (2019) Interpretable sparse SIR for digitized functional data. *Statistics and Computing*, **29**(2), 255–267.

See Also

`sparseSIR`, `SISIR`, `tune.ridgeSIR`

Examples

```
set.seed(1140)
tsteps <- seq(0, 1, length = 50)
simulate_bm <- function() return(c(0, cumsum(rnorm(length(tsteps)-1, sd=1))))
x <- t(replicate(50, simulate_bm()))
beta <- cbind(sin(tsteps*3*pi/2), sin(tsteps*5*pi/2))
y <- log(abs(x %*% beta[ ,1])) + sqrt(abs(x %*% beta[ ,2]))
y <- y + rnorm(50, sd = 0.1)
res_ridge <- ridgeSIR(x, y, H = 10, d = 2, mu2 = 10^8)
res_ridge
```

`sfcb` *sfcb*

Description

`sfcb` performs interval selection based on random forests

Usage

```
sfcb(
  X,
  Y,
  group.method = c("adjclust", "cclustofvar"),
  summary.method = c("pls", "basics", "cclustofvar"),
  selection.method = c("none", "boruta", "relief"),
  at = round(0.15 * ncol(X)),
```

```
  range.at = NULL,
  seed = NULL,
  repeats = 5,
  keep.time = TRUE,
  verbose = TRUE,
  parallel = FALSE
)
```

Arguments

X	input predictors (matrix or data.frame)
Y	target variable (vector whose length is equal to the number of rows in X)
group.method	group method. Default to "adjclust"
summary.method	summary method. Default to "pls"
selection.method	selection method. Default to "none" (no selection performed)
at	number of groups targeted for output results (integer). Not used when range.at is not NULL
range.at	(vector of integer) sequence of the numbers of groups for output results
seed	random seed (integer)
repeats	number of repeats for the final random forest computation
keep.time	keep computational times for each step of the method? (logical; default to TRUE)
verbose	print messages? (logical; default to TRUE)
parallel	not implemented yet

Value

an object of class "SFCB" with elements:

dendro	a dendrogram corresponding to the method chosen in group.method
groups	a list of length length(range.at) (or of length 1 if range.at == NULL) that contains the clusterings of input variables for the selected group numbers
summaries	a list of the same length than $groups that contains the summarized predictors according to the method chosen in summary.methods
selected	a list of the same length than $groups that contains the names of the variable selected by selection.method if it is not equal to "none"
mse	a data.frame with repeats $\times$ length($groups) rows that contains Mean Squared Errors of the repeats random forests fitted for each number of groups
importance	a list of the same length than $groups that contains a data.frame providing variable importances for the variables in selected groups in repeats columns (one for each iteration of the random forest method). When summary.method == "basics", importance for mean and sd are provided in separated columns, in which case, the number of columns is equal to 2repeats
computational.times	a vector with 4 values corresponding to the computational times of (respectively) the group, summary, selection, and RF steps. Only if keep.time == TRUE
call	function call

Author(s)

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References

Servien, R. and Vialaneix, N. (2024) A random forest approach for interval selection in functional regression. *Statistical Analysis and Data Mining*, **17**(4), e11705. doi:10.1002/sam.11705

Examples

```
data(truffles)
if (requireNamespace("CORElearn", quietly = TRUE)) {
  out1 <- sfcb(rainfall, truffles, group.method = "adjclust",
               summary.method = "pls", selection.method = "relief")
}
out2 <- sfcb(rainfall, truffles, group.method = "adjclust",
             summary.method = "basics", selection.method = "none",
             range.at = c(5, 7))
```

SFCB-class *Methods for SFCB objects*

Description

Print, plot, manipulate or compute quality for outputs of the sfcb function (SFCB object)

Usage

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

## S3 method for class 'SFCB'
print(x, ...)

## S3 method for class 'SFCB'
plot(
  x,
  ...,
  plot.type = c("dendrogram", "selection", "importance", "quality"),
  sel.type = c("importance", "selection"),
  threshold = "none",
  shape.imp = c("boxplot", "histogram"),
  quality.crit = "mse"
)

extract_at(object, at)

quality(object, ground_truth, threshold = NULL)
```

Arguments

object	a SFCB object
...	not used
x	a SFCB object
plot.type	type of the plot. Default to "dendrogram" (see Details)
sel.type	when plot.type == "selection", criterion on which to base the selection. Default to "importance"
threshold	numeric value. If not NULL, selection of variables to compute qualities is based on a threshold of importance values extract_at
shape.imp	when plot.type == "importance", type of plot to represent the importance. Default to "boxplot"
quality.crit	character vector (length 1 or 2) indicating one or two quality criteria to display. The values have to be taken in {"mse", "time", "Precision", "Recall", "ARI", "NMI"}. If "time" is chosen, it can not be associated with any other criterion
at	numeric vector. Set of the number of intervals to extract for
ground_truth	numeric vector of ground truth. Target variables to compute qualities correspond to non-zero entries of this vector

Details

The plot functions can be used in four different ways to extract information from the SFCB object:

- plot.type == "dendrogram" displays the dendrogram obtained at the clustering step of the method. Depending on the cases, the dendrogram comes with additional information on clusters, variable selections and/or importance values;
- plot.type == "selection" displays either the evolution of the importance for the simulation with the best (smallest) MSE for each time step in the range of the functional predictor or the evolution of the selected intervals along the whole range of the functional prediction also for the best MSE;
- plot.type == "importance" displays a summary of the importance values over the whole range of the functional predictor and for the different experiments. This summary can take the form of a boxplot or of an histogram;
- plot.type == "quality" displays one or two quality distribution with respect to the different experiments and different number of intervals.

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References

Servien, R. and Vialaneix, N. (2023) A random forest approach for interval selection in functional regression. Preprint.

See Also

sfcb

Examples

```
data(truffles)
if (requireNamespace("CORElearn", quietly = TRUE)) {
  out1 <- sfcb(rainfall, truffles, group.method = "adjclust",
               summary.method = "pls", selection.method = "relief")
  summary(out1)

  plot(out1)
  plot(out1, plot.type = "selection")
  plot(out1, plot.type = "importance")
}

out2 <- sfcb(rainfall, truffles, group.method = "adjclust",
             summary.method = "basics", selection.method = "none",
             range.at = c(5, 7))
out3 <- extract_at(out2, at = 6)
summary(out3)
```

SISIR *Interval Sparse SIR*

Description

SISIR performs an automatic search of relevant intervals

Usage

```
SISIR(
  object,
  inter_len = rep(1, nrow(object$EDR)),
  sel_prop = 0.05,
  itermax = Inf,
  minint = 2,
  parallel = TRUE,
  ncores = NULL
)
```

Arguments

object	an object of class ridgeRes as obtained from the function ridgeSIR
inter_len	(numeric) vector with interval lengths for the initial state. Default is to set one interval for each variable (all intervals have length 1)

sel_prop	fraction of the coefficients that will be considered as strong zeros and strong non zeros. Default to 0.05
itermax	maximum number of iterations. Default to Inf
minint	minimum number of intervals. Default to 2
parallel	whether the computation should be performed in parallel or not. Logical. Default is FALSE
ncores	number of cores to use if parallel = TRUE. If left to NULL, all available cores minus one are used

Details

Different quality criteria used to select the best models among a list of models with different interval definitions. Quality criteria are: log-likelihood (loglik), cross-validation error as provided by the function glmnet, two versions of the AIC (AIC and AIC2) and of the BIC (BIC and BIC2) in which the number of parameters is either the number of non null intervals or the number of non null parameters with respect to the original variables

Value

S3 object of class SISIR: a list consisting of

sEDR the estimated EDR spaces (a list of p x d matrices)

alpha the estimated shrinkage coefficients (a list of vectors)

intervals the interval lengths (a list of vectors)

quality a data frame with various qualities for the model. The chosen quality measures are the same than for the function sparseSIR plus the number of intervals nbint

init_sel_prop initial fraction of the coefficients which are considered as strong zeros or strong non zeros

rSIR same as the input object

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References

Picheny, V., Servien, R. and Villa-Vialaneix, N. (2016) Interpretable sparse SIR for digitized functional data. *Statistics and Computing*, **29**(2), 255–267.

See Also

ridgeSIR, sparseSIR

Examples

```
set.seed(1140)
tsteps <- seq(0, 1, length = 200)
nsim <- 100
simulate_bm <- function() return(c(0, cumsum(rnorm(length(tsteps)-1, sd=1))))
x <- t(replicate(nsim, simulate_bm()))
beta <- cbind(sin(tsteps*3*pi/2), sin(tsteps*5*pi/2))
beta[((tsteps < 0.2) | (tsteps > 0.5)), 1] <- 0
beta[((tsteps < 0.6) | (tsteps > 0.75)), 2] <- 0
y <- log(abs(x %*% beta[ ,1]) + 1) + sqrt(abs(x %*% beta[ ,2]))
y <- y + rnorm(nsim, sd = 0.1)
res_ridge <- ridgeSIR(x, y, H = 10, d = 2, mu2 = 10^8)
res_fused <- SISIR(res_ridge, rep(1, ncol(x)), ncores = 2)
res_fused
```

SISIRres *Print SISIRres object*

Description

Print a summary of the result of SISIRres (SISIRres object)

Usage

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

## S3 method for class 'SISIRres'
print(x, ...)
```

Arguments

object	a SISIRres object
...	not used
x	a SISIRres object

Author(s)

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See Also

SISIR

sparseRes *Print sparseRes object*

Description

Print a summary of the result of sparseSIR (sparseRes object)

Usage

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

## S3 method for class 'sparseRes'
print(x, ...)
```

Arguments

object	a sparseRes object
...	not used
x	a sparseRes object

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See Also

sparseSIR

sparseSIR *sparse SIR*

Description

sparseSIR performs the second step of the method (shrinkage of ridge SIR results

Usage

```
sparseSIR(
  object,
  inter_len,
  adaptive = FALSE,
  sel_prop = 0.05,
  parallel = FALSE,
  ncores = NULL
)
```

Arguments

object	an object of class ridgeRes as obtained from the function ridgeSIR
inter_len	(numeric) vector with interval lengths
adaptive	should the function returns the list of strong zeros and non strong zeros (logical). Default to FALSE
sel_prop	used only when adaptive = TRUE. Fraction of the coefficients that will be considered as strong zeros and strong non zeros. Default to 0.05
parallel	whether the computation should be performed in parallel or not. Logical. Default is FALSE
ncores	number of cores to use if parallel = TRUE. If left to NULL, all available cores minus one are used

Value

S3 object of class sparseRes: a list consisting of

sEDR the estimated EDR space (a p x d matrix)

alpha the estimated shrinkage coefficients (a vector having a length similar to inter_len)

quality a vector with various qualities for the model (see Details)

adapt_res if adaptive = TRUE, a list of two vectors:

- nonzeros indexes of variables that are strong non zeros
- zeros indexes of variables that are strong zeros

parameters a list of hyper-parameters for the method:

- inter_len lengths of intervals
- sel_prop if adaptive = TRUE, fraction of the coefficients which are considered as strong zeros or strong non zeros

rSIR same as the input object

fit a list for LASSO fit with:

- glmnet result of the glmnet function
- lambda value of the best Lasso parameter by CV
- x exploratory variable values as passed to fit the model

@details Different quality criteria used to select the best models among a list of models with different interval definitions. Quality criteria are: log-likelihood (loglik), cross-validation error as provided by the function glmnet, two versions of the AIC (AIC and AIC2) and of the BIC (BIC and BIC2) in which the number of parameters is either the number of non null intervals or the number of non null parameters with respect to the original variables.

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References

Picheny, V., Servien, R., and Villa-Vialaneix, N. (2019) Interpretable sparse SIR for digitized functional data. *Statistics and Computing*, **29**(2), 255–267.

See Also

ridgeSIR, project.sparseRes, SISIR

Examples

```
set.seed(1140)
tsteps <- seq(0, 1, length = 200)
nsim <- 100
simulate_bm <- function() return(c(0, cumsum(rnorm(length(tsteps)-1, sd=1))))
x <- t(replicate(nsim, simulate_bm()))
beta <- cbind(sin(tsteps*3*pi/2), sin(tsteps*5*pi/2))
beta[((tsteps < 0.2) | (tsteps > 0.5)), 1] <- 0
beta[((tsteps < 0.6) | (tsteps > 0.75)), 2] <- 0
y <- log(abs(x %*% beta[ ,1]) + 1) + sqrt(abs(x %*% beta[ ,2]))
y <- y + rnorm(nsim, sd = 0.1)
res_ridge <- ridgeSIR(x, y, H = 10, d = 2, mu2 = 10^8)
res_sparse <- sparseSIR(res_ridge, rep(10, 20))
```

---

truffles *Dataset "Truffles"*

Description

Yearly truffles production and corresponding monthly rainfall information of the Perigord black truffle in the Vaucluse (France) between 1924 and 1949.

Format

3 datasets are provided:

- `rainfall`: a data frame with 15 columns (months from January Year n to March Year n+1) and 25 rows (production years from 1924/1925 to 1948/1949). Data correspond to cumulated rainfall in mm;
- `truffles`: a vector with 25 values corresponding to the total production (in kg) of truffles in the truffle patch of T. melanosporum de Pernes-Les-Fontaines (Vaucluse, France);
- `beta`: 0/1 vector with 15 values indicated the months during which the rainfall has the most important influence on the truffle production, as provided by experts.

Details

This dataset has been made available by courtesy of the authors of the publication [Baragatti *et al.*, 2019]. Meteorological data have been provided by Meteo France https://meteofrance.com (Orange meteorological station) and truffle production data are courtesy of the truffle patch.

References

Baragatti M., Grollemund P.M., Montpied P., Dupouey J.L., Gravier J., Murat C., Le Tacon F. (2019) Influence of annual climatic variations, climate changes, and sociological factors on the production of the Perigord black truffle (*Tuber melanosporum Vittad.*) from 1903-1904 to 1988-1989 in the Vaucluse (France), *Mycorrhiza*, **29**(2), 113-125.

Examples

```
data(truffles)
summary(truffles)
plot(1:15, rainfall[1, ], type = "l", xlab = "month", ylab = "rainfall (mm)")
```

---

tune.ridgeSIR *Cross-Validation for ridge SIR*

Description

`tune.ridgeSIR` performs a Cross Validation for ridge SIR estimation

Usage

```
tune.ridgeSIR(
  x,
  y,
  listH,
  list_mu2,
  list_d,
  nfolds = 10,
  parallel = TRUE,
  ncores = NULL
)
```

Arguments

`x`	explanatory variables (numeric matrix or data frame)
`y`	target variable (numeric vector)
`listH`	list of the number of slices to be tested (numeric vector)
`list_mu2`	list of ridge regularization parameters to be tested (numeric vector)
`list_d`	list of the dimensions to be tested (numeric vector)
`nfolds`	number of folds for the cross validation. Default is 10
`parallel`	whether the computation should be performed in parallel or not. Logical. Default is FALSE
`ncores`	number of cores to use if `parallel = TRUE`. If left to NULL, all available cores minus one are used

Value

a data frame with tested parameters and corresponding CV error and estimation of R(d)

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References

Picheny, V., Servien, R. and Villa-Vialaneix, N. (2016) Interpretable sparse SIR for digitized functional data. *Statistics and Computing*, **29**(2), 255–267.

See Also

ridgeSIR

Examples

```
set.seed(1115)
tsteps <- seq(0, 1, length = 200)
nsim <- 100
simulate_bm <- function() return(c(0, cumsum(rnorm(length(tsteps)-1, sd=1))))
x <- t(replicate(nsim, simulate_bm()))
beta <- cbind(sin(tsteps*3*pi/2), sin(tsteps*5*pi/2))
y <- log(abs(x %*% beta[ ,1])) + sqrt(abs(x %*% beta[ ,2]))
y <- y + rnorm(nsim, sd = 0.1)
list_mu2 <- 10^(0:10)
listH <- c(5, 10)
list_d <- 1:4
set.seed(1129)

res_tune <- tune.ridgeSIR(x, y, listH, list_mu2, list_d, nfolds = 10,
                          parallel = TRUE, ncores = 2)
```

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