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Description Implementation of multiple approaches to perform inference in high-dimensional models.

Depends scalreg

DependsNote scalreg does not correctly import lars etc, so we need to depend on it

Imports grDevices, graphics, stats, parallel, MASS, glmnet, linprog

Suggests Matrix

SuggestsNote for tests only

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Description

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Details

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Maintainer:	Lukas Meier <meier@stat.math.ethz.ch>
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Author(s)

Lukas Meier, Ruben Dezeure, Nicolai Meinshausen, Martin Mächler, Peter Bühlmann, Maintainer: Lukas Meier <meier@stat.math.ethz.ch>

References

Dezeure, R., Bühlmann, P., Meier, L. and Meinshausen, N. (2015) High-dimensional inference: confidence intervals, p-values and R-software hdi. *Statistical Science* **30**, 533–558.

Meinshausen, N., Meier, L. and Bühlmann, P. (2009) P-values for high-dimensional regression. *Journal of the American Statistical Association* **104**, 1671–1681.

Meinshausen, N. (2015) Group-bound: confidence intervals for groups of variables in sparse high-dimensional regression without assumptions on the design. *Journal of the Royal Statistical Society: Series B*, **77**(5), 923–945.

Meinshausen, N. and Bühlmann, P. (2010) Stability selection (with discussion). *Journal of the Royal Statistical Society: Series B* **72**, 417–473.

`boot.lasso.proj` *P-values based on the bootstrapped lasso projection method*

Description

Compute p-values based on the lasso projection method, also known as the de-sparsified Lasso, using the bootstrap to approximate the distribution of the estimator.

Usage

```
boot.lasso.proj(x, y, family = "gaussian", standardize = TRUE,
                multiplecorr.method = "WY",
                parallel = FALSE, ncores = getOption("mc.cores", 2L),
                betainit = "cv lasso", sigma = NULL, Z = NULL, verbose = FALSE,
                return.Z = FALSE, robust= FALSE,
                B = 1000, boot.shortcut = FALSE,
                return.bootdist = FALSE, wild = FALSE,
                gaussian.stub = FALSE)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`family`	family
`standardize`	Should design matrix be standardized to unit column standard deviation.
`multiplecorr.method`	Either "WY" or any of `p.adjust.methods`.
`parallel`	Should parallelization be used? (logical)
`ncores`	Number of cores used for parallelization.
`betainit`	Either a numeric vector, corresponding to a sparse estimate of the coefficient vector, or the method to be used for the initial estimation, "scaled lasso" or "cv lasso".
`sigma`	Estimate of the standard deviation of the error term. This estimate needs to be compatible with the initial estimate (see betainit) provided or calculated. Otherwise, results will not be correct.
`Z`	user input, also see `return.Z` below
`verbose`	A boolean to enable reporting on the progress of the computations. (Only prints out information when Z is not provided by the user)
`return.Z`	An option to return the intermediate result which only depends on the design matrix x. This intermediate results can be used when calling the function again and the design matrix is the same as before.
`robust`	Uses a robust variance estimation procedure to be able to deal with model misspecification.

`B`	The number of bootstrap samples to be used.
`boot.shortcut`	A boolean to enable the computational shortcut for the bootstrap. If set to true, the lasso is not re-tuned for each bootstrap iteration, but it uses the tuning parameter computed on the original data instead.
`return.bootdist`	A boolean specifying if one is to return the computed bootstrap distributions to the estimator. (Matrix size: ncol(x)*B) If the multiple testing method was chosen to be WY, the bootstrap distribution computer under the complete null hypothesis is returned as well. This option is required if one wants to compute confidence intervals afterwards.
`wild`	Perform the wild bootstrap based on N(0,1) distributed random variables
`gaussian.stub`	DEVELOPER OPTION. Only enable if you know what you are doing. A boolean to run stub code instead of actually bootstrapping the estimator. It generates a finite sample distribution for each estimate by sampling B samples from N(0,\hat{s.e.}_j^2). (Note: we do not sample from the multivariate gaussian with the covariance matrix. Therefore, no dependencies are modelled at all.) Useful for debugging and for checking if the bootstrap is way off for some reason.

Value

`pval`	Individual p-values for each parameter.
`pval.corr`	Multiple testing corrected p-values for each parameter.
`sigmahat`	$\widehat{\sigma}$ coming from the scaled lasso.
`Z`	Only different from NULL if the option return.Z is on. This is an intermediate result from the computation which only depends on the design matrix x. These are the residuals of the nodewise regressions.
`B`	The number of bootstrap samples used.
`boot.shortcut`	If the bootstrap shortcut has been used or not.
`lambda`	What tuning parameter was used for the bootstrap shortcut. NULL if no shortcut was used or if no valid lambda was available to use for the shortcut.
`cboot.dist`	Only different from NULL if the option return.bootdist is on. This is a ncol(x)*B matrix where each row contains the computed centered bootstrap distribution for that estimate.
`cboot.dist.underH0`	Only different from NULL if the option return.bootdist is on and if the multiple testing method is WY. This is a ncol(x)*B matrix where each row contains the computed centered bootstrap distribution for that estimate. These bootstrap distributions were computed under the complete null hypothesis (b_1 = ... = b_p = 0).

Author(s)

Ruben Dezeure

References

van de Geer, S., Bühlmann, P., Ritov, Y. and Dezeure, R. (2014) On asymptotically optimal confidence regions and tests for high-dimensional models. *Annals of Statistics* **42**, 1166–1202._

Zhang, C., Zhang, S. (2014) Confidence intervals for low dimensional parameters in high dimensional linear models. *Journal of the Royal Statistical Society: Series B* **76**, 217–242.

Bühlmann, P. and van de Geer, S. (2015) High-dimensional inference in misspecified linear models. *Electronic Journal of Statistics* **9**, 1449–1473.

Dezeure, R., Bühlmann, P. and Zhang, C. (2016) High-dimensional simultaneous inference with the bootstrap *http://arxiv.org/abs/1606.03940*

Examples

```
x <- matrix(rnorm(100 * 10), nrow = 100, ncol = 10)
y <- x[,1] + x[,2] + rnorm(100)


fit.lasso <- boot.lasso.proj(x, y)
which(fit.lasso$pval.corr < 0.05) # typically: '1' and '2' and no other



## Use the computational shortcut for the bootstrap to speed up
## computations
fit.lasso.shortcut <- boot.lasso.proj(x, y, boot.shortcut = TRUE)
which(fit.lasso.shortcut$pval.corr < 0.05) # typically: '1' and '2' and no other



## Return the bootstrap distribution as well and compute confidence intervals based on it
fit.lasso.allinfo <- boot.lasso.proj(x, y, return.bootdist = TRUE)
confint(fit.lasso.allinfo, level = 0.95)
confint(fit.lasso.allinfo, parm = 1:3)

## Use the scaled lasso for the initial estimate
fit.lasso.scaled <- boot.lasso.proj(x, y, betainit = "scaled lasso")
which(fit.lasso.scaled$pval.corr < 0.05)

## Use a robust estimate for the standard error
fit.lasso.robust <- boot.lasso.proj(x, y, robust = TRUE)
which(fit.lasso.robust$pval.corr < 0.05)
```

`clusterGroupBound` *Hierarchical structure group tests in linear model*

Description

Computes confidence intervals for the l1-norm of groups of linear regression coefficients in a hierarchical clustering tree.

Usage

```
clusterGroupBound(x, y, method = "average",
                  dist = as.dist(1 - abs(cor(x))), alpha = 0.05,
                  eps = 0.1, hcloutput, nsplit = 11,
                  s = min(10, ncol(x) - 1),
                  silent = FALSE, setseed = TRUE, lpSolve = TRUE)
```

Arguments

`x`	numeric design matrix of the regression $n \times p$ with p columns for p predictor variables and n rows corresponding to n observations.
`y`	numeric response variable of length n.
`method`	a `character` string; the method used for constructing the hierarchical clustering tree (default: `"average"` for "average linkage") via `hclust`. Alternatively, you can provide your own hierarchical clustering through the optional argument `hcloutput`.
`dist`	a distance matrix can be specified on which the hierarchical clustering will be based (see `dist`). The default option is that the distance between variables will be calculated as 1 less the absolute correlation matrix. Alternatively, you can provide your own hierarchical clustering through the optional argument `hcloutput`.
`alpha`	numeric level in $(0, 1)$ at which the test / confidence intervals are to be constructed.
`eps`	a level of eps*alpha is used and the values of different splits are aggregated using the (1-eps) quantile. See reference below for more details.
`hcloutput`	optionally, the value of a `hclust()` call. If it is provided, the arguments `dist` and `method` are ignored.
`nsplit`	the number of data splits used.
`s`	the dimensionality of the projection that is used. Lower values lead to faster computation and if $n > 50$, then `s` is set to 50 if left unspecified, to avoid lengthy computations.
`silent`	logical enabling progress output.
`setseed`	a logical; if this is true (recommended), then the same random seeds are used for all groups, which makes the confidence intervals simultaneously valid over all groups of variables tested.
`lpSolve`	logical; only set it to false if `lpSolve()` is not working on the current machine: setting it to false will result in much slower computations; only use on small problems.

Value

Returns a list with components

`groupNumber`	The index of the group tested in the original hierarchical clustering tree
`members`	A list containing the variables that belong into each testes group

`noMembers`	A vector containing the number of members in each group
`lowerBound`	The lower bound on the l1-norm in each group
`position`	The position on the x-axis of each group (used for plotting)
`leftChild`	Gives the index of the group that corresponds to the left child node in the tested tree (negative values correspond to leaf nodes)
`rightChild`	Same as `leftCHild` for the right child of each node
`isLeaf`	Logical vector. Is `TRUE` for a group if it is a leaf node in the tested tree or if both child nodes have a zero lower bound on their group l1-norm

Author(s)

Nicolai Meinshausen

References

Meinshausen, N. (2015); JRSS B, see `groupBound`.

See Also

Use `groupBound` to compute the lower bound for selected groups of variables whereas you use this `clusterGroupBound` to test all groups in a hierarchical clustering tree.

Examples

```
## Create a regression problem with correlated design (n = 10, p = 3):
## a block of size 2 and a block of size 1, within-block correlation is 0.99

set.seed(29)
p   <- 3
n   <- 10

Sigma <- diag(p)
Sigma[1,2] <- Sigma[2,1] <- 0.99

x <- matrix(rnorm(n * p), nrow = n) %*% chol(Sigma)

## Create response with active variable 1
beta    <- rep(0, p)
beta[1] <- 5

y  <- as.numeric(x %*% beta + rnorm(n))

out <- clusterGroupBound(x, y, nsplit = 4) ## use larger value for nsplit!

## Plot and print the hierarchical group-test
plot(out)
print(out)
out$members
out$lowerBound
```

fdr.adjust *Function to calculate FDR adjusted p-values*

Description

Calculates FDR adjusted p-values similar to R-function p.adjust but *without* adjustment for multiplicity.

Usage

```
fdr.adjust(p)
```

Arguments

`p`	Vector of p-values.

Details

It is assumed that the p-values are already corrected for multiplicity. P-values with a value of 1 are currently ignored.

Value

Vector of p-values.

Author(s)

Lukas Meier

References

Meinshausen, N., Meier, L. and Bühlmann, P. (2009), *P-values for high-dimensional regression*, Journal of the American Statistical Association 104, 1671-1681.

See Also

`p.adjust`

Examples

```
x <- matrix(rnorm(100 * 1000), nrow = 100, ncol = 1000)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)

## Multi-splitting with lasso.firstq as model selector function
fit.multi <- multi.split(x, y, model.selector =lasso.firstq,
                         args.model.selector = list(q = 10))
p.adjust <- fdr.adjust(fit.multi$pval.corr)
```

`glm.pval` *Function to calculate p-values for a generalized linear model.*

Description

Calculates (classical) p-values for an ordinary generalized linear model in the n > p situation.

Usage

```
glm.pval(x, y, family = "binomial", verbose = FALSE, ...)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`family`	As in `glm`.
`verbose`	Logical. Should information be printed out if algorithm did not converge?
`...`	Additional arguments to be passed to `glm`.

Details

A model with intercept is fitted but the p-value of the intercept is not reported in the output.

Value

Vector of p-values (not including the intercept).

Author(s)

Lukas Meier

See Also

`hdi`

Examples

```
## ...
```

groupBound *Lower bound on the l1-norm of groups of regression variables*

Description

Computes a lower bound that forms a one-sided confidence interval for the group l1-norm of a specified group of regression parameters. It is assumed that errors have a Gaussian distribution with unknown noise level. The underlying vector that inference is made about is the l1-sparsest approximation to the noiseless data.

Usage

```
groupBound(x, y, group, alpha = 0.05, eps = 0.1, nsplit = 11,
           s = min(10, ncol(x) - 1), setseed = TRUE,
           silent = FALSE, lpSolve = TRUE, parallel = FALSE,
           ncores = getOption("mc.cores", 2L))
```

Arguments

`x`	numeric design matrix of the regression $n \times p$ with p columns for p predictor variables and n rows corresponding to n observations.
`y`	numeric response variable of length n.
`group`	either a numeric vector with entries in $\{1, ..., p\}$ or a `list` with such numeric vectors. If `group` is a numeric vector, this is the group of variables for which a lower bound is computed. If `group` is a list, the lower bound is computed for each group in the list.
`alpha`	numeric level in $(0, 1)$ at which the test / confidence interval is computed.
`eps`	a level of eps * alpha is used and the values of different splits are aggregated using the (1 - eps) quantile. See reference below for more details.
`nsplit`	the number of data splits used.
`s`	the dimensionality of the projection that is used. Lower values lead to faster computation and if $n > 50$, then `s` is set to 50 if left unspecified, to avoid lengthy computations.
`setseed`	a logical; if this is true (recommended), then the same random seeds are used for all groups, which makes the confidence intervals simultaneously valid over all groups of variables tested.
`silent`	logical enabling progress output.
`lpSolve`	logical; only set it to false if `lpSolve()` is not working on the current machine: setting it to false will result in much slower computations; only use on small problems.
`parallel`	should parallelization be used? (logical)
`ncores`	number of cores used for parallelization.

Details

The data are split since the noise level is unknown. On the first part of the random split, a cross-validated lasso solution is computed, using the **glmnet** implementation. This estimator is used as an initial estimator on the second half of the data. Results at level `alpha` are aggregated over `nsplit` splits via the median of results at levels `alpha/2`.

Value

If `group` is a single numeric vector, a scalar containg the lower bound for this group of variables is returned. If `group` is a list, a numeric vector is retuned where each entry corresponds to the group of variables defined in the same order in `group`.

Author(s)

Nicolai Meinshausen

References

Meinshausen, N. (2015) Group bound: confidence intervals for groups of variables in sparse high dimensional regression without assumptions on the design. *Journal of the Royal Statistical Society: Series B*, **77**, 923–945; doi: 10.1111/rssb.12094.

See Also

Use `clusterGroupBound` to test all groups in a hierarchical clustering tree.

Examples

```
## Create a regression problem with correlated design: p = 6, n = 50,
## block size B = 3 and within-block correlation of rho = 0.99
p   <- 6
n   <- 50
B   <- 3
rho <- 0.99

ind   <- rep(1:ceiling(p / B), each = B)[1:p]
Sigma <- diag(p)

for (ii in unique(ind)){
  id <- which(ind == ii)
  Sigma[id, id] <- rho
}
diag(Sigma) <- 1

x <- matrix(rnorm(n * p), nrow = n) %*% chol(Sigma)

## Create response with active variable 1
beta    <- rep(0, p)
beta[1] <- 5

y  <- as.numeric(x %*% beta + rnorm(n))
```

```
## Compute lower bounds:

## Lower bound for the L1-norm of *all* variables 1-6 of the sparsest
## optimal vector
nsplit <- 4  ## to make example run fast (use larger value)
lowerBoundAll <- groupBound(x, y, 1:p, nsplit = nsplit)
cat("\nlower bound for all variables 1-6: ", lowerBoundAll, "\n")

## Compute additional lower bounds:
q()## Lower bounds for variable 1 itself, then group {1,3}, 1-2, 1-3, 2-6,
lowerBound <- groupBound(x, y, list(1, c(1,3), 1:2, 1:3, 2:6),
                         nsplit = nsplit)
cat("lower bound for the groups\n\t {1}, {1,3}, {1,2}, {1..3}, {2..6}:\n\t",
    format(formatC(c(lowerBound))), "\n")
```

hdi — *Function to perform inference in high-dimensional (generalized) linear models*

Description

Perform inference in high-dimensional (generalized) linear models using various approaches.

Usage

```
hdi(x, y, method = "multi.split", B = NULL, fraction = 0.5,
    model.selector = NULL, EV = NULL, threshold = 0.75,
    gamma = seq(0.05, 0.99, by = 0.01),
    classical.fit = NULL,
    args.model.selector = NULL, args.classical.fit = NULL,
    verbose = FALSE, ...)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`method`	Multi-splitting ("multi.split") or stability-selection ("stability").
`B`	Number of sample-splits (for "multi.split") or sub-sample iterations (for "stability"). Default is 50 ("multi.split")or 100 ("stability"). Ignored otherwise.
`fraction`	Fraction of data used at each of the B iterations.
`model.selector`	Function to perform model selection. Default is `lasso.cv` ("multi.split") and `lasso.firstq` ("stability"). Function must have at least two arguments: x (the design matrix) and y (the response vector). Return value is the index vector of selected columns. See `lasso.cv` and `lasso.firstq` for examples. Additional arguments can be passed through `args.model.selector`.

`EV`	(only for "stability"). Bound(s) for expected number of false positives . Can be a vector.
`threshold`	(only for "stability"). Bound on selection frequency.
`gamma`	(only for "multi.split"). Vector of gamma-values.
`classical.fit`	(only for "multi.split"). Function to calculate (classical) p-values. Default is `lm.pval`. Function must have at least two arguments: x (the design matrix) and y (the response vector). Return value is the vector of p-values. See `lm.pval` for an example. Additional arguments can be passed through `args.classical.fit`.
`args.model.selector`	Named list of further arguments for function `model.selector`.
`args.classical.fit`	Named list of further arguments for function `classical.fit`.
`verbose`	Should information be printed out while computing (logical).
`...`	Other arguments to be passed to the underlying functions.

Value

`pval`	(only for "multi.split"). Vector of p-values.
`gamma.min`	(only for "multi.split"). Value of gamma where minimal p-values was attained.
`select`	(only for "stability"). List with selected predictors for the supplied values of EV.
`EV`	(only for "stability"). Vector of corresponding values of EV.
`thresholds`	(only for "stability"). Used thresholds.
`freq`	(only for "stability"). Vector of selection frequencies.

Author(s)

Lukas Meier

References

Meinshausen, N., Meier, L. and Bühlmann, P. (2009) P-values for high-dimensional regression. *Journal of the American Statistical Association* **104**, 1671–1681.

Meinshausen, N. and Bühlmann, P. (2010) Stability selection (with discussion). *Journal of the Royal Statistical Society: Series B* **72**, 417–473.

See Also

`stability`, `multi.split`

Examples

```
x <- matrix(rnorm(100 * 200), nrow = 100, ncol = 200)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)

## Multi-splitting with lasso.firstq as model selector function
fit.multi <- hdi(x, y, method = "multi.split",
                  model.selector =lasso.firstq,
                  args.model.selector = list(q = 10))
fit.multi
fit.multi$pval.corr[1:10] ## the first 10 p-values

## Stability selection
fit.stab <- hdi(x, y, method = "stability", EV = 2)
fit.stab
fit.stab$freq[1:10] ## frequency of the first 10 predictors
```

---

lasso.cv — *Select Predictors via (10-fold) Cross-Validation of the Lasso*

Description

Performs (n-fold) cross-validation of the lasso (via `cv.glmnet`) and determines the prediction optimal set of parameters.

Usage

```
lasso.cv(x, y,
          nfolds = 10,
          grouped = nrow(x) > 3*nfolds,
          ...)
```

Arguments

`x`	numeric design matrix (without intercept) of dimension $n \times p$.
`y`	response vector of length n.
`nfolds`	the number of folds to be used in the cross-validation
`grouped`	corresponds to the `grouped` argument to `cv.glmnet`. This has a smart default such that glmnet does not give a warning about too small sample size.
`...`	further arguments to be passed to `cv.glmnet`.

Details

The function basically only calls `cv.glmnet`, see source code.

Value

Vector of selected predictors.

Author(s)

Lukas Meier

See Also

hdi which uses `lasso.cv()` by default; cv.glmnet. An alternative for `hdi()`: lasso.firstq.

Examples

```
x <- matrix(rnorm(100 * 1000), nrow = 100, ncol = 1000)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)
sel <- lasso.cv(x, y)
sel
```

`lasso.firstq` *Determine the first q Predictors in the Lasso Path*

Description

Determines the q predictors that enter the lasso path first.

Usage

```
lasso.firstq(x, y, q, ...)
```

Arguments

`x`	numeric design matrix (without intercept) of dimension $n \times p$.
`y`	response vector of length n.
`q`	number of predictors that should be selected, a positive integer.
`...`	optional additional arguments to be passed to glmnet.

Details

The `lasso.firstq` function calls glmnet in a special way and simply postprocesses its nonzero predictor list, see its source code.

Value

Vector of selected predictors.

Author(s)

Lukas Meier

See Also

hdi; the default choice for `hdi()`, lasso.cv. glmnet

Examples

```
x <- matrix(rnorm(100 * 1000), nrow = 100, ncol = 1000)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)
sel <- lasso.firstq(x, y, q = 5)
sel # 5 integers from {1,2, ..., 1000},  including '1' and '2', typically
```

`lasso.proj` *P-values based on lasso projection method*

Description

Compute p-values based on the lasso projection method, also known as the de-sparsified Lasso, using an asymptotic gaussian approximation to the distribution of the estimator.

Usage

```
lasso.proj(x, y, family = "gaussian", standardize = TRUE,
           multiplecorr.method = "holm", N = 10000,
           parallel = FALSE, ncores = getOption("mc.cores", 2L),
           betainit = "cv lasso", sigma = NULL, Z = NULL, verbose = FALSE,
           return.Z = FALSE, suppress.grouptesting = FALSE, robust = FALSE,
    do.ZnZ = FALSE)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`family`	family
`standardize`	Should design matrix be standardized to unit column standard deviation.
`multiplecorr.method`	Either "WY" or any of `p.adjust.methods`.
`N`	Number of empirical samples (only used if multiplecorr.method == "WY")
`parallel`	Should parallelization be used? (logical)
`ncores`	Number of cores used for parallelization.
`betainit`	Either a numeric vector, corresponding to a sparse estimate of the coefficient vector, or the method to be used for the initial estimation, "scaled lasso" or "cv lasso".
`sigma`	Estimate of the standard deviation of the error term. This estimate needs to be compatible with the initial estimate (see betainit) provided or calculated. Otherwise, results will not be correct.
`Z`	user input, also see `return.Z` below
`verbose`	A boolean to enable reporting on the progress of the computations. (Only prints out information when Z is not provided by the user)

`return.Z`	An option to return the intermediate result which only depends on the design matrix x. This intermediate results can be used when calling the function again and the design matrix is the same as before.
`suppress.grouptesting`	A boolean to optionally suppress the preparations made for testing groups. This will avoid quite a bit of computation and memory usage. The output will also be smaller.
`robust`	Uses a robust variance estimation procedure to be able to deal with model misspecification.
`do.ZnZ`	Use a slightly different way of choosing tuning parameters to compute Z, called Z&Z based on Zhang and Zhang (2014). This choice of tuning parameter results in a slightly higher variance of the estimator. More concretely, it achieves a 25 variance of the estimator (over j=1..ncol(x)) in comparison to tuning with cross-validation.

Value

`pval`	Individual p-values for each parameter.
`pval.corr`	Multiple testing corrected p-values for each parameter.
`groupTest`	Function to perform groupwise tests. Groups are indicated using an index vector with entries in 1,...,p or a list thereof.
`clusterGroupTest`	Function to perform groupwise tests based on hierarchical clustering. You can either provide a distance matrix and clustering method or the output of hierarchical clustering from the function `hclust` as for `clusterGroupBound`. P-values are adjusted for multiple testing.
`sigmahat`	$\widehat{\sigma}$ coming from the scaled lasso.
`Z`	Only different from NULL if the option return.Z is on. This is an intermediate result from the computation which only depends on the design matrix x. These are the residuals of the nodewise regressions.

Author(s)

Ruben Dezeure

References

van de Geer, S., Bühlmann, P., Ritov, Y. and Dezeure, R. (2014) On asymptotically optimal confidence regions and tests for high-dimensional models. *Annals of Statistics* **42**, 1166–1202._

Zhang, C., Zhang, S. (2014) Confidence intervals for low dimensional parameters in high dimensional linear models. *Journal of the Royal Statistical Society: Series B* **76**, 217–242.

Bühlmann, P. and van de Geer, S. (2015) High-dimensional inference in misspecified linear models. *Electronic Journal of Statistics* **9**, 1449–1473.

Examples

```
x <- matrix(rnorm(100 * 10), nrow = 100, ncol = 10)
y <- x[,1] + x[,2] + rnorm(100)
fit.lasso <- lasso.proj(x, y)
which(fit.lasso$pval.corr < 0.05) # typically: '1' and '2' and no other

## Group-wise testing of the first two coefficients
fit.lasso$groupTest(1:2)

##Compute confidence intervals
confint(fit.lasso, level = 0.95)


## Hierarchical testing using distance matrix based on
## correlation matrix
out.clust <- fit.lasso$clusterGroupTest()
plot(out.clust)

## Fit the lasso projection method without doing the preparations
## for group testing (saves time and memory)
fit.lasso.faster <- lasso.proj(x, y, suppress.grouptesting = TRUE)

## Use the scaled lasso for the initial estimate
fit.lasso.scaled <- lasso.proj(x, y, betainit = "scaled lasso")
which(fit.lasso.scaled$pval.corr < 0.05)

## Use a robust estimate for the standard error
fit.lasso.robust <- lasso.proj(x, y, robust = TRUE)
which(fit.lasso.robust$pval.corr < 0.05)


## Perform the Z&Z version of the lasso projection method
fit.lasso <- lasso.proj(x, y, do.ZnZ = TRUE)

which(fit.lasso$pval.corr < 0.05) # typically: '1' and '2' and no other
```

`lm.ci` *Function to calculate confidence intervals for ordinary multiple linear regression.*

Description

Calculates (classical) confidence intervals for an ordinary multiple linear regression model in the n > p situation.

Usage

```
lm.ci(x, y, level = 0.95, ...)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`level`	Coverage level.
`...`	Additional arguments to be passed to `lm`.

Details

A model with intercept is fitted but the p-value of the intercept is not reported in the output.

Value

Matrix of confidence interval bounds (not including the intercept).

Author(s)

Lukas Meier

See Also

`hdi`

Examples

```
x <- matrix(rnorm(100 * 5), nrow = 100, ncol = 5)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)
ci <- lm.ci(x, y)
ci
```

`lm.pval` *Function to calculate p-values for ordinary multiple linear regression.*

Description

Calculates (classical) p-values for an ordinary multiple linear regression in the n > p situation.

Usage

```
lm.pval(x, y, exact = TRUE, ...)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`exact`	Logical. TRUE if p-values based on t-distribution should be calculated. FALSE if normal distribution should be used as approximation.
`...`	Additional arguments to be passed to `lm`.

Details

A model with intercept is fitted but the p-value of the intercept is not reported in the output.

Value

Vector of p-values (not including the intercept).

Author(s)

Lukas Meier

See Also

`hdi`

Examples

```
x <- matrix(rnorm(100 * 5), nrow = 100, ncol = 5)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)
pval <- lm.pval(x, y)
pval
```

`multi.split` *Calculate P-values Based on Multi-Splitting Approach*

Description

Calculate p-values and confidence intervals based on the multi-splitting approach

Usage

```
multi.split(x, y, B = 100, fraction = 0.5, ci = TRUE, ci.level = 0.95,
            model.selector = lasso.cv,
            classical.fit = lm.pval, classical.ci = lm.ci,
            parallel = FALSE, ncores = getOption("mc.cores", 2L),
            gamma = seq(ceiling(0.05 * B) / B, 1 - 1 / B, by = 1 / B),
            args.model.selector = NULL, args.classical.fit = NULL,
            args.classical.ci = NULL,
            return.nonaggr = FALSE, return.selmodels = FALSE,
            repeat.max = 20,
            verbose = FALSE)
```

Arguments

`x`	numeric design matrix (without intercept).
`y`	numeric response vector.
`B`	the number of sample-splits, a positive integer.
`fraction`	a number in $(0, 1)$, the fraction of data used at each sample split for the model selection process. The remaining data is used for calculating the p-values.
`ci`	logical indicating if a confidence interval should be calculated for each parameter.
`ci.level`	(if `ci` is true:) a number in $(0, 1)$, typically close to 1, the desired coverage level of the confidence intervals.
`model.selector`	a `function` to perform model selection, with default `lasso.cv`. The function must have at least two arguments, `x` (the design matrix) and `y` (the response vector). Return value is the index vector of selected columns. See `lasso.cv` and `lasso.firstq` for an example. Additional arguments can be passed via `args.model.selector`.
`classical.fit`	a `function` to calculate (classical) p-values. Default is `lm.pval`. The function must have at least two arguments, `x` (the design matrix) and `y` (the response vector), and return the vector of p-values. See `lm.pval` for an example. Additional arguments can be passed through `args.classical.fit`.
`classical.ci`	a `function` to calculate (classical) confidence intervals. Default is `lm.ci`. The function must have at least 3 arguments, `x` (the design matrix), `y` (the response vector) and `level` (the coverage level), and return the matrix of confidence intervals. See `lm.ci` for an example. Additional arguments can be passed through `args.classical.ci`.
`parallel`	logical indicating if parallelization via `mclapply` should be used.
`ncores`	number of cores used for parallelization as `mc.cores` in `mclapply()`.
`gamma`	vector of gamma-values. In case gamma is a scalar, the value Q_j instead of P_j is being calculated (see reference below).
`args.model.selector`	named `list` of further arguments for function `model.selector`.
`args.classical.fit`	named `list` of further arguments for function `classical.fit`.
`args.classical.ci`	named `list` of further arguments for function `classical.ci`.
`return.nonaggr`	`logical` indicating if the unadjusted p-values be returned.
`return.selmodels`	`logical` indicating if the selected models (at each split) should be returned. Necessary for the `clusterGroupTest()` part of the result.
`repeat.max`	positive integer indicating the maximal number of split trials. Should not matter in regular cases, but necessary to prevent infinite loops in borderline cases.
`verbose`	should information be printed out while computing? (logical).

Value

`pval.corr`	Vector of multiple testing corrected p-values.
`gamma.min`	Value of gamma where minimal p-values was attained.
`clusterGroupTest`	Function to perform groupwise tests based on hierarchical clustering. You can either provide a distance matrix and clustering method or the output of hierarchical clustering from the function `hclust` as for `clusterGroupBound`. P-values are adjusted for multiple testing.

Author(s)

Lukas Meier, Ruben Dezeure, Jacopo Mandozzi

References

Meinshausen, N., Meier, L. and Bühlmann, P. (2009) P-values for high-dimensional regression. *Journal of the American Statistical Association* **104**, 1671–1681.

Mandozzi, J. and Bühlmann, P. (2015) A sequential rejection testing method for high-dimensional regression with correlated variables. To appear in the International Journal of Biostatistics. Preprint arXiv:1502.03300

See Also

`lasso.cv`, `lasso.firstq`; `lm.pval`, `lm.ci`.

Examples

```
n <-  40 # a bit small, to keep example "fast"
p <- 256
x <- matrix(rnorm(n * p), nrow = n, ncol = p)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(n)

## Multi-splitting with lasso.firstq as model selector function
## 'q' must be specified
fit.multi <- multi.split(x, y, model.selector = lasso.firstq,
                         args.model.selector = list(q = 10))
fit.multi
head(fit.multi$pval.corr, 10) ## the first 10 p-values
ci. <- confint(fit.multi)
head(ci.) # the first 6
stopifnot(all.equal(ci.,
     with(fit.multi, cbind(lci, uci)), check.attributes=FALSE))


## Use default 'lasso.cv' (slower!!) -- incl cluster group testing:
system.time(fit.m2 <- multi.split(x, y, return.selmodels = TRUE))# 9 sec (on "i7")
head(fit.m2$pval.corr) ## the first  6  p-values
head(confint(fit.m2))  ## the first  6  95% conf.intervals

## Now do clustergroup testing
```

```
clGTst <- fit.m2$clusterGroupTest
names(envGT <- environment(clGTst))# about 14
if(!interactive()) # if you are curious (and advanced):
  print(ls.str(envGT), max = 0)
stopifnot(identical(clGTst, envGT$clusterGroupTest))
ccc <- clGTst()
str(ccc)
ccc$hh   # the clustering
has.1.or.2 <- sapply(ccc$clusters,
                     function(j.set) any(c(1,2) %in% j.set))
ccc$pval[ has.1.or.2] ## all very small
ccc$pval[!has.1.or.2] ## all 1
```

plot.clusterGroupBound

Plot output of hierarchical testing of groups of variables

Description

The `plot()` method for "`clusterGroupBound`" objects plots the outcome of applying a lower bound on the l1-norm on groups of variables in a hierarchical clustering tree.

Usage

```
## S3 method for class 'clusterGroupBound'
plot(x, cexfactor = 1, yaxis = "members",
     xlab = "", col = NULL, pch = 20, ...)
```

Arguments

`x`	an object of `class` "`clusterGroupBound`", as resulting from `clusterGroupBound()`.
`cexfactor`	numeric expansion factor for the size of the node symbols.
`yaxis`	a string; for the default "`members`", the hierarchical tree is shown as function of cluster size on the y-axis, whereas the node sizes are proportional to the lower l1-norm of the respective groups of variables. If `yaxis` takes any different value, then this is reversed and the tree is shown against the lower l1-norm on the y-axis, while node sizes are now proportional to the number of elements in each cluster.
`xlab`	label used for the x-axis; by default none.
`col`	the colour of the symbols for the nodes.
`pch`	the plot symbol (see `points`) of the symbols for the nodes.
`...`	optional additional arguments passed to `plot.default`.

Value

Nothing is returned

Author(s)

Nicolai Meinshausen <meinshausen@stat.math.ethz.ch>

See Also

Use `clusterGroupBound()` to test all groups in a hierarchical clustering tree. Use `groupBound()` to compute the lower bound for selected groups of variables.

Examples

```
## Create a regression problem with correlated design (n = 10, p = 3):
## a block of size 2 and a block of size 1, within-block correlation is 0.99

set.seed(29)
p   <- 3
n   <- 10

Sigma <- diag(p)
Sigma[1,2] <- Sigma[2,1] <- 0.99

x <- matrix(rnorm(n * p), nrow = n) %*% chol(Sigma)

## Create response with active variable 1
beta    <- rep(0, p)
beta[1] <- 5

y  <- as.numeric(x %*% beta + rnorm(n))

## Compute the lower bound for all groups in a hierarchical clustering tree
cgb5 <- clusterGroupBound(x, y, nsplit = 4) ## use larger value for nsplit!

## Plot the tree with y-axis proportional to the (log) of the number of
## group members and node sizes proportional to the lower l1-norm bound.
plot(cgb5)

## Show the lower bound on the y-axis and node sizes proportional to
## number of group members
plot(cgb5, yaxis = "")
```

`riboflavin` *Riboflavin data set*

Description

Dataset of riboflavin production by Bacillus subtilis containing $n = 71$ observations of $p = 4088$ predictors (gene expressions) and a one-dimensional response (riboflavin production).

Usage

```
data(riboflavin)
```

Format

y Log-transformed riboflavin production rate (original name: q_RIBFLV).

x (Co-)variables measuring the logarithm of the expression level of 4088 genes.

Details

Data kindly provided by DSM (Switzerland).

References

Bühlmann, P., Kalisch, M. and Meier, L. (2014) *High-dimensional statistics with a view towards applications in biology*. Annual Review of Statistics and its Applications **1**, 255–278

Examples

```
data(riboflavin)
```

---

ridge.proj *P-values based on ridge projection method*

Description

Compute p-values for lasso-type regression coefficients based on the ridge projection method.

Usage

```
ridge.proj(x, y, family = "gaussian", standardize = TRUE,
           lambda = 1, betainit = "cv lasso", sigma = NULL,
           suppress.grouptesting = FALSE,
           multiplecorr.method = "holm", N = 10000)
```

Arguments

`x`	design matrix (without intercept).
`y`	response vector.
`family`	family
`standardize`	Should design matrix be standardized to unit column standard deviation (logical)?
`lambda`	Value of penalty parameter lambda (ridge regression).
`betainit`	Either a numeric vector, corresponding to a sparse estimate of the coefficient vector, or the method to be used for the initial estimation, "scaled lasso" or "cv lasso".

`sigma`	Estimate of the standard deviation of the error term. This estimate needs to be compatible with the initial estimate (see betainit) provided or calculated. Otherwise, results won't be correct.
`suppress.grouptesting`	A boolean to optionally suppress the preparations made for testing groups. This will avoid quite a bit of computation and memory usage. The output will also be smaller.
`multiplecorr.method`	Either "WY" or any of `p.adjust.methods`.
`N`	number of empirical samples (only used if `multiplecorr.method = "WY"`).

Value

`pval`	Individual p-values for each parameter.
`pval.corr`	Multiple testing corrected p-values for each parameter.
`groupTest`	Function to perform groupwise tests. Groups are indicated using an index vector with entries in $1, \ldots, p$ or a list thereof.
`clusterGroupTest`	Function to perform groupwise tests based on hierarchical clustering. You can either provide a distance matrix and clustering method or the output of hierarchical clustering from the function `hclust` as for `clusterGroupBound`. P-values are adjusted for multiple testing.
`sigmahat`	$\widehat{\sigma}$ coming from the scaled lasso.

Author(s)

Peter Buehlmann, Ruben Dezeure, Lukas Meier

References

Bühlmann, P. (2013) Statistical significance in high-dimensional linear models. *Bernoulli* **19**, 1212–1242.

Examples

```
x <- matrix(rnorm(100 * 100), nrow = 100, ncol = 100)
y <- x[,1] + x[,2] + rnorm(100)
fit.ridge <- ridge.proj(x, y)
which(fit.ridge$pval.corr < 0.05)

## Use the scaled lasso for the initial estimate
fit.ridge.scaled  <- ridge.proj(x, y, betainit = "scaled lasso")
which(fit.ridge.scaled$pval.corr < 0.05)

## Group-wise testing of the first two coefficients
fit.ridge$groupTest(1:2)

## Hierarchical testing using distance matrix based on
## correlation matrix
```

```
out.clust <- fit.ridge$clusterGroupTest()
plot(out.clust)

## Fit the method without doing the preparations
## for group testing (saves time and memory)
fit.ridge.faster <- ridge.proj(x, y, suppress.grouptesting = TRUE)
```

---

rXb *Generate Data Design Matrix X and Coefficient Vector β*

Description

Generate a random design matrix X and coefficient vector β useful for simulations of (high dimensional) linear models. In particular, the function `rXb()` can be used to exactly recreate the reference linear model datasets of the hdi paper.

Usage

```
rXb(n, p, s0,
    xtype = c("toeplitz", "exp.decay", "equi.corr"),
    btype = "U[-2,2]",
    permuted = FALSE, iteration = NA, do2S = TRUE,
    x.par = switch(xtype,
                   "toeplitz"  = 0.9,
                   "equi.corr" = 0.8,
                   "exp.decay" = c(0.4, 5)),
   verbose = TRUE)

rX(n, p, xtype, permuted, do2S = TRUE,
   par = switch(xtype,
                "toeplitz"  = 0.9,
                "equi.corr" = 0.8,
                "exp.decay" = c(0.4, 5)))
```

Arguments

`n`	integer; the sample size n (paper had always `n = 100`).
`p`	integer; the number of coefficients in the linear model. (paper had always `p = 500`).
`s0`	integer number of *nonzero* coefficients desired in the model; hence at most `p`.
`xtype`	a `character` string specifying the type of design matrix one wants to generate. Must be one of `"toeplitz"`, `"equi.corr"` or `"exp.decay"`.
`btype`	a `character` string specifying the type of nonzero coefficients ("beta") one wants to generate. In the hdi paper, this has been one of "U[-2,2]", "U[0,2]", "U[0,4]", "bfix1", "bfix2" and "bfix10". In general, any string of the form `"U[a,b]"` or `"bfix<c>"` is allowed, where `a`, `b`, and `<c>` must be numbers (with $a \leq b$).

`permuted`	logical specifying if the columns of the design matrix should be permuted.
`iteration`	integer or `NA` specifying if seeds should be set to generate reproducible realizations of the design type and coefficients type. `NA` corresponds to not setting seeds. Iteration numbers 1 to 50 correspond to the setups from the paper. If a seed is set, the original `.Random.seed` at the point of entering the function is saved and is restored upon exit of the data generation. If `NA`, the current `.Random.seed` is taken as usual in R.
`do2S`	logical indicating if in the case of `xtype`s `"toeplitz"` or `"equi.corr"`, the $p \times p$ covariance matrix should be inverted twice. Must be true, to regenerate the X matrices from the hdi paper exactly "to the last bit".
`x.par, par`	the parameters to be used for the design matrix. Must be a numeric vector of length one or two. The default uses the parameters also used in the hdi paper.
`verbose`	should the function give a message if seeds are being set? (logical).

Details

Generation of the design matrix X:
For all `xtype`'s, the X matrix will be multivariate normal, with mean zero and (co)variance matrix $\Sigma =$`C` determined from `xtype`, `x.par` and p as follows:

`xtype = "toeplitz"`: `C <- par ^ abs(toeplitz(0:(p-1)))`

`xtype = "equi.corr"`: $\Sigma_{i,j} =$ `par` for $i \neq j$, and $= 1$ for $i = j$, i.e., on the diagonal.

`xtype = "exp.decay"`: `C <- solve(par[1] ^ abs(toeplitz(0:(p-1)) / par[2]))`

Value

For `rXb()`: A `list` with components

x the generated $n \times p$ design matrix X.

beta the generated coefficient vector β ('beta').

For `rX()`: the generated $n \times p$ design matrix X.

Author(s)

Ruben Dezeure <dezeure@stat.math.ethz.ch>

References

Dezeure, R., Bühlmann, P., Meier, L. and Meinshausen, N. (2015) High-dimensional inference: confidence intervals, p-values and R-software hdi. *Statistical Science* **30**, 533–558.

Examples

```
## Generate the first realization of the linear model with design matrix
## type Toeplitz and coefficients type uniform between -2 and 2

dset <- rXb(n = 80, p = 20, s0 = 3,
            xtype = "toeplitz", btype = "U[-2,2]")
x <- dset$x
```

```
beta <- dset$beta

## generate 100 response vectors of this linear model
y <- as.vector( x %*% beta ) + replicate(100, rnorm(nrow(x)))

## Use  'beta_min' fulfilling  beta's  (non standard 'btype'):
str(ds2 <- rXb(n = 50, p = 12, s0 = 3,
               xtype = "exp.decay", btype = "U[0.1, 5]"))

## Generate a design matrix of type "toeplitz"
set.seed(3) # making it reproducible
X3 <- rX(n = 800, p = 500, xtype = "toeplitz", permuted = FALSE)

## permute the columns
set.seed(3)
Xp <- rX(n = 800, p = 500, xtype = "toeplitz", permuted = TRUE)
```

`stability` *Function to perform stability selection*

Description

Function to perform stability selection

Usage

```
stability(x, y, EV, threshold = 0.75, B = 100, fraction = 0.5,
          model.selector = lasso.firstq, args.model.selector = NULL,
          parallel = FALSE, ncores = getOption("mc.cores", 2L),
          verbose = FALSE)
```

Arguments

`x`	Design matrix (without intercept).
`y`	Response vector.
`EV`	Bound for expected number of false positives.
`threshold`	Threshold for selection frequency. Must be in (0.5, 1).
`B`	Number of sub-sample iterations.
`fraction`	Fraction of data used at each of the B sub-samples.
`model.selector`	Function to perform model selection. Default is `lasso.firstq`. User supplied function must have at least three arguments: x (the design matrix), y (the response vector) and q (the maximal model size). Return value is the index vector of selected columns. See `lasso.firstq` for an example. Additional arguments can be passed through `args.model.selector`.
`args.model.selector`	Named list of further arguments for function `model.selector`.

`parallel`	Should parallelization be used? (logical)
`ncores`	Number of cores used for parallelization.
`verbose`	Should information be printed out while computing (logical).

Value

`selected`	Vector of selected predictors.
`freq`	Vector of selection frequencies.
`q`	Size of fitted models in order to control error rate at desired level.

Author(s)

Lukas Meier

References

Meinshausen, N. and Bühlmann, P. (2010) Stability selection (with discussion). *Journal of the Royal Statistical Society: Series B* **72**, 417–473.

Bühlmann, P., Kalisch, M. and Meier, L. (2014) *High-dimensional statistics with a view towards applications in biology*. Annual Review of Statistics and its Applications **1**, 255–278

Examples

```
x <- matrix(rnorm(100 * 1000), nrow = 100, ncol = 1000)
y <- x[,1] * 2 + x[,2] * 2.5 + rnorm(100)
fit.stab <- stability(x, y, EV = 1)
fit.stab
fit.stab$freq[1:10] ## selection frequency of the first 10 predictors
```

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