Package 'sigaR'

September 24, 2012

Type Package

Title statistics for integrative genomics analyses in R

Version 1.0.0

Date 2012-03-19

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Description Facilites the joint analysis of high-throughput data from multiple molecular levels. Contains functions for manipulation of objects, various analysis types, and some visualization.

License GPL (>= 2)

LazyLoad yes

URL http://www.few.vu.nl/~wvanwie

Depends Biobase, CGHbase, corpcor (>= 1.6.2), methods

Imports graphics, marray, MASS, mvtnorm, quadprog, snowfall, stats

biocViews Microarray, Bioinformatics, DifferentialExpression, aCGH,GeneExpression, Pathways

R topics documented:

`sigaR-package` *statistics for integrative genomics analyses in R*

Description

The package facilitates several types of integrative analysis of high-throughput data from various molecular levels. In addition, it includes functions for data management and visualization.

Details

Package:	sigaR
Type:	Package
Version:	1.0
Date:	2011-04-15
License:	What license is it under?
LazyLoad:	yes

Author(s)

Author: Wessel N. van Wieringen Maintainer: Wessel N. van Wieringen <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Van de Wiel, M.A. (2009), "Non-parametric testing for DNA copy number induced differential mRNA gene expression", *Biometrics*, 65(1), 19-29.

Van Wieringen, W.N., Berkhof, J., Van de Wiel, M.A. (2010), "A random coefficients model for regional co-expression associated with DNA copy number", *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue1, Article 25, 1-28.

Van Wieringen, W.N., Van der Vaart, A.W. (2011), "Statistical analysis of the cancer cell's molecular entropy using high-throughput data", *Bioinformatics*, 27(4), 556-563.

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

.RCMloss-method *Internal function*

Description

Internal function.

Note

Not to be called by the user.

---

cghCall2maximumSubset *Maximum subsetting cghCall-objects.*

Description

Limit an cghCall object to a subset of its features, selecting those features with the most deviating copy number signal.

Usage

```
cghCall2maximumSubset(CNdata, featuresAndWeights, chr, bpstart, bpend, ncpus = 1, verbose=TRUE)
```

Arguments

CNdata	Object of class cghCall.
featuresAndWeights	Object of class list. Each list item is a matrix. The first column of this matrix contains the row numbers of features to be maintained in the cghCall-object. The second column contains the weights of each features, to be used in the calculation of the weighted average copy number signal.
chr	Column in the slot featureData of the cghCall-object specifying the chromosome information of the features.
bpstart	Column in the slot featureData of the cghCall-object specifying the start basepair information of the features.
bpend	Column in the slot featureData of the cghCall-object specifying the end basepair information of the features.
ncpus	Number of cpus to be used in computations.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

Per entry of the `featuresAndWeights`-object and per sample the feature with the maximum absolute segmented DNA copy number signal is selected.

Value

Object of class `cghCall`, restricted to the specified subset of features.

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

`matchAnn2Ann`

Examples

```
# load data
data(pollackCN16)

# extract genomic information from ExpressionSet-object
chr <- fData(pollackCN16)[,1]
bpstart <- fData(pollackCN16)[,2]
bpend <- fData(pollackCN16)[,3]

# find unique genomic locations
uniqInfo <- uniqGenomicInfo(chr, bpstart, bpend, verbose = FALSE)

# subset cghCall-object to features with unique genomic locations
pollackCN16 <- cghCall2maximumSubset(pollackCN16, uniqInfo, 1, 2, 3)
```

---

cghCall2order *Genomic ordering of cghCall-objects.*

Description

Orders the features within a `cghCall`-object in accordance with their genomic order.

Usage

```
cghCall2order(CNdata, chr, bpstart, verbose=TRUE)
```

Arguments

CNdata	Object of class cghCall.
chr	Column in the slot featureData of the cghCall-object specifying the chromosome information of the features.
bpstart	Column in the slot featureData of the cghCall-object specifying the start basepair information of the features.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class cghCall, now genomically ordered.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van de Wiel, M.A., Kim, K.I., Vosse, S.J., Van Wieringen, W.N., Wilting, S.M. , Ylstra, B. (2007), "CGHcall: an algorithm for calling aberrations for multiple array CGH tumor profiles", Bioinformatics, 23, 892-894.

See Also

cghCall.

Examples

```
# load data
data(pollackCN16)

# order the copy number data genomically
pollackCN16 <- cghCall2order(pollackCN16, 1, 2)
```

---

cghCall2subset *Subsetting cghCall-objects.*

Description

Limit an cghCall object to a subset of its features.

Usage

```
cghCall2subset(CNdata, featureSubset, verbose=TRUE)
```

Arguments

CNdata	Object of class cghCall.
featureSubset	Object of class numeric, containing the row numbers of features to be maintained in the cghCall-object.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class cghCall, restricted to the specified subset of features.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van de Wiel, M.A., Kim, K.I., Vosse, S.J., Van Wieringen, W.N., Wilting, S.M. , Ylstra, B. (2007), "CGHcall: an algorithm for calling aberrations for multiple array CGH tumor profiles", Bioinformatics, 23, 892-894.

See Also

cghCall.

Examples

```
# load data
data(pollackCN16)

# order the copy number data genomically
pollackCN16 <- cghCall2subset(pollackCN16, c(1:50))
```

---

cghCall2weightedSubset

Weighted subsetting cghCall-objects.

Description

Limit an cghCall object to a subset of its features, using weighted averaging of the copy number signal.

Usage

```
cghCall2weightedSubset(CNdata, featuresAndWeights, chr, bpstart, bpend, ncpus = 1, verbose=TRUE)
```

Arguments

CNdata	Object of class cghCall.
featuresAndWeights	Object of class list. Each list item is a matrix. The first column of this matrix contains the row numbers of features to be maintained in the cghCall-object. The second column contains the weights of each features, to be used in the calculation of the weighted average copy number signal.
chr	Column in the slot featureData of the cghCall-object specifying the chromosome information of the features.
bpstart	Column in the slot featureData of the cghCall-object specifying the start basepair information of the features.

bpend	Column in the slot `featureData` of the `cghCall`-object specifying the end base-pair information of the features.
ncpus	Number of cpus to be used in computations.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class `cghCall`, restricted to the specified subset of features.

Warning

The `phenoData`, `experimentData`, and other slots of the `cghCall`-object are currently not passed on to the subsetted object.

Note

This is a more intricate version of the `cghCall2subset` function. They exists parallel because this function is (much) slower than its counterpart.

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

`cghCall2subset`

Examples

```
# load data
data(pollackCN16)

# extract genomic information from ExpressionSet-object
chr <- fData(pollackCN16)[,1]
bpstart <- fData(pollackCN16)[,2]
bpend <- fData(pollackCN16)[,3]

# find unique genomic locations
uniqInfo <- uniqGenomicInfo(chr, bpstart, bpend, verbose = FALSE)

# subset cghCall-object to features with unique genomic locations
pollackCN16 <- cghCall2weightedSubset(pollackCN16, uniqInfo, 1, 2, 3)
```

CNGEheatmaps *Parellel CN and GE heatmap plotting*

Description

Heatmaps of DNA copy number and gene expression data are plotted together.

Usage

```
CNGEheatmaps(CNdata, GEdata, location = "mode", colorbreaks = "equiquantiles")
```

Arguments

CNdata	Object of class cghCall, containing (among others) annotion and call probabilities. Features should be matched with those of the accompanying ExpressionSet-object (as may be done using the matchCGHcall2ExpressionSet-function).
GEdata	Object of class ExpressionSet. Features should be matched with those of the accompanying cghCall-object (as may be done using the matchCGHcall2ExpressionSet-function).
location	Parameter (median, mean, or mode) specifying how the center of the gene expression heatmap color-scheme is determined.
colorbreaks	Parameter specifying how the color distribution of the gene expression heatmap is determined, either equiquantiles or equidistant.

Details

The DNA copy number data heatmap is generated as follows. The DNA copy number data are used to determine the genomic segments exhibiting no difference in DNA copy number between the array elements that map to that segment. This resembles the dimension reduction technique employed in the CGHregions-package. Consequently, within a segment the DNA copy number for one sample is constant, but may vary between samples. Note that a region may comprise of a whole chromosome, but also of a focal amplication. It is the DNA copy number signature of the segments that is depicted in the heatmap of the DNA copy number data.

For the gene expression heatmap segments as constructed for the array CGH data are adopted. For each segment-sample combination the expression levels of the genes that map to that segment are averaged. Next, the gene expression data is also collapsed to the segment format. It is this collapsed and averaged expression data that is depicted in the corresponding heatmap.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van de Wiel, M.A., Van Wieringen, W.N. (2007), "CGHregions: dimension reduction for array CGH data with minimal information loss", *Cancer Informatics*, 2, 55-63.

Van Wieringen, W.N., Van de Wiel, M.A. (2009), "Non-parametric testing for DNA copy number induced differential mRNA gene expression", *Biometrics*, 65(1), 19-29.

See Also

cghCall, ExpressionSet, matchCGHcall2ExpressionSet, profilesPlot,

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# plot heatmaps
CNGEheatmaps(pollackCN16, pollackGE16, location = "mode", colorbreaks = "equiquantiles")
```

---

entropyTest *One-sided two-sample test for entropy comparison*

Description

A one-sided two-sample test compares the entropy of a (high-dimensional) multivariate random variable between two groups. The test is one-sided: one group is a priori suspected to have a larger entropy. The null distribution is obtained via an efficient permutation resampling algorithm.

Usage

```
entropyTest(Y, id, nPerm = 1000, method = "normal", k0 = 1, k1 = 1, center = TRUE, lowCiThres=0.
```

Arguments

Y	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits.
id	An indicator variable for the two groups to be compared. The groups should be coded as 0 and 1. There is an asymmetric interest in the groups: the group indicated by 1 is believed to exhibit a larger entropy.
nPerm	Number of permutations.
method	Distributional assumption under which entropy is to be estimated.
k0	k-nearest neighbor parameter for group comprising of samples indicated by a zero in the indicator variable id.
k1	k-nearest neighbor parameter for group comprising of samples indicated by a one in the indicator variable id.
center	Logical indicator: should the rows of Y be centered at zero?
lowCiThres	A value between 0 and 1. Determines speed of efficient p-value calculation. If the probability of a p-value being below lowCiThres is smaller than 0.001 (read: the test is unlikely to become significant), the permutation analysis is terminated and a p-value of 1.00 is reported.
ncpus	Number of cpus used for the permutations.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of entTest-class.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Van der Vaart, A.W. (2011), "Statistical analysis of the cancer cell's molecular entropy using high-throughput data", *Bioinformatics*, 27(4), 556-563.

Van Wieringen, W.N., Van de Wiel, M.A., Van der Vaart, A.W. (2008), "A test for partial differential expression", *Journal of the American Statistical Association*, 103(483), 1039-1049.

See Also

hdEntropy

Examples

```
# load data
data(pollackGE16)
Y <- exprs(pollackGE16)

# assign samples to groups
id <- sample(c(0,1), 41, replace=TRUE)

# perform testing and print test results
testRes <- entropyTest(t(Y), id, nPerm = 5, method="knn")
summary(testRes)
```

---

entTest-class *Class "entTest" for storing the results of the function entropyTest.*

Description

The class entTest is the output of a call to entropyTest. It stores results from a hypothesis test.

Slots

statistic: Object of class "numeric". Observed test statistic (i.e., estimated mutual information).

p.value: Object of class "numeric". P-value for the mutual information test.

null.dist: Object of class "numeric". The permutation null distribution for the test statistic.

nperm: Object of class "numeric". Number of permutation used for p-value calculation.

remark: Object of class "character". Tells whether the permutation algorithm was terminated prematurely or not.

Methods

summary signature(object = "entTest"): Prints the test results.

Author(s)

Wessel van Wieringen: <w.vanwieringen@vumc.nl>

See Also

entTest

Examples

```
showClass("entTest")
```

---

expandMatching2singleIDs

Expand matching to single entries

Description

In case a feature of platform 1 has been matched to multiple features of another platform, instead of averaging the data from these features, one may consider maintaining all features, each matched individually the feature of platform 1. This function modifies the results from the matching function matchAnn2Ann to facilitate this. The result can than directly be used in the subsetting functions cghCall2weightedSubset and ExpressionSet2weightedSubset.

Usage

```
expandMatching2singleIDs(matchedIDs)
```

Arguments

matchedIDs	An object of class list, as returned by the matchAnn2Ann-function.

Value

An object of class list, similar to that returned by the matchAnn2Ann-function.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

matchAnn2Ann, cghCall2weightedSubset, ExpressionSet2weightedSubset.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# extract genomic information from cghCall-object
chr1 <- fData(pollackCN16)[,1]
bpstart1 <- fData(pollackCN16)[,2]
bpend1 <- fData(pollackCN16)[,3]

# extract genomic information from ExpressionSet-object
chr2 <- fData(pollackGE16)[,1]
bpstart2 <- fData(pollackGE16)[,2]
bpend2 <- fData(pollackGE16)[,3]

# match features from both platforms
matchedFeatures <- matchAnn2Ann(chr1, bpstart1, bpend1, chr2, bpstart2, bpend2, method = "distance", maxDis

# expand
matchedFeatures <- expandMatching2singleIDs(matchedFeatures)
```

ExpressionSet2order *Genomic ordering of ExpressionSet-objects.*

Description

Orders the features within a ExpressionSet-object in accordance with their genomic order.

Usage

```
ExpressionSet2order(GEdata, chr, bpstart, verbose=TRUE)
```

Arguments

GEdata	Object of class ExpressionSet.
chr	Column in the slot featureData of the ExpressionSet-object specifying the chromosome information of the features.
bpstart	Column in the slot featureData of the ExpressionSet-object specifying the start basepair information of the features.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class ExpressionSet, now genomically ordered.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

See Also

ExpressionSet.

Examples

```
# load data
data(pollackGE16)

# order the copy number data genomically
pollackGE16 <- ExpressionSet2order(pollackGE16, 1, 2)
```

ExpressionSet2subset *Subsetting ExpressionSet-objects.*

Description

Limit an ExpressionSet object to a subset of its features.

Usage

```
ExpressionSet2subset(GEdata, featureSubset, verbose=TRUE)
```

Arguments

GEdata	Object of class ExpressionSet.
featureSubset	Object of class numeric, containing the row numbers of features to be maintained in the ExpressionSet-object.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class ExpressionSet, restricted to the specified subset of features.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

See Also

ExpressionSet.

Examples

```
# load data
data(pollackGE16)

# order the copy number data genomically
pollackGE16 <- ExpressionSet2subset(pollackGE16, c(1:50))
```

ExpressionSet2weightedSubset
Weighted subsetting ExpressionSet-objects.

Description

Limit an ExpressionSet object to a subset of its features, using weighted averaging of the expression signal.

Usage

```
ExpressionSet2weightedSubset(GEdata, featuresAndWeights, chr, bpstart, bpend, ncpus = 1, verbose
```

Arguments

GEdata	Object of class ExpressionSet.
featuresAndWeights	Object of class list. Each list item is a matrix. The first column of this matrix contains the row numbers of features to be maintained in the ExpressionSet-object. The second column contains the weights of each features, to be used in the calculation of the weighted average gene expression signal.
chr	Column in the slot featureData of the ExpressionSet-object specifying the chromosome information of the features.
bpstart	Column in the slot featureData of the ExpressionSet-object specifying the start basepair information of the features.
bpend	Column in the slot featureData of the ExpressionSet-object specifying the end basepair information of the features.
ncpus	Number of cpus to be used in computations.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

Annotation information of features with multiplicity larger than one is compressed as follows. It is assumed that all features map to the same chromosome, leaving no ambiguity. The start base pair of the "new" feature is the smallest start base pair of features from which it has been formed. The end base pair of the "new" feature is the largest end base pair of features from which it has been formed.

Value

Object of class ExpressionSet, restricted to the specified subset of features.

Warning

The phenoData, experimentData, and other slots of the ExpressionSet-object are currently not passed on to the subsetted object.

Note

This is a more intricate version of the ExpressionSet2subset function. They exists parallel because this function is much slower than its counterpart.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

`ExpressionSet2subset`

Examples

```
# load data
data(pollackGE16)

# extract genomic information from ExpressionSet-object
chr <- fData(pollackGE16)[,1]
bpstart <- fData(pollackGE16)[,2]
bpend <- fData(pollackGE16)[,3]

# find unique genomic locations
uniqInfo <- uniqGenomicInfo(chr, bpstart, bpend, verbose = FALSE)

# subset ExpressionSet-object to features with unique genomic locations
pollackGE16 <- ExpressionSet2weightedSubset(pollackGE16, uniqInfo, 1, 2, 3)
```

`getSegFeatures` *Identical signature features selection from cghCall-object.*

Description

Given an example, selects features (contiguous to the example) with the same signature (as the example) across samples from an `cghCall`-object.

Usage

```
getSegFeatures(featureNo, CNdata, verbose=TRUE)
```

Arguments

`featureNo`	Row number of example feature.
`CNdata`	Object of class `cghCall`.
`verbose`	Logical indicator: should intermediate output be printed on the screen?

Value

Object of class `numeric`, containing the row numbers of those contiguous features with the same segmented log2-ratio signatures as `featureNo` across samples.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Berkhof, J., Van de Wiel, M.A. (2010), "A random coefficients model for regional co-expression associated with DNA copy number", *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue1, Article 25, 1-28.

See Also

cghCall, RCMestimation.

Examples

```
# load data
data(pollackCN16)

# feature of interest
featureNo <- 7

# extract all features with identical copy number signature (over the samples)
getSegFeatures(featureNo, pollackCN16)
```

---

hdEntropy *Entropy estimation.*

Description

The (differential) entropy of a high-dimensional multivariate random variable is estimated from a (high-dimensional matrix) under a normality or k-NN distributional assumption.

Usage

```
hdEntropy(Y, method = "normal", k = 1, center = TRUE, indKnn = TRUE)
```

Arguments

Y	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits.
method	Distributional assumption under which entropy is to be estimated.
k	k-nearest neighbor parameter.
center	Logical indicator: should the rows of Y be centered at zero?
indKnn	Logical indicator: should samples' individual contributions to the k-NN entropy be reported?

Value

The entropy estimate is returned as a numeric.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Van der Vaart, A.W. (2011), "Statistical analysis of the cancer cell's molecular entropy using high-throughput data", *Bioinformatics*, 27(4), 556-563.

See Also

entropyTest.

Examples

```
data(pollackGE16)
hdEntropy(t(exprs(pollackGE16)), method="knn")
```

---

hdMI *Mutual information estimation.*

Description

The mutual information between two high-dimensional mutivariate random variables is estimated from two (high-dimensional matrix) under a normality or k-NN distributional assumption.

Usage

```
hdMI(Y, X, method = "normal", k = 1, center = TRUE, rescale = TRUE)
```

Arguments

Y	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits.
X	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits. The number of columns of X must be identical to that of Y.
method	Distributional assumption under which mutual information is to be estimated.
k	k-nearest neighbor parameter.
center	Logical indicator: should the rows of Y and X be centered at zero? Applied only under the normality assumption.
rescale	Logical indicator: should Y and X be rescaled to have the same scale? Applied only under the k-NN assumption.

Value

The mutual information estimate is returned as a numeric.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Van der Vaart, A.W. (2011), "Statistical analysis of the cancer cell's molecular entropy using high-throughput data", *Bioinformatics*, 27(4), 556-563.

See Also

mutInfTest.

Examples

```
data(pollackCN16)
data(pollackGE16)
hdMI(t(exprs(pollackGE16)), t(copynumber(pollackCN16)), method="knn")
```

---

matchAnn2Ann *Genomic location matching of two sets of features*

Description

Genomic location matching of two sets of features

Usage

```
matchAnn2Ann(chr1, bpstart1, bpend1, chr2, bpstart2, bpend2, method = "distance", maxDist = 1000
```

Arguments

chr1	Object of class numeric containing chromosome information of features from set 1.
bpstart1	Object of class numeric containing start base pair information of features from set 1. Of same length as chr1.
bpend1	Object of class numeric containing end base pair information of features from set 1. Of same length as chr1.
chr2	Object of class numeric containing chromosome information of features from set 2.
bpstart2	Object of class numeric containing start base pair information of features from set 2. Of same length as chr2.
bpend2	Object of class numeric containing end base pair information of features from set 2. Of same length as chr2.
method	Matching method to be applied, either "distance" or "overlap". See below for details.
maxDist	Maximum number of bases two features are allowed to be separated for a match. Only used in combination with method="distance".
minPerc	Minimum percentage of overlap between two features required for a match. Only used in combination with method="overlap".
reference	Platform that is taken as a reference in the calculation of the percentage, should equal 1 or two, referring to the platform.
ncpus	Number of cpus to be used in the computation.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

The features of set 1 (chr1, bpstart1, bpend1) are matched to the features of set 2 (chr2, bpstart2, bpend2). That is, for every feature in set 2, features in set 1 are sought.

In case method="distance", the midpoint of set 1 and set 2 features are calculated and for each feature of set 2 all features of set 1 with midpoints not further than maxDist are selected. If there are no features in set 1 satisfying this criterion, the feature of set 2 that could not be matched is discarded.

If method="overlap", each feature of set 1 is matched to the feature of set 2 on the basis of the percentage of overlap. All features of set 1 with a percentage exceeding minPerc are selected. In case no feature in set 1 had any overlap with the features from set 2, the feature of set 2 that could not be matched is discarded.

Value

An object of class list. Each list item is a three-column matrix with the matched features information. The first column contains feature numbers of set 1 in the order as supplied. The second column contains feature numbers of set 2 in the order as supplied. Each row thus has two entries. The first entry contains the feature number of set 1 that has been matched to second entry, representing the feature number of set 2. The third column contains either the percentage of overlap (method="overlap") or the distance between the the midpoints of the two features (method="distance").

Warning

Base pair information of features from both sets should be on the same scale!

Features with incomplete annotation information are removed before matching. For clarity, they are not included in the object with matched features.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

matchCGHcall2ExpressionSet

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# extract genomic information from cghCall-object
chr1 <- fData(pollackCN16)[,1]
bpstart1 <- fData(pollackCN16)[,2]
bpend1 <- fData(pollackCN16)[,3]
```

```
# extract genomic information from ExpressionSet-object
chr2 <- fData(pollackGE16)[,1]
bpstart2 <- fData(pollackGE16)[,2]
bpend2 <- fData(pollackGE16)[,3]

# match features from both platforms
matchedFeatures <- matchAnn2Ann(chr1, bpstart1, bpend1, chr2, bpstart2, bpend2, method = "distance", maxDis
```

`matchCGHcall2ExpressionSet`

Genomic location matching of CN and GE data

Description

Integrative CN-GE analysis requires the copy number data of all genes on the expression array to be available. `intCNGEan.match` matches the features of the copy number platform to the genes of the expression array. This is done using their genomic locations on the basis of either proximity or overlap.

Usage

```
matchCGHcall2ExpressionSet(CNdata, GEdata, CNchr, CNbpstart, CNbpend, GEchr, GEbpstart, GEbpend,
```

Arguments

`CNdata`	Object of class `cghCall`, containing (among others) annotion and call probabilities.
`GEdata`	Object of class `ExpressionSet`.
`CNchr`	Column in the slot `featureData` of the `cghCall`-object specifying the chromosome information of the features.
`CNbpstart`	Column in the slot `featureData` of the `cghCall`-object specifying the start basepair information of the features.
`CNbpend`	Column in the slot `featureData` of the `cghCall`-object specifying the end basepair information of the features.
`GEchr`	Column in the slot `featureData` of the `ExpressionSet`-object specifying the chromosome information of the features.
`GEbpstart`	Column in the slot `featureData` of the `ExpressionSet`-object specifying the start basepair information of the features.
`GEbpend`	Column in the slot `featureData` of the `ExpressionSet`-object specifying the end basepair information of the features.
`method`	Matching method to be applied, either `"distance"`, `"overlap"` or `"overlapPlus"`. See below for details.
`reference`	Platform that is taken as a reference in the calculation of the percentage, should equal 1 or two, referring to the platform.
`ncpus`	Number of cpus to be used in the computation.
`verbose`	Logical indicator: should intermediate output be printed on the screen?

Details

Ideally full annotation information (chromosome number, start base pair, end base pair) for both copy number and gene expression data is available. In case only start base pair information is available, let `CNbpend` and `GEbpend` refer to the same columns as `CNbpstart` and `GEbpstart`. Base pair information of copy number and expression data should be on the same scale.

Matching occurs on the basis of genomic locations. In case `method="distance"`, the midpoint of CN and GE features are calculated and for each gene on the expression array the closest feature of the copy number platform is selected. If `method="overlap"`, each gene in the `ExpressionSet`-object is matched to the feature from the copy number platform with the maximum percentage of overlap. If the maximum percentage of overlap equals zero, the gene is not included in the matched objects. If `method="overlapPlus"`, the features are first matched by their percentage of overlap (as with the `method="overlap"`-option). For all non-matched GE features its closest two CN features (one down- and one upstream) are determined. If the copy number signature of these two CN features is identical, intrapolation seems reasonable, and and the GE feature is matched to the closest of these two CN features. Hence, `method="overlapPlus"` makes use of the copy number data, consequently, matching may be different for different data sets.

Value

A two-column matrix with the matched features entries. The first column contains feature numbers of the `cghCall`-object. The second column contains feature numbers of the `ExpressionSet`-object. Each row thus has two entries. The first entry contains the feature number of the `cghCall`-object that has been matched to second entry, representing the feature number of the `ExpressionSet`-object.

Warning

Features with incomplete annotation information are removed before matching. For clarity, they are not included in the objects with matched features.

Note

The matching process implemented here is different from the one implemented in the (depreciated) `ACEit`-package (Van Wieringen et al., 2006).

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

References

Van Wieringen, W.N., Belien, J.A.M., Vosse, S.J., Achame, E.M., Ylstra, B. (2006), "ACE-it: a tool for genome-wide integration of gene dosage and RNA expression data", *Bioinformatics*, 22(15), 1919-1920.

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

`cghCall`, `ExpressionSet`

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# match features from both platforms
featureMatch <- matchCGHcall2ExpressionSet(pollackCN16, pollackGE16, 1, 2, 3, 1, 2, 3)
```

`merge2cghCalls` *Merge two cghCall-objects into one cghCall-object*

Description

Merge two cghCall-objects into one cghCall-object.

Usage

```
merge2cghCalls(CNdata1, CNdata2, verbose=TRUE)
```

Arguments

`CNdata1`	Object of class `cghCall`.
`CNdata2`	Object of class `cghCall`.
`verbose`	Logical indicator: should intermediate output be printed on the screen?

Details

Data of the two objects is assumed to originate from the same samples, and are presented in the same order.

Only the experimental data and annotation information is inherited by the merged object.

Value

Object of class `cghCall`, restricted to the specified subset of features.

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

References

Van de Wiel, M.A., Kim, K.I., Vosse, S.J., Van Wieringen, W.N., Wilting, S.M. , Ylstra, B. (2007), "CGHcall: an algorithm for calling aberrations for multiple array CGH tumor profiles", Bioinformatics, 23, 892-894.

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

`cghCall`.

Examples

```
# load data
data(pollackCN16)

# create two cghCall-objects
ids1 <- sample(1:dim(pollackCN16)[1], 10)
CNdata1 <- pollackCN16[ids1,]
CNdata2 <- pollackCN16[-ids1,]

# order the copy number data genomically
pollackCN16 <- merge2cghCalls(CNdata1, CNdata2)
```

`merge2ExpressionSets` *Merge two ExpressionSet-objects into one ExpressionSet-object*

Description

Merge two ExpressionSet-objects into one ExpressionSet-object

Usage

```
merge2ExpressionSets(GEdata1, GEdata2, verbose=TRUE)
```

Arguments

`GEdata1`	Object of class `ExpressionSet`.
`GEdata2`	Object of class `ExpressionSet`.
`verbose`	Logical indicator: should intermediate output be printed on the screen?

Details

Data of the two objects is assumed to originate from the same samples, and are presented in the same order.

Only the experimental data and annotation information is inherited by the merged object.

Value

Object of class `ExpressionSet`, restricted to the specified subset of features.

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

References

Van de Wiel, M.A., Kim, K.I., Vosse, S.J., Van Wieringen, W.N., Wilting, S.M. , Ylstra, B. (2007), "CGHcall: an algorithm for calling aberrations for multiple array CGH tumor profiles", Bioinformatics, 23, 892-894.

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

ExpressionSet.

Examples

```
# load data
data(pollackGE16)

# create two cghCall-objects
ids1 <- sample(1:dim(pollackGE16)[1], 10)
GEdata1 <- pollackGE16[ids1,]
GEdata2 <- pollackGE16[-ids1,]

# order the copy number data genomically
pollackGE16 <- merge2ExpressionSets(GEdata1, GEdata2)
```

---

miTest-class *Class "miTest" for storing the results of the function mutInfTest.*

Description

The class miTest is the output of a call to mutInfTest. It stores results from a hypothesis test.

Slots

statistic: Object of class "numeric". Observed test statistic (i.e., estimated mutual information).

p.value: Object of class "numeric". P-value for the mutual information test.

null.dist: Object of class "numeric". The permutation null distribution for the test statistic.

nperm: Object of class "numeric". Number of permutation used for p-value calculation.

remark: Object of class "character". Tells whether the permutation algorithm was terminated prematurely or not.

Methods

summary signature(object = "miTest"): Prints the test results.

Author(s)

Wessel van Wieringen: <w.vanwieringen@vumc.nl>

See Also

mutInfTest

Examples

```
showClass("miTest")
```

mutInfTest *Test for mutual information*

Description

A test evaluates the significance of the mutual information between two (high-dimensional) multivariate random variables. The null distribution is obtained via an efficient permutation resampling algorithm.

Usage

```
mutInfTest(Y, X, nPerm = 1000, method = "normal", k = 1, center = TRUE, rescale = TRUE, lowCiThr
```

Arguments

Y	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits.
X	(High-dimensional) matrix. Columns are assumed to represent the samples, and rows represent the samples' genes or traits. The number of columns of X must be identical to that of Y.
nPerm	Number of permutations.
method	Distributional assumption under which mutual information is to be estimated.
k	k-nearest neighbor parameter.
center	Logical indicator: should the rows of Y and X be centered at zero? Applied only under the normality assumption.
rescale	Logical indicator: should Y and X be rescaled to have the same scale? Applied only under the k-NN assumption.
lowCiThres	A value between 0 and 1. Determines speed of efficient p-value calculation. If the probability of a p-value being below lowCiThres is smaller than 0.001 (read: the test is unlikely to become significant), the permutation analysis is terminated and a p-value of 1.00 is reported.
ncpus	Number of cpus used for the permutations.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

Object of miTest-class.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Van der Vaart, A.W. (2011), "Statistical analysis of the cancer cell's molecular entropy using high-throughput data", *Bioinformatics*, 27(4), 556-563.

Van Wieringen, W.N., Van de Wiel, M.A., Van der Vaart, A.W. (2008), "A test for partial differential expression", *Journal of the American Statistical Association*, 103(483), 1039-1049.

See Also

hdMI

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)
Y <- t(exprs(pollackGE16))
X <- t(copynumber(pollackCN16))

# perform testing and print test results
testRes <- mutInfTest(Y, X, nPerm = 1000)
summary(testRes)
```

---

nBreakpoints *Number of breakpoints*

Description

The number of samples with at least one breakpoint is calculated for each transcipt.

Usage

```
nBreakpoints(featuresAndWeights, CNdata)
```

Arguments

featuresAndWeights	Object of class list. Each list item is a matrix. The first column of this matrix contains the row numbers of features to be maintained in subsetting of the cghCall-object. The second column contains the weights of each features, to be used in the calculation of the weighted average copy number signal.
CNdata	Object of class cghCall

Details

For each item of the object featuresAndWeights the segmented data from the cghCall-object is used to determine whether a sample exhibits a breakpoint for this transcript.

Value

Object of class numeric containing the number of samples with at least one breakpoint. It is of the same length as the featuresAndWeights-object.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

matchAnn2Ann.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# extract genomic information from cghCall-object
chr1 <- fData(pollackCN16)[,1]
bpstart1 <- fData(pollackCN16)[,2]
bpend1 <- fData(pollackCN16)[,3]

# extract genomic information from ExpressionSet-object
chr2 <- fData(pollackGE16)[,1]
bpstart2 <- fData(pollackGE16)[,2]
bpend2 <- fData(pollackGE16)[,3]

# match features from both platforms
matchedIDs <- matchAnn2Ann(chr1, bpstart1, bpend1, chr2, bpstart2, bpend2, method = "distance", maxDist = 1

# extract ids for object subsetting
matchedIDsCN <- lapply(matchedIDs, function(Z){ return(Z[, -1, drop=FALSE]) })

# calculate the number of breakpoints
nBreakpoints(matchedIDsCN, pollackCN16)
```

---

pollackCN16 *Breast cancer data (copy number)*

Description

Copy number data of chromosome 16 the breast cancer data set. Called using CGHcall with default settings, contains 240 features and 41 samples.

Usage

```
data(pollackCN16)
```

Format

An object of class cghCall.

Source

Pollack, J. R., Sorlie, T., Perou, C. M., Rees, C. A., Jeffrey, S. S., Lonning, P. E., Tibshirani, R., Botstein, D., Borresen- Dale, A. L., Brown, P. O. (2002), "Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors", *PNAS*, 99, 12963-12968.

References

Van de Wiel, M. A., Kim, K. I., Vosse, S. J., Van Wieringen, W. N., Wilting, S. M., Ylstra, B. (2007), "CGHcall: Calling aberrations for array CGH tumor profiles", *Bioinformatics*, 23, 892-894.

Examples

```
data(pollackCN16)
```

---

pollackGE16 *Breast cancer data (gene expression)*

Description

Gene expression data of chromosome 16 of the breast cancer data set; contains 240 features and 41 samples.

Usage

```
data(pollackGE16)
```

Format

An object of class `ExpressionSet`.

Source

Pollack, J.R., Sorlie, T., Perou, C.M., Rees, C.A., Jeffrey, S.S., Lonning, P.E., Tibshirani, R., Botstein, D., Borresen- Dale, A.L., Brown, P.O. (2002), "Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors", *PNAS*, 99, 12963-12968.

Examples

```
data(pollackGE16)
```

profilesPlot *CN-GE profiles plot*

Description

Plots a sample's copy number and gene expression data side-by-side. This visualizes the relation between CN and GE within an individual sample.

Usage

```
profilesPlot(CNdata, GEdata, sampleNo, chr = 0, verbose=TRUE)
```

Arguments

CNdata	Object of class cghCall, containing (among others) annotion and call probabilities. Features should be matched with those of the accompanying ExpressionSet-object (as may be done using the matchCGHcall2ExpressionSet-function).
GEdata	Object of class ExpressionSet. Features should be matched with those of the accompanying cghCall-object (as may be done using the matchCGHcall2ExpressionSet-function).
sampleNo	Sample number of sample to be plotted. Corresponds to the order in which samples appear the CNdata- and GEdata-objects.
chr	Chromosome number for which the profiles are to be plotted. Default chr=0 for whole genome plotting.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

The blue lines in the gene expression profile plot are the median expressions of genes that map to the same copy number segment.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

See Also

cghCall, ExpressionSet

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# plot CN and GE profiles alongside
profilesPlot(pollackCN16, pollackGE16, 23, 16)
```

RCMestimation *Fitting of the random coefficients model.*

Description

The parameters of the random coefficients model are estimated by means of the maximum likelihood method. The implemented maximum likelihood procedure has been optimized with respect to computational efficiency and memory usage.

Usage

```
RCMestimation(Y, X, R, hypothesis = "H2", shrinkType = "none", estType = "normal", corType = "un
```

Arguments

Y	The matrix containing the (e.g., expression) data (number of columns equal to number of features, number of rows equal to number of samples).
X	The design matrix (number of rows equal to number of samples, number of columns equal to number of covariates).
R	The linear constraint matrix (number of columns equal to the number of covariates).
hypothesis	The hypothesis under which the model is fitted: H0 (H0 : R beta = 0 & tau2 = 0), H1 (H1 : R beta >= 0 & tau2 = 0), H2 (H2 : R beta >= 0 & tau2 >= 0).
shrinkType	The type of shrinkage to be applied to the error variances: none (shrinkage parameter is set equal to zero: no shrinkage), opt (shrinkage parameter is chosen to minimize the mean squared error criterion) or full (shrinkage parameter is set equal to one).
estType	Type of estimation, either normal (non-robust) or robust.
corType	Correlation structure to be used, either unif or ar1.
maxNoIt	Maximum number of iterations in the ML procedure.
minSuccDist	Minimum distance between estimates of two successive iterations to be achieved.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

Details on the type of random coefficients model that is actually fitted are specified in the reference below.

Value

Object of class rcmFit.

Note

In case a covariate for the intercept is included in the design matrix X we strongly recommend the center, per feature, the data around zero.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Berkhof, J., Van de Wiel, M.A. (2010), "A random coefficients model for regional co-expression associated with DNA copy number", *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue1, Article 25, 1-28.

See Also

RCMrandom, RCMtest, rcmTest.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# select features belonging to a region
ids <- getSegFeatures(20, pollackCN16)

# extract segmented log2 ratios of the region
X <- t(segmented(pollackCN16)[ids[1], , drop=FALSE])

# extract segmented log2 ratios of the region
Y <- exprs(pollackGE16)[ids,]

# center the expression data (row-wise)
Y <- t(Y - apply(Y, 1, mean))

# specify the linear constraint matrix
R <- matrix(1, nrow=1)

# fit the random coefficients model to the random data
RCMresults <- RCMestimation(Y, X, R)
```

---

rcmFit-class *Class "rcmFit" for storing the results of the function RCMestimation.*

Description

The class rcmFit is the output of a call to RCMestimation. It stores results from fitting a random coefficients model.

Slots

betas: Object of class "numeric". Vector of estimated global regression coefficients for each of the covariates in the design matrix.

tau2s: Object of class "numeric". Vector of estimated regression coefficient variances for each of the covariates in the design matrix X.

sigma2s: Object of class "numeric". Vector of estimated error variances for all genes.

rho: Object of class "numeric". Estimated correlation parameter between the error of two contiguous features.

av.sigma2s: Object of class "numeric". Average of the unshrunken estimated error variances.

`shrinkage`: Object of class `"numeric"`. Applied shrinkage parameters in fitting the model.

`loglik`: Object of class `"numeric"`. The log-likelihood of the fitted model.

`corType`: Object of class `"character"`. Correlation structure of the error used.

`X`: Object of class `"matrix"`. The design matrix.

Methods

.RCMloss `signature(object = "rcmFit")`: Calculates the log-likelihood associated with the fitted model.

RCMrandom `signature(object = "rcmFit")`: Samples from the distribution induced by the fitted model.

summary `signature(object = "rcmFit")`: Prints the estimation result.

Author(s)

Wessel N. van Wieringen: `<w.vanwieringen@vumc.nl>`

See Also

`RCMestimation`, `RCMrandom`.

Examples

```
showClass("rcmFit")
```

`RCMrandom` *Random data from the random coefficients model.*

Description

The significance of hypotheses regarding parameters of the random coefficients model is assessed by means of the parametric bootstrap. Hereto random data from the fitted model under the null hypothesis of interest are drawn. This function provides.

Usage

```
RCMrandom(object)
```

Arguments

`object`	Object of class `rcmFit`.

Details

Details on the type of random coefficients model from which data are drawn are specified in the reference below.

Value

A `matrix` of dimension (number of genes) times (number of samples).

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Berkhof, J., Van de Wiel, M.A. (2010), "A random coefficients model for regional co-expression associated with DNA copy number", *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue1, Article 25, 1-28.

See Also

RCMestimation, rcmFit.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# select features belonging to a region
ids <- getSegFeatures(20, pollackCN16)

# extract segmented log2 ratios of the region
X <- t(segmented(pollackCN16)[ids[1], , drop=FALSE])

# extract segmented log2 ratios of the region
Y <- exprs(pollackGE16)[ids,]

# center the expression data (row-wise)
Y <- t(Y - apply(Y, 1, mean))

# specify the linear constraint matrix
R <- matrix(1, nrow=1)

# fit the random coefficients model to the random data
RCMresults <- RCMestimation(Y, X, R)

# draw random data
Yrandom <- RCMrandom(RCMresults)
```

RCMrandom-method *Methods for Function RCMrandom*

Description

Methods for function RCMrandom

Methods

signature(object = "rcmFit") Draws random data of same dimension as data on which the rcmFit-object was fitted.

RCMtest *Hypothesis testing within the random coefficient model.*

Description

Function that evaluates various hypothesis within the random coefficients model via bootstrap re-sampling.

Usage

```
RCMtest(Y, X, R, testType = "I", nBoot = 100, lowCiThres = 0.1, shrinkType = "none", estType = "
```

Arguments

Y	The matrix containing the (e.g., expression) data (number of columns equal to number of features, number of rows equal to number of samples).
X	The design matrix (number of rows equal to number of samples, number of columns equal to number of covariates).
R	The linear constraint matrix (number of columns equal to the number of covariates).
testType	The hypothesis to be tested: I (H0 : R beta = 0 & tau2 = 0) vs. (H2 : R beta >= 0 V tau2 >= 0), II (H0 : R beta = 0 & tau2 = 0) vs. (H1 : R beta >= 0 & tau2 = 0), III (H1 : R beta >= 0 & tau2 = 0) vs. (H2 : R beta >= 0 & tau2 >= 0).
nBoot	Number of bootstraps.
lowCiThres	A value between 0 and 1. Determines speed of efficient p-value calculation. If the probability of a p-value being below lowCiThres is smaller than 0.001 (read: the test is unlikely to become significant), bootstrapping is terminated and a p-value of 1.00 is reported.
shrinkType	The type of shrinkage to be applied to the error variances: none (shrinkage parameter is set equal to zero: no shrinkage), opt (shrinkage parameter is chosen to minimize the mean squared error criterion) or full (shrinkage parameter is set equal to one).
estType	Type of estimation, either normal (non-robust) or robust.
corType	Correlation structure to be used, either unif or ar1.
maxNoIt	Maximum number of iterations in the ML procedure.
minSuccDist	Minimum distance between estimates of two successive iterations to be achieved.
returnNullDist	Logical indicator: should the null distribution be returned?
ncpus	Number of cpus used for the bootstrap.
verbose	Logical indicator: should intermediate output be printed on the screen?

Details

Details on the type of random coefficients model that is actually fitted are specified in the reference below.

Value

Object of class rcmTest.

Warning

In case a covariate for the intercept is included in the design matrix `X` we strongly recommend the center, per feature, the data around zero.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Berkhof, J., Van de Wiel, M.A. (2010), "A random coefficients model for regional co-expression associated with DNA copy number", *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue1, Article 25, 1-28.

Van Wieringen, W.N., Van de Wiel, M.A., Van der Vaart, A.W. (2008), "A test for partial differential expression", *Journal of the American Statistical Association*, 103(483), 1039-1049.

See Also

`RCMestimation`, `RCMrandom`, `rcmTest`.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# select features belonging to a region
ids <- getSegFeatures(20, pollackCN16)

# extract segmented log2 ratios of the region
X <- t(segmented(pollackCN16)[ids[1], , drop=FALSE])

# extract segmented log2 ratios of the region
Y <- exprs(pollackGE16)[ids,]

# center the expression data (row-wise)
Y <- t(Y - apply(Y, 1, mean))

# specify the linear constraint matrix
R <- matrix(1, nrow=1)

# fit the random coefficients model to the random data
RCMresults <- RCMestimation(Y, X, R)

# test for significance of effect of X on Y
RCMtestResults <- RCMtest(Y, X, R, nBoot=2)
summary(RCMtestResults)
```

`rcmTest-class` *Class "rcmTest" for storing the results of the function RCMtest.*

Description

The class `rcmTest` is the output of a call to `RCMtest`. It stores results from a hypothesis test.

Slots

`statistic`: Object of class `"numeric"`. Observed test statistic (i.e., estimated mutual information).

`p.value`: Object of class `"numeric"`. P-value for the mutual information test.

`betas`: Object of class `"numeric"`. Vector of estimated global regression coefficients for each of the covariates in the design matrix.

`tau2s`: Object of class `"numeric"`. Vector of estimated regression coefficient variances for each of the covariates in the design matrix.

`sigma2s`: Object of class `"numeric"`. Vector of estimated error variances for all features.

`rho`: Object of class `"numeric"`. Estimated correlation parameter between the error of two contiguous features.

`av.sigma2s`: Object of class `"numeric"`. Average of the unshrunken estimated error variances.

`shrinkage`: Object of class `"numeric"`. Type of shrinkage applied in the estimation.

`loglik`: Object of class `"numeric"`. The log-likelihood of the fitted model.

`nBoot`: Object of class `"numeric"`. Number of bootstraps used for p-value calculation.

`corType`: Object of class `"character"`. Correlation structure used in the fitted model.

`null.dist`: Object of class `"numeric"`. The permutation null distribution for the test statistic.

`remark`: Object of class `"character"`. Tells whether the bootstrapping was terminated prematurely or not.

Methods

summary `signature(object = "rcmTest")`: Prints the test results.

Author(s)

Wessel van Wieringen: `<w.vanwieringen@vumc.nl>`

See Also

`RCMtest`

Examples

```
showClass("rcmTest")
```

splitMatchingAtBreakpoints
Split matching at breakpoints

Description

In case a feature of platform 1 has been matched to multiple features of another platform, instead of averaging the data from these features, one may consider splitting the data at breakpoints within genes. This function modifies the results from the matching function matchAnn2Ann to facilitate this. The result can than directly be used in the subsetting functions cghCall2weightedSubset and ExpressionSet2weightedSubset.

Usage

```
splitMatchingAtBreakpoints(matchedIDs, CNdata)
```

Arguments

matchedIDs	An object of class list, as returned by the matchAnn2Ann-function.
CNdata	Object of class cghCall.

Value

An object of class list, similar to that returned by the matchAnn2Ann-function.

Author(s)

Wessel N. van Wieringen: <w.vanwieringen@vumc.nl>

References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

matchAnn2Ann, cghCall2weightedSubset, ExpressionSet2weightedSubset.

Examples

```
# load data
data(pollackCN16)
data(pollackGE16)

# extract genomic information from cghCall-object
chr1 <- fData(pollackCN16)[,1]
bpstart1 <- fData(pollackCN16)[,2]
bpend1 <- fData(pollackCN16)[,3]

# extract genomic information from ExpressionSet-object
chr2 <- fData(pollackGE16)[,1]
bpstart2 <- fData(pollackGE16)[,2]
```

```
bpend2 <- fData(pollackGE16)[,3]

# match features from both platforms
matchedFeatures <- matchAnn2Ann(chr1, bpstart1, bpend1, chr2, bpstart2, bpend2, method = "distance", maxDis

# expand
matchedFeatures <- splitMatchingAtBreakpoints(matchedFeatures, pollackCN16)
```

---

summary-method *Methods for Function summary*

Description

Methods for function summary

Methods

signature(object = "ANY") Regular.

signature(object = "entTest") Print output.

signature(object = "miTest") Print output.

signature(object = "rcmFit") Print output.

signature(object = "rcmTest") Print output.

---

uniqGenomicInfo *Unique genomic location information*

Description

Finds unique genomic location information.

Usage

```
uniqGenomicInfo(chr, bpstart, bpend, verbose = FALSE)
```

Arguments

chr	Object of class numeric containing chromosome information of features.
bpstart	Object of class numeric containing start base pair information of features. Of same length as chr.
bpend	Object of class numeric containing end base pair information of features. Of same length as chr.
verbose	Logical indicator: should intermediate output be printed on the screen?

Value

An object of class list. Each list item is a four-column matrix with the matched features information. The first column contains feature numbers of features with identical genomic location. The second, third and fourth column contain the chromosome, start and end base pair information of the features (should be the same for each feature).

Author(s)

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References

Van Wieringen, W.N., Unger, K., Leday, G.G.R., Krijgsman, O., De Menezes, R.X., Ylstra, B., Van de Wiel, M.A. (2011), "Matching of array CGH and gene expression microarray features for the purpose of integrative analysis", *submitted for publication*.

See Also

ExpressionSet2weightedSubset, cghCall2weightedSubset

Examples

```
# load data
data(pollackGE16)

# extract genomic information from ExpressionSet-object
chr <- fData(pollackGE16)[,1]
bpstart <- fData(pollackGE16)[,2]
bpend <- fData(pollackGE16)[,3]

# find unique genomic locations
uniqInfo <- uniqGenomicInfo(chr, bpstart, bpend, verbose = FALSE)
```

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