

Package ‘a4Core’

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Type Package

Title Automated Affymetrix Array Analysis Core Package

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Description Automated Affymetrix Array Analysis Core Package

Depends methods, Biobase, glmnet

biocViews Bioinformatics, Microarray

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confusionMatrix	<i>Generic function to produce a confusion matrix (related to a classification problem)</i>
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Description

Generic function to produce a confusion matrix (related to a classification problem)

Usage

```
confusionMatrix(x, ...)
```

Arguments

x object (usually a model fit object) that contains all information needed to produce the confusion matrix.

... further arguments for a specific method

Author(s)

Tobias Verbeke

simulateData

Simulate Data for Package Testing and Demonstration Purposes

Description

Simulate Data for Package Testing and Demonstration Purposes

Usage

```
simulateData(nCols = 40, nRows = 1000, nEffectRows = 5, nNoEffectCols = 5,
             betweenClassDifference = 1, withinClassSd = 0.5)
```

Arguments

nCols number of samples; currently this should be an even number

nRows number of features (genes)

nEffectRows number of differentially expressed features

nNoEffectCols number of samples for which the profile of a differentially expressed feature will be set similar to the other class

betweenClassDifference Average mean difference between the two classes to simulate a certain signal in the features for which an effect was introduced; the default is set to 1

withinClassSd Within class standard deviation used to add a certain noise level to the features for which an effect was introduced; the default standard deviation is set to 0.5

Value

object of class ExpressionSet with the characteristics specified

Note

The simulation assumes the variances are equal between the two classes. Heterogeneity could easily be introduced in the simulation if this would be requested by the users.

Author(s)

W. Talloen and T. Verbeke

Examples

```
someEset <- simulateData(nCols = 40, nRows = 1000, nEffectRows = 5, nNoEffectCols = 5)
someEset
```

topTable	<i>S4 Generic for obtaining a top table</i>
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Description

a top table is a rectangular object (e.g. data frame) which lists the top n most relevant variables

Usage

```
topTable(fit, n, ...)
```

Arguments

fit	object for which to obtain a top table, generally a fit object for a given model class
n	number of features (variables) to list in the top table, ranked by importance
...	further arguments for specific methods

Author(s)

Tobias Verbeke

topTable-methods	<i>Methods for topTable</i>
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Description

Methods for topTable. topTable extracts the top n most important features for a given classification or regression procedure

Arguments

fit	object resulting from a classification or regression procedure
n	number of features that one wants to extract from a table that ranks all features according to their importance in the classification or regression model; defaults to 10 for limma objects

Methods

glmnet and lognet

glmnet objects are produced by lassoClass (a4Classif) or lassoReg (a4Base)

fit = "glmnet", n = "numeric" lognet objects are produced by lassoClass (a4Classif) or lassoReg (a4Base)

fit = "elnet", n = "numeric" lognet objects are produced by lassoClass (a4Classif) or lassoReg (a4Base)

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