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
License GPL-3
biocViews Microarray
NeedsCompilation no

R topics documented:

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

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

Usage

confusionMatrix(x, ...)

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simulateData

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

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
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

Methods

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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