

# Package ‘a4Core’

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**Type** Package

**Title** Automated Affymetrix Array Analysis Core Package

**Version** 1.61.0

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**Description** Utility functions for the Automated Affymetrix Array Analysis set of packages.

**Imports** Biobase, glmnet, methods, stats

**Suggests** knitr, rmarkdown

**License** GPL-3

**biocViews** Microarray, Classification

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

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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

**Value**

A confusion matrix

**Author(s)**

Tobias Verbeke

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simulateData	<i>Simulate Data for Package Testing and Demonstration Purposes</i>
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**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
```

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topTable

*S4 Generic for obtaining a top table*

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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

**Value**

Top table with top n relevant variable.

**Author(s)**

Tobias Verbeke

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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

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

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

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