

# Package ‘a4Core’

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**Type** Package  
**Title** Automated Affymetrix Array Analysis Core Package  
**Version** 1.15.0  
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**Description** Automated Affymetrix Array Analysis Core Package  
**Depends** methods, Biobase, glmnet  
**License** GPL-3  
**biocViews** Microarray  
**NeedsCompilation** no

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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

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simulateData

*Simulate Data for Package Testing and Demonstration Purposes*

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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

**Author(s)**

Tobias Verbeke

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topTable-methods

*Methods for topTable*

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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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