

# Package ‘metagenomeSeq’

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**Title** Statistical analysis for sparse high-throughput sequencing

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**Description** metagenomeSeq is designed to determine features (be it Operational Taxonomic Unit (OTU), species, etc.) that are differentially abundant between two or more groups of multiple samples. metagenomeSeq is designed to address the effects of both normalization and under-sampling of microbial communities on disease association detection and the testing of feature correlations.

**License** Artistic-2.0

**Depends** R(>= 3.0), Biobase, limma, glmnet, methods, RColorBrewer

**Suggests** annotate, BiocGenerics, biomformat, knitr, gss, testthat (>= 0.8), vegan, interactiveDisplay, IHW

**Imports** parallel, matrixStats, foreach, Matrix, gplots, graphics,  
grDevices, stats, utils, Wrench

**VignetteBuilder** knitr

**URL** <https://github.com/nosson/metagenomeSeq/>

**BugReports** <https://github.com/nosson/metagenomeSeq/issues>

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## Contents

metagenomeSeq-package . . . . .	3
aggregateBySample . . . . .	4
aggregateByTaxonomy . . . . .	5
biom2MRexperiment . . . . .	6
calcNormFactors . . . . .	7
calcPosComponent . . . . .	7
calcShrinkParameters . . . . .	8
calcStandardError . . . . .	8
calculateEffectiveSamples . . . . .	9
calcZeroAdjustment . . . . .	9
calcZeroComponent . . . . .	10
correctIndices . . . . .	10
correlationTest . . . . .	11
cumNorm . . . . .	12
cumNormMat . . . . .	13
cumNormStat . . . . .	13
cumNormStatFast . . . . .	14
doCountMStep . . . . .	15
doEStep . . . . .	16
doZeroMStep . . . . .	16
exportMat . . . . .	17
exportStats . . . . .	18
expSummary . . . . .	19
extractMR . . . . .	19
filterData . . . . .	20
fitDO . . . . .	21
fitFeatureModel . . . . .	22
fitFeatureModelResults-class . . . . .	23
fitLogNormal . . . . .	23
fitMultipleTimeSeries . . . . .	24
fitPA . . . . .	25
fitSSTimeSeries . . . . .	26
fitTimeSeries . . . . .	27
fitZeroLogNormal . . . . .	29
fitZig . . . . .	30
fitZigResults-class . . . . .	31
getCountDensity . . . . .	32
getEpsilon . . . . .	32
getNegativeLogLikelihoods . . . . .	33
getPi . . . . .	34
getZ . . . . .	34
isItStillActive . . . . .	35
libSize . . . . .	36
libSize<- . . . . .	36
loadBiom . . . . .	37
loadMeta . . . . .	38
loadMetaQ . . . . .	38
loadPhenoData . . . . .	39
lungData . . . . .	40
makeLabels . . . . .	40

mergeMRexperiments . . . . .	41
mergeTable . . . . .	41
metagenomeSeq-deprecated . . . . .	42
mouseData . . . . .	42
MRcoefs . . . . .	43
MRcounts . . . . .	44
MRexperiment . . . . .	45
MRexperiment2biom . . . . .	46
MRfulltable . . . . .	47
MRihw . . . . .	48
MRihw,fitFeatureModelResults-method . . . . .	48
MRihw,fitZigResults-method . . . . .	49
MRtable . . . . .	49
newMRexperiment . . . . .	51
normFactors . . . . .	52
normFactors<- . . . . .	53
plotBubble . . . . .	53
plotClassTimeSeries . . . . .	54
plotCorr . . . . .	55
plotFeature . . . . .	56
plotGenus . . . . .	57
plotMRheatmap . . . . .	59
plotOrd . . . . .	60
plotOTU . . . . .	61
plotRare . . . . .	62
plotTimeSeries . . . . .	63
posteriorProbs . . . . .	64
returnAppropriateObj . . . . .	64
ssFit . . . . .	65
ssIntervalCandidate . . . . .	66
ssPerm . . . . .	67
ssPermAnalysis . . . . .	67
trapz . . . . .	68
ts2MRexperiment . . . . .	69
uniqueFeatures . . . . .	70
wrenchNorm . . . . .	71
zigControl . . . . .	71
<b>Index</b>	<b>73</b>

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metagenomeSeq-package *Statistical analysis for sparse high-throughput sequencing*

---

## Description

metagenomeSeq is designed to determine features (be it Operational Taxonomic Unit (OTU), species, etc.) that are differentially abundant between two or more groups of multiple samples. metagenomeSeq is designed to address the effects of both normalization and under-sampling of microbial communities on disease association detection and the testing of feature correlations.

A user's guide is available, and can be opened by typing `vignette("metagenomeSeq")`

The metagenomeSeq package implements novel normalization and statistical methodology in the following papers.

**Author(s)**

Paulson, JN <jpaulson@umiacs.umd.edu>; Pop, M; Corrada Bravo, H

**References**

Paulson, Joseph N., O. Colin Stine, Hector Corrada Bravo, and Mihai Pop. "Differential abundance analysis for microbial marker-gene surveys." *Nature methods* (2013).

---

aggregateBySample      *Aggregates a MRExperiment object or counts matrix to by a factor.*

---

**Description**

Using the phenoData information in the MRExperiment, calling aggregateBySample on a MRExperiment and a particular phenoData column (i.e. 'diet') will aggregate counts using the aggfun function (default rowMeans). Possible aggfun alternatives include rowMeans and rowMedians.

**Usage**

```
aggregateBySample(obj, fct, aggfun = rowMeans, out = "MRExperiment")
```

```
aggSamp(obj, fct, aggfun = rowMeans, out = "MRExperiment")
```

**Arguments**

obj	A MRExperiment object or count matrix.
fct	phenoData column name from the MRExperiment object or if count matrix object a vector of labels.
aggfun	Aggregation function.
out	Either 'MRExperiment' or 'matrix'

**Value**

An aggregated count matrix or MRExperiment object where the new pData is a vector of 'fct' levels.

**Examples**

```
data(mouseData)
aggregateBySample(mouseData[1:100,], fct="diet", aggfun=rowSums)
# not run
# aggregateBySample(mouseData, fct="diet", aggfun=matrixStats::rowMedians)
# aggSamp(mouseData, fct='diet', aggfun=rowMaxs)
```

---

aggregateByTaxonomy    *Aggregates a MRExperiment object or counts matrix to a particular level.*

---

### Description

Using the featureData information in the MRExperiment, calling aggregateByTaxonomy on a MRExperiment and a particular featureData column (i.e. 'genus') will aggregate counts to the desired level using the aggfun function (default colSums). Possible aggfun alternatives include colMeans and colMedians.

### Usage

```
aggregateByTaxonomy(
  obj,
  lvl,
  alternate = FALSE,
  norm = FALSE,
  log = FALSE,
  aggfun = colSums,
  sl = 1000,
  featureOrder = NULL,
  returnFullHierarchy = TRUE,
  out = "MRExperiment"
)

aggTax(
  obj,
  lvl,
  alternate = FALSE,
  norm = FALSE,
  log = FALSE,
  aggfun = colSums,
  sl = 1000,
  featureOrder = NULL,
  returnFullHierarchy = TRUE,
  out = "MRExperiment"
)
```

### Arguments

obj	A MRExperiment object or count matrix.
lvl	featureData column name from the MRExperiment object or if count matrix object a vector of labels.
alternate	Use the rowname for undefined OTUs instead of aggregating to "no_match".
norm	Whether to aggregate normalized counts or not.
log	Whether or not to log2 transform the counts - if MRExperiment object.
aggfun	Aggregation function.
sl	scaling value, default is 1000.

featureOrder Hierarchy of levels in taxonomy as fData colnames  
 returnFullHierarchy Boolean value to indicate return single column of fData or all columns of hierarchy  
 out Either 'MRExperiment' or 'matrix'

**Value**

An aggregated count matrix.

**Examples**

```
data(mouseData)
aggregateByTaxonomy(mouseData[1:100,], lvl="class", norm=TRUE, aggfun=colSums)
# not run
# aggregateByTaxonomy(mouseData, lvl="class", norm=TRUE, aggfun=colMedians)
# aggTax(mouseData, lvl='phylum', norm=FALSE, aggfun=colSums)
```

---

biom2MRExperiment      *Biom to MRExperiment objects*

---

**Description**

Wrapper to convert biom files to MRExperiment objects.

**Usage**

```
biom2MRExperiment(obj)
```

**Arguments**

obj                    The biom object file.

**Value**

A MRExperiment object.

**See Also**

[loadMeta](#) [loadPhenoData](#) [newMRExperiment](#) [loadBiom](#)

**Examples**

```
library(biomformat)
rich_dense_file = system.file("extdata", "rich_dense_otu_table.biom", package = "biomformat")
x = biomformat::read_biom(rich_dense_file)
biom2MRExperiment(x)
```

---

calcNormFactors	<i>Cumulative sum scaling (css) normalization factors</i>
-----------------	---

---

**Description**

Return a vector of the the sum up to and including a quantile.

**Usage**

```
calcNormFactors(obj, p = cumNormStatFast(obj))
```

**Arguments**

obj	An MExperiment object or matrix.
p	The pth quantile.

**Value**

Vector of the sum up to and including a sample's pth quantile.

**See Also**

[fitZig](#) [cumNormStatFast](#) [cumNorm](#)

**Examples**

```
data(mouseData)
head(calcNormFactors(mouseData))
```

---

calcPosComponent	<i>Positive component</i>
------------------	---------------------------

---

**Description**

Fit the positive (log-normal) component

**Usage**

```
calcPosComponent(mat, mod, weights)
```

**Arguments**

mat	A matrix of normalized counts
mod	A model matrix
weights	Weight matrix for samples and counts

**See Also**

[fitZeroLogNormal](#) [fitFeatureModel](#)

---

calcShrinkParameters    *Calculate shrinkage parameters*

---

### Description

Calculate the shrunken variances and variance of parameters of interest across features.

### Usage

```
calcShrinkParameters(fit, coef, mins2, exclude = NULL)
```

### Arguments

fit	A matrix of fits as outputted by calcZeroComponent or calcPosComponent
coef	Coefficient of interest
mins2	minimum variance estimate
exclude	Vector of features to exclude when shrinking

### See Also

[fitZeroLogNormal](#) [fitFeatureModel](#)

---

calcStandardError    *Calculate the zero-inflated log-normal statistic's standard error*

---

### Description

Calculat the se for the model. Code modified from "Adjusting for covariates in zero-inflated gamma and zero-inflated log-normal models for semicontinuous data", ED Mills

### Usage

```
calcStandardError(mod, fitln, fitzero, coef = 2, exclude = NULL)
```

### Arguments

mod	The zero component model matrix
fitln	A matrix with parameters from the log-normal fit
fitzero	A matrix with parameters from the logistic fit
coef	Coefficient of interest
exclude	List of features to exclude

### See Also

[fitZeroLogNormal](#) [fitFeatureModel](#)



---

 calculateEffectiveSamples

*Estimated effective samples per feature*


---

**Description**

Calculates the number of estimated effective samples per feature from the output of a fitZig run. The estimated effective samples per feature is calculated as the  $\sum 1^n$  ( $n$  = number of samples)  $1 - z_i$  where  $z_i$  is the posterior probability a feature belongs to the technical distribution.

**Usage**

```
calculateEffectiveSamples(obj)
```

**Arguments**

obj                    The output of fitZig run on a MRexperiment object.

**Value**

A list of the estimated effective samples per feature.

**See Also**

[fitZig](#) [MRcoefs](#) [MRfulltable](#)

---

calcZeroAdjustment

*Calculate the zero-inflated component's adjustment factor*


---

**Description**

Calculate the log ratio of average marginal probabilities for each sample having a positive count. This becomes the adjustment factor for the log fold change.

**Usage**

```
calcZeroAdjustment(fitln, fitzero, mod, coef, exclude = NULL)
```

**Arguments**

fitln                    A matrix with parameters from the log-normal fit  
 fitzero                    A matrix with parameters from the logistic fit  
 mod                      The zero component model matrix  
 coef                      Coefficient of interest  
 exclude                    List of features to exclude

**See Also**

[fitZeroLogNormal](#) [fitFeatureModel](#)

---

calcZeroComponent      *Zero component*

---

### Description

Fit the zero (logistic) component

### Usage

```
calcZeroComponent(mat, mod, weights)
```

### Arguments

mat	A matrix of normalized counts
mod	A model matrix
weights	Weight matrix for samples and counts

### See Also

[fitZeroLogNormal](#) [fitFeatureModel](#)

---

correctIndices      *Calculate the correct indices for the output of correlationTest*

---

### Description

Consider the upper triangular portion of a matrix of size  $n \times n$ . Results from the `correlationTest` are output as the combination of two vectors, correlation statistic and p-values. The order of the output is 1vs2, 1vs3, 1vs4, etc. The `correctIndices` returns the correct indices to fill a correlation matrix or correlation-pvalue matrix.

### Usage

```
correctIndices(n)
```

### Arguments

n	The number of features compared by <code>correlationTest</code> ( <code>nrow(mat)</code> ).
---	---

### Value

A vector of the indices for an upper triangular matrix.

### See Also

[correlationTest](#)

**Examples**

```

data(mouseData)
mat = MRcounts(mouseData)[55:60,]
cors = correlationTest(mat)
ind = correctIndices(nrow(mat))

cormat = as.matrix(dist(mat))
cormat[cormat>0] = 0
cormat[upper.tri(cormat)][ind] = cors[,1]
table(cormat[1,-1] - cors[1:5,1])

```

---

correlationTest	<i>Correlation of each row of a matrix or MRexperiment object</i>
-----------------	---

---

**Description**

Calculates the (pairwise) correlation statistics and associated p-values of a matrix or the correlation of each row with a vector.

**Usage**

```

correlationTest(
  obj,
  y = NULL,
  method = "pearson",
  alternative = "two.sided",
  norm = TRUE,
  log = TRUE,
  cores = 1,
  override = FALSE,
  ...
)

```

**Arguments**

obj	A MRexperiment object or count matrix.
y	Vector of length ncol(obj) to compare to.
method	One of 'pearson', 'spearman', or 'kendall'.
alternative	Indicates the alternative hypothesis and must be one of 'two.sided', 'greater' (positive) or 'less' (negative). You can specify just the initial letter.
norm	Whether to aggregate normalized counts or not - if MRexperiment object.
log	Whether or not to log <sub>2</sub> transform the counts - if MRexperiment object.
cores	Number of cores to use.
override	If the number of rows to test is over a thousand the test will not commence (unless override==TRUE).
...	Extra parameters for mclapply.

**Value**

A matrix of size choose(number of rows, 2) by 2. The first column corresponds to the correlation value. The second column the p-value.

**See Also**

[correctIndices](#)

**Examples**

```
# Pairwise correlation of raw counts
data(mouseData)
cors = correlationTest(mouseData[1:10,],norm=FALSE,log=FALSE)
head(cors)

mat = MRcounts(mouseData)[1:10,]
cormat = as.matrix(dist(mat)) # Creating a matrix
cormat[cormat>0] = 0 # Creating an empty matrix
ind = correctIndices(nrow(mat))
cormat[upper.tri(cormat)][ind] = cors[,1]
table(cormat[1,-1] - cors[1:9,1])

# Correlation of raw counts with a vector (library size in this case)
data(mouseData)
cors = correlationTest(mouseData[1:10,],libSize(mouseData),norm=FALSE,log=FALSE)
head(cors)
```

---

cumNorm

*Cumulative sum scaling normalization*

---

**Description**

Calculates each column's quantile and calculates the sum up to and including that quantile.

**Usage**

```
cumNorm(obj, p = cumNormStatFast(obj))
```

**Arguments**

obj                    An MRexperiment object.  
p                        The pth quantile.

**Value**

Object with the normalization factors stored as a vector of the sum up to and including a sample's pth quantile.

**See Also**

[fitZig](#) [cumNormStat](#)

**Examples**

```
data(mouseData)
mouseData <- cumNorm(mouseData)
head(normFactors(mouseData))
```

---

cumNormMat	<i>Cumulative sum scaling factors.</i>
------------	--

---

**Description**

Calculates each column's quantile and calculates the sum up to and including that quantile.

**Usage**

```
cumNormMat(obj, p = cumNormStatFast(obj), sl = 1000)
```

**Arguments**

obj	A matrix or MRExperiment object.
p	The pth quantile.
sl	The value to scale by (default=1000).

**Value**

Returns a matrix normalized by scaling counts up to and including the pth quantile.

**See Also**

[fitZig](#) [cumNorm](#)

**Examples**

```
data(mouseData)
head(cumNormMat(mouseData))
```

---

cumNormStat	<i>Cumulative sum scaling percentile selection</i>
-------------	--

---

**Description**

Calculates the percentile for which to sum counts up to and scale by. `cumNormStat` might be deprecated one day. Deviates from methods in Nature Methods paper by making use row means for generating reference.

**Usage**

```
cumNormStat(obj, qFlag = TRUE, pFlag = FALSE, rel = 0.1, ...)
```

**Arguments**

obj	A matrix or MRExperiment object.
qFlag	Flag to either calculate the proper percentile using R's step-wise quantile function or approximate function.
pFlag	Plot the relative difference of the median deviance from the reference.
rel	Cutoff for the relative difference from one median difference from the reference to the next
...	Applicable if pFlag == TRUE. Additional plotting parameters.

**Value**

Percentile for which to scale data

**See Also**

[fitZig](#) [cumNorm](#) [cumNormStatFast](#)

**Examples**

```
data(mouseData)
p = round(cumNormStat(mouseData,pFlag=FALSE),digits=2)
```

---

cumNormStatFast

*Cumulative sum scaling percentile selection*

---

**Description**

Calculates the percentile for which to sum counts up to and scale by. Faster version than available in cumNormStat. Deviates from methods described in Nature Methods by making use of ro means for reference.

**Usage**

```
cumNormStatFast(obj, pFlag = FALSE, rel = 0.1, ...)
```

**Arguments**

obj	A matrix or MRExperiment object.
pFlag	Plot the median difference quantiles.
rel	Cutoff for the relative difference from one median difference from the reference to the next.
...	Applicable if pFlag == TRUE. Additional plotting parameters.

**Value**

Percentile for which to scale data

**See Also**

[fitZig](#) [cumNorm](#) [cumNormStat](#)

**Examples**

```
data(mouseData)
p = round(cumNormStatFast(mouseData,pFlag=FALSE),digits=2)
```

---

doCountMStep

*Compute the Maximization step calculation for features still active.*


---

**Description**

Maximization step is solved by weighted least squares. The function also computes counts residuals.

**Usage**

```
doCountMStep(z, y, mmCount, stillActive, fit2 = NULL, dfMethod = "modified")
```

**Arguments**

<code>z</code>	Matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).
<code>y</code>	Matrix (m x n) of count observations.
<code>mmCount</code>	Model matrix for the count distribution.
<code>stillActive</code>	Boolean vector of size M, indicating whether a feature converged or not.
<code>fit2</code>	Previous fit of the count model.
<code>dfMethod</code>	Either 'default' or 'modified' (by responsibilities)

**Details**

Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The density is defined as  $f_{\text{zig}}(y_{ij} = \pi_j(S_j) * f_0(y_{ij}) + (1 - \pi_j(S_j)) * f_{\text{count}}(y_{ij}; \mu_i, \sigma_i^2)$ . The log-likelihood in this extended model is  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 | \text{data})$ .

**Value**

Update matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).

**See Also**

[fitZig](#)

---

doEStep *Compute the Expectation step.*

---

### Description

Estimates the responsibilities  $z_{ij} = \frac{\pi_j \cdot I_0(y_{ij})}{\pi_j \cdot I_0(y_{ij}) + (1 - \pi_j) \cdot f_{\text{count}}(y_{ij})}$

### Usage

```
doEStep(countResiduals, zeroResiduals, zeroIndices)
```

### Arguments

countResiduals Residuals from the count model.  
 zeroResiduals Residuals from the zero model.  
 zeroIndices Index (matrix m x n) of counts that are zero/non-zero.

### Details

Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The density is defined as  $f_{\text{zig}}(y_{ij} = \pi_j(S_j) \cdot f_0(y_{ij}) + (1 - \pi_j(S_j)) \cdot f_{\text{count}}(y_{ij}; \mu_i, \sigma_i^2)$ . The log-likelihood in this extended model is  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 \mid \text{data})$ .

### Value

Updated matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).

### See Also

[fitZig](#)

---

doZeroMStep *Compute the zero Maximization step.*

---

### Description

Performs Maximization step calculation for the mixture components. Uses least squares to fit the parameters of the mean of the logistic distribution.  $\pi_j = \frac{\sum_i M_{ij}}{\sum_i M_{ij}}$  Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The density is defined as  $f_{\text{zig}}(y_{ij} = \pi_j(S_j) \cdot f_0(y_{ij}) + (1 - \pi_j(S_j)) \cdot f_{\text{count}}(y_{ij}; \mu_i, \sigma_i^2)$ . The log-likelihood in this extended model is  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 \mid \text{data})$ .



**Usage**

```
doZeroMStep(z, zeroIndices, mmZero)
```

**Arguments**

z	Matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).
zeroIndices	Index (matrix m x n) of counts that are zero/non-zero.
mmZero	The zero model, the model matrix to account for the change in the number of OTUs observed as a linear effect of the depth of coverage.

**Value**

List of the zero fit (zero mean model) coefficients, variance - scale parameter (scalar), and normalized residuals of length `sum(zeroIndices)`.

**See Also**

[fitZig](#)

---

exportMat

*Export the normalized MRexperiment dataset as a matrix.*

---

**Description**

This function allows the user to take a dataset of counts and output the dataset to the user's workspace as a tab-delimited file, etc.

**Usage**

```
exportMat(
  obj,
  log = TRUE,
  norm = TRUE,
  sep = "\t",
  file = "~/Desktop/matrix.tsv"
)
```

**Arguments**

obj	A MRexperiment object or count matrix.
log	Whether or not to log transform the counts - if MRexperiment object.
norm	Whether or not to normalize the counts - if MRexperiment object.
sep	Separator for writing out the count matrix.
file	Output file name.

**Value**

NA

**See Also**[cumNorm](#)**Examples**

```
data(lungData)
dataDirectory <- system.file("extdata", package="metagenomeSeq")
exportMat(lungData[,1:5], file=file.path(dataDirectory, "tmp.tsv"))
head(read.csv(file=file.path(dataDirectory, "tmp.tsv"), sep="\t"))
```

---

**exportStats***Various statistics of the count data.*

---

**Description**

A matrix of values for each sample. The matrix consists of sample ids, the sample scaling factor, quantile value, the number identified features, and library size (depth of coverage).

**Usage**

```
exportStats(obj, p = cumNormStat(obj), file = "~/Desktop/res.stats.tsv")
```

**Arguments**

<b>obj</b>	A MRexperiment object with count data.
<b>p</b>	Quantile value to calculate the scaling factor and quantiles for the various samples.
<b>file</b>	Output file name.

**Value**

None.

**See Also**[cumNorm quantile](#)**Examples**

```
data(lungData)
dataDirectory <- system.file("extdata", package="metagenomeSeq")
exportStats(lungData[,1:5], file=file.path(dataDirectory, "tmp.tsv"))
head(read.csv(file=file.path(dataDirectory, "tmp.tsv"), sep="\t"))
```

---

expSummary	<i>Access MRExperiment object experiment data</i>
------------	---

---

**Description**

The expSummary vectors represent the column (sample specific) sums of features, i.e. the total number of reads for a sample, libSize and also the normalization factors, normFactor.

**Usage**

```
expSummary(obj)
```

**Arguments**

obj                    a MRExperiment object.

**Value**

Experiment summary table

**Author(s)**

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**Examples**

```
data(mouseData)  
expSummary(mouseData)
```

---

extractMR	<i>Extract the essentials of an MRExperiment.</i>
-----------	---

---

**Description**

Extract the essentials of an MRExperiment.

**Usage**

```
extractMR(obj)
```

**Arguments**

obj                    MRExperiment-class object.

**Value**

A list containing:

counts : Count data

- librarySize : The column sums / library size / sequencing depth
- normFactors : The normalization scaling factors
- pheno : phenotype table
- feat : feature table

**Examples**

```
data(mouseData)
head(metagenomeSeq::extractMR(mouseData))
```

---

<code>filterData</code>	<i>Filter datasets according to no. features present in features with at least a certain depth.</i>
-------------------------	---

---

**Description**

Filter the data based on the number of present features after filtering samples by depth of coverage. There are many ways to filter the object, this is just one way.

**Usage**

```
filterData(obj, present = 1, depth = 1000)
```

**Arguments**

<code>obj</code>	A MRexperiment object or count matrix.
<code>present</code>	Features with at least 'present' positive samples.
<code>depth</code>	Sampls with at least this much depth of coverage

**Value**

A MRexperiment object.

**Examples**

```
data(mouseData)
filterData(mouseData)
```

---

fitDO

*Wrapper to calculate Discovery Odds Ratios on feature values.*


---

### Description

This function returns a data frame of p-values, odds ratios, lower and upper confidence limits for every row of a matrix. The discovery odds ratio is calculated as using Fisher's exact test on actual counts. The test's hypothesis is whether or not the discovery of counts for a feature (of all counts) is found in greater proportion in a particular group.

### Usage

```
fitDO(obj, cl, norm = TRUE, log = TRUE, adjust.method = "fdr", cores = 1, ...)
```

### Arguments

obj	A MRexperiment object with a count matrix, or a simple count matrix.
cl	Group comparison
norm	Whether or not to normalize the counts - if MRexperiment object.
log	Whether or not to log2 transform the counts - if MRexperiment object.
adjust.method	Method to adjust p-values by. Default is "FDR". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">p.adjust</a> for more details.
cores	Number of cores to use.
...	Extra options for makeCluster

### Value

Matrix of odds ratios, p-values, lower and upper confidence intervals

### See Also

[cumNorm](#) [fitZig](#) [fitPA](#) [fitMeta](#)

### Examples

```
data(lungData)
k = grep("Extraction.Control", pData(lungData)$SampleType)
lungTrim = lungData[, -k]
lungTrim = lungTrim[-which(rowSums(MRcounts(lungTrim)>0)<20), ]
res = fitDO(lungTrim, pData(lungTrim)$SmokingStatus);
head(res)
```

---

fitFeatureModel	<i>Computes differential abundance analysis using a zero-inflated log-normal model</i>
-----------------	--

---

### Description

Wrapper to actually run zero-inflated log-normal model given a MRexperiment object and model matrix. User can decide to shrink parameter estimates.

### Usage

```
fitFeatureModel(obj, mod, coef = 2, B = 1, szero = FALSE, spos = TRUE)
```

### Arguments

obj	A MRexperiment object with count data.
mod	The model for the count distribution.
coef	Coefficient of interest to grab log fold-changes.
B	Number of bootstraps to perform if >1. If >1 performs permutation test.
szero	TRUE/FALSE, shrink zero component parameters.
spos	TRUE/FALSE, shrink positive component parameters.

### Value

A list of objects including:

- call - the call made to fitFeatureModel
- fitZeroLogNormal - list of parameter estimates for the zero-inflated log normal model
- design - model matrix
- taxa - taxa names
- counts - count matrix
- pvalues - calculated p-values
- permutedfits - permuted z-score estimates under the null

### See Also

[cumNorm](#)

### Examples

```
data(lungData)
lungData = lungData[,-which(is.na(pData(lungData)$SmokingStatus))]
lungData=filterData(lungData,present=30,depth=1)
lungData <- cumNorm(lungData, p=.5)
s <- normFactors(lungData)
pd <- pData(lungData)
mod <- model.matrix(~1+SmokingStatus, data=pd)
lungres1 = fitFeatureModel(lungData,mod)
```

---

 fitFeatureModelResults-class

*Class "fitFeatureModelResults" – a formal class for storing results from a fitFeatureModel call*

---

### Description

This class contains all of the same information expected from a fitFeatureModel call, but it is defined in the S4 style as opposed to being stored as a list.

### Slots

call the call made to fitFeatureModel  
 fitZeroLogNormal list of parameter estimates for the zero-inflated log normal model  
 design model matrix  
 taxa taxa names  
 counts count matrix  
 pvalues calculated p-values  
 permutedFits permuted z-score estimates under the null

---

 fitLogNormal

*Computes a log-normal linear model and permutation based p-values.*

---

### Description

Wrapper to perform the permutation test on the t-statistic. This is the original method employed by metastats (for non-sparse large samples). We include CSS normalization though (optional) and log2 transform the data. In this method the null distribution is not assumed to be a t-dist.

### Usage

```
fitLogNormal(obj, mod, useCSSoffset = TRUE, B = 1000, coef = 2, sl = 1000)
```

### Arguments

obj	A MRexperiment object with count data.
mod	The model for the count distribution.
useCSSoffset	Boolean, whether to include the default scaling parameters in the model or not.
B	Number of permutations.
coef	The coefficient of interest.
sl	The value to scale by (default=1000).

### Value

Call made, fit object from lmFit, t-statistics and p-values for each feature.

**Examples**

```
# This is a simple demonstration
data(lungData)
k = grep("Extraction.Control", pData(lungData)$SampleType)
lungTrim = lungData[,-k]
k = which(rowSums(MRcounts(lungTrim)>0)<30)
lungTrim = cumNorm(lungTrim)
lungTrim = lungTrim[-k,]
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
fit = fitLogNormal(obj = lungTrim, mod=mod, B=1)
```

---

fitMultipleTimeSeries *Discover differentially abundant time intervals for all bacteria*

---

**Description**

Calculate time intervals of significant differential abundance over all bacteria of a particularly specified level (lvl). If not lvl is specified, all OTUs are analyzed. Warning, function can take a while

**Usage**

```
fitMultipleTimeSeries(obj, lvl = NULL, B = 1, featureOrder = NULL, ...)
```

**Arguments**

obj	metagenomeSeq MRExperiment-class object.
lvl	Vector or name of column in featureData of MRExperiment-class object for aggregating counts (if not OTU level).
B	Number of permutations to perform.
featureOrder	Hierarchy of levels in taxonomy as fData colnames
...	Options for <a href="#">fitTimeSeries</a> , except feature.

**Value**

List of lists of matrices of time point intervals of interest, Difference in abundance area and p-value, fit, area permutations.

A list of lists for which each includes:

- timeIntervals - Matrix of time point intervals of interest, area of differential abundance, and pvalue.
- data - Data frame of abundance, class indicator, time, and id input.
- fit - Data frame of fitted values of the difference in abundance, standard error estimates and timepoints interpolated over.
- perm - Differential abundance area estimates for each permutation.
- call - Function call.



**See Also**

[cumNorm](#) [fitSSTimeSeries](#) [fitTimeSeries](#)

**Examples**

```
data(mouseData)
res = fitMultipleTimeSeries(obj=mouseData, lvl='phylum', class="status",
                             id="mouseID", time="relativeTime", B=1)
```

---

fitPA

*Wrapper to run fisher's test on presence/absence of a feature.*


---

**Description**

This function returns a data frame of p-values, odds ratios, lower and upper confidence limits for every row of a matrix.

**Usage**

```
fitPA(obj, cl, thres = 0, adjust.method = "fdr", cores = 1, ...)
```

**Arguments**

obj	A MRexperiment object with a count matrix, or a simple count matrix.
cl	Group comparison
thres	Threshold for defining presence/absence.
adjust.method	Method to adjust p-values by. Default is "FDR". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">p.adjust</a> for more details.
cores	Number of cores to use.
...	Extra parameters for makeCluster

**Value**

Matrix of odds ratios, p-values, lower and upper confidence intervals

**See Also**

[cumNorm](#) [fitZig](#) [fitDO](#) [fitMeta](#)

**Examples**

```
data(lungData)
k = grep("Extraction.Control", pData(lungData)$SampleType)
lungTrim = lungData[,-k]
lungTrim = lungTrim[-which(rowSums(MRcounts(lungTrim)>0)<20),]
res = fitPA(lungTrim, pData(lungTrim)$SmokingStatus);
head(res)
```

fitSSTimeSeries

*Discover differentially abundant time intervals using SS-Anova***Description**

Calculate time intervals of interest using SS-Anova fitted models. Fitting is performed using Smoothing Spline ANOVA (SS-Anova) to find interesting intervals of time. Given observations at different time points for two groups, fitSSTimeSeries calculates a function that models the difference in abundance between two groups across all time. Using permutations we estimate a null distribution of areas for the time intervals of interest and report significant intervals of time. Use of the function for analyses should cite: "Finding regions of interest in high throughput genomics data using smoothing splines" Talukder H, Paulson JN, Bravo HC. (In preparation)

**Usage**

```
fitSSTimeSeries(
  obj,
  formula,
  feature,
  class,
  time,
  id,
  lvl = NULL,
  include = c("class", "time:class"),
  C = 0,
  B = 1000,
  norm = TRUE,
  log = TRUE,
  sl = 1000,
  featureOrder = NULL,
  ...
)
```

**Arguments**

obj	metagenomeSeq MExperiment-class object.
formula	Formula for ssanova. Of the form: abundance ~ ... where ... includes any pData slot value.
feature	Name or row of feature of interest.
class	Name of column in phenoData of MExperiment-class object for class membership.
time	Name of column in phenoData of MExperiment-class object for relative time.
id	Name of column in phenoData of MExperiment-class object for sample id.
lvl	Vector or name of column in featureData of MExperiment-class object for aggregating counts (if not OTU level).
include	Parameters to include in prediction.
C	Value for which difference function has to be larger or smaller than (default 0).
B	Number of permutations to perform

norm	When aggregating counts to normalize or not.
log	Log2 transform.
sl	Scaling value.
featureOrder	Hierarchy of levels in taxonomy as fData colnames
...	Options for ssanova

### Value

List of matrix of time point intervals of interest, Difference in abundance area and p-value, fit, area permutations, and call.

A list of objects including:

- timeIntervals - Matrix of time point intervals of interest, area of differential abundance, and pvalue.
- data - Data frame of abundance, class indicator, time, and id input.
- fit - Data frame of fitted values of the difference in abundance, standard error estimates and timepoints interpolated over.
- perm - Differential abundance area estimates for each permutation.
- call - Function call.

### See Also

[cumNorm](#) [ssFit](#) [ssIntervalCandidate](#) [ssPerm](#) [ssPermAnalysis](#) [plotTimeSeries](#)

### Examples

```
data(mouseData)
res = fitSSTimeSeries(obj=mouseData,feature="Actinobacteria",
  class="status",id="mouseID",time="relativeTime",lvl='class',B=2)
```

---

fitTimeSeries

*Discover differentially abundant time intervals*

---

### Description

Calculate time intervals of significant differential abundance. Currently only one method is implemented (ssanova). fitSSTimeSeries is called with method="ssanova".

### Usage

```
fitTimeSeries(
  obj,
  formula,
  feature,
  class,
  time,
  id,
  method = c("ssanova"),
```

```

lvl = NULL,
include = c("class", "time:class"),
C = 0,
B = 1000,
norm = TRUE,
log = TRUE,
sl = 1000,
featureOrder = NULL,
...
)

```

### Arguments

obj	metagenomeSeq MRExperiment-class object.
formula	Formula for ssanova. Of the form: abundance ~ ... where ... includes any pData slot value.
feature	Name or row of feature of interest.
class	Name of column in phenoData of MRExperiment-class object for class membership.
time	Name of column in phenoData of MRExperiment-class object for relative time.
id	Name of column in phenoData of MRExperiment-class object for sample id.
method	Method to estimate time intervals of differentially abundant bacteria (only ssanova method implemented currently).
lvl	Vector or name of column in featureData of MRExperiment-class object for aggregating counts (if not OTU level).
include	Parameters to include in prediction.
C	Value for which difference function has to be larger or smaller than (default 0).
B	Number of permutations to perform.
norm	When aggregating counts to normalize or not.
log	Log2 transform.
sl	Scaling value.
featureOrder	Hierarchy of levels in taxonomy as fData colnames
...	Options for ssanova

### Value

List of matrix of time point intervals of interest, Difference in abundance area and p-value, fit, area permutations, and call.

A list of objects including:

- timeIntervals - Matrix of time point intervals of interest, area of differential abundance, and pvalue.
- data - Data frame of abundance, class indicator, time, and id input.
- fit - Data frame of fitted values of the difference in abundance, standard error estimates and timepoints interpolated over.
- perm - Differential abundance area estimates for each permutation.
- call - Function call.

**See Also**

[cumNorm](#) [fitSSTimeSeries](#) [plotTimeSeries](#)

**Examples**

```
data(mouseData)
res = fitTimeSeries(obj=mouseData,feature="Actinobacteria",
  class="status",id="mouseID",time="relativeTime",lvl='class',B=2)
```

---

fitZeroLogNormal	<i>Compute the log fold-change estimates for the zero-inflated log-normal model</i>
------------------	---

---

**Description**

Run the zero-inflated log-normal model given a MRexperiment object and model matrix. Not for the average user, assumes structure of the model matrix.

**Usage**

```
fitZeroLogNormal(obj, mod, coef = 2, szero = TRUE, spos = TRUE)
```

**Arguments**

obj	A MRexperiment object with count data.
mod	The model for the count distribution.
coef	Coefficient of interest to grab log fold-changes.
szero	TRUE/FALSE, shrink zero component parameters.
spos	TRUE/FALSE, shrink positive component parameters.

**Value**

A list of objects including:

- logFC - the log fold-change estimates
- adjFactor - the adjustment factor based on the zero component
- se - standard error estimates
- fitln - parameters from the log-normal fit
- fitzero - parameters from the logistic fit
- zeroRidge - output from the ridge regression
- posRidge - output from the ridge regression
- tauPos - estimated  $\tau^2$  for positive component
- tauZero - estimated  $\tau^2$  for zero component
- exclude - features to exclude for various reasons, e.g. all zeros
- zeroExclude - features to exclude for various reasons, e.g. all zeros

**See Also**

[cumNorm](#) [fitFeatureModel](#)

---

fitZig

*Computes the weighted fold-change estimates and t-statistics.*


---

### Description

Wrapper to actually run the Expectation-maximization algorithm and estimate  $f_{\text{count}}$  fits. Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The density is defined as  $f_{\text{zig}}(y_{ij} = \pi_j(S_j) * f_0(y_{ij}) + (1 - \pi_j(S_j)) * f_{\text{count}}(y_{ij}; \mu_i, \sigma_i^2)$ . The log-likelihood in this extended model is:  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 \mid \text{data})$ .

### Usage

```
fitZig(
  obj,
  mod,
  zeroMod = NULL,
  useCSSoffset = TRUE,
  control = zigControl(),
  useMixedModel = FALSE,
  ...
)
```

### Arguments

obj	A MRexperiment object with count data.
mod	The model for the count distribution.
zeroMod	The zero model, the model to account for the change in the number of OTUs observed as a linear effect of the depth of coverage.
useCSSoffset	Boolean, whether to include the default scaling parameters in the model or not.
control	The settings for fitZig.
useMixedModel	Estimate the correlation between duplicate features or replicates using duplicateCorrelation.
...	Additional parameters for duplicateCorrelation.

### Value

A list of objects including:

- call - the call made to fitZig
- fit - 'MLArrayLM' Limma object of the weighted fit
- countResiduals - standardized residuals of the fit
- z - matrix of the posterior probabilities
- eb - output of eBayes, moderated t-statistics, moderated F-statistics, etc
- taxa - vector of the taxa names
- counts - the original count matrix input

- zeroMod - the zero model matrix
- zeroCoef - the zero model fitted results
- stillActive - convergence
- stillActiveNLL - nll at convergence
- dupcor - correlation of duplicates

### See Also

[cumNorm](#) [zigControl](#)

### Examples

```
# This is a simple demonstration
data(lungData)
k = grep("Extraction.Control",pData(lungData)$SampleType)
lungTrim = lungData[,-k]
k = which(rowSums(MRcounts(lungTrim)>0)<30)
lungTrim = cumNorm(lungTrim)
lungTrim = lungTrim[-k,]
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
# The maxit is not meant to be 1 - this is for demonstration/speed
settings = zigControl(maxit=1,verbose=FALSE)
fit = fitZig(obj = lungTrim,mod=mod,control=settings)
```

---

fitZigResults-class    *Class "fitZigResults" – a formal class for storing results from a fitZig call*

---

### Description

This class contains all of the same information expected from a fitZig call, but it is defined in the S4 style as opposed to being stored as a list.

### Slots

call    the call made to fitZig  
fit    'MLArrayLM' Limma object of the weighted fit  
countResiduals    standardized residuals of the fit  
z    matrix of the posterior probabilities. It is defined as  $\$z_{ij} = \text{pr}(\text{delta}_{ij}=1 \mid \text{data})$   
zUsed    used in [getZ](#)  
eb    output of eBayes, moderated t-statistics, moderated F-statistics, etc  
taxa    vector of the taxa names  
counts    the original count matrix input  
zeroMod    the zero model matrix  
zeroCoef    the zero model fitted results  
stillActive    convergence  
stillActiveNLL    nll at convergence  
dupcor    correlation of duplicates

---

getCountDensity	<i>Compute the value of the count density function from the count model residuals.</i>
-----------------	--

---

### Description

Calculate density values from a normal:  $f(x) = 1/(\sqrt{2\pi}\sigma) e^{-((x - \mu)^2/(2\sigma^2))}$ . Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The density is defined as  $f_{\text{zig}}(y_{ij} = \pi_j(S_j) \cdot f_0(y_{ij}) + (1 - \pi_j(S_j)) \cdot f_{\text{count}}(y_{ij}; \mu_i, \sigma_i^2)$ . The log-likelihood in this extended model is  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 \mid \text{data})$ .

### Usage

```
getCountDensity(residuals, log = FALSE)
```

### Arguments

residuals	Residuals from the count model.
log	Whether or not we are calculating from a log-normal distribution.

### Value

Density values from the count model residuals.

### See Also

[fitZig](#)

---

getEpsilon	<i>Calculate the relative difference between iterations of the negative log-likelihoods.</i>
------------	--

---

### Description

Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The log-likelihood in this extended model is  $(1 - \delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1 - \delta_{ij}) \log (1 - \pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij} = 1 \mid \text{data})$ .

### Usage

```
getEpsilon(nll, nllold)
```

### Arguments

nll	Vector of size M with the current negative log-likelihoods.
nllold	Vector of size M with the previous iterations negative log-likelihoods.



**Value**

Vector of size M of the relative differences between the previous and current iteration nll.

**See Also**

[fitZig](#)

---

getNegativeLogLikelihoods

*Calculate the negative log-likelihoods for the various features given the residuals.*

---

**Description**

Maximum-likelihood estimates are approximated using the EM algorithm where we treat mixture membership  $\delta_{ij} = 1$  if  $y_{ij}$  is generated from the zero point mass as latent indicator variables. The log-likelihood in this extended model is  $(1-\delta_{ij}) \log f_{\text{count}}(y; \mu_i, \sigma_i^2) + \delta_{ij} \log \pi_j(s_j) + (1-\delta_{ij}) \log (1-\pi_j(s_j))$ . The responsibilities are defined as  $z_{ij} = \text{pr}(\delta_{ij}=1 \mid \text{data and current values})$ .

**Usage**

```
getNegativeLogLikelihoods(z, countResiduals, zeroResiduals)
```

**Arguments**

z	Matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).
countResiduals	Residuals from the count model.
zeroResiduals	Residuals from the zero model.

**Value**

Vector of size M of the negative log-likelihoods for the various features.

**See Also**

[fitZig](#)

---

getPi	<i>Calculate the mixture proportions from the zero model / spike mass model residuals.</i>
-------	--

---

**Description**

$F(x) = 1 / (1 + \exp(-(x-m)/s))$  (the CDF of the logistic distribution). Provides the probability that a real-valued random variable  $X$  with a given probability distribution will be found at a value less than or equal to  $x$ . The output are the mixture proportions for the samples given the residuals from the zero model.

**Usage**

```
getPi(residuals)
```

**Arguments**

residuals      Residuals from the zero model.

**Value**

Mixture proportions for each sample.

**See Also**

[fitZig](#)

---

getZ	<i>Calculate the current Z estimate responsibilities (posterior probabilities)</i>
------	--

---

**Description**

Calculate the current Z estimate responsibilities (posterior probabilities)

**Usage**

```
getZ(z, zUsed, stillActive, nll, nllUSED)
```

**Arguments**

**z**      Matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0).

**zUsed**      Matrix (m x n) of estimate responsibilities (probabilities that a count comes from a spike distribution at 0) that are actually used (following convergence).

**stillActive**      A vector of size M booleans saying if a feature is still active or not.

**nll**      Vector of size M with the current negative log-likelihoods.

**nllUSED**      Vector of size M with the converged negative log-likelihoods.

**Value**

A list of updated zUsed and nllUSED.

**See Also**

[fitZig](#)

---

isItStillActive	<i>Function to determine if a feature is still active.</i>
-----------------	--

---

**Description**

In the Expectation Maximization routine features posterior probabilities routinely converge based on a tolerance threshold. This function checks whether or not the feature's negative log-likelihood (measure of the fit) has changed or not.

**Usage**

```
isItStillActive(eps, tol, stillActive, stillActiveNLL, nll)
```

**Arguments**

eps	Vector of size M (features) representing the relative difference between the new nll and old nll.
tol	The threshold tolerance for the difference
stillActive	A vector of size M booleans saying if a feature is still active or not.
stillActiveNLL	A vector of size M recording the negative log-likelihoods of the various features, updated for those still active.
nll	Vector of size M with the current negative log-likelihoods.

**Value**

None.

**See Also**

[fitZig](#)

---

libSize	<i>Access sample depth of coverage from MRExperiment object</i>
---------	---

---

**Description**

Access the libSize vector represents the column (sample specific) sums of features, i.e. the total number of reads for a sample or depth of coverage. It is used by [fitZig](#).

**Usage**

```
libSize(object)
```

**Arguments**

object	a MRExperiment object
--------	-----------------------

**Value**

Library sizes

**Author(s)**

Joseph N. Paulson

**Examples**

```
data(lungData)
head(libSize(lungData))
```

---

libSize<-	<i>Replace the library sizes in a MRExperiment object</i>
-----------	---

---

**Description**

Function to replace the scaling factors, aka the library sizes, of samples in a MRExperiment object.

**Usage**

```
## S4 replacement method for signature 'MRExperiment,numeric'
libSize(object) <- value
```

**Arguments**

object	a MRExperiment object
value	vector of library sizes

**Value**

vector library sizes

**Author(s)**

Joseph N. Paulson

**Examples**

```
data(lungData)
head(libSize(lungData)<- rnorm(1))
```

---

loadBiom

*Load objects organized in the Biom format.*

---

**Description**

Wrapper to load Biom formatted object.

**Usage**

```
loadBiom(file)
```

**Arguments**

file            The biom object filepath.

**Value**

A MRExperiment object.

**See Also**

[loadMeta](#) [loadPhenoData](#) [newMRExperiment](#) [biom2MRExperiment](#)

**Examples**

```
#library(biomformat)
rich_dense_file = system.file("extdata", "rich_dense_otu_table.biom", package = "biomformat")
x = loadBiom(rich_dense_file)
x
```

---

loadMeta	<i>Load a count dataset associated with a study.</i>
----------	--

---

**Description**

Load a matrix of OTUs in a tab delimited format

**Usage**

```
loadMeta(file, sep = "\t")
```

**Arguments**

file	Path and filename of the actual data file.
sep	File delimiter.

**Value**

A list with objects 'counts' and 'taxa'.

**See Also**

[loadPhenoData](#)

**Examples**

```
dataDirectory <- system.file("extdata", package="metagenomeSeq")  
lung = loadMeta(file.path(dataDirectory, "CHK_NAME.otus.count.csv"))
```

---

loadMetaQ	<i>Load a count dataset associated with a study set up in a Qiime format.</i>
-----------	---

---

**Description**

Load a matrix of OTUs in Qiime's format

**Usage**

```
loadMetaQ(file)
```

**Arguments**

file	Path and filename of the actual data file.
------	--

**Value**

An list with 'counts' containing the count data, 'taxa' containing the otu annotation, and 'otus'.

**See Also**

[loadMeta](#) [loadPhenoData](#)

**Examples**

```
# see vignette
```

---

loadPhenoData	<i>Load a clinical/phenotypic dataset associated with a study.</i>
---------------	--

---

**Description**

Load a matrix of metadata associated with a study.

**Usage**

```
loadPhenoData(file, tran = TRUE, sep = "\t")
```

**Arguments**

file	Path and filename of the actual clinical file.
tran	Boolean. If the covariates are along the columns and samples along the rows, then tran should equal TRUE.
sep	The separator for the file.

**Value**

The metadata as a dataframe.

**See Also**

[loadMeta](#)

**Examples**

```
dataDirectory <- system.file("extdata", package="metagenomeSeq")
clin = loadPhenoData(file.path(dataDirectory,"CHK_clinical.csv"),tran=TRUE)
```

---

lungData

*OTU abundance matrix of samples from a smoker/non-smoker study*


---

**Description**

This is a list with a matrix of OTU counts,otu names, taxa annotations for each OTU, and phenotypic data. Samples along the columns and OTUs along the rows.

**Format**

A list of OTU matrix, taxa, otus, and phenotypes

**Value**

MRExperiment-class object of 16S lung samples.

**References**

<http://www.ncbi.nlm.nih.gov/pubmed/21680950>

---

makeLabels

*Function to make labels simpler*


---

**Description**

Beginning to transition to better axes for plots

**Usage**

```
makeLabels(x = "samples", y = "abundance", norm, log)
```

**Arguments**

x	string for the x-axis
y	string for the y-axis
norm	is the data normalized?
log	is the data logged?

**Value**

vector of x,y labels

**Examples**

```
metagenomeSeq::makeLabels(norm=TRUE,log=TRUE)
```



---

mergeMRExperiments	<i>Merge two MRExperiment objects together</i>
--------------------	--

---

**Description**

This function will take two MRExperiment objects and merge them together finding common OTUs. If there are OTUs not found in one of the two MRExperiments then a message will announce this and values will be coerced to zero for the second table.

**Usage**

```
mergeMRExperiments(x, y)
```

**Arguments**

x	MRExperiment-class object 1.
y	MRExperiment-class object 2.

**Value**

Merged MRExperiment-class object.

**Examples**

```
data(mouseData)
newobj = mergeMRExperiments(mouseData, mouseData)
newobj

# let me know if people are interested in an option to merge by keys instead of row names.
data(lungData)
newobj = mergeMRExperiments(mouseData, lungData)
newobj
```

---

mergeTable	<i>Merge two tables</i>
------------	-------------------------

---

**Description**

Merge two tables

**Usage**

```
mergeTable(x, y)
```

**Arguments**

x	Table 1.
y	Table 2.

**Value**

Merged table

---

metagenomeSeq-deprecated

*Deprecated functions in the metagenomeSeq package.*

---

### Description

These functions may be removed completely in the next release.

### Usage

```
deprecated_metagenomeSeq_function(x, value, ...)
```

### Arguments

x	For assignment operators, the object that will undergo a replacement (object inside parenthesis).
value	For assignment operators, the value to replace with (the right side of the assignment).
...	For functions other than assignment operators, parameters to be passed to the modern version of the function (see table).

---

mouseData

*OTU abundance matrix of mice samples from a diet longitudinal study*

---

### Description

This is a list with a matrix of OTU counts, taxa annotations for each OTU, otu names, and vector of phenotypic data. Samples along the columns and OTUs along the rows.

### Format

A list of OTU matrix, taxa, otus, and phenotypes

### Value

MRExperiment-class object of 16S mouse samples.

### References

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2894525/>

MRcoefs

*Table of top-ranked features from fitZig or fitFeatureModel***Description**

Extract a table of the top-ranked features from a linear model fit. This function will be updated soon to provide better flexibility similar to limma's topTable.

**Usage**

```
MRcoefs(
  obj,
  by = 2,
  coef = NULL,
  number = 10,
  taxa = obj@taxa,
  uniqueNames = FALSE,
  adjustMethod = "fdr",
  alpha = 0.1,
  group = 0,
  eff = 0,
  numberEff = FALSE,
  counts = 0,
  file = NULL
)
```

**Arguments**

obj	Output of fitFeatureModel or fitZig.
by	Column number or column name specifying which coefficient or contrast of the linear model is of interest.
coef	Column number(s) or column name(s) specifying which coefficient or contrast of the linear model to display.
number	The number of bacterial features to pick out.
taxa	Taxa list.
uniqueNames	Number the various taxa.
adjustMethod	Method to adjust p-values by. Default is "FDR". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">p.adjust</a> for more details. Additionally, options using independent hypothesis weighting (IHW) are available. See <a href="#">MRihw</a> for more details.
alpha	Value for p-value significance threshold when running IHW. The default is set to 0.1
group	One of five choices, 0,1,2,3,4. 0: the sort is ordered by a decreasing absolute value coefficient fit. 1: the sort is ordered by the raw coefficient fit in decreasing order. 2: the sort is ordered by the raw coefficient fit in increasing order. 3: the sort is ordered by the p-value of the coefficient fit in increasing order. 4: no sorting.
eff	Filter features to have at least a "eff" quantile or number of effective samples.

numberEff	Boolean, whether eff should represent quantile (default/FALSE) or number.
counts	Filter features to have at least 'counts' counts.
file	Name of output file, including location, to save the table.

**Value**

Table of the top-ranked features determined by the linear fit's coefficient.

**See Also**

[fitZig](#) [fitFeatureModel](#) [MRtable](#) [MRfulltable](#)

**Examples**

```
data(lungData)
k = grep("Extraction.Control",pData(lungData)$SampleType)
lungTrim = lungData[,-k]
lungTrim=filterData(lungTrim,present=30)
lungTrim=cumNorm(lungTrim,p=0.5)
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
fit = fitZig(obj = lungTrim,mod=mod)
head(MRcoefs(fit))
####
fit = fitFeatureModel(obj = lungTrim,mod=mod)
head(MRcoefs(fit))
```

---

MRcounts

*Accessor for the counts slot of a MRexperiment object*


---

**Description**

The counts slot holds the raw count data representing (along the rows) the number of reads annotated for a particular feature and (along the columns) the sample.

**Usage**

```
MRcounts(obj, norm = FALSE, log = FALSE, sl = 1000)
```

**Arguments**

obj	a MRexperiment object.
norm	logical indicating whether or not to return normalized counts.
log	TRUE/FALSE whether or not to log2 transform scale.
sl	The value to scale by (default=1000).

**Value**

Normalized or raw counts

**Author(s)**

Joseph N. Paulson, [jpaulson@umiacs.umd.edu](mailto:jpaulson@umiacs.umd.edu)

**Examples**

```
data(lungData)
head(MRcounts(lungData))
```

---

MRexperiment

*Class "MRexperiment" – a modified eSet object for the data from high-throughput sequencing experiments*

---

**Description**

This is the main class for metagenomeSeq.

**Objects from the Class**

Objects should be created with calls to [newMRexperiment](#).

**Extends**

Class eSet (package 'Biobase'), directly. Class VersionedBiobase (package 'Biobase'), by class "eSet", distance 2. Class Versioned (package 'Biobase'), by class "eSet", distance 3.

**Methods**

Class-specific methods.

- [ Subset operation, taking two arguments and indexing the sample and variable. Returns an MRexperiment object, including relevant metadata. Setting drop=TRUE generates an error. Subsetting the data, the experiment summary slot is repopulated and pData is repopulated after calling factor (removing levels not present).

**Note**

Note: This is a summary for reference. For an explanation of the actual usage, see the vignette.

MRexperiments are the main class in use by metagenomeSeq. The class extends eSet and provides additional slots which are populated during the analysis pipeline.

MRexperiment dataset are created with calls to [newMRexperiment](#). MRexperiment datasets contain raw count matrices (integers) accessible through [MRcounts](#). Similarly, normalized count matrices can be accessed (following normalization) through [MRcounts](#) by calling norm=TRUE. Following an analysis, a matrix of posterior probabilities for counts is accessible through [posteriorProbs](#).

The normalization factors used in analysis can be recovered by [normFactors](#), as can the library sizes of samples (depths of coverage), [libSize](#).

Similarly to other RNASeq bioconductor packages available, the rows of the matrix correspond to a feature (be it OTU, species, gene, etc.) and each column an experimental sample. Pertinent clinical information and potential confounding factors are stored in the phenoData slot (accessed via pData).

To populate the various slots in an MRexperiment several functions are run. 1) `cumNormStat` calculates the proper percentile to calculate normalization factors. The `cumNormStat` slot is populated. 2) `cumNorm` calculates the actual normalization factors using `p = cumNormStat`.

Other functions will place subsequent matrices (normalized counts (`cumNormMat`), posterior probabilities (`posteriorProbs`))

As mentioned above, MRexperiment is derived from the virtual class, `eSet` and thereby has a `phenoData` slot which allows for sample annotation. In the `phenoData` data frame factors are stored. The normalization factors and library size information is stored in a slot called `expSummary` that is an annotated data frame and is repopulated for subsetted data.

## Examples

```
# See vignette
```

---

MRexperiment2biom	<i>MRexperiment to biom objects</i>
-------------------	-------------------------------------

---

## Description

Wrapper to convert MRexperiment objects to biom objects.

## Usage

```
MRexperiment2biom(
  obj,
  id = NULL,
  norm = FALSE,
  log = FALSE,
  sl = 1000,
  qiimeVersion = TRUE
)
```

## Arguments

<code>obj</code>	The MRexperiment object.
<code>id</code>	Optional id for the biom matrix.
<code>norm</code>	normalize count table
<code>log</code>	log2 transform count table
<code>sl</code>	scaling factor for normalized counts.
<code>qiimeVersion</code>	Format <code>fData</code> according to QIIME specifications (assumes only taxonomy in <code>fData</code> ).

## Value

A biom object.

## See Also

[loadMeta](#) [loadPhenoData](#) [newMRexperiment](#) [loadBiom](#) [biom2MRexperiment](#)

---

MRfulltable	<i>Table of top microbial marker gene from linear model fit including sequence information</i>
-------------	--

---

### Description

Extract a table of the top-ranked features from a linear model fit. This function will be updated soon to provide better flexibility similar to `limma`'s `topTable`. This function differs from `link{MRcoefs}` in that it provides other information about the presence or absence of features to help ensure significant features called are moderately present.

### Usage

```
MRfulltable(
  obj,
  by = 2,
  coef = NULL,
  number = 10,
  taxa = obj@taxa,
  uniqueNames = FALSE,
  adjustMethod = "fdr",
  group = 0,
  eff = 0,
  numberEff = FALSE,
  ncounts = 0,
  file = NULL
)
```

### Arguments

<code>obj</code>	Output of <code>fitFeatureModel</code> or <code>fitZig</code> .
<code>by</code>	Column number or column name specifying which coefficient or contrast of the linear model is of interest.
<code>coef</code>	Column number(s) or column name(s) specifying which coefficient or contrast of the linear model to display.
<code>number</code>	The number of bacterial features to pick out.
<code>taxa</code>	Taxa list.
<code>uniqueNames</code>	Number the various taxa.
<code>adjustMethod</code>	Method to adjust p-values by. Default is "FDR". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">p.adjust</a> for more details.
<code>group</code>	One of five choices: 0,1,2,3,4. 0: the sort is ordered by a decreasing absolute value coefficient fit. 1: the sort is ordered by the raw coefficient fit in decreasing order. 2: the sort is ordered by the raw coefficient fit in increasing order. 3: the sort is ordered by the p-value of the coefficient fit in increasing order. 4: no sorting.
<code>eff</code>	Filter features to have at least a "eff" quantile or number of effective samples.
<code>numberEff</code>	Boolean, whether <code>eff</code> should represent quantile (default/FALSE) or number.
<code>ncounts</code>	Filter features to those with at least 'counts' counts.
<code>file</code>	Name of output file, including location, to save the table.

**Value**

Table of the top-ranked features determined by the linear fit's coefficient.

**See Also**

[fitZig](#) [fitFeatureModel](#) [MRcoefs](#) [MRtable](#) [fitPA](#)

**Examples**

```
data(lungData)
k = grep("Extraction.Control",pData(lungData)$SampleType)
lungTrim = lungData[,-k]
lungTrim=filterData(lungTrim,present=30)
lungTrim=cumNorm(lungTrim,p=0.5)
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
fit = fitZig(obj = lungTrim,mod=mod)
head(MRfulltable(fit))
####
fit = fitFeatureModel(obj = lungTrim,mod=mod)
head(MRfulltable(fit))
```

---

MRihw

*MRihw runs IHW within a MRcoefs() call*

---

**Description**

Function used in MRcoefs() when "IHW" is set as the p value adjustment method

**Usage**

```
MRihw(obj, ...)
```

**Arguments**

obj	Either a fitFeatureModelResults or fitZigResults object
...	other parameters

---

MRihw,fitFeatureModelResults-method

*MRihw runs IHW within a MRcoefs() call*

---

**Description**

Function used in MRcoefs() when "IHW" is set as the p value adjustment method

**Usage**

```
## S4 method for signature 'fitFeatureModelResults'
MRihw(obj, p, adjustMethod, alpha)
```



**Arguments**

obj	Either a fitFeatureModelResults or fitZigResults object
p	a vector of pvalues extracted from obj
adjustMethod	Value specifying which adjustment method and which covariate to use for IHW pvalue adjustment. For obj of class <code>fitFeatureModelResults-class</code> , options are "ihw-abundance" (median feature count per row) and "ihw-ubiquity" (number of non-zero features per row). For obj of class <code>fitZigResults-class</code> , options are "ihw-abundance" (weighted mean per feature) and "ihw-ubiquity" (number of non-zero features per row).
alpha	pvalue significance level specified for IHW call. Default is 0.1

---

 MRihw,fitZigResults-method

*MRihw runs IHW within a MRcoefs() call*

---

**Description**

Function used in MRcoefs() when "IHW" is set as the p value adjustment method

**Usage**

```
## S4 method for signature 'fitZigResults'
MRihw(obj, p, adjustMethod, alpha)
```

**Arguments**

obj	Either a fitFeatureModelResults or fitZigResults object
p	a vector of pvalues extracted from obj
adjustMethod	Value specifying which adjustment method and which covariate to use for IHW pvalue adjustment. For obj of class <code>fitFeatureModelResults-class</code> , options are "ihw-abundance" (median feature count per row) and "ihw-ubiquity" (number of non-zero features per row). For obj of class <code>fitZigResults-class</code> , options are "ihw-abundance" (weighted mean per feature) and "ihw-ubiquity" (number of non-zero features per row).
alpha	pvalue significance level specified for IHW call. Default is 0.1

---

 MRtable

*Table of top microbial marker gene from linear model fit including sequence information*

---

**Description**

Extract a table of the top-ranked features from a linear model fit. This function will be updated soon to provide better flexibility similar to limma's topTable. This function differs from `link{MRcoefs}` in that it provides other information about the presence or absence of features to help ensure significant features called are moderately present.

**Usage**

```
MRtable(
  obj,
  by = 2,
  coef = NULL,
  number = 10,
  taxa = obj@taxa,
  uniqueNames = FALSE,
  adjustMethod = "fdr",
  group = 0,
  eff = 0,
  numberEff = FALSE,
  ncounts = 0,
  file = NULL
)
```

**Arguments**

obj	Output of fitFeatureModel or fitZig.
by	Column number or column name specifying which coefficient or contrast of the linear model is of interest.
coef	Column number(s) or column name(s) specifying which coefficient or contrast of the linear model to display.
number	The number of bacterial features to pick out.
taxa	Taxa list.
uniqueNames	Number the various taxa.
adjustMethod	Method to adjust p-values by. Default is "FDR". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">p.adjust</a> for more details.
group	One of five choices, 0,1,2,3,4. 0: the sort is ordered by a decreasing absolute value coefficient fit. 1: the sort is ordered by the raw coefficient fit in decreasing order. 2: the sort is ordered by the raw coefficient fit in increasing order. 3: the sort is ordered by the p-value of the coefficient fit in increasing order. 4: no sorting.
eff	Filter features to have at least a "eff" quantile or number of effective samples.
numberEff	Boolean, whether eff should represent quantile (default/FALSE) or number.
ncounts	Filter features to have at least 'counts' of counts.
file	Name of file, including location, to save the table.

**Value**

Table of the top-ranked features determined by the linear fit's coefficient.

**See Also**

[fitZig](#) [fitFeatureModel](#) [MRcoefs](#) [MRfulltable](#)

**Examples**

```

data(lungData)
k = grep("Extraction.Control",pData(lungData)$SampleType)
lungTrim = lungData[,-k]
lungTrim=filterData(lungTrim,present=30)
lungTrim=cumNorm(lungTrim,p=0.5)
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
fit = fitZig(obj = lungTrim,mod=mod)
head(MRtable(fit))
####
fit = fitFeatureModel(obj = lungTrim,mod=mod)
head(MRtable(fit))

```

---

newMRExperiment	<i>Create a MRExperiment object</i>
-----------------	-------------------------------------

---

**Description**

This function creates a MRExperiment object from a matrix or data frame of count data.

**Usage**

```

newMRExperiment(
  counts,
  phenoData = NULL,
  featureData = NULL,
  libSize = NULL,
  normFactors = NULL
)

```

**Arguments**

counts	A matrix or data frame of count data. The count data is representative of the number of reads annotated for a feature (be it gene, OTU, species, etc). Rows should correspond to features and columns to samples.
phenoData	An AnnotatedDataFrame with pertinent sample information.
featureData	An AnnotatedDataFrame with pertinent feature information.
libSize	libSize, library size, is the total number of reads for a particular sample.
normFactors	normFactors, the normalization factors used in either the model or as scaling factors of sample counts for each particular sample.

**Details**

See [MRExperiment-class](#) and eSet (from the Biobase package) for the meaning of the various slots.

**Value**

an object of class MRExperiment

**Author(s)**

Joseph N Paulson

**Examples**

```
cnts = matrix(abs(rnorm(1000)),nc=10)
obj <- newMRExperiment(cnts)
```

---

normFactors

*Access the normalization factors in a MRExperiment object*

---

**Description**

Function to access the scaling factors, aka the normalization factors, of samples in a MRExperiment object.

**Usage**

```
normFactors(object)
```

**Arguments**

object            a MRExperiment object

**Value**

Normalization scaling factors

**Author(s)**

Joseph N. Paulson

**Examples**

```
data(lungData)
head(normFactors(lungData))
```

---

normFactors<-	<i>Replace the normalization factors in a MRExperiment object</i>
---------------	---

---

**Description**

Function to replace the scaling factors, aka the normalization factors, of samples in a MRExperiment object.

**Usage**

```
## S4 replacement method for signature 'MRExperiment,numeric'  
normFactors(object) <- value
```

**Arguments**

object	a MRExperiment object
value	vector of normalization scaling factors

**Value**

Normalization scaling factors

**Author(s)**

Joseph N. Paulson

**Examples**

```
data(lungData)  
head(normFactors(lungData)<- rnorm(1))
```

---

plotBubble	<i>Basic plot of binned vectors.</i>
------------	--------------------------------------

---

**Description**

This function plots takes two vectors, calculates the contingency table and plots circles sized by the contingency table value. Optional significance vectors of the values significant will shade the circles by proportion of significance.

**Usage**

```
plotBubble(  
  yvector,  
  xvector,  
  sigvector = NULL,  
  nbreaks = 10,  
  ybreak = quantile(yvector, p = seq(0, 1, length.out = nbreaks)),  
  xbreak = quantile(xvector, p = seq(0, 1, length.out = nbreaks)),
```

```

    scale = 1,
    local = FALSE,
    ...
  )

```

### Arguments

yvector	A vector of values represented along y-axis.
xvector	A vector of values represented along x-axis.
sigvector	A vector of the names of significant features (names should match x/yvector).
nbreaks	Number of bins to break yvector and xvector into.
ybreak	The values to break the yvector at.
xbreak	The values to break the xvector at.
scale	Scaling of circle bin sizes.
local	Boolean to shade by significant bin numbers (TRUE) or overall proportion (FALSE).
...	Additional plot arguments.

### Value

A matrix of features along rows, and the group membership along columns.

### See Also

[plotMRheatmap](#)

### Examples

```

data(mouseData)
mouseData = mouseData[which(rowSums(mouseData)>139),]
sparsity = rowMeans(MRcounts(mouseData)==0)
lor = log(fitPA(mouseData,cl=pData(mouseData)[,3])$oddsRatio)
plotBubble(lor,sparsity,main="lor ~ sparsity")
# Example 2
x = runif(100000)
y = runif(100000)
plotBubble(y,x)

```

---

plotClassTimeSeries    *Plot abundances by class*

---

### Description

Plot the abundance of values for each class using a spline approach on the estimated full model.

**Usage**

```
plotClassTimeSeries(
  res,
  formula,
  xlab = "Time",
  ylab = "Abundance",
  color0 = "black",
  color1 = "red",
  include = c("1", "class", "time:class"),
  ...
)
```

**Arguments**

res	Output of fitTimeSeries function
formula	Formula for ssanova. Of the form: abundance ~ ... where ... includes any pData slot value.
xlab	X-label.
ylab	Y-label.
color0	Color of samples from first group.
color1	Color of samples from second group.
include	Parameters to include in prediction.
...	Extra plotting arguments.

**Value**

Plot for abundances of each class using a spline approach on estimated null model.

**See Also**

[fitTimeSeries](#)

**Examples**

```
data(mouseData)
res = fitTimeSeries(obj=mouseData, feature="Actinobacteria",
  class="status", id="mouseID", time="relativeTime", lvl='class', B=10)
plotClassTimeSeries(res, pch=21, bg=res$data$class, ylim=c(0, 8))
```

---

plotCorr	<i>Basic correlation plot function for normalized or unnormalized counts.</i>
----------	---

---

**Description**

This function plots a heatmap of the "n" features with greatest variance across rows.

**Usage**

```
plotCorr(obj, n, norm = TRUE, log = TRUE, fun = cor, ...)
```

**Arguments**

obj	A MRExperiment object with count data.
n	The number of features to plot. This chooses the "n" features with greatest variance.
norm	Whether or not to normalize the counts - if MRExperiment object.
log	Whether or not to log2 transform the counts - if MRExperiment object.
fun	Function to calculate pair-wise relationships. Default is pearson correlation
...	Additional plot arguments.

**Value**

plotted correlation matrix

**See Also**

[cumNormMat](#)

**Examples**

```
data(mouseData)
plotCorr(obj=mouseData,n=200,cexRow = 0.4,cexCol = 0.4,trace="none",dendrogram="none",
         col = colorRampPalette(brewer.pal(9, "RdBu"))(50))
```

---

plotFeature

*Basic plot function of the raw or normalized data.*

---

**Description**

This function plots the abundance of a particular OTU by class. The function is the typical manhattan plot of the abundances.

**Usage**

```
plotFeature(
  obj,
  otuIndex,
  classIndex,
  col = "black",
  sort = TRUE,
  sortby = NULL,
  norm = TRUE,
  log = TRUE,
  sl = 1000,
  ...
)
```



**Arguments**

obj	A MRExperiment object with count data.
otuIndex	The row to plot
classIndex	A list of the samples in their respective groups.
col	A vector to color samples by.
sort	Boolean, sort or not.
sortby	Default is sort by library size, alternative vector for sorting
norm	Whether or not to normalize the counts - if MRExperiment object.
log	Whether or not to log2 transform the counts - if MRExperiment object.
sl	Scaling factor - if MRExperiment and norm=TRUE.
...	Additional plot arguments.

**Value**

counts and classindex

**See Also**

[cumNorm](#)

**Examples**

```
data(mouseData)
classIndex=list(Western=which(pData(mouseData)$diet=="Western"))
classIndex$BK=which(pData(mouseData)$diet=="BK")
otuIndex = 8770

par(mfrow=c(2,1))
dates = pData(mouseData)$date
plotFeature(mouseData, norm=FALSE, log=FALSE, otuIndex, classIndex,
col=dates, sortby=dates, ylab="Raw reads")
```

---

plotGenus

*Basic plot function of the raw or normalized data.*

---

**Description**

This function plots the abundance of a particular OTU by class. The function uses the estimated posterior probabilities to make technical zeros transparent.

**Usage**

```
plotGenus(
  obj,
  otuIndex,
  classIndex,
  norm = TRUE,
  log = TRUE,
```

```

no = 1:length(otuIndex),
labs = TRUE,
xlab = NULL,
ylab = NULL,
jitter = TRUE,
jitter.factor = 1,
pch = 21,
...
)

```

### Arguments

obj	An MRExperiment object with count data.
otuIndex	A list of the otus with the same annotation.
classIndex	A list of the samples in their respective groups.
norm	Whether or not to normalize the counts - if MRExperiment object.
log	Whether or not to log <sub>2</sub> transform the counts - if MRExperiment object.
no	Which of the otuIndex to plot.
labs	Whether to include group labels or not. (TRUE/FALSE)
xlab	xlabel for the plot.
ylab	ylabel for the plot.
jitter	Boolean to jitter the count data or not.
jitter.factor	Factor value for jitter
pch	Standard pch value for the plot command.
...	Additional plot arguments.

### Value

plotted data

### See Also

[cumNorm](#)

### Examples

```

data(mouseData)
classIndex=list(controls=which(pData(mouseData)$diet=="BK"))
classIndex$cases=which(pData(mouseData)$diet=="Western")
otuIndex = grep("Strep",fData(mouseData)$family)
otuIndex=otuIndex[order(rowSums(MRcounts(mouseData)[otuIndex,]),decreasing=TRUE)]
plotGenus(mouseData,otuIndex,classIndex,no=1:2,xaxt="n",norm=FALSE,ylab="Strep normalized log(cpt)")

```

---

plotMRheatmap	<i>Basic heatmap plot function for normalized counts.</i>
---------------	---

---

### Description

This function plots a heatmap of the 'n' features with greatest variance across rows (or other statistic).

### Usage

```
plotMRheatmap(obj, n, norm = TRUE, log = TRUE, fun = sd, ...)
```

### Arguments

obj	A MRexperiment object with count data.
n	The number of features to plot. This chooses the 'n' features of greatest positive statistic.
norm	Whether or not to normalize the counts - if MRexperiment object.
log	Whether or not to log2 transform the counts - if MRexperiment object.
fun	Function to select top 'n' features.
...	Additional plot arguments.

### Value

plotted matrix

### See Also

[cumNormMat](#)

### Examples

```
data(mouseData)
trials = pData(mouseData)$diet
heatmapColColors=brewer.pal(12,"Set3")[as.integer(factor(trials))];
heatmapCols = colorRampPalette(brewer.pal(9, "RdBu"))(50)
#### version using sd
plotMRheatmap(obj=mouseData,n=200,cexRow = 0.4,cexCol = 0.4,trace="none",
              col = heatmapCols,ColSideColors = heatmapColColors)
#### version using MAD
plotMRheatmap(obj=mouseData,n=50,fun=mad,cexRow = 0.4,cexCol = 0.4,trace="none",
              col = heatmapCols,ColSideColors = heatmapColColors)
```

---

plotOrd	<i>Plot of either PCA or MDS coordinates for the distances of normalized or unnormalized counts.</i>
---------	--

---

### Description

This function plots the PCA / MDS coordinates for the "n" features of interest. Potentially uncovering batch effects or feature relationships.

### Usage

```
plotOrd(
  obj,
  tran = TRUE,
  comp = 1:2,
  norm = TRUE,
  log = TRUE,
  usePCA = TRUE,
  useDist = FALSE,
  distfun = stats::dist,
  dist.method = "euclidian",
  n = NULL,
  ...
)
```

### Arguments

obj	A MRExperiment object or count matrix.
tran	Transpose the matrix.
comp	Which components to display
norm	Whether or not to normalize the counts - if MRExperiment object.
log	Whether or not to log2 the counts - if MRExperiment object.
usePCA	TRUE/FALSE whether to use PCA or MDS coordinates (TRUE is PCA).
useDist	TRUE/FALSE whether to calculate distances.
distfun	Distance function, default is stats::dist
dist.method	If useDist==TRUE, what method to calculate distances.
n	Number of features to make use of in calculating your distances.
...	Additional plot arguments.

### Value

coordinates

### See Also

[cumNormMat](#)

**Examples**

```
data(mouseData)
c1 = pData(mouseData)[,3]
plot0rd(mouseData, tran=TRUE, useDist=TRUE, pch=21, bg=factor(c1), usePCA=FALSE)
```

---

plotOTU

*Basic plot function of the raw or normalized data.*


---

**Description**

This function plots the abundance of a particular OTU by class. The function uses the estimated posterior probabilities to make technical zeros transparent.

**Usage**

```
plotOTU(
  obj,
  otu,
  classIndex,
  log = TRUE,
  norm = TRUE,
  jitter.factor = 1,
  pch = 21,
  labs = TRUE,
  xlab = NULL,
  ylab = NULL,
  jitter = TRUE,
  ...
)
```

**Arguments**

obj	A MRexperiment object with count data.
otu	The row number/OTU to plot.
classIndex	A list of the samples in their respective groups.
log	Whether or not to log <sub>2</sub> transform the counts - if MRexperiment object.
norm	Whether or not to normalize the counts - if MRexperiment object.
jitter.factor	Factor value for jitter.
pch	Standard pch value for the plot command.
labs	Whether to include group labels or not. (TRUE/FALSE)
xlab	xlabel for the plot.
ylab	ylabel for the plot.
jitter	Boolean to jitter the count data or not.
...	Additional plot arguments.

**Value**

Plotted values

**See Also**[cumNorm](#)**Examples**

```

data(mouseData)
classIndex=list(controls=which(pData(mouseData)$diet=="BK"))
classIndex$cases=which(pData(mouseData)$diet=="Western")
# you can specify whether or not to normalize, and to what level
plotOTU(mouseData,otu=9083,classIndex,norm=FALSE,main="9083 feature abundances")

```

plotRare

*Plot of rarefaction effect***Description**

This function plots the number of observed features vs. the depth of coverage.

**Usage**

```
plotRare(obj, cl = NULL, ...)
```

**Arguments**

obj	A MRexperiment object with count data or matrix.
cl	Vector of classes for various samples.
...	Additional plot arguments.

**Value**

Library size and number of detected features

**See Also**

[plotOrd](#), [plotMRheatmap](#), [plotCorr](#), [plotOTU](#), [plotGenus](#)

**Examples**

```

data(mouseData)
cl = factor(pData(mouseData)[,3])
res = plotRare(mouseData,cl=cl,pch=21,bg=cl)
tmp=lapply(levels(cl), function(lv) lm(res[,"ident"]~res[,"libSize"]-1, subset=cl==lv))
for(i in 1:length(levels(cl))){
  abline(tmp[[i]], col=i)
}
legend("topleft", c("Diet 1","Diet 2"), text.col=c(1,2),box.col=NA)

```

---

plotTimeSeries	<i>Plot difference function for particular bacteria</i>
----------------	---

---

### Description

Plot the difference in abundance for significant features.

### Usage

```
plotTimeSeries(  
  res,  
  C = 0,  
  xlab = "Time",  
  ylab = "Difference in abundance",  
  main = "SS difference function prediction",  
  ...  
)
```

### Arguments

res	Output of fitTimeSeries function
C	Value for which difference function has to be larger or smaller than (default 0).
xlab	X-label.
ylab	Y-label.
main	Main label.
...	Extra plotting arguments.

### Value

Plot of difference in abundance for significant features.

### See Also

[fitTimeSeries](#)

### Examples

```
data(mouseData)  
res = fitTimeSeries(obj=mouseData,feature="Actinobacteria",  
  class="status",id="mouseID",time="relativeTime",lvl='class',B=10)  
plotTimeSeries(res)
```

---

posteriorProbs      *Access the posterior probabilities that results from analysis*

---

**Description**

Accessing the posterior probabilities following a run through `fitZig`

**Usage**

```
posteriorProbs(obj)
```

**Arguments**

obj                    a MRExperiment object.

**Value**

Matrix of posterior probabilities

**Author(s)**

Joseph N. Paulson

**Examples**

```
# This is a simple demonstration
data(lungData)
k = grep("Extraction.Control", pData(lungData)$SampleType)
lungTrim = lungData[,-k]
k = which(rowSums(MRcounts(lungTrim)>0)<30)
lungTrim = cumNorm(lungTrim)
lungTrim = lungTrim[-k,]
smokingStatus = pData(lungTrim)$SmokingStatus
mod = model.matrix(~smokingStatus)
# The maxit is not meant to be 1 -- this is for demonstration/speed
settings = zigControl(maxit=1, verbose=FALSE)
fit = fitZig(obj = lungTrim, mod=mod, control=settings)
head(posteriorProbs(lungTrim))
```

---

returnAppropriateObj      *Check if MRExperiment or matrix and return matrix*

---

**Description**

Function to check if object is a MRExperiment class or matrix

**Usage**

```
returnAppropriateObj(obj, norm, log, sl = 1000)
```



**Arguments**

obj	a MExperiment or matrix object
norm	return a normalized MExperiment matrix
log	return a log transformed MExperiment matrix
sl	scaling value

**Value**

Matrix

**Examples**

```
data(lungData)
head(returnAppropriateObj(lungData,norm=FALSE,log=FALSE))
```

---

ssFit	<i>smoothing-splines anova fit</i>
-------	------------------------------------

---

**Description**

Sets up a data-frame with the feature abundance, class information, time points, sample ids and returns the fitted values for the fitted model.

**Usage**

```
ssFit(
  formula,
  abundance,
  class,
  time,
  id,
  include = c("class", "time:class"),
  pd,
  ...
)
```

**Arguments**

formula	Formula for ssanova. Of the form: abundance ~ ... where ... includes any pData slot value.
abundance	Numeric vector of abundances.
class	Class membership (factor of group membership).
time	Time point vector of relative times (same length as abundance).
id	Sample / patient id.
include	Parameters to include in prediction.
pd	Extra variable.
...	Extra parameters for ssanova function (see ?ssanova).

**Value**

A list containing:

data : Inputed data

- fit : The interpolated / fitted values for timePoints
- se : The standard error for CI intervals
- timePoints : The time points interpolated over

**See Also**

[cumNorm](#) [fitTimeSeries](#) [ssPermAnalysis](#) [ssPerm](#) [ssIntervalCandidate](#)

**Examples**

```
# Not run
```

---

```
ssIntervalCandidate    calculate interesting time intervals
```

---

**Description**

Calculates time intervals of interest using SS-Anova fitted confidence intervals.

**Usage**

```
ssIntervalCandidate(fit, standardError, timePoints, positive = TRUE, C = 0)
```

**Arguments**

fit	SS-Anova fits.
standardError	SS-Anova se estimates.
timePoints	Time points interpolated over.
positive	Positive region or negative region (difference in abundance is positive/negative).
C	Value for which difference function has to be larger or smaller than (default 0).

**Value**

Matrix of time point intervals of interest

**See Also**

[cumNorm](#) [fitTimeSeries](#) [ssFit](#) [ssPerm](#) [ssPermAnalysis](#)

**Examples**

```
# Not run
```

---

ssPerm	<i>class permutations for smoothing-spline time series analysis</i>
--------	---

---

**Description**

Creates a list of permuted class memberships for the time series permutation tests.

**Usage**

```
ssPerm(df, B)
```

**Arguments**

df	Data frame containing class membership and sample/patient id label.
B	Number of permutations.

**Value**

A list of permuted class memberships

**See Also**

[cumNorm](#) [fitTimeSeries](#) [ssFit](#) [ssPermAnalysis](#) [ssIntervalCandidate](#)

**Examples**

```
# Not run
```

---

ssPermAnalysis	<i>smoothing-splines anova fits for each permutation</i>
----------------	--

---

**Description**

Calculates the fit for each permutation and estimates the area under the null (permuted) model for interesting time intervals of differential abundance.

**Usage**

```
ssPermAnalysis(  
  data,  
  formula,  
  permList,  
  intTimes,  
  timePoints,  
  include = c("class", "time:class"),  
  ...  
)
```

**Arguments**

data	Data used in estimation.
formula	Formula for ssanova. Of the form: abundance ~ ... where ... includes any pData slot value.
permList	A list of permuted class memberships
intTimes	Interesting time intervals.
timePoints	Time points to interpolate over.
include	Parameters to include in prediction.
...	Options for ssanova

**Value**

A matrix of permuted area estimates for time intervals of interest.

**See Also**

[cumNorm](#) [fitTimeSeries](#) [ssFit](#) [ssPerm](#) [ssIntervalCandidate](#)

**Examples**

```
# Not run
```

---

trapez

*Trapezoidal Integration*


---

**Description**

Compute the area of a function with values 'y' at the points 'x'. Function comes from the pracma package.

**Usage**

```
trapez(x, y)
```

**Arguments**

x	x-coordinates of points on the x-axis
y	y-coordinates of function values

**Value**

Approximated integral of the function from 'min(x)' to 'max(x)'. Or a matrix of the same size as 'y'.

**Examples**

```
# Calculate the area under the sine curve from 0 to pi:
n <- 101
x <- seq(0, pi, len = n)
y <- sin(x)
trapz(x, y)           #=> 1.999835504

# Use a correction term at the boundary: -h^2/12*(f'(b)-f'(a))
h <- x[2] - x[1]
ca <- (y[2]-y[1]) / h
cb <- (y[n]-y[n-1]) / h
trapz(x, y) - h^2/12 * (cb - ca) #=> 1.999999969
```

---

ts2MRExperiment	<i>With a list of fitTimeSeries results, generate an MRExperiment that can be plotted with metavizr</i>
-----------------	---

---

**Description**

With a list of fitTimeSeries results, generate an MRExperiment that can be plotted with metavizr

**Usage**

```
ts2MRExperiment(
  obj,
  sampleNames = NULL,
  sampleDescription = "timepoints",
  taxonomyLevels = NULL,
  taxonomyHierarchyRoot = "bacteria",
  taxonomyDescription = "taxonomy",
  featuresOfInterest = NULL,
  featureDataOfInterest = NULL
)
```

**Arguments**

obj	Output of fitMultipleTimeSeries
sampleNames	Sample names for plot
sampleDescription	Description of samples for plot axis label
taxonomyLevels	Feature names for plot
taxonomyHierarchyRoot	Root of feature hierarchy for MRExperiment
taxonomyDescription	Description of features for plot axis label
featuresOfInterest	The features to select from the fitMultipleTimeSeries output
featureDataOfInterest	featureData for the resulting MRExperiment

**Value**

MRExperiment that contains fitTimeSeries data, featureData, and phenoData

**See Also**

[fitTimeSeries](#) [fitMultipleTimeSeries](#)

**Examples**

```
data(mouseData)
res = fitMultipleTimeSeries(obj=mouseData, lvl='phylum', class="status",
                           id="mouseID", time="relativeTime", B=1)
obj = ts2MRExperiment(res)
obj
```

---

uniqueFeatures	<i>Table of features unique to a group</i>
----------------	--

---

**Description**

Creates a table of features, their index, number of positive samples in a group, and the number of reads in a group. Can threshold features by a minimum no. of reads or no. of samples.

**Usage**

```
uniqueFeatures(obj, cl, nsamples = 0, nreads = 0)
```

**Arguments**

obj	Either a MRExperiment object or matrix.
cl	A vector representing assigning samples to a group.
nsamples	The minimum number of positive samples.
nreads	The minimum number of raw reads.

**Value**

Table of features unique to a group

**Examples**

```
data(mouseData)
head(uniqueFeatures(mouseData[1:100,], cl=pData(mouseData)[,3]))
```

---

wrenchNorm	<i>Computes normalization factors using wrench instead of cumNorm</i>
------------	---

---

**Description**

Calculates normalization factors using method published by M. Sentil Kumar et al. (2018) to compute normalization factors which considers compositional bias introduced by sequencers.

**Usage**

```
wrenchNorm(obj, condition)
```

**Arguments**

obj	an MRexperiment object
condition	case control label that wrench uses to calculate normalization factors

**Value**

an MRexperiment object with updated normalization factors. Accessible by `normFactors`.

**See Also**

[cumNorm](#) [fitZig](#)

**Examples**

```
data(mouseData)
mouseData <- wrenchNorm(mouseData, condition = mouseData$diet)
head(normFactors(mouseData))
```

---

zigControl	<i>Settings for the fitZig function</i>
------------	---

---

**Description**

Settings for the fitZig function

**Usage**

```
zigControl(
  tol = 1e-04,
  maxit = 10,
  verbose = TRUE,
  dfMethod = "modified",
  pvalMethod = "default"
)
```

**Arguments**

tol	The tolerance for the difference in negative log likelihood estimates for a feature to remain active.
maxit	The maximum number of iterations for the expectation-maximization algorithm.
verbose	Whether to display iterative step summary statistics or not.
dfMethod	Either 'default' or 'modified' (by responsibilities).
pvalMethod	Either 'default' or 'bootstrap'.

**Value**

The value for the tolerance, maximum no. of iterations, and the verbose warning.

**Note**

[fitZig](#) makes use of `zigControl`.

**See Also**

[fitZig](#) [cumNorm](#) [plotOTU](#)

**Examples**

```
control = zigControl(tol=1e-10,maxit=10,verbose=FALSE)
```



# Index

- \* **package**
  - metagenomeSeq-package, 3
- [,MRexperiment,ANY,ANY,ANY-method (MRexperiment), 45
- [,MRexperiment-method (MRexperiment), 45
- aggregateBySample, 4
- aggregateByTaxonomy, 5
- aggSamp (aggregateBySample), 4
- aggTax (aggregateByTaxonomy), 5
- biom2MRexperiment, 6, 37, 46
- calcNormFactors, 7
- calcPosComponent, 7
- calcShrinkParameters, 8
- calcStandardError, 8
- calculateEffectiveSamples, 9
- calcZeroAdjustment, 9
- calcZeroComponent, 10
- colMeans,MRexperiment-method (MRexperiment), 45
- colSums,MRexperiment-method (MRexperiment), 45
- correctIndices, 10, 12
- correlationTest, 10, 11
- corTest (correlationTest), 11
- cumNorm, 7, 12, 13–15, 18, 21, 22, 25, 27, 29, 31, 46, 57, 58, 62, 66–68, 71, 72
- cumNormMat, 13, 46, 56, 59, 60
- cumNormStat, 12, 13, 15, 46
- cumNormStatFast, 7, 14, 14
- deprecated\_metagenomeSeq\_function (metagenomeSeq-deprecated), 42
- doCountMStep, 15
- doEStep, 16
- doZeroMStep, 16
- exportMat, 17
- exportMatrix (exportMat), 17
- exportStats, 18
- expSummary, 19
- expSummary,MRexperiment-method (expSummary), 19
- extractMR, 19
- filterData, 20
- fitDO, 21, 25
- fitFeatureModel, 7–10, 22, 29, 44, 48, 50
- fitFeatureModelResults-class, 23
- fitLogNormal, 23
- fitMeta, 21, 25
- fitMeta (metagenomeSeq-deprecated), 42
- fitMultipleTimeSeries, 24, 70
- fitPA, 21, 25, 48
- fitSSTimeSeries, 25, 26, 29
- fitTimeSeries, 24, 25, 27, 55, 63, 66–68, 70
- fitZeroLogNormal, 7–10, 29
- fitZig, 7, 9, 12–17, 21, 25, 30, 32–36, 44, 48, 50, 64, 71, 72
- fitZigResults-class, 31
- genusPlot (plotGenus), 57
- getCountDensity, 32
- getEpsilon, 32
- getNegativeLogLikelihoods, 33
- getPi, 34
- getZ, 31, 34
- isItStillActive, 35
- libSize, 36, 45
- libSize,MRexperiment-method (MRexperiment), 45
- libSize<-, 36
- libSize<-,MRexperiment,numeric-method (libSize<-), 36
- load\_biom (metagenomeSeq-deprecated), 42
- load\_meta (metagenomeSeq-deprecated), 42
- load\_metaQ (metagenomeSeq-deprecated), 42
- load\_phenoData (metagenomeSeq-deprecated), 42
- loadBiom, 6, 37, 46
- loadMeta, 6, 37, 38, 39, 46
- loadMetaQ, 38
- loadPhenoData, 6, 37–39, 39, 46
- lungData, 40

- makeLabels, 40
- mergeMRExperiments, 41
- mergeTable, 41
- metagenomeSeq (metagenomeSeq-package), 3
- metagenomeSeq-deprecated, 42
- metagenomeSeq-package, 3
- metagenomicLoader (loadMeta), 38
- mouseData, 42
- MRcoefs, 9, 43, 48, 50
- MRcounts, 44, 45
- MRcounts, MRExperiment-method  
(MRcounts), 44
- MRExperiment, 45
- MRExperiment-class (MRExperiment), 45
- MRExperiment2biom, 46
- MRfulltable, 9, 44, 47, 50
- MRihw, 43, 48
- MRihw, fitFeatureModelResults-method,  
48
- MRihw, fitZigResults-method, 49
- MRtable, 44, 48, 49
  
- newMRExperiment, 6, 37, 45, 46, 51
- normFactors, 45, 52, 71
- normFactors, MRExperiment-method  
(MRExperiment), 45
- normFactors<-, 53
- normFactors<-, MRExperiment, numeric-method  
(normFactors<-), 53
  
- p.adjust, 21, 25, 43, 47, 50
- phenoData (loadPhenoData), 39
- plotBubble, 53
- plotClassTimeSeries, 54
- plotCorr, 55, 62
- plotFeature, 56
- plotGenus, 57, 62
- plotMRheatmap, 54, 59, 62
- plotOrd, 60, 62
- plotOTU, 61, 62, 72
- plotRare, 62
- plotTimeSeries, 27, 29, 63
- posteriorProbs, 45, 46, 64
- posteriorProbs, MRExperiment-method  
(posteriorProbs), 64
  
- qiimeLoader (loadMetaQ), 38
- quantile, 18
  
- returnAppropriateObj, 64
- rowMeans, MRExperiment-method  
(MRExperiment), 45
- rowSums, MRExperiment-method  
(MRExperiment), 45
  
- settings2 (zigControl), 71
- ssFit, 27, 65, 66–68
- ssIntervalCandidate, 27, 66, 66, 67, 68
- ssPerm, 27, 66, 67, 68
- ssPermAnalysis, 27, 66, 67, 67
  
- trapz, 68
- ts2MRExperiment, 69
  
- uniqueFeatures, 70
  
- wrenchNorm, 71
  
- zigControl, 31, 71