

# Package ‘ReducedExperiment’

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**Type** Package

**Title** Containers and tools for dimensionally-reduced -omics representations

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**Description** Provides SummarizedExperiment-like containers for storing and manipulating dimensionally-reduced assay data. The ReducedExperiment classes allow users to simultaneously manipulate their original dataset and their decomposed data, in addition to other method-specific outputs like feature loadings. Implements utilities and specialised classes for the application of stabilised independent component analysis (sICA) and weighted gene correlation network analysis (WGCNA).

**License** GPL (>= 3)

**Encoding** UTF-8

**Depends** R (>= 4.4.0), SummarizedExperiment, methods

**Imports** WGCNA, ica, moments, clusterProfiler, msigdb, RColorBrewer, car, lme4, lmerTest, pheatmap, biomaRt, stats, grDevices, BiocParallel, ggplot2, patchwork, BiocGenerics, S4Vectors

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---

```
.DollarNames.FactorisedExperiment
```

*Command line completion for \$*

---

**Description**

Command line completion for \$. This function is not intended to be used directly by users but provides auto-completion capabilities. Autocompletes based on column data names (i.e., the column names of the colData).

**Usage**

```
## S3 method for class 'FactorisedExperiment'
.DollarNames(x, pattern = "")

## S3 method for class 'ModularExperiment'
.DollarNames(x, pattern = "")

## S3 method for class 'ReducedExperiment'
.DollarNames(x, pattern = "")
```

**Arguments**

x	The <a href="#">ReducedExperiment</a> object.
pattern	Search pattern.

**Value**

The names of the matching columns of colData.

**See Also**

[utils::.DollarNames\(\)](#)

---

assessSoftThreshold	<i>Assess soft thresholding power for WGCNA</i>
---------------------	---

---

**Description**

A wrapper around [pickSoftThreshold](#), allowing assessment and automatic selection of soft-thresholding power. Extends the function to accept a [SummarizedExperiment](#) as input and additionally considers mean connectivity when selecting the soft-thresholding power to recommend.

## Usage

```
assessSoftThreshold(
  X,
  assay_name = "normal",
  powerVector = 1:30,
  RsquaredCut = 0.85,
  max_mean_connectivity = 100,
  cor_type = "pearson",
  networkType = "signed",
  maxBlockSize = 30000,
  verbose = 0,
  ...
)
```

## Arguments

X	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to WGCNA. X should have rows as features and columns as samples.
assay_name	If X is a <a href="#">SummarizedExperiment</a> , then this should be the name of the assay to be subject to WGCNA.
powerVector	a vector of soft thresholding powers for which the scale free topology fit indices are to be calculated.
RsquaredCut	desired minimum scale free topology fitting index $R^2$ .
max_mean_connectivity	The maximal mean connectivity required. Used to select the soft-thresholding power.
cor_type	The type of correlation to be used to generate a correlation matrix during network formation. One of "pearson" ( <a href="#">cor</a> ) and "bicor" ( <a href="#">bicor</a> ).
networkType	network type. Allowed values are (unique abbreviations of) "unsigned", "signed", "signed hybrid". See <a href="#">adjacency</a> .
maxBlockSize	The chunk size (in terms of the number of features/genes) to process the data. The default (30000) should process standard transcriptomic datasets in a single chunk. Results may differ if the number of features exceeds the chunk size. Lower values of this parameter will use less memory to calculate networks.
verbose	integer level of verbosity. Zero means silent, higher values make the output progressively more and more verbose.
...	Additional arguments to be passed to <a href="#">pickSoftThreshold</a> .

## Details

The [pickSoftThreshold](#) function estimates the power by selecting the lowest value with a minimum scale free topology fitting index exceeding RsquaredCut. The assessSoftThreshold function mirrors this behaviour when max\_mean\_connectivity is NULL. When max\_mean\_connectivity is specified, however, we additionally require that the selected power does not exceed this connectivity threshold.

## Value

Returns a data.frame, generated by [pickSoftThreshold](#), with scale free topology fitting indices and connectivity statistics. Additionally contains a column, estimated\_power, indicating the rec-

ommended power to use (see details). We suggest manually considering suitability of the soft-thresholding power rather than solely relying on this automated approach.

### Author(s)

Jack Gisby

### See Also

[WGCNA::pickSoftThreshold\(\)](#), [runWGCNA\(\)](#)

### Examples

```
# Get the airway data as a SummarizedExperiment (with a subset of features)
set.seed(2)
airway_se <- ReducedExperiment:::getAirwayData(n_features = 500)

# Select soft-thresholding power to use (use capture.output to hide WGCNA's prints)
WGCNA::disableWGCNAThreads()
invisible(capture.output(fit_indices <- assessSoftThreshold(airway_se)))

print(fit_indices)
print(paste0("Estimated power: ", fit_indices$Power[fit_indices$estimated_power]))
```

---

assignments

*Get and set module feature assignments*

---

### Description

Retrieves a vector of features (usually genes) named by the modules they belong to. Assignment can be used to modify all or part of the vector.

### Usage

```
## S4 method for signature 'ModularExperiment'
assignments(object, as_list = FALSE)

## S4 replacement method for signature 'ModularExperiment'
assignments(object) <- value
```

### Arguments

object	<a href="#">ModularExperiment</a> object.
as_list	If TRUE, the results are returned as a list, with an entry for each module containing a list of features.
value	New value to replace existing assignments.

### Value

A vector with values representing features and names representing feature assignments (i.e., modules).

**Author(s)**

Jack Gisby

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me <- ReducedExperiment:::.createRandomisedModularExperiment(100, 50, 10)
me

# Assignment of features to groups/modules
assignments(me)

# We can reassign a feature to a new module if we like:
names(assignments(me))[6] <- "new_module"
assignments(me)[1:10]

# We shouldn't, however, attempt to change the feature names here:
# assignments(me)[5] <- "modified_gene_name"

# Instead, we should change the object's feature names as so:
featureNames(me)[5] <- "modified_gene_name"
assignments(me)[1:10]
```

---

associateComponents     *Runs linear models for components and sample-level data*

---

**Description**

Runs either standard linear or linear mixed models, with reduced components (e.g., factors or modules) as the outcomes and sample-level information (e.g., treatment, disease status) as predictors.

**Usage**

```
associateComponents(
  re,
  formula,
  method = "lm",
  scale_reduced = TRUE,
  center_reduced = TRUE,
  type = "II",
  adj_method = "BH",
  ...
)
```

**Arguments**

re	An object inheriting from <a href="#">ReducedExperiment</a> .
formula	The model formula to apply. Only the right hand side of the model need be specified (e.g., "~ x + y"). The left hand side (outcome) represents the components themselves. The variables in this formula should be present in the colData of re.

method	If "lm", then the <a href="#">lm</a> function is used to run linear models (in tandem with <a href="#">Anova</a> for running anovas on the model terms). If "lmer", then linear mixed models are run through <a href="#">lmer</a> .
scale_reduced	If TRUE, the reduced data are scaled (to have a standard deviation of 1) before modelling.
center_reduced	If TRUE, the reduced data are centered (to have a mean of 0) before modelling.
type	The type of anova to be applied to the terms of the linear model.
adj_method	The method for adjusting for multiple testing. Passed to the <a href="#">p.adjust</a> method parameter.
...	Additional arguments passed to <a href="#">lmer</a> , given that method is set to "lmer".

### Details

Multiple testing adjustment is performed separately for each term in the model across all factors. In other words, p-values are adjusted for the number of factors, but not the number of model terms. If you are testing a large number of terms, you could consider applying a custom adjustment method or using penalised regression.

### Value

Returns a list with the entry "models" including a list of the model objects, "anovas" containing the output of anova-based testing, and "summaries" containing the results of running summary on the models.

### Author(s)

Jack Gisby

### See Also

[stats::lm\(\)](#), [car::Anova\(\)](#), [lmerTest::lmer\(\)](#)

### Examples

```
# Create FactorisedExperiment with random data (100 features, 50 samples,
# 10 factors)
set.seed(1)
fe <- ReducedExperiment:::.createRandomisedFactorisedExperiment(100, 50, 10)
fe

# Create a sample-level variable describing some sort of treatment
colData(fe)$treated <- c(rep("control", 25), rep("treatment", 25))
colData(fe)$treated <- factor(colData(fe)$treated, c("control", "treatment"))

# Increase the value of factor 1 for the treated samples, simulating some
# kind of treatment-related effect picked up by factor analysis
reduced(fe)[, 1][colData(fe)$treated == "treatment"] <-
  reduced(fe)[, 1][colData(fe)$treated == "treatment"] +
  rnorm(25, mean = 1.5, sd = 0.1)

# Create a sample-level variable describing a covariate we want to adjust for
# We will make the treated patients slightly older on average
colData(fe)$age <- 0
colData(fe)$age[colData(fe)$treated == "control"] <- rnorm(25, mean = 35, sd = 8)
```

```
colData(fe)$age[colData(fe)$treated == "treatment"] <- rnorm(25, mean = 40, sd = 8)

# Associate the factors with sample-level variable in the colData
lm_res <- associateComponents(
  fe,
  formula = "~ treated + age", # Our model formula
  method = "lm", # Use a linear model
  adj_method = "BH" # Adjust our p-values with Benjamini-Hochberg
)

# We see that treatment is significantly associated with factor 1 (adjusted
# p-value < 0.05) and is higher in the treated patients. Age is not
# significantly associated with factor 1, but there is a slight positive
# relationship
print(head(lm_res$summaries[
  ,
  c("term", "component", "estimate", "stderr", "pvalue", "adj_pvalue")
]))

# But what if these aren't 50 independent patients, but rather 25 patients
# sampled before and after treatment? We can account for this using a
# linear mixed model, which can account for repeated measures and paired
# designs

# First we add in this information
colData(fe)$patient_id <- c(paste0("patient_", 1:25), paste0("patient_", 1:25))

# Then we run the linear mixed model with a random intercept for patient
lmm_res <- associateComponents(
  fe,
  formula = "~ treated + age + (1 | patient_id)", # Add a random intercept
  method = "lmer", # Use a linear mixed model
  adj_method = "BH"
)

# We used a different method, but can obtain a similar summary output
print(head(lmm_res$summaries[
  ,
  c("term", "component", "estimate", "stderr", "pvalue", "adj_pvalue")
]))
```

---

calcEigengenes

*Calculate eigengenes for new data*


---

## Description

Calculates eigengenes for modules in new data. By default, eigengenes are calculated from scratch using PCA, in a similar manner to the [moduleEigengenes](#) function. The function also offers a projection approach, which functions in a similar fashion to the predict method of [prcomp](#).

## Usage

```
## S4 method for signature 'ModularExperiment,matrix'
```



```

calcEigengenes(
  object,
  newdata,
  project = FALSE,
  scale_reduced = TRUE,
  return_loadings = FALSE,
  scale_newdata = NULL,
  center_newdata = NULL,
  realign = TRUE,
  min_module_genes = 10
)

## S4 method for signature 'ModularExperiment,data.frame'
calcEigengenes(
  object,
  newdata,
  project = FALSE,
  scale_reduced = TRUE,
  return_loadings = FALSE,
  scale_newdata = NULL,
  center_newdata = NULL,
  realign = TRUE,
  min_module_genes = 10
)

## S4 method for signature 'ModularExperiment,SummarizedExperiment'
calcEigengenes(
  object,
  newdata,
  project = FALSE,
  scale_reduced = TRUE,
  assay_name = "normal",
  scale_newdata = NULL,
  center_newdata = NULL,
  realign = TRUE,
  min_module_genes = 10
)

## S4 method for signature 'ModularExperiment'
predict(object, newdata, ...)

```

### Arguments

object	A <a href="#">ModularExperiment</a> object. By default, the scale and center slots are used to apply the original transformation to the new data. The loadings slot of this class will be used if project is TRUE.
newdata	New data for eigengenes to be calculated in. Must be a data.frame or matrix with features as rows and samples as columns, or a <a href="#">SummarizedExperiment</a> object. Assumes that the rows of newdata match those of the <a href="#">ModularExperiment</a> object.
project	If FALSE (default), calculate eigengenes from scratch in the new dataset using an approach similar to <a href="#">moduleEigengenes</a> (i.e., performing PCA for each module

	in newdata). If FALSE, perform projection, using PCA rotation matrix from the original data to calculate module eigengenes. Projection approach is experimental.
scale_reduced	Whether or not the reduced data should be scaled after calculation.
return_loadings	If TRUE, additionally returns the feature loadings for the eigengenes.
scale_newdata	Controls whether the newdata are scaled. If NULL, performs scaling based on the <a href="#">ModularExperiment</a> object's scale slot. The value of this argument will be passed to the scale argument of <a href="#">scale</a> .
center_newdata	Controls whether the newdata are centered. If NULL, performs centering based on the <a href="#">ModularExperiment</a> object's center slot. The value of this argument will be passed to the center argument of <a href="#">scale</a> .
realign	If project is TRUE, this argument is ignored. Else, controls whether eigengenes are realigned after PCA is performed to ensure the resultant signatures are positively correlated with average expression of the module. Similar to the align argument of <a href="#">moduleEigengenes</a> .
min_module_genes	If project is FALSE, this argument is ignored. Else, controls the minimum number of genes required in a module for projection. Projected eigengenes are not calculated for modules with sizes below this threshold.
assay_name	If a <a href="#">SummarizedExperiment</a> object is passed as new data, this argument indicates which assay should be used for projection.
...	Additional arguments to be passed to <a href="#">calcEigengenes</a> .

### Details

If scale\_newdata and center\_newdata are left as NULL, then the projection method assumes that the newdata are on the same scale as the original data of the object. It will therefore use the values of the center and scale slots of the object. For instance, if the scale slot is TRUE, the newdata will be scaled. If the scale slot is a vector, the values of this vector will be applied to scale the newdata.

### Value

If return\_loadings is TRUE, returns a list with the "reduced" matrix and "loadings" vector (one value per feature). If FALSE, returns only the reduced matrix.

The reduced matrix has samples as rows and modules as columns. If newdata was a matrix or data.frame, this will be returned as a matrix. If a [SummarizedExperiment](#) object was passed instead, then a [ModularExperiment](#) object will be created containing this matrix in its reduced slot.

### Author(s)

Jack Gisby

### See Also

[projectData](#), [moduleEigengenes](#)

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me_1 <- ReducedExperiment:::.createRandomisedModularExperiment(100, 50, 10)

# Generate a new dataset with the same features (100 rows) but different
# samples/observations (20 columns)
X_2 <- ReducedExperiment:::.makeRandomData(100, 20, "gene", "sample")

# We can use the projection approach to calculate the eigengenes for
# the modules identified in dataset 1 for the samples in dataset 2
# This approach is based on the module loadings
me_2_project <- calcEigengenes(me_1, X_2, project = TRUE)
me_2_project[1:5, 1:5]

# Alternatively, we can calculate eigengenes from scratch in the second
# dataset. This still uses the modules identified in the first dataset (me_1)
# but does not make use of the loadings. This approach is similar to
# that applied by WGCNA::moduleEigengenes.
me_2_eig <- calcEigengenes(me_1, X_2, project = FALSE)
me_2_eig[1:5, 1:5]
```

---

cbind,FactorisedExperiment-method

*Combine ReducedExperiment objects by columns or rows*


---

**Description**

Combines [ReducedExperiment](#) objects by columns (samples) or rows (features).

**Usage**

```
## S4 method for signature 'FactorisedExperiment'
cbind(..., deparse.level = 1)

## S4 method for signature 'FactorisedExperiment'
rbind(..., deparse.level = 1)

## S4 method for signature 'ModularExperiment'
cbind(..., deparse.level = 1)

## S4 method for signature 'ModularExperiment'
rbind(..., deparse.level = 1)

## S4 method for signature 'ReducedExperiment'
cbind(..., deparse.level = 1)

## S4 method for signature 'ReducedExperiment'
rbind(..., deparse.level = 1)
```

**Arguments**

... A series of [ReducedExperiment](#) objects to be combined. See [cbind,SummarizedExperiment-method](#) for further details.

deparse.level Integer, see [cbind](#).

**Details**

cbind assumes that objects have identical features and components (i.e., factors or modules). If they are not, an error is returned.

So, this means that the feature-level slots should be equivalent, for example the assay rownames and values of the loadings available in [FactorisedExperiment](#) and [ModularExperiment](#) objects. The component slots should also be equivalent, such as the column names of the reduced matrix or the column names of the aforementioned factor loadings matrix.

rbind assumes that objects have identical samples and components. If they are not, an error is returned. This means that the sample-level slots should be equivalent, including for example the assay column names.

The [SummarizedExperiment](#) package includes separate methods for cbind ([cbind,SummarizedExperiment-method](#)) and ([combineRows](#)). The latter is supposed to be more flexible, permitting differences in the number and identity of the rows. For [ReducedExperiment](#) objects we only implement a single, less flexible, method that assumes the rows and components (i.e., factors or modules) are identical across objects. Attempting to apply combineRows to a [ReducedExperiment](#) object will result in the objects being treated as if they were [SummarizedExperiments](#), and a single [SummarizedExperiment](#) object will be returned.

**Value**

Returns a single [ReducedExperiment](#) object containing all of the columns in the objects passed to cbind.

**Author(s)**

Jack Gisby

**See Also**

[base::cbind\(\)](#), [base::rbind\(\)](#), [cbind,SummarizedExperiment-method](#), [rbind,SummarizedExperiment-method](#)

**Examples**

```
# Create randomised containers with different numbers of samples
i <- 300 # Number of features
k <- 10 # Number of components (i.e., factors/modules)

# Same features and components, different samples (30 vs. 50 columns)
re_1 <- ReducedExperiment:::createRandomisedReducedExperiment(i, 50, k)
re_2 <- ReducedExperiment:::createRandomisedReducedExperiment(i, 30, k)

# Make a new object with 80 columns
cbind(re_1, re_2)

# Create randomised containers with different numbers of features
j <- 100 # Number of samples
```

```

k <- 10 # Number of components (i.e., factors/modules)

# Same features and components, different samples (30 vs. 50 columns)
re_3 <- ReducedExperiment:::.createRandomisedReducedExperiment(200, j, k)
re_4 <- ReducedExperiment:::.createRandomisedReducedExperiment(150, j, k)
reduced(re_3) <- reduced(re_4) # rbind assumes identical reduced data

# Make a new object with 80 columns
rbind(re_3, re_4)

# We can apply combineRows and combineCols to `ReducedExperiment` objects
# but the resulting object will be a `SummarizedExperiment`
combineCols(re_1, re_2)
combineRows(re_3, re_4)

```

---

```
componentNames<-,FactorisedExperiment-method
```

*Get names of dimensionally-reduced components*

---

## Description

Retrieves the feature names post-dimensionality reduction In the case of module analysis, these are the names of the gene modules; in the case of factor analysis, these are the names of the factors.

## Usage

```

## S4 replacement method for signature 'FactorisedExperiment'
componentNames(object) <- value

## S4 replacement method for signature 'ModularExperiment'
componentNames(object) <- value

## S4 method for signature 'ModularExperiment'
moduleNames(object)

## S4 replacement method for signature 'ModularExperiment'
moduleNames(object) <- value

## S4 method for signature 'ReducedExperiment'
componentNames(object)

## S4 replacement method for signature 'ReducedExperiment'
componentNames(object) <- value

```

## Arguments

object	A <a href="#">ReducedExperiment</a> object.
value	New value to replace existing names.

**Details**

componentNames is valid for all [ReducedExperiment](#) objects, whereas moduleNames is only valid for [ModularExperiments](#).

**Value**

A vector containing the names of the components.

**Author(s)**

Jack Gisby

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

rand_assay_data <- ReducedExperiment:::makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

stopifnot(all.equal(componentNames(re), colnames(rand_reduced_data)))

print(paste0("Component name at [2]: ", componentNames(re)[2]))
componentNames(re)[2] <- "custom_component_name"
print(paste0("Component name at [2]: ", componentNames(re)[2]))
```

---

dendrogram

*Get the dendrogram stored in a ModularExperiment*


---

**Description**

Get the dendrogram stored in a ModularExperiment

**Usage**

```
## S4 method for signature 'ModularExperiment'
dendrogram(object)

## S4 replacement method for signature 'ModularExperiment'
dendrogram(object) <- value
```

**Arguments**

object	A <a href="#">ModularExperiment</a> object.
value	New value to replace existing dendrogram.

**Value**

Returns a dendrogram describing relationships between genes. Usually produced through hierarchical clustering using the [blockwiseModules](#) function.

**Author(s)**

Jack Gisby

**See Also**

[WGCNA::blockwiseModules\(\)](#), [stats::hclust\(\)](#)

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me <- ReducedExperiment:::createRandomisedModularExperiment(100, 50, 10)
me

# The dendrogram is usually produced during module discovery, but we can
# assign any dendrogram to the slot. Let's do hierarchical clustering on the
# features in our object and assign it
dendrogram(me) <- hclust(dist(assay(me)))
dendrogram(me)

# Can use default plotting approach
plot(dendrogram(me))

# Or class method that calls WGCNA::plotDendroAndColors
plotDendro(me)
```

---

dim,ReducedExperiment-method

*Get the dimensions of a Reducedexperiment object*

---

**Description**

Get the dimensions of a Reducedexperiment object

**Usage**

```
## S4 method for signature 'ReducedExperiment'
dim(x)
```

**Arguments**

x                      A [ReducedExperiment](#) object.

**Value**

Returns a named vector containing the dimensions of the samples, features and reduced dimensions.

**Author(s)**

Jack Gisby

**Examples**

```
# Create a randomised ReducedExperiment
re <- ReducedExperiment:::createRandomisedReducedExperiment(100, 50, 10)

# Get the dimensions
dim(re)
```

---

estimateFactors	<i>Perform dimensionality reduction using Independent Component Analysis</i>
-----------------	--

---

**Description**

Performs independent component analysis (ICA) and packages both the input data and subsequent results into a [FactorisedExperiment](#) container. Calls [runICA](#) to perform the analysis; see its documentation page for more information on the ICA method, parameters and outputs.

**Usage**

```
estimateFactors(
  X,
  nc,
  center_X = TRUE,
  scale_X = FALSE,
  assay_name = "normal",
  ...
)
```

**Arguments**

X	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to ICA. X should have rows as features and columns as samples.
nc	The number of components to be identified. See <a href="#">estimateStability</a> for a method to estimate the optimal number of components.
center_X	If TRUE, X is centered (i.e., features / rows are transformed to have a mean of 0) prior to ICA. Generally recommended.
scale_X	If TRUE, X is scaled (i.e., features / rows are transformed to have a standard deviation of 1) before ICA.
assay_name	If X is a <a href="#">SummarizedExperiment</a> , then this should be the name of the assay to be subject to ICA.
...	Additional arguments to be passed to <a href="#">runICA</a> .



**Value**

A [FactorisedExperiment](#) is returned containing the input data (i.e., the original data matrix in addition to other slots if a [SummarizedExperiment](#) was used as input). Additionally contains the results of factor analysis, stored in the reduced and loadings slots. The center\_X, scale\_X and stability slots may also be filled depending on the arguments given to estimateFactors.

**Author(s)**

Jack Gisby

**See Also**

[runICA\(\)](#), [ica::ica\(\)](#)

**Examples**

```
# Get a random matrix with rnorm, with 100 rows (features)
# and 20 columns (observations)
X <- ReducedExperiment:::makeRandomData(100, 20, "feature", "obs")

# Estimate 5 factors based on the data matrix
set.seed(1)
fe_1 <- estimateFactors(X, nc = 5)
fe_1

# Convert the data matrix to a SummarizedExperiment, then estimate 5 factors
se <- SummarizedExperiment(assays = list("normal" = X))
set.seed(1)
fe_2 <- estimateFactors(se, nc = 5)
fe_2
```

---

estimateStability

*Estimate stability of factors as a function of the number of components*

---

**Description**

Estimates the stability of factors over a range of component numbers to aid in the identification of the optimal factor number. Based on the Most Stable Transcriptome Dimension (MSTD) approach (see details).

**Usage**

```
estimateStability(
  X,
  min_components = 10,
  max_components = 60,
  by = 2,
  n_runs = 30,
  resample = FALSE,
  mean_stability_threshold = NULL,
  center_X = TRUE,
```

```

scale_X = FALSE,
assay_name = "normal",
BPPARAM = BiocParallel::SerialParam(),
verbose = TRUE,
...
)

```

## Arguments

<code>X</code>	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to ICA. <code>X</code> should have rows as features and columns as samples.
<code>min_components</code>	The minimum number of components to estimate the stability for.
<code>max_components</code>	The maximum number of components to estimate the stability for.
<code>by</code>	The number by which to increment the numbers of components tested.
<code>n_runs</code>	The number of times to run ICA to estimate factors and quantify stability. Ignored if <code>use_stability</code> is FALSE.
<code>resample</code>	If TRUE, a bootstrap approach is used to estimate factors and quantify stability. Else, random initialisation of ICA is employed. Ignored if <code>use_stability</code> is FALSE.
<code>mean_stability_threshold</code>	A threshold for the mean stability of factors.
<code>center_X</code>	If TRUE, <code>X</code> is centered (i.e., features / rows are transformed to have a mean of 0) prior to ICA. Generally recommended.
<code>scale_X</code>	If TRUE, <code>X</code> is scaled (i.e., features / rows are transformed to have a standard deviation of 1) before ICA.
<code>assay_name</code>	If <code>X</code> is a <a href="#">SummarizedExperiment</a> , then this should be the name of the assay to be subject to ICA.
<code>BPPARAM</code>	A class containing parameters for parallel evaluation. Uses <a href="#">SerialParam</a> by default, running only a single ICA computation at a time. Ignored if <code>use_stability</code> is FALSE.
<code>verbose</code>	If TRUE, shows a progress bar that updates for each number of components tested. Note that the time taken may not be linear, because the time taken to run ICA generally increases with the number of components.
<code>...</code>	Additional arguments to be passed to <a href="#">runICA</a> .

## Details

Runs the stability-based ICA algorithm (see [runICA](#)) for a range of component numbers. Estimates stability for each, allowing for selection of the optimal number of components to be used for ICA. The results of this function can be plotted by [plotStability](#).

This algorithm is based on the Most Stable Transcriptome Dimension (MSTD) approach (<https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-017-4112-9>).

The function automatically selects a number of components based on `mean_stability_threshold`. However, this choice should be made after visualising the stabilities as a function of the number of components, which may be done using [plotStability](#). The aforementioned MSTD paper provides additional context and advice for choosing the number of components based on these results.

**Value**

Returns a list containing:

**stability** A data.frame indicating factor stabilities as a function of the number of components.

**selected\_nc** a naive estimate for the optimal number of components based on the mean\_stability\_threshold.

**Author(s)**

Jack Gisby

**See Also**

[runICA\(\)](#), [plotStability\(\)](#)

**Examples**

```
# Get a random matrix with rnorm, with 200 rows (features)
# and 100 columns (observations)
X <- ReducedExperiment:::makeRandomData(200, 100, "feature", "obs")

# Estimate stability across 10 to 30 components
# Note: We could have provided a SummarizedExperiment object instead of a matrix
stab_res_1 <- estimateStability(
  X,
  min_components = 10,
  max_components = 30,
  n_runs = 5,
  verbose = FALSE
)
```

---

FactorisedExperiment-class

*FactorisedExperiment: A container for the results of factor analysis*

---

**Description**

A container inheriting from the [ReducedExperiment](#) class, that contains one or more data matrices, to which factor analysis has been applied to identify a reduced set of features. A [FactorisedExperiment](#) can be created directly in a similar manner to a [SummarizedExperiment](#). Alternatively, the [estimateFactors](#) function can be used to both apply factor analysis and generate a [FactorisedExperiment](#) from the results.

**Usage**

```
FactorisedExperiment(
  reduced = new("matrix"),
  scale = TRUE,
  center = TRUE,
  loadings = new("matrix"),
  stability = NULL,
  ...
)
```

**Arguments**

reduced	A matrix, produced by factor analysis, with rows representing samples and columns representing factors.
scale	Either a boolean, representing whether or not the original data has been scaled to unit variance, or a numeric vector indicating the standard deviations of the original features (as produced by <a href="#">scale</a> .)
center	Either a boolean, representing whether or not the original data has been centered to have a mean of 0, or a numeric vector indicating the means of the original features (as produced by <a href="#">scale</a> .)
loadings	A matrix, produced by factor analysis, with rows representing features and columns representing factors.
stability	A vector containing some measure of stability or variance explained for each factor. If factor analysis was performed using <a href="#">estimateFactors</a> and use_stability = TRUE, this slot will indicate the stability of the factors across multiple runs of ICA.
...	Additional arguments to be passed to <a href="#">ReducedExperiment</a> .

**Value**

Constructor method returns a [FactorisedExperiment](#) object.

**Author(s)**

Jack Gisby

**See Also**

[ReducedExperiment\(\)](#), [ModularExperiment\(\)](#), [estimateFactors\(\)](#)

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

# In this case we use random assay, reduced and loadings data, but in
# practice these will likely be the result of applying some kind of factor
# analysis to the assay data (e.g., gene expression data) from some study.
rand_assay_data <- ReducedExperiment:::makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::makeRandomData(j, k, "sample", "factor")
rand_loadings <- ReducedExperiment:::makeRandomData(i, k, "gene", "factor")

fe <- FactorisedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data,
  loadings = rand_loadings
)

fe
```

---

getAlignedFeatures	<i>Get feature alignments with factors</i>
--------------------	--

---

## Description

Retrieves features (usually genes) and their alignment (loadings) with the factors. Allows for the selection of features whose alignments are high relative to other features. Useful for functional interpretation of factors.

## Usage

```
## S4 method for signature 'FactorisedExperiment'
getAlignedFeatures(
  object,
  loading_threshold = 0.5,
  proportional_threshold = 0.01,
  feature_id_col = "rownames",
  format = "list",
  center_loadings = FALSE
)
```

## Arguments

object	A <a href="#">FactorisedExperiment</a> object.
loading_threshold	A value between 0 and 1 indicating the proportion of the maximal loading to be used as a threshold. A value of 0.5 (default) means that genes will be selected if their factor alignment (derived from the loadings slot) exceeds or equals 50% of the maximally aligned feature.
proportional_threshold	A value between 0 and 1 indicating the maximal proportion of features to be returned. A value of 0.01 (default) means that a maximum of 1% of the input features (usually genes) will be returned for each factor. These will be the genes in the top percentile with respect to the loadings
feature_id_col	The column in <code>rowData(object)</code> that will be used as a feature ID. Setting this to "rownames" (default) instead uses <code>rownames(object)</code> .
format	A string specifying the format in which to return the results. See the value section below.
center_loadings	If TRUE, loadings will be centered column-wise to have a mean of 0.

## Value

If the format argument is "list", then a list will be returned with an entry for each factor, each containing a vector of input features. Otherwise, if format is "data.frame", a data.frame is returned with a row for each gene-factor combination. The format argument can also be a function to be applied to the output data.frame before returning the results.

## Author(s)

Jack Gisby

**See Also**

[getCommonFeatures\(\)](#)

**Examples**

```
# Get a random matrix with rnorm, with 100 rows (features)
# and 20 columns (observations)
X <- ReducedExperiment:::makeRandomData(100, 20, "feature", "obs")

# Estimate 5 factors based on the data matrix
fe <- estimateFactors(X, nc = 5)

# Get the genes highly aligned with each factor as a list
aligned_features <- getAlignedFeatures(fe, proportional_threshold = 0.03)
aligned_features

# Can also view as a data.frame
head(getAlignedFeatures(fe, format = "data.frame", proportional_threshold = 0.03))
```

---

getCentrality

*Get correlation of features with module eigengenes*


---

**Description**

Provides a wrapper around [signedKME](#). Provides a measure of module centrality/connectivity of each feature. Calculates correlation (Pearson's  $r$ ) of each feature with the module eigengene (i.e., the column of reduced to which the feature belongs).

**Usage**

```
## S4 method for signature 'ModularExperiment'
getCentrality(object, assay_name = "normal", feature_id_col = "rownames")
```

**Arguments**

object	A <a href="#">ModularExperiment</a> object.
assay_name	The name of the assay to be used for calculation of module centrality.
feature_id_col	The column in <code>rowData(object)</code> that will be used as a feature ID. Setting this to "rownames" (default) instead uses <code>rownames(object)</code> .

**Value**

Returns a `data.frame` with columns for feature,  $r$  (signed correlation with the eigengene),  $rsq$  (squared correlation with the eigengene),  $rank_r$  (feature rank based on  $r$ ) and  $rank_rsq$  (feature rank based on  $rsq$ ).

**Author(s)**

Jack Gisby

**See Also**

[WGCNA::signedKME\(\)](#)

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me <- ReducedExperiment:::.createRandomisedModularExperiment(100, 50, 10)
me

# Calculate centrality of each feature for the corresponding module
head(getCentrality(me))
```

---

getCommonFeatures	<i>Get common factor features</i>
-------------------	-----------------------------------

---

**Description**

Function to count how many genes are aligned with multiple factors.

**Usage**

```
getCommonFeatures(factor_features)
```

**Arguments**

factor\_features

A data.frame as returned by [getAlignedFeatures](#).

**Value**

A data.frame for each factor pair with the numbers and proportions of the genes in the input that overlap.

**Author(s)**

Jack Gisby

**See Also**

[plotCommonFeatures\(\)](#), [getAlignedFeatures\(\)](#)

**Examples**

```
# Get a random matrix with rnorm, with 100 rows (features)
# and 20 columns (observations)
X <- ReducedExperiment:::.makeRandomData(100, 20, "feature", "obs")

# Estimate 5 factors based on the data matrix
fe <- estimateFactors(X, nc = 5)

# Get the genes highly aligned with each factor
```

```
aligned_features <- getAlignedFeatures(
  fe,
  format = "data.frame",
  proportional_threshold = 0.3
)

# Identify overlap between common features for each factor
common_features <- getCommonFeatures(aligned_features)
head(common_features)
```

---

getGeneIDs

*Gets alternative gene annotations from biomaRt*


---

## Description

Uses [getBM](#) to get alternative gene IDs for [ReducedExperiment](#) objects. The new annotations are added as columns to the input object's rowData

## Usage

```
## S4 method for signature 'ReducedExperiment'
getGeneIDs(
  object,
  gene_id_col = "rownames",
  gene_id_type = "ensembl_gene_id",
  ids_to_get = c("hgnc_symbol", "entrezgene_id"),
  dataset = "hsapiens_gene_ensembl",
  mart = NULL,
  biomaRt_out = NULL
)
```

## Arguments

object	<a href="#">ReducedExperiment</a> object.
gene_id_col	The column in rowData(object) that will be used to query biomaRt. Setting this to "rownames" instead uses rownames(object) for matching.
gene_id_type	The type of attribute to be used to query with biomaRt. See the filters argument of <a href="#">getBM</a> .
ids_to_get	The type of attribute to get from biomaRt. See the attributes argument of <a href="#">getBM</a> .
dataset	The Ensembl dataset to retrieve. See the dataset argument of <a href="#">useEnsembl</a> . If mart is not NULL, this argument is ignored.
mart	An optional mart object to use. See the mart argument of <a href="#">getBM</a> . If provided, this object is used to query biomaRt for the conversion of gene IDs. If biomaRt_out is not NULL, this argument is ignored.
biomaRt_out	An optional data.frame containing the output of a call to <a href="#">getBM</a> . If provided, this object is used for the conversion of gene IDs.



**Value**

Returns the original object, with additional variables added to the rowData slot.

**Author(s)**

Jack Gisby

**See Also**

`biomaRt::useEnsembl()`, `biomaRt::getBM()`

**Examples**

```
set.seed(2)
airway <- ReducedExperiment:::getAirwayData(n_features = 500)

set.seed(1)
airway_fe <- estimateFactors(airway, nc = 2, use_stability = FALSE, method = "imax")

# rowData before getting additional gene IDs
rowData(airway_fe)

# For this example we run `getGeneIDs` using a preloaded biomaRt query
# (`biomart_out`) to avoid actually querying ensembl during testing
# Note: do not use this file for your actual data
biomart_out <- readRDS(system.file(
  "extdata",
  "biomart_out.rds",
  package = "ReducedExperiment"
))
airway_fe <- getGeneIDs(airway_fe, biomart_out = biomart_out)

# rowData after getting additional gene IDs
rowData(airway_fe)
```

---

getMsigdbT2G

---

*Get TERM2GENE dataframe from MSigDB*


---

**Description**

Gets pathways from the MSigDB database in the format required by clusterProfiler enrichment functions, such as [enricher](#) and [GSEA](#). May be used as input to [runEnrich](#). By default, retrieves the C2 canonical pathways.

**Usage**

```
getMsigdbT2G(
  species = "Homo sapiens",
  category = "C2",
  subcategory = NULL,
  subcategory_to_remove = "CGP",
  gene_id = "ensembl_gene"
)
```

**Arguments**

species	The species for which to obtain MSigDB pathways. See <a href="#">msigdb</a> for more details.
category	The MSigDB category to retrieve pathways for. See <a href="#">msigdb</a> for more details.
subcategory	The MSigDB subcategory to retrieve pathways for. See <a href="#">msigdb</a> for more details.
subcategory_to_remove	If not NULL, this is a character string indicating a subcategory to be removed from the results of <a href="#">msigdb</a> .
gene_id	The name to be given to the gene_id column of the resulting data.frame.

**Value**

Returns a data.frame, where the gs\_name column indicates the name of a pathway, and the gene\_id column indicates genes that belong to said pathway.

**Author(s)**

Jack Gisby

**Examples**

```
pathways <- getMsigdbT2G(
  species = "Homo sapiens",
  category = "C2",
  subcategory_to_remove = "CGP",
  gene_id = "ensembl_gene"
)

# A data.frame indicating gene-pathway mappings for use in pathway analysis
head(pathways)
```

---

identifyModules	<i>Apply dimensionality reduction using Weighted Gene Correlation Network Analysis</i>
-----------------	--

---

**Description**

Performs Weighted gene correlation network analysis (WGCNA) and packages both the input data and subsequent results into a [ModularExperiment](#). Calls [runWGCNA](#) to perform the analysis; see its documentation page for more information on the ICA method, parameters and outputs.

**Usage**

```
identifyModules(
  X,
  power,
  center_X = TRUE,
  scale_X = TRUE,
  assay_name = "normal",
  ...
)
```

**Arguments**

<code>X</code>	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to WGCNA. <code>X</code> should have rows as features and columns as samples.
<code>power</code>	An integer representing the soft-thresholding power to be used to define modules. See the <a href="#">assessSoftThreshold</a> function for aid in determining this parameter.
<code>center_X</code>	If TRUE, <code>X</code> is centered (i.e., features / rows are transformed to have a mean of 0) prior to WGCNA.
<code>scale_X</code>	If TRUE, <code>X</code> is scaled (i.e., features / rows are transformed to have a standard deviation of 1) before WGCNA.
<code>assay_name</code>	If <code>X</code> is a <a href="#">SummarizedExperiment</a> , then this should be the name of the assay to be subject to WGCNA.
<code>...</code>	Additional arguments to be passed to <a href="#">runWGCNA</a> .

**Value**

A [ModularExperiment](#) is returned containing the input data (i.e., the original data matrix in addition to other slots if a [SummarizedExperiment](#) was used as input). Additionally contains the results of module analysis, stored in the reduced and assignments slots. The `center_X`, `scale_X`, `loadings`, `threshold` and `dendrogram` slots may also be filled depending on the arguments given to `identifyModules`.

**Author(s)**

Jack Gisby

**See Also**

[runWGCNA\(\)](#), [WGCNA::blockwiseModules\(\)](#), [WGCNA::pickSoftThreshold\(\)](#)

**Examples**

```
# Get the airway data as a SummarizedExperiment (with a subset of features)
set.seed(2)
airway_se <- ReducedExperiment:::getAirwayData(n_features = 500)

# Select soft-thresholding power to use (use capture.output to hide WGCNA's prints)
WGCNA::disableWGCNAThreads()
invisible(capture.output(fit_indices <- assessSoftThreshold(airway_se)))
estimated_power <- fit_indices$Power[fit_indices$estimated_power]

# Identify modules using WGCNA
airway_me <- identifyModules(airway_se, verbose = 0, power = estimated_power)
airway_me
```

---

loadings,FactorisedExperiment-method  
*Get and set loadings*

---

## Description

Method for getting and setting loadings for a [ReducedExperiment](#) object.

## Usage

```
## S4 method for signature 'FactorisedExperiment'
loadings(
  object,
  scale_loadings = FALSE,
  center_loadings = FALSE,
  abs_loadings = FALSE
)

## S4 replacement method for signature 'FactorisedExperiment'
loadings(object) <- value

## S4 method for signature 'ModularExperiment'
loadings(
  object,
  scale_loadings = FALSE,
  center_loadings = FALSE,
  abs_loadings = FALSE
)

## S4 replacement method for signature 'ModularExperiment'
loadings(object) <- value
```

## Arguments

object	<a href="#">ReducedExperiment</a> object or an object that inherits from this class.
scale_loadings	If TRUE, loadings will be scaled to have a standard deviation of 1. If the loadings are a matrix, this operation is performed column-wise.
center_loadings	If TRUE, loadings will be centered to have a mean of 0. If the loadings are a matrix, this operation is performed column-wise.
abs_loadings	If TRUE, the absolute values of the loadings will be returned.
value	New value to replace existing loadings.

## Details

When available, the module loadings provide the values of the rotation matrix (usually generated by [prcomp](#)) used to calculate the sample-level module vectors available in the reduced slot. Normally, these loadings are calculated for each module separately, so their values are not comparable across modules.

**Value**

If object is a [FactorisedExperiment](#), the loadings matrix will be returned, with features as rows and reduced components as columns. If object is a [ModularExperiment](#), the loadings will be returned as a vector, with a value for each feature (usually genes).

**Author(s)**

Jack Gisby

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me <- ReducedExperiment:::createRandomisedModularExperiment(100, 50, 10)
me

# Retrieve the loadings
loadings(me)[1:10]

# Change a loading
loadings(me)[9] <- 8
loadings(me)[1:10]
```

---

ModularExperiment-class

*ModularExperiment: A container for the results of module analysis*

---

**Description**

A container inheriting from the [ReducedExperiment](#) class, that contains one or more data matrices, to which module analysis has been applied to identify a reduced set of features. A [ModularExperiment](#) can be created directly in a similar manner to a [SummarizedExperiment](#). Alternatively, the [identifyModules](#) function can be used to both define modules and generate a [ModularExperiment](#) from the results.

**Usage**

```
ModularExperiment(
  reduced = new("matrix"),
  scale = TRUE,
  center = TRUE,
  loadings = NULL,
  assignments = character(),
  dendrogram = NULL,
  threshold = NULL,
  ...
)
```

**Arguments**

reduced	A matrix, produced by module analysis, with rows representing samples and columns representing module expression profiles. Typically, this matrix contains "eigengenes" produced by the Weighted Gene Correlation Network Analysis (WGCNA) approach, as is applied by <a href="#">identifyModules</a> .
scale	Either a boolean, representing whether or not the original data has been scaled to unit variance, or a numeric vector indicating the standard deviations of the original features (as produced by <a href="#">scale</a> .)
center	Either a boolean, representing whether or not the original data has been centered to have a mean of 0, or a numeric vector indicating the means of the original features (as produced by <a href="#">scale</a> .)
loadings	A numeric vector representing the loadings used to generate module expression profiles. Typically, these values are obtained from the rotation matrix produced by <a href="#">prcomp</a> , which is used to identify the first principal component of each module. The vector names represent features.
assignments	A vector of features, named according to the module to which the feature belongs.
dendrogram	Either NULL, or the dendrogram used to identify modules from the original data.
threshold	Either NULL, or a matrix produced by <a href="#">pickSoftThreshold</a> indicating the parameters used for network construction.
...	Additional arguments to be passed to <a href="#">ReducedExperiment</a> .

**Value**

Constructor method returns a ModularExperiment object.

**Author(s)**

Jack Gisby

**See Also**

[ReducedExperiment\(\)](#), [FactorisedExperiment\(\)](#), [identifyModules\(\)](#)

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of modules

# In this case we use random assay data and reduced data (i.e., module
# eigengenes). We also randomly assign each feature to a module. In practice,
# we would identify modules and eigengenes using a method like WGCNA applied
# to the analysis of assay data (e.g., gene expression data) from some study.
rand_assay_data <- ReducedExperiment:::makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::makeRandomData(j, k, "sample", "module")
rand_assignments <- paste0("gene_", seq_len(i))
names(rand_assignments) <- paste0("module_", round(stats::runif(i, 1, k), 0))

me <- ModularExperiment(
  assays = list("normal" = rand_assay_data),
```

```

        reduced = rand_reduced_data,
        assignments = rand_assignments
    )

me

```

---

modulePreservation	<i>Get module preservation statistics</i>
--------------------	---

---

## Description

Tests whether a set of modules defined in the reference dataset are preserved in the test dataset. Provides a convenient wrapper around `modulePreservation` for `ModularExperiment` and `SummarizedExperiment` objects.

## Usage

```

modulePreservation(
  reference_dataset,
  test_dataset,
  reference_assay_name = "normal",
  test_assay_name = "normal",
  module_assignments = NULL,
  greyName = "module_0",
  goldName = "random",
  networkType = "signed",
  corFnc = "cor",
  savePermutedStatistics = FALSE,
  ...
)

```

## Arguments

reference_dataset	The dataset that was used to define the modules. Must be a <code>data.frame</code> or <code>matrix</code> with features as rows and samples as columns, or a <code>ModularExperiment</code> or <code>SummarizedExperiment</code> object.
test_dataset	The dataset that will be used to test for module preservation. Must be a <code>data.frame</code> or <code>matrix</code> with features as rows and samples as columns, or a <code>SummarizedExperiment</code> object. The features of <code>test_dataset</code> should be the same as <code>reference_dataset</code> and in the same order.
reference_assay_name	If the reference dataset is a <code>ModularExperiment</code> or <code>SummarizedExperiment</code> object, this argument specifies which assay slot was used to define the modules.
test_assay_name	If the reference dataset is a <code>ModularExperiment</code> or <code>SummarizedExperiment</code> object, this argument specifies which assay slot is to be used in preservation tests.
module_assignments	If the reference dataset is not a <code>ModularExperiment</code> object, this argument is necessary to specify the module assignments.

greyName	The name of the "module" of unassigned genes. Usually "module_0" (Reduced-Experiment default) or "grey" (WGCNA default). See <a href="#">modulePreservation</a> .
goldName	The name to be used for the "gold" module (which is made up of a random sample of all network genes). See <a href="#">modulePreservation</a> .
networkType	A string referring to the type of WGCNA network used for the reference and test datasets. One of "unsigned", "signed" or "signed hybrid". See <a href="#">adjacency</a> . See <a href="#">modulePreservation</a> .
corFnc	A string referring to the function to be used to calculate correlation. One of "cor" or "bicor". See <a href="#">modulePreservation</a> .
savePermutedStatistics	If TRUE, saves the permutation statistics as a .RData file. See <a href="#">modulePreservation</a> .
...	Additional arguments to be passed to <a href="#">modulePreservation</a> .

**Value**

A data.frame containing preservation statistics, as described by [modulePreservation](#).

**Author(s)**

Jack Gisby

**Examples**

```
# Get random ModularExperiments with rnorm, with 100 rows (features),
# 20 columns (observations) and 5/10 modules
me_1 <- ReducedExperiment:::createRandomisedModularExperiment(100, 20, 5)
me_2 <- ReducedExperiment:::createRandomisedModularExperiment(100, 20, 10)

# Test module preservation (test modules from dataset 1 in dataset 2)
mp <- modulePreservation(me_1, me_2, verbose = 0, nPermutations = 3)
```

---

```
names<-,FactorisedExperiment-method
  Get feature names
```

---

**Description**

Gets and sets feature names (i.e., rownames, usually genes).

**Usage**

```
## S4 replacement method for signature 'FactorisedExperiment'
names(x) <- value

## S4 replacement method for signature 'FactorisedExperiment'
featureNames(x) <- value

## S4 replacement method for signature 'FactorisedExperiment'
rownames(x) <- value
```



```
## S4 replacement method for signature 'ModularExperiment'
names(x) <- value

## S4 replacement method for signature 'ModularExperiment'
featureNames(x) <- value

## S4 replacement method for signature 'ModularExperiment'
rownames(x) <- value

## S4 method for signature 'ReducedExperiment'
featureNames(x)

## S4 replacement method for signature 'ReducedExperiment'
names(x) <- value

## S4 replacement method for signature 'ReducedExperiment'
rownames(x) <- value

## S4 replacement method for signature 'ReducedExperiment'
ROWNAMES(x) <- value

## S4 replacement method for signature 'ReducedExperiment'
featureNames(x) <- value
```

### Arguments

x	<a href="#">ReducedExperiment</a> object.
value	New value to replace existing names.

### Value

A vector containing the names of the features.

### Author(s)

Jack Gisby

### Examples

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

rand_assay_data <- ReducedExperiment:::makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

# Methods return equivalent results
```

```

stopifnot(all.equal(featureNames(re), rownames(rand_assay_data)))
stopifnot(all.equal(rownames(re), rownames(rand_assay_data)))
stopifnot(all.equal(names(re), rownames(rand_assay_data)))

# We can change the feature name at a particular position
print(paste0("Feature name at position 55: ", featureNames(re)[55]))
featureNames(re)[55] <- "custom_feature_name"
print(paste0("Reduced data at position 55: ", featureNames(re)[55]))

```

---

nModules,ModularExperiment-method

*Prints individual lengths of samples, components and features*


---

## Description

Prints individual lengths of samples, components and features

## Usage

```

## S4 method for signature 'ModularExperiment'
nModules(object)

## S4 method for signature 'ReducedExperiment'
nComponents(object)

## S4 method for signature 'ReducedExperiment'
nSamples(object)

## S4 method for signature 'ReducedExperiment'
nFeatures(object)

```

## Arguments

object [ReducedExperiment](#) object.

## Value

The number of samples (nSamples), features (nFeatures) or dimensionally-reduced components (nComponents) are returned.

## Author(s)

Jack Gisby

## See Also

[dim,ReducedExperiment-method](#)

**Examples**

```
# Create a randomised ReducedExperiment
re <- ReducedExperiment:::.createRandomisedReducedExperiment(100, 50, 10)

# Get the dimensions
nComponents(re) # 10
nSamples(re) # 50
nFeatures(re) # 10

# For a ModularExperiment we can alternatively use nModules
me <- ReducedExperiment:::.createRandomisedModularExperiment(100, 50, 10)
nComponents(me) # 10
nModules(me) # 10
```

---

plotCommonFeatures	<i>Heatmap comparing commonality across factors</i>
--------------------	---

---

**Description**

Heatmap comparing commonality across factors

**Usage**

```
plotCommonFeatures(
  common_features,
  filename = NA,
  color = (grDevices::colorRampPalette(RColorBrewer::brewer.pal(n = 7, name =
    "YlOrRd")))(100)
)
```

**Arguments**

common_features	
filename	The output of <a href="#">getCommonFeatures</a> .
color	The colour palette to be used in the heatmap.

**Value**

An object generated by [pheatmap](#).

**Author(s)**

Jack Gisby

**See Also**

[getCommonFeatures\(\)](#), [getAlignedFeatures\(\)](#)

## Examples

```
# Get a random matrix with rnorm, with 100 rows (features)
# and 20 columns (observations)
X <- ReducedExperiment:::makeRandomData(100, 20, "feature", "obs")

# Estimate 5 factors based on the data matrix
fe <- estimateFactors(X, nc = 5)

# Get the genes highly aligned with each factor
aligned_features <- getAlignedFeatures(
  fe,
  format = "data.frame",
  proportional_threshold = 0.3
)

# Identify overlap between common features for each factor
common_features <- getCommonFeatures(aligned_features)

# Plot the common features as a heatmap
plotCommonFeatures(common_features)
```

---

plotDendro

*Plot a dendrogram stored in a ModularExperiment*


---

## Description

Plots the dendrogram in the dendrogram slot of a [ModularExperiment](#) object using the [plotDendroAndColors](#) function.

## Usage

```
## S4 method for signature 'ModularExperiment'
plotDendro(
  object,
  groupLabels = "Module colors",
  dendroLabels = FALSE,
  hang = 0.03,
  addGuide = TRUE,
  guideHang = 0.05,
  color_func = WGCNA::labels2colors,
  modules_are_colors = FALSE,
  ...
)
```

## Arguments

object	<a href="#">ModularExperiment</a> object.
groupLabels	Module label axis label. See <a href="#">plotDendroAndColors</a> .
dendroLabels	If TRUE, shows feature names in the dendrogram. See <a href="#">plotDendroAndColors</a> .
hang	The fraction of the plot height by which labels should hang below the rest of the plot. See <a href="#">plot.hclust</a> .

addGuide	If TRUE, adds vertical guide lines to the dendrogram. See <a href="#">plotDendroAndColors</a> .
guideHang	The fraction of the dendrogram's height to leave between the top end of the guide line and the dendrogram merge height. See <a href="#">plotDendroAndColors</a> .
color_func	Function for converting module names to colors. Only used if modules_are_colors is FALSE.
modules_are_colors	If TRUE, expects the module names to be colors. Else, assumes that module names are numbers that can be converted into colours by color_func.
...	Additional arguments to be passed to <a href="#">plotDendroAndColors</a> .

**Value**

A plot produced by [plotDendroAndColors](#).

**Author(s)**

Jack Gisby

**See Also**

[WGCNA::plotDendroAndColors\(\)](#), [plot.hclust](#)

**Examples**

```
# Create ModularExperiment with random data (100 features, 50 samples,
# 10 modules)
me <- ReducedExperiment:::.createRandomisedModularExperiment(100, 50, 10)
me

# The dendrogram is usually produced during module discovery, but we can
# assign any dendrogram to the slot. Let's do hierarchical clustering on the
# features in our object and assign it
dendrogram(me) <- hclust(dist(assay(me)))
dendrogram(me)

# Plot the dendrogram - modules are random in this instance, but in general
# features within a module should cluster together
plotDendro(me)
```

---

plotModulePreservation

*Plot module preservation statistics*

---

**Description**

Plot module preservation statistics

**Usage**

```
plotModulePreservation(
  modulePreservation_results,
  show_random = TRUE,
  remove_module = NULL
)
```

**Arguments**

`modulePreservation_results` The output of [modulePreservation](#)

`show_random` If TRUE, shows the random module in the plots.

`remove_module` The name of a module to be hidden from the plots.

**Value**

Two ggplot2 plot objects combined by patchwork. Plots the module preservation statistics generated by [modulePreservation](#).

**Author(s)**

Jack Gisby

**Examples**

```
# Get random ModularExperiments with rnorm, with 100 rows (features),
# 20 columns (observations) and 5/10 modules
me_1 <- ReducedExperiment:::.createRandomisedModularExperiment(100, 20, 5)
me_2 <- ReducedExperiment:::.createRandomisedModularExperiment(100, 20, 10)

# Test module preservation (test modules from dataset 1 in dataset 2)
mp <- modulePreservation(me_1, me_2, verbose = 0, nPermutations = 3)

# No significant preservation, since these were random modules
plotModulePreservation(mp)
```

---

plotStability

*Plot component stability as a function of the number of components*

---

**Description**

Plots the results of [estimateStability](#). See this function's documentation for more information.

**Usage**

```
plotStability(
  stability,
  plot_path = NULL,
  stability_threshold = NULL,
  mean_stability_threshold = NULL,
  height = 4,
```

```

    width = 10,
    ...
  )

```

### Arguments

stability	The results of <a href="#">estimateStability</a> .
plot_path	The path at which the plot will be saved
stability_threshold	Plots a stability threshold, below which components can be pruned by <a href="#">runICA</a> .
mean_stability_threshold	Plots a stability threshold, which is used by <a href="#">estimateStability</a> to provide a naive estimate for the optimal number of components.
height	The height of the plot, to be passed to <a href="#">ggsave</a> .
width	The width of the plot, to be passed to <a href="#">ggsave</a> .
...	Additional arguments to be passed to <a href="#">ggsave</a> .

### Value

Returns a list of three plots as ggplot2 objects:

**combined\_plot** The two other plots combined with patchwork.

**stability\_plot** A plot in which each line indicates stability as a function of the number of components. A line is shown for each number of components tested.

**mean\_plot** The average component stability as a function of the number of components.

### Author(s)

Jack Gisby

### Examples

```

# Get a random matrix with rnorm, with 200 rows (features)
# and 100 columns (observations)
X <- ReducedExperiment::makeRandomData(200, 100, "feature", "obs")

# Estimate stability across 10 to 30 components
stab_res <- estimateStability(
  X,
  min_components = 10,
  max_components = 30,
  n_runs = 5,
  verbose = FALSE
)

# Intraclass stability similar to extraclass since this is random data
plotStability(stab_res)$combined_plot

```

projectData

*Project new data using pre-defined factors***Description**

Uses a projection approach to calculate factors in new data. Functions in a similar fashion to the predict method of [prcomp](#). The transposed newdata are multiplied by the original loadings matrix.

**Usage**

```
## S4 method for signature 'FactorisedExperiment,matrix'
projectData(
  object,
  newdata,
  standardise_reduced = TRUE,
  scale_newdata = NULL,
  center_newdata = NULL
)

## S4 method for signature 'FactorisedExperiment,data.frame'
projectData(
  object,
  newdata,
  standardise_reduced = TRUE,
  scale_newdata = NULL,
  center_newdata = NULL
)

## S4 method for signature 'FactorisedExperiment,SummarizedExperiment'
projectData(
  object,
  newdata,
  standardise_reduced = TRUE,
  scale_newdata = NULL,
  center_newdata = NULL,
  assay_name = "normal"
)

## S4 method for signature 'FactorisedExperiment'
predict(object, newdata, ...)
```

**Arguments**

object	A <a href="#">FactorisedExperiment</a> object. The loadings slot of this class will be used for projection. Additionally, by default, the scale and center slots are used to apply the original transformation to the new data.
newdata	New data for projection. Must be a data.frame or matrix with features as rows and samples as columns, or a <a href="#">SummarizedExperiment</a> object. Assumes that the rows of newdata match those of the <a href="#">FactorisedExperiment</a> object.



standardise_reduced	Whether or not the reduced data should be standardised (i.e., transformed to have a mean of 0 and standard deviation of 1) after calculation.
scale_newdata	Controls whether the newdata are scaled. If NULL, performs scaling based on the FactorisedExperiment object's scale slot. The value of this argument will be passed to the scale argument of <a href="#">scale</a> .
center_newdata	Controls whether the newdata are centered. If NULL, performs centering based on the FactorisedExperiment object's center slot. The value of this argument will be passed to the center argument of <a href="#">scale</a> .
assay_name	If a <a href="#">SummarizedExperiment</a> object is passed as new data, this argument indicates which assay should be used for projection.
...	Additional arguments to be passed to projectData.

### Details

If scale\_newdata and center\_newdata are left as NULL, then the projection method assumes that the newdata are on the same scale as the original data of the object. It will therefore use the values of the center and scale slots of the object. For instance, if the scale slot is TRUE, the newdata will be scaled. If the scale slot is a vector, the values of this vector will be applied to scale the newdata.

### Value

Calculates a matrix with samples as rows and factors as columns. If newdata was a matrix or data.frame, this will be returned as a matrix. If a [SummarizedExperiment](#) object was passed instead, then a FactorisedExperiment object will be created containing this matrix in its reduced slot.

### Author(s)

Jack Gisby

### See Also

[calcEigengenes](#), [stats::prcomp](#)

### Examples

```
# Get two random matrices with rnorm
# 1: 100 rows (features) and 20 columns (observations)
X_1 <- ReducedExperiment:::.makeRandomData(100, 20, "feature", "obs")

# Both matrices must have the same features, but they may have different obs
# 2: 100 rows (features) and 30 columns (observations)
X_2 <- ReducedExperiment:::.makeRandomData(100, 30, "feature", "obs")

# Estimate 5 factors based on the data matrix
fe_1 <- estimateFactors(X_1, nc = 5)
fe_1

# Project the fe_1 factors for the samples in X_2
projected_data <- projectData(fe_1, X_2)
projected_data
```

---

reduced	<i>Get and set reduced data</i>
---------	---------------------------------

---

## Description

Retrieves the reduced data matrix, with samples as rows and reduced components as columns. Setter method can be used to replace or modify all or part of the matrix.

## Usage

```
## S4 method for signature 'ReducedExperiment'
reduced(object, scale_reduced = FALSE, center_reduced = FALSE)

## S4 replacement method for signature 'ReducedExperiment'
reduced(object) <- value
```

## Arguments

object	An object that inherits from <a href="#">ReducedExperiment</a> .
scale_reduced	If TRUE, data will be scaled column-wise to have a standard deviation of 0.
center_reduced	If TRUE, data will be centered column-wise to have a mean of 0.
value	New value to replace existing reduced data matrix.

## Value

A matrix with samples/observations as rows and columns referring to the dimensionally-reduced components.

## Author(s)

Jack Gisby

## See Also

[ReducedExperiment\(\)](#)

## Examples

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

rand_assay_data <- ReducedExperiment:::makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

stopifnot(all.equal(reduced(re), rand_reduced_data))
```

```
print(paste0("Reduced data at position (2, 2): ", reduced(re)[2, 2]))
reduced(re)[2, 2] <- 5
print(paste0("Reduced data at position (2, 2): ", reduced(re)[2, 2]))
```

---

#### ReducedExperiment-class

*ReducedExperiment: A container for dimensionally-reduced representations*

---

### Description

Inherits from [SummarizedExperiment](#), a container for one or more matrices with features as rows (e.g., genes) and columns as samples. Additional information on features and samples are contained in [DataFrame](#) tables. The `ReducedExperiment` extends [SummarizedExperiment](#) by additionally providing access to a "reduced" data matrix, in which rows represent samples and columns represent a second set of dimensionally-reduced features.

The methods available for [SummarizedExperiment](#) objects are also available for `ReducedExperiment` and its children, which include [FactorisedExperiment](#) and [ModularExperiment](#).

Typically, `ReducedExperiment` objects contain two main assays. The first is, by default, named "normal" and contains some type of normalised assay data, such as gene expression. The second is "transformed", which is typically the result of applying scaling and/or centering to the normalised data matrix.

### Usage

```
ReducedExperiment(reduced = new("matrix"), scale = TRUE, center = TRUE, ...)
```

### Arguments

<code>reduced</code>	A matrix, usually the result of some type of dimensionality-reduction, with rows representing samples and columns representing a new set of features.
<code>scale</code>	Either a boolean, representing whether or not the original data has been scaled to unit variance, or a numeric vector indicating the standard deviations of the original features (as produced by <a href="#">scale</a> .)
<code>center</code>	Either a boolean, representing whether or not the original data has been centered to have a mean of 0, or a numeric vector indicating the means of the original features (as produced by <a href="#">scale</a> .)
<code>...</code>	Additional arguments to be passed to <a href="#">SummarizedExperiment</a> .

### Value

Constructor method returns a [ReducedExperiment](#) object.

### Author(s)

Jack Gisby

**See Also**

[FactorisedExperiment\(\)](#), [ModularExperiment\(\)](#)

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

# In this case we use random assay and reduced data, but in
# practice these will likely be the result of applying some kind of
# dimensionality-reduction method to the assay data (e.g., gene
# expression data) from some study.
rand_assay_data <- ReducedExperiment:::.makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::.makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

re
```

---

runEnrich

*Functional enrichment analyses for dimensionally-reduced data*


---

**Description**

Method for applying pathway enrichment analysis to components identified through dimensionality reduction (e.g., factors or modules). Enrichment analyses are applied to each component separately.

**Usage**

```
## S4 method for signature 'FactorisedExperiment'
runEnrich(
  object,
  method = "gsea",
  feature_id_col = "rownames",
  center_loadings = FALSE,
  abs_loadings = FALSE,
  loading_threshold = 0.5,
  proportional_threshold = 0.01,
  as_dataframe = FALSE,
  ...
)

## S4 method for signature 'ModularExperiment'
runEnrich(
  object,
  method = "overrepresentation",
```

```

    feature_id_col = "rownames",
    as_dataframe = FALSE,
    ...
)

```

## Arguments

object	<a href="#">FactorisedExperiment</a> or <a href="#">ModularExperiment</a> object.
method	The method to use for identifying enriched pathways. One of "overrepresentation" or "gsea". The "overrepresentation" method calls <a href="#">enricher</a> whereas the "gsea" method calls <a href="#">GSEA</a> . Note that "gsea" is not available for modules.
feature_id_col	The column in <code>rowData(object)</code> that will be used as a feature ID. Setting this to "rownames" (default) instead uses <code>rownames(object)</code> .
center_loadings	If TRUE, loadings will be centered column-wise to have a mean of 0.
abs_loadings	If TRUE, the absolute values of the loadings will be used for enrichment analysis. If FALSE, the signed loadings will be used for GSEA enrichment. Note that, regardless of the value of this term, the process used to select genes for overrepresentation analysis will be based on absolute loadings.
loading_threshold	See <a href="#">getAlignedFeatures</a> . Only relevant for overrepresentation analysis.
proportional_threshold	See <a href="#">getAlignedFeatures</a> . Only relevant for overrepresentation analysis.
as_dataframe	If TRUE, the results will be returned as a <code>data.frame</code> . Otherwise, the results will be returned as a list of objects created by either <a href="#">enricher</a> , in the case of overrepresentation analysis, or <a href="#">GSEA</a> , in the case of GSEA.
...	Additional arguments to be passed to <a href="#">GSEA</a> (if <code>method == "gsea"</code> ) or <a href="#">enricher</a> (if <code>method == "overrepresentation"</code> ).

## Details

When running module analysis, the overrepresentation method identifies pathways that are overrepresented in each module.

For factor analysis, the overrepresentation method first identifies the genes most highly aligned with each factor (using [getAlignedFeatures](#)), then uses the resulting gene lists to perform overrepresentation analysis. The GSEA method instead uses the entire set of factor loadings, and identifies pathways that are overrepresented in the tails of this distribution.

## Value

If `as_dataframe` is TRUE, the results will be returned as a `data.frame`. Otherwise, the results will be returned as a list of objects created by either [enricher](#), in the case of overrepresentation analysis, or [GSEA](#), in the case of GSEA.

## Author(s)

Jack Gisby

## See Also

[getMsigdbT2G\(\)](#)

## Examples

```

set.seed(2)
airway <- ReducedExperiment:::getAirwayData(n_features = 2000)
airway_fe <- estimateFactors(
  airway,
  nc = 2,
  use_stability = FALSE,
  method = "imax"
)

# Get pathways (e.g., by using ReducedExperiment::getMsigdbT2G())
t2g <- read.csv(system.file(
  "extdata",
  "msigdb_t2g_filtered.csv",
  package = "ReducedExperiment"
))

# Run overrepresentation analysis
overrep_res <- runEnrich(
  airway_fe,
  method = "overrepresentation",
  feature_id_col = "rownames",
  as_dataframe = TRUE,
  p_cutoff = 0.1,
  TERM2GENE = t2g,
  universe = rownames(airway_fe)
)

head(overrep_res)

```

---

runICA

---

*Run standard or stabilised Independent Component Analysis*


---

## Description

Runs ICA through [ica](#). If `use_stability` is `FALSE`, then `X` is passed directly to [ica](#) and a standard ICA analysis is performed. If `use_stability` is `TRUE`, then the stabilised ICA procedure is carried out (see details).

## Usage

```

runICA(
  X,
  nc,
  use_stability = FALSE,
  resample = FALSE,
  method = "fast",
  stability_threshold = NULL,
  center_X = TRUE,
  scale_X = FALSE,
  reorient_skewed = TRUE,
  scale_components = TRUE,

```

```

    scale_reduced = TRUE,
    n_runs = 30,
    BPPARAM = BiocParallel::SerialParam(),
    ...
)

```

## Arguments

<code>X</code>	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to ICA. <code>X</code> should have rows as features and columns as samples.
<code>nc</code>	The number of components to be identified. See <a href="#">estimateStability</a> for a method to estimate the optimal number of components.
<code>use_stability</code>	Whether to use a stability-based approach to estimate factors. See details for further information.
<code>resample</code>	If TRUE, a bootstrap approach is used to estimate factors and quantify stability. Else, random initialisation of ICA is employed. Ignored if <code>use_stability</code> is FALSE.
<code>method</code>	The ICA method to use. Passed to <a href="#">ica</a> , the options are "fast", "imax" or "jade".
<code>stability_threshold</code>	A stability threshold for pruning factors. Factors with a stability below this threshold will be removed. If used, the threshold can lead to fewer factors being returned than that specified by <code>nc</code> .
<code>center_X</code>	If TRUE, <code>X</code> is centered (i.e., features / rows are transformed to have a mean of 0) prior to ICA. Generally recommended.
<code>scale_X</code>	If TRUE, <code>X</code> is scaled (i.e., features / rows are transformed to have a standard deviation of 1) before ICA.
<code>reorient_skewed</code>	If TRUE, factors are reorientated to ensure that the loadings of each factor (i.e., the source signal matrix) have positive skew. Helps ensure that the most influential features for each factor are positively associated with it.
<code>scale_components</code>	If TRUE, the loadings are standardised (to have a mean of 0 and standard deviation of 1).
<code>scale_reduced</code>	If TRUE, the reduced data (mixture matrix) are standardised (to have a mean of 0 and standard deviation of 1).
<code>n_runs</code>	The number of times to run ICA to estimate factors and quantify stability. Ignored if <code>use_stability</code> is FALSE.
<code>BPPARAM</code>	A class containing parameters for parallel evaluation. Uses <a href="#">SerialParam</a> by default, running only a single ICA computation at a time. Ignored if <code>use_stability</code> is FALSE.
<code>...</code>	Additional arguments to be passed to <a href="#">ica</a> .

## Details

Function performs ICA for a data matrix. If `use_stability` is TRUE, then ICA is performed multiple times with either: i) random initialisation (default); or ii) bootstrap resampling of the data (if `resample` is TRUE).

Note that the seed must be set if reproducibility is needed. Specifically, one can use `set.seed` prior to running standard ICA (`use_stability = FALSE`) or set the `RNGseed` argument of `BPPARAM` when running stabilised ICA (`use_stability = TRUE`).

The stability-based ICA algorithm is similar to the ICASSO approach (<https://www.cs.helsinki.fi/u/ahyvarin/papers/Himberg03.pdf>) that is implemented in the stabilized-ica Python package (<https://github.com/ncaptier/stabilized-ica/tree/master>).

In short, the stability-based algorithm consists of:

- Running ICA multiple times with either random initialisation or bootstrap resampling of the input data.
- Clustering the resulting factors across all runs based on the signature matrix.
- Calculating intra- (aics) and extra- (aeacs) cluster stability, and defining the final cluster stability as  $aics - aeacs$ .
- Calculating the cluster centroid as the factor with the highest intra-cluster stability.
- Optionally removing factors below a specified stability threshold (`stability_threshold`).

Results from this function should be broadly similar to those generated by other implementations of stabilised ICA, although they will not be identical. Notable differences include:

**ICA algorithm** Differences in the underlying implementation of ICA.

**Stability threshold** The `stability_threshold` argument, if specified, removes unstable components. Such a threshold is not used by stabilized-ica.

**Mixture matrix recovery** ICA is generally formulated as  $X = MS$ , where  $X$  is the input data,  $M$  is the mixture matrix (reduced data) and  $S$  is the source signal matrix (feature loadings). The stabilised ICA approach first calculates a source signal matrix before recovering the mixture matrix. To do this, other implementations, including that of the stabilized-ica package, multiply  $X$  by the pseudo-inverse of  $S$ . Such an operation is implemented in the `ginv` function of the MASS R package. In the development of ReducedExperiment, we noticed that taking the inverse of  $S$  often failed, particularly when there were correlated factors. For this reason, we instead formulate the mixture matrix as  $M = XS$ . After standardisation of  $M$ , both approaches return near-identical results, given that the matrix inverse was successfully calculated.

## Value

A list containing the following:

**M** The mixture matrix (reduced data) with samples as rows and columns as factors.

**S** The source signal matrix (loadings) with rows as features and columns as factors.

**stab** If `use_stability` is TRUE, "stab" will be a component of the list. It is a vector indicating the relative stability, as described above.

## Author(s)

Jack Gisby

## See Also

`ica::ica()`, `estimateStability()`

## Examples

```
# Get a random matrix with rnorm, with 100 rows (features)
# and 20 columns (observations)
X <- ReducedExperiment:::makeRandomData(100, 20, "feature", "obs")
```



```
# Run standard ICA on the data with 5 components
set.seed(1)
ica_res <- runICA(X, nc = 5, use_stability = FALSE)

# Run stabilised ICA on the data with 5 components (low runs for example)
ica_res_stab <- runICA(X, nc = 5, use_stability = TRUE, n_runs = 5,
  BPPARAM = BiocParallel::SerialParam(RNGseed = 1))
```

runWGCNA

*Run WGCNA for a data matrix*

## Description

Runs WGCNA. Largely a wrapper for the [blockwiseModules](#) function that reformats data into a format convenient for creating a [ModularExperiment](#) object and changes module names from colours to numbers by default.

## Usage

```
runWGCNA(
  X,
  power,
  cor_type = "pearson",
  networkType = "signed",
  module_labels = "numbers",
  maxBlockSize = 30000,
  verbose = 0,
  standardise_reduced = TRUE,
  ...
)
```

## Arguments

X	Either a <a href="#">SummarizedExperiment</a> object or a matrix containing data to be subject to WGCNA. X should have rows as features and columns as samples.
power	soft-thresholding power for network construction.
cor_type	The type of correlation to be used to generate a correlation matrix during network formation. One of "pearson" ( <a href="#">cor</a> ) and "bicor" ( <a href="#">bicor</a> ).
networkType	network type. Allowed values are (unique abbreviations of) "unsigned", "signed", "signed hybrid". See <a href="#">adjacency</a> .
module_labels	Specifies whether the modules should be named based on "numbers" or "colours". If module_labels is set to "numbers", then "module_0" represents unclustered genes, whereas if it is set to "colours" then "grey" represents unclustered genes.
maxBlockSize	The chunk size (in terms of the number of features/genes) to process the data. See <a href="#">blockwiseModules</a> for more details. The default (30000) should process standard transcriptomic datasets in a single chunk. Results may differ if the number of features exceeds the chunk size. Lower values of this parameter may use less memory to calculate networks.

`verbose` integer level of verbosity. Zero means silent, higher values make the output progressively more and more verbose.

`standardise_reduced` If TRUE, the reduced data (eigengenes) are standardised to have a mean of 0 and a standard deviation of 1.

... Additional arguments to be passed to [blockwiseModules](#).

### Details

Note that if `module_labels` is set to "numbers", then "module\_0" represents unclustered genes, whereas if it is set to "colours" then "grey" represents unclustered genes.

The function also stores the loadings matrices generated when PCA is performed for each module to calculate eigengenes. These loadings can be used to recalculate the reduced data matrix (eigengenes).

### Value

Returns a list containing:

"E" The reduced data (eigengenes).

"L" The module loadings. This represents the values of the PCA rotation matrix for the first principal component generated for each module.

"assignments" A named vector representing the assignments of genes to modules.

### Author(s)

Jack Gisby

### See Also

[WGCNA::blockwiseModules\(\)](#), [assessSoftThreshold\(\)](#), [WGCNA::pickSoftThreshold\(\)](#),

### Examples

```
# Get the airway data as a SummarizedExperiment (with a subset of features)
set.seed(2)
airway_se <- ReducedExperiment:::getAirwayData(n_features = 500)

# Choose an appropriate soft-thresholding power
WGCNA::disableWGCNAThreads()
fit_indices <- assessSoftThreshold(airway_se)
estimated_power <- fit_indices$Power[fit_indices$estimated_power]

# Identify modules using the airway expression matrix
wgcna_res <- runWGCNA(
  assay(airway_se, "normal"),
  verbose = 0,
  power = estimated_power
)

# We find just one module for this small dataset (module_0 indicates unclustered genes)
table(names(wgcna_res$assignments))
```

---

sampleNames	<i>Get sample names</i>
-------------	-------------------------

---

**Description**

Retrieves sample names (colnames).

**Usage**

```
## S4 method for signature 'ReducedExperiment'
sampleNames(x)

## S4 replacement method for signature 'ReducedExperiment'
sampleNames(x) <- value

## S4 replacement method for signature 'ReducedExperiment'
colnames(x) <- value
```

**Arguments**

**x** [ReducedExperiment](#) object.  
**value** New value to replace existing names.

**Value**

A vector containing the names of the features.

**Author(s)**

Jack Gisby

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

rand_assay_data <- ReducedExperiment:::.makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::.makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

stopifnot(all.equal(sampleNames(re), colnames(rand_assay_data)))
stopifnot(all.equal(colnames(re), colnames(rand_assay_data)))

print(paste0("Sample name at [80]: ", sampleNames(re)[80]))
sampleNames(re)[80] <- "custom_feature_name"
print(paste0("Sample data at [80]: ", sampleNames(re)[80]))
```

---

`show`*Prints a summary of a `ReducedExperiment` object*

---

## Description

Prints a summary of a `ReducedExperiment` object

## Usage

```
## S4 method for signature 'ReducedExperiment'
show(object)
```

## Arguments

`object`            [ReducedExperiment](#) object.

## Value

A character summary describing the object.

## Author(s)

Jack Gisby

## Examples

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of factors

rand_assay_data <- ReducedExperiment:::.makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::.makeRandomData(j, k, "sample", "component")

re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

# Equivalent to `show(re)`
re
```

---

`stability`*Get and setting the stability values for factors*

---

## Description

Get and setting the stability values for factors

## Usage

```
## S4 method for signature 'FactorisedExperiment'  
stability(object)  
  
## S4 replacement method for signature 'FactorisedExperiment'  
stability(object) <- value
```

## Arguments

<code>object</code>	<a href="#">FactorisedExperiment</a> object.
<code>value</code>	New value to replace existing stability vector.

## Value

A vector with a value for each factor indicating the factor stability. More details are available from the [estimateStability](#) help page.

## Author(s)

Jack Gisby

## See Also

[estimateStability\(\)](#)

## Examples

```
# Get a random matrix with rnorm, with 100 rows (features)  
# and 20 columns (observations)  
X <- ReducedExperiment:::makeRandomData(100, 20, "feature", "obs")  
  
# Run stabilised ICA on the data with 5 components  
fe <- estimateFactors(X, nc = 5, use_stability = TRUE)  
  
stability(fe)  
  
stability(fe)[2] <- 10  
stability(fe)
```

---

[,FactorisedExperiment,ANY,ANY,ANY-method]

*Extract and replace parts of ReducedExperiment objects*


---

## Description

Method permits slicing of [ReducedExperiment](#) objects.

## Usage

```
## S4 method for signature 'FactorisedExperiment,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]

## S4 replacement method for signature 'FactorisedExperiment,ANY,ANY,FactorisedExperiment'
x[i, j, k, ...] <- value

## S4 method for signature 'ModularExperiment,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]

## S4 replacement method for signature 'ModularExperiment,ANY,ANY,ModularExperiment'
x[i, j, k, ...] <- value

## S4 method for signature 'ReducedExperiment,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]

## S4 replacement method for signature 'ReducedExperiment,ANY,ANY,ReducedExperiment'
x[i, j, k, ...] <- value
```

## Arguments

x	<a href="#">ReducedExperiment</a> object.
i	Slicing by rows (features, usually genes).
j	Slicing by columns (samples/observations).
k	Slicing by reduced dimensions.
...	Additional arguments to be passed to the parent method.
drop	Included for consistency with other slicing methods.
value	Value to be used to replace part of the object.

## Value

A [ReducedExperiment](#) object, potentially sliced by rows (i), columns (j) and components (k).

## Author(s)

Jack Gisby

**Examples**

```
# Create randomised data with the following dimensions
i <- 300 # Number of features
j <- 100 # Number of samples
k <- 10 # Number of components (i.e., factors/modules)

rand_assay_data <- ReducedExperiment:::.makeRandomData(i, j, "gene", "sample")
rand_reduced_data <- ReducedExperiment:::.makeRandomData(j, k, "sample", "component")

# Create a randomised ReducedExperiment container
re <- ReducedExperiment(
  assays = list("normal" = rand_assay_data),
  reduced = rand_reduced_data
)

# Slice our object by rows (1:50), columns (1:20) and components (1:5)
# re[i, j, k, ...]
sliced_re <- re[1:50, 1:20, 1:5]
sliced_re

# We can also assign our subsetted object back to the original
re[1:50, 1:20, 1:5] <- sliced_re
re
```

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