

# Package: miloR (via r-universe)

June 15, 2024

**Type** Package

**Title** Differential neighbourhood abundance testing on a graph

**Version** 2.1.0

**Description** Milo performs single-cell differential abundance testing. Cell states are modelled as representative neighbourhoods on a nearest neighbour graph. Hypothesis testing is performed using either a negative binomial generalized linear model or negative binomial generalized linear mixed model.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**URL** <https://marionilab.github.io/miloR>

**BugReports** <https://github.com/MarioniLab/miloR/issues>

**biocViews** SingleCell, MultipleComparison, FunctionalGenomics, Software

**LinkingTo** Rcpp, RcppArmadillo

**Depends** R (>= 4.0.0), edgeR

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**Suggests** testthat, mvtnorm, scater, scran, covr, knitr, rmarkdown, uwot, scuttle, BiocStyle, MouseGastrulationData, MouseThymusAgeing, magick, RCurl, MASS, curl, scRNAseq, graphics

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**NeedsCompilation** no

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'miloR-package.R' 'methods.R' 'plotNhoods.R' 'sim\_discrete.R'  
 'sim\_family.R' 'sim\_nbgLmm.R' 'sim\_trajectory.R' 'testNhoods.R'  
 'testDiffExp.R' 'utils.R' 'buildNhoodGraph.R'  
 'annotateNhoods.R' 'groupNhoods.R' 'findNhoodGroupMarkers.R'  
 'RcppExports.R' 'miloR.R'

**VignetteBuilder** knitr

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miroR-package *The miroR package*

**Description**

The **miroR** package provides modular functions to perform differential abundance testing on replicated single-cell experiments. For details please see the vignettes `vignette("miro_demo", package="miroR")` and `vignette("miro_gastrulation", package="miroR")`.

**Value**

The miroR package

**Author(s)**

Mike Morgan & Emma Dann

annotateNhoods *Add annotations from colData to DA testing results*

**Description**

This function assigns a categorical label to neighbourhoods in the differential abundance results data.frame (output of `testNhoods`), based on the most frequent label among cells in each neighbourhood. This can be useful to stratify DA testing results by cell types or samples. Also the fraction of cells carrying that label is stored.

**Usage**

```
annotateNhoods(x, da.res, coldata_col, subset.nhoods = NULL)
```

**Arguments**

<code>x</code>	A <code>Milo</code> object containing single-cell gene expression and neighbourhoods.
<code>da.res</code>	A <code>data.frame</code> containing DA results, as expected from running <code>testNhoods</code> .
<code>coldata_col</code>	A character scalar determining which column of <code>colData(x)</code> stores the annotation to be added to the neighbourhoods
<code>subset.nhoods</code>	A character, numeric or logical vector that will subset the annotation to the specific nhoods. If a character vector these should correspond to row names of <code>nhoodCounts</code> . If a logical vector then these should have the same length as <code>nrow</code> of <code>nhoodCounts</code> . If numeric, then these are assumed to correspond to indices of <code>nhoodCounts</code> - if the maximal index is greater than <code>nrow(nhoodCounts(x))</code> an error will be produced. This is necessary if <code>testNhoods</code> was run using <code>subset.nhoods=...</code>

**Details**

For each neighbourhood, this calculates the most frequent value of `colData(x)[coldata_col]` among cells in the neighbourhood and assigns that value as annotation for the neighbourhood, adding a column in the `da.res` `data.frame`. In addition, a `coldata_col_fraction` column will be added, storing the fraction of cells carrying the assigned label. While in practice neighbourhoods are often homogeneous, one might choose to remove an annotation label when the fraction of cells with the label is too low (e.g. below 0.6).

**Value**

A `data.frame` of model results (as `da.res` input) with two new columns: (1) `coldata_col` storing the assigned label for each neighbourhood; (2) `coldata_col_fraction` storing the fraction of cells in the neighbourhood with the assigned label.

**Author(s)**

Emma Dann

**Examples**

NULL

---

`buildFromAdjacency`      *Build a graph from an input adjacency matrix*

---

**Description**

Construct a kNN-graph from an input adjacency matrix - either binary or distances between NNs.

**Arguments**

x	An n X n matrix of single-cells, where values represent edges between cells; 0 values are taken to mean no edge between cells. If the matrix is not binary, then it is assumed the values are distances; 0 retain the same meaning. This behaviour can be toggled using <code>is.binary=TRUE</code> .
k	(optional) Scalar value that represents the number of nearest neighbours in the original graph. This can also be inferred directly from the adjacency matrix x.
is.binary	Logical scalar indicating if the input matrix is binary or not.

**Details**

This function will take a matrix as input and construct the kNN graph that it describes. If the matrix is not symmetric then the graph is assumed to be directed, whereas if the matrix is not binary, i.e. all 0's and 1's then the input values are taken to be distances between graph vertices; 0 values are assumed to represent a lack of edge between vertices.

**Value**

A `Milo` with the graph slot populated.

**Author(s)**

Mike Morgan

**Examples**

```
r <- 1000
c <- 1000
k <- 35
m <- floor(matrix(runif(r*c), r, c))
for(i in seq_along(1:r)){
  m[i, sample(1:c, size=k)] <- 1
}

milo <- buildFromAdjacency(m)
```

---

buildGraph

*Build a k-nearest neighbour graph*

---

**Description**

This function is borrowed from the old `buildKNNGraph` function in `scran`. Instead of returning an `igraph` object it populates the graph and distance slots in a `Milo` object. If the input is a `SingleCellExperiment` object or a matrix then it will return a *de novo* `Milo` object with the same slots filled.

**Usage**

```

buildGraph(
  x,
  k = 10,
  d = 50,
  transposed = FALSE,
  get.distance = FALSE,
  reduced.dim = "PCA",
  BNPARAM = KmknnParam(),
  BSPARAM = bsparam(),
  BPPARAM = SerialParam()
)

```

**Arguments**

x	A matrix, <a href="#">SingleCellExperiment</a> or Milo object containing feature X cell gene expression data.
k	An integer scalar that specifies the number of nearest-neighbours to consider for the graph building.
d	The number of dimensions to use if the input is a matrix of cells X reduced dimensions. If this is provided, transposed should also be set=TRUE.
transposed	Logical if the input x is transposed with rows as cells.
get.distance	A logical scalar whether to compute distances during graph construction.
reduced.dim	A character scalar that refers to a specific entry in the reduceDim slot of the <a href="#">Milo</a> object.
BNPARAM	refer to <a href="#">buildKNNGraph</a> for details.
BSPARAM	refer to <a href="#">buildKNNGraph</a> for details.
BPPARAM	refer to <a href="#">buildKNNGraph</a> for details.

**Details**

This function computes a k-nearest neighbour graph. Each graph vertex is a single-cell connected by the edges between its neighbours. Whilst a kNN-graph is strictly directed, we remove directionality by forcing all edge weights to 1; this behaviour can be overridden by providing `directed=TRUE`.

If you wish to use an alternative graph structure, such as a shared-NN graph I recommend you construct this separately and add to the relevant slot in the [Milo](#) object.

**Value**

A [Milo](#) object with the graph and distance slots populated.

**Author(s)**

Mike Morgan, with KNN code written by Aaron Lun & Jonathan Griffiths.

## Examples

```
library(SingleCellExperiment)
ux <- matrix(rpois(12000, 5), ncol=200)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo <- buildGraph(milo, d=30, transposed=TRUE)

milo
```

---

buildNhoodGraph	<i>Build an abstracted graph of neighbourhoods for visualization</i>
-----------------	--

---

## Description

Build an abstracted graph of neighbourhoods for visualization

## Usage

```
buildNhoodGraph(x, overlap = 1)
```

## Arguments

x	A <a href="#">Milo</a> object with a non-empty nhoods slot.
overlap	A numeric scalar that thresholds graph edges based on the number of overlapping cells between neighbourhoods.

## Details

This constructs a weighted graph where nodes represent neighbourhoods and edges represent the number of overlapping cells between two neighbourhoods.

## Value

A [Milo](#) object containing an igraph graph in the nhoodGraph slot.

## Author(s)

Emma Dann

## Examples

```
NULL
```

---

calcNhoodDistance      *Calculate within neighbourhood distances*

---

### Description

This function will calculate Euclidean distances between single-cells in a neighbourhood using the same dimensionality as was used to construct the graph. This step follows the makeNhoods call to limit the number of distance calculations required.

### Usage

```
calcNhoodDistance(x, d, reduced.dim = NULL, use.assay = "logcounts")
```

### Arguments

x	A <a href="#">Milo</a> object with a valid graph slot. If reduced.dims is not provided and there is no valid populated reducedDim slot in x, then this is computed first with d + 1 principal components.
d	The number of dimensions to use for computing within-neighbourhood distances. This should be the same value used construct the graph.
reduced.dim	If x is an <a href="#">Milo</a> object, a character indicating the name of the reducedDim slot in the <a href="#">Milo</a> object to use as (default: 'PCA'). Otherwise this should be an N X P matrix with rows in the same order as the columns of the input Milo object x.
use.assay	A character scalar defining which assay slot in the <a href="#">Milo</a> to use

### Value

A [Milo](#) object with the distance slots populated.

### Author(s)

Mike Morgan, Emma Dann

### Examples

```
library(SingleCellExperiment)
ux <- matrix(rpois(12000, 5), ncol=200)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo <- buildGraph(milo, d=30, transposed=TRUE)
milo <- makeNhoods(milo)
milo <- calcNhoodDistance(milo, d=30)

milo
```



---

calcNhoodExpression     *Average expression within neighbourhoods*

---

### Description

This function calculates the mean expression of each feature in the Milo object stored in the assays slot. Neighbourhood expression data are stored in a new slot nhoodExpression.

### Usage

```
calcNhoodExpression(x, assay = "logcounts", subset.row = NULL, exprs = NULL)
```

### Arguments

x	A Milo object with nhoods slot populated, alternatively a NxM indicator matrix of N cells and M nhoods.
assay	A character scalar that describes the assay slot to use for calculating neighbourhood expression.
subset.row	A logical, integer or character vector indicating the rows of x to use for summarizing over cells in neighbourhoods.
exprs	If x is a list of neighbourhoods, exprs is a matrix of genes X cells to use for calculating neighbourhood expression.

### Details

This function computes the mean expression of each gene, subset by subset.rows where present, across the cells contained within each neighbourhood.

### Value

A [Milo](#) object with the nhoodExpression slot populated.

### Author(s)

Mike Morgan

### Examples

```
require(SingleCellExperiment)
m <- matrix(rnorm(100000), ncol=100)
milo <- Milo(SingleCellExperiment(assays=list(logcounts=m)))
milo <- buildGraph(m, k=20, d=30)
milo <- makeNhoods(milo)
milo <- calcNhoodExpression(milo)
dim(nhoodExpression(milo))
```

---

checkSeparation	<i>Check for separation of count distributions by variables</i>
-----------------	---

---

### Description

Check the count distributions for each nhoo according to a test variable of interest. This is important for checking if there is separation in the GLMM to inform either nhoo subsetting or re-computation of the NN-graph and refined nhoo.

### Arguments

<code>x</code>	<code>Milo</code> object with a non-empty <code>nhooCounts</code> slot.
<code>design.df</code>	A <code>data.frame</code> containing meta-data in which <code>condition</code> is a column variable. The rownames must be the same as, or a subset of, the colnames of <code>nhooCounts(x)</code> .
<code>condition</code>	A character scalar of the test variable contained in <code>design.df</code> . This should be a factor variable if it is numeric or character it will be cast to a factor variable.
<code>min.val</code>	A numeric scalar that sets the minimum number of counts across condition level samples, below which separation is defined.
<code>factor.check</code>	A logical scalar that sets the factor variable level checking. See <i>details</i> for more information.

### Details

This function checks across nhoo for separation based on the separate levels of an input factor variable. It checks if `condition` is a factor variable, and if not it will cast it to a factor. Note that the function first checks for the number of unique values - if this exceeds  $> 50$  error is generated. Users can override this behaviour with `factor.check=FALSE`.

### Value

A logical vector of the same length as `ncol(nhooCounts(x))` where *TRUE* values represent nhoo where separation is detected. The output of this function can be used to subset nhoo-based analyses e.g. `testNhoo(..., subset.nhoo=checkSeparation(x, ...))`.

### Author(s)

Mike Morgan

### Examples

```
library(SingleCellExperiment)
ux.1 <- matrix(rpois(12000, 5), ncol=400)
ux.2 <- matrix(rpois(12000, 4), ncol=400)
ux <- rbind(ux.1, ux.2)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))
```

```

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                             reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)
milo <- calcNhooDistance(milo, d=10)

cond <- rep("A", ncol(milo))
cond.a <- sample(1:ncol(milo), size=floor(ncol(milo)*0.25))
cond.b <- setdiff(1:ncol(milo), cond.a)
cond[cond.b] <- "B"
meta.df <- data.frame(Condition=cond, Replicate=c(rep("R1", 132), rep("R2", 132), rep("R3", 136)))
meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")

test.meta <- data.frame("Condition"=c(rep("A", 3), rep("B", 3)), "Replicate"=rep(c("R1", "R2", "R3"), 2))
test.meta$Sample <- paste(test.meta$Condition, test.meta$Replicate, sep="_")
rownames(test.meta) <- test.meta$Sample

check.sep <- checkSeparation(milo, design.df=test.meta, condition='Condition')
sum(check.sep)

```

---

computePvalue

*Compute the p-value for the fixed effect parameters*


---

### Description

Based on the asymptotic t-distribution, compute the 2-tailed p-value that estimate  $\neq 0$ . This function is not intended to be used directly, but is included for reference or if an alternative estimate of the degrees of freedom is available.

### Usage

```
computePvalue(Zscore, df)
```

### Arguments

Zscore	A numeric vector containing the Z scores for each fixed effect parameter
df	A numeric vector containing the estimated degrees of freedom for each fixed effect parameter

### Details

Based on sampling from a 2-tailed t-distribution with df degrees of freedom, compute the probability that the calculated Zscore is greater than or equal to what would be expected from random chance.

**Value**

Numeric vector of p-values, 1 per fixed effect parameter

**Author(s)**

Mike Morgan & Alice Kluzer

**Examples**

NULL

---

countCells	<i>Count cells in neighbourhoods</i>
------------	--------------------------------------

---

**Description**

This function quantifies the number of cells in each neighbourhood according to an input experimental design. This forms the basis for the differential neighbourhood abundance testing.

**Usage**

```
countCells(x, samples, meta.data = NULL)
```

**Arguments**

x	A <a href="#">Milo</a> object with non-empty graph and nhoods slots.
samples	Either a string specifying which column of data should be used to identify the experimental samples for counting, or a named vector of sample ids mapping each single cell to it's respective sample.
meta.data	A cell X variable data.frame containing study meta-data including experimental sample IDs. Assumed to be in the same order as the cells in the input <a href="#">Milo</a> object.

**Details**

This function generates a counts matrix of nhoods X samples, and populates the nhoodCounts slot of the input [Milo](#) object. This matrix is used down-stream for differential abundance testing.

**Value**

A [Milo](#) object containing a counts matrix in the nhoodCounts slot.

**Author(s)**

Mike Morgan, Emma Dann

**Examples**

```

library(igraph)
m <- matrix(rnorm(100000), ncol=100)
milo <- buildGraph(t(m), k=20, d=10)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)

cond <- rep("A", nrow(m))
cond.a <- sample(seq_len(nrow(m)), size=floor(nrow(m)*0.25))
cond.b <- setdiff(seq_len(nrow(m)), cond.a)
cond[cond.b] <- "B"
meta.df <- data.frame(Condition=cond, Replicate=c(rep("R1", 330), rep("R2", 330), rep("R3", 340)))
meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")
milo

```

---

findNhoodGroupMarkers *Identify post-hoc neighbourhood marker genes*

---

**Description**

This function will perform differential gene expression analysis on groups of neighbourhoods. Adjacent and concordantly DA neighbourhoods can be defined using groupNhoods or by the user. Cells *between* these aggregated groups are compared. For differential gene expression based on an input design *within* DA neighbourhoods see [testDiffExp](#).

**Usage**

```

findNhoodGroupMarkers(
  x,
  da.res,
  assay = "logcounts",
  aggregate.samples = FALSE,
  sample_col = NULL,
  subset.row = NULL,
  gene.offset = TRUE,
  subset.nhoods = NULL,
  subset.groups = NULL,
  na.function = "na.pass"
)

```

**Arguments**

**x** A [Milo](#) object containing single-cell gene expression and neighbourhoods.

**da.res** A data.frame containing DA results, as expected from running testNhoods, as a NhoodGroup column specifying the grouping of neighbourhoods, as expected from

<code>assay</code>	A character scalar determining which assays slot to extract from the <code>Milo</code> object to use for DGE testing.
<code>aggregate.samples</code>	logical indicating wheather the expression values for cells in the same sample and neighbourhood group should be merged for DGE testing. This allows to perform testing exploiting the replication structure in the experimental design, rather than treating single-cells as independent replicates. The function used for aggregation depends on the selected gene expression assay: if <code>assay="counts"</code> the expression values are summed, otherwise we take the mean.
<code>sample_col</code>	a character scalar indicating the column in the <code>colData</code> storing sample information (only relevant if <code>aggregate.samples==TRUE</code> )
<code>subset.row</code>	A logical, integer or character vector indicating the rows of <code>x</code> to use for sumamrizing over cells in neighbourhoods.
<code>gene.offset</code>	A logical scalar the determines whether a per-cell offset is provided in the DGE GLM to adjust for the number of detected genes with expression $> 0$ .
<code>subset.nhoods</code>	A logical, integer or character vector indicating which neighbourhoods to subset before aggregation and DGE testing (default: <code>NULL</code> ).
<code>subset.groups</code>	A character vector indicating which groups to test for markers (default: <code>NULL</code> )
<code>na.function</code>	A valid NA action function to apply, should be one of <code>na.fail</code> , <code>na.omit</code> , <code>na.exclude</code> , <code>na.pass</code> .

### Details

Using a one vs. all approach, each aggregated group of cells is compared to all others using the single-cell log normalized gene expression with a GLM (for details see [limma-package](#)), or the single-cell counts using a negative binomial GLM (for details see [edgeR-package](#)). When using the latter it is recommended to set `gene.offset=TRUE` as this behaviour adjusts the model offsets by the number of detected genes in each cell.

### Value

A `data.frame` of DGE results containing a log fold change and adjusted p-value for each aggregated group of neighbourhoods. If `return.groups` then the return value is a list with the slots `groups` and `dge` containing the aggregated neighbourhood groups per single-cell and marker gene results, respectively.

*Warning:* If all neighbourhoods are grouped together, then it is impossible to run `findNhoodMarkers`. In this (hopefully rare) instance, this function will return a warning and return `NULL`.

### Examples

```
NULL
```

---

findNhoodMarkers      *Identify post-hoc neighbourhood marker genes*

---

## Description

This function will perform differential gene expression analysis on differentially abundant neighbourhoods, by first aggregating adjacent and concordantly DA neighbourhoods, then comparing cells *between* these aggregated groups. For differential gene expression based on an input design *within* DA neighbourhoods see [testDiffExp](#).

## Arguments

x	A <a href="#">Milo</a> object containing single-cell gene expression and neighbourhoods.
da.res	A <code>data.frame</code> containing DA results, as expected from running <code>testNhoods</code> .
da.fdr	A numeric scalar that determines at what FDR neighbourhoods are declared DA for the purposes of aggregating across concordantly DA neighbourhoods.
assay	A character scalar determining which assays slot to extract from the <a href="#">Milo</a> object to use for DGE testing.
aggregate.samples	logical indicating whether the expression values for cells in the same sample and neighbourhood group should be merged for DGE testing. This allows to perform testing exploiting the replication structure in the experimental design, rather than treating single-cells as independent replicates. The function used for aggregation depends on the selected gene expression assay: if <code>assay="counts"</code> the expression values are summed, otherwise we take the mean.
sample_col	a character scalar indicating the column in the <code>colData</code> storing sample information (only relevant if <code>aggregate.samples==TRUE</code> )
overlap	A scalar integer that determines the number of cells that must overlap between adjacent neighbourhoods for merging.
lfc.threshold	A scalar that determines the absolute log fold change above which neighbourhoods should be considered 'DA' for merging. Default=NULL
merge.discord	A logical scalar that overrides the default behaviour and allows adjacent neighbourhoods to be merged if they have discordant log fold change signs. Using this argument is generally discouraged, but may be useful for constructing an empirical null group of cells, regardless of DA sign.
subset.row	A logical, integer or character vector indicating the rows of <code>x</code> to use for summarizing over cells in neighbourhoods.
gene.offset	A logical scalar that determines whether a per-cell offset is provided in the DGE GLM to adjust for the number of detected genes with expression > 0.
return.groups	A logical scalar that returns a <code>data.frame</code> of the aggregated groups per single-cell. Cells that are members of non-DA neighbourhoods contain NA values.
subset.nhoods	A logical, integer or character vector indicating which neighbourhoods to subset before aggregation and DGE testing.

na.function	A valid NA action function to apply, should be one of na.fail, na.omit, na.exclude, na.pass.
compute.new	A logical scalar indicating whether to force computing a new neighbourhood adjacency matrix if already present.

### Details

Louvain clustering is applied to the neighbourhood graph. This graph is first modified based on two criteria: 1) neighbourhoods share at least overlap number of cells, and 2) the DA log fold change sign is concordant. This behaviour can be modulated by setting overlap to be more or less stringent. Additionally, a threshold on the log fold-changes can be set, such that lfc.threshold is required to retain edges between adjacent neighbourhoods. Note: adjacent neighbourhoods will never be merged with opposite signs.

Using a one vs. all approach, each aggregated group of cells is compared to all others using the single-cell log normalized gene expression with a GLM (for details see [limma-package](#)), or the single-cell counts using a negative binomial GLM (for details see [edgeR-package](#)). When using the latter it is recommended to set gene.offset=TRUE as this behaviour adjusts the model offsets by the number of detected genes in each cell.

### Value

A data.frame of DGE results containing a log fold change and adjusted p-value for each aggregated group of neighbourhoods. If return.groups then the return value is a list with the slots groups and dge containing the aggregated neighbourhood groups per single-cell and marker gene results, respectively.

*Warning:* If all neighbourhoods are grouped together, then it is impossible to run findNhoodMarkers. In this (hopefully rare) instance, this function will return a warning and return NULL.

### Author(s)

Mike Morgan & Emma Dann

### Examples

```
library(SingleCellExperiment)
ux.1 <- matrix(rpois(12000, 5), ncol=400)
ux.2 <- matrix(rpois(12000, 4), ncol=400)
ux <- rbind(ux.1, ux.2)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))
colnames(sce) <- paste0("Cell", seq_len(ncol(sce)))
milo <- Milo(sce)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)
milo <- calcNhoodDistance(milo, d=10)

cond <- rep("A", ncol(milo))
```



```

cond.a <- sample(seq_len(ncol(milo)), size=floor(ncol(milo)*0.25))
cond.b <- setdiff(seq_len(ncol(milo)), cond.a)
cond[cond.b] <- "B"
meta.df <- data.frame(Condition=cond, Replicate=c(rep("R1", 132), rep("R2", 132), rep("R3", 136)))
meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")

test.meta <- data.frame("Condition"=c(rep("A", 3), rep("B", 3)), "Replicate"=rep(c("R1", "R2", "R3"), 2))
test.meta$Sample <- paste(test.meta$Condition, test.meta$Replicate, sep="_")
rownames(test.meta) <- test.meta$Sample
da.res <- testNhoods(milo, design=~0 + Condition, design.df=test.meta[colnames(nhoodCounts(milo)), ])

nhood.dge <- findNhoodMarkers(milo, da.res, overlap=1, compute.new=TRUE)
nhood.dge

```

---

fitGeneticPLGlm

*GLMM parameter estimation using pseudo-likelihood with a custom covariance matrix*


---

## Description

Iteratively estimate GLMM fixed and random effect parameters, and variance component parameters using Fisher scoring based on the Pseudo-likelihood approximation to a Normal loglikelihood. This function incorporates a user-defined covariance matrix, e.g. a kinship matrix for genetic analyses.

## Usage

```

fitGeneticPLGlm(
  Z,
  X,
  K,
  muvec,
  offsets,
  curr_beta,
  curr_theta,
  curr_u,
  curr_sigma,
  curr_G,
  y,
  u_indices,
  theta_conv,
  rlevels,
  curr_disp,
  REML,
  maxit,
  solver,
  vardist
)

```

**Arguments**

Z	mat - sparse matrix that maps random effect variable levels to observations
X	mat - sparse matrix that maps fixed effect variables to observations
K	mat - sparse matrix that defines the known covariance patterns between individual observations. For example, a kinship matrix will then adjust for the known/estimated genetic relationships between observations.
muvec	vec vector of estimated phenotype means
offsets	vec vector of model offsets
curr_beta	vec vector of initial beta estimates
curr_theta	vec vector of initial parameter estimates
curr_u	vec of initial u estimates
curr_sigma	vec of initial sigma estimates
curr_G	mat c X c matrix of variance components
y	vec of observed counts
u_indices	List a List, each element contains the indices of Z relevant to each RE and all its levels
theta_conv	double Convergence tolerance for parameter estimates
rlevels	List containing mapping of RE variables to individual levels
curr_disp	double Dispersion parameter estimate
REML	bool - use REML for variance component estimation
maxit	int maximum number of iterations if theta_conv is FALSE
solver	string which solver to use - either HE (Haseman-Elston regression) or Fisher scoring
vardist	string which variance form to use NB = negative binomial, P=Poisson [not yet implemented]/

**Details**

Fit a NB-GLMM to the counts provided in *y*. The model uses an iterative approach that switches between the joint fixed and random effect parameter inference, and the variance component estimation. A pseudo-likelihood approach is adopted to minimise the log-likelihood of the model given the parameter estimates. The fixed and random effect parameters are estimated using Hendersons mixed model equations, and the variance component parameters are then estimated with the specified solver, i.e. Fisher scoring, Haseman-Elston or constrained Haseman-Elston regression. As the domain of the variance components is  $[0, +\text{Inf}]$ , any negative variance component estimates will trigger the switch to the HE-NNLS solver until the model converges.

**Value**

A list containing the following elements (note: return types are dictated by Rcpp, so the R types are described here):

FE: numeric vector of fixed effect parameter estimates.

RE: list of the same length as the number of random effect variables. Each slot contains the best linear unbiased predictors (BLUPs) for the levels of the corresponding RE variable.

Sigma: numeric vector of variance component estimates, 1 per random effect variable. For this model the last variance component corresponds to the input  $K$  matrix.

converged: logical scalar of whether the model has reached the convergence tolerance or not.

Iter: numeric scalar with the number of iterations that the model ran for. Is strictly  $\leq \text{max.iter}$ .

Dispersion: numeric scalar of the dispersion estimate computed off-line

Hessian: matrix of 2nd derivative elements from the fixed and random effect parameter inference.

SE: matrix of standard error estimates, derived from the hessian, i.e. the square roots of the diagonal elements.

t: numeric vector containing the compute t-score for each fixed effect variable.

COEFF: matrix containing the coefficient matrix from the mixed model equations.

P: matrix containing the elements of the REML projection matrix.

Vpartial: list containing the partial derivatives of the (pseudo)variance matrix with respect to each variance component.

Ginv: matrix of the inverse variance components broadcast to the full  $Z$  matrix.

Vsinv: matrix of the inverse pseudovariance.

Winv: matrix of the inverse elements of  $W = D^{-1} V D^{-1}$

VCOV: matrix of the variance-covariance for all model fixed and random effect variable parameter estimates. This is required to compute the degrees of freedom for the fixed effect parameter inference.

CONVLIST: list of list containing the parameter estimates and differences between current and previous iteration estimates at each model iteration. These are included for each fixed effect, random effect and variance component parameter. The list elements for each iteration are: *ThetaDiff, SigmaDiff, beta, u, sigma*.

**Author(s)**

Mike Morgan

**Examples**

NULL

---

fitGLMM

*Perform differential abundance testing using a NB-generalised linear mixed model*

---

**Description**

This function will perform DA testing per-nhood using a negative binomial generalised linear mixed model

**Usage**

```
fitGLMM(
  X,
  Z,
  y,
  offsets,
  init.theta = NULL,
  Kin = NULL,
  random.levels = NULL,
  REML = FALSE,
  glmm.control = list(theta.tol = 1e-06, max.iter = 100, init.sigma = NULL, init.beta =
    NULL, init.u = NULL, solver = NULL),
  dispersion = 1,
  geno.only = FALSE,
  solver = NULL
)
```

**Arguments**

X	A matrix containing the fixed effects of the model.
Z	A matrix containing the random effects of the model.
y	A matrix containing the observed phenotype over each neighborhood.
offsets	A vector containing the (log) offsets to apply normalisation for different numbers of cells across samples.
init.theta	A column vector (m X 1 matrix) of initial estimates of fixed and random effect coefficients
Kin	A n x n covariance matrix to explicitly model variation between observations
random.levels	A list describing the random effects of the model, and for each, the different unique levels.
REML	A logical value denoting whether REML (Restricted Maximum Likelihood) should be run. Default is TRUE.
glmm.control	A list containing parameter values specifying the theta tolerance of the model, the maximum number of iterations to be run, initial parameter values for the fixed (init.beta) and random effects (init.u), and glmm solver (see details).
dispersion	A scalar value for the initial dispersion of the negative binomial.
geno.only	A logical value that flags the model to use either just the matrix 'Kin' or the supplied random effects.
solver	a character value that determines which optimisation algorithm is used for the variance components. Must be either HE (Haseman-Elston regression) or Fisher (Fisher scoring).

**Details**

This function runs a negative binomial generalised linear mixed effects model. If mixed effects are detected in testNhoods, this function is run to solve the model. The solver defaults to the *Fisher* optimiser, and in the case of negative variance estimates it will switch to the non-negative least squares

(NNLS) Haseman-Elston solver. This behaviour can be pre-set by passing `glmm.control$solver="HE"` for Haseman-Elston regression, which is the recommended solver when a covariance matrix is provided, or `glmm.control$solver="HE-NNLS"` which is the constrained HE optimisation algorithm.

### Value

A list containing the GLMM output, including inference results. The list elements are as follows:

FE: numeric vector of fixed effect parameter estimates.

RE: list of the same length as the number of random effect variables. Each slot contains the best linear unbiased predictors (BLUPs) for the levels of the corresponding RE variable.

Sigma: numeric vector of variance component estimates, 1 per random effect variable.

converged: logical scalar of whether the model has reached the convergence tolerance or not.

Iter: numeric scalar with the number of iterations that the model ran for. Is strictly  $\leq \text{max.iter}$ .

Dispersion: numeric scalar of the dispersion estimate computed off-line

Hessian: matrix of 2nd derivative elements from the fixed and random effect parameter inference.

SE: matrix of standard error estimates, derived from the hessian, i.e. the square roots of the diagonal elements.

t: numeric vector containing the compute t-score for each fixed effect variable.

COEFF: matrix containing the coefficient matrix from the mixed model equations.

P: matrix containing the elements of the REML projection matrix.

Vpartial: list containing the partial derivatives of the (pseudo)variance matrix with respect to each variance component.

Ginv: matrix of the inverse variance components broadcast to the full Z matrix.

Vsinv: matrix of the inverse pseudovariance.

Winv: matrix of the inverse elements of  $W = D^{-1} V D^{-1}$

VCOV: matrix of the variance-covariance for all model fixed and random effect variable parameter estimates. This is required to compute the degrees of freedom for the fixed effect parameter inference.

DF: numeric vector of the number of inferred degrees of freedom. For details see [Satterthwaite\\_df](#).

PVALS: numeric vector of the compute p-values from a t-distribution with the inferred number of degrees of freedom.

ERROR: list containing Rcpp error messages - used for internal checking.

### Author(s)

Mike Morgan

### Examples

```
data(sim_nbg1mm)
random.levels <- list("RE1"=paste("RE1", levels(as.factor(sim_nbg1mm$RE1)), sep="_"),
                    "RE2"=paste("RE2", levels(as.factor(sim_nbg1mm$RE2)), sep="_"))
X <- as.matrix(data.frame("Intercept"=rep(1, nrow(sim_nbg1mm)), "FE2"=as.numeric(sim_nbg1mm$FE2)))
```

```

Z <- as.matrix(data.frame("RE1"=paste("RE1", as.numeric(sim_nbgglm$RE1), sep="_"),
                          "RE2"=paste("RE2", as.numeric(sim_nbgglm$RE2), sep="_")))
y <- sim_nbgglm$Mean.Count
dispersion <- 0.5

glmm.control <- glmmControl.defaults()
glmm.control$theta.tol <- 1e-6
glmm.control$max.iter <- 15
model.list <- fitGLMM(X=X, Z=Z, y=y, offsets=rep(0, nrow(X)), random.levels=random.levels,
                     REML = TRUE, glmm.control=glmm.control, dispersion=dispersion, solver="Fisher")
model.list

```

---

fitPLGlm

*GLMM parameter estimation using pseudo-likelihood*


---

### Description

Iteratively estimate GLMM fixed and random effect parameters, and variance component parameters using Fisher scoring based on the Pseudo-likelihood approximation to a Normal loglikelihood.

### Usage

```

fitPLGlm(
  Z,
  X,
  muvec,
  offsets,
  curr_beta,
  curr_theta,
  curr_u,
  curr_sigma,
  curr_G,
  y,
  u_indices,
  theta_conv,
  rlevels,
  curr_disp,
  REML,
  maxit,
  solver,
  vardist
)

```

### Arguments

Z mat - sparse matrix that maps random effect variable levels to observations  
X mat - sparse matrix that maps fixed effect variables to observations

<code>muvec</code>	vec vector of estimated phenotype means
<code>offsets</code>	vec vector of model offsets
<code>curr_beta</code>	vec vector of initial beta estimates
<code>curr_theta</code>	vec vector of initial parameter estimates
<code>curr_u</code>	vec of initial u estimates
<code>curr_sigma</code>	vec of initial sigma estimates
<code>curr_G</code>	mat c X c matrix of variance components
<code>y</code>	vec of observed counts
<code>u_indices</code>	List a List, each element contains the indices of Z relevant to each RE and all its levels
<code>theta_conv</code>	double Convergence tolerance for parameter estimates
<code>rlevels</code>	List containing mapping of RE variables to individual levels
<code>curr_disp</code>	double Dispersion parameter estimate
<code>REML</code>	bool - use REML for variance component estimation
<code>maxit</code>	int maximum number of iterations if <code>theta_conv</code> is FALSE
<code>solver</code>	string which solver to use - either HE (Haseman-Elston regression) or Fisher scoring
<code>vardist</code>	string which variance form to use NB = negative binomial, P=Poisson [not yet implemented.]

## Details

Fit a NB-GLMM to the counts provided in `y`. The model uses an iterative approach that switches between the joint fixed and random effect parameter inference, and the variance component estimation. A pseudo-likelihood approach is adopted to minimise the log-likelihood of the model given the parameter estimates. The fixed and random effect parameters are estimated using Henderson's mixed model equations, and the variance component parameters are then estimated with the specified solver, i.e. Fisher scoring, Haseman-Elston or constrained Haseman-Elston regression. As the domain of the variance components is  $[0, +\infty]$ , any negative variance component estimates will trigger the switch to the HE-NNLS solver until the model converges.

## Value

A list containing the following elements (note: return types are dictated by Rcpp, so the R types are described here):

**FE:** numeric vector of fixed effect parameter estimates.

**RE:** list of the same length as the number of random effect variables. Each slot contains the best linear unbiased predictors (BLUPs) for the levels of the corresponding RE variable.

**Sigma:** numeric vector of variance component estimates, 1 per random effect variable.

**converged:** logical scalar of whether the model has reached the convergence tolerance or not.

**Iters:** numeric scalar with the number of iterations that the model ran for. Is strictly  $\leq \text{max.iters}$ .

**Dispersion:** numeric scalar of the dispersion estimate computed off-line

Hessian: matrix of 2nd derivative elements from the fixed and random effect parameter inference.

SE: matrix of standard error estimates, derived from the hessian, i.e. the square roots of the diagonal elements.

t: numeric vector containing the compute t-score for each fixed effect variable.

COEFF: matrix containing the coefficient matrix from the mixed model equations.

P: matrix containing the elements of the REML projection matrix.

Vpartial: list containing the partial derivatives of the (pseudo)variance matrix with respect to each variance component.

Ginv: matrix of the inverse variance components broadcast to the full Z matrix.

Vsinv: matrix of the inverse pseudovariance.

Winv: matrix of the inverse elements of  $W = D^{-1} V D^{-1}$

VCOV: matrix of the variance-covariance for all model fixed and random effect variable parameter estimates. This is required to compute the degrees of freedom for the fixed effect parameter inference.

CONVLIST: list of list containing the parameter estimates and differences between current and previous iteration estimates at each model iteration. These are included for each fixed effect, random effect and variance component parameter. The list elements for each iteration are: *ThetaDiff*, *SigmaDiff*, *beta*, *u*, *sigma*.

**Author(s)**

Mike Morgan

**Examples**

NULL

---

`glmmControl.defaults` *glmm control default values*

---

**Description**

This will give the default values for the GLMM solver

**Usage**

`glmmControl.defaults(...)`

**Arguments**

... see `fitGLMM` for details



**Details**

The default values for the parameter estimation convergence is  $1e-6$ , and the maximum number of iterations is 100. In practise if the solver converges it generally does so fairly quickly on moderately well conditioned problems. The default solver is Fisher scoring, but this will switch (with a warning produced) to the NNLS Haseman-Elston solver if negative variance estimates are found.

**Value**

list containing the default values GLMM solver. This can be saved in the user environment and then passed to `testNhoods` directly to modify the convergence criteria of the solver that is used.

`theta.tol`: numeric scalar that sets the convergence threshold for the parameter inference - this is applied globally to fixed and random effect parameters, and to the variance estimates.

`max.iter`: numeric scalar that sets the maximum number of iterations that the NB-GLMM will run for.

`solver`: character scalar that sets the solver to use. Valid values are *Fisher*, *HE* or *HE-NNLS*. See `fitGLMM` for details.

**Author(s)**

Mike Morgan

**Examples**

```
mmcontrol <- glmControl.defaults()
mmcontrol
mmcontrol$solver <- "HE-NNLS"
mmcontrol
```

---

graphSpatialFDR      *Control the spatial FDR*

---

**Description**

Borrowing heavily from cydar which corrects for multiple-testing using a weighting scheme based on the volumetric overlap over hyperspheres. In the instance of graph neighbourhoods this weighting scheme can use graph connectivity or incorporate different within-neighbourhood distances for the weighted FDR calculation.

**Arguments**

<code>x.nhoods</code>	A list of vertices and the constituent vertices of their neighbourhood
<code>graph</code>	The kNN graph used to define the neighbourhoods
<code>pvalues</code>	A vector of p-values calculated from a GLM or other appropriate statistical test for differential neighbourhood abundance

k	A numeric integer that determines the kth nearest neighbour distance to use for the weighted FDR. Only applicable when using <code>weighting="k-distance"</code> .
weighting	A string scalar defining which weighting scheme to use. Choices are: max, k-distance, neighbour-distance or graph-overlap.
reduced.dimensions	(optional) A matrix of cells X reduced dimensions used to calculate the kNN graph. Only necessary if this function is being used outside of <code>testNhoods</code> where the <code>Milo</code> object is not available
distances	(optional) A matrix of cell-to-cell distances or a list of distance matrices, 1 per neighbourhood. Only necessary if this function is being used outside of <code>testNhoods</code> where the <code>Milo</code> object is not available.
indices	(optional) A list of neighbourhood index vertices in the same order as the input neighbourhoods. Only used for the k-distance weighting.

### Details

Each neighbourhood is weighted according to the weighting scheme defined. k-distance uses the distance to the kth nearest neighbour of the index vertex, neighbour-distance uses the average within-neighbourhood Euclidean distance in reduced dimensional space, max uses the largest within-neighbourhood distance from the index vertex, and graph-overlap uses the total number of cells overlapping between neighborhoods (distance-independent measure). The frequency-weighted version of the BH method is then applied to the p-values, as in `cydar`.

### Value

A vector of adjusted p-values

### Author(s)

Adapted by Mike Morgan, original function by Aaron Lun

### Examples

NULL

---

groupNhoods

*Group neighbourhoods*

---

### Description

This function groups overlapping and concordantly DA neighbourhoods, using the louvain community detection algorithm.

**Usage**

```
groupNhoods(
  x,
  da.res,
  da.fdr = 0.1,
  overlap = 1,
  max.lfc.delta = NULL,
  merge.discord = FALSE,
  subset.nhoods = NULL,
  compute.new = FALSE,
  na.function = "na.pass"
)
```

**Arguments**

<code>x</code>	A <a href="#">Milo</a> object containing single-cell gene expression and neighbourhoods.
<code>da.res</code>	A data.frame containing DA results, as expected from running <code>testNhoods</code> .
<code>da.fdr</code>	A numeric scalar that determines at what FDR neighbourhoods are declared DA for the purposes of aggregating across concordantly DA neighbourhoods.
<code>overlap</code>	A scalar integer that determines the number of cells that must overlap between adjacent neighbourhoods for merging.
<code>max.lfc.delta</code>	A scalar that determines the absolute difference in log fold change below which neighbourhoods should not be considered adjacent. Default=NULL
<code>merge.discord</code>	A logical scalar that overrides the default behaviour and allows adjacent neighbourhoods to be merged if they have discordant log fold change signs. Using this argument is generally discouraged, but may be useful for constructing an empirical null group of cells, regardless of DA sign.
<code>subset.nhoods</code>	A logical, integer or character vector indicating which neighbourhoods to subset before grouping. All other neighbourhoods will be assigned NA
<code>compute.new</code>	A logical scalar indicating whether to force computing a new neighbourhood adjacency matrix if already present.
<code>na.function</code>	A valid NA action function to apply, should be one of <code>na.fail</code> , <code>na.omit</code> , <code>na.exclude</code> , <code>na.pass</code> (default='na.pass').

**Details**

Louvain clustering is applied to the neighbourhood graph. This graph is first modified based on two criteria: 1) neighbourhoods share at least `overlap` number of cells, and 2) the DA log fold change sign is concordant. This behaviour can be modulated by setting `overlap` to be more or less stringent. Additionally, a threshold on the log fold-changes can be set, such that `max.lfc.delta` is required to retain edges between adjacent neighbourhoods. Note: adjacent neighbourhoods will never be merged with opposite signs.

**Value**

A data.frame of model results (as `da.res` input) with a new column storing the assigned group label for each neighbourhood (`NhoodGroup` column)

**Author(s)**

Emma Dann & Mike Morgan

---

initialiseG

*Construct the initial G matrix*

---

**Description**

This function maps the variance estimates onto the full  $c \times q$  levels for each random effect. This ensures that the matrices commute in the NB-GLMM solver. This function is included for reference, and should not be used directly

**Usage**

```
initialiseG(cluster_levels, sigmas, Kin = NULL)
```

**Arguments**

`cluster_levels` A list containing the random effect levels for each variable

`sigmas` A matrix of  $c \times 1$ , i.e. a column vector, containing the variance component estimates

`Kin` A matrix containing a user-supplied covariance matrix

**Details**

Broadcast the variance component estimates to the full  $c \times q \times c \times q$  matrix.

**Value**

matrix of the full broadcast variance component estimates.

**Author(s)**

Mike Morgan & Alice Kluzer

**Examples**

```
data(sim_nbg1mm)
random.levels <- list("RE1"=paste("RE1", levels(as.factor(sim_nbg1mm$RE1)), sep="_"),
                    "RE2"=paste("RE2", levels(as.factor(sim_nbg1mm$RE2)), sep="_"))
rand.sigma <- matrix(runif(2), ncol=1)
rownames(rand.sigma) <- names(random.levels)
big.G <- initialiseG(random.levels, rand.sigma)
dim(big.G)
```

---

<code>initializeFullZ</code>	<i>Construct the full Z matrix</i>
------------------------------	------------------------------------

---

### Description

Using a simplified version of the  $n \times c$   $Z$  matrix, with one column per variable, construct the fully broadcast  $n \times (c \times q)$  binary matrix that maps each individual onto the random effect variable levels. It is not intended for this function to be called by the user directly, but it can be useful to debug mappings between random effect levels and input variables.

### Usage

```
initializeFullZ(Z, cluster_levels, stand.cols = FALSE)
```

### Arguments

<code>Z</code>	A $n \times c$ matrix containing the numeric or character levels
<code>cluster_levels</code>	A list that maps the column names of $Z$ onto the individual levels
<code>stand.cols</code>	A logical scalar that determines if $Z^*$ should be computed which is the row-centered and scaled version of the full $Z$ matrix

### Details

To make sure that matrices commute it is necessary to construct the full  $n \times c \times q$  matrix. This is a binary matrix where each level of each random effect occupies a column, and the samples/observations are mapped onto the correct levels based on the input  $Z$ .

### Value

matrix Fully broadcast  $Z$  matrix with one column per random effect level for all random effect variables in the model.

### Author(s)

Mike Morgan & Alice Kluzer

### Examples

```
data(sim_nbglmm)
random.levels <- list("RE1"=paste("RE1", levels(as.factor(sim_nbglmm$RE1)), sep="_"),
                    "RE2"=paste("RE2", levels(as.factor(sim_nbglmm$RE2)), sep="_"))
Z <- as.matrix(data.frame("RE1"=paste("RE1", as.numeric(sim_nbglmm$RE1), sep="_"),
                        "RE2"=paste("RE2", as.numeric(sim_nbglmm$RE2), sep="_")))
fullZ <- initializeFullZ(Z, random.levels)
dim(Z)
dim(fullZ)
```

---

 makeNhoods

*Define neighbourhoods on a graph (fast)*


---

## Description

This function randomly samples vertices on a graph to define neighbourhoods. These are then refined by either computing the median profile for the neighbourhood in reduced dimensional space and selecting the nearest vertex to this position (`refinement_scheme = "reduced_dim"`), or by computing the vertex with the highest number of triangles within the neighborhood (`refinement_scheme = "graph"`). Thus, multiple neighbourhoods may be collapsed down together to prevent over-sampling the graph space.

## Usage

```
makeNhoods(
  x,
  prop = 0.1,
  k = 21,
  d = 30,
  refined = TRUE,
  reduced_dims = "PCA",
  refinement_scheme = "reduced_dim"
)
```

## Arguments

<code>x</code>	A <a href="#">Milo</a> object with a non-empty graph slot. Alternatively an <code>igraph</code> object on which neighbourhoods will be defined.
<code>prop</code>	A double scalar that defines what proportion of graph vertices to randomly sample. Must be $0 < \text{prop} < 1$ .
<code>k</code>	An integer scalar - the same <code>k</code> used to construct the input graph.
<code>d</code>	The number of dimensions to use if the input is a matrix of cells <code>X</code> reduced dimensions.
<code>refined</code>	A logical scalar that determines the sampling behavior, default= <code>TRUE</code> implements a refined sampling scheme, specified by the <code>refinement_scheme</code> argument.
<code>reduced_dims</code>	If <code>x</code> is an <a href="#">Milo</a> object, a character indicating the name of the <code>reducedDim</code> slot in the <a href="#">Milo</a> object to use as (default: <code>'PCA'</code> ). If <code>x</code> is an <code>igraph</code> object, a matrix of vertices <code>X</code> reduced dimensions with <code>rownames()</code> set to correspond to the cellIDs.
<code>refinement_scheme</code>	A character scalar that defines the sampling scheme, either <code>"reduced_dim"</code> or <code>"graph"</code> . Default is <code>"reduced_dim"</code> .

**Details**

This function randomly samples graph vertices, then refines them to collapse down the number of neighbourhoods to be tested. The refinement behaviour can be turned off by setting `refine=FALSE`, however, we do not recommend this as neighbourhoods will contain a lot of redundancy and lead to an unnecessarily larger multiple-testing burden.

**Value**

A `Milo` object containing a list of vertices and the indices of vertices that constitute the neighbourhoods in the `nhoods` slot. If the input is a `igraph` object then the output is a matrix containing a list of vertices and the indices of vertices that constitute the neighbourhoods.

**Author(s)**

Emma Dann, Mike Morgan

**Examples**

```
require(igraph)
m <- matrix(rnorm(100000), ncol=100)
milo <- buildGraph(m, d=10)

milo <- makeNhoods(milo, prop=0.1)
milo
```

---

matrix.trace	<i>Compute the trace of a matrix</i>
--------------	--------------------------------------

---

**Description**

Exactly what it says on the tin - compute the sum of the matrix diagonal

**Usage**

```
matrix.trace(x)
```

**Arguments**

`x`                    A matrix

**Details**

It computes the matrix trace of a square matrix.

**Value**

numeric scalar of the matrix trace.

**Author(s)**

Mike Morgan

**Examples**

```
matrix.trace(matrix(runif(9), ncol=3, nrow=3))
```

Milo-class

*The Milo constructor***Description**

The Milo class extends the SingleCellExperiment class and is designed to work with neighbourhoods of cells. Therefore, it inherits from the [SingleCellExperiment](#) class and follows the same usage conventions. There is additional support for cell-to-cell distances via distance, and the KNN-graph used to define the neighbourhoods.

**Usage**

```
Milo(
  ...,
  graph = list(),
  nhooDistances = Matrix(0L, sparse = TRUE),
  nhooDs = Matrix(0L, sparse = TRUE),
  nhooCounts = Matrix(0L, sparse = TRUE),
  nhooIndex = list(),
  nhooExpression = Matrix(0L, sparse = TRUE),
  .k = NULL
)
```

**Arguments**

...	Arguments passed to the Milo constructor to fill the slots of the base class. This should be either a <a href="#">SingleCellExperiment</a> or matrix of features X cells
graph	An igraph object or list of adjacent vertices that represents the KNN-graph
nhooDistances	A list containing sparse matrices of cell-to-cell distances for cells in the same neighbourhoods, one list entry per neighbourhood.
nhooDs	A list of graph vertices, each containing the indices of the constituent graph vertices in the respective neighbourhood
nhooCounts	A matrix of neighbourhood X sample counts of the number of cells in each neighbourhood derived from the respective samples
nhooIndex	A list of cells that are the neighborhood index cells.
nhooExpression	A matrix of gene X neighbourhood expression.
.k	An integer value. The same value used to build the k-NN graph if already computed.



**Details**

In this class the underlying structure is the gene/feature X cell expression data. The additional slots provide a link between these single cells and the neighbourhood representation. This can be further extended by the use of an abstracted graph for visualisation that preserves the structure of the single-cell KNN-graph

A Milo object can also be constructed by inputting a feature X cell gene expression matrix. In this case it simply constructs a SingleCellExperiment and fills the relevant slots, such as reducedDims.

**Value**

a Milo object

**Author(s)**

Mike Morgan

**Examples**

```
library(SingleCellExperiment)
ux <- matrix(rpois(12000, 5), ncol=200)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo
```

---

Milo-methods

*Get and set methods for Milo objects*

---

**Description**

Get and set methods for Milo object slots. Generally speaking these methods are used internally, but they allow the user to assign their own externally computed values - should be used *with caution*.

**Value**

See individual methods for return values

## Getters

In the following descriptions `x` is always a [Milo](#) object.

- `graph(x)`: Returns an `igraph` object representation of the KNN-graph, with number of vertices equal to the number of single-cells.
- `nhoodDistances(x)`: Returns a list of sparse matrix of cell-to-cell distances between nearest neighbours, one list entry per neighbourhood. Largely used internally for computing the k-distance weighting in `graphSpatialFDR`.
- `nhoodCounts(x)`: Returns a  $N \times M$  sparse matrix of cell counts in each of  $N$  neighbourhoods with respect to the  $M$  experimental samples defined.
- `nhoodExpression(x)`: Returns a  $G \times N$  matrix of gene expression values.
- `nhoodIndex(x)`: Returns a list of the single-cells that are the neighbourhood indices.
- `nhoodReducedDim(x)`: Returns an  $N \times P$  matrix of reduced dimension positions. Either generated by `projectNhoodExpression(x)` or by providing an  $N \times P$  matrix (see setter method below).
- `nhoods(x)`: Returns a sparse matrix of  $C \times N$  mapping of  $C$  single-cells to  $N$  neighbourhoods.
- `nhoodGraph(x)`: Returns an `igraph` object representation of the graph of neighbourhoods, with number of vertices equal to the number of neighbourhoods.
- `nhoodAdjacency(x)`: Returns a matrix of  $N$  by  $N$  neighbourhoods with entries of 1 where neighbourhoods share cells, and 0 elsewhere.

## Setters

In the following descriptions `x` is always a [Milo](#) object.

- `graph(x) <- value`: Populates the `graph` slot with `value` - this should be a valid graph representation in either `igraph` or `list` format.
- `nhoodDistances(x) <- value`: Replaces the internally computed neighbourhood distances. This is normally computed internally during graph building, but can be defined externally. Must be a list with one entry per neighbourhood containing the cell-to-cell distances for the cells within that neighbourhood.
- `nhoodCounts(x) <- value`: Replaces the neighbourhood counts matrix. This is normally computed and assigned by `countCells`, however, it can also be user-defined.
- `nhoodExpression(x) <- value`: Replaces the `nhoodExpression` slot. This is calculated internally by `calcNhoodExpression`, which calculates the mean expression. An alternative summary function can be used to assign an alternative in this way.
- `nhoodIndex(x) <- value`: Replaces the list of neighbourhood indices. This is provided purely for completeness, and is usually only set internally in `makeNhoods`.
- `nhoodReducedDim(x) <- value`: Replaces the reduced dimensional representation or projection of neighbourhoods. This can be useful for externally computed projections or representations.
- `nhoods(x) <- value`: Replaces the neighbourhood matrix. Generally use of this function is discouraged, however, it may be useful for users to define their own bespoke neighbourhoods by some means.
- `nhoodGraph(x) <- value`: Populates the `nhoodGraph` slot with `value` - this should be a valid graph representation in either `igraph` or `list` format.
- `nhoodAdjacency(x) <- value`: Populates the `nhoodAdjacency` slot with `value` - this should be a  $N$  by  $N$  matrix with elements denoting which neighbourhoods share cells

**Miscellaneous**

A collection of non-getter and setter methods that operate on [Milo](#) objects.

show(x): Prints information to the console regarding the [Milo](#) object.

**Author(s)**

Mike Morgan

**Examples**

```
example(Milo, echo=FALSE)
show(milo)
```

milor

*milor*

**Description**

Milo performs single-cell differential abundance testing. Cell states are modelled as representative neighbourhoods on a nearest neighbour graph. Hypothesis testing is performed using a negative binomial generalized linear model.

plotDAbeeswarm

*Visualize DA results as a beeswarm plot*

**Description**

This function constructs a beeswarm plot using the ggplot engine to visualise the distribution of log fold changes across neighbourhood annotations.

**Usage**

```
plotDAbeeswarm(da.res, group.by = NULL, alpha = 0.1, subset.nhoods = NULL)
```

**Arguments**

- da.res            a data.frame of DA testing results
- group.by        a character scalar determining which column of da.res to use for grouping. This can be a column added to the DA testing results using the ‘annotateNhoods’ function. If da.res[,group.by] is a character or a numeric, the function will coerce it to a factor (see details) (default: NULL, no grouping)
- alpha            significance level for Spatial FDR (default: 0.1)
- subset.nhoods   A logical, integer or character vector indicating a subset of nhoods to show in plot (default: NULL, no subsetting)

**Details**

The `group.by` variable will be coerced to a factor. If you want the variables in `group.by` to be in a given order make sure you set the column to a factor with the levels in the right order before running the function.

**Value**

a `ggplot` object

**Author(s)**

Emma Dann

**Examples**

NULL

---

plotNhoodCounts	<i>Plot the number of cells in a neighbourhood per sample and condition</i>
-----------------	---

---

**Description**

Plot the number of cells in a neighbourhood per sample and condition

**Usage**

```
plotNhoodCounts(x, subset.nhoods, design.df, condition, n_col = 3)
```

**Arguments**

<code>x</code>	A <a href="#">Milo</a> object with a non-empty <code>nhoodCounts</code> slot.
<code>subset.nhoods</code>	A logical, integer or character vector indicating the rows of <code>nhoodCounts(x)</code> to use for plotting. If you use a logical vector, make sure the length matches <code>nrow(nhoodCounts(x))</code> .
<code>design.df</code>	A <code>data.frame</code> which matches samples to a condition of interest. The row names should correspond to the samples. You can use the same <code>design.df</code> that you already used in the <code>testNhoods</code> function.
<code>condition</code>	String specifying the condition of interest Has to be a column in the design.
<code>n_col</code>	Number of columns in the output <code>ggplot</code> .

**Value**

A `ggplot-class` object

**Author(s)**

Nick Hirschmüller

**Examples**

```

require(SingleCellExperiment)
ux.1 <- matrix(rpois(12000, 5), ncol=300)
ux.2 <- matrix(rpois(12000, 4), ncol=300)
ux <- rbind(ux.1, ux.2)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)
milo <- calcNhoodDistance(milo, d=10)

cond <- sample(c("A", "B", "C"), 300, replace=TRUE)

meta.df <- data.frame(Condition=cond, Replicate=c(rep("R1", 100), rep("R2", 100), rep("R3", 100)))
meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")

design.mtx <- data.frame("Condition"=c(rep("A", 3), rep("B", 3), rep("C", 3)),
                       "Replicate"=rep(c("R1", "R2", "R3"), 3))
design.mtx$SampID <- paste(design.mtx$Condition, design.mtx$Replicate, sep="_")
rownames(design.mtx) <- design.mtx$SampID

plotNhoodCounts(x = milo,
               subset.nhoods = c(1,2),
               design.df = design.mtx,
               condition = "Condition")

```

---

plotNhoodExpressionDA *Visualize gene expression in neighbourhoods*

---

**Description**

Plots the average gene expression in neighbourhoods, sorted by DA fold-change

Plots the average gene expression in neighbourhood groups

**Usage**

```

plotNhoodExpressionDA(
  x,
  da.res,

```

```

    features,
    alpha = 0.1,
    subset.nhoods = NULL,
    cluster_features = FALSE,
    assay = "logcounts",
    scale_to_1 = FALSE,
    show_rownames = TRUE,
    highlight_features = NULL
  )

plotNhoodExpressionGroups(
  x,
  da.res,
  features,
  alpha = 0.1,
  subset.nhoods = NULL,
  cluster_features = FALSE,
  assay = "logcounts",
  scale_to_1 = FALSE,
  show_rownames = TRUE,
  highlight_features = NULL,
  grid.space = "free"
)

```

### Arguments

<code>x</code>	A <a href="#">Milo</a> object
<code>da.res</code>	a data.frame of DA testing results
<code>features</code>	a character vector of features to plot (they must be in <code>rownames(x)</code> )
<code>alpha</code>	significance level for Spatial FDR (default: 0.1)
<code>subset.nhoods</code>	A logical, integer or character vector indicating a subset of nhoods to show in plot (default: NULL, no subsetting)
<code>cluster_features</code>	logical indicating whether features should be clustered with hierarchical clustering. If FALSE then the order in features is maintained (default: FALSE)
<code>assay</code>	A character scalar that describes the assay slot to use for calculating neighbourhood expression. (default: logcounts) Of note: neighbourhood expression will be computed only if the requested features are not in the <code>nhoodExpression</code> slot of the milo object. If you wish to plot average neighbourhood expression from a different assay, you should run <code>calcNhoodExpression(x)</code> with the desired assay.
<code>scale_to_1</code>	A logical scalar to re-scale gene expression values between 0 and 1 for visualisation.
<code>show_rownames</code>	A logical scalar whether to plot rownames or not. Generally useful to set this to <code>show_rownames=FALSE</code> when plotting many genes.

highlight_features	A character vector of feature names that should be highlighted on the right side of the heatmap. Generally useful in conjunction to show_rownames=FALSE, if you are interested in only a few features
grid.space	a character setting the space parameter for facet.grid ('fixed' for equally sized facets, 'free' to adapt the size of facet to number of neighbourhoods in group)

**Value**

a ggplot object

a ggplot object

**Author(s)**

Emma Dann

**Examples**

NULL

NULL

---

plotNhoodGraph	<i>Plot graph of neighbourhood</i>
----------------	------------------------------------

---

**Description**

Visualize graph of neighbourhoods

**Usage**

```
plotNhoodGraph(  
  x,  
  layout = "UMAP",  
  colour_by = NA,  
  subset.nhoods = NULL,  
  size_range = c(0.5, 3),  
  node_stroke = 0.3,  
  ...  
)
```

**Arguments**

x	A <a href="#">Milo</a> object
layout	this can be (a) a character indicating the name of the reducedDim slot in the <a href="#">Milo</a> object to use for layout (default: 'UMAP') (b) an igraph layout object
colour_by	this can be a data.frame of milo results or a character corresponding to a column in colData
subset.nhoods	A logical, integer or character vector indicating a subset of nhoods to show in plot (default: NULL, no subsetting). This is necessary if testNhoods was run using subset.nhoods=...
size_range	a numeric vector indicating the range of node sizes to use for plotting (to avoid overplotting in the graph)
node_stroke	a numeric indicating the desired thickness of the border around each node
...	arguments to pass to ggraph

**Value**

a ggplot-class object

**Author(s)**

Emma Dann

**Examples**

NULL

---

plotNhoodGraphDA	<i>Plot Milo results on graph of neighbourhood</i>
------------------	--

---

**Description**

Visualize log-FC estimated with differential nhood abundance testing on embedding of original single-cell dataset.

**Usage**

```
plotNhoodGraphDA(x, milo_res, alpha = 0.05, res_column = "logFC", ...)
```

**Arguments**

x	A <a href="#">Milo</a> object
milo_res	a data.frame of milo results
alpha	significance level for Spatial FDR (default: 0.05)
res_column	which column of milo_res object to use for color (default: logFC)
...	arguments to pass to plotNhoodGraph



**Value**

a ggplot object

**Author(s)**

Emma Dann

**Examples**

NULL

---

plotNhoodGroups      *Plot graph of neighbourhoods coloring by nhoodGroups*

---

**Description**

Visualize grouping of neighbourhoods obtained with groupNhoods

**Usage**

```
plotNhoodGroups(x, milo_res, show_groups = NULL, ...)
```

**Arguments**

- x                    A [Milo](#) object
- milo\_res            a data.frame of milo results containing the nhoodGroup column
- show\_groups        a character vector indicating which groups to plot all other neighbourhoods will be gray
- ...                   arguments to pass to plotNhoodGraph

**Value**

a ggplot object

**Author(s)**

Emma Dann

**Examples**

NULL

---

`plotNhoodMA`*Visualize DA results as an MAplot*

---

**Description**

Make an MAplot to visualise the relationship between DA log fold changes and neighbourhood abundance. This is a useful way to diagnose issues with the DA testing, such as large compositional biases and/or issues relating to large imbalances in numbers of cells between condition labels/levels.

**Usage**

```
plotNhoodMA(da.res, alpha = 0.05, null.mean = 0)
```

**Arguments**

<code>da.res</code>	A data.frame of DA testing results
<code>alpha</code>	A numeric scalar that represents the Spatial FDR threshold for statistical significance.
<code>null.mean</code>	A numeric scalar determining the expected value of the log fold change under the null hypothesis. <code>default=0</code> .

**Details**

MA plots provide a useful means to evaluate the distribution of log fold changes after differential abundance testing. In particular, they can be used to diagnose global shifts that occur in the presence of confounding between the number of cells acquired and the experimental variable of interest. The expected null value for the log FC distribution (grey dashed line), along with the mean observed log fold change for non-DA neighbourhoods (purple dashed line) are plotted for reference. The deviation between these two lines can give an indication of biases in the results, such as in the presence of a single strong region of DA leading to an increase in false positive DA neighbourhoods in the opposite direction.

**Value**

a ggplot object

**Author(s)**

Mike Morgan

**Examples**

```
NULL
```

---

plotNhoodSizeHist	<i>Plot histogram of neighbourhood sizes</i>
-------------------	--

---

### Description

This function plots the histogram of the number of cells belonging to each neighbourhood

### Usage

```
plotNhoodSizeHist(milo, bins = 50)
```

### Arguments

milo	A <a href="#">Milo</a> object with a non-empty nhoods slot.
bins	number of bins for geom_histogram

### Value

A ggplot-class object

### Author(s)

Emma Dann

### Examples

```
require(igraph)
require(SingleCellExperiment)
ux.1 <- matrix(rpois(12000, 5), ncol=400)
ux.2 <- matrix(rpois(12000, 4), ncol=400)
ux <- rbind(ux.1, ux.2)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))
colnames(sce) <- paste0("Cell", seq_len(ncol(sce)))
milo <- Milo(sce)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)

milo <- makeNhoods(milo, d=10, prop=0.1)
plotNhoodSizeHist(milo)
```

---

Satterthwaite\_df      *Compute degrees of freedom using Satterthwaite method*

---

### Description

This function is not intended to be called by the user, and is included for reference

### Usage

```
Satterthwaite_df(
  coeff.mat,
  mint,
  cint,
  SE,
  curr_sigma,
  curr_beta,
  V_partial,
  V_a,
  G_inv,
  random.levels
)
```

### Arguments

coeff.mat	A matrix class object containing the coefficient matrix from the mixed model equations
mint	A numeric scalar of the number of fixed effect variables in the model
cint	A numeric scalar of the number of random effect variables in the model
SE	A $1 \times \text{mint}$ matrix, i.e. column vector, containing the standard errors of the fixed effect parameter estimates
curr_sigma	A $1 \times \text{cint}$ matrix, i.e. column vector, of the variance component parameter estimates
curr_beta	A $1 \times \text{mint}$ matrix, i.e. column vector, of the fixed effect parameter estimates
V_partial	A list of the partial derivatives for each fixed and random effect variable in the model
V_a	A $c+m \times c+m$ variance-covariance matrix of the fixed and random effect variable parameter estimates
G_inv	A $n \times c$ $\times$ $n \times c$ inverse matrix containing the variance component estimates
random.levels	A list containing the mapping between the random effect variables and each respective set of levels for said variable.

**Details**

The Satterthwaite degrees of freedom are computed, which estimates the numbers of degrees of freedom in the NB-GLMM based on ratio of the squared standard errors and the product of the Jacobians of the variance-covariance matrix from the fixed effect variable parameter estimation with full variance-covariance matrix. For more details see Satterthwaite FE, Biometrics Bulletin (1946) Vol 2 No 6, pp110-114.

**Value**

matrix containing the inferred number of degrees of freedom for the specific model.

**Author(s)**

Mike Morgan & Alice Kluzer

**Examples**

NULL

---

sim\_discrete

*sim\_discrete*

---

**Description**

Simulated discrete groups data

**Usage**

```
data(sim_discrete)
```

**Format**

A list containing a [Milo](#) object in the "mylo" slot, and a `data.frame` containing experimental meta-data in the "meta" slot.

**Details**

Data are simulated single-cells in 4 distinct groups of cells. Cells in each group are assigned to 1 of 2 conditions: *A* or *B*. Specifically, the cells in block 1 are highly abundant in the *A* condition, whilst cells in block 4 are most abundant in condition *B*.

**Examples**

NULL

---

 sim\_family

*sim\_family*


---

**Description**

Simulated counts data from a series of simulated family trees

**Usage**

```
data(sim_family)
```

**Format**

A list containing a `data.frame` in the "DF" slot containing the mean counts and meta-data, and a `matrix` containing the kinship matrix across all families in the "IBD" slot.

**Details**

Data are simulated counts from 30 families and includes X and Z design matrices, as well as a single large kinship matrix. Kinships between family members are dictated by the simulated family, i.e. sibs=0.5, parent-sib=0.5, sib-grandparent=0.25, etc. These kinships, along with 2 other random effects, are used to induce a defined covariance between simulated observations as such:

Z:= random effect design matrix, n X q G:= matrix of variance components, including kinship matrix

$LL^T = \text{Chol}(ZGZ^T)$  := the Cholesky decomposition of the random effect contribution to the sample covariance Ysim:= simulated means based on  $\exp(\text{offset} + X\beta + Zb)$  Y = LYsim := simulated means with defined covariance

**Examples**

```
NULL
```

---

 sim\_nbgllmm

*sim\_nbgllmm*


---

**Description**

Simulated counts data from a NB-GLMM for a single trait

**Usage**

```
data(sim_nbgllmm)
```

**Format**

A data.frame *sim\_nbglmm* containing the following columns:

Mean: numeric containing the base mean computed as the linear combination of the simulated fixed and random effect weights multiplied by their respective weight matrices.

Mean.Count: numeric containing the integer count values randomly sampled from a negative binomial distribution with mean = *Mean* and dispersion = *r*

r: numeric containing the dispersion value used to simulate the integer counts in *Mean.Count*.

Intercept: numeric of all 1s which can be used to set the intercept term in the X design matrix.

FE1: numeric a binary fixed effect variable taking on values [0, 1]

FE2: numeric a continuous fixed effect variables

RE1: numeric a random effect variable with 10 levels

RE2: numeric a random effect variable with 7 levels

**Details**

Data are simulated counts from 50 samples in a single data frame, from which the X and Z design matrices, can be constructed (see examples). There are 2 random effects and 2 fixed effect variables used to simulate the count trait.

**Examples**

```
data(sim_nbglmm)
head(sim_nbglmm)
```

---

sim_trajectory	<i>Simulated linear trajectory data</i>
----------------	---

---

**Description**

Data are simulated single-cells along a single linear trajectory. Cells are simulated from 5 groups, and assigned to 1 of 2 conditions; *A* or *B*. Data were generated using in the `simulate_linear_trajectory` function in the `dyntoy` package.

**Usage**

```
data(sim_trajectory)
```

**Format**

A list containing a `Milo` object in the "mylo" slot, and a data.frame containing experimental meta-data in the "meta" slot.

**References**

<https://github.com/dynverse/dyntoy>

**Examples**

```
NULL
```

---

testDiffExp

*Perform post-hoc differential gene expression analysis*

---

**Description**

This function will perform differential gene expression analysis within differentially abundant neighbourhoods, by first aggregating adjacent and concordantly DA neighbourhoods, then comparing cells *within* these aggregated groups for differential gene expression using the input design. For comparing *between* DA neighbourhoods see [findNhoodMarkers](#).

**Usage**

```
testDiffExp(
  x,
  da.res,
  design,
  meta.data,
  model.contrasts = NULL,
  assay = "logcounts",
  subset.nhoods = NULL,
  subset.row = NULL,
  gene.offset = TRUE,
  n.coef = NULL,
  na.function = "na.pass"
)
```

**Arguments**

x	A <a href="#">Milo</a> object containing single-cell gene expression and neighbourhoods.
da.res	A data.frame containing DA results, as expected from running testNhoods.
design	A formula or model.matrix object describing the experimental design for differential gene expression testing. The last component of the formula or last column of the model matrix are by default the test variable. This behaviour can be overridden by setting the model.contrasts argument. This should be the same as was used for DA testing.
meta.data	A cell X variable data.frame containing single-cell meta-data to which design refers. The order of rows (cells) must be the same as the <a href="#">Milo</a> object columns.



<code>model.contrasts</code>	A string vector that defines the contrasts used to perform DA testing. This should be the same as was used for DA testing.
<code>assay</code>	A character scalar determining which assays slot to extract from the <code>Milo</code> object to use for DGE testing.
<code>subset.nhoods</code>	A logical, integer or character vector indicating which neighbourhoods to subset before aggregation and DGE testing (default: <code>NULL</code> ).
<code>subset.row</code>	A logical, integer or character vector indicating the rows of <code>x</code> to use for summarizing over cells in neighbourhoods.
<code>gene.offset</code>	A logical scalar that determines whether a per-cell offset is provided in the DGE GLM to adjust for the number of detected genes with expression $> 0$ .
<code>n.coef</code>	A numeric scalar referring to the coefficient to select from the DGE model. This is especially pertinent when passing an ordered variable and only one specific type of effects are to be tested.
<code>na.function</code>	A valid NA action function to apply, should be one of <code>na.fail</code> , <code>na.omit</code> , <code>na.exclude</code> , <code>na.pass</code> .

### Details

Adjacent neighbourhoods are first merged based on two criteria: 1) they share at least overlap number of cells, and 2) the DA log fold change sign is concordant. This behaviour can be modulated by setting `overlap` to be more or less stringent. Additionally, a threshold on the log fold-changes can be set, such that `lfc.threshold` is required to merge adjacent neighbourhoods. Note: adjacent neighbourhoods will never be merged with opposite signs unless `merge.discord=TRUE`.

Within each aggregated group of cells differential gene expression testing is performed using the single-cell log normalized gene expression with a GLM (for details see [limma-package](#)), or the single-cell counts using a negative binomial GLM (for details see [edgeR-package](#)). When using single-cell data for DGE it is recommended to set `gene.offset=TRUE` as this behaviour adjusts the model by the number of detected genes in each cell as a proxy for differences in capture efficiency and cellular RNA content.

### Value

A list containing a data frame of DGE results for each aggregated group of neighbourhoods.

### Author(s)

Mike Morgan & Emma Dann

### Examples

```
data(sim_discrete)

milo <- Milo(sim_discrete$SCE)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)

meta.df <- sim_discrete$meta
```

```

meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")

test.meta <- data.frame("Condition"=c(rep("A", 3), rep("B", 3)), "Replicate"=rep(c("R1", "R2", "R3"), 2))
test.meta$Sample <- paste(test.meta$Condition, test.meta$Replicate, sep="_")
rownames(test.meta) <- test.meta$Sample
da.res <- testNhoods(milo, design=~Condition, design.df=test.meta[colnames(nhoodCounts(milo)), ])
da.res <- groupNhoods(milo, da.res, da.fdr=0.1)
nhood.dge <- testDiffExp(milo, da.res, design=~Condition, meta.data=meta.df)
nhood.dge

```

---

testNhoods	<i>Perform differential neighbourhood abundance testing</i>
------------	---

---

### Description

This will perform differential neighbourhood abundance testing after cell counting.

### Arguments

x	A <a href="#">Milo</a> object with a non-empty <code>nhoodCounts</code> slot.
design	A formula or <code>model.matrix</code> object describing the experimental design for differential abundance testing. The last component of the formula or last column of the model matrix are by default the test variable. This behaviour can be overridden by setting the <code>model.contrasts</code> argument
design.df	A <code>data.frame</code> containing meta-data to which design refers to
kinship	(optional) An $n \times X \times n$ matrix containing pair-wise relationships between observations, such as expected relationships or computed from SNPs/SNVs/other genetic variants. Row names and column names should correspond to the column names of <code>nhoods(x)</code> and <code>rownames</code> of <code>design.df</code> .
min.mean	A scalar used to threshold neighbourhoods on the minimum average cell counts across samples.
model.contrasts	A string vector that defines the contrasts used to perform DA testing. For a specific comparison we recommend a single contrast be passed to <code>testNhoods</code> . More details can be found in the vignette <code>milo_contrasts</code> .
fdr.weighting	The spatial FDR weighting scheme to use. Choice from <code>max</code> , <code>neighbour-distance</code> , <code>graph-overlap</code> or <code>k-distance</code> (default). If none is passed no spatial FDR correction is performed and returns a vector of NAs.
robust	If <code>robust=TRUE</code> then this is passed to <code>edgeR</code> and <code>limma</code> which use a robust estimation for the global quasiliikelihood dispersion distribution. See <code>edgeR</code> and Phipson et al, 2013 for details.

norm.method	A character scalar, either "logMS", "TMM" or "RLE". The "logMS" method normalises the counts across samples using the log columns sums of the count matrix as a model offset. "TMM" uses the trimmed mean of M-values normalisation as described in Robinson & Oshlack, 2010, whilst "RLE" uses the relative log expression method by Anders & Huber, 2010, to compute normalisation factors relative to a reference computed from the geometric mean across samples. The latter methods provides a degree of robustness against false positives when there are very large compositional differences between samples.
cell.sizes	A named numeric vector of cell numbers per experimental samples. Names should correspond to the columns of nhoodCounts. This can be used to define the model normalisation factors based on a set of numbers instead of the colSums(nhoodCounts(x)). The example use-case is when performing an analysis of a subset of nhoods while retaining the need to normalisation based on the numbers of cells collected for each experimental sample to avoid compositional biases. Infinite or NA values will give an error.
reduced.dim	A character scalar referring to the reduced dimensional slot used to compute distances for the spatial FDR. This should be the same as used for graph building.
REML	A logical scalar that controls the variance component behaviour to use either restricted maximum likelihood (REML) or maximum likelihood (ML). The former is recommended to account for the bias in the ML variance estimates.
glmm.solver	A character scalar that determines which GLMM solver is applied. Must be one of: Fisher, HE or HE-NNLS. HE or HE-NNLS are recommended when supplying a user-defined covariance matrix.
max.iters	A scalar that determines the maximum number of iterations to run the GLMM solver if it does not reach the convergence tolerance threshold.
max.tol	A scalar that determines the GLMM solver convergence tolerance. It is recommended to keep this number small to provide some confidence that the parameter estimates are at least in a feasible region and close to a <i>local</i> optimum
subset.nhoods	A character, numeric or logical vector that will subset the analysis to the specific nhoods. If a character vector these should correspond to row names of nhoodCounts. If a logical vector then these should have the same length as nrow of nhoodCounts. If numeric, then these are assumed to correspond to indices of nhoodCounts - if the maximal index is greater than nrow(nhoodCounts(x)) an error will be produced.
fail.on.error	A logical scalar the determines the behaviour of the error reporting. Used for debugging only.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying the arguments for parallelisation. By default this will evaluate using <code>SerialParam()</code> . See detailson how to use parallelisation in testNhoods.

## Details

This function wraps up several steps of differential abundance testing using the edgeR functions. These could be performed separately for users who want to exercise more control over their DA testing. By default this function sets the `lib.sizes` to the `colSums(x)`, and uses the Quasi-Likelihood

F-test in `glmQLFTest` for DA testing. FDR correction is performed separately as the default multiple-testing correction is inappropriate for neighbourhoods with overlapping cells. The GLMM testing cannot be performed using `edgeR`, however, a separate function `fitGLMM` can be used to fit a mixed effect model to each nhood (see `fitGLMM` docs for details).

Parallelisation is currently only enabled for the NB-LMM and uses the `BiocParallel` paradigm. In general the GLM implementation in `glmQLFit` is sufficiently fast that it does not require parallelisation. Parallelisation requires the user to pass a `BiocParallelParam` object with the parallelisation arguments contained therein. This relies on the user to specify how parallelisation - for details see the `BiocParallel` package.

## Value

A data frame of model results, which contain:

**logFC:** Numeric, the log fold change between conditions, or for an ordered/continuous variable the per-unit change in (normalized) cell counts per unit-change in experimental variable.

**logCPM:** Numeric, the log counts per million (CPM), which equates to the average log normalized cell counts across all samples.

**F:** Numeric, the F-test statistic from the quasi-likelihood F-test implemented in `edgeR`.

**PValue:** Numeric, the unadjusted p-value from the quasi-likelihood F-test.

**FDR:** Numeric, the Benjamini & Hochberg false discovery weight computed from `p.adjust`.

**Nhood:** Numeric, a unique identifier corresponding to the specific graph neighbourhood.

**SpatialFDR:** Numeric, the weighted FDR, computed to adjust for spatial graph overlaps between neighbourhoods. For details see [graphSpatialFDR](#).

## Author(s)

Mike Morgan

## Examples

```
library(SingleCellExperiment)
ux.1 <- matrix(rpois(12000, 5), ncol=400)
ux.2 <- matrix(rpois(12000, 4), ncol=400)
ux <- rbind(ux.1, ux.2)
vx <- log2(ux + 1)
pca <- prcomp(t(vx))

sce <- SingleCellExperiment(assays=list(counts=ux, logcounts=vx),
                           reducedDims=SimpleList(PCA=pca$x))

milo <- Milo(sce)
milo <- buildGraph(milo, k=20, d=10, transposed=TRUE)
milo <- makeNhoods(milo, k=20, d=10, prop=0.3)
milo <- calcNhoodDistance(milo, d=10)

cond <- rep("A", ncol(milo))
cond.a <- sample(1:ncol(milo), size=floor(ncol(milo)*0.25))
cond.b <- setdiff(1:ncol(milo), cond.a)
```

```
cond[cond.b] <- "B"
meta.df <- data.frame(Condition=cond, Replicate=c(rep("R1", 132), rep("R2", 132), rep("R3", 136)))
meta.df$SampID <- paste(meta.df$Condition, meta.df$Replicate, sep="_")
milo <- countCells(milo, meta.data=meta.df, samples="SampID")

test.meta <- data.frame("Condition"=c(rep("A", 3), rep("B", 3)), "Replicate"=rep(c("R1", "R2", "R3"), 2))
test.meta$Sample <- paste(test.meta$Condition, test.meta$Replicate, sep="_")
rownames(test.meta) <- test.meta$Sample
da.res <- testNhoods(milo, design=~Condition, design.df=test.meta[colnames(nhoodCounts(milo)), ], norm.method="T")
da.res
```

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