

Package ‘miloR’

October 14, 2021

Type Package

Title Differential neighbourhood abundance testing on a graph

Version 1.0.0

Description This package 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.

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

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miloR-package	<i>The miloR package</i>
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Description

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

Author(s)

Mike Morgan & Emma Dann

annotateNhoods	<i>Add annotations from colData to DA testing results</i>
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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)
```

Arguments

<code>x</code>	A Milo 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>coldata_col</code>	A character scalar determining which column of <code>colData(x)</code> stores the annotation to be added to the neighbourhoods

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

<code>buildFromAdjacency</code>	<i>Build a graph from an input adjacency matrix</i>
---------------------------------	---

Description

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

Arguments

<code>x</code>	An $n \times n$ 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> .
<code>k</code>	(optional) Scalar value that represents the number of nearest neighbours in the original graph. This can also be inferred directly from the adjacency matrix <code>x</code> .
<code>is.binary</code>	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 `scrn`. 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 = KmknParam(),
  BSPARAM = bsparam(),
  BPPARAM = SerialParam()
)

```

Arguments

<code>x</code>	A matrix, SingleCellExperiment or <code>Milo</code> object containing feature X cell gene expression data.
<code>k</code>	An integer scalar that specifies the number of nearest-neighbours to consider for the graph building.
<code>d</code>	The number of dimensions to use if the input is a matrix of cells X reduced dimensions. If this is provided, <code>transposed</code> should also be set=TRUE.
<code>transposed</code>	Logical if the input <code>x</code> is transposed with rows as cells.
<code>get.distance</code>	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 Milo object.
BNPARAM	refer to buildKNNGraph for details.
BSPARAM	refer to buildKNNGraph for details.
BPPARAM	refer to buildKNNGraph 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 Milo 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	<i>Calculate within neighbourhood distances</i>
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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 Milo 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 to construct the graph.
reduced.dim	If x is an Milo object, a character indicating the name of the reducedDim slot in the Milo 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 Milo 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

<code>x</code>	A <code>Milo</code> object with <code>nhoods</code> slot populated, alternatively a $N \times M$ indicator matrix of N cells and M <code>nhoods</code> .
<code>assay</code>	A character scalar that describes the assay slot to use for calculating neighbourhood expression.
<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>exprs</code>	If <code>x</code> is a list of neighbourhoods, <code>exprs</code> is a matrix of genes \times 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))
```

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

<code>x</code>	A <code>Milo</code> object with non-empty graph and nhoods slots.
<code>samples</code>	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 its respective sample.
<code>meta.data</code>	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 <code>Milo</code> 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

<code>x</code>	A Milo 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> , as a <code>NhoodGroup</code> column specifying the grouping of neighbourhoods, as expected from
<code>assay</code>	A character scalar determining which assays slot to extract from the Milo 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 summarizing 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.

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 Milo 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 Milo 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 <code>na.fail</code> , <code>na.omit</code> , <code>na.exclude</code> , <code>na.pass</code> .
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

```

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

x.nhoods	A list of vertices and the constituent vertices of their neighbourhood
graph	The kNN graph used to define the neighbourhoods
pvalues	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: <code>max</code> , <code>k-distance</code> , <code>neighbour-distance</code> .
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, while neighbour-distance uses the average within-neighbourhood Euclidean distance in reduced dimensional space, and max uses the largest within-neighbourhood distance from the index vertex. 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

x	A Milo object containing single-cell gene expression and neighbourhoods.
da.res	A data.frame containing DA results, as expected from running testNhoods.
da.fdr	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

makeNhoods

Define neighbourhoods on a graph (fast)

Description

This function randomly samples vertices on a graph to define neighbourhoods. These are then refined by computing the median profile for the neighbourhood in reduced dimensional space and selecting the nearest vertex to this position. 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")
```


Arguments

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

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 `isIndex` slot. If the input is a `igraph` object then the output is 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
```

matrixORMatrix-class *The Milo container class*

Description

The Milo container class

Slots

graph An igraph object that represents the kNN graph
 nhoods A CxN binary sparse matrix mapping cells to the neighbourhoods they belong to
 nhoodDistances An list of PxN sparse matrices of Euclidean distances between vertices in each neighbourhood, one matrix per neighbourhood
 nhoodCounts An NxM sparse matrix of cells counts in each neighbourhood across M samples
 nhoodIndex A list of the index vertices for each neighbourhood
 nhoodExpression An GxN matrix of genes X neighbourhoods containing average gene expression levels across cells in each neighbourhood
 nhoodReducedDim a list of reduced dimensional representations of neighbourhoods, including projections into lower dimension space
 nhoodGraph an igraph object that represents the graph of neighbourhoods
 .k A hidden slot that stores the value of k used for graph building

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(),
  nhoodDistances = Matrix(0L, sparse = TRUE),
  nhoods = Matrix(0L, sparse = TRUE),
  nhoodCounts = Matrix(0L, sparse = TRUE),
  nhoodIndex = list(),
  nhoodExpression = 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 SingleCellExperiment or matrix of features X cells
graph	An igraph object or list of adjacent vertices that represents the KNN-graph
nhoodDistances	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
nhoodCounts	A matrix of neighbourhood X sample counts of the number of cells in each neighbourhood derived from the respective samples
nhoodIndex	A list of cells that are the neighborhood index cells.
nhoodExpression	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
```

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*.

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)
```

<code>plotDAbeeswarm</code>	<i>Visualize DA results as a beeswarm plot</i>
-----------------------------	--

Description

Visualize DA results as a beeswarm plot

Usage

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

Arguments

<code>da.res</code>	a data.frame of DA testing results
<code>group.by</code>	a character scalar determining which column of <code>da.res</code> to use for grouping. This can be a column added to the DA testing results using the <code>'annotateNhoods'</code> function. If <code>da.res[,group.by]</code> is a character or a numeric, the function will coerce it to a factor (see details) (default: <code>NULL</code> , no grouping)
<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 <code>nhoods</code> to show in plot (default: <code>NULL</code> , 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

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

x	A Milo object
da.res	a data.frame of DA testing results
features	a character vector of features to plot (they must be in rownames(x))
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)
cluster_features	logical indicating whether features should be clustered with hierarchical clustering. If FALSE then the order in features is maintained (default: FALSE)
assay	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 nhoodExpression 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.
scale_to_1	A logical scalar to re-scale gene expression values between 0 and 1 for visualisation.
show_rownames	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 <code>show_rownames=FALSE</code> , if you are interested in only a few features
grid.space	a character setting the space parameter for <code>facet.grid</code> ('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
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 Milo object
layout	this can be (a) a character indicating the name of the reducedDim slot in the Milo 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)
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 *Plot Milo results on graph of neighbourhood*

Description

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

Visualize grouping of neighbourhoods obtained with groupNhoods

Usage

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

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

Arguments

x	A Milo object
milo_res	a data.frame of milo results containing the nhoodGroup column
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
show_groups	a character vector indicating which groups to plot all other neighbourhoods will be gray

Value

a ggplot object

a ggplot object

Author(s)

Emma Dann

Emma Dann

Examples

NULL

NULL

plotNhoodMA	<i>Visualize DA results as an MAplot</i>
-------------	--

Description

Visualize DA results as an MAplot

Usage

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

Arguments

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

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 *Plot histogram of neighbourhood sizes*

Description

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

Usage

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

Arguments

`milo` A [Milo](#) 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)
```

sim_discrete	<i>sim_discrete</i>
--------------	---------------------

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_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	<i>Perform post-hoc differential gene expression analysis</i>
-------------	---

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 Milo 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 Milo 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

Perform differential neighbourhood abundance testing

Description

This will perform differential neighbourhood abundance testing after cell counting.

Arguments

x	A Milo 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
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.
fdr.weighting	The spatial FDR weighting scheme to use. Choice from <code>max</code> , <code>neighbour-distance</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 quasilielihood dispersion distribution. See <code>edgeR</code> and Phipson et al, 2013 for details.
norm.method	A character scalar, either <code>"logMS"</code> , <code>"TMM"</code> or <code>"RLE"</code> . The <code>"logMS"</code> method normalises the counts across samples using the log columns sums of the count matrix as a model offset. <code>"TMM"</code> uses the trimmed mean of M-values normalisation as described in Robinson & Oshlack, 2010, whilst <code>"RLE"</code> 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.

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.

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="_")
```



```
mil0 <- 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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