Package 'dreamlet'

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Type Package

Title Scalable differential expression analysis of single cell transcriptomics datasets with complex study designs

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Description Recent advances in single cell/nucleus transcriptomic technology has enabled collection of cohort-scale datasets to study cell type specific gene expression differences associated disease state, stimulus, and genetic regulation. The scale of these data, complex study designs, and low read count per cell mean that characterizing cell type specific molecular mechanisms requires a user-frieldly, purpose-build analytical framework. We have developed the dreamlet package that applies a pseudobulk approach and fits a regression model for each gene and cell cluster to test differential expression across individuals associated with a trait of interest. Use of precision-weighted linear mixed models enables accounting for repeated measures study designs, high dimensional batch effects, and varying sequencing depth or observed cells per biosample.

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`aggregateNonCountSignal` *Aggregation of single-cell signals*

Description

Aggregation of single-cell to pseudobulk data for non-count data.

Usage

```
aggregateNonCountSignal(
  sce,
  assay = NULL,
  sample_id = NULL,
  cluster_id = NULL,
  min.cells = 10,
  min.signal = 0.01,
  min.samples = 4,
  min.prop = 0.4,
  verbose = TRUE,
```

```
  BPPARAM = SerialParam(progressbar = verbose)
)
```

Arguments

sce	a SingleCellExperiment.
assay	character string specifying the assay slot to use as input data. Defaults to the 1st available (assayNames(x)[1]).
sample_id	character string specifying which variable to use as sample id
cluster_id	character string specifying which variable to use as cluster id
min.cells	minimum number of observed cells for a sample to be included in the analysis
min.signal	minimum signal value for a gene to be considered expressed in a sample. Proper value for this cutoff depends on the type of signal value
min.samples	minimum number of samples passing cutoffs for cell cluster to be retained
min.prop	minimum proportion of retained samples with non-zero counts for a gene to be
verbose	logical. Should information on progress be reported?
BPPARAM	a BiocParallelParam object specifying how aggregation should be parallelized.

Details

The dreamlet workflow can also be applied to non-count data. In this case, a signal is averaged across all cells from a given sample and cell type. Here aggregateNonCountSignal() performs the roles of aggregateToPseudoBulk() followed by processAssays() but using non-count data.

For each cell cluster, samples with at least min.cells are retained. Only clusters with at least min.samples retained samples are kept. Features are retained if they have at least min.signal in at least min.prop fraction of the samples.

The precision of a measurement is the inverse of its sampling variance. The precision weights are computed as 1/sem^2, where sem = sd(signal) / sqrt(n), signal stores the values averaged across cells, and n is the number of cells.

Value

a dreamletProcessedData object

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
# using non-count signal
pb.signal <- aggregateNonCountSignal(example_sce,
  assay = "logcounts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(pb.signal, ~group_id)
```

aggregateToPseudoBulk *Aggregation of single-cell to pseudobulk data*

Description

Aggregation of single-cell to pseudobulk data. Adapted from `muscat::aggregateData` and has same syntax and results. But can be much faster for `SingleCellExperiment` backed by H5AD files using on-disk storage.

Usage

```
aggregateToPseudoBulk(
  x,
  assay = NULL,
  sample_id = NULL,
  cluster_id = NULL,
 fun = c("sum", "mean", "median", "prop.detected", "num.detected", "sem", "number"),
  scale = FALSE,
  verbose = TRUE,
  BPPARAM = SerialParam(progressbar = verbose),
  checkValues = TRUE,
  h5adBlockSizes = 1e+09
)
```

Arguments

`x`	a `SingleCellExperiment`.
`assay`	character string specifying the assay slot to use as input data. Defaults to the 1st available (`assayNames(x)[1]`).
`sample_id`	character string specifying which variable to use as sample id
`cluster_id`	character string specifying which variable to use as cluster id
`fun`	a character string. Specifies the function to use as summary statistic. Passed to `summarizeAssayByGroup2`.
`scale`	logical. Should pseudo-bulks be scaled with the effective library size & multiplied by 1M?
`verbose`	logical. Should information on progress be reported?
`BPPARAM`	a `BiocParallelParam` object specifying how aggregation should be parallelized.
`checkValues`	logical. Should we check that signal values are positive integers?
`h5adBlockSizes`	set the automatic block size block size (in bytes) for DelayedArray to read an H5AD file. Larger values use more memory but are faster.

Details

Adapted from `muscat::aggregateData` and has similar syntax and same results. This is much faster for `SingleCellExperiment` backed by H5AD files using `DelayedMatrix` because this summarizes counts using `DelayedMatrixStats`. But this function also includes optmizations for `sparseMatrix` used by `Seurat` by using `sparseMatrixStats`.

Keeps variables from `colData()` that are constant within `sample_id`. For example, sex will be constant for all cells from the same `sample_id`, so it is retained as a variable in the pseudobulk result. But number of expressed genes varies across cells within each `sample_id`, so it is dropped from `colData()`. Instead the mean value per cell type is stored in `metadata(pb)$aggr_means`, and these can be included in regression formulas downstream. In that case, the value of the covariates used per sample will depend on the cell type analyzed.

Value

a SingleCellExperiment.

Aggregation parameters (`assay`, `by`, `fun`, `scaled`) are stored in `metadata()$agg_pars`, where `by = c(cluster_id, sample_id)`. The number of cells that were aggregated are accessible in `int_colData()$n_cells`.

Author(s)

Gabriel Hoffman, Helena L Crowell & Mark D Robinson

References

Crowell, HL, Soneson, C, Germain, P-L, Calini, D, Collin, L, Raposo, C, Malhotra, D & Robinson, MD: Muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. *Nature Communications* **11(1):6077** (2020). doi: https://doi.org/10.1038/s41467-020-19894-4

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# pseudobulk data from each cell type
# is stored as its own assay
pb

# aggregate by cluster only,
# collapsing all samples into the same pseudobulk
pb2 <- aggregateToPseudoBulk(example_sce,
 cluster_id = "cluster_id",
 verbose = FALSE)

pb2
#
```

aggregateVar *Per-sample variance of single-cell counts*

Description

Aggregation function for single-cell log-normalized counts to calculate per-sample variance for dreamlet.

Usage

```
aggregateVar(
  sce,
  assay = NULL,
  cluster_id = NULL,
  sample_id = NULL,
  min.cells = 10,
  min.var = 0.01,
  min.samples = 4,
  min.prop = 0.4,
  verbose = TRUE,
  BPPARAM = SerialParam(progressbar = verbose)
)
```

Arguments

sce	a SingleCellExperiment.
assay	character string specifying the assay slot to use as input data. Defaults to the 1st available (assayNames(x)[1]).
cluster_id	character string specifying which variable to use as cluster id
sample_id	character string specifying which variable to use as sample id
min.cells	minimum number of observed cells for a sample to be included in the analysis
min.var	minimum variance for a gene to be considered expressed in a sample
min.samples	minimum number of samples passing cutoffs for cell cluster to be retained
min.prop	minimum proportion of retained samples with non-zero counts for a gene to be
verbose	logical. Should information on progress be reported?
BPPARAM	a BiocParallelParam object specifying how aggregation should be parallelized.

Details

The dreamlet workflow can also be applied to model gene expression variance. In this case, a per-sample per-gene variance is calculated across all cells from a given sample and cell type. Here aggregateVar() performs the roles of aggregateToPseudoBulk() followed by processAssays() but using log-normalized count data.

For each cell cluster, samples with at least min.cells are retained. Only clusters with at least min.samples retained samples are kept. Features are retained if they have at least min.var in at least min.prop fraction of the samples.

The precision of a measurement is the inverse of its sampling variance. The precision weights are computed as 1/sem^2, where sem = sd / sqrt(n) and n is the number of cells.

Value

a dreamletProcessedData object

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# Compute variance for each sample and cell cluster
pbVar <- aggregateVar(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)
```

---

as.dreamletResult *Convert list of regression fits to* dreamletResult

---

Description

Convert list of regression fits to dreamletResult for downstream analysis

Usage

```
as.dreamletResult(fitList, df_details = NULL)
```

Arguments

fitList	list of regression fit with dream()
df_details	data.frame storing assay details

Details

Useful for combining multiple runs of dreamletCompareClusters() into a single dreamletResult for downstream analysis

Value

object of class dreamletResult

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
```

```
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# first comparison
ct.pairs <- c("B cells", "CD14+ Monocytes")
fit <- dreamletCompareClusters(pb, ct.pairs, method = "fixed")

# second comparison
ct.pairs2 <- c("B cells", "CD8 T cells")
fit2 <- dreamletCompareClusters(pb, ct.pairs2, method = "fixed")

# Make a list storing each result with a meaningful name
fitList <- list()

id <- paste0("[", ct.pairs[1], "]_vs_[", ct.pairs[2], "]")
fitList[[id]] <- fit

id <- paste0("[", ct.pairs2[1], "]_vs_[", ct.pairs2[2], "]")
fitList[[id]] <- fit2

# create a dreamletResult form this list
res.compare <- as.dreamletResult(fitList)
res.compare
```

---

assay,dreamletResult,ANY-method

Get assay

Description

Get assay

Get assay

Get assays by name

Usage

```
## S4 method for signature 'dreamletResult,ANY'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'dreamletProcessedData,ANY'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'vpDF,ANY'
assay(x, i, withDimnames = TRUE, ...)
```

Arguments

x	vpDF object
i	number indicating index, or string indicating assay

withDimnames	not used
...	other arguments

Value

return ith assay

`assayNames,dreamletResult-method`
Get assayNames

Description

Get assayNames

Get assayNames

Get assayNames

Usage

```
## S4 method for signature 'dreamletResult'
assayNames(x, ...)

## S4 method for signature 'dreamletProcessedData'
assayNames(x, ...)

## S4 method for signature 'vpDF'
assayNames(x, ...)
```

Arguments

x	vpDF object
...	additional arguments

Value

array of assay names

`buildClusterTreeFromPB`
Hierarchical clustering on cell types from pseudobulk

Description

Perform hierarchical clustering on cell types from pseudobulk by aggregating read counts from each cell type.

Usage

```
buildClusterTreeFromPB(
  pb,
 method = c("complete", "ward.D", "single", "average", "mcquitty", "median", "centroid",
    "ward.D2"),
 dist.method = c("euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski"),
  assays = assayNames(pb)
)
```

Arguments

pb	SingleCellObject storing pseudobulk for each cell type in in assay() field
method	clustering method for hclust()
dist.method	distance metric
assays	which assays to include

Value

hierarchical clustering object of class hclust

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Hierarchical clustering of cell types
hcl <- buildClusterTreeFromPB(pb)

plot(hcl)
```

---

cellCounts *Extract cell counts*

Description

Extract matrix of cell counts from SingleCellExperiment

Usage

```
cellCounts(x)
```

Arguments

x	a SingleCellExperiment

Value

matrix of cell counts with samples as rows and cell types as columns

See Also

computeCellCounts()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# get matrix of cell counts for each sample
cellCounts(pb)
```

---

cellSpecificityValues-class

Class cellSpecificityValues

Description

Class cellSpecificityValues cell type specificity values for each gene and cell type

Value

none

`cellTypeSpecificity` *Get cell type specificity of gene expression*

Description

For each gene, compute fraction of overall expression attributable to each cell type

Usage

```
cellTypeSpecificity(pb, ...)
```

Arguments

pb	`SingleCellExperiment` of pseudobulk data where easy `assay` is a cell type.
...	other arguments passed to `edgeR::calcNormFactors()`

Details

Sum counts for each cell type, and compute the fraction of counts-per-million attributable to each cell type for each gene

Value

matrix of the fraction of expression attributable to each cell type for each gene.

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Compute cell type specificity of each gene
df <- cellTypeSpecificity(pb)

# Violin plot of specificity scores for each cell type
# Dashed line indicates genes that are equally expressed
# across all cell types.  For K cell types, this is 1/K
plotViolin(df)

# Compute the maximum specificity score for each gene
scoreMax <- apply(df, 1, max)
head(scoreMax)

# For each cell type, get most specific gene
```

```
genes <- rownames(df)[apply(df, 2, which.max)]

# Barplot of 5 genes
plotPercentBars(df, genes = genes)

# heatmap of 5 genes that are most cell type specific
dreamlet::plotHeatmap(df, genes = genes)
```

---

checkFormula *Check variables in a formula*

Description

Check that variables in formula are present in the data

Usage

```
checkFormula(formula, data)
```

Arguments

formula	formula of variables to check
data	data.frame storing variables in the formula

Value

If formula is valid, return TRUE. Else throw error

Examples

```
# Valid formula
dreamlet:::checkFormula(~speed, cars)

# Not valid formula
# dreamlet:::checkFormula( ~ speed + a, cars)
```

---

coefNames *Get coefficient names*

Description

Get coefficient names

Usage

```
coefNames(obj)

## S4 method for signature 'dreamletResult'
coefNames(obj)
```

Arguments

obj	A dreamletResult object

Value

array storing names of coefficients

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show coefficients estimated for each cell type
coefNames(res.dl)
```

---

colData,dreamletProcessedData-method

Extract colData from dreamletProcessedData

Description

Extract colData from dreamletProcessedData

Usage

```
## S4 method for signature 'dreamletProcessedData'
colData(x, ...)
```

Arguments

x	A dreamletProcessedData object
...	other arguments

Value

object from colData field

colData<-,dreamletProcessedData,ANY-method

Set colData

Description

Set colData of dreamletProcessedData, and check for same dimensions and rownames

Usage

```
## S4 replacement method for signature 'dreamletProcessedData,ANY'
colData(x, ...) <- value
```

Arguments

x	dreamletProcessedData object
...	other arguments
value	data.frame or object that can be coerced to it

Value

none

compositePosteriorTest

Perform composite test on results from mashr

Description

Perform composite test evaluating the specificity of an effect. Evalute the posterior probability that an a non-zero effect present in _all_ or _at least one_ condition in the inclusion set, but _no conditions_ in the exclusion set.

Usage

```
compositePosteriorTest(
  x,
  include,
  exclude = NULL,
  test = c("at least 1", "all")
)
```

Arguments

x	"dreamlet_mash_result" from run_mash()
include	array of conditions in the inclusion set
exclude	array of conditions in the exclusion set. Defaults to NULL for no exclusion
test	evaluate the posterior probability of a non-zero effect in "at least 1" or "all" conditions

Details

The posterior probabilities for all genes and conditions is obtained as `1-lFSR`. Let `prob` be an array storing results for one gene. The probability that _no_ conditions in the exclusion set are non-zero is `prod(1 - prob[exclude])`. The probability that _all_ conditions in the inclusion set are non-zero is `prod(prob[include])`. The probability that _at least one_ condition in the inclusion set is non-zero is `1 - prod(1 - prob[include])`. The composite test is the product of the probabilties computed from the inclusion and exclusion sets.

See description in section Identifying shared and cell type specific genetic regulatory effects of Zeng, et al. (https://doi.org/10.1101/2024.11.02.24316590).

See Also

`run_mash()`

Examples

```
library(muscat)
library(mashr)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce[1:100, ],
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# run MASH model
# This can take 10s of minutes on real data
# This small datasets should take ~30s
res_mash <- run_mash(res.dl, "group_idstim")

# Composite test based on posterior probabilities
# to identify effect present in *at least 1* monocyte type
# and *NO* T-cell type.
include <- c("CD14+ Monocytes", "FCGR3A+ Monocytes")
exclude <- c("CD4 T cells", "CD8 T cells")

# Perform composite test
prob <- compositePosteriorTest(res_mash, include, exclude)

# examine the lFSR for top gene
get_lfsr(res_mash$model)[which.max(prob), , drop = FALSE]

# Test if *all* cell types have non-zero effect
```

```
prob <- compositePosteriorTest(res_mash, assayNames(res.dl))
```

`computeCellCounts` *Get cell counts with metadata*

Description

Get cell counts with metadata for each sample

Usage

```
computeCellCounts(sce, annotation, sampleIDs)
```

Arguments

`sce`	`SingleCellExperiment`
`annotation`	string indicating column in `colData(sce)` storing cell type annotations
`sampleIDs`	string indicating column in `colData(sce)` storing sample identifers

Value

`matrix` storing cell counts

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

counts <- computeCellCounts(example_sce, "cluster_id", "sample_id")

counts[1:4, 1:4]
```

`computeLogCPM` *Compute log normalized counts*

Description

Compute normalized counts as log2 counts per million

Usage

```
computeLogCPM(
  sce,
  lib.size = colSums2(counts(sce)),
  prior.count = 2,
  scaledByLib = FALSE
)
```

Arguments

sce	SingleCellExperiment with counts stored as counts(sce)
lib.size	library size for each cell
prior.count	average count to be added to each observation to avoid taking log of zero
scaledByLib	if TRUE, scale pseudocount by lib.size. Else do standard constant pseudocount addition

Details

This function gives same result as edgeR::cpm(counts(sce), log=TRUE)

Value

matrix of log CPM values

See Also

also edgeR::cpm()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

logcounts(example_sce) <- computeLogCPM(example_sce)
```

---

computeNormCounts *Compute normalized counts*

Description

Compute normalized counts as counts per million

Usage

```
computeNormCounts(sce)
```

Arguments

sce	SingleCellExperiment with counts stored as counts(sce)

Details

This function gives same result as edgeR::cpm(counts(sce), log=FALSE)

Value

matrix of CPM values

See Also

also edgeR::cpm()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

normcounts(example_sce) <- computeNormCounts(example_sce)
```

---

details *Extract details from dreamletProcessedData*

Description

Extract details from dreamletProcessedData

Usage

```
details(object)

## S4 method for signature 'dreamletProcessedData'
details(object)

## S4 method for signature 'dreamletResult'
details(object)

## S4 method for signature 'vpDF'
details(object)
```

Arguments

object	A dreamletProcessedData object

Value

Extract detailed information from some classes

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
```

```
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# For each cell type, number of samples retained,
# and variables retained
details(res.proc)
```

`diffVar,dreamletResult-method`
Test differential variance

Description

Test the association between a covariate of interest and the response's deviation from expectation.

Usage

```
## S4 method for signature 'dreamletResult'
diffVar(
  fit,
  method = c("AD", "SQ"),
  scale = c("leverage", "none"),
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

`fit`	model fit from `dream()`
`method`	transform the residuals using absolute deviation ("AD") or squared deviation ("SQ").
`scale`	scale each observation by "leverage", or no scaling ("none")
`BPPARAM`	parameters for parallel evaluation
`...`	other parameters passed to `dream()`

Details

This method performs a test of differential variance between two subsets of the data, in a way that generalizes to multiple categories, continuous variables and metrics of spread beyond variance. For the two category test, this method is simular to Levene's test. This model was adapted from Phipson, et al (2014), extended to linear mixed models, and adapted to be compatible with `variancePartition::dream()` and `dreamlet::dreamlet()`.

This method is composed of multiple steps where 1) a typical linear (mixed) model is fit with `dreamlet()`, 2) residuals are computed and transformed based on an absolute value or squaring transform, 3) a second regression is performed with `dreamlet()` to test if a variable is associated with increased deviation from expectation. Both regression take advantage of the `dreamlet()` linear (mixed) modelling framework followed by empirical Bayes shrinkage that extends the `limma::voom()` framework.

Note that `diffVar()` takes the results of the first regression as a parameter to use as a starting point.

References

Phipson B, Oshlack A (2014). "DiffVar: a new method for detecting differential variability with application to methylation in cancer and aging." *Genome biology*, **15**(9), 1–16.

See Also

`variancePartition::diffVar()`

`variancePartition::diffVar()`, `missMethyl::diffVar()`

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# Differential variance analysis
# result is a dreamlet fit
res.dvar <- diffVar(res.dl)

# Examine results
res.dvar

# Examine details for each assay
details(res.dvar)

# show coefficients estimated for each cell type
coefNames(res.dvar)

# extract results using limma-style syntax
# combines all cell types together
# adj.P.Val gives study-wide FDR
topTable(res.dvar, coef = "group_idstim", number = 3)

# Plot top hit to see differential variance
# Note that this is a toy example with only 4 samples
cellType <- "CD4 T cells"
gene <- "DYNLRB1"

y <- res.proc[[cellType]]$E[gene, ]
x <- colData(res.proc)$group_id
```

```
boxplot(y ~ x,
  xlab = "Stimulation status",
  ylab = "Gene expression",
  main = paste(cellType, gene)
)
#
```

`dreamlet` *Differential expression for each assay*

Description

Perform differential expression for each assay using linear (mixed) models

Usage

```
dreamlet(
  x,
  formula,
  data = colData(x),
  assays = assayNames(x),
  contrasts = NULL,
  min.cells = 10,
  robust = FALSE,
  quiet = FALSE,
  BPPARAM = SerialParam(),
  use.eBayes = TRUE,
  ...
)

## S4 method for signature 'dreamletProcessedData'
dreamlet(
  x,
  formula,
  data = colData(x),
  assays = assayNames(x),
  contrasts = NULL,
  min.cells = 10,
  robust = FALSE,
  quiet = FALSE,
  BPPARAM = SerialParam(),
  use.eBayes = TRUE,
  ...
)
```

Arguments

`x`	SingleCellExperiment or dreamletProcessedData object
`formula`	regression formula for differential expression analysis
`data`	metadata used in regression formula

assays	array of assay names to include in analysis. Defaults to assayNames(x)
contrasts	character vector specifying contrasts specifying linear combinations of fixed effects to test. This is fed into makeContrastsDream(formula, data, contrasts=contrasts)
min.cells	minimum number of observed cells for a sample to be included in the analysis
robust	logical, use eBayes method that is robust to outlier genes
quiet	show messages
BPPARAM	parameters for parallel evaluation
use.eBayes	should eBayes be used on result? (defualt: TRUE)
...	other arguments passed to dream

Details

Fit linear (mixed) model on each cell type separately. For advanced use of contrasts see variancePartition::makeCont and vignette https://gabrielhoffman.github.io/variancePartition/articles/dream.html#advanced-hypothesis-testing-1.

Value

Object of class dreamletResult storing results for each cell type

See Also

variancePartition::dream(), variancePartition::makeContrastsDream()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# Examine results
res.dl

# Examine details for each assay
details(res.dl)

# show coefficients estimated for each cell type
coefNames(res.dl)
```

```
# extract results using limma-style syntax
# combines all cell types together
# adj.P.Val gives study-wide FDR
topTable(res.dl, coef = "group_idstim", number = 3)
```

`dreamletCompareClusters` *Differential expression between pair of assays*

Description

Perform differential expression between a pair of assays using linear (mixed) models

Usage

```
dreamletCompareClusters(
  pb,
  assays,
  method = c("fixed", "random", "none"),
  formula = ~0,
  collapse = TRUE,
  min.cells = 10,
  min.count = 10,
  min.samples = 4,
  isCounts = TRUE,
  normalize.method = "TMM",
  robust = FALSE,
  quiet = FALSE,
  contrasts = c(compare = paste("cellClustertest - cellClusterbaseline")),
  BPPARAM = SerialParam(),
  errorsAsWarnings = FALSE,
  ...
)
```

Arguments

pb	pseudobulk data as SingleCellExperiment object
assays	array of two entries specifying assays (i.e. cell clusters) to compare, or a list of two sets of assays.
method	account for repeated measures from donors using a "random" effect, a "fixed" effect, or "none"
formula	covariates to include in the analysis.
collapse	if TRUE (default), combine all cell clusters within the test set, and separately the baseline set. If FALSE, estimate coefficient for each cell cluster and then identify differential expression using linear contrasts with `variancePartition::makeContrastsDream(`
min.cells	minimum number of observed cells for a sample to be included in the analysis
min.count	minimum number of reads for a gene to be consider expressed in a sample. Passed to `edgeR::filterByExpr`

min.samples	minimum number of samples passing cutoffs for cell cluster to be retained
isCounts	logical, indicating if data is raw counts
normalize.method	normalization method to be used by calcNormFactors
robust	logical, use eBayes method that is robust to outlier genes
quiet	show messages
contrasts	cell type is encoded in variable cellCluster with levels test and baseline. contrasts specifies contrasts passed to variancePartition::makeContrastsDream(). Note, advanced users only.
BPPARAM	parameters for parallel evaluation
errorsAsWarnings	if TRUE, convert error to a warning and return NULL
...	other arguments passed to dream

Details

Analyze pseudobulk data to identify differential gene expression between two cell clusters or sets of clusters while modeling the cross-donor expression variation and other aspects of the study design.

dreamletCompareClusters() is useful for finding genes that are differentially expressed betweeen cell clusters and estimating their fold change. However, the p-values and number of differentially expressed genes are problematic for two reasons, so users must be careful not to overinterpret them:

1. Cell clusters are typically identified with the same gene expression data used for this differential expression analysis between clusters. The same data is used both for discovery and testing, and this means that the p-values from the differential expression analysis will not be uniform under the null. This will produce a lot of findings with small p-values even in the absence of true biological differences.
2. The dreamlet package is designed for large datasets with many subjects. The sample sizes from cohort studies are an order of magnitude larger than typical single cell studies. This means that these analyses have huge power to detect even subtle difference in expression between cell clusters. While cluster-specific marker genes are often discovered from an handful of samples, the dreamlet package is applicable to 100s or 1000s of subjects.

method indicates the regression method used to test differential expression between sets of cell clusters. Since the same biosample will usually be represented in both sets of cell clusters, method determines how the paired design is modeled. For method = "mixed", the sample is modeled as a random effect: ~ (1|Sample) + ... For method = "fixed", the sample is modeled as a fixed effect: ~ Sample + ... For method = "none", the pairing is ignored.

When collapse=TRUE (default) combine all cell clusters within the test set, and separately the baseline set, and estimate a coefficient indicating the differential expression between sets for a given gene. If collapse=FALSE, estimate a coefficient for each cell type and then identify differential expression using linear contrasts with variancePartition::makeContrastsDream().

Value

Object of class dreamletResult storing results for each comparison

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Evaluate the specificity of each gene for each cluster
df_cts <- cellTypeSpecificity(pb)

# compare first two assays (i.e. cell types)
ct.pairs <- c("B cells", "CD14+ Monocytes")

# run comparison
# use method = 'fixed' here since it is faster
fit <- dreamletCompareClusters(pb, ct.pairs, method = "fixed")

# Extract top 10 differentially expressed genes
# The coefficient 'compare' is the value logFC between test and baseline:
# compare = cellClustertest - cellClusterbaseline
res <- topTable(fit, coef = "compare", number = 10)

# genes with highest logFC are most highly expressed in
# B cells compared to CD14+ Monocytes
head(res)

dreamlet::plotHeatmap(df_cts, genes = rownames(res)[1:5])

# compare B cells versus the rest of the cell types
# 'rest' is a keyword indicating all other assays
fit <- dreamletCompareClusters(pb, c("B cells", "rest"), method = "fixed")

res <- topTable(fit, coef = "compare", number = 10)

# genes with highest logFC are most highly expressed in
# B cells compared to all others
head(res)

# Get genes upregulated in B cells
idx <- with(res, which(logFC > 0))[1:5]
dreamlet::plotHeatmap(df_cts, genes = rownames(res)[idx])

lst <- list(
  test = c("CD14+ Monocytes", "FCGR3A+ Monocytes"),
  baseline = c("CD4 T cells", "CD8 T cells")
)

# compare 2 monocyte clusters to two T cell clusters
fit <- dreamletCompareClusters(pb, lst, method = "fixed")
```

```
res <- topTable(fit, coef = "compare", number = 10)

# genes with highest logFC are most highly expressed in
# monocytes compared to T cells
head(res)

# Get genes upregulated in monocytes
idx <- with(res, which(logFC > 0))[1:5]
dreamlet::plotHeatmap(df_cts, genes = rownames(res)[idx])
```

`dreamletProcessedData-class` *Class dreamletProcessedData*

Description

Class `dreamletProcessedData`

Value

none

none

`dreamletResult-class` *Class dreamletResult*

Description

Class `dreamletResult` stores results produced by `dreamlet()` to give a standard interface for downstream analysis

Class `dreamletResult` stores results produced by `dreamlet()` to give a standard interface for downstream analysis

Value

none

none

`dreamlet_mash_result-class` *Class dreamlet_mash_result*

Description

Class `dreamlet_mash_result`

Value

`dreamlet_mash_result` class

dropRedundantTerms *Drop redundant terms from the model*

Description

Detect co-linear fixed effects and drop the last one

Usage

```
dropRedundantTerms(formula, data, tol = 0.001)
```

Arguments

formula	original formula
data	data.frame
tol	tolerance to test difference of correlation from 1 or -1

Value

a formula, possibly with terms omitted.

Examples

```
# Valid formula
dropRedundantTerms(~ group + extra, sleep)
```

equalFormulas *Check if two formulas are equal*

Description

Check if two formulas are equal by evaluating the formulas and extracting terms

Usage

```
equalFormulas(formula1, formula2)
```

Arguments

formula1	first formula
formula2	second formula

Value

boolean value indciating of formulas are equivalent

Examples

```
# These formulas are equivalent
formula1 <- ~ Size + 1
formula2 <- ~ 1 + Size

dreamlet:::equalFormulas(formula1, formula2)
```

`extractData` *Extract normalized expression and* `colData`

Description

Extract normalized expression and `colData`

Extract normalized (i.e. log2 CPM) expression and `colData` from `dreamletProcessedData`

Usage

```
extractData(x, assay, cols = colnames(colData(x)), genes = rownames(x))

## S4 method for signature 'dreamletProcessedData,character'
extractData(
  x,
  assay,
  cols = colnames(colData(x)),
  genes = rownames(assay(x, assay))
)
```

Arguments

`x`	`dreamletProcessedData` object
`assay`	assay to extract
`cols`	columns in `colData(x)` to extract. defaults to all columns as `colnames(colData(x))`
`genes`	genes to extract from `assay(x, assay)$E`. defaults to all genes as `rownames(x)`

Value

`data.frame` or `DataFrame` of merged expression and colData

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
```

```
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Extract all:
# Extract tibble of colData merged with expression.
# variables and genes are stored as columns, samples as rows
df_merge <- extractData(res.proc, "B cells")

# first few columns
df_merge[, 1:6]

# Extract subset:
df_merge <- extractData(res.proc, "B cells", cols = "group_id", genes = c("SSU72", "U2AF1"))

df_merge

# Boxplot of expression
boxplot(SSU72 ~ group_id, df_merge)
#
```

`fitVarPart` *Variance Partition analysis for each assay*

Description

Perform Variance Partition analysis for each assay

Usage

```
fitVarPart(
  x,
  formula,
  data = colData(x),
  assays = assayNames(x),
  quiet = FALSE,
  BPPARAM = SerialParam(),
  ...
)

## S4 method for signature 'dreamletProcessedData'
fitVarPart(
  x,
  formula,
  data = colData(x),
  assays = assayNames(x),
  quiet = FALSE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

x	SingleCellExperiment or dreamletProcessedData object
formula	regression formula for differential expression analysis
data	metadata used in regression formula
assays	array of assay names to include in analysis. Defaults to assayNames(x)
quiet	show messages
BPPARAM	parameters for parallel evaluation
...	other arguments passed to dream

Value

Object of class vpDF inheriting from DataFrame storing the variance fractions for each gene and cell type.

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# variance partitioning analysis
vp <- fitVarPart(res.proc, ~group_id)

# Show variance fractions at the gene-level for each cell type
genes <- vp$gene[2:4]
plotPercentBars(vp[vp$gene %in% genes, ])

# Summarize variance fractions genome-wide for each cell type
plotVarPart(vp)
```

---

getTreat,dreamletResult-method

Test if coefficient is different from a specified value

Description

Test if coefficient is different from a specified value

Usage

```
## S4 method for signature 'dreamletResult'
getTreat(fit, lfc = log2(1.2), coef = NULL, number = 10, sort.by = "p")
```

Arguments

fit	dreamletResult object
lfc	a minimum log2-fold-change below which changes not considered scientifically meaningful
coef	which coefficient to test
number	number of genes to return
sort.by	column to sort by

Value

DataFrame storing hypothesis test for each gene and cell type

See Also

limma::topTreat(), variancePartition::getTreat()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show coefficients estimated for each cell type
coefNames(res.dl)

# extract results using limma-style syntax
# combines all cell types together
# adj.P.Val gives study-wide FDR
getTreat(res.dl, coef = "group_idstim", number = 3)
```

metadata,dreamletProcessedData-method *Extract metadata from* dreamletProcessedData

Description

Extract metadata from dreamletProcessedData

Usage

```
## S4 method for signature 'dreamletProcessedData'
metadata(x)
```

Arguments

x	A dreamletProcessedData object

Value

object from metadata field

meta_analysis *Meta-analysis across multiple studies*

Description

Meta-analysis across multiple studies

Usage

```
meta_analysis(
  x,
  method = "FE",
  group = c("ID", "assay"),
  control = list(maxiter = 2000)
)
```

Arguments

x	data.frame rbind'ing results across genes, cell types and datasets
method	meta-analysis method. Values are fed into metafor::rma(), except for 'RE2C' which calls remaCor::RE2C().
group	colums in x to group by. For results from dreamlet::topTable(), results are aggregrated by gene and cell type (i.e. 'ID' and 'assay'). If x is not from this function, this argument allows the function to group results properly
control	passed to rma(..,control)

Details

'FE': fixed effects meta-analysis

'REML': random effects meta-analysis

'RE2C': joint testing of fixed and random effects

Examples

```
library(dreamlet)
library(muscat)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
# just 'CD14+ Monocytes' for speed
res.proc <- processAssays(pb, ~group_id, assays = "CD14+ Monocytes")

# dreamlet
res.dl <- dreamlet(res.proc, ~group_id)

tab1 <- topTable(res.dl, coef = "group_idstim", number = Inf)
tab1$Dataset <- "1"

# Results from a second cohort
# Here, just a copy of the same results for simplicity
tab2 <- tab1
tab2$Dataset <- "2"

# rbind
tab_combined <- rbind(tab1, tab2)

# Perform fixed effects meta-analysis
res <- meta_analysis(tab_combined, method = "FE")

res[1:3, ]
```

---

outlier *Multivariate outlier detection*

Description

Detect multivariante outliers using Mahalanobis distance using mean and covariance estimated either with standard or robust methods.

Usage

```
outlier(data, robust = FALSE, ...)
```

Arguments

data	matrix of data
robust	use robust covariance method, defaults to FALSE
...	arguments passed to MASS::cov.rob()

Details

The distance follow a chisq distrubtion under the null with standard method for mean and covariance. It is approximate if the robust method is used. So use qchisq(p = 0.999 , df = k) to get cutoff to keep 99.9% of samples under the null for data with k=2 columns.

Value

data.frame storing chisq and z-score for each entry indicating deviation from the mean. The z-score is computed by evaluating the p-value of chisq statistic and converting it into a z-score

Examples

```
data <- matrix(rnorm(200), 100, 2)

res <- outlier(data)

res[1:4,]
```

---

outlierByAssay *Outlier analysis for each assay*

Description

Compute outlier score for each sample in each assay using outlier() run on the top principal components. Mahalanobis distance is used for outlier detect and multivariate normal assumption is used to compute p-values

Usage

```
outlierByAssay(object, assays = names(object), nPC = 2, robust = FALSE, ...)
```

Arguments

object	dreamletProcessedData from processAssays()
assays	assays / cell types to analyze
nPC	number of PCs to uses for outlier score with outlier()
robust	use robust covariance method, defaults to FALSE
...	arguments passed to MASS::cov.rob()

Value

`ID`: sample identifier

`assay`: specify assay

`PCs`: principal components

`chisq`: mahalanobis distance that is distributed as chisq(k) k = nPC if the data is multivariate gaussian

`z`: z-score corresponding to the chisq distance

See Also

`outlier()`

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Compute PCs and outlier scores
outlierByAssay( res.proc, c("B cells", "CD14+ Monocytes"))
```

---

plotBeeswarm *Beeswarm plot of effect sizes for each assay*

Description

Beeswarm plot of effect sizes for each assay, colored by sign and FDR

Usage

```
plotBeeswarm(res.dl, coef, fdr.range = 4, assays = assayNames(res.dl))
```

Arguments

`res.dl`	`dreamletResult` object from `dreamlet()`
`coef`	coefficient name fed to `topTable()`
`fdr.range`	range for coloring FDR
`assays`	which assays to plot

Value

ggplot2 of logFC by assay

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# Beeswarm plot of effect sizes for each assay,
# colored by sign and FDR
plotBeeswarm(res.dl, "group_idstim")
```

---

plotCellComposition *Bar plot of cell compositions*

Description

Bar plot of cell compositions

Usage

```
plotCellComposition(obj, col, width = NULL)

## S4 method for signature 'SingleCellExperiment'
plotCellComposition(obj, col, width = NULL)

## S4 method for signature 'matrix'
plotCellComposition(obj, col, width = NULL)

## S4 method for signature 'data.frame'
plotCellComposition(obj, col, width = NULL)
```

Arguments

obj	matrix of [cells] x [samples] or SingleCellExperiment from aggregateToPseudoBulk
col	array of colors. If missing, use default colors. If names(col) is the same as arrayNames(obj), then colors will be assigned by assay name#'
width	specify width of bars

Value

Barplot showing cell fractions

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# show cell composition bar plots
plotCellComposition(pb)

# extract cell counts
df_cellCounts <- cellCounts(pb)

# show cell composition bar plots
plotCellComposition(df_cellCounts)
```

---

plotForest *Forest plot*

Description

Forest plot

Usage

```
plotForest(x, gene, coef, ...)

## S4 method for signature 'dreamletResult'
plotForest(x, gene, coef, assays = names(x), ylim = NULL)

## S4 method for signature 'dreamlet_mash_result'
plotForest(x, gene, coef, assays = colnames(x$logFC.original), ylim = NULL)
```

Arguments

x	result from dreamlet
gene	gene to show results for
coef	coefficient to test with topTable
...	other arguments
assays	array of assays to plot
ylim	limits for the y axis

Value

Plot showing effect sizes

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show coefficients estimated for each cell type
coefNames(res.dl)

# Show estimated log fold change with in each cell type
plotForest(res.dl, gene = "ISG20", coef = "group_idstim")
```

---

plotGeneHeatmap *Heatmap of genes and assays*

Description

Heatmap of genes and assays

Usage

```
plotGeneHeatmap(
  x,
  coef,
  genes,
  assays = assayNames(x),
  zmax = NULL,
  transpose = FALSE
)

## S4 method for signature 'dreamletResult'
plotGeneHeatmap(
  x,
  coef,
  genes,
  assays = assayNames(x),
  zmax = NULL,
  transpose = FALSE
)
```

Arguments

x	A dreamletResult object
coef	column number or column name specifying which coefficient or contrast of the linear model is of interest.
genes	array of genes to include in plot
assays	array of assay names to include in analysis. Defaults to assayNames(x)
zmax	maximum z.std value
transpose	(default: FALSE) Use 'coord_flip()' to flip axies

Value

Heatmap plot for specified genes and assays

Heatmap plot for specified genes and assays

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)
```

```
# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# Heatmap for specified subset of genes
plotGeneHeatmap(res.dl, coef = "group_idstim", genes = rownames(pb)[1:15])
```

`plotHeatmap` *Plot heatmap*

Description

Plot heatmap

Usage

```
plotHeatmap(
  x,
  genes = rownames(x),
  color = "darkblue",
  assays = colnames(x),
  useFillScale = TRUE
)

## S4 method for signature 'cellSpecificityValues'
plotHeatmap(
  x,
  genes = rownames(x),
  color = "darkblue",
  assays = colnames(x),
  useFillScale = TRUE
)

## S4 method for signature 'data.frame'
plotHeatmap(
  x,
  genes = rownames(x),
  color = "darkblue",
  assays = colnames(x),
  useFillScale = TRUE
)

## S4 method for signature 'matrix'
plotHeatmap(
  x,
  genes = rownames(x),
  color = "darkblue",
  assays = colnames(x),
  useFillScale = TRUE
)
```

Arguments

x	fractions for each gene
genes	name of genes to plot
color	color of heatmap
assays	array of assays to plot
useFillScale	default TRUE. add scale_fill_gradient() to plot

Value

heatmap

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Compute cell type specificity of each gene
df <- cellTypeSpecificity(pb)

# For each cell type, get most specific gene
genes <- rownames(df)[apply(df, 2, which.max)]

# heatmap of 5 genes that are most cell type specific
dreamlet::plotHeatmap(df, genes = genes)
```

---

plotPCA *Plot PCA of gene expression for an assay*

Description

Compute PCA of gene expression for an assay, and plot samples coloring by outlier score

Usage

```
## S4 method for signature 'list'
plotPCA(
  object,
  assays = names(object),
  nPC = 2,
  robust = FALSE,
  ...,
```

```
  maxOutlierZ = 20,
  nrow = 2,
  size = 2,
  fdr.cutoff = 0.05
)
```

Arguments

object	dreamletProcessedData from processAssays() or a list from residuals()
assays	assays / cell types to analyze
nPC	number of PCs to uses for outlier score with outlier()
robust	use robust covariance method, defaults to FALSE
...	arguments passed to MASS::cov.rob()
maxOutlierZ	cap outlier z-scores at this value for plotting to maintain consistent color scale
nrow	number of rows in plot
size	size passed to geom_point()
fdr.cutoff	FDR cutoff to determine outlier

See Also

outlierByAssay()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# PCA to identify outliers
# from normalized expression
plotPCA( res.proc, c("B cells", "CD14+ Monocytes"))

# Run on regression residuals
#----------------------------

# Regression analysis
fit = dreamlet(res.proc, ~ group_id)

# Extract regression residuals
residsObj = residuals(fit)
```

```
# PCA on residuals
plotPCA( residsObj, c("B cells", "CD14+ Monocytes"))
```

`plotPercentBars,vpDF-method`
Bar plot of variance fractions

Description

Bar plot of variance fractions for a subset of genes

Usage

```
## S4 method for signature 'vpDF'
plotPercentBars(
  x,
  col = c(ggColorHue(ncol(x) - 3), "grey85"),
  genes = unique(x$gene),
  width = NULL,
  ncol = 3,
  ...
)

## S4 method for signature 'cellSpecificityValues'
plotPercentBars(
  x,
  col = ggColorHue(ncol(x)),
  genes = rownames(x),
  width = NULL,
  ...
)
```

Arguments

`x`	`vpDF` object returned by `fitVarPart()`
`col`	color of bars for each variable
`genes`	name of genes to plot
`width`	specify width of bars
`ncol`	number of columns in the plot
`...`	other arguments

Value

Bar plot showing variance fractions for each gene

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# variance partitioning analysis
vp <- fitVarPart(res.proc, ~group_id)

# Show variance fractions at the gene-level for each cell type
plotPercentBars(vp, genes = vp$gene[2:4], ncol = 2)
```

`plotProjection` *Plot 2D projection*

Description

Plot 2D projection (i.e. UMAP, tSNE) for millions of cells efficiently

Usage

```
plotProjection(
  sce,
  type,
  annotation,
  pointsize = 0,
  pixels = c(512, 512),
  legend.position = "none",
  text = TRUE,
  order
)
```

Arguments

`sce`	`SingleCellExperiment`
`type`	field in `reducedDims(sce)` to plot
`annotation`	column in `colData(sce)` to annotate each cell
`pointsize`	Radius of rasterized point. Use `0` for single pixels(fastest).
`pixels`	Vector with X and Y resolution of the raster, default `c(512,512)`

legend.position
: legend.position: the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)

text
: show annotation as text. Default TRUE

order
: specify order of levels for annotation

Details

Uses scattermore::geom_scattermore() to plot millions of points efficiently

Value

ggplot2 plot of the projection

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

plotProjection(example_sce, "TSNE", "cluster_id", 1)
```

---

plotVarPart,DataFrame-method
Violin plot of variance fractions

Description

Violin plot of variance fraction for each gene and each variable

Usage

```
## S4 method for signature 'DataFrame'
plotVarPart(
  obj,
  col = c(ggColorHue(base::ncol(obj) - 3), "grey85"),
  label.angle = 20,
  main = "",
  ylab = "",
  convertToPercent = TRUE,
  ncol = 3,
  ...
)
```

Arguments

obj
: varParFrac object returned by fitExtractVarPart or extractVarPart

col
: vector of colors

label.angle
: angle of labels on x-axis

main
: title of plot

ylab	text on y-axis
convertToPercent	multiply fractions by 100 to convert to percent values
ncol	number of columns in the plot
...	additional arguments

Value

Violin plot showing variance fractions

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# variance partitioning analysis
vp <- fitVarPart(res.proc, ~group_id)

# Summarize variance fractions genome-wide for each cell type
plotVarPart(vp)
```

---

plotViolin *Plot Violins*

Description

Plot Violins

Usage

```
plotViolin(x, ...)

## S4 method for signature 'cellSpecificityValues'
plotViolin(x, assays = colnames(x))
```

Arguments

x	fractions for each gene
...	other arguments
assays	array of assays to plot

Value

Violin plot

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Compute cell type specificity of each gene
df <- cellTypeSpecificity(pb)

# Violin plot of specificity scores for each cell type
# Dashed line indicates genes that are equally expressed
# across all cell types.  For K cell types, this is 1/K
plotViolin(df)
```

---

plotVolcano *Volcano plot for each cell type*

Description

Volcano plot for each cell type

Usage

```
plotVolcano(
  x,
  coef,
  nGenes = 5,
  size = 12,
  minp = 9.99999999999997e-311,
  cutoff = 0.05,
  ncol = 3,
  ...
)

## S4 method for signature 'list'
plotVolcano(
  x,
  coef,
  nGenes = 5,
  size = 12,
```

```
  minp = 9.99999999999997e-311,
  cutoff = 0.05,
  ncol = 3,
  assays = names(x),
  ...
)

## S4 method for signature 'MArrayLM'
plotVolcano(
  x,
  coef,
  nGenes = 5,
  size = 12,
  minp = 9.99999999999997e-311,
  cutoff = 0.05,
  ncol = 3,
  ...
)

## S4 method for signature 'dreamlet_mash_result'
plotVolcano(
  x,
  coef,
  nGenes = 5,
  size = 12,
  minp = 1e-16,
  cutoff = 0.05,
  ncol = 3,
  assays = colnames(x$logFC.original),
  ...
)
```

Arguments

x	result from dreamlet
coef	coefficient to test with topTable
nGenes	number of genes to highlight in each volcano plot
size	text size
minp	minimum p-value to show on the y-axis
cutoff	adj.P.Val cutoff to distinguish significant from non-significant genes
ncol	number of columns in the plot
...	arguments passed to facet_wrap(). Useful for specifying scales = "free_y"
assays	which assays to plot

Value

Volcano plot for each cell type

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show coefficients estimated for each cell type
coefNames(res.dl)

# volcano plot for each cell type
plotVolcano(res.dl, coef = "group_idstim")

# volcano plot for first two cell types
plotVolcano(res.dl[1:2], coef = "group_idstim")
```

---

plotVoom *Plot voom curves from each cell type*

Description

Plot voom curves from each cell type

Usage

```
plotVoom(x, ncol = 3, alpha = 0.5, ...)

## S4 method for signature 'dreamletProcessedData'
plotVoom(x, ncol = 3, alpha = 0.5, assays = names(x))

## S4 method for signature 'EList'
plotVoom(x, ncol = 3, alpha = 0.5)
```

Arguments

x	dreamletProcessedData
ncol	number of columns in the plot

alpha	transparency of points
...	other arguments
assays	which assays to plot

Value

Plot of mean-variance trend

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Show mean-variance trend from voom
plotVoom(res.proc)

# plot for first two cell types
plotVoom(res.proc[1:2])
```

---

print,dreamletResult-method

Print object

Description

Print object

Print object

Usage

```
## S4 method for signature 'dreamletResult'
print(x, ...)

## S4 method for signature 'dreamletProcessedData'
print(x, ...)
```

Arguments

x	dreamletProcessedData object
...	other arguments

Value

print data stored in object

`processAssays` *Processing SingleCellExperiment to dreamletProcessedData*

Description

For raw counts, estimate precision weights using linear mixed model weighting by number of cells observed for each sample. For normalized data, only weight by number of cells.

Usage

```
processAssays(
  sceObj,
  formula,
  assays = assayNames(sceObj),
  min.cells = 5,
  min.count = 5,
  min.samples = 4,
  min.prop = 0.4,
  isCounts = TRUE,
  normalize.method = "TMM",
  span = "auto",
  quiet = FALSE,
  weightsList = NULL,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

sceObj	SingleCellExperiment object
formula	regression formula for differential expression analysis
assays	array of assay names to include in analysis. Defaults to assayNames(sceObj)
min.cells	minimum number of observed cells for a sample to be included in the analysis
min.count	used to compute a CPM threshold of CPM.cutoff = min.count/median(lib.size)*1e6. Passed to edgeR::filterByExpr()
min.samples	minimum number of samples passing cutoffs for cell cluster to be retained
min.prop	minimum proportion of retained samples with CPM > CPM.cutoff
isCounts	logical, indicating if data is raw counts
normalize.method	normalization method to be used by calcNormFactors

span	Lowess smoothing parameter using by variancePartition::voomWithDreamWeights()
quiet	show messages
weightsList	list storing matrix of precision weights for each cell type. If NULL precision weights are set to 1
BPPARAM	parameters for parallel evaluation
...	other arguments passed to dream

Details

For each cell cluster, samples with at least min.cells are retained. Only clusters with at least min.samples retained samples are kept. Genes are retained if they have at least min.count reads in at least min.prop fraction of the samples. Current values are reasonable defaults, since genes that don't pass these cutoffs are very underpowered for differential expression analysis and only increase the multiple testing burden. But values of min.cells = 2 and min.count = 2 are also reasonable to include more genes in the analysis.

The precision weights are estimated using the residuals fit from the specified formula. These weights are robust to changes in the formula as long as the major variables explaining the highest fraction of the variance are included.

If weightsList is NULL, precision weights are set to 1 internally.

Value

Object of class dreamletProcessedData storing voom-style normalized expression data

See Also

voomWithDreamWeights()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)
#
```

processOneAssay *Processing expression data from assay*

Description

For raw counts, filter genes and samples, then estimate precision weights using linear mixed model weighting by number of cells observed for each sample. For normalized data, only weight by number of cells

Usage

```
processOneAssay(
  y,
  formula,
  data,
  n.cells,
  min.cells = 5,
  min.count = 2,
  min.samples = 4,
  min.prop = 0.4,
  min.total.count = 15,
  isCounts = TRUE,
  normalize.method = "TMM",
  span = "auto",
  quiet = TRUE,
  weights = NULL,
  rescaleWeightsAfter = FALSE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

y	matrix of counts or log2 CPM
formula	regression formula for differential expression analysis
data	metadata used in regression formula
n.cells	array of cell count for each sample
min.cells	minimum number of observed cells for a sample to be included in the analysis
min.count	used to compute a CPM threshold of CPM.cutoff = min.count/median(lib.size)*1e6. Passed to edgeR::filterByExpr()
min.samples	minimum number of samples passing cutoffs for cell cluster to be retained
min.prop	minimum proportion of retained samples with CPM > CPM.cutoff
min.total.count	minimum total count required per gene for inclusion
isCounts	logical, indicating if data is raw counts
normalize.method	normalization method to be used by calcNormFactors
span	Lowess smoothing parameter using by variancePartition::voomWithDreamWeights()

quiet	show messages
weights	matrix of precision weights
rescaleWeightsAfter	default = FALSE, should the output weights be scaled by the input weights
BPPARAM	parameters for parallel evaluation
...	other arguments passed to dream

Value

EList object storing log2 CPM and precision weights

See Also

processAssays()

---

removeConstantTerms *Remove constant terms from formula*

Description

Remove constant terms from formula. Also remove categorical variables with a max of one example per category

Usage

```
removeConstantTerms(formula, data)
```

Arguments

formula	original formula
data	data.frame

Details

Adapted from MoEClust::drop_constants

Value

a formula, possibly with terms omitted.

Examples

```
# Valid formula
removeConstantTerms(~ group + extra, sleep)

# there is no variation in 'group' in this dataset
removeConstantTerms(~ group + extra, sleep[1:3, ])
```

`residuals,dreamletResult-method`
Extract residuals from `dreamletResult`

Description

Extract residuals from `dreamletResult`

Usage

```
## S4 method for signature 'dreamletResult'
residuals(object, y, ..., type = c("response", "pearson"))
```

Arguments

`object`	`dreamletResult` object
`y`	`dreamletProcessedData` object
`...`	other arguments
`type`	compute either `"response"` residuals or `"pearson"` residuals.

Details

`"response"` residuals are the typical residuals returned from `lm()`. `"pearson"` residuals divides each residual value by its estimated standard error. This requires specifying `y`

Value

residuals from model fit

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# extract typical residuals for each assay (i.e. cell type)
```

```
# Return list with entry for each assay with for retained samples and genes
resid.lst <- residuals(res.dl)

# Get Pearson residuals:
# typical residuals scaled by the standard deviation
residPearson.lst <- residuals(res.dl, res.proc, type = "pearson")
```

`run_mash` *Run mash analysis on dreamlet results*

Description

Run mash analysis on dreamlet results

Usage

```
run_mash(fit, coefList)
```

Arguments

`fit`	result from `dreamlet()`
`coefList`	coefficient to be analyzed. Assumes 1) the null distribution of the two coefficients is simular, 2) the effects sizes are on the same scale, and 3) the effect estimates should be shrunk towards each other. If these are not satisfied, run separately on each coefficient

Details

Apply mashr analysis (Urbut et al. 2019) on the joint set of coefficients for each gene and cell type. `mashr` is a Bayesian statistical method that borrows strength across tests (i.e. genes and cell types) by learning the distribution of non-zero effects based the obesrved logFC and standard errors. The method then estimates the posterior distributions of each coefficient based on the observed value and the genome-wide emprical distribution.

`mashr` has been previously applied to differential expression in GTEx data using multiple tissues from the same set of donors (Oliva et al. 2020).

In single cell data, a given gene is often not sufficiently expressed in all cell types. So it is not evaluated in a subsets of cell types, and its coefficient value is `NA`. Since mashr assumes coefficients and standard errors for every gene and cell type pair, entries with these missing values are set to have `coef = 0`, and `se = 1e6`. The output of mashr is then modified to set the corresponding values to `NA`, to avoid nonsensical results downstream.

Based on empirical analysis, `mashr` is most useful for prioritizing genes based on their cell type specificity using `compositePosteriorTest()`. `mashr` tends to overshink and push the estimated effect size from mutliple cell types towards a common value. This is not ideal for identifying differentially expressed genes in a given cell type, due to the overshinkage.

Value

a list storing the `mashr` model as `model` and the original coefficients as `logFC.original`

References

Oliva M, Munoz-Aguirre M, Kim-Hellmuth S, Wucher V, Gewirtz AD, Cotter DJ, Parsana P, Kasela S, Balliu B, Vinuela A, others (2020). "The impact of sex on gene expression across human tissues." *Science*, **369**(6509), eaba3066. https://doi.org/10.1126/science.aba3066.

Urbut SM, Wang G, Carbonetto P, Stephens M (2019). "Flexible statistical methods for estimating and testing effects in genomic studies with multiple conditions." *Nature genetics*, **51**(1), 187–195. https://doi.org/10.1038/s41588-018-0268-8.

See Also

compositePosteriorTest(), mashr::mash_estimate_corr_em(), mashr::cov_canonical, mashr::mash_set_dat

Examples

```
library(muscat)
library(mashr)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce[1:100, ],
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# run MASH model
# This can take 10s of minutes on real data
# This small datasets should take ~30s
res_mash <- run_mash(res.dl, "group_idstim")

# extract statistics from mashr model
# NA values indicate genes not sufficiently expressed
# in a given cell type

# original logFC
head(res_mash$logFC.original)

# posterior mean for logFC
head(get_pm(res_mash$model))

# how many gene-by-celltype tests are significant
# i.e.  if a gene is significant in 2 celltypes, it is counted twice
table(get_lfsr(res_mash$model) < 0.05, useNA = "ifany")

# how many genes are significant in at least one cell type
```

```
table(apply(get_lfsr(res_mash$model), 1, min, na.rm = TRUE) < 0.05)

# how many genes are significant in each cell type
apply(get_lfsr(res_mash$model), 2, function(x) sum(x < 0.05, na.rm = TRUE))

# examine top set of genes
# which genes are significant in at least 1 cell type
sort(names(get_significant_results(res_mash$model)))[1:10]

# Lets examine ENO1
# There is a lot of variation in the raw logFC
res_mash$logFC.original["ENO1", ]

# posterior mean after borrowing across cell type and genes
get_pm(res_mash$model)["ENO1", ]

# forest plot based on mashr results
plotForest(res_mash, "ENO1")

# volcano plot based on mashr results
# yaxis uses local false sign rate (lfsr)
plotVolcano(res_mash)

# Comment out to reduce package runtime
# gene set analysis using mashr results
# library(zenith)
# go.gs = get_GeneOntology("CC", to="SYMBOL")
# df_gs = zenith_gsa(res_mash, go.gs)

# Heatmap of results
# plotZenithResults(df_gs, 2, 1)
```

`seeErrors` *Get error text*

Description

Get error text

Usage

```
seeErrors(obj)

## S4 method for signature 'dreamletResult'
seeErrors(obj)

## S4 method for signature 'dreamletProcessedData'
seeErrors(obj)

## S4 method for signature 'vpDF'
seeErrors(obj)
```

Arguments

obj	A dreamletResult object

Value

tibble storing error text

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show errors
# but none are reported
res.err = seeErrors(res.dl)
```

---

show,dreamletResult-method

Show object

Description

Show object

Show object

Usage

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

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

Arguments

object	dreamletProcessedData object

Value

show data stored in object

---

sortCols,vpDF-method *Sort variance partition statistics*

Description

Sort variance partition statistics

Usage

```
## S4 method for signature 'vpDF'
sortCols(
  x,
  FUN = sum,
  decreasing = TRUE,
  last = c("Residuals", "Measurement.error"),
  ...
)
```

Arguments

x	object returned by fitVarPart()
FUN	function giving summary statistic to sort by. Defaults to sum
decreasing	logical. Should the sorting be increasing or decreasing?
last	columns to be placed on the right, regardless of values in these columns
...	other arguments to sort

Value

data.frame with columns sorted by mean value, with Residuals in last column

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)
```

```
# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# variance partitioning analysis
vp <- fitVarPart(res.proc, ~group_id)

# Summarize variance fractions genome-wide for each cell type
plotVarPart(sortCols(vp))
```

`stackAssays` *Stack assays from pseudobulk*

Description

Stack assays from pseudobulk to perform analysis across cell types

Usage

```
stackAssays(pb, assays = assayNames(pb))
```

Arguments

pb	pseudobulk `SingleCellExperiment` from `aggregateToPseudoBulk()`
assays	array of assay names to include in analysis. Defaults to `assayNames(pb)`

Value

pseudobulk `SingleCellExperiment` cbind'ing expression values and rbind'ing colData. The column `stackedAssay` in `colData()` stores the assay information of the stacked data.

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# Replace space with underscore, and remove "+" to avoid issue downstream
example_sce$cluster_id <- gsub(" ", "_", example_sce$cluster_id)
example_sce$cluster_id <- gsub("\\+", "", example_sce$cluster_id)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# Stack assays for joint analysis
pb.stack <- stackAssays(pb)
```

```
# voom-style normalization
# stackedAssay (i.e. cell type) can now be included as a covariate
res.proc <- processAssays(pb.stack, ~ group_id + stackedAssay)

# Examine coding of covariates
# colData:
head(colData(res.proc))

# Examine coding of covariates
# metadata:
head(metadata(res.proc))

# Variance partitioning analysis
# Model contribution of Donor (id), stimulation status (group_id), and cell type (stackedAssay)
form <- ~ (1|id) + (1|group_id) + (1|stackedAssay)
vp <- fitVarPart(res.proc, form)

# Summarize variance fractions across cell types
plotVarPart(sortCols(vp))

# Interaction analysis allows group_id
# to have a different effect within each stackedAssay
form <- ~ (1|id) + (1|group_id) + (1|stackedAssay) + (1|group_id:stackedAssay)
vp2 <- fitVarPart(res.proc, form)

plotVarPart(sortCols(vp2))

plotVarPart(sortCols(vp2))

# Differential expression analysis
# Testing differences between cell types

# In a real data you want to test the full model,
# but this dataset is too small
form <- ~ (1|id) + (1|group_id) + (1|stackedAssay) + group_id:stackedAssay + 0

# In this small dataset, just test simulation-by-celltype interaction term
# Here, test if the effect of stimulation (i.e. difference between stimulated and
# controls) is different between B cells and monocytes
contrasts <- c(Diff = "(group_idstim:stackedAssayB_cells - group_idctrl:stackedAssayB_cells) -
(group_idstim:stackedAssayCD14_Monocytes - group_idstim:stackedAssayCD14_Monocytes)")
form <- ~ group_id:stackedAssay + 0
fit <- dreamlet( res.proc, form, contrasts = contrasts)

# Top genes
topTable(fit, coef='Diff', number=3)

# Plot example
df <- extractData(res.proc, assay = "stacked", genes = c("ISG20"))

df <- df[df$stackedAssay %in% c("B_cells", "CD14_Monocytes"),]

ggplot(df, aes(group_id, ISG20)) +
  geom_boxplot() +
  theme_bw() +
  theme(aspect.ratio=1) +
  facet_wrap( ~ stackedAssay)
```

tabToMatrix *Convert results table to matrix*

Description

Convert results table to matrix

Usage

```
tabToMatrix(tab, col, rn = "ID", cn = "assay")
```

Arguments

tab	results table from topTable()
col	which column to extract
rn	column id storing rownames
cn	column id storing colnames

Value

matrix storing values of column col in rows defind by rn and columns defined by cn

topTable,dreamletResult-method *Table of Top Genes from dreamlet fit*

Description

Extract a table of the top-ranked genes from a dreamlet fit.

Usage

```
## S4 method for signature 'dreamletResult'
topTable(
  fit,
  coef = NULL,
  number = 10,
  genelist = NULL,
  adjust.method = "BH",
  sort.by = "P",
  resort.by = NULL,
  p.value = 1,
  lfc = 0,
  confint = FALSE
)
```

Arguments

fit	dreamletResult object
coef	coef
number	number
genelist	genelist
adjust.method	adjust.method
sort.by	sort.by
resort.by	resort.by
p.value	p.value
lfc	lfc
confint	confint

Value

data.frame storing hypothesis test for each gene and cell type

See Also

limma::topTable(), variancePartition::topTable()

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# show coefficients estimated for each cell type
coefNames(res.dl)

# extract results using limma-style syntax
# combines all cell types together
# adj.P.Val gives study-wide FDR
topTable(res.dl, coef = "group_idstim", number = 3)
```

vpDF-class *Class vpDF*

Description

Class vpDF stores results for each gene for each assay

Value

none

none

zenith_gsa,dreamletResult,GeneSetCollection-method *Perform gene set analysis using zenith*

Description

Perform a competitive gene set analysis accounting for correlation between genes.

Usage

```
## S4 method for signature 'dreamletResult,GeneSetCollection'
zenith_gsa(
  fit,
  geneSets,
  coefs,
  use.ranks = FALSE,
  n_genes_min = 10,
  inter.gene.cor = 0.01,
  progressbar = TRUE,
  ...
)

## S4 method for signature 'dreamlet_mash_result,GeneSetCollection'
zenith_gsa(
  fit,
  geneSets,
  coefs,
  use.ranks = FALSE,
  n_genes_min = 10,
  inter.gene.cor = 0.01,
  progressbar = TRUE,
  ...
)
```

Arguments

fit	results from dreamlet()
geneSets	GeneSetCollection
coefs	coefficients to test using topTable(fit, coef=coefs[i])
use.ranks	do a rank-based test TRUE or a parametric test FALSE? default: FALSE
n_genes_min	minimum number of genes in a geneset
inter.gene.cor	if NA, estimate correlation from data. Otherwise, use specified value
progressbar	if TRUE, show progress bar
...	other arguments

Details

This code adapts the widely used camera() analysis (Wu and Smyth 2012) in the limma package (Ritchie et al. 2015) to the case of linear (mixed) models used by variancePartition::dream().

Value

data.frame of results for each gene set and cell type

data.frame of results for each gene set and cell type

Examples

```
library(muscat)
library(SingleCellExperiment)

data(example_sce)

# create pseudobulk for each sample and cell cluster
pb <- aggregateToPseudoBulk(example_sce,
  assay = "counts",
  cluster_id = "cluster_id",
  sample_id = "sample_id",
  verbose = FALSE
)

# voom-style normalization
res.proc <- processAssays(pb, ~group_id)

# Differential expression analysis within each assay,
# evaluated on the voom normalized data
res.dl <- dreamlet(res.proc, ~group_id)

# Load Gene Ontology database
# use gene 'SYMBOL', or 'ENSEMBL' id
# use get_MSigDB() to load MSigDB
library(zenith)
go.gs <- get_GeneOntology("CC", to = "SYMBOL")

# Run zenith gene set analysis on result of dreamlet
res_zenith <- zenith_gsa(res.dl, go.gs, "group_idstim", progressbar = FALSE)

# for each cell type select 3 genesets with largest t-statistic
# and 1 geneset with the lowest
```

```
# Grey boxes indicate the gene set could not be evaluted because
#    to few genes were represented
plotZenithResults(res_zenith, 3, 1)
```

`[,dreamletResult,ANY,ANY,ANY-method`
Subset with brackets

Description

Subset with brackets

Subset with brackets

Usage

```
## S4 method for signature 'dreamletResult,ANY,ANY,ANY'
x[i]

## S4 method for signature 'dreamletProcessedData,ANY,ANY,ANY'
x[i]
```

Arguments

x	`dreamletProcessedData` object
i	indeces to extract

Value

entries stored at specified index

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