Package 'spoon'

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Title Address the Mean-variance Relationship in Spatial Transcriptomics Data

Version 1.5.0

Description This package addresses the mean-variance relationship in spatially resolved transcriptomics data. Precision weights are generated for individual observations using Empirical Bayes techniques. These weights are used to rescale the data and covariates, which are then used as input in spatially variable gene detection tools.

URL https://github.com/kinnaryshah/spoon

BugReports https://github.com/kinnaryshah/spoon/issues

Imports SpatialExperiment, BRISC, nnSVG, BiocParallel, Matrix, methods, SummarizedExperiment, stats, utils, scuttle

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Encoding UTF-8

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`generate_weights` *Generate weights*

Description

Generate weights on the observation level for each gene

Usage

```
generate_weights(
  input,
  spatial_coords = NULL,
  assay_name = "counts",
  stabilize = TRUE,
  n_threads = 1,
  BPPARAM = NULL
)
```

Arguments

`input`	either a SpatialExperiment object which contains a counts matrix, or a counts matrix
`spatial_coords`	matrix containing columns of spatial coordinates, needed if input is a matrix
`assay_name`	if using a SpatialExperiment object, name of the assay in which the counts matrix is stored
`stabilize`	when TRUE, stabilize weights to avoid extrapolation (highly recommended)
`n_threads`	default = 1, number of threads for parallelization
`BPPARAM`	optional additional argument for parallelization to use BiocParallel

Details

This function generates weights for each observation, which are used as input to scale the data and covariates

Value

weights matrix

Examples

```
library(nnSVG)
library(STexampleData)
library(SpatialExperiment)
library(BRISC)
library(BiocParallel)
library(scuttle)


spe <- Visium_humanDLPFC()

# keep spots over tissue
spe <- spe[, colData(spe)$in_tissue == 1]

# filter low-expressed and mitochondrial genes
spe <- filter_genes(spe)

# calculate logcounts (log-transformed normalized counts) using scran package
spe <- computeLibraryFactors(spe)
spe <- logNormCounts(spe)

known_genes <- c("MOBP", "PCP4", "SNAP25", "HBB", "IGKC", "NPY")
ix_known <- which(rowData(spe)$gene_name %in% known_genes)
ix <- c(ix_known)

spe <- spe[ix, ]

spe <- spe[, colSums(logcounts(spe)) > 0]

#EXAMPLE 1 USING SPATIAL EXPERIMENT

set.seed(1)
weights_1 <- generate_weights(input = spe,
                              stabilize = TRUE)

#EXAMPLE 2 USING MATRIX

counts_mat <- counts(spe)
logcounts_mat <- logcounts(spe)
coords_mat <- spatialCoords(spe)

set.seed(1)
weights_2 <- generate_weights(input = counts_mat,
                              spatial_coords = coords_mat,
                              stabilize = TRUE)
```

`weighted_nnSVG` *Weighted nnSVG*

Description

Run nnSVG for SVG detection using the weights

Usage

```
weighted_nnSVG(
  input,
  spatial_coords = NULL,
  assay_name = "logcounts",
  w,
  n_threads = 1,
  BPPARAM = MulticoreParam(workers = 1)
)
```

Arguments

input	either a SpatialExperiment object which contains a logcounts matrix, or a logcounts matrix
spatial_coords	matrix containing columns of spatial coordinates, needed if input is a matrix
assay_name	if using a SpatialExperiment object, name of the assay in which the logcounts matrix is stored
w	weights matrix
n_threads	default = 1, number of threads for parallelization
BPPARAM	optional additional argument for parallelization to use BiocParallel

Details

This function incorporates weights for each observation to run nnSVG

Value

either spe with weighted nnSVG statistics, or matrix with weighted nnSVG statistics

Examples

```
library(nnSVG)
library(STexampleData)
library(SpatialExperiment)
library(BRISC)
library(BiocParallel)
library(scuttle)
library(Matrix)

spe <- Visium_humanDLPFC()

# keep spots over tissue
spe <- spe[, colData(spe)$in_tissue == 1]

# filter low-expressed and mitochondrial genes
spe <- filter_genes(spe)

# calculate logcounts (log-transformed normalized counts) using scran package
spe <- computeLibraryFactors(spe)
spe <- logNormCounts(spe)

known_genes <- c("MOBP", "PCP4", "SNAP25", "HBB", "IGKC", "NPY")
ix_known <- which(rowData(spe)$gene_name %in% known_genes)
```

```
ix <- c(ix_known)

spe <- spe[ix, ]

spe <- spe[, colSums(logcounts(spe)) > 0]

#EXAMPLE 1 USING SPATIAL EXPERIMENT

set.seed(1)
weights_1 <- generate_weights(input = spe,
                              stabilize = TRUE)
spe_results <- weighted_nnSVG(input = spe,
                              w = weights_1,
                              BPPARAM = MulticoreParam(workers = 1,
                                                       RNGseed = 4))

# display results
rowData(spe_results)


#EXAMPLE 2 USING MATRIX

counts_mat <- counts(spe)
logcounts_mat <- logcounts(spe)
coords_mat <- spatialCoords(spe)

set.seed(1)
weights_2 <- generate_weights(input = counts_mat,
                              spatial_coords = coords_mat,
                              stabilize = TRUE)
results <- weighted_nnSVG(input = logcounts_mat,
                          spatial_coords = coords_mat,
                          w = weights_2,
                          BPPARAM = MulticoreParam(workers = 1, RNGseed = 4))

# display results
print(results)
```

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