Package ‘standR’

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Title  Spatial transcriptome analyses of Nanostring’s DSP data in R

Version  1.6.0

Description  standR is an user-friendly R package providing functions to assist conducting good-practice analysis of Nanostring’s GeoMX DSP data. All functions in the package are built based on the SpatialExperiment object, allowing integration into various spatial transcriptomics-related packages from Bioconductor. standR allows data inspection, quality control, normalization, batch correction and evaluation with informative visualizations.

biocViews  Spatial, Transcriptomics, GeneExpression, DifferentialExpression, QualityControl, Normalization, ExperimentHubSoftware

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standR-package  Tools for analyzing NanoString’s GeoMX spatial transcriptomics data

Description

standR implements a series of functions to facilitate inspection, analysis and visualization of the NanoString’s GeoMX DSP datasets. standR takes the either the csv files from the Nanostring or DGEList object as input, allowing for multiple methods to be analyzed together.
Details

**standR** represents the GeoMX DSP data as `SpatialExperiment` objects, which can easily be integrated with a wide variety of Bioconductor packages. **standR** generates various plots, such as QC distribution plots, dimension reduction plots and RLE plots, for quality control of genes and region of interest (ROI) samples. Multiple normalization and batch correction methods are also provided in the package as well, with the ability to compute statistics for assessing the normalization/batch correction results.

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---

### addPerROIQC

#### Add QC statistics to the Spatial Experiment object

**Description**

Add QC statistics to the Spatial Experiment object

**Usage**

```r
addPerROIQC(
  spe_object,
  sample_fraction = 0.9,
  rm_genes = TRUE,
  min_count = 5,
  design = NULL
)
```

**Arguments**

- `spe_object`: A `SpatialExperiment` object
- `sample_fraction`: Double. Genes with low count in more than this threshold of the samples will be removed. Default is 0.9
- `rm_genes`: Logical. Decide whether genes with low count in more than `sample_fraction` of the samples are removed from the dataset. Default is TRUE.
- `min_count`: Integer. Minimum read count to calculate count threshold. Default is 5.
- `design`: Generate using `model.matrix`, if this is specify, `edgeR::filterByExpr` will be used to filter genes.

**Value**

A `SpatialExperiment` object
computeClusterEvalStats

Calculate statistics for evaluating batch correction

Description

Calculate statistics for evaluating batch correction

Usage

computeClusterEvalStats(
  spe_object,
  foiColumn,
  precomputed = NULL,
  n_dimension = c(1, 2),
  assay = 2
)

Arguments

spe_object A Spatial Experiment object.
foiColumn A column name indicating the factor of interest to be tested, can be biological factor or batch factor.
precomputed a dimensional reduction results from stats::prcomp. result in reducedDims(object) to plot. Default is NULL, we will compute for you.
n_dimension The top n dimensions to be plotted
assay a numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).

Value

A dataframe object containing the clustering evaluating statistics.

Examples

library(scater)
data("dkd_spe_subset")
computeClusterEvalStats(dkd_spe_subset, "SlideName")

data("dkd_spe_subset")
spe_filtered <- addPerROIQC(dkd_spe_subset)
spe_filtered

**Description**

standR-package has 1 datasets:

- dkd_spe_subset Example subset of a GeoMX DSP WTA dataset,

**Usage**

data("dkd_spe_subset")

**Format**

A SpatialExperiment object with 3000 rows and 70 samples:

**Source**


**Examples**

data(dkd_spe_subset)

drawPCA

**Description**

Compute and plot the results of a PCA analysis on gene expression data

**Usage**

drawPCA(object, dims = c(1, 2), ...)

```r
## S4 method for signature 'ExpressionSet'
drawPCA(object, dims = c(1, 2), precomputed = NULL, textScale = 1, ...)
```

```r
## S4 method for signature 'SummarizedExperiment'
drawPCA(
    object,
    dims = c(1, 2),
    assay = 1,
```
drawPCA

```r
precomputed = NULL,
textScale = 1,
...
)

## S4 method for signature 'SingleCellExperiment'
drawPCA(
  object,
  dims = c(1, 2),
  assay = 1,
  precomputed = NULL,
  textScale = 1,
  ...
)

## S4 method for signature 'SpatialExperiment'
drawPCA(
  object,
  dims = c(1, 2),
  assay = 1,
  precomputed = NULL,
  textScale = 1,
...
)
```

**Arguments**

- `object` a DGEList, SummarizedExperiment or ExpressionSet object containing gene expression data.
- `dims` a numeric, containing 2 values specifying the dimensions to plot.
- `...` aesthetic mappings to pass to `ggplot2::aes_string()`.
- `precomputed` a dimensional reduction results from `stats::prcomp`. result in `reducedDims(object)` to plot.
- `textScale` a numeric, specifying the relative scale factor to apply to text on the plot.
- `assay` a numeric or character, specifying the assay to use (for `SummarizedExperiment` and its derivative classes).

**Value**

a `ggplot2` object

**Examples**

```r
data("dkd_spe_subset")
drawPCA(dkd_spe_subset)
```
findBestK

Description

Testing multiple K for RUV4 batch correction to find the best K.

Usage

findBestK(
  spe,
  maxK = 10,
  factor_of_int,
  factor_batch,
  NCGs,
  point_size = 3,
  line_col = "black",
  point_col = "black",
  text_size = 13
)

Arguments

- **spe**: A Spatial Experiment object.
- **maxK**: Integer. The max k to test, will test k from 1 to maxK, by default is 10.
- **factor_of_int**: Column name(s) to indicate the factors of interest. This is required for the RUV4 method.
- **factor_batch**: Column name to indicate the batch.
- **NCGs**: Negative control genes. This is required for the RUV4 method.
- **point_size**: Numeric. Plotting parameter.
- **line_col**: Character. Plotting parameter.
- **point_col**: Character. Plotting parameter.
- **text_size**: Numeric. Plotting parameter.

Value

A ggplot object.

Examples

data("dkd_spe_subset")
spe <- findNCGs(dkd_spe_subset, top_n = 100)
findBestK(spe,
  factor_of_int = c("disease_status"),
  factor_batch = "SlideName", NCGs = S4Vectors::metadata(spe)$NCGs
)
**findNCGs**  
*Get negative control genes from each batch of the data*

**Description**
Get negative control genes from each batch of the data

**Usage**

```r
findNCGs(spe, n_assay = 2, batch_name = "SlideName", top_n = 200)
```

**Arguments**

- `spe`  
  A Spatial Experiment object.
- `n_assay`  
  Integer to indicate the nth count table in the assay(spe) to be used.
- `batch_name`  
  Column name indicating batches.
- `top_n`  
  Integer indicate how many genes to be included as negative control genes.

**Value**

A Spatial Experiment object, containing negative control genes in the metadata.

**Examples**

```r
data("dkd_spe_subset")
spe <- findNCGs(dkd_spe_subset, top_n = 100)
S4Vectors::metadata(spe)$NCGs
```

---

**geomxBatchCorrection**  
*Batch correction for GeoMX data*

**Description**
Batch correction for GeoMX data
Usage

geomxBatchCorrection(
  spe,
  k,
  factors,
  NCGs,
  n_assay = 2,
  batch = NULL,
  batch2 = NULL,
  covariates = NULL,
  design = matrix(1, ncol(spe), 1),
  method = c("RUV4", "Limma", "RUVg"),
  isLog = TRUE
)

Arguments

spe A Spatial Experiment object.

k The number of unwanted factors to use. Can be 0. This is required for the RUV4 method.

factors Column name(s) to indicate the factors of interest. This is required for the RUV4 method.

NCGs Negative control genes. This is required for the RUV4 method.

n_assay Integer to indicate the nth count table in the assay(spe) to be used.

batch A vector indicating batches. This is required for the Limma method.

batch2 A vector indicating the second series of batches. This is specific for the Limma method.

covariates A matrix or vector of numeric covariates to be adjusted for.

design A design matrix relating to treatment conditions to be preserved, can be generated using stats::model.matrix function with all biological factors included.

method Can be either RUV4 or Limma or RUVg, by default is RUV4.

isLog Logical vector, indicating if the count table is log or not.

Value

A Spatial Experiment object, containing the normalized count and normalization factor. For method RUV4 and RUVg, the W matrices will be saved in the colData of the object.

Note

The normalised count is not intended to be used directly for linear modelling. For linear modelling, it is better to include the batch factors/W matrices in the linear model.
gumxNorm

Perform normalization to GeoMX data

**Description**
Perform normalization to GeoMX data

**Usage**
gumxNorm(
  spe_object,  
  method = c(“TMM”, “RPKM”, “TPM”, “CPM”, “upperquartile”, “sizefactor”),
  log = TRUE
)

**Arguments**
- **spe_object**  A SpatialExperiment object.
- **method**  Normalization method to use. Options: TMM, RPKM, TPM, CPM, upperquartile, sizefactor. RPKM and TPM require gene length information, which should be added into rowData(spe). Note that TMM here is TMM + CPM.
- **log**  Log-transformed or not.

**Value**
A SpatialExperiment object, with the second assay being the normalized count matrix. The normalised count is stored in the assay slot called “logcounts” by default. With method TMM and sizefactor, the norm.factor will be saved in the metadata of the SpatialExperiment object.

**Examples**
data(“dkd_spe_subset”)
spe <- findNCGs(dkd_spe_subset, top_n = 100)
spe_ruv <- gumxBatchCorrection(spe,
  k = 3,
  factors = c(“disease_status”, “region”),
  NCGs = S4Vectors::metadata(spe)$NCGs
)

**References**

Note

The normalised count is not intended to be used directly for linear modelling. For linear modelling, it is better to include the normalized factors in the "norm.factors" column of the DGEList object.

References


Examples

data("dkd_spe_subset")

spe_tmm <- geomxNorm(dkd_spe_subset, method = "TMM")
spe_upq <- geomxNorm(dkd_spe_subset, method = "upperquartile")
spe_deseqnorm <- geomxNorm(dkd_spe_subset, method = "sizefactor")

\section*{Description}

Compare and evaluate different batch corrected data with plotting.

\section*{Usage}

\begin{verbatim}
plotClusterEvalStats(
  spe_list,
  bio_feature_name,
  batch_feature_name,
  data_names,
  colors = NA
)
\end{verbatim}

\section*{Arguments}

\begin{verbatim}
spe_list A list of Spatial Experiment object.
bio_feature_name The common biological variation name.
batch_feature_name The common batch variation name.
data_names Data names.
colors Color values of filing the bars.
\end{verbatim}
plotDR

Compute and plot the results of any dimension reduction methods on gene expression data

Description

Compute and plot the results of any dimension reduction methods on gene expression data

Usage

plotDR(object, dims = c(1, 2), ...)

## S4 method for signature 'SingleCellExperiment'
plotDR(object, dims, dimred = "PCA", textScale = 1, ...)

## S4 method for signature 'SpatialExperiment'
plotDR(object, dims, dimred = "PCA", textScale = 1, ...)

Arguments

object a DGEList, SummarizedExperiment or ExpressionSet object containing gene expression data.
dims a numeric, containing 2 values specifying the dimensions to plot.
... aesthetic mappings to pass to ggplot2::aes_string().
dimred a string or integer scalar indicating the reduced dimension result in reducedDims(object) to plot.
textScale a numeric, specifying the relative scale factor to apply to text on the plot.

Value

a ggplot2 object
plotGeneQC

Examples

```
library(scater)
data("dkd_spe_subset")
spe <- scater::runPCA(dkd_spe_subset)
plotDR(spe, dimred = "PCA")
```

plotGeneQC  

Plot gene-wise QC plot

Description

Plot gene-wise QC plot

Usage

```
plotGeneQC(
  spe, 
  top_n = 9, 
  ordannots = c(), 
  point_size = 1, 
  line_type = "dashed", 
  line_col = "darkred", 
  line_cex = 1, 
  hist_col = "black", 
  hist_fill = "skyblue", 
  bin_num = 30, 
  text_size = 13, 
  layout_ncol = 1, 
  layout_nrow = 2, 
  layout_height = c(1, 1), 
  ... 
)
```

Arguments

- **spe**: A SpatialExperiment object.
- **top_n**: Integer. Indicating the top n genes will be plotted. Default is 9.
- **ordannots**: variables or computations to sort samples by (tidy style).
- **point_size**: Numeric. Point size.
- **line_type**: Character. Line types for ggplot.
- **line_col**: Color for line.
- **line_cex**: Cex for line.
- **hist_col**: Color for histogram.
**plotMDS**

```r
hist_fill  Fill for histogram.
bin_num    Bin numbers for histogram.
text_size  Text size.
layout_ncol Integer. Column number for layout. Default is 1.
layout_nrow Integer. Row number for layout. Default is 2.
layout_height Vector of numerics with length of 2. Default is c(1, .4).
...        aesthetic mappings to pass to `ggplot2::aes()` of the dot plots.
```

**Value**

A ggplot object

**Examples**

```r
data("dkd_spe_subset")
spe <- addPerROIQC(dkd_spe_subset)
plotGeneQC(spe)
```

---

**Description**

Compute and plot the results of a MDS analysis on gene expression data

**Usage**

```r
plotMDS(
    object,
    dims = c(1, 2),
    precomputed = NULL,
    textScale = 1,
    assay = 1,
    ...
)
```

## S4 method for signature 'DGEList'

```r
plotMDS(
    object,
    dims = c(1, 2),
    precomputed = NULL,
    textScale = 1,
    assay = 1,
    ...
)
```
## S4 method for signature 'ExpressionSet'

plotMDS(
  object,
  dims = c(1, 2),
  precomputed = NULL,
  textScale = 1,
  assay = 1,
  ...
)

## S4 method for signature 'SummarizedExperiment'

plotMDS(
  object,
  dims = c(1, 2),
  precomputed = NULL,
  textScale = 1,
  assay = 1,
  ...
)

## S4 method for signature 'SingleCellExperiment'

plotMDS(
  object,
  dims = c(1, 2),
  precomputed = NULL,
  textScale = 1,
  assay = 1,
  ...
)

## S4 method for signature 'SpatialExperiment'

plotMDS(
  object,
  dims = c(1, 2),
  precomputed = NULL,
  textScale = 1,
  assay = 1,
  ...
)

### Arguments

- **object**
  - a DGEList, SummarizedExperiment or ExpressionSet object containing gene expression data.

- **dims**
  - a numeric, containing 2 values specifying the dimensions to plot.

- **precomputed**
  - a dimensional reduction results from either limma::plotMDS.

- **textScale**
  - a numeric, specifying the relative scale factor to apply to text on the plot.
assay a numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).

... aesthetic mappings to pass to ggplot2::aes_string().

Value

a ggplot2 object

Examples

data("dkd_spe_subset")
standR::plotMDS(dkd_spe_subset)

---------

plotPairPCA  Plot pair-wise PCA plots for multiple dimensions

---------

Description

Plot pair-wise PCA plots for multiple dimensions

Usage

plotPairPCA(
spe_object,
n_dimension = 3,
precomputed = NULL,
assay = 2,
title = NA,
title.size = 14,
rmduplabs = FALSE,
flipcoord = FALSE,
...
)

Arguments

  spe_object     A SpatialExperiment object.
  n_dimension    The top n dimensions to be plotted
  precomputed    a dimensional reduction results from stats::prcomp. result in reducedDims(object) to plot. Default is NULL, we will compute for you.
  assay          a numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).
  title          Character vector, title to put at the top.
  title.size     Numeric vector, size of the title.
  rmduplabs      Remove duplicated labels from the plot. FALSE by default.
  flipcoord      Flip the xy coordinates. FALSE by default.
  ...            aesthetic mappings to pass to ggplot2::aes().
plotPCAbiplot

Value

A ggplot object.

Examples

data("dkd_spe_subset")
plotPairPCA(dkd_spe_subset)

Description

Plot PCA bi plot

Usage

plotPCAbiplot(
  spe_object,
  n_loadings = 10,
  dims = c(1, 2),
  precomputed = NULL,
  assay = 1,
  arrow_x = 0,
  arrow_y = 0,
  ...
)

Arguments

   spe_object A SpatialExperiment object.
   n_loadings Plot the top n gene loadings
   dims       The top n dimensions to be plotted
   precomputed a dimensional reduction results from stats::prcomp. result in reducedDims(object) to plot. Default is NULL, we will compute for you.
   assay      a numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).
   arrow_x    a numeric, indicating the x coordinate of the base of the arrow.
   arrow_y    a numeric, indicating the y coordinate of the base of the arrow.
   ...        aesthetic mappings to pass to ggplot2::aes().

Value

A ggplot object.
Examples

data("dkd_spe_subset")
plotPCAbiplot(dkd_spe_subset)

plotRLExpr Compute and plot relative log expression (RLE) values of gene expression data

Description

Compute and plot relative log expression (RLE) values of gene expression data

Usage

plotRLExpr(object, ordannots = c(), ...)

## S4 method for signature 'DGEList'
plotRLExpr(object, ordannots = c(), ...)

## S4 method for signature 'ExpressionSet'
plotRLExpr(object, ordannots = c(), ...)

## S4 method for signature 'SummarizedExperiment'
plotRLExpr(object, ordannots, assay = 1, ...)

Arguments

object a DGEList, SummarizedExperiment or ExpressionSet object containing gene expression data.
ordannots variables or computations to sort samples by (tidy style).
... aesthetic mappings to pass to ggplot2::aes_string().
assay a numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).

Value

a ggplot2 object, containing the RLE plot.

Examples

data("dkd_spe_subset")
plotRLExpr(dkd_spe_subset)
plotROIQC  

Plot Sample-wise QC plot

Description

Plot Sample-wise QC plot

Usage

plotROIQC(
  spe_object,
  x_axis = "AOINucleiCount",
  y_axis = "lib_size",
  x_lab = "AOINucleiCount",
  y_lab = "Library size",
  x_threshold = NULL,
  y_threshold = NULL,
  regression_col = "purple",
  hist_col = "black",
  hist_fill = "white",
  bin_num = 50,
  threshold_col = "red",
  threshold_linetype = "dashed",
  layout_ncol = 2,
  layout_nrow = 2,
  layout_height = c(0.8, 2.5),
  layout_width = c(2.5, 0.8),
  ...
)

Arguments

spe_object  A SpatialExperiment object.
x_axis      Numeric feature to plot as x axis.
y_axis      Numeric feature to plot as y axis.
x_lab       Label name for x axis.
y_lab       Label name for y axis.
x_threshold Threshold to draw.
y_threshold Threshold to draw.
regression_col Color for the regression line.
hist_col    Color for the histograms.
hist_fill   Fill for the histograms.
bin_num     Bin numbers for the histograms.
threshold_col Threshold line color.
plotSampleInfo

threshold_linetype
Threshold line type.

layout_ncol Column number layout.

layout_nrow Row number layout.

layout_height Height layout.

layout_width Width layout.

... aesthetic mappings to pass to ggplot2::aes() of the dot plots.

Value
A ggplot object.

Examples

library(ggplot2)
library(patchwork)
data("dkd_spe_subset")
spe <- addPerROIQC(dkd_spe_subset)

plotROIQC(spe)

plotSampleInfo
Plot the user-defined meta data using alluvium plot

Description
Plot the user-defined meta data using alluvium plot

Usage
plotSampleInfo(spe_object, column2plot, textsize = 3)

Arguments

spe_object A SpatialExperiment object.
column2plot Which columns to plot.
textsize text size.

Value
A ggplot object
Examples

```r
library(ggalluvial)

data("dkd_spe_subset")
plotSampleInfo(dkd_spe_subset, column2plot = c("SlideName", "disease_status", "region"))
```

plotScreePCA
Plot the PCA scree plot.

Description
Plot the PCA scree plot.

Usage

```r
plotScreePCA(
  spe_object,
  dims = ncol(spe_object),
  precomputed = NULL,
  assay = 1,
  bar_color = "black",
  bar_fill = "royalblue",
  bar_width = 0.8,
  point_col = "tomato3",
  line_col = "tomato3",
  point_size = 2
)
```

Arguments

- `spe_object` A SpatialExperiment object.
- `dims` The top n dimensions to be plotted.
- `precomputed` A dimensional reduction results from stats::prcomp. result in reducedDims(object) to plot. Default is NULL, we will compute for you.
- `assay` A numeric or character, specifying the assay to use (for SummarizedExperiment and its derivative classes).
- `bar_color` Color for bar.
- `bar_fill` Fill for bar.
- `bar_width` Bar width.
- `point_col` Color for point.
- `line_col` Color for line.
- `point_size` Point size.
**Value**

A ggplot object.

**Examples**

```r
data("dkd_spe_subset")
plotScreePCA(dkd_spe_subset, dims = 10)
```

---

**prepareSpatialDecon**

*Preparing the inputs for SpatialDecon for doing deconvolution on spatial data*

**Description**

Preparing the inputs for SpatialDecon for doing deconvolution on spatial data

**Usage**

```r
prepareSpatialDecon(
  spe,
  assay2use = "logcounts",
  negProbeName = "NegProbe-WTX",
  pool = NA
)
```

**Arguments**

- **spe**  
  SpatialExperiment object.
- **assay2use**  
  The name of the assay to use. By default is logcounts.
- **negProbeName**  
  The name of the negative probe gene. By default is NegProbe-WTX.
- **pool**  
  A vector indicates the pools of the genes. This is required when there are more than one Negative Probes.

**Value**

A list of two dataframes. The first data.frame is the normalised count, the second data.frame is the background for the data.

**Examples**

```r
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "standR")
countFile <- eh[['EH7364']]  
sampleAnnoFile <- eh[['EH7365']]`
```


```r
spe <- readGeoMx(countFile, sampleAnnoFile, rmNegProbe = FALSE)
out <- prepareSpatialDecon(spe)
```

---

**readGeoMx**  
*Import GeoMX DSP data into a spatial experiment object from file paths*

**Description**

Import GeoMX DSP data into a spatial experiment object from file paths.

**Usage**

```r
readGeoMx(
  countFile,
  sampleAnnoFile,
  featureAnnoFile = NA,
  rmNegProbe = TRUE,
  NegProbeName = "NegProbe-WTX",
  colnames.as.rownames = c("TargetName", "SegmentDisplayName", "TargetName"),
  coord.colnames = c("ROICoordinateX", "ROICoordinateY")
)
```

**Arguments**

- `countFile`: tsv file or a dataframe object. Count matrix, with samples in columns and features/genes in rows. The first column is gene names/ids.
- `sampleAnnoFile`: tsv file or a dataframe object. Sample annotations.
- `rmNegProbe`: Logical. Default is `TRUE`, indicating there are negative probe genes in the data.
- `NegProbeName`: Character. Name of negative probe genes, default is `NegProbe-WTX`.
- `colnames.as.rownames`: Vector of characters, length of 3. Column names used to capture gene names, sample names and gene names in countFile, sampleAnnoFile and featureAnnoFile, respectively.
- `coord.colnames`: Vector of characters, length of 2. Column names used to capture ROI coordinates.

**Value**

A SpatialExperiment object.
Examples

library(ExperimentHub)

eh <- ExperimentHub()
query(eh, "standR")
countFile <- eh["EH7364"]
sampleAnnoFile <- eh["EH7365"]

spe <- readGeoMx(countFile, sampleAnnoFile, rmNegProbe = FALSE)

readGeoMxFromDGE

Import GeoMX DSP data into a spatial experiment object from DGEList object

Description

Import GeoMX DSP data into a spatial experiment object from DGEList object

Usage

readGeoMxFromDGE(dge_object, spatialCoord = NULL)

Arguments

dge_object a DGEList object (created using edgeR::DGEList).
spatialCoord a matrix with coordinates of samples, rowname must be consistent with the col-

Value

A SpatialExperiment object.

Examples

# making a simple DGEList object
ng <- 1000
ns <- 10
Counts <- matrix(rnbinom(ng * ns, mu = 5, size = 2), ng, ns)
rownames(Counts) <- seq(ng)
y <- edgeR::DGEList(counts = Counts, group = rep(seq(2), each = 5))

# transfer into spatial experiment object
coords <- matrix(rnorm(2 * ns), 10, 2)
spe <- readGeoMxFromDGE(dge_object = y, spatialCoord = coords)
spe
**spe2dge**

Transfer SpatialExperiment object into DGEList object for DE analysis

**Usage**

spe2dge(spe)

**Arguments**

- **spe**: SpatialExperiment object.

**Value**

A DGEList.

**Examples**

```r
data("dkd_spe_subset")

spe_tmm <- geomxNorm(dkd_spe_subset, method = "TMM")
dge <- spe2dge(spe_tmm)
```
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