

# Package ‘scGSEA’

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**Type** Package

**Title** Gene Set Enrichment Analysis (GSEA) of Single-Cell RNA-Seq Data

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**Description** The package provides methods for gene set enrichment analysis of single-cell RNA-Seq data, including statistical methods, and visualization functions.

**License** GPL (>= 3)

**Depends** SeqGSEA (>= 1.23.2), SingleCellExperiment, Seurat (>= 3.0.1)

**Imports** Biobase, methods, biomaRt

**biocViews** Sequencing, SingleCell, RNASeq, scRNAseq, GeneSetEnrichment, GeneExpression, ImmunoOncology

**RoxygenNote** 7.3.2

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`add.scGESA.to.obj`      *Add scGESA results to single cell object*

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**Description**

This functions adds scGESA results to single cell object

**Usage**

```
add.scGESA.to.obj(sc.obj, gs.obj)
```

**Value**

a 'SeqGeneSet' object with data added to slot `sc.ES.perm` and `sc.normFlag` reset as TRUE

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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`gene.signature`      *gene signature score*

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**Description**

gene signature score

**Usage**

```
gene.signature(  
  sc.obj,  
  gene.list,  
  permute.time = 1000,  
  mean.bin.num = 6,  
  var.bin.num = 6  
)
```

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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getGSgenelist	<i>Get gene list from a 'SeqGeneSet' object</i>
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**Description**

This function extracts a list of genes in geneSet(s) specified by GeneSetName.

**Usage**

```
getGSgenelist(gs.obj, GeneSetName)
```

**Arguments**

gs.obj	a 'SeqGeneSet' object
GeneSetName	Name(s) of geneSet(s)

**Value**

a vector of gene names

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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scCalES	<i>Calculate ES score</i>
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**Description**

This function is used to calculate ES score for each cell and each gene set

**Usage**

```
scCalES(sc.obj, gs.obj, weighted.type = 0)
```

**Arguments**

sc.obj	either a 'Seurat' or a 'SingleCellExperiment' object
gs.obj	a 'SeqGeneSet' object
weighted.type	the weighted type in GSEA

**Value**

a 'SeqGeneSet' object with data added to slot sc.ES

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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scCalSignif	<i>Calculate ES significance</i>
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**Description**

This function calculates ES significance, including p-value, FDR, and FWER

**Usage**

```
scCalSignif(gs.obj)
```

**Value**

a ‘SeqGeneSet’ object with data added to slots sc.pval, sc.FDR, and sc.FWER

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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scESnorm	<i>ES score normalizaton</i>
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**Description**

This function calculates ES scores for a permuted data sets, which is then used for normalization of the observed ES scores

**Usage**

```
scESnorm(
  sc.obj,
  gs.obj,
  weighted.type = 0,
  perm.time = ncol(sc.obj@scale.data),
  seed = 1234
)
```

**Arguments**

sc.obj	either a ‘Seurat’ or a ‘SingleCellExperiment’ object
gs.obj	a ‘SeqGeneSet’ object
weighted.type	the weighted type in GSEA
perm.time	the number of permutations, with default value the number of cells
seed	the seed for random sampling

**Value**

a 'SeqGeneSet' object with data added to slot sc.ES.perm and sc.normFlag reset as TRUE

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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scESPlot

*Plot showing (normalized) enrichment scores of a specified gene set for each cell in low-dimension, in a single-cell experiment*

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**Description**

The function is to generate a scatter plot of enrichment scores of a specified gene set for each cell in low-dimension, in a single-cell experiment.

**Usage**

```
scESPlot(sc.obj, gs.obj, gene.set=gs.obj@GSNames, cols.use = c("blue", "green", "yellow", "red"), redu
```

**Arguments**

sc.obj

gs.obj

**Author(s)**

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**See Also**

[GSEnrichAnalyze](#), [scESPlotGeneSet](#)

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scGSEA.scale.data

*Scale gene expression for scGSEA*

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**Description**

This function normalizes single cell gene expression levels across cells for each gene.

**Usage**

```
scGSEA.scale.data(obj, gene_expr_frac = 0.1, kNN = 21)
```

**Arguments**

obj                    either a 'Seurat' or a 'SingleCellExperiment' object

gene\_expr\_frac       filtering out genes if the non-zero fraction less than this number

kNN                   the k nearest neighbors for data smoothing/denoising.

**Value**

the obj with added data in slot 'assay' of 'Seurat' and 'metadata' of 'SingleCellExperiment'

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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scLoadGS

*Load and store gene sets for scGSEA*


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**Description**

This function loads gene sets and creates a 'SeqGeneSet' object

**Usage**

```
scLoadGS(
  geneset.file,
  sc.obj,
  geneID.type = c("gene.symbol", "ensembl"),
  use.HVG = FALSE,
  genesetsize.min = 5,
  genesetsize.max = 1000
)
```

**Arguments**

geneset.file        the file path and name of GeneSet in .gmt format

sc.obj              either a 'Seurat' or a 'SingleCellExperiment' object

geneID.type        the gene ID type, currently support gene symbol and Ensembl

use.HVG            logical, using highly variable genes only or not

genesetsize.min    minimum number of genes in a gene set, gene set with smaller than this number of genes will be excluded

genesetsize.max    maximum number of genes in a gene set, gene set with greater than this number of genes will be excluded

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**Value**

a 'SeqGeneSet' object

**Author(s)**

Xi Wang (xi.wang at dkfz.de)

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