Package ‘signifinder’

May 9, 2024

Type Package

Title Collection and implementation of public transcriptional cancer signatures

Version 1.6.0

Description signifinder is an R package for computing and exploring a compendium of tumor signatures. It allows to compute a variety of signatures, based on gene expression values, and return single-sample scores. Currently, signifinder contains more than 60 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

License AGPL-3

biocViews GeneExpression, GeneTarget, ImmunoOncology, BiomedicalInformatics, RNASeq, Microarray, ReportWriting, Visualization, SingleCell, Spatial, GeneSignaling

Imports AnnotationDbi, BiocGenerics, ComplexHeatmap, consensusOV, cowplot, DGEnobj.utils, dplyr, ensembldb, ggplot2, ggridges, GSVA, IRanges, magrittr, matrixStats, maxstat, methods, openair, org.Hs.eg.db, patchwork, RColorBrewer, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, sparrow, SpatialExperiment, stats, SummarizedExperiment, survival, survminer, viridis

Encoding UTF-8

RoxygenNote 7.3.1

Depends R (>= 4.3.0)

LazyData false

Suggests BiocStyle, edgeR, grid, kableExtra, knitr, limma, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

BugReports https://github.com/CaluraLab/signifinder/issues

URL https://github.com/CaluraLab/signifinder
git_url https://git.bioconductor.org/packages/signifinder

Contents

signifinder-package ........................................... 3
ADOSign ...................................................... 4
APMSign ....................................................... 5
ASCSign ......................................................... 6
autophagySign ................................................ 7
availableSignatures .......................................... 8
breastStateSign .............................................. 9
cellCycleSign ................................................ 10
chemokineSign ............................................... 11
CINSign ......................................................... 12
CISSign ......................................................... 13
CombinedSign ................................................ 13
consensusOVSign ............................................. 14
correlationSignPlot ......................................... 15
COXISSign ...................................................... 16
DNArepSign .................................................... 17
ECMSign ......................................................... 18
EMTSign ......................................................... 18
evaluationSignPlot .......................................... 20
expandedImmuneSign ........................................ 21
ferroptosisSign ............................................... 21
geneHeatmapSignPlot ....................................... 22
getSignGenes ................................................. 24
glioCellStateSign ............................................ 24
glycolysisSign ............................................... 25
heatmapSignPlot ............................................. 26
HRDSSign ...................................................... 27
hypoxiaSign .................................................. 28
ICBResponseSign ............................................ 29
IFNSign ......................................................... 30
immuneCytSign ............................................... 30
immunoScoreSign ............................................ 31
IPRESSign ....................................................... 32
**Description**

signifinder is an R package for computing and exploring a compendium of tumor signatures. It allows to compute a variety of signatures, based on gene expression values, and return single-sample scores. Currently, signifinder contains more than 60 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

**Author(s)**

**Maintainer:** Stefania Pirrotta <stefania.pirrotta@phd.unipd.it> (ORCID)

Authors:

- Enrica Calura <enrica.calura@unipd.it> (ORCID)
See Also

Useful links:

- [https://github.com/CaluraLab/signifinder](https://github.com/CaluraLab/signifinder)
- Report bugs at [https://github.com/CaluraLab/signifinder/issues](https://github.com/CaluraLab/signifinder/issues)

---

ADOSign  
Adenosine Signaling Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

```
ADOSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```

Arguments

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay`: integer scalar or string indicating which assay of dataset to use.
- `...`: other arguments passed on to the `gsvaParam` function.

Value

If `dataset` is a `SummarizedExperiment` object, then scores are added in the `colData` section. If `dataset` is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```
data(ovse)
ADOSign(dataset = ovse)
```
**APMSign**

**Antigen Processing Machinery Signature**

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
APMSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Wang",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)
```

**Arguments**

- `dataset` Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype` character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `inputType` character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- `author` character string saying the first author of the signature publication. Check it in `availableSignatures`.
- `whichAssay` integer scalar or string indicating which assay of dataset to use.
- `hgReference` character string saying the human reference genome. Either one of "hg19" or "hg38".
- `...` other arguments passed on to the `gsvaParam` function.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.
Examples

```r
data(ovse)
APMSign(dataset = ovse)
```

---

**ASCSign**

*Adult Stem Cell Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
ASCSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset` Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype` character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay` integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
ASCSign(dataset = ovse)
```
autophagySign

autophagySign  Autophagy Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

autophagySign(
  dataset,
  nametype = "SYMBOL",
  author = "Xu",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

author  character string saying the first author of the signature publication. Check it in availableSignatures.

whichAssay  integer scalar or string indicating which assay of dataset to use.

hgReference  character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
autophagySign(dataset = ovse)
availableSignatures  

Description

It returns a table with all the information of the signatures collected in signifinder.

Usage

```r
availableSignatures(
  tumor = NULL,
  tissue = NULL,
  topic = NULL,
  requiredInput = NULL,
  description = TRUE
)
```

Arguments

tumor character vector saying the type of tumors for which signatures are developed. Used to filter the signatures in the table.
tissue character vector saying the type of tissues for which signatures are developed. Used to filter the signatures in the table.
topic character vector saying the signature topics. Used to filter the signatures in the table.
requiredInput character string saying the type of data required in input by the signature. Either one of "microarray", "rnaseq" or "sc". Used to filter the signatures in the table.
description logical. If TRUE it shows the signature's description.

Value

A data frame with 12 variables:

- `signature` name of the signature
- `scoreLabel` label of the signature when added inside colData section
- `functionName` name of the function to use to compute the signature
- `topic` main cancer topic of the signature
- `tumor` tumor type for which the signature was developed
- `tissue` tumor tissue for which the signature was developed
- `cellType` cell type for which the signature was developed
- `requiredInput` type of data with which the signature was developed
- `transformationStep` data transformation step performed inside the function starting from the user’s 'normArray' or 'normCounts' data
- `author` first author of the work in which the signature is described
- `reference` reference of the work
- `description` signature description and how to evaluate its score ...
breastStateSign

Examples

availableSignatures()

breastStateSign  Breast Cancer Cellular States Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

breastStateSign(  
dataset,  
nametype = "SYMBOL",  
whichAssay = "norm_expr",  
isMalignant = NULL,  
hgReference = "hg38"  
)

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay  integer scalar or string indicating which assay of dataset to use.

isMalignant  logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.

hgReference  character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
cellCycleSign

Cell-cycle Signature classifier

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

```r
cellCycleSign(
  dataset,
  nametype = "SYMBOL",
  author = "Lundberg",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **author**: character string saying the first author of the signature publication. Check it in availableSignatures.
- **inputType**: character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

```r
data(ovse)
cellCycleSign(dataset = ovse, inputType = "rnaseq")
```
chemokineSign

chemokineSign  Chemokine Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

```r
chemokineSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

inputType  character string saying the type of data you are using. Either one of "microarray" or "rnaseq".

whichAssay  integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
chemokineSign(dataset = ovse, inputType = "rnaseq")
```
**CINSign**

**Chromosomal instability Signature**

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
cinSign(
    dataset,
    nametype = "SYMBOL",
    inputType = "microarray",
    whichAssay = "norm_expr"
)
```

**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **inputType**: character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
cinSign(dataset = ovse, inputType = "rnaseq")```
**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
CISSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset` Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype` character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay` integer scalar or string indicating which assay of dataset to use.

**Value**

If `dataset` is a `SummarizedExperiment` object, then scores are added in the `colData` section. If `dataset` is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
CISSign(dataset = ovse)
```

---

**CombinedSign**

**EMT-Inflammation Combined Signature**

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`. 

---

**CISSign**

**CIS (carcinoma-in situ) Signature**
Usage

```
CombinedSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  weighted = FALSE
)
```

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay integer scalar or string indicating which assay of dataset to use.

hgReference character string saying the human reference genome. Either one of "hg19" or "hg38".

weighted logical value, saying whether the score should be calculated with or without weights.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```
data(ovse)
CombinedSign(dataset = ovse)
```

---

**consensusOVSign**  

**ConsensusOV Signature**

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

```
consensusOVSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```
correlationSignPlot

Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.
- **...**: optional parameters to be passed to `get.subtypes`.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
consensusOVSign(dataset = ovse)
```

correlationSignPlot `Correlation Plot`

Description

Given multiple signatures, the function plots signatures correlations.

Usage

```r
correlationSignPlot(
  data,
  whichSign = NULL,
  sampleAnnot = NULL,
  selectByAnnot = NULL
)
```

Arguments

- **data**: an object of type `SummarizedExperiment`. Output of the signatures functions.
- **whichSign**: character vector saying the signatures to plot. If not specified, all the signatures inside data will be plotted. Other signatures not computed with signifinder can be added in the vector if they are also included in the colData section of data.
- **sampleAnnot**: character vector containing samples' annotations.
- **selectByAnnot**: character string saying the subgroup from 'sampleAnnot' used to compute the correlation plot.
Value

An object of class "openair".

Examples

data(ovse)
correlationSignPlot(data = ovse)

COXISSign  COX-2-associated Inflammatory Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

COXISSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay  integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
COXISSign(dataset = ovse)
DNArepSign

DNA Repair Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

DNArepSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

inputType character string saying the type of data you are using. Either one of "microarray" or "rnaseq".

whichAssay integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
DNArepSign(dataset = ovse, inputType = "rnaseq")
ECMSign  
*Extracellular Matrix Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
ECMSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```

**Arguments**

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay`: integer scalar or string indicating which assay of dataset to use.
- `...`: other arguments passed on to the `ssgseaParam` function.

**Value**

If `dataset` is a `SummarizedExperiment` object, then scores are added in the `colData` section. If `dataset` is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
ECMSign(dataset = ovse)
```

EMTSign  
*Epithelial-Mesenchymal Transition Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.
EMTSign

Usage

EMTSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Miow",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)

Arguments

- **dataset** Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.

- **nametype** character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **inputType** character string saying the type of data you are using. Either one of "microarray" or "rnaseq".

- **author** character string saying the first author of the signature publication. Check it in `availableSignatures`.

- **whichAssay** integer scalar or string indicating which assay of dataset to use.

- **hgReference** character string saying the human reference genome. Either one of "hg19" or "hg38".

- **...** other arguments passed on to the `ssgseaParam` function.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

data(ovse)
EMTSign(dataset = ovse, inputType = "rnaseq")
evaluationSignPlot  Evaluation Plot

Description

A multipanel plot that shows: (i) a value of the goodness of a signature for the user’s dataset. This is a combination of the parameters shown in the other panels; (ii) the percentage of genes from the signature gene list that are actually available in the dataset; (iii) the percentage of zero values in the signature genes, for each sample; (iv) the correlation between signature scores and the sample total read counts; (v) the correlation between signature scores and the percentage of the sample total zero values.

Usage

evaluationSignPlot(
    data, 
    nametype = "SYMBOL", 
    whichSign = NULL, 
    whichAssay = "norm_expr", 
    sampleAnnot = NULL, 
    selectByAnnot = NULL
)

Arguments

data an object of type SummarizedExperiment. Output of the signatures functions.
nametype character string saying the type of gene name ID (row names in data). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichSign character vector saying the signatures to plot. These must be signatures computed with signifier. If not specified, all the signatures inside data will be plotted.
whichAssay integer scalar or string indicating which assay of data to use.
sampleAnnot character vector containing samples’ annotations.
selectByAnnot character string saying the subgroup from ‘sampleAnnot’ used to compute the evaluation plot.

Value

A ggplot object.

Examples

data(ovse)
evaluationSignPlot(data = ovse)
expandedImmuneSign

**expansedImmuneSign**  
*ExpandedImmune Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function **availableSignatures**.

**Usage**

expandedImmuneSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")

**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type **SummarizedExperiment**, **SingleCellExperiment** or **SpatialExperiment** where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a **SummarizedExperiment** object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a **SummarizedExperiment** object is created in which scores are added in the colData section.

**Examples**

```r
data(ovse)
expandedImmuneSign(dataset = ovse)
```

---

ferroptosisSign

**Ferroptosis Signature**

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function **availableSignatures**.
Usage

```r
ferroptosisSign(
    dataset,
    nametype = "SYMBOL",
    inputType = "rnaseq",
    author = "Ye",
    whichAssay = "norm_expr",
    hgReference = "hg38"
)
```

Arguments

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.
- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `inputType`: character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- `author`: character string saying the first author of the signature publication. Check it in `availableSignatures`.
- `whichAssay`: integer scalar or string indicating which assay of dataset to use.
- `hgReference`: character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
ferroptosisSign(dataset = ovse)
```

Description

Given one or multiple signatures, the function returns a heatmap of the expression values of the genes included in each of them.
geneHeatmapSignPlot

Usage

geneHeatmapSignPlot(
  data,
  nametype = "SYMBOL",
  whichSign,
  logCount = FALSE,
  whichAssay = "norm_expr",
  splitBySign = FALSE,
  sampleAnnot = NULL,
  splitBySampleAnnot = FALSE,
  ...
)

Arguments

data an object of type SummarizedExperiment. Output of the signatures functions.
nametype character string saying the type of gene name ID (row names in data). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichSign character vector saying the signatures to plot. These must be signatures computed with signifinder.
logCount logical. If TRUE it shows logarithms of expression values.
whichAssay integer scalar or string indicating which assay of data to use.
splitBySign logical. If TRUE it splits rows by signatures.
sampleAnnot vector containing samples' annotations.
splitBySampleAnnot logical. If TRUE it splits columns by samples' annotations.
...
other parameters specific of the function Heatmap.

Value

A Heatmap-class object.

Examples

data(ovse)
geneHeatmapSignPlot(data = ovse, whichSign = "Ferroptosis_Ye")
getSignGenes | Get Signature Gene List

Description
This function returns the list of genes of a signature.

Usage
getSignGenes(whichSign)

Arguments
whichSign | name of the signature. The names are those in column 'signature' from the table which is obtained by availableSignatures.

Value
A dataframe object with "SYMBOL" in the first column. Some signatures have also additional columns: "coeff" for coefficients that weigh the gene contributions; "class" for a classification that divides the signature in two or more groups. Few signatures have other specific columns.

Examples
getSignGenes("EMT_Miow")

glioCellStateSign | Glioblastoma Cellular States Signature

Description
This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage
glioCellStateSign(
dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  isMalignant = NULL,
  hgReference = "hg38"
)
**glycolysisSign**

**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.
- **nametype**: Character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **whichAssay**: Integer scalar or string indicating which assay of dataset to use.
- **isMalignant**: Logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.
- **hgReference**: Character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
glycolysisSign
```

---

**glycolysisSign** *Glycolysis Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
glycolysisSign(
  dataset,
  nametype = "SYMBOL",
  author = "Zhang",
  whichAssay = "norm_expr"
)
```
**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called `norm_expr`.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **author**: character string saying the first author of the signature publication. Check it in `availableSignatures`.

- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
glycolysisSign(dataset = ovse)
```

---

**Description**

Given one or multiple signatures, the function returns a heatmap of scores. Since each signature has its own method to compute the score then to plot several signatures together the scores are transformed into z-score, individually for each signature.

**Usage**

```r
heatmapSignPlot(
  data,
  whichSign = NULL,
  clusterBySign = NULL,
  sampleAnnot = NULL,
  signAnnot = NULL,
  splitBySampleAnnot = FALSE,
  ...
)
```
HRDSSign

Arguments

data an object of type SummarizedExperiment. Output of the signatures functions.
whichSign character vector saying the signatures to plot. If not specified, all the signatures inside data will be plotted. Other signatures not computed with signifinder can be added in the vector if they are also included in the colData section of data.
clusterBySign character vector saying one or more signatures to use to cluster columns.
sampleAnnot vector containing samples’ annotations.
signAnnot character vector of signature’s annotations. One or more between: "signature", "topic", "tumor", "tissue".
splitBySampleAnnot logical. If TRUE it splits columns by samples’ annotations.
...
other parameters specific of the function Heatmap.

Value

A Heatmap-class object.

Examples

data(ovse)
heatmapSignPlot(data = ovse)

---

HRDSSign Homologous Recombination Deficiency Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

HRDSSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.
nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay integer scalar or string indicating which assay of dataset to use.
Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

data(ovse)
HRDSSign(dataset = ovse)

**hypoxiaSign**

_Hypoxia Signature_

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
hypoxiaSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

**Arguments**

- **dataset** Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype** character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **inputType** character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- **whichAssay** integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.
ICBResponseSign

**Examples**

```r
data(ovse)
hypoxiaSign(dataset = ovse, inputType = "rnaseq")
```

---

<table>
<thead>
<tr>
<th>ICBResponseSign</th>
<th>ICB Response Signature</th>
</tr>
</thead>
</table>

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
ICBResponseSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay`: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
ICBResponseSign(dataset = ovse)
```
### Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

### Usage

```r
IFNSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

### Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

### Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

### Examples

```r
data(ovse)
IFNSign(dataset = ovse)
```

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`. 

---
Usage

```
immuneCytSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Rooney",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond
to genes and columns correspond to samples. Alternatively, an object of type
SummarizedExperiment, SingleCellExperiment or SpatialExperiment where
the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either
one of "SYMBOL", "ENTREZID" or "ENSEMBL".

inputType  character string saying the type of data you are using. Either one of "microarray"
or "rnaseq".

author  character string saying the first author of the signature publication. Check it in
availableSignatures.

whichAssay  integer scalar or string indicating which assay of dataset to use.

hgReference  character string saying the human reference genome. Either one of "hg19" or
"hg38".

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If
dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores
are added in the colData section.

Examples

```
data(ovse)
immuneCytSign(dataset = ovse, inputType = "rnaseq")
```

---

### immunoScoreSign

**Immunogenic Signature**

Description

This signature is computed accordingly to the reference paper, to have more details explore the
function availableSignatures.
Usage

```r
immunoScoreSign(
  dataset,
  nametype = "SYMBOL",
  author = "Hao",
  inputType = "rnaseq",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **author**: character string saying the first author of the signature publication. Check it in `availableSignatures`.
- **inputType**: character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.
- **hgReference**: character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
immunoScoreSign(dataset = ovse)
```

---

**IPRESSign**  
**IPRES Signature**

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`. 
Usage

IPRESSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.
nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay integer scalar or string indicating which assay of dataset to use.
hgReference character string saying the human reference genome. Either one of "hg19" or "hg38".
... other arguments passed on to the ssgseaParam function.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
IPRESSign(dataset = ovse)

<table>
<thead>
<tr>
<th>IPSOVSign</th>
<th>IPSOV Signature</th>
</tr>
</thead>
</table>

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.
Usage

IPSOVSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr",
  ...
)

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

inputType character string saying the type of data you are using. Either one of "microarray" or "rnaseq".

whichAssay integer scalar or string indicating which assay of dataset to use.

... other arguments passed on to the ssgseaParam function.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
IPSOVSign(dataset = ovse)

IPSSign

<table>
<thead>
<tr>
<th>ImmunoPhenoScore Signature</th>
</tr>
</thead>
</table>

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.
IRGSign

Usage

IRGSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)

Arguments

dataset  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay  integer scalar or string indicating which assay of dataset to use.

hgReference  character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
IPSSign(dataset = ovse)

IRGSign

Immune-Related Genes Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

IRGSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
IRGSign(dataset = ovse)
```

---

**ISCSign**

*Adult Intestinal Stem Cell Signature*

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

```r
ISCSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
lipidMetabolismSign

inputType character string saying the type of data you are using. Either one of "microarray" or "rnaseq".

whichAssay integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
lipidMetabolismSign(dataset = ovse)

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

lipidMetabolismSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
lipidMetabolismSign(dataset = ovse)
**LRRC15CAFSign**  
*LRRC15 CAF Signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
LRRC15CAFSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- `whichAssay`: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
LRRC15CAFSign(dataset = ovse)
```

---

**matrisomeSign**  
*Core Matrisome Gene signature*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
matrisomeSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```
**melStateSign**

**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
matisomeSign(dataset = ovse)
```

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
melStateSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  isMalignant = NULL,
  hgReference = "hg38"
)
```

**Arguments**

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
**MITFlowPTENnegSign**

integer scalar or string indicating which assay of dataset to use.

logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.

character string saying the human reference genome. Either one of "hg19" or "hg38".

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

```r
MITFlowPTENnegSign
```

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

**Usage**

```r
MITFlowPTENnegSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- `whichAssay`: integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.
**Examples**

```r
data(ovse)
MITFlowPTENnegSign(dataset = ovse)
```

---

### mitoticIndexSign  

*Mitotic Index*

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
mitoticIndexSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

- `dataset`  
  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- `nametype`  
  Character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- `whichAssay`  
  Integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
mitoticIndexSign(dataset = ovse)
```
# Melanocytic Plasticity Signature

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

## Usage

```r
MPSSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

## Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.
- **hgReference**: character string saying the human reference genome. Either one of "hg19" or "hg38".

## Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

## Examples

```r
data(ovse)
MPSSign(dataset = ovse)
```
**multipleSign**

**Multiple Signatures Computation**

### Description

This function computes all the signatures for a specific 'inputType'. Further, it is possible to select specific signatures setting the 'tumor', the 'tissue' and/or the 'topic'.

### Usage

```r
multipleSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "rnaseq",
  whichAssay = "norm_expr",
  whichSign = NULL,
  tumor = NULL,
  tissue = NULL,
  topic = NULL,
  ...
)
```

### Arguments

- **dataset**: Expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment`.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **inputType**: character vector saying the type of data you are using. When working with bulk data this should be either one of "microarray" or "rnaseq". When working with single-cell data and spatial transcriptomics data this could be "sc" to compute only signatures developed by single-cell data or c("rnaseq","sc") to compute all the signatures.

- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

- **whichSign**: character vector saying the signatures to compute.

- **tumor**: character vector saying the tumor types. Signatures from that tumors will be computed (this can also be "pan-cancer").

- **tissue**: character vector saying the tumor tissues. Signatures from that tissues will be computed (this can also be "pan-tissue").

- **topic**: character vector saying signatures topics. Signatures having that topics will be computed.

- **...**: other arguments passed on to the signature functions.
Value

A SummarizedExperiment object in which the signatures’ scores are added in the colData section.

Examples

data(ovse)
multipleSign(dataset = ovse)
multipleSign(dataset = ovse, tissue = "ovary")

Description

Given signatures’ scores, it returns a scatterplot of samples’ scores and a barplot of the density distribution of samples’ scores.

Usage

oneSignPlot(data, whichSign, statistics = NULL)

Arguments

data an object of type SummarizedExperiment. Output of the signatures functions.

whichSign character string saying the signature to plot. This must be a signature computed with signifinder.

statistics character string saying the statistics to be plotted in the graph. Either one of "mean", "median" or "quantiles".

Value

A ggplot object.

Examples

data(ovse)
oneSignPlot(data = ovse, whichSign = "Ferroptosis_Ye")
Example expression data.

Description

This is an example dataset containing gene expression values (in normalized counts, TPM, CPM, and FPKM) of 40 ovarian cancer (OVC) patients extracted from the Cancer Genome Atlas (TCGA) database. This dataset should be used only with example purpose. RNA sequencing OVC data were retrieved using curatedTCGAData package. Data were then normalized with the betweenLaneNormalization function. To lighten the dataset, the consensusOVSign function was computed, which return 4 different scores, one for each OVC subtype (Chen et al, 2018, Clinical Cancer Research) and the 10 samples with the highest scores were selected for each subgroup. Further, only the genes used for the signatures computation were kept. Finally, all the signatures available in signifinder for OVC plus all the pan-cancer signatures were computed. Further details in signifinder/inst/scripts/howToGenerateOvse.Rmd.

Usage

data(ovse)

Format

An object of class SummarizedExperiment with 3180 rows and 40 columns.

---

PassONSign  

passON Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

PassONSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)

---

ovse
Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

- **whichAssay**: integer scalar or string indicating which assay of dataset to use.

- **hgReference**: character string saying the human reference genome. Either one of "hg19" or "hg38".

- **...**: other arguments passed on to the `ssgseaParam` function.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
PassOnSign(dataset = ovse)
```

---

**pyroptosisSign**  
*Pyroptosis Signature*

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

```r
pyroptosisSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "rnaseq",
  author = "Ye",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```
Arguments

- **dataset**: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- **nametype**: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- **inputType**: character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- **author**: character string saying the first author of the signature publication. Check it in `availableSignatures`.
- **whichAssay**: integer scalar or string indicating which assay of dataset to use.
- **hgReference**: character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
pyroptosisSign(dataset = ovse)
```

### Description

Given multiple signatures, the function plots scores density distribution.

### Usage

```r
ridgelineSignPlot(
  data,  # Required
  whichSign = NULL,
  groupByAnnot = NULL,
  selectByAnnot = NULL,
  ...  # Additional arguments
)
```
Arguments

data
whichSign
groupByAnnot
selectByAnnot
... other parameters specific of the functions `geom_density_ridges` and `geom_density_ridges_gradient`.

Value

A `ggplot` object.

Examples

data(ovse)
ridgelineSignPlot(data = ovse)

---

stemCellCD49fSign  

CD49fHi Basal Stem Cell Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

stemCellCD49fSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")

Arguments

dataset

Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

nametype

character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay

integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.
survivalSignPlot

Examples

data(ovse)
stemCellCD49fSign(dataset = ovse)

survivalSignPlot       Survival Plot

Description

Given a signature and samples’ survival data, the function plots survival curves for that signature. This is a wrapper around `survfit`, that creates survival curves from a model formula. Here, the response variable in the formula is a survival object created by `Surv`. Survival curves are then passed to the `ggsurvplot` function. For details about the statistics see `survfit` and `Surv`.

Usage

```
survivalSignPlot(
  data,
  survData,
  whichSign,
  cutpoint = "mean",
  sampleAnnot = NULL,
  selectByAnnot = NULL
)
```

Arguments

data an object of type SummarizedExperiment. Output of the signatures functions.
survData a dataframe with samples on rows and two columns. The first column holds survival data of time, indicating the follow up times; the second holds data of the survival status, normally 0=alive and 1=dead. For further details check `Surv` function.
whichSign character string saying the signature to plot. This must be a signature computed with signifinder.
cutpoint a character string (one of: "median", "mean" and "optimal") or a numeric value, which divide samples between high scores and low scores. The function computes the threshold with the method indicated or employs the values directly supplied by the user. Based on that number, it divides samples. In case of "optimal" the `maxstat.test` function will be used to estimate the cutpoint which separates samples best.
sampleAnnot a categorical vector containing samples’ annotations named with samples names equal to the row names used in `survData`.
selectByAnnot character string saying the subgroup from `sampleAnnot` used to compute the survival analysis.
Value

A `ggplot` object.

Examples

data(ovse)
mysurvData <- cbind(ovse$os, ovse$status)
rownames(mysurvData) <- rownames(SummarizedExperiment::colData(ovse))
survivalSignPlot(
  data = ovse,
  survData = mysurvData,
  whichSign = "Ferroptosis_Ye"
)

---

**TGFBSign**

*Pan-Fibroblast TGFB Response Signature*

Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

`TGFBSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")`

Arguments

dataset Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.

nametype character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

whichAssay integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

data(ovse)
TGFBSign(dataset = ovse)
TinflamSign

Description

This signature is computed accordingly to the reference paper, to have more details explore the function availableSignatures.

Usage

TinflamSign(
  dataset,
  nametype = "SYMBOL",
  author = "Ayers",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)

Arguments

dataset
  Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type SummarizedExperiment, SingleCellExperiment or SpatialExperiment where the normalized expression values should be in an assay called 'norm_expr'.

nametype
  character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

author
  character string saying the first author of the signature publication. Check it in availableSignatures.

whichAssay
  integer scalar or string indicating which assay of dataset to use.

hgReference
  character string saying the human reference genome. Either one of "hg19" or "hg38".

Value

If dataset is a SummarizedExperiment object, then scores are added in the colData section. If dataset is a data frame or a matrix, then a SummarizedExperiment object is created in which scores are added in the colData section.

Examples

data(ovse)
TinflamSign(dataset = ovse)
**TLSSign**

**Tertiary Lymphoid Structures (TLS) Signature**

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

**Usage**

```r
tlssign(  
  dataset,  
  nametype = "SYMBOL",  
  inputType = "rnaseq",  
  whichAssay = "norm_expr"
)
```

**Arguments**

- `dataset` Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype` character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `inputType` character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
- `whichAssay` integer scalar or string indicating which assay of dataset to use.

**Value**

If `dataset` is a `SummarizedExperiment` object, then scores are added in the `colData` section. If `dataset` is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

**Examples**

```r
data(ovse)
TLSSign(dataset = ovse)
```
Description

This signature is computed accordingly to the reference paper, to have more details explore the function `availableSignatures`.

Usage

`VEGFSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")`

Arguments

- `dataset`: Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type `SummarizedExperiment`, `SingleCellExperiment` or `SpatialExperiment` where the normalized expression values should be in an assay called 'norm_expr'.
- `nametype`: character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
- `whichAssay`: integer scalar or string indicating which assay of dataset to use.

Value

If dataset is a `SummarizedExperiment` object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a `SummarizedExperiment` object is created in which scores are added in the `colData` section.

Examples

```r
data(ovse)
VEGFSign(dataset = ovse)
```
Index

* datasets
  * ovse, 45

* internal
  * signifinder-package, 3

ADOSign, 4
APMSign, 5
ASCSSign, 6
autophagySign, 7
availableSignatures, 4–7, 8, 9–14, 16–19, 21, 22, 24–42, 45–48, 50–53
betweenLaneNormalization, 45
breastStateSign, 9
cellCycleSign, 10
chemokineSign, 11
CINSign, 12
CISSign, 13
colData, 4–7, 9–19, 21, 22, 25, 26, 28–42, 44, 46–48, 50–53
CombinedSign, 13
consensusOVSign, 14, 45
correlationSignPlot, 15
COXISSign, 16
curatedTCGADATA, 45
DNArepSign, 17
ECMSign, 18
EMTSign, 18
evaluationSignPlot, 20
expandedImmuneSign, 21
ferroptosisSign, 21
geneHeatmapSignPlot, 22
genos_besides_ridges, 48
genos_besides_ridges_gradient, 48
get.subtypes, 15
getSignGenes, 24
ggplot, 20, 44, 48, 50
ggsurvplot, 49
gliocellStateSign, 24
glycolysisSign, 25
gsvaParam, 4, 5
Heatmap, 23, 27
heatmapSignPlot, 26
HRDSSign, 27
hypoxiaSign, 28
ICBResponseSign, 29
IFNSign, 30
immuneCytSign, 30
immunoScoreSign, 31
IPRESSign, 32
IPSOVSign, 33
IPSSign, 34
IRGSign, 35
ISCSign, 36
lipidMetabolismSign, 37
LRRC15CAFSign, 38
matrisomeSign, 38
maxstat.test, 49
melStateSign, 39
MITFlowPTENnegSign, 40
mitoticIndexSign, 41
MPSSign, 42
multipleSign, 43
oneSignPlot, 44
ovse, 45
PassONSsign, 45
pyroptosisSign, 46
ridgelineSignPlot, 47
signifinder (signifinder-package), 3
signifinder-package, 3
SingleCellExperiment, 4–7, 9–19, 21, 22, 25–43, 46–48, 50–53
SpatialExperiment, 4–7, 9–19, 21, 22, 25–43, 46–48, 50–53
ssgseaParam, 18, 19, 33, 34, 46
stemCellCD49fSign, 48
SummarizedExperiment, 4–7, 9–23, 25–44, 46–53
Surv, 49
survfit, 49
survivalSignPlot, 49

TGFBSign, 50
TinflamSign, 51
TLSSign, 52

VEGFSign, 53