Package ‘signifinder’

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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 46 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

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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 46 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

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See Also

Useful links:

- https://github.com/CaluraLab/signifinder
- Report bugs at https://github.com/CaluraLab/signifinder/issues
ASCSign  
**Adult Stem Cell Signature**

**Description**

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

**Usage**

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  
**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

```r
data(ovse)
autophagySign(dataset = ovse)
```
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" or "rnaseq". Used to filter the signatures in the table.
description logical. If TRUE it shows the signature’s description.

Value

A data frame with 47 rows and 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 ...

Examples

```r
availableSignatures()
```
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  

Chemokine Signature

Description

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

Usage

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

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

_Cromosomal 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")
```
**CISSign**

*CIS (carcinoma-in situ) Signature*

**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)
```

**consensusOVSign**

*ConsensusOV Signature*

**Description**

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

**Usage**

```r
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.
DNArepSign

Description

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

Usage

```r
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.
ECMSign

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

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 gsva 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)
ECMSign(dataset = ovse)
EMTSign

**Description**

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

**Usage**

```r
EMTSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Miow",
  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".
- `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.
- `...` other arguments passed on to the `gsva` 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)
EMTSign(dataset = ovse, inputType = "rnaseq")
```
Description

Given multiple signatures, it returns a multipanel plot that shows: (i) the percentage of genes from the signature gene list that are actually available in the dataset; (ii) the log2 average expressions of these genes; (iii) the percentage of zero values in them; (iv) the correlation between scores and total read counts; (v) the correlation between scores and the percentage of 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 signifinder. 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  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

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

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

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.

Value

A Heatmap-class object.

Examples

data(ovse)
geneHeatmapSignPlot(data = ovse, whichSign = "Ferroptosis_Ye"
**Glioblastoma Cellular States Signature**

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

**Usage**

```r
glioCellStateSign(
  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)
```
glycolysisSign

Glycolysis Signature

Description

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

Usage

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

data(ovse)
glycolysisSign(dataset = ovse)
heatmapSignPlot

**Global Heatmap of Signatures’ scores.**

**Description**

Given one or multiple signatures, the function returns a heatmap of scores.

**Usage**

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

**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**

```r
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.

Examples

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

---

### IFNSign

#### IFN-gamma Signature

**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")
```
**immuneCytSign**

**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)
```

---

**immuneCytSign**

**Immune Cytolytic Activity Signature**

**Description**

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

**Usage**

```r
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'.

immunoScoreSign

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

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)
```

Description

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

Usage

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

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 `gsva` 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)
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**

```r
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 `gsva` 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)
IPSSign(dataset = ovse)
```

**Description**

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

**Usage**

```r
IPSSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```
**ISCSign**

**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)
IPSSign(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'.

---
**li**pidMetabolismSign

- **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)
ISCSSign(dataset = ovse, inputType = "rnaseq")
```

**Description**

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

**Usage**

```r
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)

matrisomeSign | Core Matrisome Gene signature

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

Usage
matrisomeSign(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)
matrisomeSign(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)
motiticIndexSign(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'.

```r
multipleSign
```
multipleSign

Usage

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 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.

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")
oneSignPlot  

Scatterplot for a single signature

Description
Given signatures’ scores, it returns a scatterplot of samples’ scores and a barplot of the density distributions 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")

ovse  

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 curatedTCGADataset 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.
PassONSign

Usage

data(ovse)

Format

An object of class SummarizedExperiment with 1456 rows and 40 columns.

Value

An object of class SummarizedExperiment.

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",
  ...
)

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 gsva 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)
PassONSign(dataset = ovse)

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.
Example

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

---

**ridgelineSignPlot**  
*Ridgeline Plot*

**Description**

Given multiple signatures, the function plots densities scores.

**Usage**

```r
ridgelineSignPlot(
  data, 
  whichSign = NULL, 
  groupByAnnot = 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.
- **groupByAnnot**
  - character vector containing samples’ annotations.
- **selectByAnnot**
  - character string saying the subgroup from 'groupByAnnot' used to compute the ridgeline plot.
- **...**
  - other parameters specific of the functions `geom_density_ridges` and `geom_density_ridges_gradient`.

**Value**

A `ggplot` object.

**Examples**

```r
data(ovse)
ridgelineSignPlot(data = ovse)
```
### Description

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

### Usage

```r
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.

### Examples

```r
data(ovse)
stemCellCD49fSign(dataset = ovse)
```

---

### 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`. 
survivalSignPlot

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"
)
**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", 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)
TLSSign(dataset = ovse)
```
**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**

```r
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)
```
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