Package ‘signifinder’

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Type Package

Title Collection and implementation of public transcriptional cancer signatures

Version 1.10.0

Description signifinder is an R package for computing and exploring a compendium of tumor signatures. It allows to compute a variety of signatures coming from public literature, based on gene expression values, and return single-sample (-cell/-spot) scores. Currently, signifinder collects more than 70 distinct signatures, relating to multiple tumors and multiple cancer processes.

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Contents

`signifinder-package` *signifinder: Collection and implementation of public transcriptional cancer signatures*

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.

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See Also

Useful links:

- https://github.com/CaluraLab/signifinder
- Report bugs at https://github.com/CaluraLab/signifinder/issues

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`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

```
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

```
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

```
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

```
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

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

`availableSignatures` *Show Available Signatures*

Description

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

Usage

```
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 ...

Examples

```
availableSignatures()
```

`CD39CD8TcellSign` *CD39+ CD8+ T cells Signature*

Description

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

Usage

```
CD39CD8TcellSign(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)
CD39CD8TcellSign(dataset = 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

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

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

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(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` *Chromosomal instability Signature*

Description

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

Usage

```
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

```
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

```
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

```
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`.

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", ...)
```

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

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

`correlationSignPlot` *Correlation Plot*

Description

Given multiple signatures, the function plots signatures correlations.

Usage

```
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 che 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

```
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

```
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`.

Usage

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

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

`geneHeatmapSignPlot` *Genes' Signatures' Heatmap*

Description

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

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 colums: "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")
```

`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. 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

```
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 che 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

```
hypoxiaSign(
  dataset,
  nametype = "SYMBOL",
  author = "Buffa",
  inputType = "microarray",
  whichAssay = "norm_expr",
  isMalignant = NULL
)
```

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

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

`ICBResponseSign` *ICB Response Signature*

Description

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

Usage

```
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

```
data(ovse)
ICBResponseSign(dataset = ovse)
```

`IFNSign` *IFN-gamma Signature*

Description

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

Usage

```
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

```
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

```
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

```
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

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

`interferonSign` *Interferon Signature*

Description

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

Usage

```
interferonSign(
  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)
```

`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)
```

`IPSOVSign` *IPSOV Signature*

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` *ImmunoPhenoScore Signature*

Description

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

Usage

```
IPSSign(
  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

```
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

```
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".

`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)
ISCSign(dataset = ovse, inputType = "rnaseq")
```

`lipidMetabolismSign` *Lipid Metabolism Signature*

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

```
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

```
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

```
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)
```

`metalSign` *Metal Response Signature*

Description

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

Usage

```
metalSign(
  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)
```

`MITFlowPTENnegSign` *MITFlow/PTENneg Signature*

Description

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

Usage

```
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

```
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

```
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

```
data(ovse)
mitoticIndexSign(dataset = ovse)
```

`MPSSign` *Melanocytic Plasticity Signature*

Description

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

Usage

```
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

```
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

```
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")
```

`oneSignPlot` *Scatterplot for a single signature*

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")
```

`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 `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.

`oxphosSign` *Oxidative Phosphorylation Signature*

Description

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

Usage

```
oxphosSign(
  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)
```

`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",
  ...
)
```

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)
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

```
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

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

`ridgelineSignPlot` *Ridgeline Plot*

Description

Given multiple signatures, the function plots scores density distribution.

Usage

```
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 che 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

```
data(ovse)
ridgelineSignPlot(data = ovse)
```

`SCSubtypeSign` *Breast Cancer Subtypes Signature*

Description

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

Usage

```
SCSubtypeSign(
  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)
```

`stateSign` *Cellular States Signature*

Description

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

Usage

```
stateSign(
  dataset,
  nametype = "SYMBOL",
  author = "Barkley",
  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".
`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.
`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)
```

`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.

Examples

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

`stressSign` *Stress Response Signature*

Description

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

Usage

```
stressSign(
  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)
```

`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` *TinflamSign Signature*

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

```
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

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

`VEGFSign` *VEGF Signature*

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

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

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