Package: signifinder (via r-universe)

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Type Package

Title Collection and implementation of public transcriptional cancer signatures

Version 1.15.0

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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`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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