

Package ‘signifinder’

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Type Package

Title Collection and implementation of public transcriptional cancer signatures

Version 1.5.3

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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Contents

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

IPSOVSign	33
IPSSign	34
IRGSign	35
ISCSign	36
lipidMetabolismSign	37
LRRC15CAFSign	38
matrisomeSign	38
melStateSign	39
MITFlowPTENnegSign	40
mitoticIndexSign	41
MPSSign	42
multipleSign	43
oneSignPlot	44
ovse	45
PassONSign	45
pyroptosisSign	46
ridgelineSignPlot	47
stemCellCD49fSign	48
survivalSignPlot	49
TGFBSign	50
TinflamSign	51
TLSSign	52
VEGFSign	53
Index	54

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>

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)
```

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	<i>Autophagy Signature</i>
---------------	----------------------------

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()
```

breastStateSign	<i>Breast Cancer Cellular States Signature</i>
-----------------	--

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

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

Arguments

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

Value

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

Examples

```
data(ovse)
```

cellCycleSign	<i>Cell-cycle Signature classifier</i>
---------------	--

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"
)
```

Arguments

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

Value

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

Examples

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

chemokineSign	<i>Chemokine Signature</i>
---------------	----------------------------

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")
```

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	<i>CIS (carcinoma-in situ) Signature</i>
---------	--

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	<i>EMT-Inflammation Combined Signature</i>
--------------	--

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 signfinder can be added in the vector if they are also included in the <code>colData</code> 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)
```

COISSign

COX-2-associated Inflammatory Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

```
COISSign(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)
COISSign(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

<code>dataset</code>	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'.
<code>nametype</code>	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
<code>inputType</code>	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
<code>whichAssay</code>	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",
  ...
)
```

Arguments

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

Value

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

Examples

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

evaluationSignPlot *Evaluation Plot*

Description

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

Usage

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

Arguments

data	an object of type SummarizedExperiment . Output of the signatures functions.
nametype	character string saying the type of gene name ID (row names in data). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichSign	character vector saying the signatures to plot. These must be signatures computed with 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	<i>Get Signature Gene List</i>
--------------	--------------------------------

Description

This function returns the list of genes of a signature.

Usage

```
getSignGenes(whichSign)
```

Arguments

`whichSign` name of the signature. The names are those in column 'signature' from the table which is obtained by [availableSignatures](#).

Value

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

Examples

```
getSignGenes("EMT_Miow")
```

glioCellStateSign	<i>Glioblastoma Cellular States Signature</i>
-------------------	---

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

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


Arguments

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

Value

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

Examples

```
data(ovse)
```

glycolysisSign	<i>Glycolysis Signature</i>
----------------	-----------------------------

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	<i>Global Heatmap of Signatures' scores.</i>
-----------------	--

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 signfinder can be added in the vector if they are also included in the colData section of data.
clusterBySign	character vector saying one or more signatures to use to cluster columns.
sampleAnnot	vector containing samples' annotations.
signAnnot	character vector of signature's annotations. One or more between: "signature", "topic", "tumor", "tissue".
splitBySampleAnnot	logical. If TRUE it splits columns by samples' annotations.
...	other parameters specific of the function Heatmap .

Value

A [Heatmap-class](#) object.

Examples

```
data(ovse)
heatmapSignPlot(data = ovse)
```

 HRDSSign

Homologous Recombination Deficiency Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

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

Arguments

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

Value

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

Examples

```
data(ovse)
HRDSSign(dataset = ovse)
```

hypoxiaSign	<i>Hypoxia Signature</i>
-------------	--------------------------

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

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

Arguments

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

ICBResponseSign	<i>ICB Response Signature</i>
-----------------	-------------------------------

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	<i>IFN-gamma Signature</i>
---------	----------------------------

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	<i>Immune Cytolytic Activity Signature</i>
---------------	--

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	<i>Immunogenic Signature</i>
-----------------	------------------------------

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)
```

 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)
```

LRR15CAFSign	<i>LRR15 CAF Signature</i>
--------------	----------------------------

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

```
LRR15CAFSign(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)
LRR15CAFSign(dataset = ovse)
```

matrisomeSign	<i>Core Matrisome Gene signature</i>
---------------	--------------------------------------

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)
```

melStateSign

Metastatic Melanoma Cellular States Signature

Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

Usage

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

Arguments

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

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	<i>Mitotic Index</i>
------------------	----------------------

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

<code>data</code>	an object of type <code>SummarizedExperiment</code> . Output of the signatures functions.
<code>whichSign</code>	character string saying the signature to plot. This must be a signature computed with <code>signifinder</code> .
<code>statistics</code>	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.

`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 "maseq".
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	<i>Ridgeline Plot</i>
-------------------	-----------------------

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 the colData section of data.
groupByAnnot	character vector containing samples' annotations.
selectByAnnot	character string saying the subgroup from 'groupByAnnot' used to compute the ridgeline plot.
...	other parameters specific of the functions geom_density_ridges and geom_density_ridges_gradient .

Value

A [ggplot](#) object.

Examples

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

stemCellCD49fSign	<i>CD49fHi Basal Stem Cell Signature</i>
-------------------	--

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)
```

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	<i>TinflamSign Signature</i>
-------------	------------------------------

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	<i>VEGF Signature</i>
----------	-----------------------

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)
```

Index

- * **datasets**
 - ovse, [45](#)
- * **internal**
 - signifinder-package, [3](#)

- ADOSign, [4](#)
- APMSign, [5](#)
- ASCSign, [6](#)
- autophagySign, [7](#)
- availableSignatures, [4–7](#), [8](#), [9–14](#), [16–19](#),
[21](#), [22](#), [24–42](#), [45–48](#), [50–53](#)

- betweenLaneNormalization, [45](#)
- breastStateSign, [9](#)

- cellCycleSign, [10](#)
- chemokineSign, [11](#)
- CINSign, [12](#)
- CISSign, [13](#)
- colData, [4–7](#), [9–19](#), [21](#), [22](#), [25](#), [26](#), [28–42](#), [44](#),
[46–48](#), [50–53](#)
- CombinedSign, [13](#)
- consensusOVSign, [14](#), [45](#)
- correlationSignPlot, [15](#)
- COXISSign, [16](#)
- curatedTCGAData, [45](#)

- DNAREPSign, [17](#)

- ECMSign, [18](#)
- EMTSign, [18](#)
- evaluationSignPlot, [20](#)
- expandedImmuneSign, [21](#)

- ferroptosisSign, [21](#)

- geneHeatmapSignPlot, [22](#)
- geom_density_ridges, [48](#)
- geom_density_ridges_gradient, [48](#)
- get.subtypes, [15](#)
- getSignGenes, [24](#)

- ggplot, [20](#), [44](#), [48](#), [50](#)
- ggsurvplot, [49](#)
- glioCellStateSign, [24](#)
- glycolysisSign, [25](#)
- gsvaParam, [4](#), [5](#)

- Heatmap, [23](#), [27](#)
- heatmapSignPlot, [26](#)
- HRDSSign, [27](#)
- hypoxiaSign, [28](#)

- ICBResponseSign, [29](#)
- IFNSign, [30](#)
- immuneCytSign, [30](#)
- immunoScoreSign, [31](#)
- IPRESSign, [32](#)
- IPSOVSign, [33](#)
- IPSSign, [34](#)
- IRGSign, [35](#)
- ISCSign, [36](#)

- lipidMetabolismSign, [37](#)
- LRRC15CAFSign, [38](#)

- matrisomeSign, [38](#)
- maxstat.test, [49](#)
- melStateSign, [39](#)
- MITFlowPTENnegSign, [40](#)
- mitoticIndexSign, [41](#)
- MPSSign, [42](#)
- multipleSign, [43](#)

- oneSignPlot, [44](#)
- ovse, [45](#)

- PassONSign, [45](#)
- pyroptosisSign, [46](#)

- ridgelineSignPlot, [47](#)

- signifinder (signifinder-package), [3](#)

signifinder-package, 3
SingleCellExperiment, 4–7, 9–19, 21, 22,
25–43, 46–48, 50–53
SpatialExperiment, 4–7, 9–19, 21, 22,
25–43, 46–48, 50–53
ssgseaParam, 18, 19, 33, 34, 46
stemCellCD49fSign, 48
SummarizedExperiment, 4–7, 9–23, 25–44,
46–53
Surv, 49
survfit, 49
survivalSignPlot, 49

TGFBSign, 50
TinflamSign, 51
TLSSign, 52

VEGFSign, 53