Package 'signifinder'

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Type Package

Title Implementations of transcriptional cancer signatures

Version 1.2.1

Description signifinder is an R package for computing and exploring a
compendium of tumor signatures. It allows to compute a variety of
signatures, based on gene expression values, and return
single-sample scores. Currently, signifinder contains 46 distinct
signatures collected from the literature, relating to multiple
tumors and multiple cancer processes.

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biocViews GeneExpression, GeneTarget, ImmunoOncology,
BiomedicalInformatics, RNASeq, Microarray, ReportWriting,
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Imports ggplot2, org.Hs.eg.db, patchwork, AnnotationDbi, BiocGenerics,
ComplexHeatmap, cowplot, DGEobj.utils, GSVA, IRanges,
SummarizedExperiment, consensusOV, dplyr, ensembldb, ggridges,
grid, magrittr, matrixStats, maxstat, methods, openair,
RColorBrewer, TxDb.Hsapiens.UCSC.hg19.knownGene,
TxDb.Hsapiens.UCSC.hg38.knownGene, stats, survival, survminer,
viridis

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RoxygenNote 7.2.3

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R **topics documented:**

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signifinder-package   *signifinder: Implementations of 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 46 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

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See Also

Useful links:

  • <https://github.com/CaluraLab/signifinder>

  • Report bugs at <https://github.com/CaluraLab/signifinder/issues>

ASCSign   *Adult Stem Cell Signature*

Description

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

Usage

```
ASCSign(dataset, nametype = "SYMBOL")
```

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".

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",
  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.

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 shows a table containing all the information of the signatures collected in the package.

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" or "rnaseq". Used to filter the signatures in the table.

description   logical. If TRUE it shows the signature's description.

Value

A data frame with 46 rows and 11 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

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()
```

---

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"
)
```

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".

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")
```

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".

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")
```

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".

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")
```

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".

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)
```

---

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", ...)
```

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".

...   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.

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)
```

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")
```

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".

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", ...)
```

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".

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

Value

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

Examples

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

EMTSign   *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",
  ...
)
```

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

Value

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

Examples

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

---

evaluationSignPlot *Evaluation Plot*

Description

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

Usage

```
evaluationSignPlot(
  data,
  nametype = "SYMBOL",
  whichSign = NULL,
  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. If not specified, all the signatures inside data will be plotted.
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")
```

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".

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",
  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]().
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,
  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.

logCount	logical. If TRUE it shows logarithms of expression values.
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")
```

---

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")
```

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`.

Value

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

Examples

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

---

heatmapSignPlot   *Global Heatmap of Signatures' scores.*

Description

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

Usage

```
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.
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")
```

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".

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", inputType = "microarray")
```

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".

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")
```

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")
```

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".

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",
  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.

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",
  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".

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", 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".

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

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

Value

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

Examples

```
data(ovse)
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", ...)
```

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".
...	other arguments passed on to the gsva function.

Value

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

Examples

```
data(ovse)
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", 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".

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)
```

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")
```

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".

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")
```

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".

Value

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

Examples

```
data(ovse)
lipidMetabolismSign(dataset = ovse)
```

---

matrisomeSign   *Core Matrisome Gene signature*

Description

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

Usage

```
matrisomeSign(dataset, nametype = "SYMBOL")
```

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".

Value

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

Examples

```
data(ovse)
matrisomeSign(dataset = ovse)
```

---

mitoticIndexSign   *Mitotic Index*

Description

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

Usage

```
mitoticIndexSign(dataset, nametype = "SYMBOL")
```

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".

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)
```

---

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",
  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 Summa-
               rizedExperiment, SingleCellExperiment or SpatialExperiment.

nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichSign	character vector saying the signatures to compute.
tumor	character vector saying the tumor types. Signatures from that tumors will be computed (this can also be "pan-cancer").
tissue	character vector saying the tumor tissues. Signatures from that tissues will be computed (this can also be "pan-tissue").
topic	character vector saying signatures topics. Signatures having that topics will be computed.
...	other arguments passed on to the signature functions.

Value

A SummarizedExperiment object in which the signatures' scores are added in the [colData](#) section.

Examples

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

---

oneSignPlot	*Scatterplot for a single signature*

Description

Given signatures' scores, it returns a scatterplot of samples' scores and a barplot of the density distributions of samples' scores.

Usage

```
oneSignPlot(data, whichSign, statistics = NULL)
```

Arguments

data	an object of type [SummarizedExperiment](#). Output of the signatures functions.
whichSign	character string saying the signature to plot.
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](#).

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", 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".

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

...
: other arguments passed on to the gsva function.

Value

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

Examples

```
data(ovse)
PassONSign(dataset = ovse)
```

---

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",
  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.

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 densities scores.

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.
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   *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")
```

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".

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.
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"
)
```

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")
```

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".

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")
```

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".

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")
```

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".

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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