Package 'mitology'

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Type Package

Title Study of mitochondrial activity from RNA-seq data

Version 1.0.0

Description mitology allows to study the mitochondrial activity throught high-throughput RNA-seq data. It is based on a collection of genes whose proteins localize in to the mitochondria. From these, mitology provides a reorganization of the pathways related to mitochondria activity from Reactome and Gene Ontology. Further a ready-to-use implementation of MitoCarta3.0 pathways is included.

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biocViews GeneExpression, RNASeq, Visualization, SingleCell, Spatial, Pathways, Reactome, GO

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Author Stefania Pirrotta [cre, aut] (ORCID:
<https://orcid.org/0009-0004-0030-217X>),
Enrica Calura [aut, fnd] (ORCID:
<https://orcid.org/0000-0001-8463-2432>)

Maintainer Stefania Pirrotta <stefania.pirrotta@unipd.it>

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`mitology-package` *mitology: Study of mitochondrial activity from RNA-seq data*

Description

mitology allows to study the mitochondrial activity throught high-throughput RNA-seq data. It is based on a collection of genes whose proteins localize in to the mitochondria. From these, mitology provides a reorganization of the pathways related to mitochondria activity from Reactome and Gene Ontology. Further a ready-to-use implementation of MitoCarta3.0 pathways is included.

Author(s)

Maintainer: Stefania Pirrotta <stefania.pirrotta@unipd.it> (ORCID)

Authors:

- Enrica Calura <enrica.calura@unipd.it> (ORCID) [funder]

See Also

Useful links:

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

getGeneSets *Get the mitochondrial gene sets*

Description

It returns the mitochondrial gene sets (in form of list or data frame) of the four possible databases: "MitoCarta", "Reactome", "GO-CC" and "GO-BP".

Usage

```
getGeneSets(
  database = "MitoCarta",
  nametype = "ENSEMBL",
  objectType = "list",
  sections = FALSE
)
```

Arguments

database	character string saying the database to use for the analysis. Either one of "MitoCarta", "Reactome", "GO-CC" and "GO-BP".
nametype	character string saying the type of gene name ID. Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
objectType	character string saying the type of needed object. Either one of "list" or "dataframe".
sections	logical. Either to keep the aggregated gene set categories or the specific gene sets. Default is FALSE.

Value

the mitochondrial gene sets.

Examples

```
MClist <- getGeneSets()
```

mitoHeatmap *Heatmap of mitochondrial gene sets.*

Description

Given a matrix of scores, it returns a heatmap of the mitochondrial gene sets.

Usage

```
mitoHeatmap(
  data,
  database = "MitoCarta",
  sampleAnnot = NULL,
  splitSamples = FALSE,
  splitSections = FALSE,
  ...
)
```

Arguments

data	matrix or data.frame with samples in columns and mitochondrial gene sets in rows.
database	character string saying the database used for the analysis. Either one of "MitoCarta", "Reactome", "GO-CC" and "GO-BP".
sampleAnnot	character vector with samples' annotation.
splitSamples	logical. If TRUE it splits samples by annotation. sampleAnnot must be provided.
splitSections	logical. If TRUE it splits gene sets by main section.
...	other parameters specific of the function Heatmap.

Value

A Heatmap-class object.

Examples

```
MClist <- getGeneSets()
n <- length(names(MClist)) * 5
rmatrix <- matrix(rnorm(n, 0), ncol = 5)
rownames(rmatrix) <- names(MClist)
colnames(rmatrix) <- paste0("Sample_", seq_len(5))
mitoHeatmap(data = rmatrix, database = "MitoCarta")
```

---

mitoTreeHeatmap *Circular heatmap on mitochondrial gene set tree.*

Description

Given a matrix of scores, it returns a circular heatmap of the mitochondrial gene sets (leaf of the database tree) or gene set groups (section of the database tree).

Usage

```
mitoTreeHeatmap(
  data,
  database = "MitoCarta",
  sections = FALSE,
  samples = NULL,
  labelNames = "sections",
  ...
)
```

Arguments

data	matrix or data.frame with samples in columns and mitochondrial gene sets in rows.
database	character string saying the database used for the analysis. Either one of "MitoCarta", "Reactome", "GO-CC" and "GO-BP".
sections	logical. Either to keep the aggregated gene set categories or the specific gene sets. Default is FALSE.
samples	character vector with the names of samples to be plotted. Otherwise all samples are plotted.
labelNames	character string that says to plot either the names of "sections" or "leaves".
...	other arguments passed on to the gheatmap function.

Value

A ggplot object.

Examples

```
MClist <- getGeneSets()
n <- length(names(MClist)) * 5
rmatrix <- matrix(rnorm(n, 0), ncol = 5)
rownames(rmatrix) <- names(MClist)
colnames(rmatrix) <- paste0("Sample_", seq_len(5))
mitoTreeHeatmap(data = rmatrix, database = "MitoCarta")
```

---

ovse *Example expression data.*

Description

This is an example dataset containing gene expression values (in normalized counts) 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 mitochondrial genes included in mitology were kept. Finally, the log fold change of the IMR versus the PRO samples were computed. Further details in mitology/inst/scripts/howToGenerateOvse.Rmd.

Usage

```
data(ovse)
```

Format

An object of class `SummarizedExperiment` with 2388 rows and 40 columns.

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