

Package ‘dorothea’

October 12, 2020

Type Package

Title Collection Of Human And Mouse TF Regulons

Version 1.0.1

Description This package contains human and mouse TF regulons.

The human regulons were curated and collected from different types of evidence such as literature curated resources, ChIP-seq peaks, TF binding site motifs and interactions inferred directly from gene expression. The mouse regulons were constructed by mapping the human gene symbols to their orthologs in mice. Those regulons can be coupled with any statistical method that aims to analyse gene sets to infer TF activity from gene expression data. Preferably the statistical method viper is used.

URL <https://github.com/saezlab/dorothea>

BugReports <https://github.com/saezlab/dorothea/issues>

Depends R (>= 4.0)

License GPL-3 + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

VignetteBuilder knitr

biocViews ExperimentData, Homo_sapiens_Data, Mus_musculus_Data

Imports dplyr, magrittr, bcellViper

Suggests Biobase, BiocStyle, knitr, pheatmap, pkgdown, Seurat, SingleCellExperiment, SummarizedExperiment, testthat (>= 2.1.0), tibble, tidyr, utils, viper

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R topics documented:

dorothea_hs	2
dorothea_mm	2
entire_database	3
run_viper	3

Index	5
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dorothea_hs	<i>Human DoRothEA</i>
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Description

A table reporting signed human TF-target interactions. This database covers in total 1395 TFs targeting 20,244 genes with 486,676 unique interactions. In addition, each TF is accompanied with an empirical confidence level that was derived from the number of supporting evidences for this TF/interaction. The range is from A (high quality) to E (low quality).

Format

A table of human TF-target interactions:

tf TF identifier as HGNC symbols

confidence Summary confidence score classifying regulons based on their quality

target target identifier as HGNC symbols

mor mode of regulation indicating the effect of a TF on the target

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/>

dorothea_mm	<i>Mouse DoRothEA</i>
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Description

A table reporting signed human TF-target interactions. This database covers in total 1179 TFs targeting 17,410 genes with 410,455 unique interactions. In addition, each TF is accompanied with an empirical confidence level that was derived from the number of supporting evidences for this TF/interaction. The range is from A (high quality) to E (low quality).

Format

A table of mouse TF-target interactions:

tf TF identifier as MGI symbols

confidence summary confidence score classifying regulons based on their quality

target target identifier as MGI symbols

mor mode of regulation indicating the effect of a TF on the target

Source

<https://www.ncbi.nlm.nih.gov/pubmed/31525460>

entire_database	<i>Entire database with associated meta data</i>
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Description

This table lists all human TF-target interactions that were derived from the four lines of evidences. Each interaction is assigned a confidence score based on the number of supporting evidences. The table provides also all required information to trace back the origin of the interaction.

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/>

run_viper	<i>VIPER wrapper</i>
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Description

This function is a convenient wrapper for the [viper](#) function using DoRothEA regulons.

Usage

```
run_viper(input, regulons, options = list(), tidy = FALSE)
```

Arguments

input	An object containing a gene expression matrix with genes (HGNC/MGI symbols) in rows and samples in columns. The object can be a simple matrix/data frame or complex objects such as ExpressionSet Seurat or SingleCellExperiment objects.
regulons	DoRothEA regulons in table format.
options	A list of named options to pass to viper such as minsize or method. These options should not include, eset or regulon.
tidy	Logical, whether computed tf activities scores should be returned in a tidy format.

Value

A matrix of normalized enrichment scores for each TF across all samples. Of note, if you provide Bioconductor objects as input the function will return this object with added tf activities at appropriate slots. e.g. Seurat object with a new assay called dorothea. For all other inputs the function will return a matrix. If tidy is TRUE the normalized enrichment scores are returned in a tidy format (not supported for Bioconductor objects).

Examples

```
# use example gene expression matrix from bcellViper package
library(bcellViper)
data(bcellViper, package = "bcellViper")
# accessing (human) dorothea regulons
# for mouse regulons: data(dorothea_mm, package = "dorothea")
data(dorothea_hs, package = "dorothea")
# run viper
tf_activities <- run_viper(dset, dorothea_hs,
  options = list(method = "scale", minsize = 4,
    eset.filter = FALSE, cores = 1,
    verbose = FALSE))
```

Index

* datasets

- dorothea_hs, [2](#)
- dorothea_mm, [2](#)
- entire_database, [3](#)

DoRothEA, [3](#)

dorothea_hs, [2](#)

dorothea_mm, [2](#)

entire_database, [3](#)

ExpressionSet, [3](#)

run_viper, [3](#)

Seurat, [3](#)

SingleCellExperiment, [3](#)

viper, [3](#)