DoRothEA is a gene regulatory network containing signed transcription factor (TF) - target gene interactions. DoRothEA regulons, the collection of a TF and its transcriptional targets, were curated and collected from different types of evidence for both human and mouse. A confidence level was assigned to each TF-target interaction based on the number of supporting evidence.


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

Depends R (&ge; 4.0)
License GPL-3 + file LICENSE
Encoding UTF-8
LazyData true
LazyDataCompression xz
RoxygenNote 7.2.3
VignetteBuilder knitr
biocViews ExperimentData, Homo_sapiens_Data, Mus_musculus_Data
Imports dplyr, magrittr, bcellViper, decoupleR,
Suggests Biobase, BiocStyle, OmnipathR, viper, knitr, pheatmap, pkgdown, rmarkdown, Seurat, SingleCellExperiment, SummarizedExperiment, testthat (&ge; 2.1.0), tibble, tidyr, utils
git_url https://git.bioconductor.org/packages/dorothea
git_branch RELEASE_3_18
git_last_commit 56660e8
git_last_commit_date 2023-10-24
Date/Publication 2023-10-26
Author Pau Badia-i-Mompel [cre] (<https://orcid.org/0000-0002-1004-3923>),
Daniel Dimitrov [aut] (<https://orcid.org/0000-0002-5197-2112>),
Christian H. Holland [aut] (<https://orcid.org/0000-0002-3060-5786>),
Luz Garcia-Alonso [aut],
Alberto Valdeolivas [ctb],
Minoo Ashtiani [ctb],
Attila Gabor [ctb]

Maintainer Pau Badia-i-Mompel <pau.badia@uni-heidelberg.de>

R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>dorothea-package</td>
<td>2</td>
</tr>
<tr>
<td>df2regulon</td>
<td>3</td>
</tr>
<tr>
<td>dorothea_hs</td>
<td>4</td>
</tr>
<tr>
<td>dorothea_hs_pancancer</td>
<td>4</td>
</tr>
<tr>
<td>dorothea_mm</td>
<td>5</td>
</tr>
<tr>
<td>dorothea_mm_pancancer</td>
<td>5</td>
</tr>
<tr>
<td>entire_database</td>
<td>6</td>
</tr>
<tr>
<td>run_viper</td>
<td>6</td>
</tr>
<tr>
<td>%&gt;+%</td>
<td>7</td>
</tr>
</tbody>
</table>

Index 8

---

dorothea-package

dorothea: Collection Of Human And Mouse TF Regulons

Description

This package contains human and mouse TF regulons.

Author(s)

Maintainer: Pau Badia-i-Mompel <pau.badia@uni-heidelberg.de> (ORCID)

Authors:

- Daniel Dimitrov <daniel.dimitrov@uni-heidelberg.de> (ORCID)
- Christian H. Holland <cholland2408@gmail.com> (ORCID)
- Luz Garcia-Alonso

Other contributors:

- Alberto Valdeolivas [contributor]
- Minoo Ashtiani [contributor]
- Attila Gabor [contributor]
df2regulon

See Also

Useful links:

- https://saezlab.github.io/dorothea/
- https://github.com/saezlab/dorothea/
- Report bugs at https://github.com/saezlab/dorothea/issues

Description

This function converts DoRothEA’s regulons that are stored in a table to the format required by the [viper](https://github.com/saezlab/dorothea/issues) function.

Usage

```
df2regulon(df)
```

Arguments

- `df`: A regulon table from dorothea package.

Value

Regulons in the viper format.

Examples

```
# accessing (human) dorothea regulons
# for mouse regulons: data(dorothea_mm, package = "dorothea")
data(dorothea_hs, package = "dorothea")
# convert to the format required by viper
viper_regulons = df2regulon(dorothea_hs)
```
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/

Description

A table reporting signed human TF-target interactions for cancer application. The difference to "dorothea_hs" is that TGCA gene expression data was used instead of GTEx to infer the networks with ARACNE. This database covers in total 1344 TFs targeting 20,582 genes with 213,230 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**  

**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**  

---

**dorothea_mm_pancancer**  

**Description**  
A table reporting signed human TF-target interactions. The difference to "dorothea_mm" is that TGCA gene expression data was used instead of GTEx to infer the networks with ARACNE. This database covers in total 1096 TFs targeting 17,695 genes with 187,955 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**  
### entire_database

*Entire database with associated meta data*

**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

*VIPER wrapper*

**Description**

This function is a convenient wrapper for the `run_viper` function using DoRothEA regulons.

**Usage**

```r
run_viper(input, regulons, options = list(), tidy = FALSE, assay_key = "RNA")
```

**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 more 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.
- **assay_key**: Only applies if the input is a `Seurat` object. It selects the name of the assay from where to extract the normalized expression data.

**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))

---

Pipe operator

Description
See magrittr::%>% for details.

Usage
lhs %>% rhs

Value
lhs

Examples
c(1:10) %>% mean()
Index

* datasets
  dorothea_hs, 4
  dorothea_hs_pancancer, 4
  dorothea_mm, 5
  dorothea_mm_pancancer, 5
  entire_database, 6

* internal
  %>%, 7
  dorothea-package, 2
  %>%, 7, 7

df2regulon, 3
DoRothEA, 6
dorothea (dorothea-package), 2
dorothea-package, 2
dorothea_hs, 4
dorothea_hs_pancancer, 4
dorothea_mm, 5
dorothea_mm_pancancer, 5
entire_database, 6
ExpressionSet, 6

run_viper, 6, 6

Seurat, 6
SingleCellExperiment, 6

viper, 3, 6