

Package ‘TargetScoreData’

June 1, 2023

Title TargetScoreData

Version 1.37.0

Author Yue Li

Maintainer Yue Li <yueli@cs.toronto.edu>

Description Precompiled and processed miRNA-overexpression fold-changes from 84 Gene Expression Omnibus (GEO) series corresponding to 6 platforms, 77 human cells or tissues, and 113 distinct miRNAs. Accompanied with the data, we also included in this package the sequence feature scores from TargetScanHuman 6.1 including the context+ score and the probabilities of conserved targeting for each miRNA-mRNA interaction. Thus, the user can use these static sequence-based scores together with user-supplied tissue/cell-specific fold-change due to miRNA overexpression to predict miRNA targets using the package TargetScore (download separately)

biocViews ExperimentData, RNASeqData, miRNAData

License GPL-2

Suggests TargetScore, gplots

git_url <https://git.bioconductor.org/packages/TargetScoreData>

git_branch devel

git_last_commit fbe6b3d

git_last_commit_date 2023-04-25

Date/Publication 2023-06-01

R topics documented:

TargetScoreData-package	2
get_miRNA_family_info	3
get_miRNA_transfection_data	4
get_precomputed_logFC	4
get_precomputed_targetScores	5
get_TargetScanHuman_contextScore	5
get_TargetScanHuman_PCT	6
get_validated_targets	6

Index	7
--------------	----------

TargetScoreData-package

Processed human microRNA perturbation data from GEO, and sequence information from TargetScan, and targetScore from TargetScore

Description

To automate the pipeline of calculating targetScore using [targetScore](#), we compiled, processed and generated miRNA-overexpression fold-changes from 84 Gene Expression Omnibus (GEO) series corresponding to 6 platforms, 77 human cells or tissues, and 113 distinct miRNAs. To our knowledge, this is by far the largest miRNA-perturbation data compendium. Accompanied with the data, we also included in this package the sequence feature scores from TargetScanHuman 6.1 including the context+ score and the probabilities of conserved targeting for each miRNA-mRNA interaction. Thus, the user can use these static sequence-based scores together with user-supplied tissue/cell-specific fold-change due to miRNA overexpression to predict miRNA targets using [targetScore](#).

Details

Package: TargetScoreData
 Type: Package
 Version: 0.99.4
 Date: 2013-07-13
 License: GPL-2

`get_TargetScanHuman_contextScore`: TargetScan context score for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

`get_TargetScanHuman_PCT`: TargetScan PCT for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

`get_miRNA_family_info`: Get miRNA family information obtained TargetScanHuman 6

`get_precomputed_targetScores`: Pre-calculated targetScores for 112 miRNAs using logFC and sequence scores from TargetScan context score and PCT from the RData files above.

`get_precomputed_logFC`: We combined all of the logFC data columns into a single N x M matrix for all of the N = 19177 RefSeq mRNAs (NM_* obtained from UCSC) and M = 286 datasets. Missing data (logFC) for some genes across studies were imputed using `impute` from `impute.knn`.

`get_miRNA_transfection_data`: Get log fold-changes (logFC) from each study organized in a list with each item corresponding to a miRNA. Notably, some miRNAs (e.g., hsa-miR-1) appear more than once in the list corresponding to different studies.

`get_validated_targets`: Get validated targets of human miRNA obtained from mirTarBase v3.5

Author(s)

Yue Li

Maintainer: Yue Li <yueli@cs.toronto.edu>

References

miRTarBase: a database curates experimentally validated microRNA-target interactions. (2011).
 miRTarBase: a database curates experimentally validated microRNA-target interactions., 39(Database
 issue), D163-9. doi:10.1093/nar/gkq1107

Friedman, R. C., Farh, K. K.-H., Burge, C. B., & Bartel, D. P. (2009). Most mammalian mRNAs are
 conserved targets of microRNAs. *Genome Research*, 19(1), 92-105. doi:10.1101/gr.082701.108

Garcia, D. M., Baek, D., Shin, C., Bell, G. W., Grimson, A., & Bartel, D. P. (2011). Weak seed-
 pairing stability and high target-site abundance decrease the proficiency of lsy-6 and other microR-
 NAs. *Nature structural & molecular biology*, 18(10), 1139-1146. doi:10.1038/nsmb.2115

Please follow the GEO series number to find the references for each microRNA-transfection dataset.

See Also

[get_TargetScanHuman_contextScore](#), [get_TargetScanHuman_PCT](#), [get_validated_targets](#),
[get_miRNA_family_info](#), [get_precomputed_targetScores](#), [get_precomputed_logFC](#), [get_miRNA_transfection_data](#)

Examples

```
ls("package:TargetScoreData")
```

```
get_miRNA_family_info MicroRNA family information
```

Description

Get human miRNA family information obtained from TargetScanHuman 6 website

Usage

```
get_miRNA_family_info(datapath = system.file("extdata/miR_Family_Info.txt", package = "TargetScoreData"))
```

Arguments

datapath data path

```
get_miRNA_transfection_data
      get_miRNA_transfection_data
```

Description

Get log fold-changes (logFC) from each study organized in a list with each item corresponding to a miRNA. Notably, some miRNAs (e.g., hsa-miR-1) appear more than once in the list corresponding to different studies.

Usage

```
get_miRNA_transfection_data(datapath = system.file("extdata/miRNA_transfection_data.RData", package =
```

Arguments

datapath	data path
----------	-----------

```
get_precomputed_logFC  get_precomputed_logFC
```

Description

We combined all of the logFC data columns into a single N x M matrix for all of the N = 19177 RefSeq mRNAs (NM_* obtained from UCSC) and M = 286 datasets. Missing data (logFC) for some genes across studies were imputed using `impute` from `impute.knn`.

Usage

```
get_precomputed_logFC(datapath = system.file("extdata/logFC.RData", package = "TargetScoreData"))
```

Arguments

datapath	data path
----------	-----------

get_precomputed_targetScores
<i>get_precomputed_targetScores</i>

Description

Pre-calculated targetScores for 112 miRNAs using logFC and sequence scores from TargetScan context score and PCT from the RData files above.

Usage

get_precomputed_targetScores(datapath = system.file("extdata/targetScores.RData", package = "TargetSc

Arguments

datapath data path

get_TargetScanHuman_contextScore
<i>get_TargetScanHuman_contextScore</i>

Description

TargetScan context score for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

Usage

get_TargetScanHuman_contextScore(datapath = system.file("extdata/TargetScanHuman_contextScore.RData"

Arguments

datapath data path

get_TargetScanHuman_PCT
<i>get_TargetScanHuman_PCT</i>

Description

TargetScan PCT for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

Usage

get_TargetScanHuman_PCT(datapath = system.file("extdata/TargetScanHuman_PCT.RData", package = "Target

Arguments

datapath	data path
----------	-----------

get_validated_targets	<i>get_validated_targets</i>
-----------------------	------------------------------

Description

Get validated targets of human miRNA obtained from mirTarBase v3.5

Usage

get_validated_targets(datapath = system.file("extdata/hsa_MTI.xls", package = "TargetScoreData"))

Arguments

datapath	data path
----------	-----------

Index

* data package

TargetScoreData-package, [2](#)

get_miRNA_family_info, [3](#), [3](#)

get_miRNA_transfection_data, [3](#), [4](#)

get_precomputed_logFC, [3](#), [4](#)

get_precomputed_targetScores, [3](#), [5](#)

get_TargetScanHuman_contextScore, [3](#), [5](#)

get_TargetScanHuman_PCT, [3](#), [6](#)

get_validated_targets, [3](#), [6](#)

targetScore, [2](#)

TargetScoreData

(TargetScoreData-package), [2](#)

TargetScoreData-package, [2](#)