Package ‘TargetScoreData’

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Title TargetScoreData

Version 1.16.0

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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

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R topics documented:

`TargetScoreData-package`

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

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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-pertubation 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)

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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 microRNAs. 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_`

Examples

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

`get_miRNA_family_info` *MicroRNA family information*

Description

Get human miRNA family information obtained frin TargetScanHuman 6 website

Usage

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

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", packa
```

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` *get_precomputed_targetScores*

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 = "Targ
```

Arguments

`datapath`	data path

`get_TargetScanHuman_contextScore` *get_TargetScanHuman_contextScore*

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.RD
```

Arguments

`datapath`	data path

`get_TargetScanHuman_PCT` *get_TargetScanHuman_PCT*

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 = "Ta
```

Arguments

`datapath`	data path

`get_validated_targets` *get_validated_targets*

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

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