Package 'miRNAtap'

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Type Package

Title miRNAtap: microRNA Targets - Aggregated Predictions

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Description The package facilitates implementation of workflows
requiring miRNA predictions, it allows to integrate ranked
miRNA target predictions from multiple sources available online
and aggregate them with various methods which improves quality
of predictions above any of the single sources. Currently
predictions are available for Homo sapiens, Mus musculus and
Rattus norvegicus (the last one through homology translation).

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Depends R (>= 3.2.0), AnnotationDbi

Imports DBI, RSQLite, stringr, sqldf, plyr, methods

Suggests topGO, org.Hs.eg.db, miRNAtap.db, testthat

biocViews Software, Classification, Microarray, Sequencing, miRNA

Roxygen list(wrap = FALSE)

NeedsCompilation no

R topics documented:

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aggregateRanks *Auxiliary targetPredictor functions*

Description

Auxiliary targetPredictor functions

Usage

```
aggregateRanks(ranks, n_valid_srcs, min_src, method = "min", promote = TRUE)
```

Arguments

ranks	data.frame with ordered scored
n_valid_srcs	number of valid sources in the dataset
min_src	minimum acceptable number fo sources
method	'min','max', or 'geom'
promote	add weights to improve accuracy of the method, default TRUE

Details

This function performs aggregation phase of target prediction for [getPredictedTargets](#) function

Value

data.frame object with aggregate ranks

Author(s)

Maciej Pajak <m.pajak@sms.ed.ac.uk>

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getPredictedTargets *Get aggregated ordered list of predicted targets for miRNA*

Description

Get aggregated ordered list of predicted targets for miRNA

Usage

```
getPredictedTargets(mirna, sources = c("pictar", "diana",
"targetscan", "miranda"), species = "mmu", min_src = 2,
method = "geom", promote = TRUE, ...)
```

Arguments

`mirna`	miRNA in a standard format
`sources`	a list of sources to use for aggregation, default c('pictar','diana','targetscan','miranda')
`species`	species in a standard three-letter acronym, 'mmu' and 'hsa' available as direct targets, 'rno' as homology translations, default 'mmu'
`min_src`	minimum number of sources required for a target to be considered, default 2
`method`	method of aggregation - choose from 'min', 'max', 'geom', 'min' is a minimum of ranks, 'max' is a maximum of ranks, and default 'geom' is based on geometric mean of the ranks, it proves to be the most accurate.
`promote`	add weights to improve accuracy of the method, default TRUE
`...`	any optional arguments

Details

This method performs aggregation of target lists from multiple sources. Aggregated list is more accurate than any list from a single source. Multiple aggregation methods are available.Direct target data from four sources for Human and Mouse is supplied through `miRNAtap.db` package, for Rat targets are derived through homology translations whenever direct ones are not available.

Value

a data.frame object where row names are entrez IDs of target genes, ranks from individual sources and aggregated rank are shown in columns. If no targets are found in any of the sources NULL and a warning is returned.

Author(s)

Maciej Pajak <m.pajak@sms.ed.ac.uk>

References

Friedman, R. C., Farh, K. K.-H., Burge, C. B., and Bartel, D. P. (2009). Most mammalian mRNAs are conserved targets of microRNAs. Genome research, 19(1):92-105.

Griffiths-Jones, S., Saini, H. K., van Dongen, S., and Enright, A. J. (2008). miRBase: tools for microRNA genomics. Nucleic acids research, 36(Database issue):D154-8.

Lall, S., Grun, D., Krek, A., Chen, K., Wang, Y.-L., Dewey, C. N., ... Rajewsky, N. (2006). A genome-wide map of conserved microRNA targets in C. elegans. Current biology : CB, 16(5):460-71.

Maragkakis, M., Vergoulis, T., Alexiou, P., Reczko, M., Plomaritou, K., Gousis, M., ... Hatzigeorgiou, A. G. (2011). DIANA-microT Web server upgrade supports Fly and Worm miRNA target prediction and bibliographic miRNA to disease association. Nucleic Acids Research, 39(Web Server issue), W145-8.

Examples

```
targets <- getPredictedTargets('let-7a',species='mmu', method = 'min')
head(targets) #top of the list with minimum aggregation
targets2 <- getPredictedTargets('let-7a',species='mmu', method='geom')
head(targets2) #top of the list with geometric mean aggregation
```

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getTargetsFromSource   *Get target list from a single source*

Description

Get target list from a single source

Usage

```
getTargetsFromSource(mirna, species = "mmu", source = "diana")
```

Arguments

mirna	miRNA in a standard format
species	species in a standard three-letter acronym, default 'mmu'
source	a list of sources to use for aggregation, default 'diana'

Details

This function queries precompiled annotation SQLite database which contains miRNA - target gene associations with their respective scores.

Value

a data.frame object with entrez IDs of target genes and their scores

Author(s)

Maciej Pajak `<m.pajak@sms.ed.ac.uk>`

References

Friedman, R. C., Farh, K. K.-H., Burge, C. B., and Bartel, D. P. (2009). Most mammalian mRNAs are conserved targets of microRNAs. Genome research, 19(1):92-105.

Griffiths-Jones, S., Saini, H. K., van Dongen, S., and Enright, A. J. (2008). miRBase: tools for microRNA genomics. Nucleic acids research, 36(Database issue):D154-8.

Lall, S., Grun, D., Krek, A., Chen, K., Wang, Y.-L., Dewey, C. N., ... Rajewsky, N. (2006). A genome-wide map of conserved microRNA targets in C. elegans. Current biology : CB, 16(5):460-71.

Maragkakis, M., Vergoulis, T., Alexiou, P., Reczko, M., Plomaritou, K., Gousis, M., ... Hatzigeorgiou, A. G. (2011). DIANA-microT Web server upgrade supports Fly and Worm miRNA target prediction and bibliographic miRNA to disease association. Nucleic Acids Research, 39(Web Server issue), W145-8.

Examples

```
targets <- getTargetsFromSource('let-7a', species='hsa', source='targetscan')
head(targets) #top of the list for TargetScan only
```

MirnaDb-class   *Database class*

Description

object of `MirnaDb` class holds the sqlite database connection, and extends `AnnotationDb` class from AnnotationDbi package. `columns`, `keys`, `keytypes` and `select` methods allow access to database tables and retrieval of miRNA target information.

`select` is the most important method, allows querying the database for predictions from a specific source and species for a given miRNA

Usage

```
columns(x)
keytypes(x)
keys(x, keytype, ...)
select(x, keys, columns, keytype, ...)

## S4 method for signature 'MirnaDb'
columns(x)

## S4 method for signature 'MirnaDb'
keytypes(x)

## S4 method for signature 'MirnaDb'
keys(x, keytype, ...)

## S4 method for signature 'MirnaDb'
select(x, keys, columns, keytype, ...)
```

Arguments

x	the `MirnaDb` object
keytype	the keytype that matches the keys used; the table in which the search should be performed.
...	any optional arguments

| keys | the key to select records for from the database - miRNA name; all possible keys (miRNAs) are returned by using the `keys` method. |
| columns | in this case same as `keytype`, the table in which the search should be performed, this value specifies the source of predictions as well as species; as with `keys`, all possible columns are returned by using the `columns` method. |

Value

string vectors, for `select` a data.frame with target genes and scores

Author(s)

Maciej Pajak <m.pajak@sms.ed.ac.uk>

Examples

```
#first load the annotations
require(miRNAtap.db)
#see all available tables
keytypes(miRNAtap.db)
```

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miRNAtap   *miRNAtap: microRNA Targets - Aggregated Predictions.*

Description

miRNAtap: microRNA Targets - Aggregated Predictions.

Details

It is a package with tools to facilitate implementation of workflows requiring miRNA prediction through access to multiple prediction results (DIANA, Targetscan, PicTar and Miranda) and their aggregation. Three aggregation methods are available: minimum, maximum and geometric mean, additional parameters provide further tuning of the results. Predictions are available for Homo sapiens, Mus musculus and Rattus norvegicus (the last one through homology translation).

Author(s)

Maciej Pajak <m.pajak@sms.ed.ac.uk>, Ian Simpson

Examples

```
#direct targets in mouse aggregated from all sources:
targets_mouse <- getPredictedTargets('let-7a',species='mmu', method='geom')
#homology-translated targets in rat aggregated from all sources
targets_rat <- getPredictedTargets('let-7a',species='mmu', method='geom')
```

---

translate   *Homology translation for miRNAtap*

Description

Homology translation for miRNAtap

Usage

```
translate(entrezes, from = "mmu", to = "rno", ...)
```

Arguments

entrezes	data.frame with entrez Gene IDs and their scores
from	origin species
to	target species
...	any optional arguments

Details

Translates gene ID using homology information from homologene.

Value

data.frame object with orthologous genes' entrez IDs and corresponding scores

Author(s)

Maciej Pajak <m.pajak@sms.ed.ac.uk>

Examples

```
mouse_genes <- data.frame(GeneID =
        c("15364", "56520", "57781", "58180", "18035", "239857"))
translate(mouse_genes, from='mmu', to='rno')
```

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