Package ‘miRNAtap’

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 (>= 3.3.0), AnnotationDbi

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

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

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aggregateRanks

Description

This function performs aggregation phase of target prediction for `getPredictedTargets`. Consensus ranking is derived from multiple individual rankings. Available methods include minimum, maximum and geometric mean with further tuning parameters which promote true positives at the top of the final ranking.

Usage

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

Arguments

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

Value

data.frame object with ranks per source and aggregate ranks

Author(s)

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getPredictedTargets

Examples

data = data.frame(GeneID=c("15364", "56520", "57781", "58180", "18035"),
                   source1scores=c(0.9,0.5,0.3,NA,NA),
                   source2scores=c(0.7,NA,0.8,0.6,0.5),
                   source3scores=c(0.5,NA,0.3,0.1,0.2))
data # dataframe with scores
aggregateRanks(data, n_valid_srcs=3, min_src=2, method='geom')
#note how gene 56520 is eliminated as it appeared in fewer than 2 sources

getPredictedTargets  Get aggregated ordered list of predicted targets for miRNA

Description

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 five 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.

Usage

generatedPredictedTargets(mirna, sources = c("pictar", "diana",
                                         "targetscan", "miranda", "mirdb"), species = "mmu", min_src = 2,
                          method = "geom", promote = TRUE, synonyms = TRUE, both_strands = FALSE, ...)

Arguments

mirna        miRNA in a standard format
sources      a list of sources to use for aggregation, default is all five sources, i.e. c('pictar', 'diana',
                  "targetscans", "miranda", "mirdb")
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', and 'geom'; 'min' is a
             minimum of ranks, 'max' is a maximum of ranks, and default 'geom' is based
             on geometric mean of the ranks which proves to be the most accurate method.
promote      add weights to improve accuracy of the method, default TRUE
synonyms     when searching for -3p miRNA automatically also searches for miRNA with the same name but ending with * (some databases list -3p miRNA this way) and other way around, similarly for -5p miRNA, default TRUE
both_strands overrides synonyms and searches for targets of both -5p and -3p strands together
...

Details

Tuning min_src parameter is an easy way of prioritising precision at the top of the list (high values) or total recall (low values). For the five default input sources, recommended values are 2, 3, or 4.
getTargetsFromSource

Value

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 are returned.

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References


Examples

targets <- getPredictedTargets('let-7a',species='hsa', method = 'min')
head(targets) #top of the list with minimum aggregation

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

Description

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

Usage

getTargetsFromSource(mirna, species = "mmu", source = "diana", synonyms = TRUE, both_strands = FALSE)
**getTargetsFromSource**

**Arguments**

- **mirna**: miRNA in a standard format
- **species**: species in a standard three-letter acronym, default 'mmu'
- **source**: a source target prediction algorithm table to query, default 'diana', other possible values are 'miranda', 'targetscan', and 'pictar'
- **synonyms**: when searching for -3p miRNA automatically also searches for miRNA with the same name but ending with * (some databases list -3p miRNA this way) and other way around, similarly for -5p miRNA, default TRUE
- **both_strands**: overrides synonyms and searches for targets of both -5p and -3p strands together

**Value**

data.frame object with entrez IDs of target genes and their scores, if there are no targets found for a given miRNA in a given table then an empty

**Author(s)**

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**References**


**Examples**

```r
targets <- getTargetsFromSource('let-7a', species='hsa', source='targetscan')
head(targets)
#top of the list of human targets of let-7a from 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
miRNAtap: microRNA Targets - Aggregated Predictions.

Description

It is a package with tools to facilitate implementation of workflows requiring miRNA prediction through access to multiple prediction results (DIANA, Targetscan, PicTar, Miranda, and miRDB) 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)

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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 = 'rno', method = 'geom')

translate

Homology transfer for miRNAtap

Description

This function maps gene entrez ID between species using homology information from Homologene.

Usage

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

entrezes  data.frame with entrez Gene IDs and their scores
from     origin species, default 'mmu', Mus musculus
to       target species, default
...      any optional arguments

Value

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

Author(s)

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Examples

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