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).
License  GPL-2
Depends  R (>= 3.3.0), AnnotationDbi
Imports  DBI, RSQLite, stringr, sqldf, plyr, methods
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biocViews  Software, Classification, Microarray, Sequencing, miRNA
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R topics documented:

- aggregateRanks
- getPredictedTargets
- getTargetsFromSource
- MirnaDb-class
- miRNAAtap
- translate

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 of 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

generatePredictedTargets(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','targetscan','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
...
any optional arguments

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.
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.

Author(s)

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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

getTargetsFromSource

Get target list from a single source

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)
**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**

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

```r
## 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

Author(s)
Maciej Pajak <m.pajak@sms.ed.ac.uk>, Ian Simpson

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

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)

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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