

# Package ‘miRNAtap’

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**Type** Package

**Title** miRNAtap: microRNA Targets - Aggregated Predictions

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**Author** Maciej Pajak, T. Ian Simpson

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

**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 (>= 3.0.0), AnnotationDbi

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

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

**biocViews** Software, Classification, Microarray, Sequencing, miRNA

**Roxygen** list(wrap = FALSE)

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aggregateRanks      *Auxiliary targetPredictor functions*

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### 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*

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### 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 = "min", 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', default 'min' is a minimum of ranks, 'max' is a maximum of ranks, and '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 miRNA`tap`.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

**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)
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
```

---

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

## 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
```

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MirnaDb-class

*Database class*

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### 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.
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.

...                any optional arguments

**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)
```

---

miRNA<sub>tap</sub>

*miRNA<sub>tap</sub>: microRNA Targets - Aggregated Predictions.*

---

**Description**

miRNA<sub>tap</sub>: 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>, T. 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)
```

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translate	<i>Homology translation for miRNA<sub>tap</sub></i>
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**Description**

Homology translation for miRNA<sub>tap</sub>

**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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