

miRNA_{Atap} example use

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Contents

| | | |
|----------|----------------------------|----------|
| 1 | Introduction | 2 |
| 2 | Installation | 2 |
| 3 | Workflow | 3 |
| 4 | Session Information | 5 |
| | References | 6 |

1 Introduction

miRNAtap package is designed to facilitate implementation of workflows requiring miRNA prediction. Aggregation of commonly used prediction algorithm outputs in a way that improves on performance of every single one of them on their own when compared against experimentally derived targets. microRNA (miRNA) is a 18-22nt long single strand that binds with RISC (RNA induced silencing complex) and targets mRNAs effectively reducing their translation rates.

Targets are aggregated from 5 most commonly cited prediction algorithms: DIANA (Maragkakis et al., 2011), Miranda (Enright et al., 2003), PicTar (Lall et al., 2006), TargetScan (Friedman et al., 2009), and miRDB (Wong and Wang, 2015).

Programmatic access to sources of data is crucial when streamlining the workflow of our analysis, this way we can run similar analysis for multiple input miRNAs or any other parameters. Not only does it allow us to obtain predictions from multiple sources straight into R but also through aggregation of sources it improves the quality of predictions.

Finally, although direct predictions from all sources are only available for *Homo sapiens* and *Mus musculus*, this package includes an algorithm that allows to translate target genes to other speices (currently only *Rattus norvegicus*) using homology information where direct targets are not available.

2 Installation

This section briefly describes the necessary steps to get miRNAtap running on your system. We assume that the user has the R program (see the R project at <http://www.r-project.org>) already installed and is familiar with it. You will need to have R 3.2.0 or later to be able to install and run miRNAtap. The miRNAtap package is available from the Bioconductor repository at <http://www.bioconductor.org>. To be able to install the package one needs first to install the core Bioconductor packages. If you have already installed Bioconductor packages on your system then you can skip the two lines below.

```
> if (!requireNamespace("BiocManager", quietly=TRUE))
+   install.packages("BiocManager")
> BiocManager::install()
```

Once the core Bioconductor packages are installed, we can install the miRNAtap and accompanying database miRNAtap.db package by

```
> if (!requireNamespace("BiocManager", quietly=TRUE))
+   install.packages("BiocManager")
> BiocManager::install("miRNAtap")
> BiocManager::install("miRNAtap.db")
```

3 Workflow

This section explains how `miRNAtap` package can be integrated in the workflow aimed at predicting which processes can be regulated by a given microRNA.

In this example workflow we'll use `miRNAtap` as well as another Bioconductor package `topGO` together with Gene Ontology (GO) annotations. In case we don't have `topGO` or GO annotations on our machine we need to install them first:

```
> if (!requireNamespace("BiocManager", quietly=TRUE))
+   install.packages("BiocManager")
> BiocManager::install("topGO")
> BiocManager::install("org.Hs.eg.db")
```

Then, let's load the required libraries

```
> library(miRNAtap)
> library(topGO)
> library(org.Hs.eg.db)
```

Now we can start the analysis. First, we will obtain predicted targets for human miRNA *miR-10b*

```
> mir = 'miR-10b'
> predictions = getPredictedTargets(mir, species = 'hsa',
+                                   method = 'geom', min_src = 2)
```

Let's inspect the top of the prediction list.

```
> head(predictions)
```

| | source_1 | source_2 | source_3 | source_4 | source_5 | rank_product | rank_final |
|--------|----------|----------|----------|----------|----------|--------------|------------|
| 627 | 103 | 10.0 | 1.0 | NA | 1 | 1.416281 | 1 |
| 79741 | NA | NA | 8.0 | 2 | NA | 2.000000 | 2 |
| 6095 | 5 | 2.5 | 73.5 | NA | 5 | 2.058173 | 3 |
| 348980 | NA | 2.5 | 20.0 | NA | NA | 3.535534 | 4 |
| 51365 | NA | 53.0 | 3.0 | 12 | 27 | 3.766392 | 5 |
| 7022 | 88 | 17.5 | 5.0 | 149 | 3 | 4.058725 | 6 |

We are using *geometric mean* aggregation method as it proves to perform best when tested against experimental data from MirBase (Griffiths-Jones et al., 2008).

We can compare it to the top of the list of the output of *minimum* method:

```
> predictions_min = getPredictedTargets(mir, species = 'hsa',
+                                       method = 'min', min_src = 2)
> head(predictions_min)
```

| | source_1 | source_2 | source_3 | source_4 | source_5 | rank_product | rank_final |
|-------|----------|----------|----------|----------|----------|--------------|------------|
| 627 | 103 | 10 | 1.0 | NA | 1 | 1 | 2.0 |
| 8897 | 1 | 183 | 282.0 | NA | NA | 1 | 2.0 |
| 79042 | NA | 107 | 99.5 | 1 | NA | 1 | 2.0 |
| 7182 | 2 | NA | NA | NA | 106 | 2 | 5.5 |
| 10739 | NA | 42 | 2.0 | NA | NA | 2 | 5.5 |
| 79741 | NA | NA | 8.0 | 2 | NA | 2 | 5.5 |

Where predictions for rat genes are not available we can obtain predictions for mouse genes and translate them into rat genes through homology. The operation happens automatically if we specify species as `rno` (for *Rattus norvegicus*)

```
> predictions_rat = getPredictedTargets(mir, species = 'rno',
+                                     method = 'geom', min_src = 2)
```

Now we can use the ranked results as input to GO enrichment analysis. For that we will use our initial prediction for human *miR-10b*

```
> rankedGenes = predictions[, 'rank_product']
> selection = function(x) TRUE
> # we do not want to impose a cut off, instead we are using rank information
> allGO2genes = annFUN.org(whichOnto='BP', feasibleGenes = NULL,
+                          mapping="org.Hs.eg.db", ID = "entrez")
> GOdata = new('topGOdata', ontology = 'BP', allGenes = rankedGenes,
+             annot = annFUN.GO2genes, GO2genes = allGO2genes,
+             geneSel = selection, nodeSize=10)
```

In order to make use of the rank information we will use Kolomonogorov Smirnov (K-S) test instead of Fisher exact test which is based only on counts.

```
> results.ks = runTest(GOdata, algorithm = "classic", statistic = "ks")
> results.ks
```

Description:

Ontology: BP

'classic' algorithm with the 'ks' test

528 GO terms scored: 5 terms with p < 0.01

Annotation data:

Annotated genes: 351

Significant genes: 351

Min. no. of genes annotated to a GO: 10

Nontrivial nodes: 528

We can view the most enriched GO terms (and potentially feed them to further steps in our workflow)

```
> allRes = GenTable(GOdata, KS = results.ks, orderBy = "KS", topNodes = 20)
> allRes[,c('GO.ID', 'Term', 'KS')]
```

| | GO.ID | Term | KS |
|----|------------|---|--------|
| 1 | GO:0044087 | regulation of cellular component biogene... | 0.0022 |
| 2 | GO:0065007 | biological regulation | 0.0025 |
| 3 | GO:0050789 | regulation of biological process | 0.0026 |
| 4 | GO:0050794 | regulation of cellular process | 0.0041 |
| 5 | GO:0042692 | muscle cell differentiation | 0.0044 |
| 6 | GO:0044093 | positive regulation of molecular functio... | 0.0111 |
| 7 | GO:0051146 | striated muscle cell differentiation | 0.0118 |
| 8 | GO:0006397 | mRNA processing | 0.0171 |
| 9 | GO:0044089 | positive regulation of cellular componen... | 0.0235 |
| 10 | GO:0043254 | regulation of protein-containing complex... | 0.0253 |
| 11 | GO:0060255 | regulation of macromolecule metabolic pr... | 0.0259 |
| 12 | GO:0006351 | DNA-templated transcription | 0.0272 |
| 13 | GO:0043085 | positive regulation of catalytic activit... | 0.0296 |
| 14 | GO:0050790 | regulation of catalytic activity | 0.0308 |
| 15 | GO:0010468 | regulation of gene expression | 0.0322 |
| 16 | GO:0048731 | system development | 0.0350 |
| 17 | GO:0006355 | regulation of DNA-templated transcriptio... | 0.0366 |
| 18 | GO:2001141 | regulation of RNA biosynthetic process | 0.0366 |
| 19 | GO:0010556 | regulation of macromolecule biosynthetic... | 0.0372 |
| 20 | GO:0051252 | regulation of RNA metabolic process | 0.0427 |

For more details about GO analysis refer to `topGO` package vignette (Alexa and Rahnenfuhrer, 2010).

Finally, we can use our predictions in a similar way for pathway enrichment analysis based on KEGG (Kanehisa and Goto, 2000), for example using Bioconductor's `KEGGprofile` (Zhao, 2012).

4 Session Information

- R version 4.5.0 beta (2025-04-02 r88102), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_GB, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Time zone: America/New_York
- TZcode source: system (glibc)
- Running under: Ubuntu 24.04.2 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.22-bioc/R/lib/libRblas.so

- LAPACK:
/usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0
- Base packages: base, datasets, grDevices, graphics, methods, stats, stats4, utils
- Other packages: AnnotationDbi 1.69.1, Biobase 2.67.0, BiocGenerics 0.53.6, GO.db 3.21.0, IRanges 2.41.3, S4Vectors 0.45.4, SparseM 1.84-2, generics 0.1.3, graph 1.85.3, miRNAatap 1.41.0, miRNAatap.db 0.99.10, org.Hs.eg.db 3.21.0, topGO 2.59.0
- Loaded via a namespace (and not attached): Biostrings 2.75.4, DBI 1.2.3, GenomeInfoDb 1.43.4, GenomeInfoDbData 1.2.14, KEGGREST 1.47.1, R6 2.6.1, RSQLite 2.3.9, Rcpp 1.0.14, UCSC.utils 1.3.1, XVector 0.47.2, bit 4.6.0, bit64 4.6.0-1, blob 1.2.4, cachem 1.1.0, chron 2.3-62, cli 3.6.4, compiler 4.5.0, crayon 1.5.3, fastmap 1.2.0, glue 1.8.0, grid 4.5.0, gsubfn 0.7, httr 1.4.7, jsonlite 2.0.0, lattice 0.22-7, lifecycle 1.0.4, magrittr 2.0.3, matrixStats 1.5.0, memoise 2.0.1, pkgconfig 2.0.3, plyr 1.8.9, png 0.1-8, proto 1.0.0, rlang 1.1.6, sqldf 0.4-11, stringi 1.8.7, stringr 1.5.1, tools 4.5.0, vctrs 0.6.5

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