miRNAtap.db: microRNA Targets - Aggregated Predictions database use

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1 Introduction

`miRNAtap.db` package provides annotation data for `miRNAtap` performing target prediction aggregation. 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.

Targets are aggregated from 4 most commonly cited prediction algorithms: DIANA (Maragkakis et al., 2011), Miranda (Enright et al., 2003), PicTar (Lall et al., 2006) and TargetScan (Friedman et al., 2009).

To read more about miRNA target prediction methods used refer to the `miRNAtap` package vignette available from http://www.bioconductor.org .

2 Installation

This section briefly describes the necessary steps to get `miRNAtap.db` 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 3.0.0 or later to be able to install and run `miRNAtap.db`. 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.

```
> source("http://bioconductor.org/biocLite.R")
> biocLite()
```

Once the core Bioconductor packages are installed, we can install the miRNAtap package by

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("miRNAtap.db")
```

3 Workflow

For the information about how to use the miRNA target data refer to the `miRNAtap` package vignette available from http://www.bioconductor.org.

4 Session Information

- R version 3.1.1 (2014-07-10), `x86_64-w64-mingw32`
- Locale: `LC_COLLATE=C`, `LC_CTYPE=English_United Kingdom.1252`, `LC_MONETARY=English_United Kingdom.1252`, `LC_NUMERIC=C`, `LC_TIME=English_United Kingdom.1252`

- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): tools 3.1.1

References

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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.

Lall, S., Grün, D., Krek, A., Chen, K., Wang, Y.-L., Dewey, C. N., Sood, P., Colombo, T., Bray, N., Macmenamin, P., Kao, H.-L., Gunsalus, K. C., Pachter, L., Piano, F., and Rajewsky, N. (2006). A genome-wide map of conserved microRNA targets in C. elegans. *Current biology : CB*, 16(5):460–71.

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