

Algorithm and workflow of miRDB

Author : Tariq Abdullah

Categories : [Algorithms](#), [miRNA Target Prediction](#)

Date : September 13, 2018

As mentioned in the previous [article](#), Micro RNAs (miRNAs) are the short endogenous RNAs (~22 nucleotides) and originate from the non-coding RNAs [1], produced in single-celled eukaryotes, viruses, plants, and animals [2]. They play significant roles in various biological processes such as degradation of mRNA [3]. Several databases exist storing a large amount of information about miRNAs, one of such databases miRBase [4] was explained in the previous article, today we will explain the algorithm of miRDB [5,6], another database for miRNA target prediction.

miRDB is an online database for miRNA target prediction and functional annotation [6]. It predicts the original results and has a wiki editing interface for miRNA annotations [6]. This wiki interface allows the community editing which results in more active and interactive database. miRDB is freely accessible at <http://mirdb.org/>.

miRDB has two databases and related web interfaces serving two main purposes [6]:

1. the retrieval of miRNA targets which are predicted by computational methods, and
2. miRNA functional annotation using wiki editing interface.

miRDB predicts the miRNA targets for five species: human, mouse, rat, chicken, and dog. It mainly focuses on the mature miRNAs because they are the functional carriers of miRNA-mediated gene regulation [6,7]. It has been reported by many studies that the miRNA having the same seed sequence targets the similar set of genes [8,9], and therefore, they are known as “functionally similar” [5]. It primarily focuses on the mature miRNAs and hence, the pages of its functional analog are organized according to the miRNAs.

How do the targets are predicted in miRDB?

miRNA sequences and nomenclature are taken from the miRBase [4]. All the database tables are linked to

other tables in miRDB. All the miRNA sequences and annotation files are taken from the NCBI databases [10,11]. mRNA 3'-UTR sequenced are imported from the GenBank files using BioPerl (<http://www.bioperl.org>) and for the genome-wide target prediction, MirTaregt2 [12] is used. Multiple mRNAs of the same gene are mapped using NCBI gene index files and the mRNA with the highest target prediction score is displayed on the website [5]. The prediction results are also made available to download as a batch file from the 'Data Download' page. Pathway data is also provided using the PANTHER database [13]. Target prediction is performed for each pathway to identify the miRNAs which are significantly associated with the pathways. A hypergeometric test is performed to find the statistical significance of the pathway-specific targets using all the genes in the genome [5].

The functional annotation page consists of miRNA sequences, genes, nomenclature, references, and experimental evidence. The expression profile results of 40 human tissues detected with RT-PCR [14] are also included in the miRDB. A new updated version of miRDB also allows the custom search using a user-provided miRNA or gene target sequence, and a search for unconventional target sites in the coding region or 5'-UTR. The miRNA data is also available to download with the current version miRDB 5.0 implementing the latest version of the target prediction tool, namely, MirTarget V3 (<http://mirdb.org/download.html>). Recently, miRDB has added 2.1 million predicted gene targets regulated by 6709 miRNAs [6].

If you would like to read further details about miRNA prediction using miRDB [click here](#). We will be discussing other miRNA databases in detail in the upcoming articles.

References

1. Bartel, D. P. (2004). MicroRNAs: genomics, biogenesis, mechanism, and function. *cell*, 116(2), 281-297.
2. Liu, B., Li, J., & Cairns, M. J. (2012). Identifying miRNAs, targets and functions. *Briefings in bioinformatics*, 15(1), 1-19.
3. He, L., & Hannon, G. J. (2004). MicroRNAs: small RNAs with a big role in gene regulation. *Nature Reviews Genetics*, 5(7), 522.
4. Sam Griffiths-Jones, Russell J. Grocock, Stijn van Dongen, Alex Bateman and Anton J. Enright. miRBase: microRNA sequences, targets, and gene nomenclature. D140–D144 *Nucleic Acids Research*, 2006, Vol. 34, Database issue. doi:10.1093/nar/gkj112
5. XIAOWEI WANG. miRDB: A microRNA target prediction and functional annotation database with a wiki interface. *RNA* (2008), 14:1012–1017. Published by Cold Spring Harbor Laboratory Press. Copyright 2008 RNA Society.
6. Wong, N., & Wang, X. (2014). miRDB: an online resource for microRNA target prediction and functional annotations. *Nucleic acids research*, 43(D1), D146-D152.
7. Bartel D. MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell* 004;116:281–97.
8. Lewis, B.P., Burge, C.B., and Bartel, D.P. 2005. Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell* 120: 15–20.
9. Linsley, P.S., Schelter, J., Burchard, J., Kibukawa, M., Martin, M.M., Bartz, S.R., Johnson, J.M., Cummins, J.M., Raymond, C.K., Dai, H., et al. 2007. Transcripts targeted by the microRNA-16 family cooperatively regulate cell cycle progression. *Mol. Cell. Biol.* 27: 2240–2252.
10. Benson, D.A., Karsch-Mizrachi, I., Lipman, D.J., Ostell, J., and Wheeler, D.L. 2007. GenBank. *Nucleic Acids Res.* 35: D21–D25. doi: 10.1093/nar/gkl986

11. Maglott, D., Ostell, J., Pruitt, K.D., and Tatusova, T. 2007. Entrez Gene: Gene-centered information at NCBI. *Nucleic Acids Res.* 35:D26–D31. doi: 10.1093/nar/gkl993.
12. Wang, X. and El Naqa, I.M. 2008. Prediction of both conserved and nonconserved microRNA targets in animals. *Bioinformatics* 34:325–332.
13. Mi, H., Lazareva-Ulitsky, B., Loo, R., Kejariwal, A., Vandergriff, J., Rabkin, S., Guo, N., Muruganujan, A., Doremieux, O., Campbell, M.J., et al. 2005. The PANTHER database of protein families, subfamilies, functions and pathways. *Nucleic Acids Res.* 33: D284–D288. doi: 10.1093/nar/gki078.
14. Liang, Y., Ridzon, D., Wong, L., and Chen, C. 2007. Characterization of microRNA expression profiles in normal human tissues. *BMC Genomics* 8: 166

Sharing is caring. Spread the love!

- [Print](#)
- [Email](#)
- [LinkedIn](#)
- [Twitter](#)
- [Facebook](#)
- [Google](#)
-