# MiRBrowser manual

Last update: Oct 20, 2014

1. Running environment miRBrowser is a Perl program, an operation system support Perl should be prepared before next step. In Linux system, Ubuntu would be preferred, Perl is natively integrated in the system, therefore, we highly recommend you running our program on this platform. However, you can also use our program pack in Windows based computer. You should preinstall a program named as ActivePerl before your running of FindTar3 or other program we provided. You can download ActivePerl from http://www.activestate.com/activeperl/downloads. Or you can directly download it from "Download Page" of FindTar3 website.

2. Installation

    The download package of miRBrowser is compressed pack in .tar.gz format, You can decompressed it using ":~$ tar -xvf ***.tar.gz" in Linux. In windows system, we provide a package containing an executable file and a folder contain accessories. Decompress them to the directory of your intention before use. For the convenience, we suggest you install miRBrowser in the directory /usr/local/bin in Linux system. After installation, you can directly double click /bin/miRBrowser.pl and select "run" to run the program in Linux or double click miRBrowser.pl in Windows. A window session should be displayed as below. (Please make sure perl-tk package has been installed!)
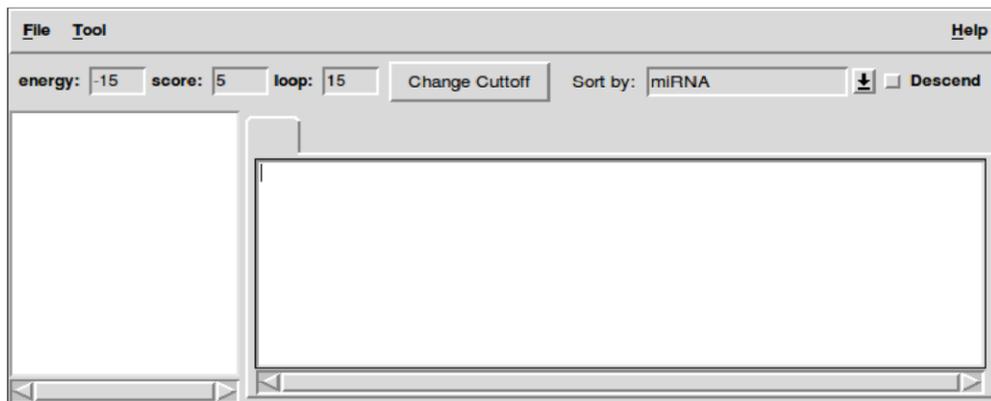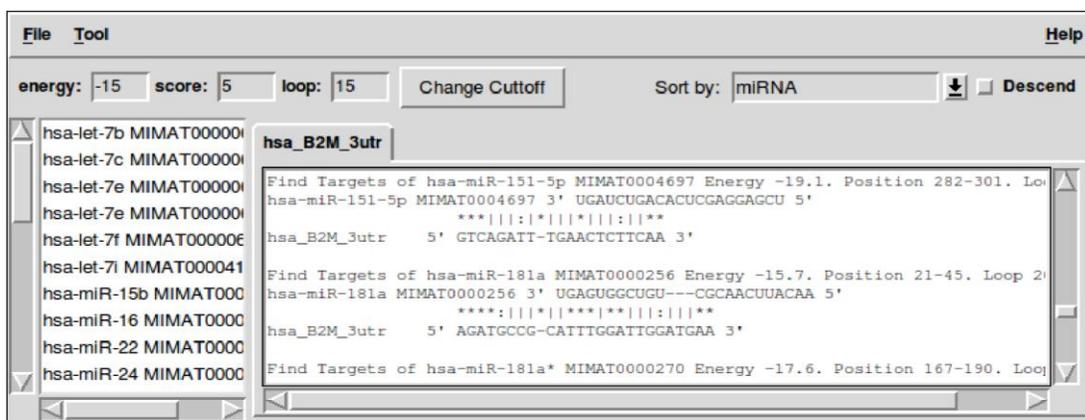

3. Open a target file

    Once being calculated by FindTar3, click "File" → "Open", and find your target file in the directory, select "OK". Then the target file should be opened and all predicted targets should be displayed in the miRBrowser. In the upper panel, we provide manual modification for cutoff free energy, dynamic programming score, and loop score on the left part displayed as "energy", "score" and "loop" respectively, and a sorting function on the right. The default values are: energy -15, score 5, loop 15.

    The free energy is the RNA secondary structure free energy calculated by RNAcofold which is a component of Vienna RNA package. A solid miRNA:MRE duplex complementary, which means higher free energy, generally help the well function of miRNA translational repression. But it is not all the case. Sometimes, a target with free energy as low as -12 kcal/mol may also have significant repression effect as well. The dynamic programming score is the value of "non-seed" region portion of miRNA:MRE duplex. We compulsory defined the priority basepair match in the 5' end of miRNA:MRE duplex. The loop score varies from 0 to 25, you can trace the detail definition of loop score from our latest publication. Although being default as 15, we highly recommended you to set it as 20 when searching for a miRNA target. According to our experimental data, loop score is a very critical issue for miRNA target function. For the details, please refer to the latest publication of our lab.

    On the right portion of this panel, we provide a sorting function. You can sort target file with miRNA name, target position on the mRNA strand, free energy value, dynamic programming score value, and loop score value. The default order is ascending, you can check the "descend" box for descending sort.

4. Count targets

    After opening a target file, you probably intend to know how these miRNA targets distribute on this mRNA strand. This function may help you. Select "Tool" → "Count Targets", a pop-out window should display as following:
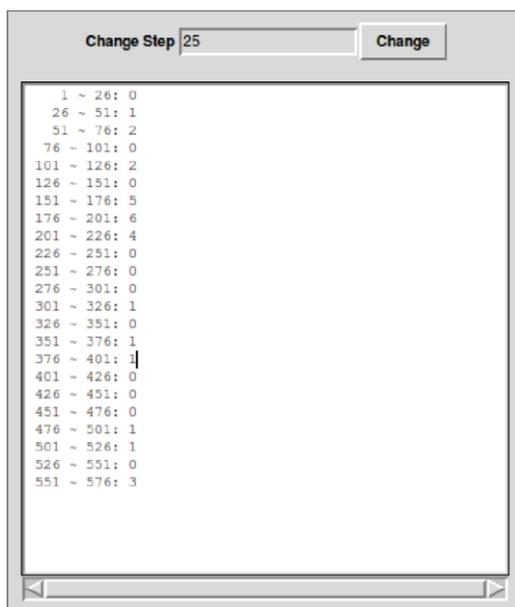
    The default step is 250nt, you can modify it at your option. With this tool, you can easily get to know which portion of the object mRNA strand has concentrated miRNA targets.

5. Show targets general information

    After opening a target file, select "Tool" → "Show Target Information", a pop-out window will be displayed, containing the information of total miRNA number which has target on this strand and the total target number under the present "cutoff" threshold.
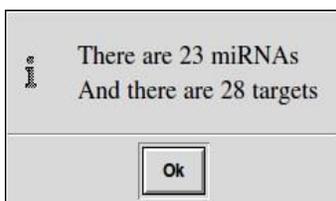

6. Select a specific miRNA

When you want to concentrate on several miRNAs but not all of them, you can click "Tool" → "Select miRNA", a pop-out window should be displayed, and you can select the specific miRNAs of your interest, then click "OK". Then, in the main window of miRBrowser, only the select miRNA targets will be displayed.
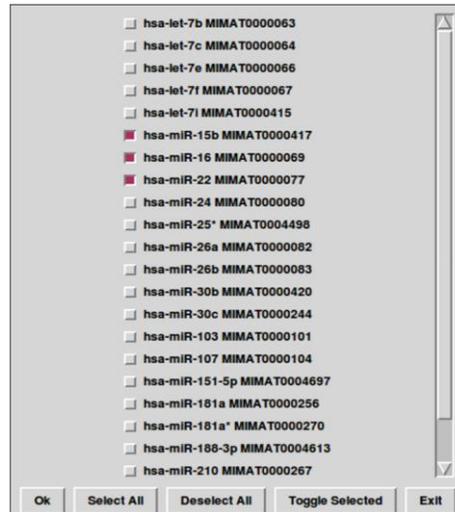
7. Change target display format
   We also provide this convenient tool for you to modify the output format of target file by selecting "Tool" → "Change Target Format" → "Edit Format". It has detail specification in the window, you can just read them. The window displays as following:
   You can even obtain the miRNA:MRE duplex structure of dynamic programming, which has been omitted in the final output window.
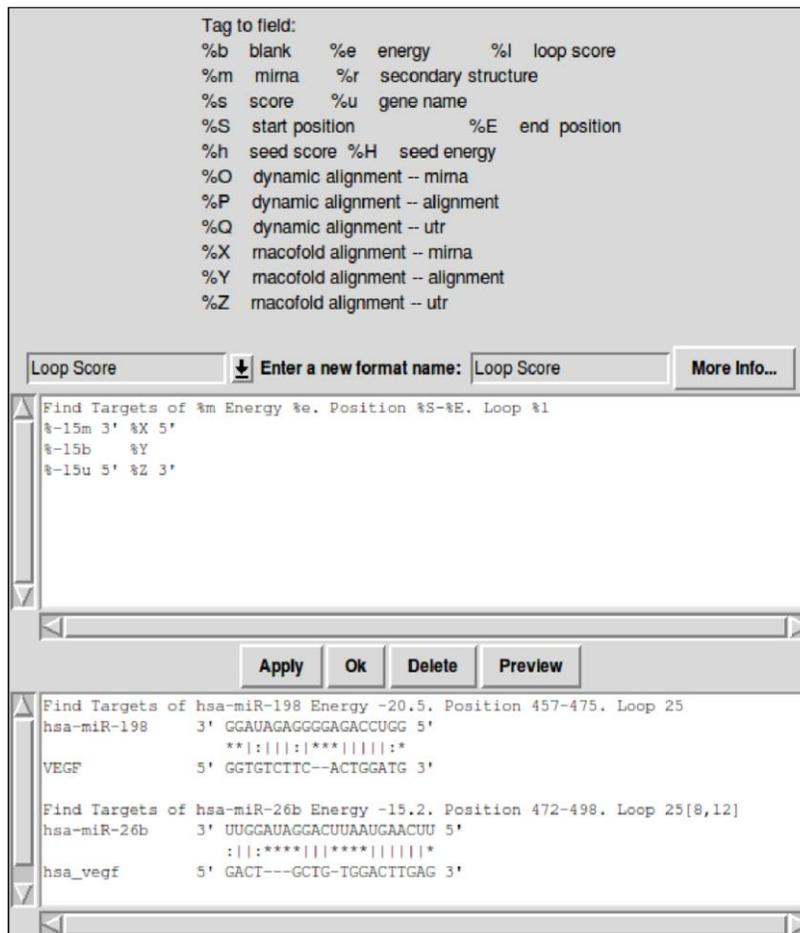
8. If you still have any question in using of miRBrowser, please contact Dr. Yaou Zhang zhangyo@sz.tsinghua.edu.cn.