

FindTar3 Manual

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NAME

FindTar3 – For predicting miRNA targets in animal mRNA 3'UTRs

SYNOPSIS

Basic Usage:

FINDTAR *miRNA_file* *3'UTR_file* -o *output_file*

Advanced:

FINDTAR [*miRNA_file* *3'UTR_file*] [-o *output_file*] [-tab|-text] [-at *at_weight*] [-gc *gc_weight*] [-gt *gt_weight*] [-mis *mismatch_weight*] [-go *gap_open*] [-ge *gap_extension*] [-energy *free energy*] [-score *dp_score*] [-loop *loopscore*] [-T *temperature*] [-noLP] [--verbose]

DESCRIPTION

FindTar3 is a program for prediction of potential miRNA target sites in mRNA 3'UTR of animal genes. FindTar3 reads RNA sequences from miRNA sequence file from *miRNA_file* and mRNA 3'UTR sequence file from *3'UTR_file*. All input files MUST be in FASTA format.

Examples of miRNA FASTA format sequence:

```
>hsa-miR-376b MIMAT0002172
AUCAUAGAGGAAAAUCCAUGUU
```

Examples of mRNA FASTA format sequence:

```
>NM_003376
CAAGCCGAGGCGGTGAGCCGGGCAGGAGGAAGGAGCCTCCCTCAGGGTTT
CGGGAAACCAGATCTCTCACCAGGAAAGACTGATACAGAACGATCGATACA
GAAACCACGCTGCCGCCACCACACCATCACCATCGACAGAACAGTCCTTA
ATCCAGAAACCTGAAATGAAGGAAGAGGAGACTCTGCGCAGAGCACTTG
GGTCCGGAGGGCGAGACTCCGGCGGAAGCATTCCCGGGCGGGTGACCCAG
CACGGTCCCTCTTGGAAATTGGATTGCGCATTTTATTTTCTTGCTGCTAA
ATCACCAGCCCCGGAAGATTAGAGATTTTATTTCTGGGATTCTGTAGA
CACACCCACCCACATACATACATTTATATATATATATATATATATATAT
AAAAATAAATATCTCTATTTTATATATATAAAAATATATATATT . . .
```

FindTar3 applied a flexible “window” for selecting miRNA:MRE seed. We predefined the p1-p8 of miRNA:MRE as the seed region, and we allowed six consecutive basepair as a effect seed (only 1 G-U wobble is allowed to appear in this six consecutive basepair, others must be Watson-Crick basepair). Each query miRNA will “slide” over the query mRNA 3'UTR sequence and find out all the seed position that meet the requirement. Therefore, dynamic programming is performed to predict the possible cover range of miRNA target and record the detail length of nucleotide cover range on the mRNA strand. Then, we compulsorily match the seed region, and calculate the RNA secondary structure of miRNA:MRE using RNAcifold in Vienna RNA Package. A central loop score strategy is performed to score all output targets. FindTar3 can output all potential miRNA targets that qualified seed criteria. Then you can read and analyze the target file in miRBrowser, another program of Yaou Lab, which provide recommendation for target selection.

OPTIONS

-h

Display help information and command line options.

-v

Display version information.

-o output_file

Select all prediction targets to output file, and you can name output target file at your intention.

- tab| -text

If you want export file for analyzing in our targets browser program miRBrowser, you should use -tab, which is also the default. You can also choose to output target file by using -text, then the target structure will display as following:

```
# version      3.11.12
# ATWeight     5
# GCWeight     5
# GTWeight     2
# MisWeight    -3
# GapOpen      -8
# GapExt       -2
# SeedEnd      8
# Temperature  37
# Fields: mirna score energy start end align energy_align seed_score seed_energy loop
structure
NM_003376
=====
hsa-miR-376b MIMAT0002172 NM_003376
Position: 1312, 1337  Score: 23  Energy: -11.7  seed: 29, -8.9

dynamic programming structure:
miRNA: UUGUACCUAAAAG--G--AGAUACUA
      |:|**|*|||**|**|:|**|*
3'UTR: AATATTTAATTTCAACTATTTATGAG

findtar final structure:
miRNA: UUGUACCUAAAAG---GAGAUACUA
      *****|**|**|**|:|**|*
3'UTR: AATATTTAATTTCAACTATTTATGAG

Secondary structure:..(((((((.....&.....)))).....))))).

Position: 1586, 1607  Score: 16  Energy: -8.3  seed: 21, -6.6

dynamic programming structure:
miRNA: UUGUACCUAAAAGGAGAUACUA
      *|:|**|*|*|*:*|:|**|*
3'UTR: TATATATATATATGTTTATGTA

findtar final structure:
miRNA: UUGUACCUAAAAGGAGAUACUA
      *****|:|**|*
3'UTR: TATATATATATATGTTTATGTA

Secondary structure:..(((((((.....)).....&.....))))..

Position: 1594, 1617  Score: 14  Energy: -10.3  seed: 29, -8.1

dynamic programming structure:
miRNA: UUGUACC--UAAAAGGAGAUACUA
      *|:|**|*|*|*:*|*|:|**|*
3'UTR: TATATGTTTATGTATATATGTGAT

findtar final structure:
miRNA: UUGUACCUAAAAGGAGAUACUA
      *****|:|**|*
3'UTR: TATGTTTATGTATATATGTGAT

Secondary structure:(((((((.....)).....&((((.....))))..))))))

<NM_003376>hsa-miR-376b MIMAT0002172 : 3 targets sites
=====
```

- at weight**
A-T base pair weight in dynamic programming, default is 5.
- gc weight**
G-C base pair weight in dynamic programming, default is 5.
- gt weight**
G-T (G-U wobble) base pair weight in dynamic programming, default is 2.
- mis mis_weight**
Base pair mismatch weight in dynamic programming, default is -3.
- go gap_open**
Gap open weight in dynamic programming, default is -8.
- ge gap_extension**
Gap extension weight in dynamic programming, default is -2.
- energy free_energy**
Output file free energy threshold, only free energy lower than the threshold can be outputted.
- score dp_score**
Output file dynamic programming score threshold, only score above the threshold can be outputted.
- loop loop_score**
Output file loop score threshold, only score above the threshold can be outputted.
- T temperature**
Temperature using to perform RNA secondary structure prediction, default is 37[°].
- noLP**
Produce structures without lonely pairs (helices of length 1). For partition function folding this only disallows pairs that can only occur isolated. Other pairs may still occasionally occur as helices of length 1. (from RNACofold manpage, Vienna RNA Package)
- verbose**
For debug use only.

VERSION

This man page documents version 3.11.12 of the FindTar3 package.

FEEDBACKS

If you have any problem in using FindTar3, please contact Dr. Yaou Zhang: zhangyo@sz.tsinghua.edu.cn.