TargetMiner:

NAME: TargetMiner

SYNOPSIS:

./TargetMiner -test <filename> -3utr <filename> -mir <filename>

DESCRIPTION:

TargetMiner is a machine learning based target prediction algorithm. The classifier Support Vector Machine (SVM) is used to classify the test data. The SVM is trained with a set of biologically validated positive (miRNA- target pairs) and newly generated negative examples (miRNA- non target pairs). A set of 90 targeting site context specific features is then extracted from the training examples. From this a set of 30 most favorable features with high F-Score is then selected to train the classifier. The robust performance of TargetMiner is achieved due to the use of a set of high quality negative training examples (miRNA-non-target).

To execute TargetMiner users have to provide three input files containing miRNA-mRNA id, 3' UTR sequence database and miRNA sequence database. Input file format can be obtained from the given example files.

TargetMiner has been successfully tested on Linux platform. It can be run on other operating system like Unix but it was not tested.

Download instructions:

1) Download the TargetMiner package into a folder of your choice.

2) Unzip and extract all its files.

3) Go to libsvm-2.88 directory. Use the command 'make'.

4) Go to TargetMiner directory. Type 'chmod +x TargetMiner'.

5) Type: ./TargetMiner -test <filename> -3utr <filename> -mir <filename> to execute TargetMiner.

Usage:

 Type: ./TargetMiner --help to see its usage.

The main parameters the tool expects are:

Test file: A Tab delimited two columns input file. First column contains the miRNA name (ex: >hsa-miR-1) and the second column contains the Refseq id (ex: NM_018362) of mRNA.

3' UTRs file: A fasta format file containing the 3'UTR sequences.

miRs file: A fasta format file containing the miRNA sequences.

The download zip file contains example files:

1) **hg18_3utr.txt:** 3'UTR database file.
2) **hsa_mirbase_list.txt:** MicroRNA sequence file.

3) **bio_verified_positive_test.txt:** Input test file containing biologically validated positive examples.
4) **bio_verified_negative_test.txt:** Input test file containing biologically validated negative examples.
5) **TargetMiner_Prediction_for_bio_verified_positive_test.html:** Tab delimited table of predictions result for biologically validated positive examples
6) **TargetMiner_Prediction_for_bio_verified_negative_test.html:** Tab delimited table of predictions result for biologically validated negative examples.

The output files are produced by the following command:

   ./TargetMiner -test bio_verified_positive_test.txt -3utr hg18_3utr.txt -mir hsa_mirbase_list.txt

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