miRNA Target Scanner Script
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Merve Elmastaş, merveelmastas@icloud.com
Salih Kasım Benli, salihkasimbenli@gmail.com

Description

MicroRNAs(miRNA) firstly discovered in *Caenorhabditis elegans*, are found in most of the eukaryotes.[1] MiRNAs are classified as non-coding, single-stranded RNAs which play essential roles in the regulation of gene expression at the post-transcriptional level via mRNA degradation or gene silencing.[2] So it is crucial to understand miRNA-target interactions. Many databases have been developed to bring miRNA targets information. There is two kind of databases one predicts computationally for instance, TargetScan, miRDB, DIANA-microT. Other collects experimentally such as miRTarBase and TarBase.

Despite of the abundance of databases, they provide thousands of predicted genes for each particular miRNA. Therefore, researchers obliged to devote extra time to select target genes that they are interested. The program collect and compare data from three different data bases which are TargetScan, miRDB and DIANA-microT that are quite popular in the literature. If it finds the genes that common in all three, it will show them with their average target scores with respect to descending order. One can also select 'only best 20 percent' in order to compare just top 20 percent in three data bases then it sorts.

Method

In order to calculate normalized and averaged values of targeting, a scan algorithm is written in Python 3 programming language[3] and with the help of Flask framework[4] it is published on the web. What the algorithm basically does is searching for the miRNA names in the databases, normalizing the targeting value if needed, and comparing and finding the intersection of scanned databases. The code is available at the following hyperlink and the serving website is available at the following hyperlink.

Results & Discussion

The program collects data from TargetScan, miRDB and DIANA-microT then compares their target genes. When the program finds the common target genes in all three then it sorts in a descending order with their average target scores in maximum 30 seconds. If it gets longer than 30 seconds the program will give an error because it is a free server. In the following updates we would figure out this error. Another thing that we desire is to add all databases to our program and implement all combinations of gene intersections.

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[1] Perron MP, Provost P. Protein interactions and complexes in human microRNA biogenesis and function. Front. Biosci. 2008;13:2537–2547. [PMC free article] [PubMed]

[2] Perron MP, Provost P. Protein interactions and complexes in human microRNA biogenesis and function. Front. Biosci. 2008;13:2537–2547. [PMC free article] [PubMed]

[3] Documentation of Python 3

[4] Documentation of Flask