Resource Summary Report

Generated by NIF on May 13, 2025

Triplet-SVM

RRID:SCR_004824
Type: Tool

Proper Citation

Triplet-SVM (RRID:SCR_004824)

Resource Information

URL: http://bioinfo.au.tsinghua.edu.cn/mirnasvm/

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Description: This program is developed for predicting a query sequence with hairpin structure as a real miRNA precursor or not. The triplet-SVM classifier analyzes the triplet elements of the query and predicts it using a SVM classifier. The SVM classifier is previously trained based on the triplet element features of a set of real miRNA precursors and a set of pseudo-miRNA hairpins. triplet-SVM classifier was written by Chenghai Xue and is free to all users but without any warranty.

Resource Type: source code, software resource

Defining Citation: PMID:16381612

Funding:

Resource Name: Triplet-SVM

Resource ID: SCR_004824

Alternate IDs: nlx_82947

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250508T064921+0000

Ratings and Alerts

No rating or validation information has been found for Triplet-SVM.

No alerts have been found for Triplet-SVM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Chen L, et al. (2019) Trends in the development of miRNA bioinformatics tools. Briefings in bioinformatics, 20(5), 1836.

Tyagi A, et al. (2018) Genome-wide discovery of tissue-specific miRNAs in clusterbean (Cyamopsis tetragonoloba) indicates their association with galactomannan biosynthesis. Plant biotechnology journal, 16(6), 1241.

Li Y, et al. (2017) Genome-wide miRNA screening reveals miR-310 family members negatively regulate the immune response in Drosophila melanogaster via co-targeting Drosomycin. Developmental and comparative immunology, 68, 34.

Jin P, et al. (2017) Transcriptome-wide analysis of microRNAs in Branchiostoma belcheri upon Vibrio parahemolyticus infection. Developmental and comparative immunology, 74, 243.

Zeng Z, et al. (2015) Survey of Natural Language Processing Techniques in Bioinformatics. Computational and mathematical methods in medicine, 2015, 674296.

Higashi S, et al. (2015) Mirinho: An efficient and general plant and animal pre-miRNA predictor for genomic and deep sequencing data. BMC bioinformatics, 16, 179.

ElGokhy SM, et al. (2014) Ensemble-based classification approach for micro-RNA mining applied on diverse metagenomic sequences. BMC research notes, 7, 286.

Rahman ME, et al. (2012) MiRANN: a reliable approach for improved classification of precursor microRNA using Artificial Neural Network model. Genomics, 99(4), 189.

Jha A, et al. (2012) miR-BAG: bagging based identification of microRNA precursors. PloS one, 7(9), e45782.

Xu JH, et al. (2008) Identification of microRNA precursors with support vector machine and string kernel. Genomics, proteomics & bioinformatics, 6(2), 121.

Jiang P, et al. (2007) MiPred: classification of real and pseudo microRNA precursors using

random forest prediction model with combined features. Nucleic acids research, 35(Web Server issue), W339.