An Excel Macro Code for the Analysis of the Density and Distance between the Homologous microRNA-Binding Sites

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ABSTRACT

We present a MACRO code (working name TW-iniRNA) to facilitate the analysis of the predicted miRNA-binding sites generated by the miRNAhrend software tools. The TW-miRNA code calculates the density of sites and the distance between the homologuos miRNA-binding sites.

Keywords: Code; MicroRNA; mRNA; Homologous

Abbreviations: miRNA: microRNA; mRNA: messenger RNA; HS: Homologous miRNA-binding sites; SNP: Single Nucleotide Polymorphism

Introduction

The computer-assisted prediction of microRNA-binding sites upon the reference genomic sequences does not reckon with the well-known by now genomic variation, which is characteristic of all biological species [1]. We developed the miRNA-mRNA complementarity alignment tool NEIL [2], and the more complex package called *miRNAhrend* [3] (https://franziskaahrend.pythonanywhere.com/). The latter one is the online-available package for the prediction and visualization of the miRNA-binding sites in any RNA sequence with their following verification by the complementarity alignment. It also allows us to identify the HS [4]. The designed TW-miRNA code (**Supplementary Data**) uses the outputs generated by *miRNAhrend* to assess the density of the HS within the selected mRNA fragments and the distance between the HS. HS are shown to act synergistically. However, it depends on the distance between HS [5], whereas overlapping HS may be considered as useless. The presence of the HS may potentially rescue the miRNA potency if one of the HS is disrupted by the SNP [4]. The proposed TW-miRNA code significantly expands the functionality of the *miRNAhrend* package tools.

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