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An integrated computational validation approach for potential novel miRNA prediction

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Abstract

MicroRNAs (miRNAs) are short, non-coding RNAs between 17bp-24bp length that regulate gene expression by targeting mRNA molecules. The regulatory functions of miRNAs are known to be majorly associated with disease phenotypes such as cancer, cell signaling, cell division, growth and other metabolisms. Novel miRNAs are defined as sequences which does not have any similarity with the existing known sequences and void of any experimental evidences. In recent decades, the advent of next-generation sequencing allows us to capture the small RNA molecules form the cells and developing methods to estimate their expression levels. Several computational algorithms are available to predict the novel miRNAs from the deep sequencing data. In this work, we integrated three novel miRNA prediction programs miRDeep, miRanalyzer and miRPRo to compare and validate their prediction efficiency. The dicer cleavage sites, alignment density, seed conservation, minimum free energy, AU-GC percentage, secondary loop scores, false discovery rates and confidence scores will be considered for comparison and evaluation. Efficiency to identify isomiRs and base pair mismatches in a strand specific manner will also be considered for the computational validation. Further, the criteria and parameters for the identification of the best possible novel miRNA with minimal false positive rates were deduced.

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