A Cost-Effective in-Silico Approach for Identification of MicroRNAs (MiRNAs) Involved in Cellular Senescence Pathway

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Accumulating evidences have shown that miRNA dysregulation occurs in the majority of human malignancies. This study aims to identify miRNAs that are involved in the cellular senescence pathway through in-silico approach. Two different bioinformatics approaches utilizing four bioinformatics software were used to identify overlapping miRNAs: Approach 1 and Approach 2. We found that the use of different bioinformatics approaches produces two different sets of results. These results imply that the use of different bioinformatics approaches approaches is not only cost-effective but also produces more thorough and robust results that act as a preliminary screening which can be very useful for downstream applications.

Keywords: miRNA dysregulation, cost-effective

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