CMEP: A database for circulating microRNA expression profiling

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In recent years, several experimental studies have revealed that the microRNAs (miRNAs) in serum, plasma, exosome and whole blood are dysregulated in various types of diseases, indicating that the circulating miRNAs may serve potential non-invasive biomarkers for disease diagnosis and prognosis. However, there is no database constructed to integrate the large-scale circulating miRNAs profiles, explore the functional pathway they involved and predict the potential biomarkers using feature selection between disease conditions. The Circulating MicroRNA Expression Profiling (CMEP) is a database for integrating, analyzing and visualizing the large-scale expression profiles of phenotype-specific circulating miRNAs. Although there have been several studies attempting to generate circulating miRNA database, they have not yet integrated the large-scale circulating miRNAs profiles and provided the biomarker-selection function using machine learning methods. To fill in this gap, we constructed the CMEP database for integrating, analyzing and visualizing the large-scale expression profiles of phenotype-specific circulating miRNAs. The CMEP database contains massive datasets manually curated from NCBI GEO including 61 datasets, 192 subsets and 9,444 samples. The CMEP provides the differential expression circulating miRNAs analysis and the KEGG functional pathway enrichment analysis. Furthermore, to provide the function of non-invasive biomarker discovery, implementation of several feature-selection methods including ridge regression, lasso regression, support vector machine and random forests. Finally, a user-friendly web interface was implemented to improve the user experience and visualize the data and results of CMEP.

Biography

Chun-Yip Tong is currently a Master’s student at National Chung Hsing University, Institute of Genomic and Bioinformatics and currently researching on circulating micro RNA non-invasive diagnosis

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