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A comprehensive pipeline for biomarker discovery using circulating miRNA microarray data

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Circulating miRNAs have the potential as cancer biomarkers but no consolidated guidelines are established for discovery analyses. Several issues (e.g. data normalization, expected miRNA up-regulation in one of classes, sample size limitation) can affect results making many approaches unsuitable. We developed a structured pipeline with innovative applications of existing bioinformatics methods including:1) an assumption-independent normalization method based on miRNA ratios in data pre-processing; 2) the combination of the results of two statistical tests (t- and Anderson Darling) to detect miRNAs with significant fold change or general distributional differences in class comparison; 3) the application of a bootstrap selection procedure together with machine learning techniques to guarantee result generalizability and study the interconnections among the selected miRNAs in class prediction. We applied the pipeline to compare hemolized and non-hemolized plasma samples, identifying four miRNAs known to be hemolysisrelated (miR-486-5p, miR-92a, miR-451, miR-16) together with a new one, miR-22.

Biography

Landoni E, third-year PhD student at the University of Milan, works as biostatistician at the Fondazione IRCCS Istituto Nazionaledei Tumori in Milan. Her research project involves the application of machine learning methods for the analysis of high-dimensional 'omics' data. In particular, her research is focused on the discovery and development of cancer molecular biomarkers, focusing on the implementation of feature selection algorithms together with the use of original and simple graphical representations of the results. Another area of her interests is nonparametric statistics, applied in particular to the fields of molecular biology and personalized medicine.

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