A Real-Time miRNA-based Machine Learning Approach for Precision Cancer Therapeutics

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Artificial intelligence has been used to identify cancer types with high accuracy, but despite this, we see increased death rates in cancer. Even though cancer is a complex and extremely heterogeneous condition, the current practice of treating cancer is a one-size-fits-all approach that is expensive, time-consuming, causes the patients to suffer, and worse, prescribed cancer drugs are ineffective 75% of the time. Advances in cancer genomics and pharmacogenomics have generated a wealth of omics data. Recent research shows that microRNAs (miRNAs), which serve to regulate gene expression, become dysregulated in cancer cells and tissues. This has led many to investigate the use of miRNAs as biomarkers for cancer detection and targeted therapy prediction. Machine learning can be used to deliver precision cancer therapeutics based on patients' genomic profiles. The solution is a machine learning platform that analyzes pharmacogenomic and miRNA data of various cancer types and predicts targeted drug efficacy with high accuracy. In this research, models were built using miRNA and drug response data of real human patients - rather than cancer cell lines and humanized mice models - from the Cancer Genome Atlas, a publicly available data repository. The machine learning algorithms tested in this research were OneVsRestClassifier, K-NearestNeighborsClassifier, AdaBoostClassifier, and DecisionTreeClassifier. An ensemble learning method combining multiple weak learners, OneVsRest was able to predict drug efficacy with the highest accuracy of 74.1%. The results show that the approach is superior to current state-of-the-art research that predicts drug efficacy based on miRNA data with an accuracy of 67%.

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