



Research Week 2020

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

Darsh Mandera

Jesuit High School

Keywords

Cancer, drug prediction, machine learning, miRNA

Abstract

Recent research shows that microRNAs (miRNAs) may be potential biomarkers of cancer. MiRNAs are noncoding RNA molecules that regulate gene expression in the post-transcriptional phase. When miRNA count is depleted, gene expression can become dysregulated, consequently leading to progression or drug resistance in cancer. Therefore, many researchers have begun to investigate the role of miRNA as a potential biomarker of cancer, and its role in targeted drug therapy.

Artificial Intelligence has emerged as a recent breakthrough to identify cancer types with high accuracy. Even though cancer is a complex and extremely heterogeneous condition, the current practice of treating cancer – which entails surgery, radiation therapy, chemotherapy, and immunotherapy – is a one-size-fits-all approach that results in the prescription of the same drug for every patient with the same type and stage of cancer. This approach is expensive, time-consuming, causes the patients to suffer, and worse, prescribed cancer drugs are ineffective for 75% of the time. Machine learning can be used to deliver precision cancer therapeutics based on genomic profiles of patient's tumors. The solution is a machine learning platform that analyzes pharmacogenomic data of various cancer types and predicts targeted drug efficacy with a high accuracy. In this research, models were built and implemented in Python and its libraries using miRNA and drug response data from the Cancer Genome Atlas, a publicly available data repository. The classification algorithms tested in this research were OneVsRest, K-Nearest-Neighbors, AdaBoost, and DecisionTree. As an ensemble learning method combining multiple weak learners, OneVsRest was able to predict drug efficacy with the highest accuracy. The results show that the approach is superior to current research that uses miRNA and machine learning to predict drug efficacy using cancer cell line data and not real patient data.