# OncoRx: An Integrative Approach to Identification of Pan-Cancer Molecular Biomarkers and Prediction of Targeted Multi-Drug Cancer Therapeutics

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The current practice of treating cancer with radiation, chemotherapy, and immunotherapy is a one-size-fits-all approach, in which patients with the same type and stage of cancer receive the same treatment. Research shows that this approach is ineffective 75% of the time. With microRNA (miRNA) having been identified as a key biomarker of cancer, precision therapeutics based on miRNA should provide the highest specificity and sensitivity by virtue of their cancer-specific expression and stability. However, identifying particular miRNAs that play a key role in driving cancer remains a challenge, as the expression of some types of miRNAs is found to be significantly different between normal tissues and tumor tissues. The focus of this research is to create a pan-cancer solution using machine learning (ML) to identify key miRNAs as biomarkers of cancer and predict drug combinations based on miRNA. Data from 80% of cancer types from The Cancer Genome Atlas with 6,280 patients, 705 miRNAs, and 230 drugs was used. Top microRNAs were identified as key biomarkers using ExtraTreesClassifier, and were validated through KEGG pathway analysis and Gene Ontology enrichment analysis. Three different models were implemented using Multi-label ML algorithms: K-NearestNeighbors, AdaBoostClassifier, and OneVsRestClassifier. OneVsRestClassifier, an ensemble learning algorithm, yielded the highest accuracy. The final model was further tuned using cross-validation through GridSearchCV and K-Fold, and by using statistical techniques like F1 Score, Jaccard Score, and Accuracy Score. The resulting solution overcomes the challenges of monotherapy and allows oncologists to prescribe anti-cancer drug combinations with high accuracy based on patients' miRNAs, yielding higher survivability.

**Awards Won:**
Second Award of $2,000