

Anti-Cancer Drug Response Prediction using Gene Expression

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Abstract: This project aims to develop and evaluate machine learning models for predicting the response of cancer cells to anti-cancer drugs, utilizing gene expression data. The project leverages publicly available datasets like the Genomics of Drug Sensitivity in Cancer (GDSC) and the Cancer Cell Line Encyclopedia (CCLE), which contain gene expression profiles and drug response measurements (e.g., IC50, AUC) for various cancer cell lines. By training machine learning algorithms on this data, the project seeks to build predictive models that can accurately identify effective drug treatments for individual cancer cell lines, contributing to the advancement of precision oncology. They emphasize the need to tailor cancer treatments to individual patients, driven by the variability in drug response due to tumor heterogeneity. Abstracts frequently mention the utilization of large-scale datasets like the Genomics of Drug Sensitivity in Cancer (GDSC) and the Cancer Cell Line Encyclopedia (CCLE). These datasets provide valuable gene expression and drug response information.

Keywords: Drug Response Prediction, Predictor Genes, Cell Line Gene Expression Data, Machine Learning (ML)