



Deep Learning Approaches for Predicting Drug Responses

Using Multi Omics Features

Student: Palaniappan Sneha **Supervisor:** Prof Jagath Chandana Rajapakse

Background:

Cancer is a pathological process resulting from the accumulation of mutations. Depending on cellular aberrations and inducement of abnormal growth, cancer is staged in the clinic for treatment selection. Treatment of cancer needs to be customised due to the complexity of each cancer. The advancement of technology has allowed the collection of biological data types at a detailed level, and the integration of omics data helps to achieve a comprehensive understanding of the underlying biological factors. The integration gives a holistic molecular perspective of the multi-omics approach to optimise cancer treatment.

Project Objectives:

DNN models were used to predict anti-cancer drug responses using the multi-omics data (six omics data) obtained from the Cancer Cell Line Encyclopedia (CCLE) and Genomics of Drug Sensitivity in Cancer (GDSC). Due to the high dimensionality nature of multi-omics data and their inherent data variations, effective multi-omics data integration is challenging. These form the motivation for this project to explore dimensionality reduction techniques and deep neural networks. Dimensionality reduction techniques were adopted to tackle the high dimensionality nature of multi-omics data. A combined deep neural network model (a) with an attention mechanism was developed to integrate the omics data to predict drug responses. This will aid to determine the most effective drug combination for personalised cancer treatment.

