A Machine Learning Approach for Predicting Drug Efficacy

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One of the most challenging problems in the field of medical science today is predicting the drugs that will work for specific cancer patients. The future of personalized cancer therapies relies on predictive computational models that can effectively simulate how a patient will respond to a targeted therapy through molecular (proteomic and transcriptomic) correlates of drug sensitivity. One novel computational model is an artificial neural network (ANN). This research study will analyze transcriptomic and proteomic effects on drug discovery and development as well as create an effective artificial neural network computational model inspired by how biological neural networks such as the human brain process information to predict the efficacy of drugs and lead to advancements in precision medicine. Specifically focusing on non-small cell lung cancer, three phases were carried out to build an effective ANN model: data collection, data preparation, and the training and testing of ANN models using various back-propagation algorithms and varying numbers of hidden neurons. Results of these trials showed that the most effective ANN model was with a Levenberg-Marquardt back-propagation algorithm at four hidden neurons. This working model can successfully help clinicians develop a personalized treatment plan for predicting the optimal drug for a patient.

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