Predicting P-Glycoprotein Inhibition Using a Message-Passing Graph Neural Network

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P-glycoprotein (P-gp) is found in various tissues throughout the body, acting as an efflux pump that actively transports substances out of cells. As a result, P-gp plays an important role in drug efficacy in many organs due to its ability to transport drugs back out of cells, decreasing their absorption. Therefore, successful drugs will be those that effectively inhibit the P-gp function, making the determination of a drug's P-gp inhibition an essential step in its development. While experimental assays performed in the laboratory are the most accurate, their slow and expensive nature paves the need for the development of a cheap, fast and precise P-gp inhibition prediction system. In this study, a graph neural network (GNN) is utilised which is able to directly learn and make predictions from the properties of atoms and bonds in the molecular structure, increasing the network's flexibility over previous approaches and hence the overall accuracy of the prediction. This study demonstrates the success of GNN in the prediction of P-gp inhibition confirmed through the highly-accurate AUC score of 0.946, improving the prediction accuracy over previous machine-learning techniques and proving its suitability to be used by medicinal chemists for drug discovery tasks.