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Korea builds deep learning model to predict adverse drug-drug interactions

06 May 2022 | News

Using gene expression data, the new model can predict how some drug-drug interactions can lead to adverse effects in the human body

The intake of multiple drugs can result in adverse health effects due to unexpected drug-drug interactions (DDIs). Now, researchers from the Gwangju Institute of Science and Technology in South Korea have developed a deep learning model that predicts DDIs based on their effects on gene expression.

Their new model is accurate and outperforms conventional prediction models. It can also predict DDIs between developmental drugs and may be useful for detecting DDIs early in the drug-discovery process.

To explain the key features of this model, researchers explain, "Our model considers the effects of drugs on genes by utilizing gene expression data, providing an explanation for why a certain pair of drugs cause DDIs. It can predict DDIs for currently approved drugs as well as for novel compounds. This way, the threats of polypharmacy can be resolved before new drugs are made available to the public."

Since all compounds do not have drug-treated gene expression signatures, this model uses a pre-trained compound generation model to generate expected drug-treated gene expressions.