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News

Machine Learning Models Help Predict Medication Responses

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Finding the best ways to treat cancer depends on our understanding of the mechanisms that prevent cancer from growing and spreading. Now, using machine learning, researchers are looking into these mechanisms in ways they never could before.

Thanks to a new study by NCI-funded researchers, you can now learn more about one of these mechanisms, called "replication stress" (RS). Put simply, RS occurs when DNA isn't able to properly form proteins—the genetic material may get its signals crossed or it may be defective and unable to make the necessary repairs.

Learn more about the study in <u>Cancer Discovery</u>. You can find the source codes at GitHub (<u>NeST-VNN repo</u> for single drug and <u>Multitask-VNN</u> for multiple drug responses).

Common chemotherapy drugs, like cisplatin, target RS to induce a condition that halts tumor growth (i.e., either by disrupting DNA's abilities or by inciting more RS).

Corresponding author, Dr. Trey Ideker, said, "With recent advances in deep learning, we're able to use an ensemble of models to predict responses to RSinducing drugs (both multiple and single drugs). This is giving us a better understanding of the mechanisms underlying cancer and how these genes/gene networks will respond—in terms of sensitivity to drugs as well as potential side-effects." <u>SUBSCRIBE TO</u> <u>UPDATES</u>

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