AI Uses Tumor Genetics for Prediction of Treatment Response

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Scientists at the University of California (UC) San Diego School of Medicine have harnessed the power of artificial intelligence to tackle a significant challenge in cancer research: predicting when tumors will develop resistance to chemotherapy. Their study, published in *Cancer Discovery*, introduces a machine learning algorithm that decodes the intricate web of genetic mutations within tumors, shedding light on their response to chemotherapy.

Chemotherapy, a widely used cancer treatment, works by disrupting the DNA replication machinery in rapidly dividing tumor cells. However, predicting which tumors might resist this treatment has been hindered by the vast array of mutations within cancer cells. The team at UC San Diego addressed this challenge by developing an algorithm that simultaneously examines numerous genetic mutations and their collective impact on a tumor's response to drugs stopping DNA replication.

The researchers focused their efforts on cervical cancer, a type known for its resistance to treatment. According to the scientists, the algorithm successfully predicted responses to cisplatin, a common chemotherapy drug, in cervical cancer tumors. Notably, it identified tumors with a high risk of treatment resistance and unveiled the underlying molecular mechanisms fueling this resistance.

Trey Ideker, PhD, a professor in the department of medicine at the UC San Diego School of Medicine, highlighted the significance of AI in understanding complex interactions within tumors. "Artificial intelligence bridges that gap in our understanding, enabling us to analyze a complex array of thousands of mutations at once," Ideker explained.

Understanding how tumors respond to drugs is challenging due to the intricate nature of DNA replication. Hundreds of proteins work collaboratively to replicate DNA, and mutations in any part of this system can alter the tumors' response to chemotherapy. To tackle this complexity, the researchers used a set of 718 genes commonly used in clinical genetic testing for cancer classification.

After training their machine learning model with publicly accessible drug response data, the researchers identified 41 molecular assemblies, or groups of collaborating proteins, where genetic alterations influence drug efficacy. Unlike previous models, this AI approach considers the broader biochemical networks crucial for cancer survival rather than focusing on individual genes or proteins.

The model's effectiveness was then put to the test in cervical cancer, where approximately 35 percent of tumors persist after treatment. The AI accurately identified tumors susceptible to therapy, leading to improved patient outcomes. Moreover, the model pinpointed tumors likely to resist treatment, providing valuable insights for personalized treatment strategies.

Importantly, the model's transparency in explaining its decision-making process emerged as a key strength. Ideker emphasized, "Unraveling an AI model's decision-making process is crucial, sometimes as important as the prediction itself."

The researchers believe that the transparency of the model not only builds trust but also identifies potential new targets for chemotherapy, paving the way for enhanced cancer treatment strategies and the exploration of novel therapeutic avenues.

Artificial intelligence | Cervical cancer | Chemotherapy

Gene mutation | Machine learning | Tumors

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