THE NUTSHELL

AI Model MutationProjector Predicts Tumor Treatment Response

An AI model trained on over 30,000 tumors from 10 different solid cancer types aims to turn complex mutation information into more effective treatment plans.

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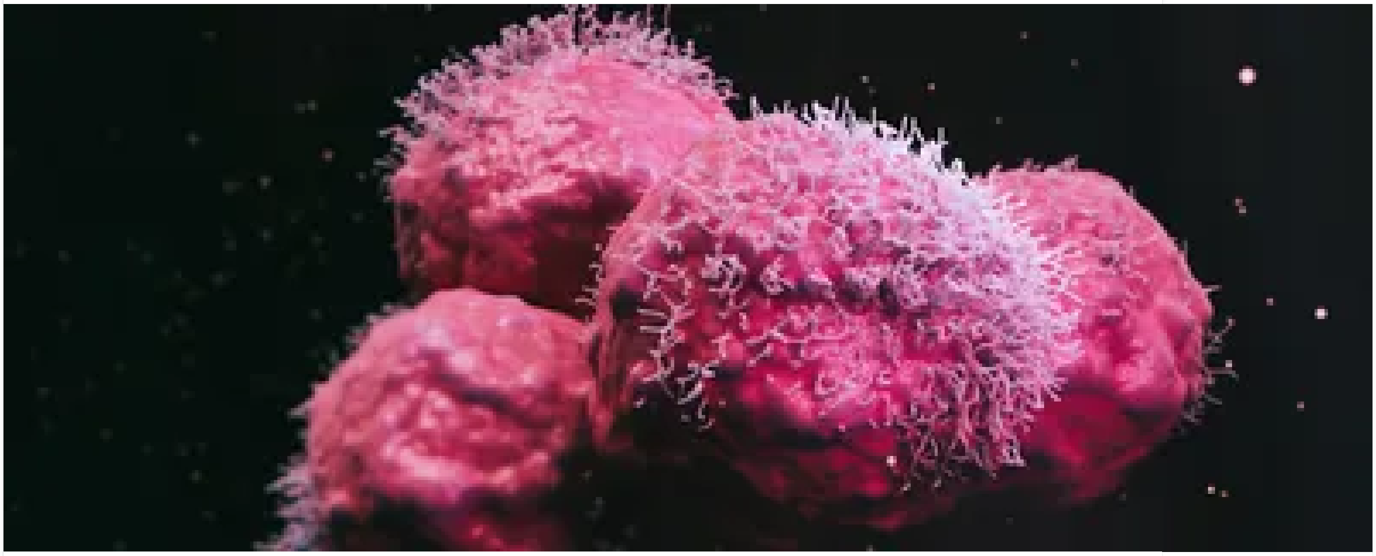

MutationProjector could help predict how tumors will respond to treatment.

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After a patient is diagnosed with cancer, modern cancer care increasingly turns to genetic testing to get more information about the tumor and guide treatment options. When there's a strong link between a genetic signature and a type of cancer, this approach can be invaluable.

But only eight percent of cancer cases are paired to an approved therapy via genetic testing approaches.

"Genetic sequencing is already routine in cancer care, but we still struggle to fully interpret the many mutations found in a patient's tumor," said Trey Ideker, a geneticist at the University of California, San Diego (UCSD), and coauthor of a new study that aims to enhance how we handle genetic data in cancer care, in a statement.

Ideker and his team have developed MutationProjector, an AI model that analyzes a tumor's genetic landscape and predicts how it will respond to a range of treatment options. The scientists trained their model on data taken from over 30,000 tumors from 10 different types of solid cancer, detailing its potential in a new study published in the journal *Cancer Discovery*.[1]

Targeting Tumor Mutations

Many cancer case decisions informed by genetic information are based on alterations to single genes of interest. But the average tumor has 11 individual genetic alterations.[2] Many of these mutations are rare, and their effects often interact to alter how a tumor responds to treatment.

Ideker's team trained MutationProjector on data from real-world cancer genetics resources totaling 30,328 cancer cases. The AI model integrated mutation information affecting 468 genes, learning associations between genes or between genes and covariates.

Ideker's team assessed how well MutationProjector could predict a tumor's response to chemotherapy and immunotherapy. They also tested whether the AI tool could separate metastatic from localized tumors.

Across several patient cohorts, including those for bladder, lung, and skin cancer, MutationProjector either exceeded or matched the performance of currently available prediction methods.

Unexpected Genes

The model based its predictions on both known and unexpected gene markers. Gene alterations that determined chemotherapy response included well-characterized DNA repair genes like *BRCA1*, as well as cell cycle regulation genes and those that influence receptor tyrosine kinase signaling pathways.

JungHo Kong, a computational biologist at UCSD and coauthor of the new study, said in the statement, “By pretraining on a large collection of tumors and integrating molecular network knowledge, MutationProjector can detect patterns that would be easy to miss with conventional biomarker approaches. That gives us a way to move from long lists of mutations toward a more functional understanding of the tumor.”

The model doesn’t just predict treatment responses; it also explains why it made those predictions, a feature that could help improve treatment strategies based on its guidance.

The team’s next steps are to expand the number of cancers the model can predict and beef up the data sources it learns from, adding clinical information such as imaging scans and electronic health records.

“Our results suggest that tumor genome foundation models may help extend the clinical value of sequencing beyond a handful of well-known genes,” Ideker said. “This could support a more comprehensive and biologically grounded approach to precision oncology.”

References

1. Kong J, et al. A foundation model of cancer genotype enables precise predictions of therapeutic response. *Cancer Discov*. 2026.
2. Pinet S, et al. Clinical management of molecular alterations identified by high throughput sequencing in patients with advanced solid tumors in treatment failure: Real-world data from a French hospital. *Front in Oncology*. 2023;13:2023.

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Meet the Author

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RJ is a freelance science writer based in Glasgow. He covers biological and biomedical science, with a focus on the complexities and curiosities of the brain and emerging AI technologies. RJ was a science writer at *Technology Networks* for six years, where he also worked on the site’s SEO and editorial AI strategies. He created the site’s podcast, Opinionated Science, in 2020. RJ has a Master’s degree in Clinical Neurosciences from the University of Cambridge.