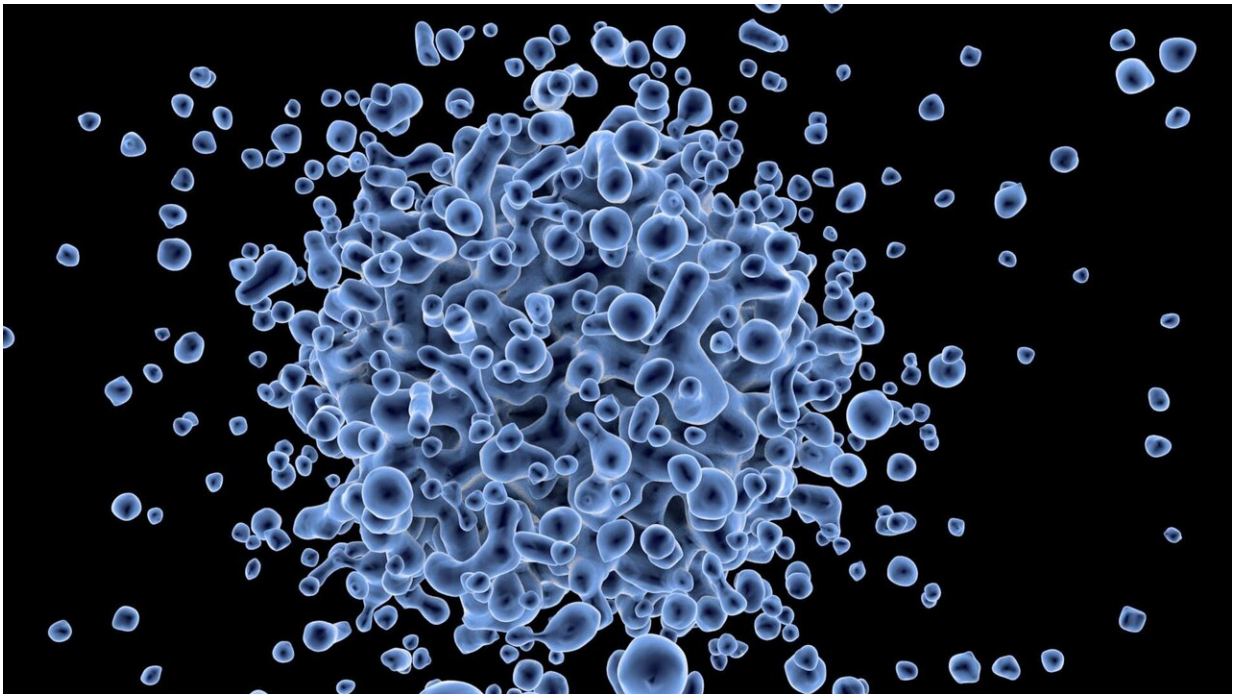


New prediction algorithm identifies previously undetected cancer driver genes

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A new study, led by researchers from the University of California, Irvine, has deepened the understanding of epigenetic mechanisms in tumorigenesis and revealed a previously undetected repertoire of cancer driver genes. The study was published this week in *Science Advances*.

Using a new prediction algorithm, called DORGE (Discovery of

Oncogenes and tumor suppressor genes using Genetic and Epigenetic features), researchers were able to identify novel [tumor suppressor genes](#) (TSGs) and oncogenes (OGs), particularly those with rare mutations, by integrating the most comprehensive collection of genetic and epigenetic data.

"Existing bioinformatics algorithms do not sufficiently leverage epigenetic features to predict [cancer](#) driver genes, despite the fact that epigenetic alterations are known to be associated with cancer driver genes," said senior author Wei Li, Ph.D., the Grace B. Bell chair and professor of bioinformatics in the Department of Biological Chemistry at the UCI School of Medicine. "Our computational algorithm integrates public data on epigenetic and genetic alternations, to improve the prediction of cancer driver genes."

Cancer results from an accumulation of key genetic alterations that disrupt the balance between cell division and apoptosis. Genes with "driver" mutations that affect cancer progression are known as cancer driver genes, and can be classified as TSGs and oncogenes OGs based on their roles in cancer progression.

This study demonstrated how cancer driver genes, predicted by DORGE, included both known cancer driver genes and novel driver genes not reported in current literature. In addition, researchers found that the novel dual-functional [genes](#), which DORGE predicted as both TSGs and OGs, are highly enriched at hubs in [protein-protein interaction](#) (PPI) and drug/compound-gene networks.

"Our DORGE algorithm, successfully leveraged public data to discover the genetic and [epigenetic alterations](#) that play significant roles in cancer driver gene dysregulation," explained Li. "These findings could be instrumental in improving cancer prevention, diagnosis and treatment efforts in the future."

More information: Jie Lyu et al, DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features, *Science Advances* (2020). [DOI: 10.1126/sciadv.aba6784](https://doi.org/10.1126/sciadv.aba6784)

Provided by University of California, Irvine

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