

IIT-M develops AI-based algorithm to identify cancer-causing alterations

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The technique will tackle the complexity and size of DNA sequencing datasets and can greatly help in pinpointing key alternations in the genomes of cancer patients



Indian Institute of Technology Madras (IIT-M) researchers have developed an artificial intelligence (AI) based mathematical model to identify cancer-causing alterations in cells. The algorithm uses a relatively unexplored technique of leveraging DNA composition to pinpoint genetic alterations responsible for cancer progression.

Explaining the rationale behind this study, Prof B Ravindran, Head, Robert Bosch Centre for Data Science and AI, IIT-M said, “One of the major challenges faced by cancer researchers involves the differentiation between the relatively small number of ‘driver’ mutations that enable the cancer cells to grow and the large number of ‘passenger’ mutations that do not have any effect on the progression of the disease.”

The researchers hope that the driver mutations predicted through their mathematical model will ultimately help discover potentially novel drug targets and will advance the notion of prescribing the “right drug to the right person at the right time.”

In this study, the researchers decided to look at this problem from a different perspective. The main goal was to discover patterns in the DNA sequences – made up of four letters, or bases, A, T, G and C surrounding a particular site of alteration.

The underlying hypothesis was that these patterns would be unique to individual types of mutations – drivers and passengers, and therefore could be modelled mathematically to distinguish between the two classes. Using sophisticated AI techniques, the researchers developed a novel prediction algorithm, NBDriver and tested its performance on several open-source cancer mutation datasets.