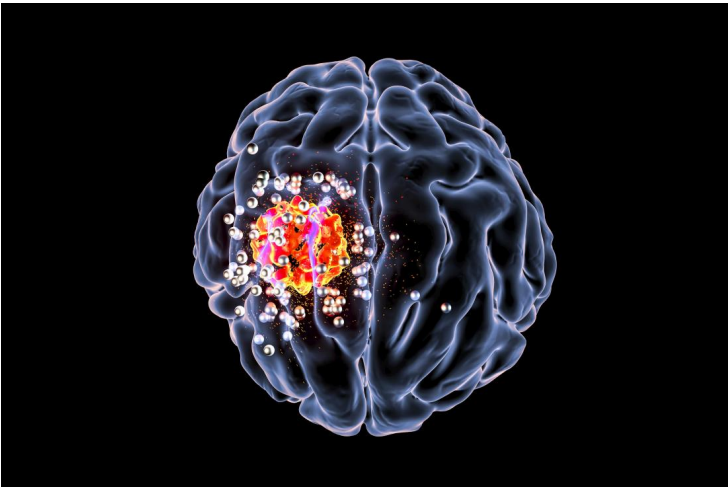


IIT-M develops machine learning tool to detect tumour in brain & spinal cord

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The web server called 'GBMDriver' is publicly available online as computational techniques need to be developed to properly identify the driver mutations of different types of cancer



A team of researchers at the Indian Institute of Technology Madras (IIT-M) has developed a Machine Learning-based computational tool for better detection of cancer-causing tumours in the brain and spinal cord. Called 'GBMDriver' (Glioblastoma Mutiforme Drivers), this tool is publicly available online.

Glioblastoma is a fast and aggressively growing tumour in the brain and spinal cord. Although there has been research undertaken to understand this tumour, therapeutic options remain limited with an expected survival rate of less than two years from the initial diagnosis.

It is important to evaluate the functional consequences of variants in proteins, which are involved in Glioblastoma to advance the therapeutic options for patients. However, functional validations to identify driver mutations (disease-causing mutations) from all the observed variants would be strenuous work.

The GBMDriver was developed specifically to identify driver mutations and passenger mutations (passenger mutations are neutral mutations) in Glioblastoma.

In order to develop this web server, a variety of factors such as amino acid properties, di- and tri-peptide motifs, conservation scores, and Position Specific Scoring Matrices (PSSM) were taken into account.

In this study, 9386 driver mutations and 8728 passenger mutations in glioblastoma were analysed. Driver mutations in glioblastoma were identified with an accuracy of 81.99 percent, in a blind set of 1809 mutants, which is better than existing computational methods. This method is completely dependent on protein sequence.