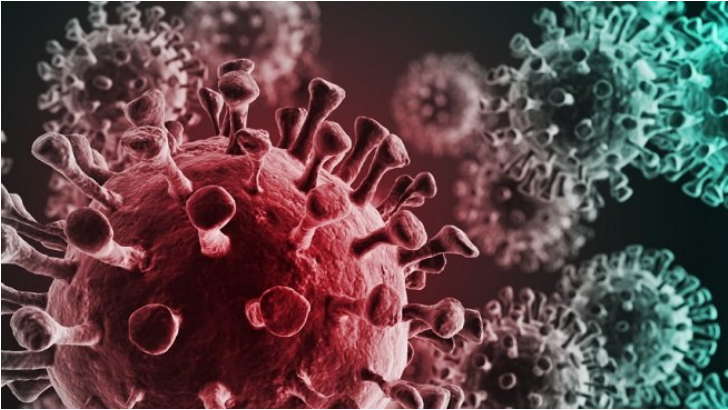


NITTTR develops viral sequence predictor to counter COVID-19

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A web-based COVID predictor to predict the sequence of viruses online



Dr Indrajit Saha, Assistant Professor in the Department of Computer Science and Engineering of National Institute of Technical Teachers' Training and Research (NITTTR), Kolkata and his team have recently developed a web-based COVID-Predictor to predict the sequence of viruses online on the basis of machine learning and analyzed 566 Indian SARS-CoV-2 genomes to find the genetic variability in terms of point mutation and Single Nucleotide Polymorphism (SNP).

The study is sponsored by Science and Engineering Research Board (SERB), a statutory body under the Department of Science and Technology (DST), which has been published in the Journal called Infection, Genetics, and Evolution. They have mainly found that 57 out of 64 SNPs are present in 6 coding regions of Indian SARS-CoV-2 genomes, and all are nonsynonymous in nature.

The scientists are on the track to identify the genetic variability in SARS-CoV-2 genomes around the globe including India, find the number of virus strains using Single Nucleotide Polymorphism (SNP), spot the potential target proteins of the virus and human host based on Protein-Protein Interactions.

The results show that the USA, England, and India are the top three countries having the geometric mean, 3.27%, 3.59%, and 5.39%, respectively, of mutation similarity score with other 72 countries. The scientists have also developed a web application for searching the mutation points in SARS-CoV-2 genomes globally and country wise.