

New software enhances efficiency, speed of genomic data analysis

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An international team of scientists, led by researchers from A*STAR's Genome Institute of Singapore (GIS) and the Bioinformatics Institute (BII), have developed SIFT 4G (SIFT for Genomes) – a software that can lead to faster genome analysis. This development was published in the scientific journal *Nature Protocols*.

While technological advances have enabled the generation of vast amounts of data on the human body and other organisms, an issue facing the scientific community is the ability to analyse such great amounts of data well.

Based on the same principles as its predecessor, SIFT 4G can prepare predictions for genomes at a much higher speed. Once the predictions are ready, they are stored in a database and are ready for [genome analysis](#). The use of graphics processing units (GPUs) instead of central processing units (CPUs) has resulted in much shorter prediction times and the ability to construct databases for a large number of organisms. SIFT 4G already has predictions available for more than 200 organisms, thereby serving a larger research community.

The increased efficiency in genome analysis will empower the research community in advancing science and developing technology that can benefit human health. The bioinformatics and genomic capabilities developed at BII and GIS enable both institutes to play a key role in quickly and accurately interpreting biological data to understand gene function, their interactions and the development of diseases.

Read full, original post: [Accelerating genome analysis](#)