New computer program can help crack precision medicine

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Credit: Australian National University

Researchers from ANU have helped develop a new computer program to find out a person's genetic make-up, bringing us a step closer to an era of precision medicine.

The program, called Flye, provides a step-by-step procedure for computers to assemble genomes—a person's complete set of genes—and

enables the process to be much faster and more accurate than current best-practice methods.

ANU researcher Dr. Yu Lin said the breakthrough would lead to better prevention, prediction and diagnosis of illnesses, as well as improved treatment, disease management and cures.

"We hope our innovation will help people to live longer and better—particularly people suffering from diseases that are not currently treatable," said Dr. Lin from the Research School of Computer Science.

"Precision medical care is advanced by personal genomics, which focuses on the unique genetic profile of individuals."

Dr. Lin said that by using long DNA sequences the new computer program would improve the reliability of genome assemblies, as well as lead to a range of biomedical applications.

"Using long DNA sequences rather than short ones taken randomly from a genome—a popular method used today—opens the door to huge advances in accuracy, speed and usefulness for a range of medical purposes and other applications," he said.

"This will open up a range of biomedical applications such as enhanced screening for genetic disorders and personalised treatments for diseases that are incurable today."

A long sequence ranges between 5,000 and 20,000 DNA letters, while short sequences are typically 200 letters. The length of genes in a human genome vary from hundreds to hundreds of thousands of letters.

Dr. Lin said the cost of computing would likely start to dominate many sequencing projects, as the price of genome sequencing continues to

drop.

"We need more efficient models and algorithms, like the one we've created, to keep computing costs as low as possible," he said.

More information: Mikhail Kolmogorov et al. Assembly of long, error-prone reads using repeat graphs, *Nature Biotechnology* (2019). DOI: 10.1038/s41587-019-0072-8

Provided by Australian National University