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Singapore leads development of AI tool for high-accuracy genome mapping

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To make complete genome assembly simpler, more scalable and more cost-effective for research worldwide

An international research team led by the A*STAR Genome Institute of Singapore (A*STAR GIS) has developed HERRO, an artificial intelligence (AI) tool that could make it easier and more cost-effective to produce complete, high-quality genome assemblies.

HERRO corrects errors in nanopore sequencing reads generated by Oxford NanoporeTechnologies (ONT) sequencers. ONT is a leading player in long-read sequencing, a technology increasingly used when scientists need to read very long stretches of DNA. These long reads help researchers study complex parts of the genome that shorter sequencing reads can find challenging, such as repetitive DNA, centromeres, and the difficult regions of the sex chromosomes.

A key differentiator is that HERRO corrects sequencing errors while preserving real genetic differences. This is especially important in humans, who carry two similar but non-identical copies of each chromosome.

Combined with up to 100-fold improvements in sequencing accuracy, meaning far fewer errors when reading DNA, this enables researchers to generate more accurate and complete genome maps using a single sequencing platform through a simpler and more cost-effective workflow, without losing biologically important information.

A*STAR GIS collaborated with Oxford Nanopore Technologies (ONT) on the HERRO project, which was jointly funded by ONT and AI Singapore.