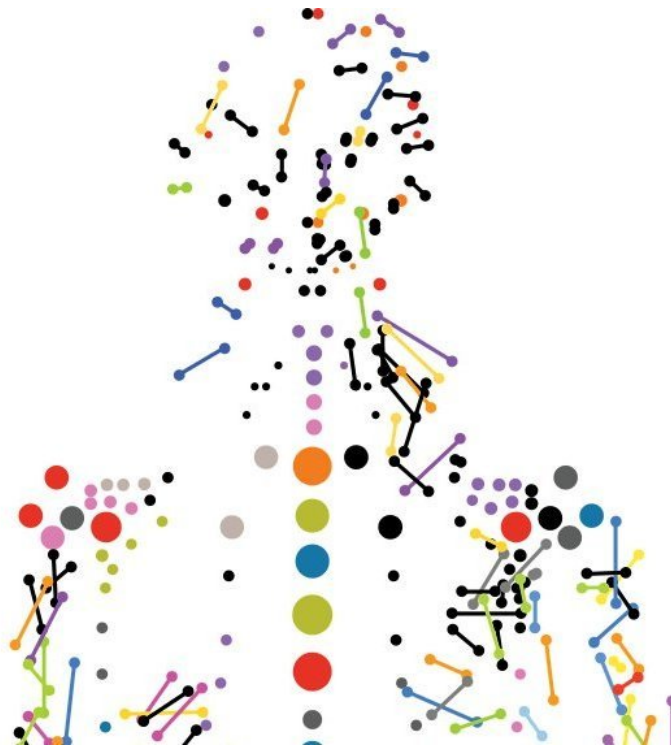


New technique promises more accurate genomes

October 23 2018



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University of Adelaide researchers have developed a new technique that will aid in a more accurate reconstruction of human genomes by determining the exact sections of the genome that come from each parent.

The new technique, published today in the journal *Nature Biotechnology*, will also allow researchers to identify further complexity within any type of genome – from plants to animals – and provide more precise reference genomes than are currently available.

Genome assembly computationally reconstructs a genome – the complete set of genes or genetic material present in a cell or organism – from the much smaller pieces of DNA that sequencing machines can read, much like putting together pieces of a jigsaw puzzle.

"Working together with colleagues from the US National Human Genome Research Institute and the US Department of Agriculture, we have yielded a complete sequence of both Brahman and Angus cattle genomes from a single crossbred individual," says Professor John Williams, Director of the Davies Research Centre, School of Animal and Veterinary Sciences, University of Adelaide's Roseworthy campus.

Brahman and Angus cattle subspecies were domesticated separately thousands of years ago and have been subjected to very different selection pressures since then: pest and drought environments in the case of the Brahman cattle and beef production in Angus cattle. These different characteristics and histories are reflected in their genomes, which makes them ideal test subjects.

"Each individual possessed two copies of each chromosome. Previous techniques have yielded genome sequences, even the [human genome sequence](#), that were a hybrid of each chromosome pair mixed together and do not accurately capture the actual sequence of a genome," says Professor Stefan Hiendler from the University of Adelaide's School of Animal and Veterinary Sciences and co-author of the paper.

"This new technique, called trio binning, gives, for the first time, a true [genome sequence](#) of each chromosome in an individual as well as the

highest quality genomes of the two cattle sub-species available to date," says Professor Hiendleder.

Trio binning takes advantage of the newest generation of sequencing technology that can "read" much longer regions of the genome—as many as 20,000 bases at a time or more—compared to a few hundred bases in previous technology. The parent's genomes are first sequenced using high-accuracy short reads to determine which parts of their genomes are unique to each parent. The offspring's genome is then sequenced using much longer reads. These reads are then sorted on which parent they were inherited from using information from the shorter sequences from the parents.

"Trio binning has completely turned previous techniques on their head as it uses a cross between the most different genomes that you can find within a species," says Professor Williams.

"Up to now, genome sequences have been constructed from individuals with minimal genetic diversity. It marks a significant advance in technological capability that has wide-reaching implications for research and medical applications.

"Trio binning will help to build a more accurate record of a person's [genome](#) variation which will improve the accuracy of genetic tests and contribute to the goal of a person's unique DNA sequence in their clinical care," says Professor Williams.

More information: Sergey Koren et al. De novo assembly of haplotype-resolved genomes with trio binning, *Nature Biotechnology* (2018). [DOI: 10.1038/nbt.4277](https://doi.org/10.1038/nbt.4277)

Provided by University of Adelaide

Citation: New technique promises more accurate genomes (2018, October 23) retrieved 10 April 2024 from <https://phys.org/news/2018-10-technique-accurate-genomes.html>

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