Oxford Nanopore Technologies
Human genomics

Genome assembly

Like a jigsaw puzzle, the larger the pieces ("reads"), the easier the assembly.

Nanopore sequencing

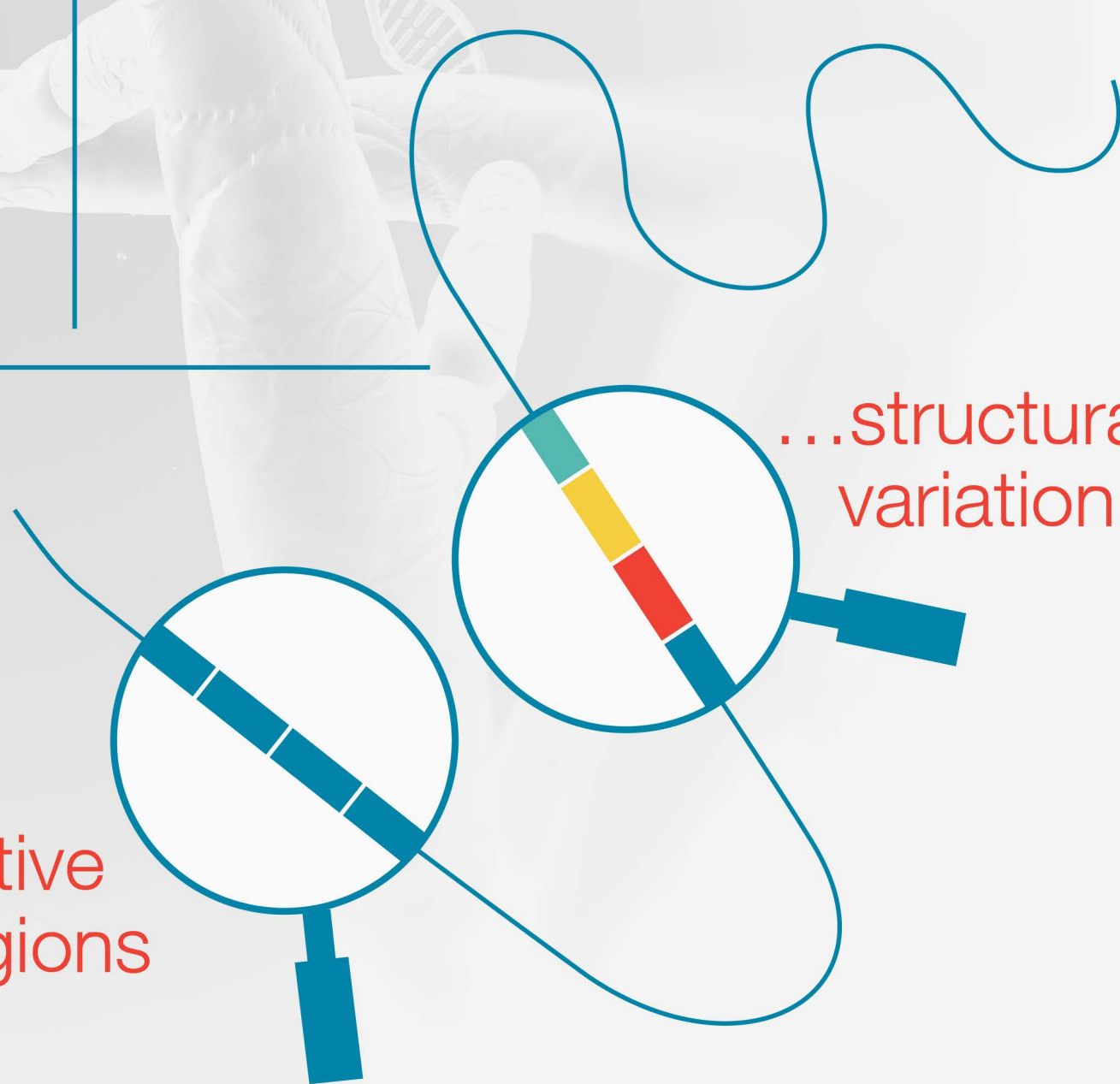Read length is equal to fragment length…

…current longest nanopore read:

>2 MB[1]

Long reads resolve large…

…structural variation

…repetitive regions

> *Using a MinION nanopore sequencer, enabled us to analyze regions of the human genome that were previously intractable with state-of-the-art sequencing methods[2].*

Short-read sequencing technology	Nanopore sequencing
Read length typically 150-300 bp	**Read length equal to DNA fragment length**
	✓ Resolve repetitive regions and structural variation
	✓ Assemble high-quality genomes with fewer gaps
	✓ Analyse haplotypes and phasing
Amplification required	**Direct, amplification-free protocols**
	✓ Detect base modifications as standard
	✓ Eliminate amplification bias
Fixed run time	**User-defined run time**
	✓ Stop sequencing when sufficient data generated
Bulk data delivery at end of run	**Real-time data streaming**
	✓ Immediate access to results

PromethION

Flexible, on-demand sequencing
Designed to run up to 48 independently addressable flow cells.

High yield, high throughput
Up to 9,600 Gb data (all 48 flow cells sequencing)*

Rapid, real-time data streaming
Immediate access to results

Cost-effective
<$1000 for human genome (30x coverage), including base modifications

MinION   GridION   PromethION

Download the white paper at
nanoporetech.com

1. Payne, A et al. 2018. Whale watching with BulkVis: A graphical viewer for Oxford Nanopore bulk fast5 files. bioRxiv 312256
2. Jain, M. et al. 2018. Nanopore sequencing and assembly of a human genome with ultra-long reads. Nat Biotechnol. 36(4)
* Based on current internal flow cell performance of 200 Gb (October 2018). Theoretical PromethION performance of up to 15 Tb.