Integrated GENOMICS Cores

Oxford Nanopore Technologies

Introducing the GridION and MiniION

The HTSF is proud to announce the addition of Oxford Nanopore's GridION and MiniION, an investment in the future of genome research. The MiniION is currently the only portable real-time device for DNA and RNA sequencing and can now generate up to 10 Gb of DNA sequence data. The GridION uses the same core technology as the MiniION but allows up to five experiments to be run simultaneously. Both devices offer new biological insights from long reads.

Overview

Oxford Nanopore provides the ability to obtain long-reads on the GridION and MiniION to provide a complete understanding of human genetic variation, allowing enhanced characterization of structural variation, repetitive regions, haplotype phasing, RNA splice variants, isoforms, and fusion transcripts (Nanopore Website).

Through powerful cutting-edge technology, Oxford Nanopore offers new opportunities in various research sectors at prices that can fit individual project's research goals. Nanopore technology offers opportunities in genome assembly and allows researchers from diverse scientific backgrounds to reap the benefits of long read and cost-efficient sequencing.

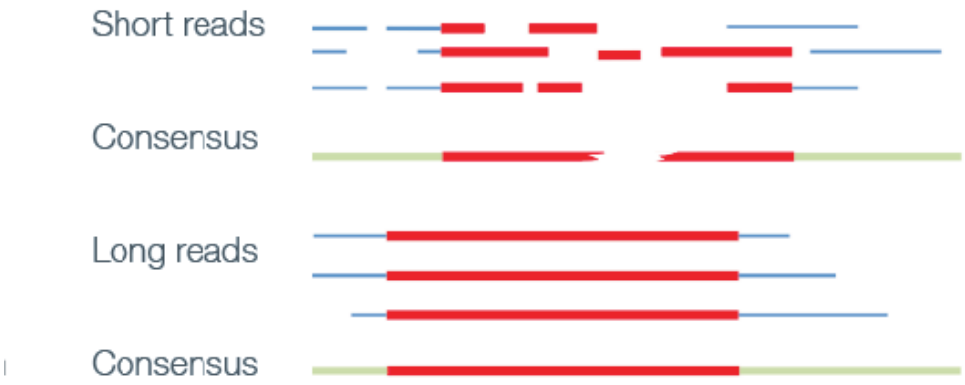
Solutions to Current Problems

Long Reads and Implications for Genome Research

Long reads from the Nanopore present numerous advantages for both de novo and alignment-based genome assembly. Currently, many existing genome assemblies were created using short-read sequencing technology. However, short-read sequencing is limited in its ability to capture large structural variation, which are vital for areas of medical research as they have been associated with several diseases such as schizophrenia and cancer. Long reads from the Nanopore can cover the whole structure variant in one read which results in more accurate genome assemblies and a better understanding of genome architecture in genomic diseases.

The longer the sequencing read, the more overlap it will have with other reads. Therefore, long-read DNA is easier to assemble than short-read DNA. Since short reads produced by traditional next generation sequencing may not cover each repetitive region, the resulting genome assemblies can be highly fragmented (Nanopore website). Through long-read sequencing, reads are more likely to span the full repetitive region allowing the creation of more accurate genome assembly (Figure 1).

Figure 1: Long read lengths are more likely to incorporate the whole repetitive region (shown in red) allowing more accurate assemply with fewer gaps.



Summary

The Oxford Nanopore offers long-read sequencing technology which solves genome assembly difficulties and improves completeness of genome assemblies compared to traditional NGS systems. This new technology provides new abilities to explore a diverse variety of experimental design options, particularly in research where structural variation is important.

To learn more about Oxford Nanopore, including sample suitability, preparation, and pricing, please contact Erin Wallace at wallacee@email.unc.edu.