**Bioinformatics of Nanopore sequencing**

**Abstract**

One of the most important sequencing technologies is nanopore that helps us in dynamic development with the use of analytical tools that help researchers to navigate this changing field.

**Introduction**

The 21 century was the beginning of next generation sequencing which increased sequencing yield. Sequencing cost depended on the length of reads that is better than sanger sequencing. The advantage of third generation enables single molecule long reads that met the needs of community so we have two competing products :

* Single molecule Real time sequencing by PacBio
* Nanopore sequencing by Oxford

Thanks to those technology it brings portability and very initial cost of Hardware but ONT also didn’t provide any analytical tools and the native base caller was in a format of FAST5 that couldn’t be handled by any software at this time. First tool that converted from the FAST5 to familiar FASTQ and FASTA is Poretools. Long reads have low sequencing accuracy so it requires computational approaches. We use algorithms and analytical to aid nanopore sequencing, and it’s not only for ONT but also they are more generic to be used with any long reads.

Here we describe a few tools developed in the recent years that are suitable for NT sequencing although it’s by no means comprehensive. We try to cover the whole range of software that reflect it diversity of the nanopore sequencing.

**Related Works**

1. We show that an electric field can drive single-stranded RNA and DNA molecules through a 2.6-nm diameter ion channel in a lipid bilayer membrane. Because the channel diameter can accommodate only a single strand of RNA or DNA, each polymer traverses the membrane as an extended chain that partially blocks the channel. The passage of each molecule is detected as a transient decrease of ionic current whose duration is proportional to polymer length. Channel blockades can therefore be used to measure polynucleotide length. With further improvements, the method could in principle provide direct, high-speed detection of the sequence of bases in single molecules of DNA or RNA.( Kasianowicz JJ, Brandin E, Branton D, Deamer DW. Characterization of individual polynucleotide molecules using a membrane channel. Proc Natl Acad Sci.)
2. Nanopore sequencing may be the next disruptive technology in genomics, owing to its ability to detect single DNA molecules without prior amplification, lack of reliance on expensive optical components, and the ability to sequence long fragments. The MinION™ from Oxford Nanopore Technologies (ONT) is the first nanopore sequencer to be commercialized and is now available to early-access users. The MinION™ is a USB-connected, portable nanopore sequencer that permits real-time analysis of streaming event data. Currently, the research community lacks a standardized toolkit for the analysis of nanopore datasets.( Loman NJ, Quinlan AR. Poretools: a toolkit for analyzing nanopore sequence data. Bioinformatics.)