**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.