

Assignment 1: Abstract and Introduction summary

- Nanopore sequencing is one of the most exciting new technologies that undergo dynamic development. It has lots of analytical tools which are becoming available for researchers. As this field is ever changing field, this paper is trying to help them by discussing a range of software available.
- As the nanopore is a new technology it came after some of other technologies. At first, there was Sanger sequencing which gets long reads but it was very slow and costs a lot, it called "First Generation Sequencing". Then, due to dynamic development of sequencing technology, came a so-called "Next Generation Sequencing" which is much easier and with less cost.
- The majority of the genomes deposited at the NCBI database are in the so-called draft form. It means that chromosomes are presented in small pieces for which order and orientation on a chromosome is unknown. so, its annotation is very difficult.
- Due to the previous problems their was a need for third generation with a single molecule long reads. In this generation their are two products, namely single molecule, real-time sequencing by PacBio and nanopore sequencing by Oxford Nanopore Technologies (ONT).
- The nanopore sequencing by Oxford Nanopore Technologies (ONT) is an exiting technology thanks to its portability and very low initial cost of hardware. Initially, ONT did not provide any analytical tools for the sequences by nanopore sequencing. So, it was provided by native base caller were in a peculiar format (FAST5) that none of the existing at that time software could handle. So, it need format conversion from FAST5 to more familiar FASTQ or FASTA formats. Many algorithms and analytical tools have been developed to aid nanopore sequences, some are specific to this method and others are more generic that can be used to any long reads.
- In this paper they try to cover the range of software that reflects diversity of the nanopore sequencing applications, grouped by tasks they can perform.