Assignment 3: Methodology and results summary

- There are some steps to make sequencing using nanopore technology.
- In first we have Base calling: which is transforming a raw signal obtained from sequencer into a string of nucleotides. As in this technology the sequencer depends on electric signals.
- Then we having Mapping: it is the process of aligning raw reads to existing sequences which is for projects involve organisms for which genomes has been already decoded.
- In the sequencing there is long reads of genes or transcripts put it still not long enough to cover the whole bacterial genome or the whole eukaryotic chromosome by a single read. So, we use Sequence Assembly, we make an assembly of raw reads in order to obtain a complete, contiguous sequences.
- In the human genomes, each of us differs from the rest by 3 million bp or 0.1%. The reference genomes are usually represented as a consensus sequence based on several individuals. In fact, mapping tools can do the variant detection but, there is some additional steps to evaluate mapping results and validate potential variant.
- In end nanopore sequencing technology promises to democratize nucleic acid sequencing. but as the sequence is raw material so, we need analytical tools. Unfortunately, most of the software developed for interpretation of the nanopore sequences require relatively high bioinformatics skills. In the growing number of tools available for the nanopore sequence analysis, the NanoPipe seems to be an exception with a simple web interface and a clear, easy to understand output files. Nevertheless, “one swallow does not make a spring” and we need more software for easy data analysis and interpretation to make sequencing fully democratized.