Assignment 1: Abstract and Introduction:

- **Long-read sequencing offers a number of advantages over short-read sequencing.**
- **Although Short-reads are effective in cost, accurate, and supported by analysis tools and pipelines, sequencing nucleic acid polymers in short fragments is difficult.**
- **Long-read technologies are good at accuracy and generate reads in excess of 10 kb, so the characteristics of long-read data should be focused on the analysis tools.**
- **This paper will study error correction, base modification detection, and long-read transcriptomics analysis and the challenges.**
- **It will Describe the principles of long-read data analysis.**
- **It also introduces open-source catalogue of long-read analysis tools: long-read-tools.org.**
- **short-read sequencers such as Illumina's NovaSeq, HiSeq, NextSeq, and MiSeq instruments ; BGI's MGISEQ and BGISEQ models ; or Thermo Fisher's Ion Torrent sequencers.**
- **long-read sequencing technologies such as Pacific Biosciences' (PacBio) single-molecule real-time (SMRT) sequencing and Oxford Nanopore Technologies' (ONT) nanopore sequencing.**
- **Long-reads can also improve de novo assembly, mapping certainty, transcript isoform identification, and detection of structural variants.**
- **we check available tools to deal with long-read sequencing projects.**