

# Task 1: Abstract and Introduction summary

- Sequencing machine is divided into short-read sequencing and Long-read sequencing
- short-read sequencers such as Illumina's NovaSeq, HiSeq, NextSeq, and MiSeq instruments BGI's MGISEQ and BGISEQ models produce reads of up to 600 bases.
- Long-read sequencing, or third-generation sequencing such as: Pacific Biosciences (PacBio), single molecule real-time (SMRT), sequencing and Oxford Nanopore Technologies (ONT), nanopore sequencing.
- long-read sequencing technologies routinely generate reads in excess of 10 kb.
- Long-read sequencing offers a number of advantages over short-read sequencing lie improving de novo assembly.
- Short-read sequencing is cost-effective, accurate, and supported by a wide range of analysis tools.
- As well as a discussion of long-read analysis that require improvements. they introduce the complementary open-source catalogue of long-read analysis tools: [long-read-tools.org](https://long-read-tools.org). The long-read-tools.org database allows users to search and filter tools based on various parameters.
- They further focus on the principles of error correction, base modification detection, and long-read transcriptomics analysis and highlight the challenges.