

## TECHNICAL TEST

**Question01:** Given a DNA string (Seq01.fasta), report the sequence:numberofrepeat of the Kmers that has equal or greater than 10 base-pair. Using argparse library (<https://docs.python.org/3/library/argparse.html>) for user inputting.

**Question02:** Building a consensus by taking 10 strings in Seq02.fasta in consideration. Use logging library to report the log file (<https://docs.python.org/3/library/logging.html>).

**Question03:** Assembly a DNA string based on 7 sequences in Seq03.fasta. Use both argparse and logging library.