- Use Biopython to answer the following assignments (you have to write your own python scripts)
    1. Download two arbitrary protein sequences and DNA sequence from NCBI in fasta format using Biopython. For the two protein sequences, please individually compute their amino acid and nuclieotide compositions and output your results in a .txt file.
    2. Download the DNA sequence from the file "Ciliate_ortholog.fasta", please perform transcription and translation using Biopython, by using the correct codon table for ciliates and report the final output (i.e., protein sequence) in the same .txt file. Note that the protein sequence should be reported in a fasta format.
    3. For each ortholog set in the file "Ciliate_ortholog.fasta": Align the translated sequence using ClustalW/Muscle and replace the amino acids with the original codons in the aligned sequence. Please write your results into a .txt file

Problem 3
- Step1: Read the file "Ciliate_ortholog.fasta" using the correct path and the appropriate Biopython module
- Step2: use Biopython to transcribe and translate (with correct codon table) the orthologs individually and write it out to a fasta file.

ATGUCCAAGGAAGCUGAAACG

ATGCCUAAGGAAGCUGAACUG

MSKEAET

MPKEAEL

Align the sequence using clustalW or Muscle

Step3a: Do a codon-based alignment for the nucleotide orthologous sequences and save as a fasta file or store it in the same program (preferred)

ATGUCC---AAGGAAGCUGAAACG

ATG---CCUAAGGAAGCUGAA---CUG

Step3b: Do a amino acid alignment for the translated orthologs and save as a fasta file or store it in the same program (preferred)

MS-KEAET

M-PKEAEL

Step4:   Read the aligned files and store the aligned codons and amino acids write it out one below the other as another fasta file

ATGUCC---AAGGAAGCUGAAACG

MS-KEAET

ATG---CCUAAGGAAGCUGAA---CUG

M-PKEAEL