Latihan Quiz Computational Biology

For given DNA sequences:

Sequence X is obtained from FASTA file (x.fasta)

Sequence Y is obtained from FASTA file (y.fasta)

The sequences might be contain ambiguous letters. Use seq = seq.replace(“<letter>”, “”) function to remove the unwanted letter from the sequence.

The ambiguous letters can be any character so filter the sequence after reading it from fasta file is a must.

Please use Biopython to do following operations:

1. Sequence Manipulation:

* Display the total length of Sequence X and Y.
* Display which index the first time the codon (CGC) appears in Sequence X and Y.
* Create a new sequence using the following task below:
  + Take the first 10 nucleotides from Sequence X and the last 5 nucleotides from Sequence X.
  + Take the first 20 nucleotides from Sequence Y and the last 3 nucleotides from Sequence Y.
  + Combine both of the string above and reverse it to a new sequence, Sequence Z.

1. Sequence Analysis & Plotting

* Display the nucleotides base (A and C) frequency for Sequence Z with a chart using matplotlib library. You are free to plot using bar or pie chart.
* Display GC and AT content percentage for Sequence Z.
* Display melting temperature for Sequence Z using Wallace method.
* Display molecular weight for Sequence Z.

1. DNA and mRNA Protein Synthesis:

* Transcribe and display the DNA sequence Z into mRNA Sequence.
* Translate and display the mRNA sequence Z into amino acids Sequence.

1. Sequence Alginment & Similarities:
   * Perform local alignment pairwise between sequence X and sequence Y and display the alignment score.
   * Perform global alignment pairwise between sequence Y and sequence Z and display the alignment score
   * Find and display the Hamming and Levenshtein distance between Sequence X and Y