

## 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.
2. Sequence Analysis & Plotting
  - Display the nucleotides base (A and C) frequency for Sequence C with a chart using matplotlib library. You are free to plot using bar or pie chart.
  - Display GC and AT content percentage for Sequence C.
  - Display melting temperature for Sequence C using Wallace method.
  - Display molecular weight for Sequence C.
3. DNA and mRNA Protein Synthesis:
  - Transcribe and display the DNA sequence C into mRNA Sequence.
  - Translate and display the mRNA sequence C into amino acids Sequence.
4. Sequence Alginment & Similarities:
  - Perform local alignment pairwise between sequence A and sequence B and display the alignment score.
  - Perform global alignment pairwise between sequence B and sequence C and display the alignment score
  - Find and display the Hamming and Levenshtein distance between Sequence A and B