**Practicum Case**

1. Parsing (fasta, gb, pdb)  
   Please parse the files provided (sequence.fasta, sequence.gb, 8z3g.pdb)  
   Show the record of each 3 file neatly  
   Let Sequence A be the seq from the fasta file  
   Let Sequence B be the seq from the gb file  
   Clean Sequence A and B so that only GCAT is allowed on the sequence
2. Create a new sequence C :  
   First, take the first 10 nucleotides from sequence A, then take 10 last nucleotides from sequence B, combine them respectively to get sequence C
3. For Sequence C :  
   Calculate the molecular weight  
   Calculate the melting temperature (NN, Wallace, GC content)  
   Transcribe and translate the sequence  
   Show the frequency of the sequence, in bar plot
4. For Sequence A and B :  
   Visualize the local alignment and the global alignment