Lab1 Part B

What is NCBI?

NCBI focuses on using biological computing to analyze genetics and protein function by using new tools and algorithms to process large amounts of data to help us better understand health and disease.

What are the tools that it supports?

According to the https://www.ncbi.nlm.nih.gov/ , it support various tool for example, Basic Local Alignment Search Tool (BLAST), Batch Entrez, E-Utilities, Genome BLAST, Genome Remapping Service, Genome Workbench, Open Reading Frame Finder (ORF Finder), Primer-BLAST, ProSplign, Sequence Viewer, Splign, and VecScreen.

Blast

blast find the similar sequence in a strain or protein sequence. The program would return a statistical significance base the database information.

FASTA

FASTA provides a heuristic search with a protein query. For blast, it almost find the ungapped sequence, and FASTA used to find similarities between less similar sequence (less optimized)

Entrez

According to the https://www.ncbi.nlm.nih.gov/, Entrez allows you to **retrieve records** from many Entrez databases by **uploading a file** of GI or accession numbers from the Nucleotide or Protein databases, or a file of unique identifiers from other Entrez databases. Search results can be saved in various formats directly to a local file on your computer.

Genebank

Genebank is an open access database that store nucleotide sequences and their protein translations information.

What PubMed and MEDLINE is and where they are used

According to the https://www.ncbi.nlm.nih.gov/, MEDLINE contains journal citations and abstracts for biomedical literature from around the world (like a database). PubMed provides free access to MEDLINE and links to full text articles when possible. They used when need to search paper for project or citation some external information.