Summary for two Youtube videos.

So, first of all, the explained content on the first video was commonly about database search on reference sequences, and downloading a content from NCBI (National Center for Biotechnology Information) database, then comparing those sequence on BLAST ( Basic Local Alignment Search Tool ). The search engine at the NCBI is capable of processing logical expression, like AND, OR, plus indexing array search is also possible. When it comes to downloading the selected sequence, we can drop them into our cart, just like when we do online shopping, and align the selected sequence in two different orders. After that, we can download the data and do the analysis or use BLAST for more research on the sequence. The NCBI provides rich support on filtering, after a quick search, we can filter out unnecessary results and choose a proper database according to our need.

On the second video, I learnt how to use uniprot.org website. This website is a database where researchers from multiple companies or individuals publish their analysis on a sequences, and the submitted data will be put into TrEMBL database automatically. TrEMBL is not reviewed and awaiting for manual review database, where SwissProt database is manually reviewed by UnProt staff. The data will be moved to SwissProt after being manually reviewed. Next, there is a free text search engine, where we can search for gene names, protein names, diseases, keywords, species or GO terms. The search gives multiple filtering options if someone wants more advanced search. When don’t know the protein name or other information about the protein but we have a portion of a sequence, then we can use a search engine called Peptide search. The viewer has two visualization modes, tabular and graphical. After we find the required sequence or a protein we download the directly from the website and use BLAST again for further research. For programmers, UniProt website has RestAPI, for protein and also for website, so we can query the website for a specific sequence using programming for faster analysis.

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