

COMP 4980 Project Proposal(#5 bioinformatic tools)

Problem and proposal

PAM and BLOSUM are the powerful global sequence alignment tools that can help analyzing the protein sequence. However, in the comp 4980 lectures this semester, the two alignments were only introduced briefly, some core mechanics were not mentioned.

In order to understand these two alignment methods. Nobutaka Kim and I are proposing to build a website like EMBOSS Needleman-Wunsch tool webpage. Thus this will be a team project and this project will contain two part. The front end website that take the protein sequences from users and display the calculated scoring metrics to the users. The second part is back end engine that read the users input and do the PAM or BLOSUM scoring metrics calculations.

Since there is already PAM and BLOSUM tool online, so we can use these online tools to check the correctness of the implemented program.

Proposed schedule:

Nov.4 - Nov.6

- Implement front end website.

- Implement Needleman-Wunsch global sequence alignment tool.

Nov.6-Nov.14

- implementing the PAM sequence alignment tool

Nov.15-20

- Implementing the BLOSUM sequence alignment tool

Nov.21-Nov.23

- Testing