

CS 466 Final Project Proposal

Team Members:

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Brief Motivation:

Our project aims to develop an interactive web platform which implements and visualizes various sequence alignment algorithms, including Global Alignment, Local Alignment, Fitting Alignment, Gap Affine Penalty Alignment, and Multiple Sequence Alignment for DNA, RNA, and protein sequences.

Planned Method/Experimentations:

For our aligner, we plan to use algorithms that were covered in class along with standard visualization techniques such as the matrix representation used in our reference aligner. Our project will be based in python. We will use the django framework for making the website. We will also make use of standard python libraries like numpy, pandas, and matplotlib for visualization.

Week 1 (November 17 - November 24):

- Set up the development environment and version control.
- Design the user interface and plan the implementation details.
- Implement Global, Local, and Fitting Alignment algorithms.

Week 2 (November 25 - December 2):

- Implement Gap Affine Penalty Alignment Algorithm
- Make improvements to the frontend and add additional features

Week 3 (December 3 - December 10):

- Develop visualization features for all alignments.
- Start working on Multiple Sequence Alignment

Week 4 (December 11 - December 15)

- Finish implementing the MSA algorithm and integrate it into the tool
- Debugging and refactoring codebase to make the tool deployment ready
- Working on the Project Report

We plan to hold regular meetings and hack sessions to ensure smooth collaboration. and effective problem-solving. Additionally, we will maintain a GitHub repository for version control and collaborative development.

References:

We base our representation on the aligner that was provided to us in class: <https://valiec.github.io/AlignmentVisualizer/index.html>