Name

Kyle Daling

Advisors Name

Filip Jagodzinski

Project Description

I will conduct research into the viability of a new constrained sequence alignment tool. This research builds off research in computational structural biology such as Basic Local Alignment Search Tool (BLAST) and the Levenshtein Distance (LD) algorithm from computer science. BLAST tries to align two sequences of DNA in the optimal arrangement. However, a biologist may want to impose some constraints on the alignment, prioritizing a certain substring of matches. This tool seeks to allow generate results subject to specified constraints. Working with another computer science student, I will update the software to operate more reliably, add additional features, and determine whether the constrained sequence alignment tool provides any benefit over existing alignment tools (Smith-Waterman algorithm, BLAST).

When and how many credits

I will perform all this research this quarter. I wish to take the Honors 490 class for 2 credits.

Plan for presentation

I want to present near the end of the quarter in an honors senior project presentation scheduled by the Honors department.

Plan for the final project

My advisor hopes to submit our research to a conference with a deadline of October 17th. Therefore, the research must be done by then. I will also perform a presentation showcasing the research I have conducted. A brief outline for the presentation is as follows:

- What is sequence alignment?
    - How does it work? Why is it hard?
    - Smith-Waterman algorithm
    - BLAST
- Why is sequence alignment important?
- What is constrained sequence alignment?
    - How does it differ from regular sequence alignment?
- What did I do?
    - Updated constrained sequence alignment tool
    - Assessed its viability
- Demo
- What's next