

# Team Project

## 605.451 Principles of Computational Biology

The students in this course are required to complete an individual or small group (less than four people) project. The project is to design, implement, and test a software tool to perform an important task in bioinformatics such as multiple sequence alignment, phylogenetic tree construction, and so on by using the methods and algorithms learned in the course.

### 1. Time Line

- a. Module 1: Project starts
- b. Module 14: All project deliverables are due including the software tool, documentation, and presentation.

### 2. Deliverables

- a. A document that provides a review of the literature on the specific task, the existing tools to the task, and the algorithms and methods you implemented in your tool to complete the task. The document should explain the rationale for selecting the particular algorithms and methods, and their advantages and disadvantages compared to existing tools.
- b. An implementation in any programming language.
- c. A presentation and demonstration (10 – 20 minutes) recorded in video, using Adobe Connect.

### 3. Grading

The project is worth 20% of your final grade. Its marking will be based on the task you selected, your solution to the task, your implementation, presentation, and documentation. Assuming a team of size two, a ten-page document should be appropriate. Here is the suggested structure for the document: 1. Introduction. 2. Problem definition. 3. Methods and algorithms. 4. Results. 5. Conclusions.

### 4. List of Projects

Here is a list of projects you can choose from. It is perfectly fine if you choose a project that is not on this list as long as the project is bioinformatics related and the algorithms or methods you are going to use are from this course.

1. Multiple sequence alignment
2. DNA database search engine
3. Phylogenetic tree construction
4. Gene search
5. Motif search
6. Microarray data analysis

