ENGR 103 – Spring 2011
Freshman Engineering Design Lab

"BioGUI: Protein Circle Plot Visualization"
Interim Progress Report

Section 19, Group 275, Project 126   **Date: May 3, 2011**

Submitted to: *Fred Allen*

David Jamison

Ahmet Sacan

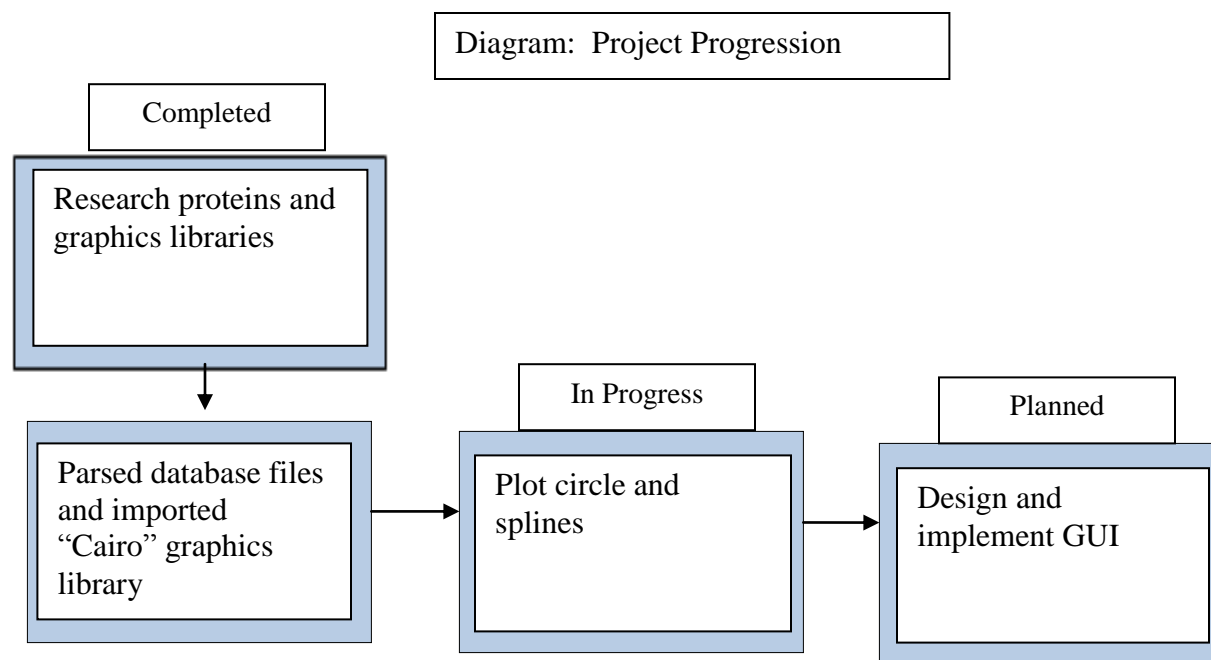**Group Members:**   *Brian Tighe*

Ethan Sena

Henry Kuns

Gavin Rapp

1. Overview

In the field of bioinformatics there is no single unifying graphical user interface system. This project is aimed towards developing small program sections that can be used to display plots based on information from data files. Other goals of this project include gaining group programming experience and developing programs to solve a realistic task.

Diagram: Project Progression

Completed

Research proteins and graphics libraries

Parsed database files and imported "Cairo" graphics library

In Progress

Plot circle and splines

Planned

Design and implement GUI

2. Ongoing and Completed Tasks

2.1 Initial Planning and Design

The first tasks that this project entailed were researching graphics libraries and planning the GUI's mechanics. The graphics library "Cairo" was chosen due to its ability to output images to different file types in addition to its simplicity compared to other libraries. Because only simple, two dimensional shapes needed to be displayed, many of the additional features of a more advanced graphics library would have been unnecessary.

After the graphics package had been chosen, it still had to be downloaded, installed, and included by the complier before any programming could begin. Another piece of software, Tortoise SVN, was required so that code could be transferred amongst the group.

2.2 Parsing Files and Using Graphics

Once the initial setup was completed, the group separated and focused on two different aspects of the program. One group worked on extracting the required information from the database files, while the other created the outline for the protein plot using the graphics library. This approach was effective because it allowed for both parts to be developed simultaneously, and there was little to no overlap between these sections.

2.3 Finding Neighbors and Drawing Text

At this point in the project, the circle plot had been created, and in order for the lines to be drawn, code needed to be written to find which molecules should be connected. Because of this, one group began to program this function, which analyzed the information obtained from the database files. At this time, the other group worked on writing text to the circle plot, so that the names of the molecules being connected could be displayed.

Figure 1

3. Upcoming Tasks

Currently, the circle plot still needs to utilize the information from the other programs to write the detail of the protein onto the circle plot, and connect them with splines.

In addition to this, the only other major task that remains is creating the GUI. This can be accomplished by either using a library to program the interface from scratch, or using a program that converts an interface that the user designs with it to code which will generate that interface.

A sample of what the circle plot might look like when completed.

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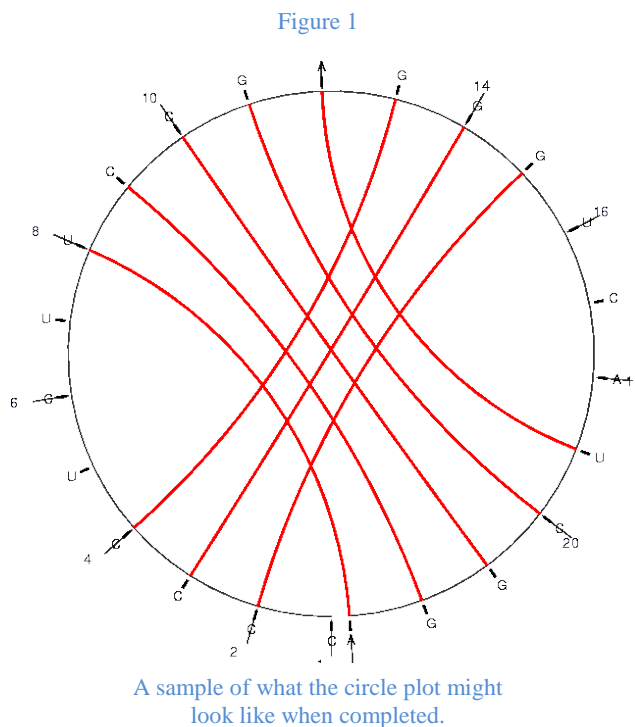
4. Timeline

The timeline for the project has remained for the most part unchanged. Weeks seven and eight have been modified slightly to include for the GUI design.

Table 1: Freshman Design Project Timeline

Task	Week									
	1	2	3	4	5	6	7	8	9	10
Circle Plot Program Design	x	x	x							
Secondary Structure Visualization				x	x	x				
Connecting with Splines & GUI design							x	x		
Final Report Preparation									x	x

5. References

[1] C. Jarabek and S. von Mammen, "Protein Painting: Aesthetic 2D Visualization of Amino Acid Sequences," University of Calgary., Calgary., Alberta, Jan. 10, 2011.

[2] G. Vreind and C. Sander, "Detection of Common Three-Dimensional Substructures in Proteins," European Molecular Biology Laboratory, Heidelberg, Germany, Feb. 23, 1991.

[3] H. Liu, X. Liu, Y. Yao, "Identification of Secretory Proteins Based on Similarity of Amino Acid Sequences," 2010 3rd International Conference on Biomedical Engineering and Informatics (BMEI), Nov. 18, 2010.

[4] R. Vivanco, N. Pizzi, "Computational performance of Java and C++ in processing large biomedical datasets" Canadian Conference on Electrical and Computer Engineering, 2002. IEEE CCECE 2002, Aug. 7, 2002.