CS 3824 Homework Assignment 3

Given: February 17, 2010

Due: February 23, 2010

General directions. The point value of each problem is shown in []. Each solution must include all details and an explanation of why the given solution is correct. In particular, write complete sentences. A correct answer without an explanation is worth no credit. The completed assignment must be placed inside the box labeled "CS 3824" outside 2160J Torgersen by 4:00 PM EST on February 23, 2010. No late homework will be accepted.

Digital preparation of your solutions is mandatory. Use of LATEX is optional, but encouraged. No matter how you prepare your homework, **please include your name.**

Use of LATEX (optional, but encouraged).

- Retrieve this LAT_EX source file, named homework3.tex, from the course web site.
- Rename the file < Your VT PID>_solvehw3.tex, For example, for the instructor, the file name would be heath_solvehw3.tex.
- Use a text editor (such as vi, emacs, or pico) to accomplish the next three steps.
- Uncomment the line
 - % \setboolean{solutions}{True}

in the document preamble by deleting the %.

• Find the line

\renewcommand{\author}{Lenwood S. Heath}

and replace the instructor's name with your name.

- $\bullet\,$ Enter your solutions where you find the LATEX comments $\,\%\,$ PUT YOUR SOLUTION HERE
- Print out and submit your solutions by 4:00 PM on February 23, 2010.

For a protein with n residues, you can define its residue-residue "contact map", which is simply an $n \times n$ matrix $A = (a_{ij})$ such that $a_{ij} = 1$ if residues (amino acids) i and j touch each other and 0, otherwise. Naturally, you assume that amino acids are labeled sequentially in the polypeptide chain.

[15] 1. Is it likely for a functional enzyme protein in its working state to have $A = (a_{ij})$ such that $a_{ij} = 1$ if and only if |i - j| = 0 or 1? Explain.

[25] 2. A 100×100 matrix $A = (a_{ij})$ is defined as $a_{ij} = 1$ if |i-j| < 6 OR if i = 25; $a_{ij} = 0$, otherwise. Can this be the contact matrix (map) of a real protein? Explain.

NOTE: No rigorous proofs required, just good logic.

If you want to know more about contact maps and are curious about what a contact map of a real protein from the protein data-bank (PDB) site¹ might look like, you may download the Macromolecular Contact tool² and play with it. It is Java-based, and should be pretty much plug-and-play. However, this is absolutely not necessary to correctly answer the questions above.

¹http://www.rcsb.org/

²http://people.cs.vt.edu/~onufriev/software.php