

CS 490/590 Bioinformatics Project VI: Neighbor Joining for Phylogenetic Trees

Description: You are to implement the Neighbor Joining algorithm on distance matrix inputs.

Specifications: The neighbor joining algorithm is described in pages 137 – 142 of your text, as part of the «On your own project ». This project is similar, except that I only require distance matrix inputs (no messing with multiple alignments, Jukes-Cantor, etc.). This restriction should also make it easier to check your correctness.

Sample inputs provided are **DM-p127.txt** and **DM-p139.txt**.

What to turn in: You must turn in a single zipped file containing your source code, a Makefile if needed for compilation, and a README file indicating how to execute your program.

Your program must be written in C/C++ or Java and compile using an open source compiler such as g++, gcc, or javac.

I will demo a Perl implementation of this project in class/lab so you will understand I/O, etc..

This assignment is due by MIDNIGHT of Thursday, November 14. Late submissions carry a -33% per day penalty.

The assignment is worth 10% of your total grade.