Translating DNA polymers to Polypeptides
Programming Assignment #1
Bio271/CS399, Spring 2002

PURPOSE
One of the primary tasks of a bioinformatician is the development of computational tools for analyzing biological data. This task requires fundamental comprehension of both the biological basis for the process being modeled and familiarity with the programming skills necessary to implement the model. The purpose of this three-week laboratory assignment is to give students an opportunity to develop one or both of these skills in a collaborative environment. This environment will provide students with an opportunity to work in interdisciplinary groups and to thus be exposed to the language and problem-solving approaches used in both computer science and biology.

ASSIGNMENT
The central dogma of molecular biology proposes a mechanism by which DNA codes for the synthesis of an organism's proteins. DNA polymers are transcribed into corresponding RNA polymers in the cell nucleus and then that are translated into chains of amino acids in cell ribosomes. Your goal is to create a program in PERL that takes as its input (via STDIN) a multiline DNA sequence and produces the sequence of amino acids that are coded for in the input DNA sequence. You MUST use the PERL pragmas "use warnings" and "use strict" in your final program.

PROGRAM GRADING
A. A program will receive a grade of "A" if it reliably produces all polypeptides coded for in any of the possible open reading frames for the sequence. The output must list these polypeptides in order of sequence length - longest to shortest. Furthermore, an A program must be well documented and robust - it should have no bugs and should rigorously check possible error conditions including illegal or nonsensical input. An "A" program must use the strict and warnings pragmas without producing warnings or errors.

B. A program will receive a grade of "B" if it reliably produces all polypeptides coded for in any of the possible open reading frames for the sequence. A B program should be well documented and robust. An "A" assignment which lacks sufficient documentation or lacks robustness will receive a B grade. A "B" program must use the strict and warnings pragmas without producing warnings or errors.

C. A program will receive a grade of "C" if it reliably produces all polypeptides coded for in the forward reading frame starting at position 1. A C program should be well documented and reasonably robust. A "B" assignment which lacks sufficient documentation or robustness will receive a C grade. An "A" or "B" assignment that produces PERL warning messages under the strict and warnings pragmas will receive a "C" grade.

D. A program will receive a grade of "D" if it successfully converts the DNA polymer into the corresponding sequence of amino acids without regard for START and STOP codons. A "C" assignment which lacks sufficient documentation or robustness will receive a D grade.

E. Programs that do not meet the minimum criteria for a "D" grade will receive an "E". IT IS REQUIRED that all programs run without producing syntax errors (crashing). Programs that produce syntax errors (no matter how ambitious in scope) will receive a failing grade on this assignment.
GROUP COLLABORATION
This assignment consists of both group interaction and individual accomplishment. Each student must turn in their own program. Students are allowed to ask ANY questions of other students in their groups. Groups are encouraged to work together to understand the problem, develop strategies and algorithms towards solving the problems, deal with programming syntax, and even to test each other's programs for robustness. Collaboration WITH OTHER MEMBERS OF YOUR GROUP is allowed and encouraged for this assignment with the following exceptions. You may not, under any circumstances, copy another student's code. You may not, under any circumstances, edit or modify another student's code. You MAY help other students "debug" code and discuss techniques and syntax to solve any problems encountered, but you MAY NOT "just fix" another student's problems. Furthermore, you MAY NOT collaborate with anyone who is not a member of your group. WSU’s standard policies for academic integrity apply except as stipulated above.

ASSIGNMENT GRADING
This homework assignment requires you to work in multi-disciplinary teams. In order to provide all students with an assessment that rewards team building and interaction, each student's overall grade will be a weighted average of their individual assignment. Two-thirds of each student's grade will be based upon the grade received for their program. One-third of each student's grade will be based upon the average of all programs received for their team.

TURNING IN PROGRAMS
All programs must be turned in by 11:59PM 4/23/02. Programs received late will loose one full letter grade for each day late. Programs can be turned in by executing the following command on your program: ~w001ted/pub/cs399/cs399_handin  <filename>.