Applying Perl

10-31-2005

Opening Discussion

- What did we talk about last class?
- Do you have any questions about the reading or was there anything in the reading you found particularly interesting?

Concluding Regular Expressions

- The base pairs of DNA are typically labeled with the letters A, C, G, and T. In the double helix, A is always bound to T and C is always bound to G. Write a subroutine that takes one strand and returns what you would have in the opposite strand.
- Perl has another regular expression type of the form tr///. The tr stands for transliteration and it does mass replacement at once to make this task a lot simpler.
- Three base pairs encode a protein (it's not really that simple, but we'll go easy for this problem). Write a subroutine that takes a sequence and counts how many time each sequence of three base pairs occurs. Assume the number of bases is a multiple of 3 to start.

Funky Control Structures

- Do you have any questions about the control structures in Perl? They allow you to do things in a lot of different ways. Some might argue too many different ways. Oddly, some of their “tricks” would work in other languages, but programmers of other languages would probably frown on them even more than Perl programmers do.

Doing Files in Perl

- Let's go back to our telephone book example now and I want you to make it so that you input the name of the file to read the telephone numbers from, not on command line, but interactively. What do we have to change in the code to make this work?
- How do we get information about files in Perl?
- What are bitwise operators? How do you use them and when do you use them?

Reminders

- Remember to turn in assignment #7 tonight.