First-Day Quiz (CS 5046, Spring 2012)

1. How do you find the length of the array @genes?

2. How do you count the number of keys in the hash %genetic_code?

3. How many values can a scalar variable store?

4. How many values can an array variable store?

5. @genes is an array variable. I want to create a reference to @genes. What is the type of this reference? Is it
   (a) a scalar,
   (b) a string,
   (c) a number,
   (d) an array,
   (e) a hash, or
   (f) some other weird thing?

6. Write a Perl command to store a reference to @genes in a variable. Let us call the variable storing the reference genes_ref. You have to decide the correct sigil to prefix genes_ref with (e.g., $, , % or something else).

7. How will you find the content of the 10th index in @genes using the genes_ref variable?
8. You have two arrays, one array \texttt{rapamycin\_up} storing the genes up-regulated in yeast upon treatment with rapamycin and the other array \texttt{heat\_shock\_up} storing the genes up-regulated in yeast upon treatment with heat shock. Write one subroutine called \texttt{condition\_compare} that takes these two arrays as arguments and returns two arrays. The first array returned is a list of genes that appear both in \texttt{rapamycin\_up} and in \texttt{heat\_shock\_up}. The second array returned is a list of genes that appear in \texttt{rapamycin\_up} but not in \texttt{heat\_shock\_up}. Also write down how you will call this subroutine. In the code for the subroutine, I am more interested in how you will pass in two arrays and return two arrays. If you have time, also fill in the rest of the code for the subroutine.