## **Randoms and Hashes**

#### 4/4/2008





## **Opening Discussion**

- Do you have any questions about the assignment?
- Do you have any questions about the reading? Note that you probably should be doing the reading because I can't cover everything in full detail during lecture.







- There are many situations in scientific computing when we want to have random numbers.
- In biology an example would be modeling mutations.
- In general models will use random sequences for elements that occur at a lower level than the model deals with. So instead of doing a detailed model of that process you do intelligent random selections. This often means using different types of random distributions.





- srand seeds the random number generator
- rand gets a random number
- Other helpful subroutines
  - scalar evaluates something in a scalar context.
  - int casts a value to an int.
- Remember parentheses can be optional.

# **Mutating DNA**

- The book runs through an example of code that takes a DNA sequence and randomly mutates it by picking random positions and substituting random bases into those positions.
- This uses a four argument version of substr that substitutes in for a segment of the original string.

### Hashes

- The third standard data type (in addition to scalar and array) in Perl is the hash.
- A hash is much like an array except that it isn't indexed by an integer, it is indexed by a string. They are sometimes called associative arrays.
- The full hash variable is preceded with a %. Use {} to index from it. When indexing you put a \$ in front because you are pulling out a scalar.
- Hashes can be initialized as a list where consecutive elements are key/value pairs. The => symbol can replace commas between key and value.







### Let's play with hashes some to see how they work.







## **Closing Remarks**

### Assignment #6 is due today.



