Homework 2: Sampling & Iteration

Biol 607

September 12, 2014

Welcome to homework 2, where you will be getting more in depth with R. Note, for some of the problems below, you'll need to learn more about the functions R has available to you via helpfiles or rooting around for more information. Time to start getting used to it, and learning how to figure out how to do something that is not immediately obvious to you! That part of learning to use this delightful data analysis beast will never entirely go away. Good luck, and I look forward to getting this by 5pm time on Tuesday.

1) Problems from Whitlock and Schluter (5 points each) Complete problems 15,17 on pg. 20 and 15,21, and 22 from pgs. 89-91. Use R where possible. Datasets (so you don't have to type things in) are available at http://www.zoology.ubc.ca/~whitlock/ABD/teaching/datasets.html (although the problem numbers are off on the datasets in some cases). Note, you may need to apply additional arguments from functions like boxplot.

2) A little R and Simulation

2.1 (10 points) The Fibonacci sequence is a classic sequence of integers in mathematics (see http://en.wikipedia.org/wiki/Fibonacci_number) where each number is the sum of the previous two numbers in the sequence before it, starting with 1,1,2,3,5... So, F1=1, F2=1 (some use F0=0, but, meh). Use a loop to give me the 30th number (F30) in the sequence.

2.2 (15 points) We've looked at the relationship between the sample size and estimation of the mean. Do the mean, median, standard deviation, and skew all appear to require the same sample size for a precise estimate? Try this with a normally distributed population with mean 10 and standard deviation of 5, and a uniform distribution between 0 and 1000. Instead of using sample, draw from the distributions directly. They are your 'population.'

For fun, `par(mfrow=c(1,4))}` will make a plotting window with 4 panels in 1 row (1 row, 4 columns). Note also that you'll need to find and load a library to estimate skew.