**Computer Lab 9 – Introduction to population genetics using microsatellites**

**Conservation Genetics (BIOL 4174 / 5174)**

Due date: 4/02/2018 at Midnight.

Submit this file via Blackboard.

Part I – Understanding our data

1. Do you notice any loci with particularly high missing data (say, >10%)? Any populations which are consistently missing a lot of data?
2. The Bonferroni adjusted alpha value is calculated by dividing your normal alpha value by the number of tests being performed. Calculate your Bonferonni adjusted alpha value. Record your value below.
3. Determine which loci appear to be out of HWE. Remember that the null hypothesis is that the population is in equilibrium.
4. After testing for HWE within each population, do you see any populations which appear out of equilibrium at many loci? List them here. What evolutionary causes might there be?
5. After running the ia() command, we should see a distribution of values in the random permutations, and a calculated value for our data (with an associated p-value). Record those values here. Do you think these loci are in linkage disequilibrium (the null hypothesis is that they aren’t)?
6. After plotting the results within each population, do you still notice much signal of linkage disequilibrium? Gray values indicate undefined values- caused by missing data or monomorphic loci within populations.

Part II – Genetic diversity and differentiation

1. After running the ggplot command, you should see box plots representing values (across loci) for several different measures of genetic distance. Qualitatively compare them here.
2. After running the corPlot() command: Do you notice some estimators which are biased by number of alleles? Do you think these estimators would perform well with loci having very high mutation rates, such as microsatellites?
3. Study your plots of pairwise D and Gst. Which populations appear to be most similar? Look at the map- do these results make sense, given their geographical locations?

Part III – Mantel Test

1. What was the result for Pearson’s r? Was this result significant?
2. Based on the results of the Mantel test, do you suspect geographic distance to be an isolating mechanism in this species? Note that I calculated a **straight-line** distance in ArcMap- why might this lead to a much lower correlation than we might have expected (Hint: What sort of organism are we working with?)