Katie Stanley

Evolution

Final Project

Initial Hypothesis

Original Hypothesis: I hypothesize that that hip dysplasia(one orthopedic disease) is a heritable characteristic that’s genotype(meant phenotype) can be followed over time in certain mammals and dog breeds.

Revised hypothesis: I hypothesize that orthopedic diseases of the hip are heritable, and their root can be traced evolutionary among certain mammals and dog breeds.

Analysis Plan: To complete this project, I would like to finish compiling the prevalence data of some of the major orthopedic diseases(osteoarthritis and hip dysplasia) for the hip found among certain mammals and dog breeds. I think that the hip dysplasia data is complete. I just must finish the osteoarthritis data. I then would like to trace the root of these orthopedic diseases evolutionary among certain mammals and dog breeds. I would hope to make a phylogeny that is focused on some general mammals and then specific dog breeds (all one phylogeny). All the mammals/breeds have been found to have a certain frequency of these orthopedic diseases of the hip based on the data present. I would like to highlight or make a box around the breeds or mammals that these orthopedic diseases show the most prevalence based upon the final three-hundred data points. I have not made this phylogeny or entered/collected all three-hundred data points into the excel sheet. I still have a hundred and seventy data points to enter an excel sheet. I have a total of a hundred and thirty data points in the excel sheet currently. I have the file read into R, I have hope to have a bar chart with those breeds/mammals that make up 90 percent of the most prevalence and a pdf saved. I also, need to look at the relationship of these variable to plot the tree. I need to make sure that these graphs test my hypothesis or get help on ideas for statistical tests or other routes that can be used for this type of data frame that might better fit this project.