**Terms, topics, or concepts you should be familiar with:**

p-value

frequentist vs Bayesian approaches

Bayes theorem

reproducibility crisis

statistic

parameter

continuous variable

discrete variable

nominal variable

ordinal variable

experimental vs observational studies

blinding

pseudoreplication

biological vs technical replicates

outliers

confounding variables

common faults in plots

sample

population

transformation

parametric

non-parametric

interaction

MCMC

**R skills you should have**

Create matrices, vectors, dataframes, and lists

Subset each of these objects

Read and write csv files

Make a high quality plot of 1, 2, or 3 variables that have a mix of continuous and discrete values

Perform a permutation or Monte Carlo test

Perform and correctly interpret the statistical tests mentioned below

**R functions you should handle with ease:**

binom.test

chisq.test

t.test (single sample, two sample, paired)

aov

lm

glm

for

if

sample

ways of testing values > < >= ! == etc.

**Example Problems**

Download the newts.repro.csv data from the website. This file contains data for matings of male newts it has their tank number, length, mass, number of mates and number of offspring. What are the important predictor(s) of offspring number?

Download the gnatocerus.male.csv data from the website this contains information on the horn size, body size, number of matings, and grandchildren of each beetle. Describe how body size effects horn size. What is the best predictor of number of grandchildren and number of mates?

Download the hiC.data.csv file from the course website. This file contains contact and size information for all chromosomes in a rattlesnake genome. Contacts are the data that we get from Hi-C sequencing and describe the fact that two pieces of DNA were close together spatially in a nucleus of a cell. Chromosomes can be divided into macro and micro based on their sizes these are indicated with the code “ma” or “mi” respectively. The columns of this dataset show in order:

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| chrom1 | chrom2 | types | chrom1.c | chrom2.c | contacts | chrom1.s | chrom2.s |
| First contact chromosome | Second contact chromosome | Ma and mi code identifying the types of chromosomes | Total contacts on first chromosome | Total contacts on second chromosome | Contacts for this pair | Size of chromosome one | Size of chromosome two |

Use a method of your choice to decide whether or not micro chromosome have a different number of contacts with other chromosomes than you expect by chance. A good starting place to think about this might be that the number of contacts a chromosome has is a function of its size.