Stephanie Thrasher, Antonio Escallon, Catherine Shea, Keegan M, Abigale Foster
In class T-tests

1. boxplot(body_mass_g ~ sex, data = penguins, main = 'Body mass of Adelie Penguins')

2. dat_ade_f= subset(dat_ade, sex == "female")

   t.test(dat_ade_f$body_mass_g, y = NULL,
   alternative = c("greater"),
   mu= 0, paired= FALSE, var.equal= FALSE,
   conf.level = 0.95)
   This is a one tailed test.
3. p-value< 2.2e-16, this means the results reject the null hypothesis and Adeile penguins have a bodymass greater than 0.

4. dat_m_adelie = na.omit(droplevels(subset(dat_ade, sex == "male")))
   t.test(dat_m_adeilie$body_mass_g, alternative = c("greater"), mu = 4000) This is a one tailed test.

5. A p-value of 0.14 means that we are accepting the null hypothesis. This means that the body mass is greater than 4000.
6. t.test(dat_ade$body_mass_g ~ dat_ade$sex)
7. Since the p-value is less than 0.05 this means the sample is normally distributed.
8. t.test(dat_ade$body_mass_g ~ dat_ade$sex, alternative = c('greater'), mu = 0)
9. t.test(dat_ade$body_mass_g ~ dat_ade$sex, alternative = c('less'), mu = 0)
10. The different p-values show whether the findings follow the null hypothesis or not. The higher p-value of 1 from question 8 rejects the null hypothesis while the p-value from question 9 means that the null hypothesis is accepted.