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| --- | --- | --- |
| **Block** | **R Code** | **Process Code** |
| 1 | #-----------------------------------------------  #Preliminary data for Fatmeter Calibration  #----------------------------------------------- | comment on nature of R script |
| 2 | install.packages("outliers") | install package for grubbs.test function |
| 2 | install.packages("lattice") | install package for equal.count, densityplot, xyplot functions |
| 2 | library(lattice) | load in package |
| 3 | #-----------------------------  # WB Lipid Analysis  #----------------------------- | comment on subsection of code |
| 3 | #upper anterior measurement Linear model | comment |
| 4 | str(PADataNoOutlier) | data inspection |
| 4 | str(PADataNoOutlierMultMeasure) | data inspection |
| 4 | plot(PADataNoOutlier) | scatterplot matrix of data |
| 4 | plot(PADataNoOutlierMultMeasure) | scatterplot matrix of data |
| 5 | linearAnterior <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUA) | lm |
| 5 | summary(linearAnterior) | summary of lm |
| 5 | linearAnterior | inspect lm |
| 5 | with(PADataNoOutlier, plot(Lipid ~ PSUA, las = 1, col = ifelse(PADataNoOutlier$`Fork Length` < 280, "red", "black"))) | plot of variables in lm, using with() and $, colors based on conditional statement |
| 5 | abline(linearAnterior) | add lm line to plot |
| 5 | rstudent(linearAnterior) | pulling off the residuals from the model |
| 5 | plot(linearAnterior) | diagnostic plot |
| 6 | #Exponential function | comment |
| 6 | expAnterior <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUA)) | lm |
| 6 | summary (expAnterior) | summary of lm |
| 6 | expAnterior | inspect lm |
| 6 | with(PADataNoOutlier, plot(Lipid ~ log(PSUA), las = 1,  col = ifelse(PADataNoOutlier$`Fork Length` < 260, "red", "black"))) | plot of variables in lm, using with() and $, colors based on conditional statement |
| 6 | abline(expAnterior) | add lm line to plot |
| 6 | summary(expAnterior) | redundant line, already included |
| 6 | plot(expAnterior) | diagnostic plot |
| 7 | #Cooks Distance for influential point identification | comment |
| 7 | cooksAnterior <- cooks.distance(expAnterior) | pull of cooks distances, store in new variable |
| 7 | plot(cooksAnterior) | scatterplot of row id & cooks distance |
| 7 | abline(h = 4\*mean(cooksAnterior, na.rm=T), col="red") | add horizontal line to plot, data summary (mean) |
| 7 | text(x=1:length(cooksAnterior)+1, y=cooksAnterior, labels=ifelse(cooksAnterior>4\*mean(cooksAnterior, na.rm=T),names(cooksAnterior),""), col="red") | add text to plot, add labels to plot, labels based on conditional statement & data summary (mean) |
| 8 | #Upper posterior measurement | comment |
| 8 | linearposterior <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUP) | lm |
| 8 | summary(linearposterior) | summary of lm |
| 8 | linearposterior | inspect lm |
| 8 | with(PADataNoOutlier, plot(Lipid~ PSUP, las = 1)) | plot of variables in lm, using with(), NO $ |
| 8 | abline(linearposterior) | add lm line to plot |
| 8 | # plot(posterior) | diagnostic plot, commented out, not relevant to variables around code |
| 9 | #Exponential posterior measurement | comment |
| 9 | expPosterior <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUP)) | lm |
| 9 | summary(expPosterior) | summary of lm |
| 9 | expPosterior | inspect lm |
| 9 | with(PADataNoOutlier, plot(Lipid ~ log(PSUP)), las = 1) | plot of variables in lm, using with(), NO $ |
| 9 | abline(expPosterior) | add lm line to plot |
| 9 | # plot(expPosterior) | diagnostic plot, commented out |
| 9 | cooksPosterior <- cooks.distance(expPosterior) | pull off cooks distances, store in new variable |
| 9 | plot(cooksPosterior) | scatterplot of row id & cooks distance |
| 9 | abline(h = 4\*mean(cooksPosterior, na.rm=T), col="red") | add horizontal line to plot, data summary (mean) |
| 9 | text(x=1:length(cooksPosterior)+1, y=cooksPosterior, labels=ifelse(cooksPosterior>4\*mean(cooksPosterior, na.rm=T),names(cooksPosterior),""), col="red") | add text to plot, add labels to plot, labels based on conditional statement & data summary (mean) |
| 9 | grubbs.test(expPosterior) | test of outliers from lm |
| 9 | #outlier test | comment |
| 9 | outlier.test(expPosterior) | test of outliers from lm |
| 10 | #CI | comment |
| 10 | # qt(.975,9) | function calculation, commented out |
| 11 | #upper middle measurements linear | comment |
| 11 | Middle <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM) | lm |
| 11 | summary(Middle) | summary of lm |
| 11 | with(PADataNoOutlier, plot(Lipid ~ PSUM, las = 1)) | plot of variables in lm, using with() |
| 12 | #upper Middle measurements only | comment |
| 12 | str(PADataNoOutlier) | data inspection, redundant already included |
| 12 | expMiddle <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | lm |
| 12 | summary(expMiddle) | summary of lm |
| 12 | with(PADataNoOutlier, plot(Lipid ~ log(PSUM), las = 1, xlab = "Whole-body Lipid Content (%)",  ylab = "UM Fatmeter Reading", col = ifelse(PADataNoOutlier$`Fork Length` < 270, "red", "black"))) | plot of variables in lm, using with(), add axis label, colors based on conditional statement |
| 12 | abline(expMiddle) | add lm line to plot |
| 12 | middle | reference to non-existant variable |
| 12 | #Cooksd middle | comment |
| 12 | cooksMiddle <- cooks.distance(expMiddle) | pull off cooks distances, store in new variable |
| 12 | plot(cooksMiddle) | scatterplot of row id & cooks distance |
| 12 | abline(h = 4\*mean(cooksMiddle, na.rm=T), col="red") | add horizontal line to plot, data summary (mean) |
| 12 | text(x=1:length(cooksMiddle)+1, y=cooksMiddle, labels=ifelse(cooksMiddle>4\*mean(cooksMiddle, na.rm=T),names(cooksMiddle),""), col="red") | add text to plot, add labels to plot, labels based on conditional statement & data summary (mean) |
| 13 | #---------------------------------  #Energy analysis of data  #--------------------------------- | subheader comment |
| 13 | #Means and sd of data | comment |
| 13 | mean(PADataNoOutlier$Energy) | data summary (mean) |
| 13 | sd(PADataNoOutlier$Energy) | data summary (sd) |
| 14 | #Anterior energy measurement | comment |
| 14 | expAnteriorE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUA)) | lm |
| 14 | summary(expAnteriorE) | summary of lm |
| 14 | with(PADataNoOutlier, plot(Energy ~ log(PSUA), las = 1)) | plot of variables in lm, using with() |
| 14 | abline(expAnteriorE) | add lm line to plot |
| 15 | #Posterior energy measurement | comment |
| 15 | expPosteriorE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUP)) | lm |
| 15 | summary(expPosteriorE) | summary of lm |
| 15 | expPosteriorE | inspect lm |
| 15 | with(PADataNoOutlier, plot(Energy ~ log(PSUP), las = 1)) | plot of variables in lm, using with() |
| 15 | abline(expPosteriorE) | add lm line to plot |
| 15 | # plot(posteriorE) | diagnostic plot, commented out |
| 16 | #OUTLIER REMOVED anterior Energy | comment |
| 16 | expAnterior2E <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUA)) | lm |
| 16 | summary(expAnterior2E) | summary of lm |
| 16 | expAnterior2E | inspect lm |
| 16 | with(PADataNoOutlier, plot(Energy ~ log(PSUA), las = 1)) | plot of variables in lm, using with() |
| 16 | abline(expAnterior2E) | add lm line to plot |
| 16 | # plot(anterior2E) | reference to non-existent variable, commented out |
| 16 | # plot(posterior2E) | reference to non-existent variable, commented out |
| 16 | # posterior2E | reference to non-existent variable, commented out |
| 17 | # #CI | comment |
| 17 | # qt(.975,9) | function calculation, commented out, redundant, already calculated |
| 18 | #Middle Data (outlier removed) | comment |
| 18 | expMiddle2E <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM)) | lm |
| 18 | summary(expMiddle2E) | summary of lm |
| 18 | expMiddle2E | inspect lm |
| 18 | with(PADataNoOutlier, plot(Energy ~ log(PSUM), las = 1)) | plot of variables in lm, using with() |
| 18 | abline(expMiddle2E) | add lm line to plot |
| 18 | # plot(middle2E) | diagnostic plot, commented out, reference to non-existent variable |
| 19 | #relationship between lipids and energy | comment |
| 19 | LMLipidEnergy <- lm(PADataNoOutlier$Energy ~ PADataNoOutlier$Lipid) | lm |
| 19 | with(PADataNoOutlier, plot(Energy ~ Lipid, las = 1)) | plot of variables in lm, using with() |
| 19 | abline(LMLipidEnergy) | add lm line to plot |
| 19 | summary(LMLipidEnergy) | summary of lm |
| 20 | #relationships with energy and condition | comment |
| 20 | lmConditionEnergy <- lm(PADataNoOutlier$Energy ~ PADataNoOutlier$KN\_\_1) | lm |
| 20 | with(PADataNoOutlier, plot(Energy ~ KN\_\_1, las = 1)) | plot of variables in lm, using with() |
| 20 | abline(lmConditionEnergy) | add lm line to plot |
| 20 | summary(lmConditionEnergy) | summary of lm |
| 21 | #relationships with lipids and condition | comment |
| 21 | lmConditionLipid <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$KN\_\_1) | lm |
| 21 | with(PADataNoOutlier, plot(Lipid ~ KN\_\_1, las = 1)) | plot of variables in lm, using with() |
| 21 | summary(lmConditionLipid) | summary of lm |
| 21 | abline(lmConditionLipid) | add lm line to plot |
| 22 | #relationship with condition and Fatmeter Anterior | comment |
| 22 | lmConditionAnterior <- lm(PADataNoOutlier$PSUA ~ PADataNoOutlier$KN\_\_1) | lm |
| 22 | with(PADataNoOutlier, plot(PSUA ~ KN\_\_1, las = 1)) | plot of variables in lm, using with() |
| 22 | abline(lmConditionAnterior) | add lm line to plot |
| 22 | summary(lmConditionAnterior) | summary of lm |
| 23 | #relationship with condition and Fatmeter Posterior | comment |
| 23 | lmConditionPosterior <- lm(PADataNoOutlier$PSUP ~ PADataNoOutlier$KN\_\_1) | lm |
| 23 | with(PADataNoOutlier, plot(PSUP ~ KN\_\_1, las = 1)) | plot of variables in lm, using with() |
| 23 | abline (lmConditionPosterior) | add lm line to plot |
| 23 | summary(lmConditionPosterior) | summary of lm |
| 24 | #relationship with condition and Fatmeter Middle | comment |
| 24 | lmConditionMiddle <- lm(PADataNoOutlier$PSUM ~ PADataNoOutlier$KN\_\_1) | lm |
| 24 | with(PADataNoOutlier, plot(PSUM ~ KN\_\_1, las = 1)) | plot of variables in lm, using with() |
| 24 | abline(lmConditionMiddle) | add lm line to plot |
| 24 | summary(lmConditionMiddle) | summary of lm |
| 25 | #combinations | comment |
| 25 | #lm P and A Fatmeter measurements, Kn, and Lipid | comment |
| 25 | lmAPKn <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUA) + log(PADataNoOutlier$PSUP) + PADataNoOutlier$KN\_\_1 + log(PADataNoOutlier$PSUM)) | lm |
| 25 | summary(lmAPKn) | summary of lm |
| 25 | plot(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUA) + log(PADataNoOutlier$PSUM) + PADataNoOutlier$KN\_\_1) | plot of variables in lm, multivariate plot, using only $ |
| 25 | abline(lmAPKn) | add lm line to plot |
| 25 | cookslmAPKn <- cooks.distance(lmAPKn) | pull off cooks distances, create new variable |
| 25 | plot(cookslmAPKn) | scatterplot of row id & cooks distance |
| 25 | abline(h = 4\*mean(cookslmAPKn, na.rm=T), col="red") | add horizontal line to plot, data summary |
| 25 | text(x=1:length(cookslmAPKn)+1, y=cookslmAPKn, labels=ifelse(cookslmAPKn>4\*mean(cookslmAPKn, na.rm=T),names(cookslmAPKn),""), col="red") | add text to plot, add labels to plot, label based on conditional statement |
| 26 | #lm of fish middle with length accounted for | comment |
| 26 | lmMidFLM <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM + PADataNoOutlier$'Fork Length' + PADataNoOutlier$Mass +  PADataNoOutlier$`Fork Length`\*PADataNoOutlier$Mass) | lm |
| 26 | summary(lmMidFLM) | summary of lm |
| 26 | lmMidFL <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM + PADataNoOutlier$'Fork Length') | lm |
| 26 | summary(lmMidFL) | summary of lm |
| 27 | #all size accounted for - Mass not helpful | comment |
| 27 | lmMidSize <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM + PADataNoOutlier$`Fork Length` +  PADataNoOutlier$Mass) | lm |
| 27 | summary(lmMidSize) | summary of lm |
| 28 | #lm of fish middle with mass accounted for | comment |
| 28 | lmMidMass <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM + PADataNoOutlier$Mass) | lm |
| 28 | summary(lmMidMass) | summary of lm |
| 29 | #lm of just fish with multiple measurements | comment |
| 29 | multMiddle <- lm(PADataNoOutlierMultMeasure$Lipid ~ PADataNoOutlierMultMeasure$PSUM) | lm |
| 29 | summary(multMiddle) | summary of lm |
| 29 | plot(PADataNoOutlierMultMeasure$Lipid ~ PADataNoOutlierMultMeasure$PSUM) | plot of variables in lm, using $ |
| 29 | abline(multMiddle) | add lm line to plot |
| 29 | multMiddleExp <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$PSUM)) | lm |
| 29 | plot(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$PSUM)) | plot of variables in lm, using $ |
| 29 | abline(multMiddleExp) | add lm line to plot |
| 30 | #lm of all measurements | comment |
| 30 | summary(multMiddleExp) | summary of lm |
| 30 | multAll <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$PSUM) + log(PADataNoOutlierMultMeasure$PSUA) + log(PADataNoOutlierMultMeasure$PSUP)) | lm |
| 30 | summary(multAll) | summary of lm |
| 30 | plot(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$PSUM) + log(PADataNoOutlierMultMeasure$PSUA) + log(PADataNoOutlierMultMeasure$PSUP)) | plot of variables in lm |
| 30 | abline(multAll) | add lm line to plot |
| 30 | avgAll <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | lm |
| 30 | summary(avgAll) | summary of lm |
| 30 | plot(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | plot of variables in lm |
| 30 | abline(avgAll) | add lm line to plot |
| 30 | avgAllKn <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$'Avg measurement') + PADataNoOutlierMultMeasure$KN\_\_1) | lm |
| 30 | summary(avgAllKn) | summary of lm |
| 30 | plot(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`) + PADataNoOutlierMultMeasure$KN\_\_1) | plot of variables in lm |
| 30 | abline(avgAllKn) | add lm line to plot |
| 31 | #alt measurements for energy | comment |
| 31 | lmAPKnE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUA) + log(PADataNoOutlier$PSUP) + PADataNoOutlier$KN\_\_1 + log(PADataNoOutlier$PSUM)) | lm |
| 31 | summary(lmAPKnE) | summary of lm |
| 32 | #lm of fish middle with length accounted for | comment |
| 32 | lmMidFLE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length`) | lm |
| 32 | summary(lmMidFLE) | summary of lm |
| 33 | #all size accounted for - Mass not helpful | comment |
| 33 | lmMidSizeE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass) | lm |
| 33 | summary(lmMidSizeE) | summary of lm |
| 34 | #lm of fish middle with mass accounted for | comment |
| 34 | lmMidMassE <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$Mass) | lm |
| 34 | summary(lmMidMassE) | summary of lm |
| 35 | #lm of just fish with multiple measurements | comment |
| 35 | multMiddleE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM)) | lm |
| 35 | summary(multMiddleE) | summary of lm |
| 35 | plot(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM)) | plot of variables in lm |
| 35 | abline(multMiddleE) | add lm line to plot |
| 35 | multMiddleExpE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM)) | lm |
| 35 | summary(multMiddleExpE) | summary of lm |
| 35 | plot(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM)) | plot of variables in lm |
| 35 | abline(multMiddleExpE) | add lm line to plot |
| 36 | #lm of all measurements | comment |
| 36 | multAllE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM) + log(PADataNoOutlierMultMeasure$PSUA) + log(PADataNoOutlierMultMeasure$PSUP)) | lm |
| 36 | summary(multAllE) | summary of lm |
| 36 | plot(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$PSUM) + log(PADataNoOutlierMultMeasure$PSUA) + log(PADataNoOutlierMultMeasure$PSUP)) | scatterplot of variables in lm |
| 36 | abline(multAllE) | add lm line to plot |
| 36 | avgAllE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | lm |
| 36 | summary(avgAllE) | summary of lm |
| 36 | plot(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | plot of variables in lm |
| 36 | abline(avgAllE) | add lm line to plot |
| 37 | #running Tukey Fences (cutoff 3) | comment |
| 38 | expAnterior | inspect previously fit lm |
| 38 | summary(expAnterior) | summary of previously fit lm |
| 39 | UMKn <- lm(log) | reference to non-existent variable |
| 40 | #LATTICE | comment |
| 40 | library(lattice) | loading package, redundant, already loaded |
| 40 | attach(PADataNoOutlier) | attaching dataset to environment |
| 40 | Length <- equal.count(PADataNoOutlier$`Fork Length`, number = 3, overlap = 0.1) | using function, creating new variable |
| 40 | str(Length) | inspecting new variable |
| 40 | densityplot(~Lipid | Length, data = PADataNoOutlier) | density plot of var1, facets for var2 |
| 40 | bwplot(Lipid~PSUM | Length, data = PADataNoOutlier, layout = c(1,3)) | boxplot with facets |
| 40 | xyplot(Lipid~PSUM | Length, data = PADataNoOutlier, layout = c(1,3)) | trellis plot of var1 vs var2, conditional on other vars |
| 41 | PADataSmall <- subset(PADataNoOutlier, PADataNoOutlier$'Fork Length' <= 292) | filter data based on quant variable, using relational statement |
| 41 | PADataMid <- subset(PADataNoOutlier, PADataNoOutlier$'Fork Length' >= 293 & PADataNoOutlier$'Fork Length' <= 324) | filter data based on quant variable, using relational statements, joined with logical (&) |
| 41 | PADataLarge <- subset(PADataNoOutlier, PADataNoOutlier$'Fork Length' >= 325) | filter data based on quant variable, using relational statement |
| 41 | Small <- lm(PADataSmall$Lipid ~ PADataSmall$PSUM) | lm |
| 41 | Small | inspect lm |
| 41 | summary(Small) | summary of lm |
| 41 | Mid <- lm(PADataMid$Lipid ~ PADataMid$PSUM) | lm |
| 41 | Mid | inspect lm |
| 41 | summary(Mid) | summary of lm |
| 41 | Large <- lm(PADataLarge$Lipid ~ PADataLarge$PSUM) | lm |
| 41 | Large | inspect lm |
| 41 | summary(Large) | summary of lm |
| 42 | #Favorite Regression | comment |
| 42 | #Middle of all measurements plus Kn | comment |
| 42 | lmKnLipidAllMidKn <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$KN\_\_1) | lm |
| 42 | summary(lmKnLipidAllMidKn) #.2389 | summary of lm, comment with hard coded number |
| 43 | #Middle of all measurements plus metric measurements | comment |
| 43 | lmMetricLipidAllMid <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass)  #+PADataNoOutlier$Mass \* PADataNoOutlier$`Fork Length`) | lm |
| 43 | summary(lmMetricLipidAllMid) #.2993 (without interaction)//(.4779 with interaction) | summary of lm, comment with hard coded number |
| 43 | plot(lm(PADataNoOutlier$Lipid ~ (log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass  + PADataNoOutlier$Mass \* PADataNoOutlier$`Fork Length`))) | plot variables in lm |
| 43 | lmMetricLipidInter <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass  +PADataNoOutlier$Mass \* PADataNoOutlier$`Fork Length`) | lm |
| 43 | lmLipidMid <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | lm |
| 43 | summary(lmLipidMid) | summary of lm |
| 43 | plot(lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM))) | plot of variables in lm |
| 44 | #Middle of all measurements on Lipid | comment |
| 44 | lmAllMid <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | lm |
| 44 | summary(lmAllMid) #.1413 | summary of lm, comment with hard coded number |
| 45 | #Avg of P and A | comment |
| 45 | lmPA <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$AvgAP)) | lm |
| 45 | summary(lmPA) #.3958 | summary of lm, comment with hard coded number |
| 46 | #Avg of AM – good | comment |
| 46 | lmAM <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$AvgAM))  summary(lmAM) #.4606 | lm |
| 47 | #Avg of MP | comment |
| 47 | lmMP <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$AvgMP)) | lm |
| 47 | summary(lmMP) #.4068 | summary of lm, comment with hard coded number |
| 48 | #Avg of AMP - good | comment |
| 48 | lmAMP <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | lm |
| 48 | summary(lmAMP) #.4113 | summary of lm, comment with hard coded number |
| 49 | #Condition Factor added to AM and AMP | comment |
| 49 | lmAMKn <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$AvgAM) + PADataNoOutlierMultMeasure$KN) | lm |
| 49 | summary(lmAMKn) #.4545 | summary of lm, comment with hard coded number |
| 49 | lmAMPKn <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`) + PADataNoOutlierMultMeasure$KN) | lm |
| 49 | summary(lmAMPKn) #.4257 | summary of lm, comment with hard coded number |
| 50 | #Length and Weight added to AM and AMP | comment |
| 50 | lmAMMetric <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$AvgAM) + PADataNoOutlierMultMeasure$`Fork Length`  + PADataNoOutlierMultMeasure$Mass + PADataNoOutlierMultMeasure$Mass \* PADataNoOutlierMultMeasure$`Fork Length`) | lm |
| 50 | summary(lmAMMetric) #.5318 | summary of lm, comment with hard coded number |
| 50 | lmAMPMetric <- lm(PADataNoOutlierMultMeasure$Lipid ~ log(PADataNoOutlierMultMeasure$`Avg measurement`) + PADataNoOutlierMultMeasure$`Fork Length`  + PADataNoOutlierMultMeasure$Mass + PADataNoOutlierMultMeasure$Mass \* PADataNoOutlierMultMeasure$`Fork Length`) | lm |
| 50 | summary(lmAMPMetric) #.4908 | summary of lm, comment with hard coded number |
| 51 | #Avg of P and A | comment |
| 51 | lmPAE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$AvgAP)) | lm |
| 51 | summary(lmPAE) #.2714 | summary of lm, comment with hard coded number |
| 52 | #Avg of AM - good | comment |
| 52 | lmAME <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$AvgAM)) | lm |
| 52 | summary(lmAME) #.3558 | summary of lm, comment with hard coded number |
| 53 | #Avg of MP - good | comment |
| 53 | lmMPE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$AvgMP)) | lm |
| 53 | summary(lmMPE) #.318 | summary of lm, comment with hard coded number |
| 54 | #Avg of AMP | comment |
| 54 | lmAMPE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$`Avg measurement`)) | lm |
| 54 | summary(lmAMPE) #.2959 | summary of lm, comment with hard coded number |
| 55 | #Condition Factor added to AM and AMP | comment |
| 55 | lmAMKnE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$AvgAM) + PADataNoOutlierMultMeasure$KN) | lm |
| 55 | summary(lmAMKnE) #.3445 | summary of lm, comment with hard coded number |
| 55 | lmAMPKnE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$`Avg measurement`) + PADataNoOutlierMultMeasure$KN) | lm |
| 55 | summary(lmAMPKnE) #.3189 | summary of lm, comment with hard coded number |
| 56 | #Length and Weight added to AM and AMP | comment |
| 56 | lmAMMetricE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$AvgAM) + PADataNoOutlierMultMeasure$`Fork Length`  + PADataNoOutlierMultMeasure$Mass + PADataNoOutlierMultMeasure$Mass \* PADataNoOutlierMultMeasure$`Fork Length`) | lm |
| 56 | summary(lmAMMetricE) #.4152 | summary of lm, comment with hard coded number |
| 56 | lmAMPMetricE <- lm(PADataNoOutlierMultMeasure$Energy ~ log(PADataNoOutlierMultMeasure$`Avg measurement`) + PADataNoOutlierMultMeasure$`Fork Length`  + PADataNoOutlierMultMeasure$Mass + PADataNoOutlierMultMeasure$Mass \* PADataNoOutlierMultMeasure$`Fork Length`) | lm |
| 56 | summary(lmAMPMetricE) #.3258 | summary of lm, comment with hard coded number |
| 57 | str(PADataNoOutlierMultMeasure) | structure of data, redundant |
| 57 | min(PADataNoOutlierMultMeasure[,3]) #301 | data summary (min), subsetting with  brackets, hard coded number, comment with hard coded number |
| 57 | min(PADataNoOutlier[,3]) #202 | data summary (min), subsetting with  brackets, hard coded number, comment with hard coded number |
| 57 | min(PADataNoOutlierMultMeasure[,10], na.rm = T) #.781 | data summary (min), subsetting with  brackets, hard coded number, comment with hard coded number |
| 57 | min(PADataNoOutlier[,11], na.rm = T) #.796 | data summary (min), subsetting with  brackets, hard coded number, comment with hard coded number |
| 57 | str(PADataNoOutlier) | structure of data, redundant |
| 59 | #residuals | comment |
| 59 | #Fork Length | comment |
| 59 | MiddleLM <- lm(Lipid ~ log(PSUM), data = PADataNoOutlier) | lm |
| 59 | str(MiddleLM) | structure of lm |
| 59 | MiddleResid <- resid(MiddleLM) | pulling off residuals, creating a new variable |
| 59 | plot(PADataNoOutlier$`Fork Length`, MiddleResid, ylab = "Residuals", xlab = "Fork Length") | plot of variables in lm |
| 59 | par(mfrow = c(2,2)) | splitting plotting window |
| 60 | #Weight | comment |
| 60 | plot(PADataNoOutlier$Mass, MiddleResid, ylab = "Residuals", xlab = "Mass") | plotting variable verses data variable, changing axis labels |
| 61 | #Kn | comment |
| 61 | plot(PADataNoOutlier$KN\_\_1, MiddleResid, ylab = "Residuals", xlab = "Kn") | plotting variable verses data variable, changing axis labels |
| 62 | #Lipid | comment |
| 62 | plot(PADataNoOutlier$Lipid, MiddleResid, ylab = "Residuals", xlab = "Lipid") | plotting variable verses data variable, changing axis labels |
| 63 | #PSUM | comment |
| 63 | plot(PADataNoOutlier$PSUM, MiddleResid, ylab = "Residuals", xlab = "PSUM") | plotting variable verses data variable, changing axis labels |
| 63 | Lipid <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM) | lm |
| 63 | plot(Lipid) | diagnostic plot |
| 63 | LipidLog <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | lm |
| 63 | plot(LipidLog) | diagnostic plot |
| 63 | plot(PADataNoOutlier$Lipid ~ PADataNoOutlier$PSUM) | plot of variables in lm |
| 63 | plot(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | plot of variables in lm |
| 64 | #PSUM + Length | comment |
| 64 | LipidLength <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length`) | lm |
| 64 | summary(LipidLength) | summary of lm |
| 65 | LipidMass <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$Mass) | lm |
| 65 | summary(LipidMass) | summary of lm |
| 66 | anovaLipidAssessment <- anova(lmAllMid, #nocomplex  LipidLength, #lowcomplex  lmMetricLipidAllMid, #midcomplex  lmMetricLipidInter #mostcomplex  ) | anova, create new variable |
| 66 | anovaLipidAssessment | inspect anova |
| 66 | plot(log(PADataNoOutlier$`Fork Length`) ~ log(PADataNoOutlier$Mass)) | plot of variables in anova |
| 66 | AIC(LipidLength, LipidMass) | use function |
| 66 | AIC(lmPA, lmAM, lmAMP, lmMP) | use function |
| 66 | anova(lmAM, lmAMMetric) | anova |
| 66 | anova(LipidLength, lmMetricLipidInter) | anova |
| 66 | summary(lmMetricLipidInter) | summary of lm, redundant |
| 67 | lmEMKN <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$KN\_\_1) | lm |
| 67 | summary(lmEMKN) | summary of lm |
| 68 | lmEMetricInter <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$Mass  + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass\*PADataNoOutlier$`Fork Length`) | lm |
| 68 | summary(lmEMetricInter) | summary of lm |
| 69 | lmEMetric <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$Mass + PADataNoOutlier$`Fork Length`) | lm |
| 69 | summary(lmEMetric) | summary of lm |
| 70 | lmEFL <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length`) | lm |
| 70 | summary(lmEFL) | summary of lm |
| 71 | lmEMass <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$Mass) | lm |
| 71 | summary(lmEMass) | summary of lm |
| 72 | lmEUMAll <- lm(PADataNoOutlier$Energy ~ log(PADataNoOutlier$PSUM)) | lm |
| 72 | summary(lmEUMAll) | summary of lm |
| 73 | lmLipidMidInter <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass +PADataNoOutlier$Mass\*PADataNoOutlier$`Fork Length`) | lm |
| 73 | summary(lmLipidMidInter) | summary of lm |
| 74 | lmLipidMid <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$`Fork Length`) | lm |
| 74 | summary(lmLipidMid) | summary of lm |
| 75 | anova(lmLipidMid, lmLipidMidInter) | anova |
| 75 | AIC(lmLipidMid, lmLipidMidInter) | use function |
| 76 | Kn <- lm(log(PADataNoOutlier$PSUM) ~ PADataNoOutlier$KN\_\_1) | lm |
| 76 | plot(log(PADataNoOutlier$PSUM) ~ PADataNoOutlier$KN\_\_1) | plot of variables in lm |
| 76 | summary(Kn) | summary of lm |
| 76 | abline(Kn) | add lm line to plot |
| 77 | lm(log(PADataNoOutlier$Lipid) ~ PADataNoOutlier$KN\_\_1 + PADataNoOutlier$`Fork Length`+ PADataNoOutlier$Mass + PADataNoOutlier$`Fork Length`\*PADataNoOutlier$Mass) | lm |
| 77 | summary(lm(log(PADataNoOutlier$Lipid) ~ PADataNoOutlier$KN\_\_1 + PADataNoOutlier$`Fork Length`+ PADataNoOutlier$Mass + PADataNoOutlier$`Fork Length`\*PADataNoOutlier$Mass)) | summary of lm, with **no** new variable created |
| 78 | lm(log(PADataNoOutlier$Lipid) ~ PADataNoOutlier$PSUM) | lm |
| 78 | summary(lm(log(PADataNoOutlier$Lipid) ~ PADataNoOutlier$PSUM)) | summary of lm, with **no** new variable created |
| 79 | plot((PADataNoOutlier$Lipid) ~ log(PADataNoOutlier$`Fork Length`)) | plot of variables in lm |
| 79 | plot((PADataNoOutlier$Lipid) ~ log(PADataNoOutlier$Mass)) | plot of variables in lm |
| 79 | plot((PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM))) | plot of variables in lm |
| 80 | log <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + log(PADataNoOutlier$Mass) + log(PADataNoOutlier$`Fork Length`) + log(PADataNoOutlier$Mass)\*log(PADataNoOutlier$`Fork Length`)) | lm |
| 80 | summary(logFL) | summary of lm, variable not yet created |
|  | summary(log) | summary of lm |
| 81 | logFL <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + log(PADataNoOutlier$`Fork Length`)) | lm |
| 82 | anova(log) | anova |
| 82 | anova(lmMetricLipidInter) | anova |
| 82 | summary(lmMetricLipidInter) | summary of lm |
| 82 | anova(lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$`Fork Length` + PADataNoOutlier$Mass)) | anova, with no new variable created |
| 82 | anova(lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$`Fork Length` \* PADataNoOutlier$Mass)) | anova, with no new variable created |
| 83 | plot(PADataNoOutlier$Lipid ~ PADataNoOutlier$`Fork Length`) | plot of variables in lm |
| 83 | plot(log(PADataNoOutlier$Lipid) ~ log(PADataNoOutlier$`Fork Length`)) | plot of variables in lm |
| 84 | KnFat <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM) + PADataNoOutlier$KN\_\_1) | lm |
| 84 | summary(KnFat) | summary of lm |
| 84 | plot(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$PSUM)) | plot of variables in lm |
| 84 | plot(KnFat) | diagnostic plot |
| 85 | Transformed <- lm((PADataNoOutlier$Lipid) ~ log(PADataNoOutlier$PSUM) + log(PADataNoOutlier$`Fork Length`) + log(PADataNoOutlier$Mass) + (log(PADataNoOutlier$`Fork Length`)\*log(PADataNoOutlier$Mass))) | lm |
| 85 | summary(Transformed) | summary of lm |
| 85 | plot(Transformed) | diagnostic plot |
| 86 | LengthMass <- lm((PADataNoOutlier$Lipid) ~ log(PADataNoOutlier$`Fork Length`) + log(PADataNoOutlier$Mass) + (log(PADataNoOutlier$`Fork Length`)\*log(PADataNoOutlier$Mass))) | lm |
| 86 | summary(LengthMass) | summary of lm |
| 87 | Kn <- lm(PADataNoOutlier$Lipid ~ PADataNoOutlier$KN\_\_1) | lm |
| 87 | abline(Kn) | add lm line to plot, no plot to add to |
| 88 | plot(PADataNoOutlier$Lipid ~ PADataNoOutlier$Mass) | plot of variables in lm |
| 88 | plot(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$Mass)) | plot of variables in lm |
| 88 | plot(PADataNoOutlier$Lipid ~ PADataNoOutlier$`Fork Length`) | plot of variables in lm |
| 88 | plot(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$`Fork Length`)) | plot of variables in lm |
| 89 | noInt <- lm(PADataNoOutlier$Lipid ~ log(PADataNoOutlier$`Fork Length`) + log(PADataNoOutlier$Mass)) | lm |
| 89 | summary(noInt) | summary of lm |
| 89 | plot(noInt) | diagnostic plot |
| 90 | large <- PADataNoOutlier[which(PADataNoOutlier$`Fork Length` >= 270 & PADataNoOutlier$'Fork Length' <= 500), ] | filter data, using indices from which(), using relational statement, joined with logical (&) |
| 90 | small <- PADataNoOutlier[which(PADataNoOutlier$'Fork Length' <= 269), ] | filter data, using indices from which(), using relational statement |
| 90 | xl <- PADataNoOutlier[which(PADataNoOutlier$`Fork Length`)] | filter data, using indices from which(), using relational statement |
| 90 | head(large) | inspect data |
| 91 | plot(large$Lipid ~ large$`Fork Length`) | scatterplot of variables in filtered data |
| 91 | plot(large$Lipid ~ log(large$`Fork Length`)) | scatterplot of variables in filtered data |
| 91 | largeLM <- lm(large$Lipid ~ large$PSUM + large$`Fork Length` + large$Mass + large$`Fork Length`\*large$Mass) | lm |
| 91 | summary(largeLM) | summary of lm |
| 91 | plot(largeLM) | diagnostic plot |
| 91 | plot(large$Lipid ~ large$Mass) | scatterplot of variables in filtered data |
| 91 | plot(large$Lipid ~ log(large$Mass)) | scatterplot of variables in filtered data |
| 91 | plot(large$Lipid ~ large$KN\_\_1) | scatterplot of variables in filtered data |
| 91 | largeLMKn <- lm(large$Lipid ~ large$PSUM + large$KN\_\_1) | lm |
| 91 | summary(largeLMKn) | summary of lm |
| 91 | plot(largeLMKn) | diagnostic plot |
| 92 | plot(small$Lipid ~ small$`Fork Length`) | scatterplot of variables in filtered data |
| 92 | plot(small$Lipid ~ small$Mass) | scatterplot of variables in filtered data |
| 93 | plot(PADataNoPrelim$Lipid ~ PADataNoPrelim$`Fork Length`) | scatterplot of variables in filtered data |
| 93 | plot(PADataNoPrelim$Lipid ~ log(PADataNoPrelim$`Fork Length`)) | scatterplot of variables in filtered data |
| 93 | plot(PADataNoPrelim$Lipid ~ log(PADataNoPrelim$Mass)) | scatterplot of variables in filtered data |
| 94 | NoPrelimLM <- lm(PADataNoPrelim$Lipid ~ log(PADataNoPrelim$PSUM) + log(PADataNoPrelim$`Fork Length`) + log(PADataNoPrelim$Mass) + log(PADataNoPrelim$`Fork Length`)\*log(PADataNoPrelim$Mass)) | lm |
| 94 | summary(NoPrelimLM) | summary of lm |
| 94 | plot(PADataNoPrelim$Lipid ~ log(PADataNoPrelim$PSUM)) | scatterplot of variables in lm |
| 95 | largeNoPrelim <- PADataNoPrelim[which(PADataNoPrelim$`Fork Length` >= 270 & PADataNoPrelim$'Fork Length' <= 500), ] | filter data, using indices from which(), relational statement, joined with logical (&) |
| 95 | smallNoPrelim <- PADataNoPrelim[which(PADataNoPrelim$'Fork Length' <= 269), ] | filter data, using indices from which(), relational statement, joined with logical (&) |
| 95 | plot(largeNoPrelim$Lipid ~ log(largeNoPrelim$`Fork Length`)) | scatterplot of variables in filtered data |
| 95 | plot(largeNoPrelim$Lipid ~ log(largeNoPrelim$Mass)) | scatterplot of variables in filtered data |
| 95 | NoPrelimLMPSUM <- lm(PADataNoPrelim$Lipid ~ log(PADataNoPrelim$PSUM)) | lm |
| 95 | summary(NoPrelimLMPSUM) | summary of lm |
| 95 | plot(NoPrelimLMPSUM) | diagnostic plot |
| 95 | NoPrelimBigLM <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`) + log(largeNoPrelim$Mass) + log(largeNoPrelim$`Fork Length`)\*log(largeNoPrelim$Mass)) | lm |
| 95 | plot(NoPrelimBigLM) | diagnostic plot |
| 95 | summary(NoPrelimBigLM) | summary of lm |
| 95 | BigPSUMLM <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM))  summary(BigPSUMLM)  BigPUSMLMKn <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$KN...13))  summary(BigPUSMLMKn)  plot(largeNoPrelim$Lipid ~ log(largeNoPrelim$KN...13))  BigPSUMlmLength <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`)) | lm |
| 95 | summary(BigPSUMlmLength) | summary of lm |
| 95 | BigPSUMlmWeight <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$Mass))  summary(BigPSUMlmWeight)  BigPSUMlmLengthWeight <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`) + log(largeNoPrelim$Mass)) | lm |
| 95 | summary(BigPSUMlmLengthWeight) | summary of lm |
| 95 | BigPSUMlmLengthWeightInt <- lm(largeNoPrelim$Lipid ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`) + log(largeNoPrelim$Mass) + log(largeNoPrelim$`Fork Length`)\*log(largeNoPrelim$Mass)) | lm |
| 95 | summary(BigPSUMlmLengthWeightInt) | summary of lm |
| 96 | anovaBigassessment <- anova(BigPSUMLM, #nocomplex  BigPSUMlmWeight, #lowcomplex  BigPSUMlmLengthWeight, #midcomplex  BigPSUMlmLengthWeightInt #mostcomplex  ) | anova, with comments on inputs, create a new variable |
| 96 | summary(anovaBigassessment) | summary of anova object |
| 96 | anovaBigassessment | inspect variable |
| 96 | plot(largeNoPrelim$`Fork Length` ~ largeNoPrelim$Mass) | scatterplot of variables in filtered data |
| 97 | #Energy | comment |
| 97 | BigEnergyLM <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM)) | lm |
| 97 | summary(BigEnergyLM) | summary of lm |
| 97 | plot(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM)) | scatterplot of variables in lm |
| 97 | BigEnergyLMKn <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$KN...13)) | lm |
| 97 | summary(BigPUSMLMKn) | summary of lm |
| 97 | plot(largeNoPrelim$Energy ~ log(largeNoPrelim$KN...13)) | scatterplot of variables in lm |
| 97 | BigEnergylmLength <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`)) | lm |
| 97 | summary(BigEnergylmLength) | summary of lm |
| 97 | BigEnergylmWeight <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$Mass)) | lm |
| 97 | summary(BigEnergylmWeight) | summary of lm |
| 97 | plot(largeNoPrelim$Energy ~ log(largeNoPrelim$Mass)) | scatterplot of variables in lm |
| 97 | BigEnergylmLengthWeight <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`) + log(largeNoPrelim$Mass)) | lm |
| 97 | summary(BigEnergylmLengthWeight) | summary of lm |
| 97 | BigEnergylmLengthWeightInt <- lm(largeNoPrelim$Energy ~ log(largeNoPrelim$PSUM) + log(largeNoPrelim$`Fork Length`) + log(largeNoPrelim$Mass) + log(largeNoPrelim$`Fork Length`)\*log(largeNoPrelim$Mass)) | lm |
| 97 | summary(BigEnergylmLengthWeightInt) | summary of lm |
| 98 | anovaBigEnergyassessment <- anova(BigEnergyLM, #nocomplex  BigEnergylmWeight, #lowcomplex  BigEnergylmLengthWeight, #midcomplex  BigEnergylmLengthWeightInt #mostcomplex  ) | anova, create new object |
| 98 | summary(anovaBigEnergyassessment) | summary of object |
| 98 | anovaBigEnergyassessment | inspect object |
| 98 | plot(largeNoPrelim$`Fork Length` ~ largeNoPrelim $Mass) | scatterplot of variables in filtered data |
| 99 | install.packages("devtools") | install package |
| 99 | # required to get packages from GitHub | comment (why need to install package) |
| 99 | devtools::install\_github("cardiomoon/ggiraphExtra") | install package from GitHub |
| 99 | # package from GitHub for interaction plot | comment on why installing package |
| 99 | library(ggiraphExtra) | loading package |
| 99 | # used to make the interaction plot | comment on what package does |
| 99 | largeNoPrelim$ | irrelevant code |
| 99 | model <- lm(lipid ~ log(fork\_length)\*log(weight), data = YOUR\_DATA) | lm |
| 99 | model <- lm(Lipid ~ log(`Fork Length`)\*log(Mass), data = largeNoPrelim) | template code from package, half filled in |
| 99 | # Fit the interaction model you are interested in | comment on what the code is doing |
| 99 | ggPredict(model, interactive = TRUE) | template code from package, not filled in |
| 99 | # Plots the interaction with different colored points and lines for the weights | comment on what the output of the function is |
| 99 | ggPredict(BigEnergylmLengthWeightInt, interactive = TRUE) | template code, filled in |