Part I:

Problem 1) Removed family “Odobenidae” and ran droplevels on dataframe.

Problem 2) This could be problematic as it introduces variation within-groups; no two representatives of the same group are necessarily the same in terms of allometric scaling. This introduces extra variation in terms of deriving a generalizable body scale relationship.

Problem 3) mod1 = lm(logpos~logpre\*Family, data = body3)

Call:

lm(formula = logpos ~ logpre \* Family, data = body3)

Residuals:

Min 1Q Median 3Q Max

-0.44052 -0.08191 -0.00373 0.07346 0.28595

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1.65626 0.18597 8.906 1.82e-13 \*\*\*

logpre 0.66924 0.03210 20.847 < 2e-16 \*\*\*

FamilyFelidae 0.15865 0.36949 0.429 0.66886

FamilyOtariidae -1.69204 0.70188 -2.411 0.01830 \*

FamilyPhocidae -0.70254 0.58627 -1.198 0.23447

logpre:FamilyFelidae 0.05497 0.07012 0.784 0.43554

logpre:FamilyOtariidae 0.30883 0.11601 2.662 0.00945 \*\*

logpre:FamilyPhocidae 0.22374 0.09916 2.256 0.02688 \*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.116 on 77 degrees of freedom

Multiple R-squared: 0.9417, Adjusted R-squared: 0.9364

F-statistic: 177.8 on 7 and 77 DF, p-value: < 2.2e-16

Problem 4) Otariidae and Phocidae

Problem 5) mod3 = lm(logpos~Family+Family:logpre -1, data=body3)

Call:

lm(formula = logpos ~ Family + Family:logpre - 1, data = body3)

Residuals:

Min 1Q Median 3Q Max

-0.44052 -0.08191 -0.00373 0.07346 0.28595

Coefficients:

Estimate Std. Error t value Pr(>|t|)

FamilyBovidae 1.65626 0.18597 8.906 1.82e-13 \*\*\*

FamilyFelidae 1.81490 0.31928 5.684 2.24e-07 \*\*\*

FamilyOtariidae -0.03578 0.67679 -0.053 0.9580

FamilyPhocidae 0.95372 0.55599 1.715 0.0903 .

FamilyBovidae:logpre 0.66924 0.03210 20.847 < 2e-16 \*\*\*

FamilyFelidae:logpre 0.72420 0.06234 11.616 < 2e-16 \*\*\*

FamilyOtariidae:logpre 0.97807 0.11147 8.774 3.27e-13 \*\*\*

FamilyPhocidae:logpre 0.89298 0.09382 9.518 1.21e-14 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.116 on 77 degrees of freedom

Multiple R-squared: 0.9996, Adjusted R-squared: 0.9996

F-statistic: 2.573e+04 on 8 and 77 DF, p-value: < 2.2e-16

Confidence intervals:

2.5 % 97.5 %

FamilyBovidae 1.2859496 2.0265667

FamilyFelidae 1.1791367 2.4506699

FamilyOtariidae -1.3834449 1.3118841

FamilyPhocidae -0.1534096 2.0608446

FamilyBovidae:logpre 0.6053125 0.7331603

FamilyFelidae:logpre 0.6000601 0.8483447

FamilyOtariidae:logpre 0.7560907 1.2000399

FamilyPhocidae:logpre 0.7061657 1.0797935

Problem 6) Slopes for Phocidae and Otariidae are noticeably different, but especially Otariidae. This may be exacerbated by the inclusion of a single data point causing a crossover between the lines for Otariidae and Bovidae; exclusion of this point may moderate the differences in slope.



#Molly Jenkins

#Assignment 4

#ENEC563

#02/27/2017

#

# 1) Read the data in and use table to see the number of counts of each family. One family has only three observations.

# i) Remove this family from the data.

# ii) If you examine the Family, you will notice that there is a "ghost" level for the family that you remove.

#Run the droplevels function on the data frame and put the output in your data frame for analysis.

#

# 2) If you run table on the Taxon variable, you will notice that some species have multiple representatives.

#There are frequently different relationships within taxa than there are among taxa for body size relationships

# i) Discuss why this would be a problem for your analysis if you are primarily concerned with among taxon relationships

# ii) To get around this problem, generate a new data frame that was one row for each Taxon and includes just the Family,

# and the mean pre- and post- diaphragmatic body length (see hint!)

# 3) Carry out a formal statistical test to determine whether the allometric exponents of the pre- and pos- diaphragmatic lengths

# are constant across the four families. For convenience,

# use log (post- diaphragmatic length) as the response (x, dep) variable and log(pre-diaphragmatic length) as a predictor (y, ind).

# 4) If you determine that the exponents are different, determine the families for which the allometric exponents are significantly different

# and the orders for which they are not.

# 5) Refit the model so that the 8 coefficients are the intercepts and slopes for each of the families.

# Generate a confidence interval for each of the slopes and determine

# which families the relationship can and cannot be distinguished from an isometric one (i.e. the slope is 1).

# 6) Summarize the 3-5.

# i) Describe in words the results of the models. Focus on any differences betwee the aquatic (Otariidae and Phocidae) and terrestrial (Bovidae and Felidae) families.

# ii) Display the results of the analysis by plotting the data and the predictions from the best fit model.

#setwd('C:/git/coursework/ENEC563/')

library(nlme)

library(dplyr)

library(ggplot2)

####Problem 1####

body = read.csv('mammalianbody.csv', header = TRUE)

table(body$Family)

body2 = body[body[,1] != "Odobenidae", ] #all rows where family is not equal to Odobenidae

unique(body2$Family) #ghost level there when category isn't!

body2 = droplevels(body2)

unique(body2$Family) #fixed

####Problem 2####

table(body2$Taxon)

#This could be problematic as it introduces variation within-groups;

#no two representatives of the same group are necessarily the same in terms of allometric scaling.

#This introduces extra variation in terms of deriving a generalizable body scale relationship.

body3 = body2 %>%

group\_by(Family,Taxon) %>%

summarize(meanpre = mean(PreL),

meanpos= mean(PosL))

####Problem 3####

body3$logpre = log(body3$meanpre)

body3$logpos = log(body3$meanpos)

mod1 = lm(logpos~logpre\*Family, data = body3) #Bovidae is intercept; separate slopes model

sink("A4\_table1.txt")

summary(lm(logpos~logpre\*Family, data = body3))

sink()

anova(mod1)

coef(mod1)

body3$preds = predict(mod1)

plot = ggplot(body3,aes(x=logpre,y=logpos,color=Family))+geom\_point()

contrasts(body3$Family)

####Problem 4####

#Otariidae and Phocidae MAY be different, but Otariidae especially

body3$fampho<-factor(body3$Family,c("Phocidae","Otariidae","Bovidae","Felidae")) #creates a new factor with Phocidae as the base level.

contrasts(body3$fampho)

####Problem 5####

mod2 = lm(logpos~logpre\*fampho, data = body3)

summary(mod2)

anova(mod2)

#additive model with Family and Family:log(pre diaphragmatic length) and removing the intercept from the model

mod3 = lm(logpos~Family+Family:logpre -1, data=body3)

sink("A4\_table2.txt")

summary(mod3)

sink()

sink("A4\_confints.txt")

confint(mod3)

sink()

#Otariidae and Phocidae both cross into negatives on the left tail; different

####Problem 6####

plot+geom\_point()+geom\_line(aes(y = predict(mod3)))

#slope for Otariidae definitely looks really noticably different