#Testing differences in Fe and Cu among mammal species

#Cu Mammal Means

Mammal\_Means\_Full\_Cu <- read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Cu csv files/Mammal\_Cu\_Raw.csv")

kruskal.test(del\_65\_Cu ~ Species, data = Mammal\_Means\_Full\_Cu)

Kruskal-Wallis rank sum test

data: del\_65\_Cu by Species

Kruskal-Wallis chi-squared = 47.05, df = 8, p-value = 1.5e-07

#Fe Mammal Means

Mammal\_Means\_Full\_Fe <- read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Fe csv files/Mammal\_Fe\_Raw.csv")

kruskal.test(del\_56\_Fe ~ Species, data = Mammal\_Means\_Full\_Fe)

Kruskal-Wallis rank sum test

data: del\_56\_Fe by Species

Kruskal-Wallis chi-squared = 41.637, df = 9, p-value = 3.829e-06

#Visualizing Mammal Means Cu

library(ggplot2)

library(gridExtra)

Mammal\_Means\_Bone\_Cu = read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Cu csv files/Mammal Means Bone Cu.csv")

Comparison\_of\_delta\_65\_Cu\_Fractionation\_in\_Mammals <- ggplot(Mammal\_Means\_Bone\_Cu,aes(y = Mean\_del\_65\_Cu, x = Species)) +

ggtitle(bquote('Comparison of '\*delta ^65\*'Cu in Mammals')) + xlab("Species") + ylab(bquote('Mean of '\*delta ^65\*'Cu Fractionation')) +

geom\_errorbar(aes(ymin = Mean\_del\_65\_Cu-Stdev\_del\_65\_Cu, ymax = Mean\_del\_65\_Cu+Stdev\_del\_65\_Cu))+ geom\_point(size = 2.5)+

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+ coord\_flip()

#Visualizing Mammal Means Fe

Mammal\_Means\_Bone\_Fe =read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Fe csv files/Mammal Means Fe.csv")

Comparison\_of\_delta\_56\_Fe\_Fractionation\_in\_Mammals <- ggplot(Mammal\_Means\_Bone\_Fe,aes(y = Mean\_del\_56\_Fe, x = Species)) +

ggtitle(bquote('Comparison of '\*delta ^56\*'Fe in Mammals')) + xlab("Species") + ylab(bquote('Mean of '\*delta ^56\*'Fe Fractionation')) +

geom\_errorbar(aes(ymin = Mean\_del\_56\_Fe-Stdev\_del\_56\_Fe, ymax = Mean\_del\_56\_Fe+Stdev\_del\_56\_Fe))+ geom\_point(size = 2.5)+

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+ coord\_flip()

#Testing differences in Fe and Cu in Humans and Rhesus Macaques

Human\_Cu\_Data =read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Cu csv files/Human Cu Data - Final .csv")

#human Fe

Human\_Fe\_Data=read.csv("C:/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Fe csv files/Human Fe Data - Final .csv")

#macaque Occipital Cu

Rhesus\_Macaque\_Occipital\_Cu=read.csv("/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Cu csv files/Rhesus Macaque Occipital Cu.csv")

#macaque teeth Cu

Rhesus\_Macaque\_Teeth\_Cu = read.csv("/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Cu csv files/Rhesus Macaque Teeth Cu.csv")

#macaque occipital Fe

Rhesus\_Macaque\_Occipital\_Fe =read.csv("/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Fe csv files/Rhesus Macaques Occipital Fe.csv")

#macaque teeth Fe

Rhesus\_Macaque\_Teeth\_Fe = read.csv("/Users/Renee/Desktop/Rutgers University/Senior Thesis/Senior Thesis/Lab Notebook/Data/Used Fe csv files/Rhesus Macaques Teeth Fe.csv")

# Visualizing Human and Rhesus Macaques Cu in Bone

Variation\_of\_delta\_65\_Cu\_in\_Human\_Bone <- ggplot(Human\_Cu\_Data, aes(x = Sex, y = del\_65\_Cu, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^65\*'Cu in Human Bone')) + xlab("Sex") +

ylab(bquote(delta ^65\*'Cu')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank()) +

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Bone <- ggplot(Rhesus\_Macaque\_Occipital\_Cu, aes(x = Sex, y = del\_65\_Cu, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^65\*'Cu in Rhesus Macaque Bone')) + xlab("Sex") +

ylab(bquote(delta ^65\*'Cu')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

grid.arrange(Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Bone,Variation\_of\_delta\_65\_Cu\_in\_Human\_Bone, nrow = 1, ncol = 2)

#Visualizing Rhesus macaques Cu in Teeth and Occipital

Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Teeth <- ggplot(Rhesus\_Macaque\_Teeth\_Cu, aes(x = Sex, y = del\_65\_Cu, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta^65\*'Cu in Rhesus Macaque Teeth')) + xlab("Sex") +

ylab(bquote(delta^65\*'Cu')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Occipital <- ggplot(Rhesus\_Macaque\_Occipital\_Cu, aes(x = Sex, y = del\_65\_Cu, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^65\*'Cu in Rhesus Macaque Occipital')) + xlab("Sex") +

ylab(bquote(delta ^65\*'Cu')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank()) + scale\_colour\_manual(values = c("male" = "black","female" = "red"))

grid.arrange(Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Teeth,Variation\_of\_delta\_65\_Cu\_in\_Rhesus\_Macaque\_Occipital, nrow = 1, ncol = 2)

#wilcoxins to test for significance of Cu variation between humans and macaques

#human bone cu

wilcox.test(Human\_Cu\_Data$del\_65\_Cu ~ Human\_Cu\_Data$Sex, data = Human\_Cu\_Data)

Wilcoxon rank sum test with continuity correction

data: Human\_Cu\_Data$del\_65\_Cu by Human\_Cu\_Data$Sex

W = 60.5, p-value = 0.04609

alternative hypothesis: true location shift is not equal to 0

#macaque bone cu

wilcox.test(Rhesus\_Macaque\_Occipital\_Cu$del\_65\_Cu ~ Rhesus\_Macaque\_Occipital\_Cu$Sex, data = Rhesus\_Macaque\_Occipital\_Cu)

Wilcoxon rank sum test

data: Rhesus\_Macaque\_Occipital\_Cu$del\_65\_Cu by Rhesus\_Macaque\_Occipital\_Cu$Sex

W = 8, p-value = 0.001451

alternative hypothesis: true location shift is not equal to 0

#macaque teeth cu

wilcox.test(Rhesus\_Macaque\_Teeth\_Cu$del\_65\_Cu ~ Rhesus\_Macaque\_Teeth\_Cu$Sex, data = Rhesus\_Macaque\_Teeth\_Cu)

Wilcoxon rank sum test

data: Rhesus\_Macaque\_Teeth\_Cu$del\_65\_Cu by Rhesus\_Macaque\_Teeth\_Cu$Sex

W = 48, p-value = 0.9118

alternative hypothesis: true location shift is not equal to 0

#Visualizing differences in bone Fe between humans and macaques

#macaques Fe in bone and teeth

Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Occipital <- ggplot(Rhesus\_Macaque\_Occipital\_Fe, aes(x = Sex, y = del\_56\_Fe, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^56\*'Fe in Rhesus Macaque Occipital')) + xlab("Sex") +

ylab(bquote(delta ^56\*'Fe')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Teeth <- ggplot(Rhesus\_Macaque\_Teeth\_Fe, aes(x = Sex, y = del\_56\_Fe, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^56\*'Fe in Rhesus Macaque Teeth')) + xlab("Sex") +

ylab(bquote(delta ^56\*'Fe')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())+

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

grid.arrange(Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Teeth,Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Occipital, nrow = 1, ncol = 2)

#fe in human and macaque bone

Variation\_of\_delta\_56\_Fe\_in\_Human\_Bone <- ggplot(Human\_Fe\_Data, aes(x = Sex, y = del\_56\_Fe, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^56\*'Fe in Human Bone')) + xlab("Sex") +

ylab(bquote(delta ^56\*'Fe')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank()) +

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Bone <- ggplot(Rhesus\_Macaque\_Occipital\_Fe, aes(x = Sex, y = del\_56\_Fe, color = Sex)) +

geom\_boxplot() + ggtitle(bquote(delta ^56\*'Fe in Rhesus Macaque Occipital')) + xlab("Sex") +

ylab(bquote(delta ^56\*'Fe')) + guides(color=guide\_legend(title="Sex")) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank()) +

scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

grid.arrange(Variation\_of\_delta\_56\_Fe\_in\_Rhesus\_Macaque\_Bone,Variation\_of\_delta\_56\_Fe\_in\_Human\_Bone, nrow = 1, ncol = 2)

#wilcoxins for significance in Fe groups

#Macaque Fe teeth

wilcox.test(Rhesus\_Macaque\_Teeth\_Fe$del\_56\_Fe ~ Rhesus\_Macaque\_Teeth\_Fe$Sex, data = Rhesus\_Macaque\_Teeth\_Fe)

Wilcoxon rank sum test

data: Rhesus\_Macaque\_Teeth\_Fe$del\_56\_Fe by Rhesus\_Macaque\_Teeth\_Fe$Sex

W = 66, p-value = 0.09472

alternative hypothesis: true location shift is not equal to 0

#Macaque Fe Occipital

wilcox.test(Rhesus\_Macaque\_Occipital\_Fe$del\_56\_Fe ~ Rhesus\_Macaque\_Occipital\_Fe$Sex, data = Rhesus\_Macaque\_Occipital\_Fe)

Wilcoxon rank sum test

data: Rhesus\_Macaque\_Occipital\_Fe$del\_56\_Fe by Rhesus\_Macaque\_Occipital\_Fe$Sex

W = 68, p-value = 0.1903

alternative hypothesis: true location shift is not equal to 0

#Human Fe bone

wilcox.test(Human\_Fe\_Data$del\_56\_Fe ~ Human\_Fe\_Data$Sex, data = Human\_Fe\_Data)

Wilcoxon rank sum test with continuity correction

data: Human\_Fe\_Data$del\_56\_Fe by Human\_Fe\_Data$Sex

W = 309.5, p-value = 0.005169

alternative hypothesis: true location shift is not equal to 0

#Modelling the success of age and/or sex predicting Cu and Fe values in teeth and bone

library(mgcv)

library(gratia)

#Plot that incorporates raw rhesus macaque vs age with GAM

Model\_3a = gam(del\_65\_Cu~s(Age, k = 6) + s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3b = gam(del\_65\_Cu~s(Age, k = 6) + te(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3c = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3d = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3e = gam(del\_65\_Cu~te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3f = gam(del\_65\_Cu~s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

AIC(Model\_3a,Model\_3b,Model\_3c,Model\_3d,Model\_3e,Model\_3f)

##Model\_3d wins

Family: gaussian

Link function: identity

Formula:

del\_65\_Cu ~ s(Age, k = 6) + te(Age, by = Sex, k = 6)

Parametric coefficients:

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

(Intercept) -1.5237 0.2116 -7.202 1.11e-05 \*\*\*

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

Approximate significance of smooth terms:

edf Ref.df F p-value

s(Age) 2.8085 3.2265 6.812 0.00585 \*\*

te(Age):Sexfemale 2.7104 3.1755 1.606 0.13144

te(Age):Sexmale 0.5243 0.5243 16.238 0.01263 \*

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

Rank: 15/16

R-sq.(adj) = 0.683 Deviance explained = 79%

GCV = 0.73056 Scale est. = 0.45975 n = 19

###make plot for model 3d####

library(visreg)

p.crude <- visreg(Model\_3d, scale='response', "Age", by="Sex",line.par = list(col = 'black'),gg=TRUE)

p.crude+geom\_point(data=Rhesus\_Macaque\_Occipital\_Cu,aes(x=Age,y=del\_65\_Cu,group=Sex,color=Sex)) +theme\_classic() +

guides(color=guide\_legend(title = "Sex")) + scale\_colour\_manual(values = c("male" = "black", "female" = "red"))

#alternative model for occipital vs sex and age (used in senior thesis)

Model\_3 = gam(del\_65\_Cu~s(Age, k = 6) + s(Age, Sex, bs = "fs", k = 6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu) #model is significant, OG paper

summary(Model\_3)

#AIC for models

Model\_3a = gam(del\_65\_Cu~s(Age, k = 6) + s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3b = gam(del\_65\_Cu~s(Age, k = 6) + te(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3c = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3d = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3e = gam(del\_65\_Cu~te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Cu)

Model\_3f = gam(del\_65\_Cu~s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

AIC(Model\_3a,Model\_3b,Model\_3c,Model\_3d,Model\_3e,Model\_3f) #Model 3d wins

Model\_6a = gam(del\_56\_Fe~s(Age, k = 6) + s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe)

Model\_6b = gam(del\_56\_Fe~s(Age, k = 6) + te(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe)

Model\_6c = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe)

Model\_6d = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Fe)

Model\_6e = gam(del\_56\_Fe~te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Fe)

Model\_6f = gam(del\_56\_Fe~s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe)

AIC(Model\_6a,Model\_6b,Model\_6c,Model\_6d,Model\_6e,Model\_6f) #Model 6d wins

Model\_Fa = gam(del\_56\_Fe~s(Age, k = 6) + s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe)

Model\_Fb = gam(del\_56\_Fe~s(Age, k = 6) + te(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe)

Model\_Fc = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe)

Model\_Fd = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Teeth\_Fe)

Model\_Fe = gam(del\_56\_Fe~te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Teeth\_Fe)

Model\_Ff = gam(del\_56\_Fe~s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe)

AIC(Model\_Fa,Model\_Fb,Model\_Fc,Model\_Fd,Model\_Fe,Model\_Ff) #Model Fb wins

Model\_C1 = gam(del\_65\_Cu~s(Age, k = 6) + s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu)

Model\_C2 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu)

Model\_C3 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu)

Model\_C4 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Teeth\_Cu)

Model\_C5 = gam(del\_65\_Cu~te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Teeth\_Cu)

Model\_C6 = gam(del\_65\_Cu~s(Age,Sex, bs="fs",k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu)

AIC(Model\_C1,Model\_C2,Model\_C3,Model\_C4,Model\_C5,Model\_C6) #Model C1 wins

library(mgcv)

library(gratia)

library(gamm4)

#Change sex column into a factor

Rhesus\_Macaque\_Occipital\_Cu$Sex = as.factor(Rhesus\_Macaque\_Occipital\_Cu$Sex)

Rhesus\_Macaque\_Occipital\_Fe$Sex = as.factor(Rhesus\_Macaque\_Occipital\_Fe$Sex)

Rhesus\_Macaque\_Teeth\_Cu$Sex = as.factor(Rhesus\_Macaque\_Teeth\_Cu$Sex)

Rhesus\_Macaque\_Teeth\_Fe$Sex = as.factor(Rhesus\_Macaque\_Teeth\_Fe$Sex)

#Conservative Models for age and sex are independent variables influencing delta fe and cu values in macaques

Model\_3c = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k = 6) + Sex,data = Rhesus\_Macaque\_Occipital\_Cu)

summary(Model\_3c) #not significant

Model\_6d = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex, k = 6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe)

summary(Model\_6d) #not significant, significance of 0.03 for age

Model\_6c = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Occipital\_Fe) #same as 6d

summary(Model\_6c) #same as 6d

Model\_Fb = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex, k = 6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe)

summary(Model\_Fb) #significant for age 0.03

Model\_Fc = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Fe) #same as Fb

summary(Model\_Fc) #same as Fb

Model\_C4 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex, k = 6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu)

summary(Model\_C4)#not significant

Model\_C3 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6) + Sex,data = Rhesus\_Macaque\_Teeth\_Cu) #model in paper, same as C4

summary(Model\_C3)

#without Sex as an independent variable, less conservative models

Model\_1 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex,k=6),data = Rhesus\_Macaque\_Occipital\_Cu)

summary(Model\_1) #significant, same as 3d, significant for age interaction and male and age interaction

Model\_2 = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex, k = 6),data = Rhesus\_Macaque\_Occipital\_Fe)

summary(Model\_2) #significant for age and male sex interaction

Model\_3 = gam(del\_56\_Fe~s(Age, k = 6) + te(Age, by=Sex, k = 6),data = Rhesus\_Macaque\_Teeth\_Fe)

summary(Model\_3) #significant for age, like model Fb

Model\_4 = gam(del\_65\_Cu~s(Age, k = 6) + te(Age, by=Sex, k = 6),data = Rhesus\_Macaque\_Teeth\_Cu)

summary(Model\_4) #not significant

#Visualizing Model Fb

ggplot(Rhesus\_Macaque\_Teeth\_Fe,aes(x=Age,y=del\_56\_Fe))+geom\_smooth(method="gam",formula=y~s(x),color="black")+

geom\_point(color="black")+

xlab("Age")+ylab(bquote(delta ^56\*'Fe'))+ggtitle(bquote('Age and '\*delta ^56\*'Fe in Teeth')) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())

#Visualizing Model 6d

ggplot(Rhesus\_Macaque\_Occipital\_Fe,aes(x=Age,y=del\_56\_Fe))+geom\_smooth(method="gam",formula=y~s(x),color="black")+

geom\_point(color="black")+

xlab("Age")+ylab(bquote(delta ^56\*'Fe'))+ggtitle(bquote('Age and '\*delta ^56\*'Fe in Occipital Bone')) +

theme\_bw()+theme(panel.grid.major=element\_blank(),panel.grid.minor=element\_blank())