Project 3, BIOS 6623

Trajectories of Onset of Memory and Other Cognitive Loss

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**Introduction**

The goal of this project is to identify trajectories of onset of memory and other cognitive loss in a population of healthy, community dwelling, and cognitively intact elders at risk of developing mild cognitive impairment (MCI) or dementia. 216 individuals entered the study, and 187 of these were included in the descriptive statistics and analysis because they had at least three measurements of the outcome of interest over the course of the study. This cognitive test of interest that was measured over time in these individuals was category fluency for animals. We were interested in determining the rate of memory decline in healthy individuals over the course of the aging process, as well as the rate of memory decline in those individuals who would be diagnosed with MCI or dementia during the course of the study. Finally, we wanted to determine the period of time before MCI or dementia diagnosis in which the rate of memory decline either changes or accelerates.

**Methods**

There were 216 individuals included at the start of the study. Only those with at least three outcomes measurements for animal category fluency were included in the analytic cohort, so 29 individuals were removed from the data set and 187 remained. The baseline demographic information at baseline for this population is reported in Table 1, with counts and percentages reported for categorical variables and means and standard deviations reported for continuous variables. The baseline values for other cognitive tests are also noted, to allow for a more detailed comparison of the two subpopulations in which individuals were and were not diagnosed with dementia during the study.

To prepare for interpretation of the models that were to be run, new variables were created. First, a new age variable was create in which the minimum age in the study, 59, was subtracted from all other ages to make the intercept more interpretable in the models. Second, a variable was created to show the difference between age at an observation and age at dementia/MCI diagnosis, which was used to plot the animal category fluency score in time leading up to diagnosis.

The time-before-diagnosis variable was also used in finding the change-point for the model—the point in time before diagnosis at which memory/cognitive scores begin to decline or change at a different pace. A model was to be fit that accounted for individuals’ age, dementia status at the end of the study, socioeconomic status as measured by the Hollingshead scale, and gender in explaining their category fluency for animals score, as well as including a term that would allow linear trends to change at some point prior to diagnosis.

To be able to allow these slopes to change at some point before dementia diagnosis, a change-point was determined for this model through likelihood-based methods. Maximum likelihood methods with Gaussian assumptions fit a variety of change points that ranged from 6 years before diagnosis to 2 years after diagnosis. The model being used to fit the change point was modeled the outcome—category fluency for animals—and adjusted for dementia status, age adjusted for minimum age of 59, the interaction between dementia status and age, socioeconomic status, gender, and the maximum of 0 and the difference between age at visit and dementia onset—if applicable—and the tested change point. To account for the repeated measures on individuals, a random intercept was fitted for each individual to account for their different starting points. Furthermore, a spatial power covariance structure was applied to the errors in the model to account for the repeated measures that occurred at differently spaced time points for individuals throughout the study.

From these methods, one change point was determined, and a final variable was created which selected the maximum of the age of onset subtracted from the age of the individual minus the change point. Then, this mixed model that was run in the bootstrap was fitted outside the bootstrap to determine the estimates for each variable based on the original data set of individuals with at least three observations.

To determine a confidence interval for the change point, 1000 iterations of a bootstrap were run that sampled with replacement from the 187 individuals in the analysis cohort, calculated the change point based on this new data set, and estimated the slope before and after the change point, as well as estimating the parameters of the model. The change-point 95% confidence interval was calculated by selecting the 2.5th and 97.5th percentiles of the bootstrap means.

These bootstrapped results were also utilized to determine more correct standard errors for the estimates compared to those in the model, which were too small because they could not account for the uncertainty of the change point. These bootstrapped standard errors were found by calculating the standard deviation of the distribution of each bootstrapped estimate. Then, p-values for each estimate were recalculated by dividing the coefficient by the recalculated standard error and then determining the probability of this value with the normal approximation.

**Results**

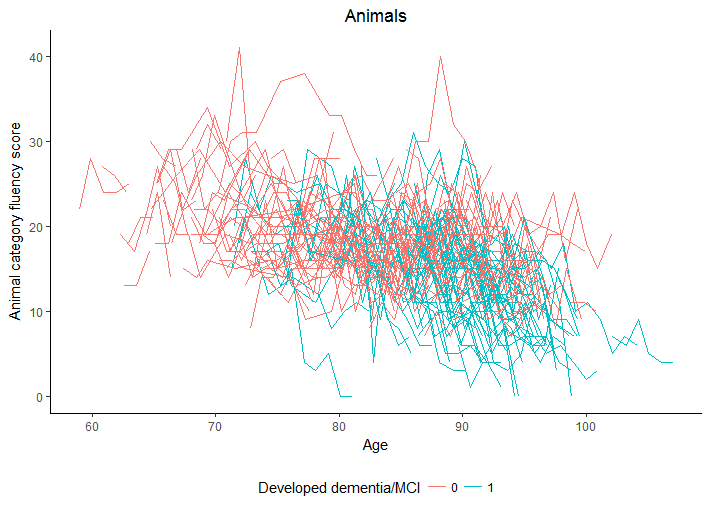
The baseline demographics for the 187 individuals included in the study are displayed in Table 1. Overall, individuals entered the study at a mean age of 80.10, and were followed for an average of approximately 17.5 visits in which the category fluency score for animals was measured over the next 8.82 years. There were more women included in the study, but a much lower proportion of women were diagnosed with dementia over the course of the study. Socioeconomic scores were fairly evenly distributed between those who were and were not diagnosed with dementia/MCI in the study. Those who were diagnosed with dementia entered the study, on average, 8 years older than those were not diagnosed, and they had lower average baseline scores in all four memory and cognitive tests that were measured at their visits, including animal category fluency.

**Table 1.** This table displays the baseline demographic information of the 187 individuals who had at least 3 measurements on the animal category fluency outcome over the course of the study.

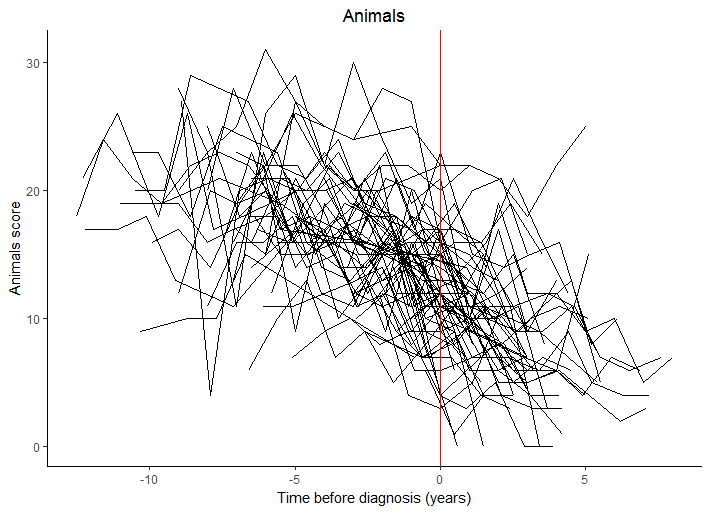
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **Overall** | **Did not develop dementia/MCI during study** | **Developed dementia/MCI during study** |
| **n** |  | 187 | 119 | 68 |
| **Number observations (mean (sd))** | | 17.49 (7.48) | 16.42 (8.22) | 19.35 (5.54) |
| **Years of follow-up (mean (sd))** | | 8.82 (4.05) | 8.23 (4.41) | 9.87 (3.08) |
| **Gender (%)** | Male | 82 (43.9) | 59 (49.6) | 23 (33.8) |
|  | Female | 105 (56.1) | 60 (50.4) | 45 (66.2) |
| **SES (mean (sd))** |  | 49.32 (11.68) | 49.66 (10.86) | 48.74 (13.07) |
| **Age (mean (sd))** |  | 80.10 (8.87) | 77.16 (8.92) | 85.24 (6.01) |
| **BlockR (mean (sd))** |  | 24.56 (9.36) | 26.52 (9.43) | 21.12 (8.22) |
| **Animals (mean (sd))** |  | 17.33 (5.11) | 18.30 (4.99) | 15.62 (4.91) |
| **LogMemI (mean (sd))** |  | 13.48 (4.36) | 14.60 (4.02) | 11.53 (4.28) |
| **LogMemII (mean (sd))** |  | 11.13 (5.00) | 12.55 (4.51) | 8.65 (4.88) |

In Figures 1 and 2, the trajectories of individuals’ category fluency for animal scores are displayed, for healthy individuals and for individuals who were diagnosed with dementia/MCI at some point in the study in Figure 1, and for only individuals who were diagnosed with dementia/MCI leading up to their diagnosis in Figure 2.

**Figure 1.** This figure displays the trajectories of individuals with at least three animal category fluency measurements in the study, colored by dementia status.



**Figure 2.** This figure displays the trajectories of animal category fluency scores leading up to dementia/MCI diagnosis for individuals who were diagnosed with dementia/MCI at some point in the study.



The results of the linear mixed model are displayed in Table 2, with the estimates determined by the model and the standard errors, and therefore p-values, determined from the bootstrapping. Only change point and age were significant predictors of category fluency for animals score (p < 0.0001; p < 0.0001). Interestingly, dementia diagnosis during the study was not a significant predictor of score, although this may likely be accounted for due to the fact that individuals who were diagnosed were older on average, and age was included as a covariate in the model.

**Table 2.** This table displays the estimates from the mixed modelwith the bootstrapped standard errors and p-values calculated from these bootstrapped errors.

|  |  |  |  |
| --- | --- | --- | --- |
| **Variable** | **Model Estimate** | **Bootstrapped Standard Error** | **p-value** |
| Intercept | 24.59 | 2.9 | <0.0001 |
| Change Point | -0.93 | 0.15 | <0.0001 |
| Gender (ref = M) | -0.56 | 0.57 | 0.3311 |
| SES | 0.04 | 0.02 | 0.0811 |
| Age - 59 | -0.18 | 0.03 | <0.0001 |
| Dementia (ref = 0) | -4.39 | 2.81 | 0.1187 |
| Interaction | 0.01 | 0.09 | 0.9493 |

The change point that was included in this mixed model, as determined by testing a variety of potential change points, was 3.9 years before diagnosis (95% CI: 5.5 years to 2.6 years before diagnosis), which suggests that there is a change in individuals’ trajectories approximately 3.9 years before their dementia/MCI diagnosis.

**Table 3.** This table displays the change point determined by maximum likelihood methods and bootstrapped change point mean and confidence interval.

|  |  |  |
| --- | --- | --- |
| **Change Point (likelihood)** | **Change point (bootstrap)** | **Bootstrapped 95% CI** |
| -3.9 | -4.05 | -5.5, -2.6 |

The slopes estimated before and after the change point of 3.9 years before diagnosis are -1.48 (95% CI: -2.63, -0.32) and -0.94 (95% CI: -1.25, -0.64), respectively, suggesting that the trajectory of category fluency for animals score decreases more slowly at first with age and then the decrease more steeply as individuals are closer to their dementia diagnosis.

**Table 4.** This table displays the bootstrapped mean and 95% confidence interval of the slopes before and after the change point.

|  |  |  |
| --- | --- | --- |
|  | **Bootstrapped mean** | **Bootstrapped 95% CI** |
| Slope before change-point | -0.94 | -1.25, -0.64 |
| Slope after change-point | -1.48 | -2.63, -0.32 |

**Conclusions**

Overall, for every one year increase in age in healthy individuals, there is an associated mean decrease of 0.18 points in animals score (95% CI: 0.24 to 0.12 point decrease). For every one year increase in age in individuals who were diagnosed with dementia/MCI in the course of the study, there is an associated mean decrease of 0.17 points in animals score before the change point, which is not significantly different from that of healthy individuals; after the change point, there is an associated mean decrease of 1.10 points in animals score per one year increase in age for this group of individuals. Finally, it is estimated that 3.9 years before diagnosis of dementia/MCI, there is an accelerated decrease in memory decline (95% CI 5.5 years to 2.6 years).

The study was limited in that subjects had to have at least 3 measurements for category fluency for animals score to be included in the study, so 29 individuals who entered the study could not be included in the analysis.

**Code**

The code for this project can be found at <https://github.com/BIOS6623-UCD/bios6623-johnsra3/tree/master/Project3/Code>.

#=============================================================#

# Project 3

# Import, explore, clean data

#=============================================================#

#=============================================================#

# Import data

#=============================================================#

library(dplyr)

library(plyr)

library(tidyr)

mci <- read.csv("C:/Users/johnsra3/Documents/School/AdvancedData/Project3Data.csv", header = T)

#=============================================================#

# Add number of visits column

#=============================================================#

freq <- as.data.frame(table(mci$id))

colnames(freq) <- c("id", "numobs")

mci <- merge(mci, freq, by = "id")

#=============================================================#

# Length of follow-up column

#=============================================================#

test <- ddply(mci, .(id), function(x) x[c(1, nrow(x)), ])

test <- test[, c(which(colnames(test) == "id"),

which(colnames(test) == "age"))]

test$whichvisit <- rep(c(1, 2), times = nrow(test)/2)

test\_wide <- spread(test, whichvisit, age)

test\_wide$followup <- test\_wide$`2` - test\_wide$`1`

mci <- merge(test\_wide, mci, by = "id")

#=============================================================#

# Create new variable stdized around minimum age

#=============================================================#

mci$age\_59 <- mci$age - 59

#=============================================================#

# Remove individuals who don't have at least 3 time points-

#=============================================================#

animals <- mci[, c(1, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 15, 16)]

animals <- animals[is.na(animals$animals) == F, ]

animals\_rows <- as.data.frame(table(animals$id))

colnames(animals\_rows) <- c("id", "num\_obs")

animals <- merge(animals, animals\_rows, by = "id")

animals <- animals[animals$num\_obs > 2, ]

animals$timeb4dem <- ifelse(animals$demind == 1,

animals$age - animals$ageonset, 0)

setwd("~/School/AdvancedData")

write.csv(mci, "MCICleaned.csv")

write.csv(animals, "AnimalsOutcome.csv")

#=============================================================#

# Project 3

# Demographics table

# Rachel Johnson

#=============================================================#

#=============================================================#

# Import data

#=============================================================#

library(tableone)

animals <- read.csv("C:/Users/johnsra3/Documents/School/AdvancedData/AnimalsOutcome.csv", header = T)

#only include baseline observations for this table

animals <- animals[order(animals$id), ]

animals <- animals[!duplicated(animals$id), ]

#=============================================================#

# Format vars for table

#=============================================================#

#Need to make following vars factors: gender, demind

animals$gender <- factor(animals$gender, levels = c("1", "2"), labels = c("Male", "Female"))

animals$demind <- factor(animals$demind, levels = c("0", "1"))

#=============================================================#

# Select vars and create table

#=============================================================#

tabvars <- c("numobs", "followup", "gender", "SES", "age", "blockR",

"animals", "logmemI", "logmemII")

tab1 <- CreateTableOne(vars = tabvars, strata = "demind", data = animals, test = F)

tab1print <- as.data.frame(print(tab1, showAllLevels = T))

tab1\_nostrat <- CreateTableOne(vars = tabvars, data = animals, test = F)

tab1nostratprint <- as.data.frame(print(tab1\_nostrat, showAllLevels = T))

tab <- cbind.data.frame(tab1nostratprint, tab1print)

tab <- tab[, -3]

colnames(tab) <- c("", "Overall", "Did not develop dementia/MCI during study",

"Developed dementia/MCI during study")

setwd("C:/Repositories/bios6623-johnsra3/Project3/Reports")

write.csv(tab, "Table1Demographics.csv")

#=============================================================#

# Project 3

# Spaghetti plots

# Rachel Johnson

#=============================================================#

#=============================================================#

# Import data

#=============================================================#

library(ggplot2)

setwd("~/School/AdvancedData")

animals <- read.csv("AnimalsOutcome.csv", header = T)

#=============================================================#

# Spaghetti plots- exploration of trajectory for all indiv

#=============================================================#

#animals

ggplot(data = animals, aes(x = age, y = animals, group = id, col = as.factor(demind))) +

geom\_line() +

theme\_classic() +

theme(panel.border = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank(),

axis.line.x = element\_line(color = "black"),

axis.line.y = element\_line(color = "black"),

plot.title = element\_text(hjust = 0.5),

legend.position = "bottom",

legend.direction = "horizontal") +

scale\_color\_discrete("Developed dementia/MCI") +

scale\_x\_continuous(name = "Age") +

scale\_y\_continuous(name = "Animal category fluency score") +

ggtitle("Animals")

#=============================================================#

# Spaghetti plots- demind = 1 time before diagnosis!

#=============================================================#

ggplot(data = animals[animals$demind == 1,], aes(x = timeb4dem, y = animals, group = id)) +

geom\_line() +

theme\_classic() +

theme(panel.border = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank(),

axis.line.x = element\_line(color = "black"),

axis.line.y = element\_line(color = "black"),

plot.title = element\_text(hjust = 0.5),

legend.position = "bottom",

legend.direction = "horizontal") +

geom\_vline(xintercept = 0, col = "red") +

scale\_x\_continuous(name = "Time before diagnosis (years)") +

scale\_y\_continuous(name = "Animals score") +

ggtitle("Animals")

#=============================================================#

# Project 3

# Functions for change points and bootstraps

# Rachel Johnson

#=============================================================#

library(nlme)

#=============================================================#

# Change point function-- note: specific to animals data set

#=============================================================#

#Create a function to search for change point and fit final change point model

cp.search\_and\_fit<-function(id, timeb4dem, age\_59, demind, ses, gender, y, cps, int){

#Place to store likelihoods from the CP search

ll<-data.frame(changepoint = rep(NA, length(cps)), ll = rep(NA, length(cps)))

#Search for the CP

for (i in 1:length(cps)){

cp <- cps[i]

timemax <- ifelse(timeb4dem > cp, timeb4dem - cp, 0)

cp.model <- lme(y ~ age\_59 + demind + int + timemax +

ses + gender, random = ~1|id,

correlation = corCAR1(form = ~age\_59), method = "REML")

ll[i, ] <- c(cp, logLik(cp.model))

}

#Plot the likelihood

plot(ll$changepoint, ll$ll, type='l', xlab='Change Point (years)', ylab='Log Likelihood')

#Find the max

cp<-ll[which(ll$ll==max(ll$ll)),'changepoint']

print(cp)

#Fit the final model

timemax <- ifelse(timeb4dem > cp, timeb4dem - cp, 0)

cp.model <- lme(y ~ age\_59 + demind + int + timemax + ses + gender, random = ~1|id,

correlation = corCAR1(form = ~age\_59), method = "REML")

return(list(cp=cp, model=cp.model))

}

#=============================================================#

# Bootstrap function for changepoint CIs

#=============================================================#

boot.function <- function(ids, dat, cps){

#Sample subjects randomly w/ replacemnt

ids.u <- unique(ids)

boot.subjects <- sample(ids.u, length(ids.u), replace = T)

#Grab the data for each of the chosen subjects

boot.dat <- NULL

for (i in 1:length(ids.u)){

temp <- cbind(i, dat[ids==boot.subjects[i],])

boot.dat <- rbind(boot.dat, temp)

}

#Repeat the analysis on the bootstrap sample

boot.model <- cp.search\_and\_fit(id = boot.dat$id, timeb4dem = boot.dat$timeb4dem, age = boot.dat$age\_59,

demind = boot.dat$demind, ses = boot.dat$ses, gender = boot.dat$gender,

y = boot.dat$y, int = boot.dat$int, cps = cps)

#Save the estimates and CP's

mod1 <- glht(boot.model$model, matrix(c(0, 0, 1, 1, 0, 0, 0), nrow = 1))

mod2 <- glht(boot.model$model, matrix(c(0, 0, 1, 0, 0, 0, 0), nrow = 1))

boot.rslt <- c(boot.model$cp,

confint(mod1)$confint[1],

confint(mod2)$confint[1],

boot.model$model$coefficient$fixed[1],

boot.model$model$coefficient$fixed[2],

boot.model$model$coefficient$fixed[3],

boot.model$model$coefficient$fixed[4],

boot.model$model$coefficient$fixed[5],

boot.model$model$coefficient$fixed[6],

boot.model$model$coefficient$fixed[7])

names(boot.rslt)<-c("Changepoint", "Slope1", "Slope2", "Intercept",

"Age\_59", "Dementia = 1", "Change-point", "SES", "Gender = 2",

"Age\_59\*Dementia = 1")

return(boot.rslt)

}

#=============================================================#

# Project 3

# Find change point for each outcome

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#=============================================================#

#=============================================================#

# Import data

#=============================================================#

library(nlme)

source("C:/Repositories/bios6623-johnsra3/Project3/Code/Functions- Change Points and Bootstrap.R")

setwd("C:/Users/johnsra3/Documents/School/AdvancedData")

#blockr <- read.csv("blockrOutcome.csv", header = T)

animals <- read.csv("AnimalsOutcome.csv", header = T)

#logmem1 <- read.csv("LogMem1Outcome.csv", header = T)

#logmem2 <- read.csv("LogMem2Outcome.csv", header = T)

#=============================================================#

# Run animals change point for only -6 to 2

#=============================================================#

cps <- seq(from = -6, to = 2, by = 0.1)

animals$gender <- factor(animals$gender)

animals$demind <- factor(animals$demind)

animals$int <- as.numeric(as.character(animals$demind)) \* animals$age\_59

#Run the function on the dataset

cp.model <- cp.search\_and\_fit(id = animals$id, timeb4dem =animals$timeb4dem, age = animals$age\_59,

demind = animals$demind, ses = animals$SES, gender = animals$gender,

y = animals$animals, cps = cps, int = animals$int)

summary(cp.model$model)

animals\_cp <- cp.model$cp

#cp = -3.9

#=============================================================#

# Prepare data set for modeling w/ cp included

#=============================================================#

#Each model will include: age\_59, demind, age\_59\*demind,

#SES, gender, max(age - ageonset + cp, 0)

animals$timemax <- animals$timeb4dem - animals\_cp

animals$timecp <- ifelse(animals$timemax < 0, 0, animals$timemax)

animals[is.na(animals)] <- ""

#=============================================================#

# Run mixed model

#=============================================================#

animals.model <- lme(animals ~ age\_59 + demind + age\_59\*demind + timecp + SES + gender, random = ~1|id,

correlation = corCAR1(form = ~age\_59), method = "REML", data = animals)

mmres <- as.data.frame(summary(animals.model)$coeff$fixed)

setwd("C:/Repositories/bios6623-johnsra3/Project3/Reports")

write.csv(mmres, "MixedModelResults.csv")

#=============================================================#

# Bootstrap change point

#=============================================================#

id <- animals$id

timeb4dem <- animals$timeb4dem

age\_59 <- animals$age\_59

demind <- animals$demind

ses <- animals$SES

gender <- animals$gender

y <- animals$animals

cps <- seq(from = -6, to = 2, by = 0.1)

int <- as.numeric(as.character(animals$demind)) \* animals$age\_59

dat <- cbind.data.frame(id, timeb4dem, age\_59, demind, ses, gender, y, int)

niter <- 10

bootstraps <- matrix(NA, ncol = 10, nrow = niter)

for (j in 1:niter){

bootstraps[j, ] <- boot.function(ids = id, dat = dat, cps = cps)

print(j)

}

#setwd("C:/Repositories/bios6623-johnsra3/Project3/Reports")

#write.csv(bootstraps, "BootstrapWithAllEstimates.csv")

#==============================================================#

# Project 3

# Work with bootstrap results

# Rachel Johnson

#==============================================================#

#==============================================================#

# Import data

#==============================================================#

setwd("C:/Repositories/bios6623-johnsra3/Project3/Reports")

mmres <- read.csv("MixedModelResults.csv", header = T)

animals\_bs <- read.csv("BootstrapWithAllEstimates.csv", header = T)

animals\_bs <- animals\_bs[, -1]

colnames(animals\_bs) <-c("Changepoint","Intercept","Change Point",

"Gender", "SES", "Age\_59",

"Interaction", "Dementia", "Slope1", "Slope2")

#==============================================================#

# Table of bootstrap results for change point

#==============================================================#

bstab <- as.data.frame(matrix(data = NA, nrow = 1, ncol = 4))

colnames(bstab) <- c("Variable", "Change Point (likelihood)", "Change point (bootstrap)",

"Bootstrapped 95% CI")

bstab[1, 1] <- c("Animals")

bstab[1, 2] <- c(-3.9)

bstab[1, 3] <- round(mean(animals\_bs[, 1]), 2)

bstab[1, 4] <- paste(paste(round(quantile(animals\_bs[, 1], 0.025), 2), ",", sep = ""),

round(quantile(animals\_bs[, 1], 0.975), 2))

bstab

write.csv(bstab, "C:/Repositories/bios6623-johnsra3/Project3/Reports/BootstrapSummaryTable.csv")

#==============================================================#

# Table of bootstrap results for updated SEs w/ model estimates

#==============================================================#

setab <- as.data.frame(matrix(data = NA, nrow = 7, ncol = 4))

colnames(setab) <- c("Variable", "Model Estimate", "Bootstrapped Standard Error", "p-value")

setab[1:7, 1] <- colnames(animals\_bs)[2:8]

setab[1, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "(Intercept)"], 2)

setab[2, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "timecp"], 2)

setab[3, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "gender2"], 2)

setab[4, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "SES"], 2)

setab[5, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "age\_59"], 2)

setab[6, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "age\_59:demind1"], 2)

setab[7, 2] <- round(mmres$summary.animals.model..coeff.fixed[mmres$X == "demind1"], 2)

setab[1, 3] <- round(sd(animals\_bs[, 2]), digits = 2)

setab[2, 3] <- round(sd(animals\_bs[, 3]), digits = 2)

setab[3, 3] <- round(sd(animals\_bs[, 4]), digits = 2)

setab[4, 3] <- round(sd(animals\_bs[, 5]), digits = 2)

setab[5, 3] <- round(sd(animals\_bs[, 6]), digits = 2)

setab[6, 3] <- round(sd(animals\_bs[, 7]), digits = 2)

setab[7, 3] <- round(sd(animals\_bs[, 8]), digits = 2)

setab[1, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "(Intercept)"])/

sd(animals\_bs[, 2])), digits = 4)

setab[2, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "timecp"])/

sd(animals\_bs[, 3])), digits = 4)

setab[3, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "gender2"])/

sd(animals\_bs[, 4])), digits = 4)

setab[4, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "SES"])/

sd(animals\_bs[, 5])), digits = 4)

setab[5, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "age\_59"])/

sd(animals\_bs[, 6])), digits = 4)

setab[6, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "age\_59:demind1"])/

sd(animals\_bs[, 7])), digits = 4)

setab[7, 4] <- round(2\*pnorm(-abs(mmres$summary.animals.model..coeff.fixed[mmres$X == "demind1"])/

sd(animals\_bs[, 8])), digits = 4)

setab

setab[c(1, 2, 5), 4] <- "<0.0001"

write.csv(setab, "ResultsTabBootstrappedSEs.csv")

#==============================================================#

# Table of bootstrap results for pre + post slope

#==============================================================#

sltab <- as.data.frame(matrix(data = NA, nrow = 2, ncol = 3))

sltab[1:2, 1] <- c("Slope after change-point", "Slope before change-point")

sltab[1, 2] <- round(mean(animals\_bs$Slope1), digits = 2)

sltab[2, 2] <- round(mean(animals\_bs$Slope2), digits = 2)

sltab[1, 3] <- paste(paste(round(mean(animals\_bs$Slope1) - 1.96 \* sd(animals\_bs$Slope1), digits = 2), ",", sep = ""),

round(mean(animals\_bs$Slope1) + 1.96 \* sd(animals\_bs$Slope1), digits = 2))

sltab[2, 3] <- paste(paste(round(mean(animals\_bs$Slope2) - 1.96 \* sd(animals\_bs$Slope2), digits = 2), ",", sep = ""),

round(mean(animals\_bs$Slope2) + 1.96 \* sd(animals\_bs$Slope2), digits = 2))

write.csv(sltab, "BootstrapSlopeTables.csv")