#Austin Dickerson

#In-Class 9-1

getwd()

setwd("C:\\Users\\Austin\\Desktop\\Virginia Tech\\CS 3654\\CMDA")

load('fdata.RData')

attach(final)

model1 <- glm(disorder ~ som1 + som2 + som3 + som4 + som5, family = "binomial")

model1

Coefficients:

(Intercept) som1 som2 som3 som4 som5

-4.7196 0.5215 1.2390 0.5441 0.5320 2.4536

#The most important features are som1, som3, and som4

#It interprets som1 as 0.5215, which means it sees it somewhat likely to be able

#to predict the disorder

model2 <- glm(disorder ~ som6 + som7 + som8 + som9, family = "binomial")

model2

Coefficients:

(Intercept) som6 som7 som8 som9

-1.544 1.941 1.092 1.167 1.192

#The most important features in this model are som7

model3 <- glm(disorder ~ som10 + som11 + som12 + som13 + som14, family = "binomial")

model3

Coefficients:

(Intercept) som10 som11 som12 som13 som14

-4.7789 1.0075 0.7396 0.5288 1.4370 1.0204

#The most important features in this model are som12

#I would say that model1 is most likely to be able to predict the disorder because

#it had the most significant features in it.