#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.