

```

library(readxl)

Copy_of_ADHD_data_Meadows <- read_excel("Copy of ADHD data Meadows.xlsx")

mydata<-Copy_of_ADHD_data_Meadows

View(mydata)

library(tidyverse)

library(summarytools)

library(dplyr)

library(xlsx)

library(ggpubr)

### Data cleaning

unique(mydata$Gender)

mydata$Gender <- gsub("(?i)F", "1", mydata$Gender)

mydata$Gender <- gsub("(?i)M", "0", mydata$Gender)

unique(mydata$`Highest Ed`)

mydata$`Highest Ed` <- gsub("(?i)Associates|(?i)HS|(?i)9", "0", mydata$`Highest Ed`)

mydata$`Highest Ed` <- gsub("(?i)BA|(?i)BS", "1", mydata$`Highest Ed`)

mydata$`Highest Ed` <- gsub("(?i)JD|(?i)MD|(?i)PHD|(?i)MASTERS|(?i)3", "2", mydata$`Highest Ed`)

unique(mydata$`adhd dx`)

mydata$`adhd dx` <- gsub("(?i)n", "0", mydata$`adhd dx`)

mydata$`adhd dx` <- gsub("(?i)y", "1", mydata$`adhd dx`)

mydata1<-subset(mydata, `adhd dx`!="q" & `adhd dx`!="Q" & `ACE Total`!="NA" & `Delay K`!="NA" &
`CAARS impulsivity`!="NA" & `caffeine`!="NA"& `Other substance`!="NA"&
`tobacco`!="NA"& `etoh`!="NA")

mydata1

```

```
unique(mydata1$`caffeine`)
```

```
mydata1$`caffeine`<- gsub("(?i)y","1", mydata1$`caffeine`)
```

```
mydata1$`caffeine`<- gsub("(?i)n","0", mydata1$`caffeine`)
```

```
unique(mydata1$`Other substance`)
```

```
mydata1$`Other substance`<- gsub("(?i)marijuana","1", mydata1$`Other substance`)
```

```
mydata1$`Other substance`<- gsub("(?i)n","0", mydata1$`Other substance`)
```

```
unique(mydata1$`tobacco`)
```

```
mydata1$`tobacco`<- gsub("(?i)y","1", mydata1$`tobacco`)
```

```
mydata1$`tobacco`<- gsub("(?i)n","0", mydata1$`tobacco`)
```

```
unique(mydata1$`etoh`)
```

```
mydata1$`etoh`<- gsub("(?i)y","1", mydata1$`etoh`)
```

```
mydata1$`etoh`<- gsub("(?i)n","0", mydata1$`etoh`)
```

```
mydata1$substance <- as.numeric(mydata1$`caffeine`) + as.numeric(mydata1$`Other  
substance`)+as.numeric(mydata1$`tobacco`)+as.numeric(mydata1$`etoh`)
```

```
mydata1$substance_yn<-as.numeric(mydata1$substance)
```

```
mydata1$substance_yn<- gsub("(?i)1|(?i)2|(?i)3","1", mydata1$substance_yn)
```

```
mydata1$substance_yn<- gsub("(?i)0","0", mydata1$substance_yn)
```

```
write.xlsx(mydata1, "/cloud/project/mydata1.xlsx")
```

```
#####QUESTION 1#####
```

```
### Descriptive statistics
```

```
summary(mydata1$`ACE Total`)
```

```
mean(mydata$Age)

summarytools::freq(mydata1$Gender, order = "freq")

summarytools::freq(mydata1$`Highest Ed`, order = "freq")

summarytools::freq(mydata1$`adhd dx`, order = "freq")
```

```
### Difference in ADHD based on gender, education and substance use

round(prop.table(table(mydata1$`adhd dx`,mydata1$Gender), 1), 2)

round(prop.table(table(mydata1$`adhd dx`,mydata1$`Highest Ed`), 1), 2)

round(prop.table(table(mydata1$`adhd dx`,mydata1$substance_yn), 1), 2)
```

```
#####QUESTION 2#####
```

```
## relationship between ACE total and ADHD_yn, ONE WAY ANOVA

hist(mydata1$`ACE Total`)

hist(log(mydata1$`ACE Total`))

ACE_ADHD<-aov(mydata1$`ACE Total` ~ mydata1$`adhd dx`, data = mydata1)

summary(ACE_ADHD)
```

```
ACE_ADHD<-aov(log(mydata1$`ACE Total`) ~ mydata1$`adhd dx`, data = mydata1)

summary(ACE_ADHD)
```

```
#####QUESTION 3#####
```

```
## plot

mydata2<-as.data.frame(mydata1)

ggplot(mydata2, aes(`ACE Total`, `CAARS impulsivity`)) + geom_point()

plot(`Delay K` ~ `ACE Total`, data = mydata2)
```

```
## correlation test

cor.test(mydata1$`ACE Total`, mydata1$`CAARS impulsivity`, method=c("pearson", "kendall",
"spearman"))
```

```
cor.test(mydata1$`ACE Total`, as.numeric(mydata1$`Delay K`), method=c("pearson", "kendall",  
"spearman"))
```

```
ace_impulse <- lm(mydata2$`CAARS impulsivity` ~ mydata2$`ACE  
Total`+mydata2$Age+mydata2$Gender+mydata2$`Highest Ed`, data = mydata2)  
summary(ace_impulse)  
par(mfrow=c(2,2))  
plot(ace_impulse)  
par(mfrow=c(1,1))
```

```
ace_delay <- lm(mydata2$`Delay K` ~ mydata2$`ACE  
Total`+mydata2$Age+mydata2$Gender+mydata2$`Highest Ed`, data = mydata2)  
summary(ace_delay)  
par(mfrow=c(2,2))  
plot(ace_delay)  
par(mfrow=c(1,1))
```

```
#####QUESTION 4#####
```

```
##substance_yn vs ACE total- one way anova
```

```
ACE_substance<-aov(mydata2$`ACE Total` ~ mydata2$`substance_yn`, data = mydata2)  
summary(ACE_substance)
```

```
ACE_substance<-aov(log(mydata1$`ACE Total`) ~ mydata1$`substance_yn`, data = mydata1)  
summary(ACE_substance)
```

```
## chi square substance yn vs adhd dx
```

```
chisq.test(mydata2$`substance_yn`, mydata2$`adhd dx`, correct=FALSE)
```