

# PSYC

## Negotiation Capstone 6

24/09/2021

```
library(car)
```

```
## Loading required package: carData
```

### Read in the csv file

```
Nego_data <- read.csv(file = "Data with Bio culture and Average Score.csv")
```

### General significant test with linear model and stepwise selection

```
Culture <- Nego_data$Bio_Culture  
Dignity <- Nego_data$Dignity  
Face <- Nego_data$Face
```

```
# linear model and test significance of factors  
model <- lm(Culture ~ (Dignity + Face)^2)
```

```
# Stepwise selection process and figure out the significant factor(s)  
# Only intercept and Dignity factor are significant in this model  
model <- step(model)
```

```
## Start:  AIC=-212.47  
## Culture ~ (Dignity + Face)^2  
##  
##           Df Sum of Sq   RSS   AIC  
## - Dignity:Face  1 0.0026338 32.809 -214.46  
## <none>                32.807 -212.47  
##  
## Step:  AIC=-214.46  
## Culture ~ Dignity + Face  
##  
##           Df Sum of Sq   RSS   AIC  
## - Face      1  0.12367 32.933 -215.91  
## <none>                32.809 -214.46  
## - Dignity   1  2.82536 35.635 -204.31
```

```
##
## Step: AIC=-215.91
## Culture ~ Dignity
##
##           Df Sum of Sq    RSS    AIC
## <none>                32.933 -215.91
## - Dignity  1      3.0669 36.000 -204.82
```

## Only dignity factor is significant

```
# print out the summary table of the reduced model
summary(model)
```

```
##
## Call:
## lm(formula = Culture ~ Dignity)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.6998 -0.4029 -0.2887  0.5285  0.7798
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.15661    0.20199  10.677 < 2e-16 ***
## Dignity      -0.13703    0.03729  -3.675 0.000334 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4766 on 145 degrees of freedom
## Multiple R-squared:  0.08519,    Adjusted R-squared:  0.07888
## F-statistic: 13.5 on 1 and 145 DF,  p-value: 0.0003345
```

## Assumption test

```
# Done the assumption test
Culture <- as.factor(Culture)
leveneTest(Dignity ~ Culture)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value    Pr(>F)
## group    1  9.5222 0.002432 **
##          145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(Face ~ Culture)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  1  1.0941 0.2973
##      145
```

## Descriptive data of face and dignity score for mono & bio culture

```
# Record data into list for mean and SD descriptive data
mono_face_culture <- c()
mono_dig_culture <- c()
bio_face_culture <- c()
bio_dig_culture <- c()

for (i in 1:length(Culture)){
  if (Culture[i] == "1"){
    mono_face_culture <- c(mono_face_culture, Face[i])
    mono_dig_culture <- c(mono_dig_culture, Dignity[i])
  } else{
    bio_face_culture <- c(bio_face_culture, Face[i])
    bio_dig_culture <- c(bio_dig_culture, Dignity[i])
  }
}
```

## SD values

```
# SD value for mono-culture of in face score
sd(mono_face_culture)
```

```
## [1] 0.8261746
```

```
# SD value for mono-culture of in dignity score
sd(mono_dig_culture)
```

```
## [1] 0.7646281
```

```
# SD value for bio-culture of in face score
sd(bio_face_culture)
```

```
## [1] 0.9952884
```

```
# SD value for bio-culture of in dignity score
sd(bio_dig_culture)
```

```
## [1] 1.275622
```

## Mean values

```
# Mean value for mono-culture of in face score  
mean(mono_face_culture)
```

```
## [1] 4.864286
```

```
# Mean value for mono-culture of in dignity score  
mean(mono_dig_culture)
```

```
## [1] 5.579365
```

```
# Mean value for bio-culture of in face score  
mean(bio_face_culture)
```

```
## [1] 5.047619
```

```
# Mean value for bio-culture of in dignity score  
mean(bio_dig_culture)
```

```
## [1] 4.957672
```

(Ignore this block if not needed)

```
info_ave <- Nego_data$Info_AVE  
emo_ave <- Nego_data$Emotion_AVE  
  
bio_info_ave <- c()  
bio_emo_ave <- c()  
mono_info_ave <- c()  
mono_emo_ave <- c()  
  
for (i in 1:length(Culture)){  
  if (Culture[i] == "1"){  
    mono_info_ave <- c(mono_info_ave, info_ave[i])  
    mono_emo_ave <- c(mono_emo_ave, emo_ave[i])  
  } else{  
    bio_info_ave <- c(bio_info_ave, info_ave[i])  
    bio_emo_ave <- c(bio_emo_ave, emo_ave[i])  
  }  
}  
  
# Drop NA value from list  
mono_emo_ave <- mono_emo_ave[-c(49, 50, 52)]  
mono_info_ave <- mono_info_ave[-c(49, 50, 52)]
```

## One-way ANOVA test on informational value for 2 mono & bio groups

## One-way ANOVA test on emotional value for 2 mono & bio groups

```
# one-way ANOVA info
one_way_info <- aov(info_ave ~ Culture)
summary(one_way_info)

##              Df Sum Sq Mean Sq F value Pr(>F)
## Culture      1  14.08   14.09    16.01 1e-04 ***
## Residuals    145 127.55    0.88
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# one-way ANOVA emo
one_way_emo <- aov(emo_ave ~ Culture)
summary(one_way_emo)

##              Df Sum Sq Mean Sq F value Pr(>F)
## Culture      1   6.48   6.479    5.306 0.0227 *
## Residuals    142 173.40    1.221
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

## Some hist plots for participants's age and gender distribution

```
dignity <- c()
bio <- c()
info_dignity <- c()
info_bio <- c()
emo_dignity <- c()
emo_bio <- c()

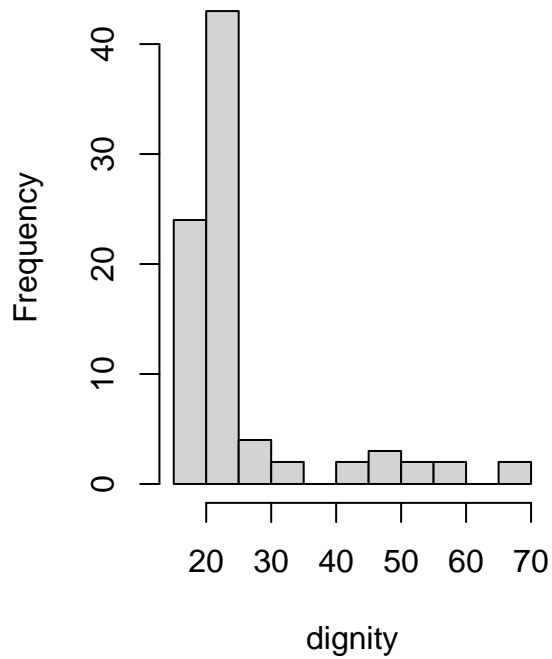
par(mfrow = c(1, 2))
for (i in 1:length(Nego_data$ResponseId)){
  if (Nego_data$Bio_Culture[i] < 2){
    dignity <- c(dignity, Nego_data$Age[i])
    info_dignity <- c(info_dignity, Nego_data$Info_AVE[i])
    emo_dignity <- c(emo_dignity, Nego_data$Emotion_AVE[i])
  }
  else{
    bio <- c(bio, Nego_data$Age[i])
    info_bio <- c(info_bio, Nego_data$Info_AVE[i])
    emo_bio <- c(emo_bio, Nego_data$Emotion_AVE[i])
  }
}
```

```
}
```

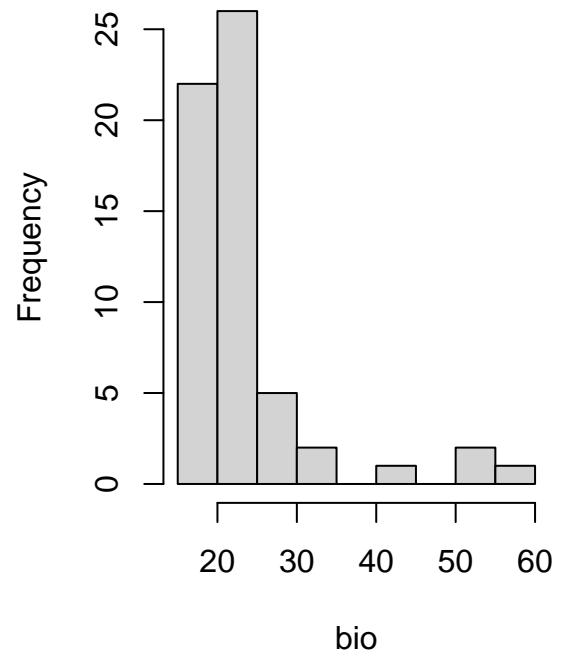
```
hist(dignity)
```

```
hist(bio)
```

**Histogram of dignity**



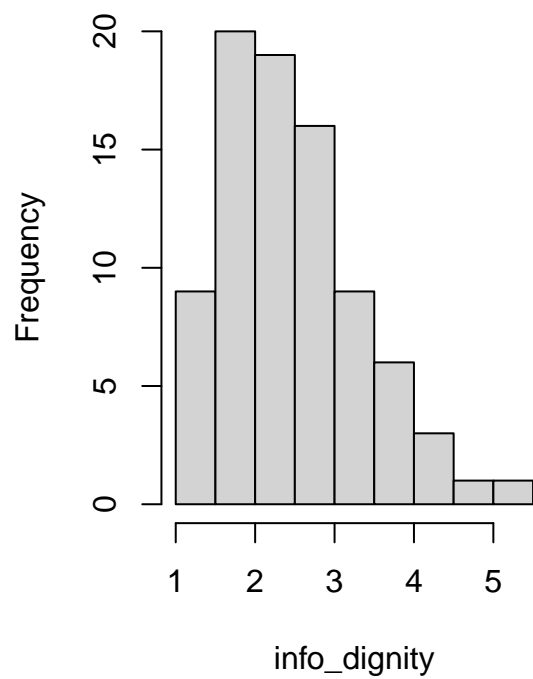
**Histogram of bio**



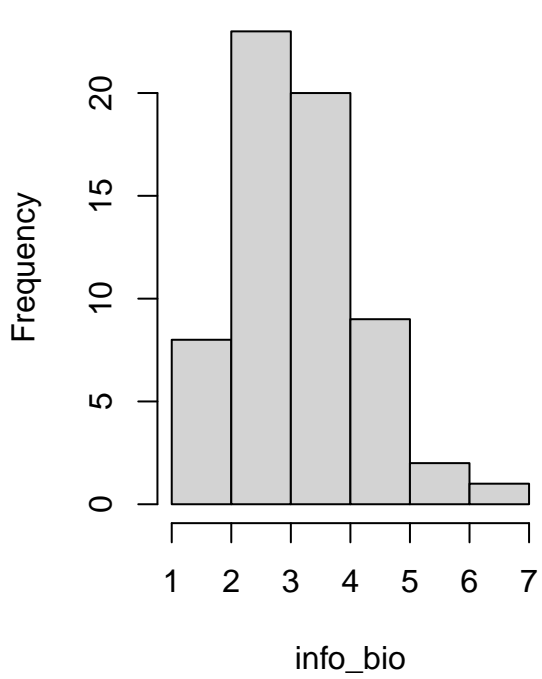
```
hist(info_dignity)
```

```
hist(info_bio)
```

**Histogram of info\_dignity**

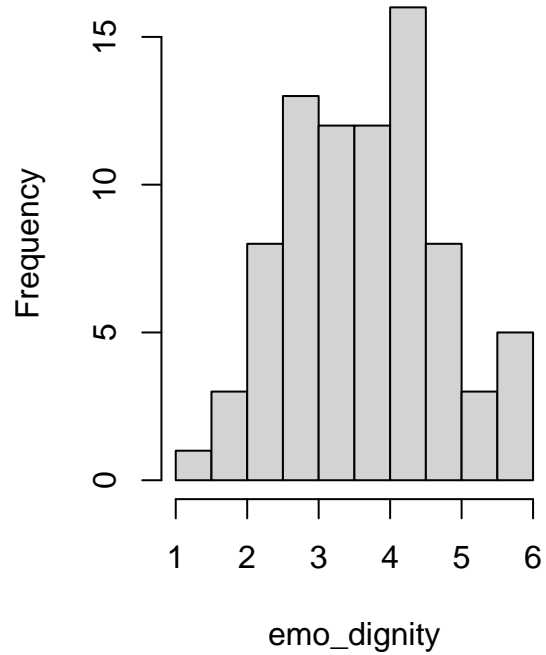


**Histogram of info\_bio**

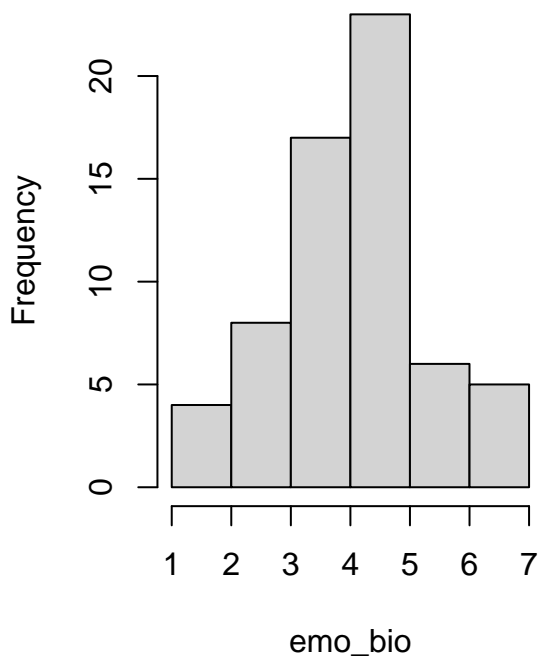


```
hist(emo_dignity)  
hist(emo_bio)
```

**Histogram of emo\_dignity**



**Histogram of emo\_bio**



```
hist(Nego_data$Gender)
```



**Histogram of Nego\_data\$Gende**

