Thesis Analysis

Rhea Sarma

11 January, 2025

Contents

Checking the relationship between BIS, BAS, meal intake and EAH intake variables.

AIM 1 : Does BIS and BAS influences eating in absence of hunger?

```
library(haven)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

1. Load dataset

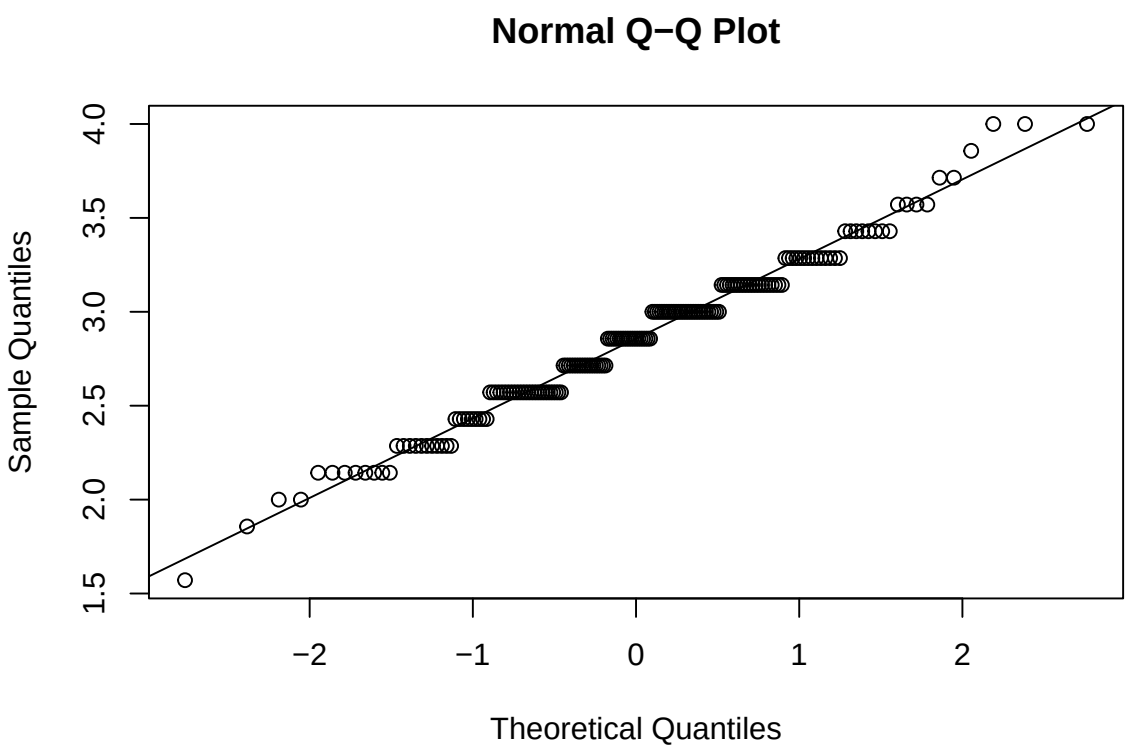
```
thesis_data<-read.csv("~/Desktop/Rhea MS thesis/MS_thesis/data/thesis_data.csv")
```

2. My IV's of interest are `bis` `bas` `bas_funseeking` `bas_drive` `bas_rewardresp`

My DV's of interest are `meal_grams_consumed` `meal_kcal_consumed` `eah_grams_consumed_foodonly` `eah_kcal_consumed`

1. Checking normality and homogeneity of variance assumptions and conducting visualizations

```r
# For variable BIS
qqnorm(thesis_data$bis)
qqline(thesis_data$bis)
```



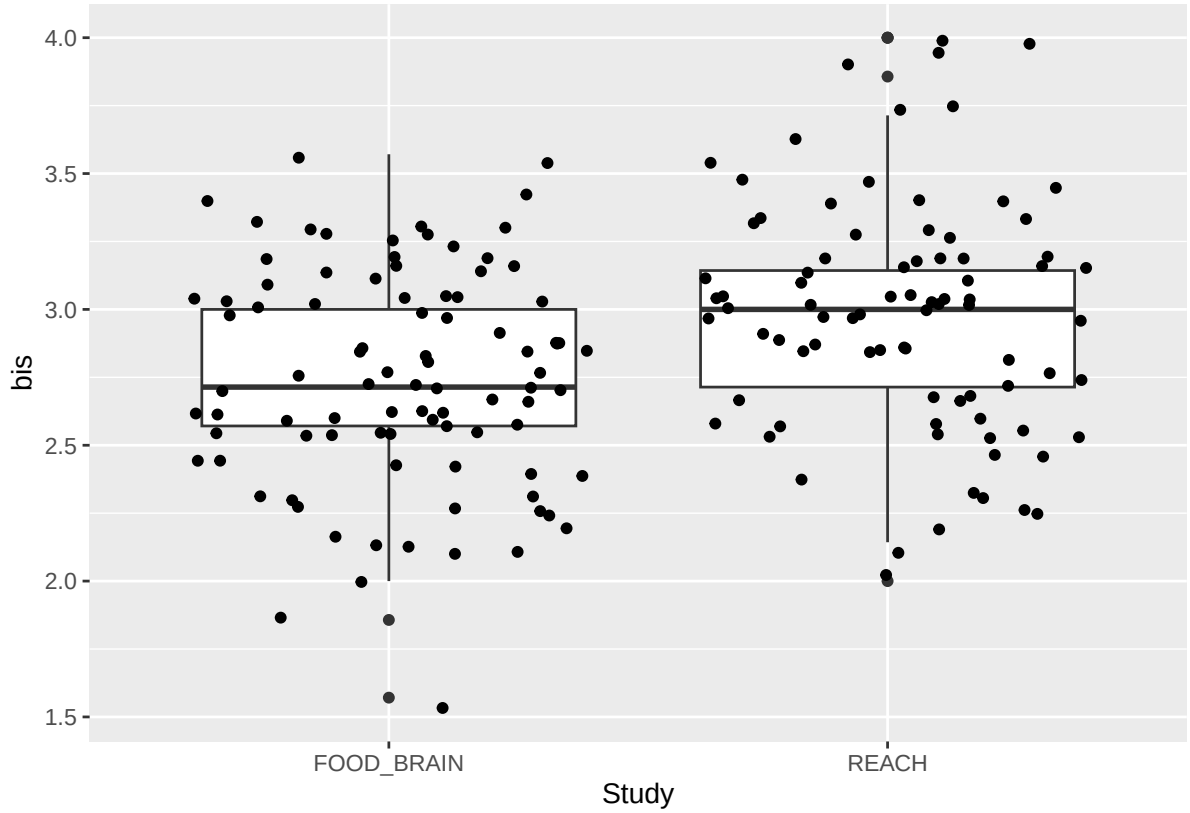

```r
shapiro.test(thesis_data$bis) #met normality
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bis
## W = 0.98488, p-value = 0.05538
```

```r
#Visualizing BIS data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=bis)) + geom_boxplot() + geom_jitter(height = NULL) #jit
```

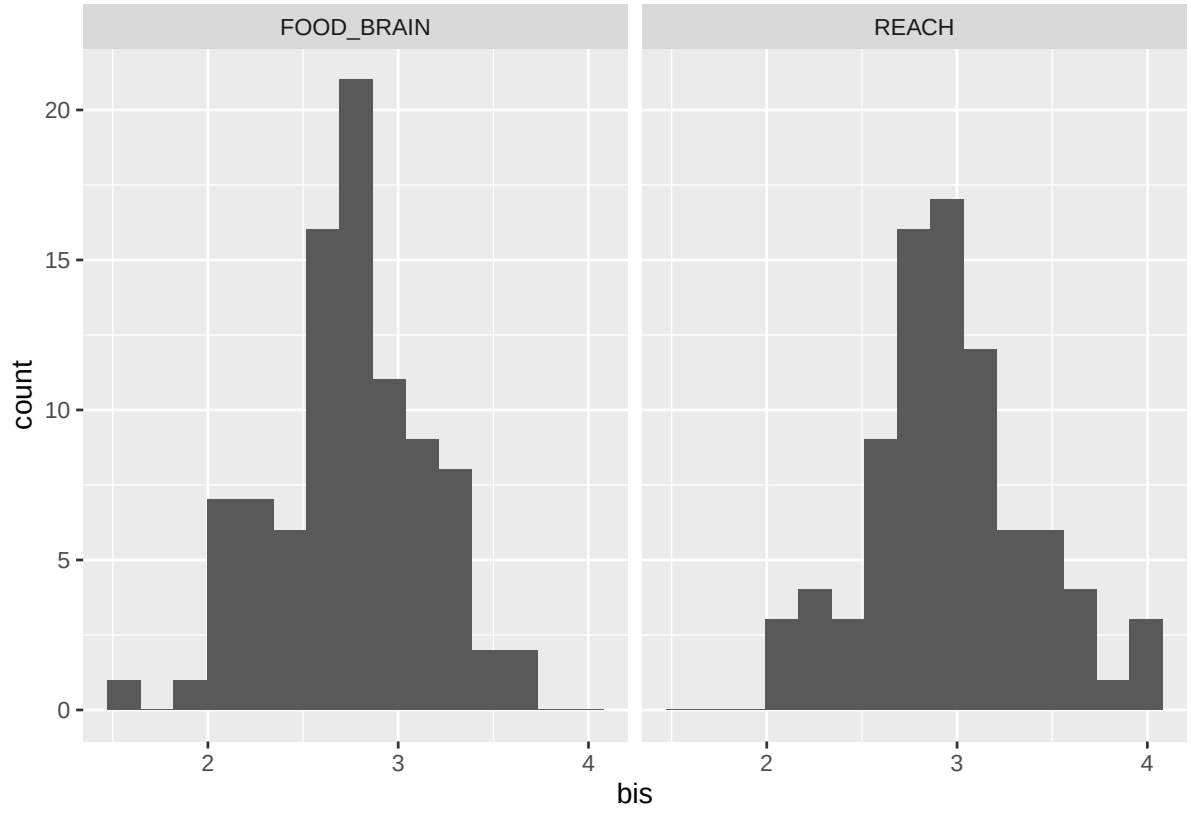
```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
```

```
## Warning: Removed 4 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

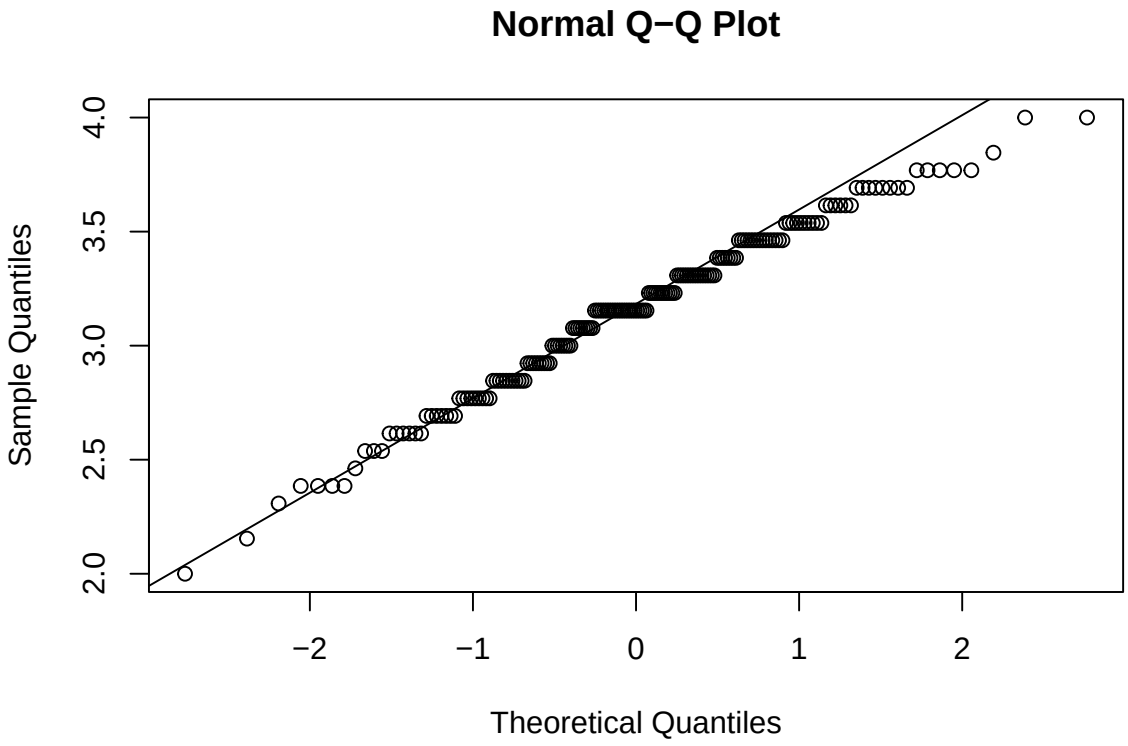



```
ggplot(thesis_data,aes(bis))+ geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (‘stat_bin()‘).
```




```
# For variable BAS
qqnorm(thesis_data$bas)
qqline(thesis_data$bas)
```



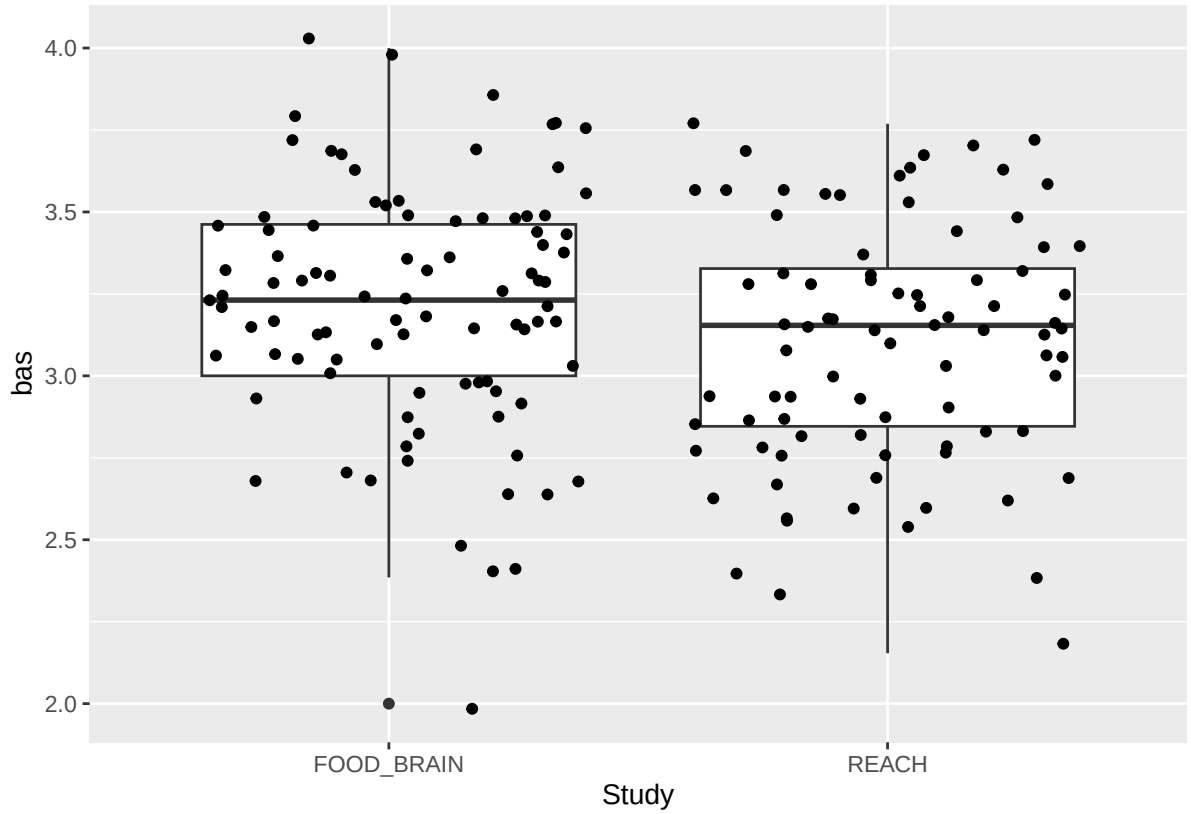
```r
shapiro.test(thesis_data$bas) #met normality
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bas
## W = 0.986, p-value = 0.07642
```

```r
#Visualizing BAS data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=bas)) + geom_boxplot() + geom_jitter(height = NULL)
```

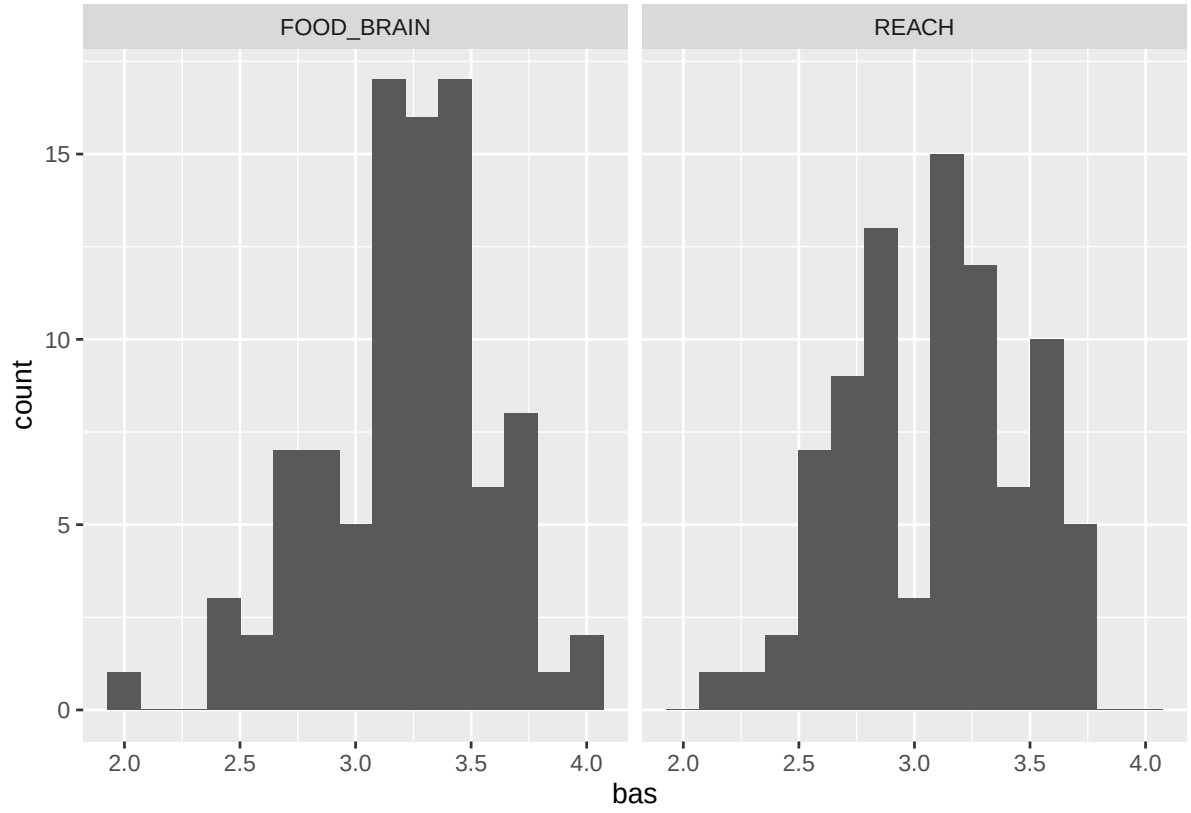
```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
```

```
## Warning: Removed 3 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

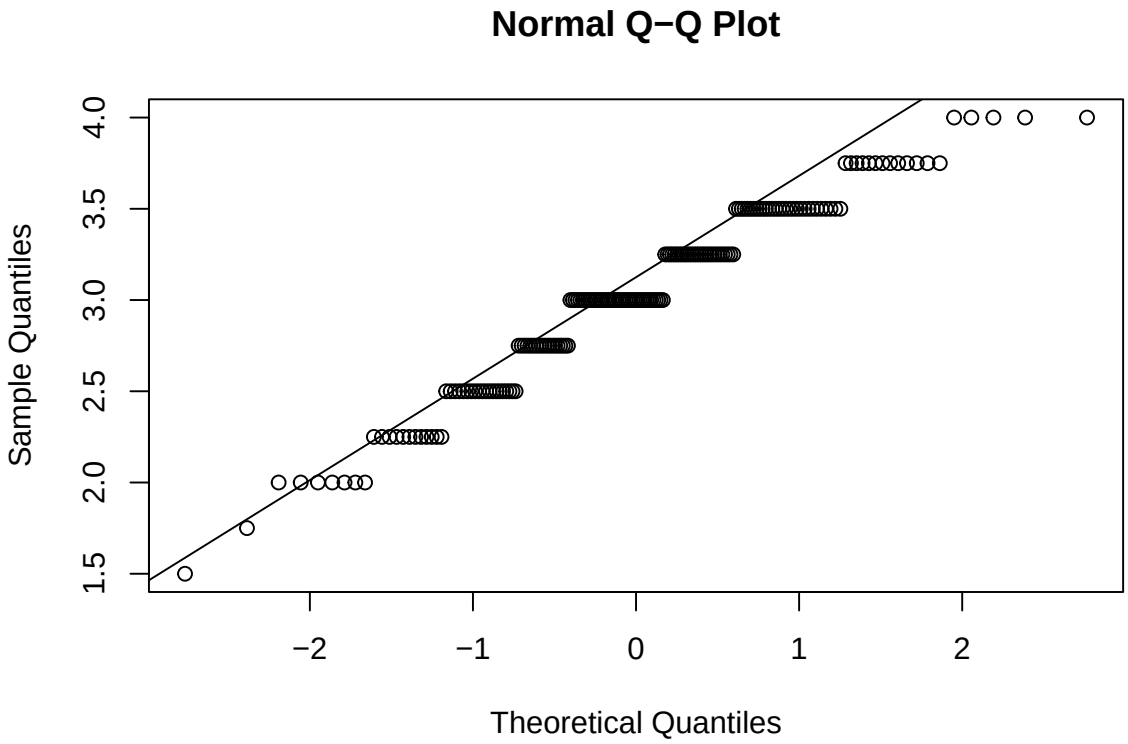



```r
ggplot(thesis_data,aes(bas))+geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```
# For variable BAS funseeking
qqnorm(thesis_data$bas_funseeking)
qqline(thesis_data$bas_funseeking)
```

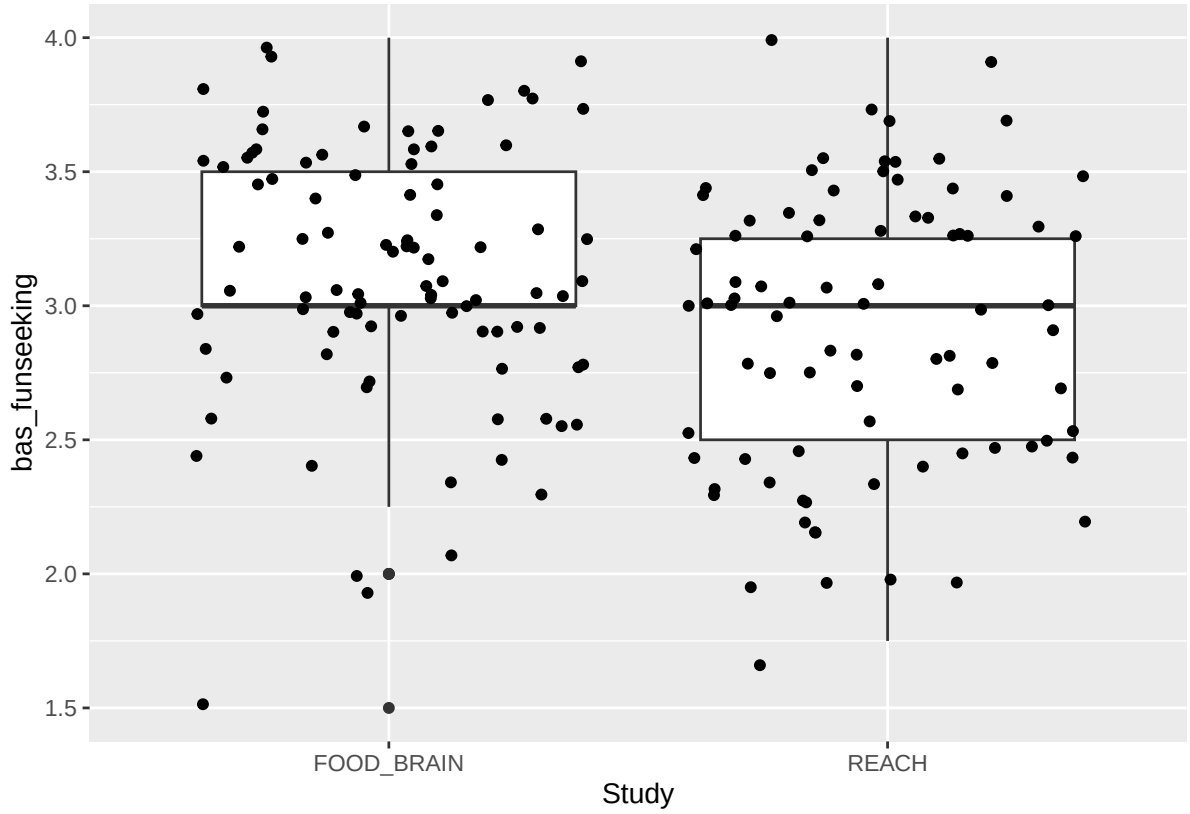


```r
shapiro.test(thesis_data$bas_funseeking) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bas_funseeking
## W = 0.96485, p-value = 0.0002044
```

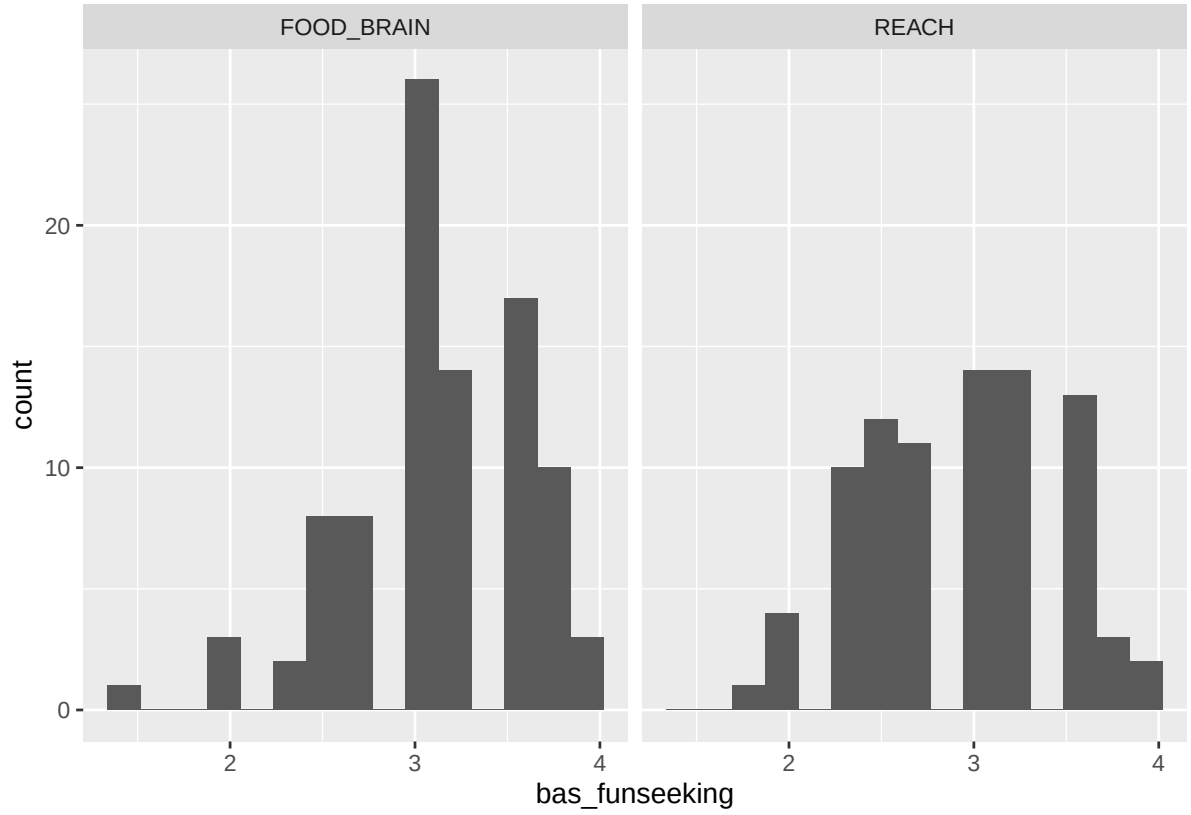
```r
#Visualizing BAS funseeking data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=bas_funseeking)) +geom_boxplot() +geom_jitter(height = NU
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
## Removed 3 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

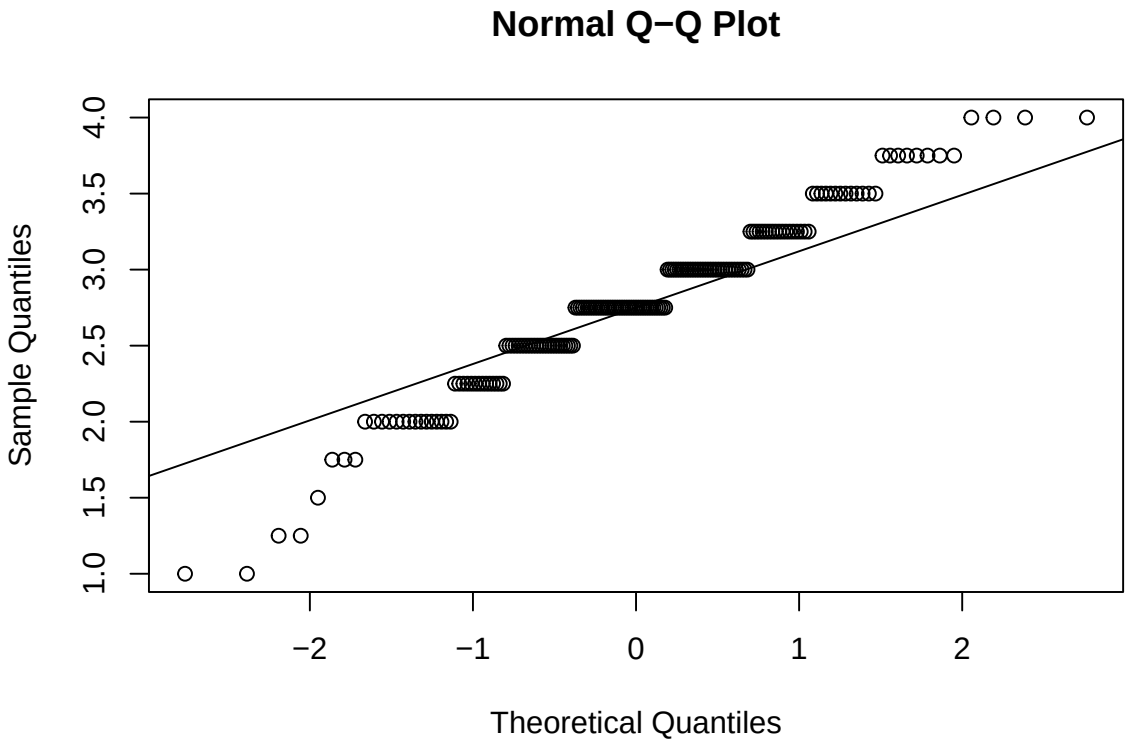



```r
ggplot(thesis_data,aes(bas_funseeking))+geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```r
# For variable BAS drive
qqnorm(thesis_data$bas_drive)
qqline(thesis_data$bas_drive)
```

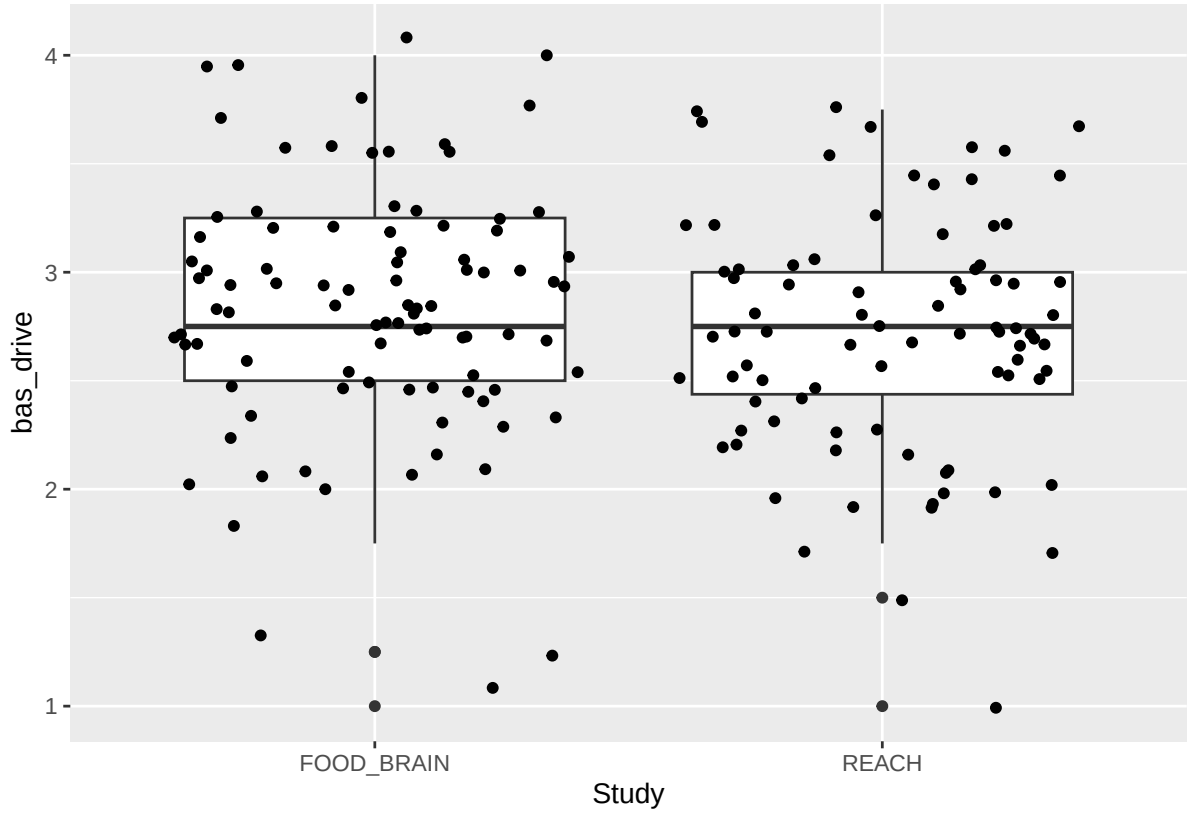


```r
shapiro.test(thesis_data$bas_drive) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bas_drive
## W = 0.9687, p-value = 0.0005395
```

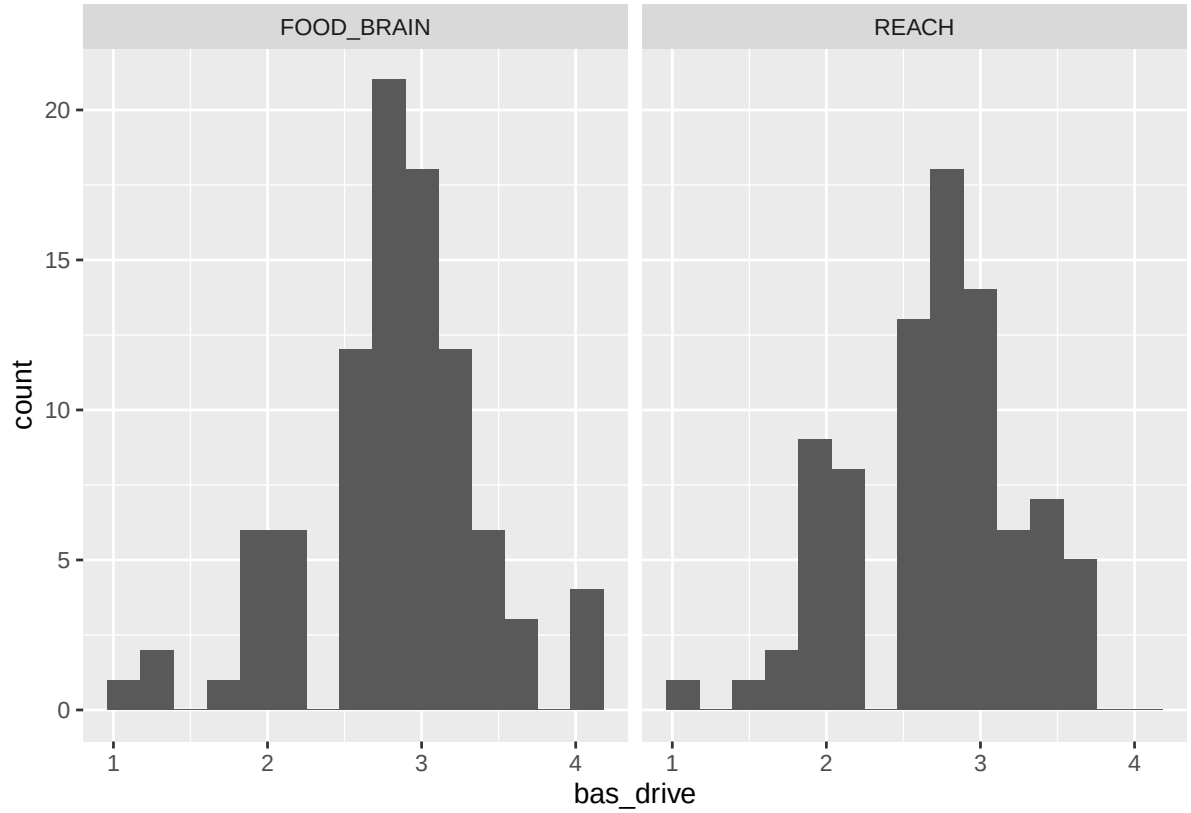
```r
#Visualizing BAS drive data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=bas_drive)) + geom_boxplot() + geom_jitter(height = NULL)
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
## Removed 3 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

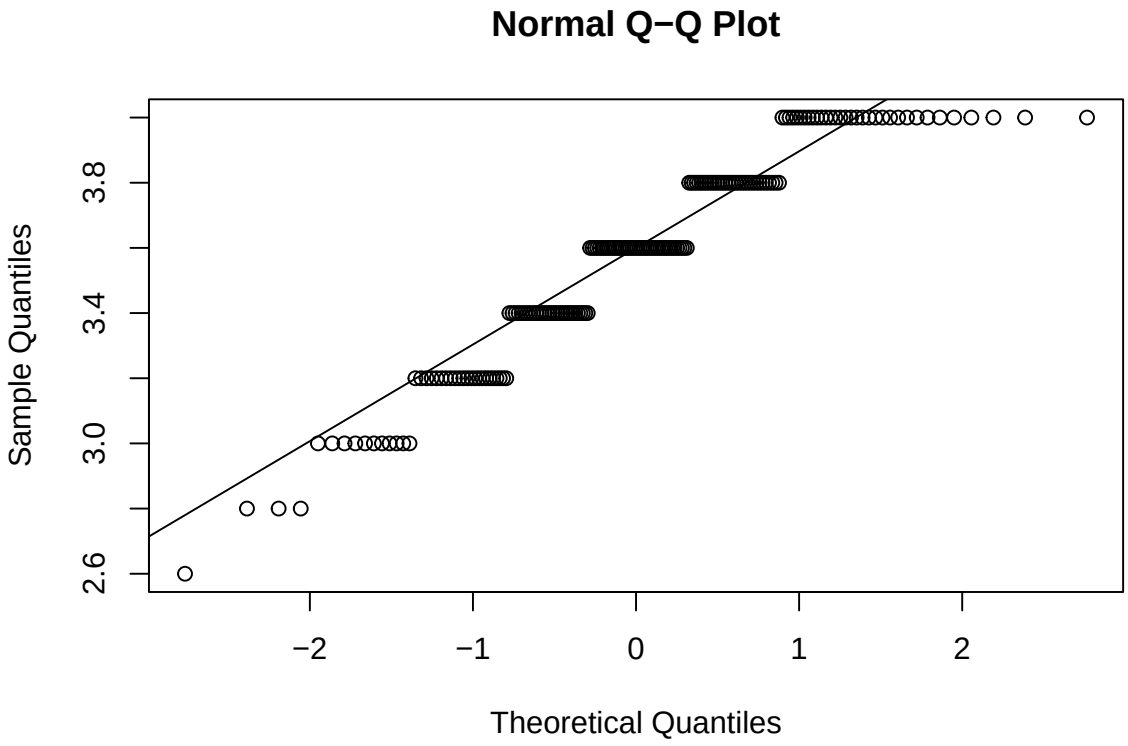



```r
ggplot(thesis_data,aes(bas_drive))+geom_histogram(bins=15)+ facet_grid(.~Study)
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```
# For variable BAS reward responsive
qqnorm(thesis_data$bas_rewardresp)
qqline(thesis_data$bas_rewardresp)
```

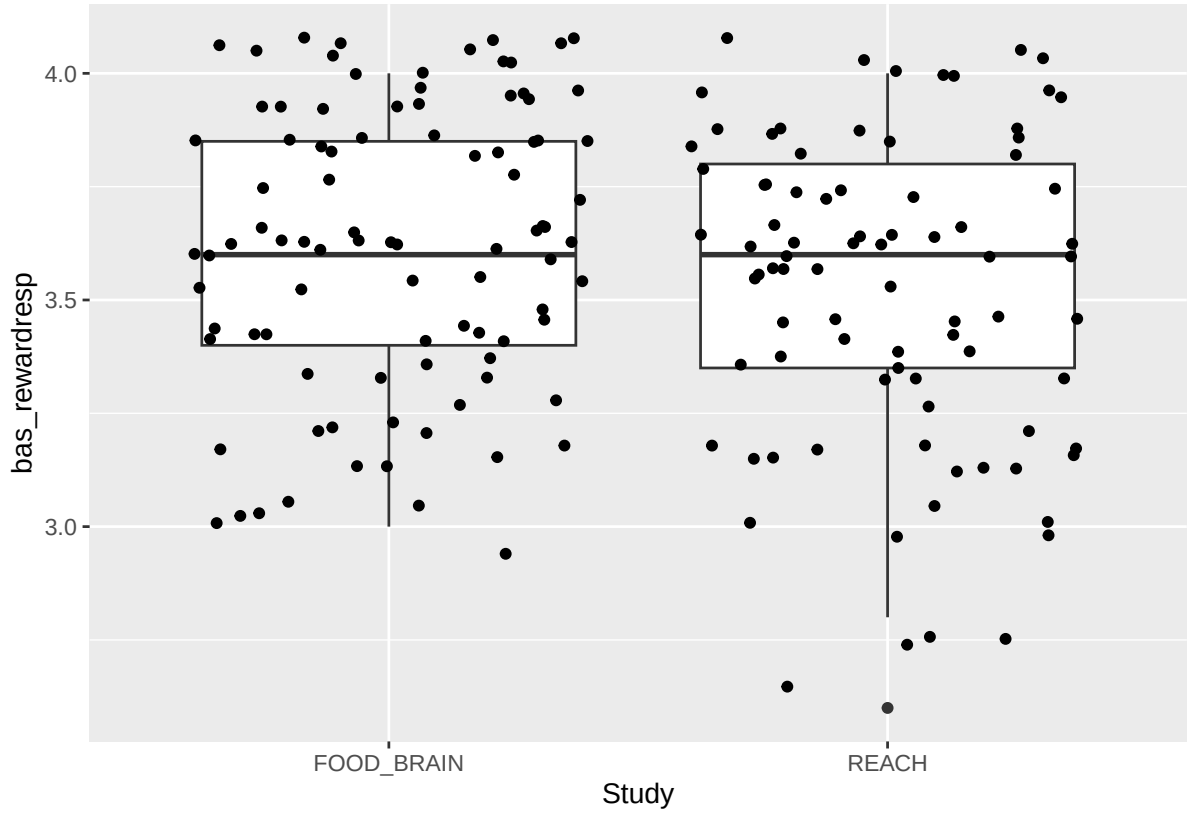


```
shapiro.test(thesis_data$bas_rewardresp) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bas_rewardresp
## W = 0.92994, p-value = 1.603e-07
```

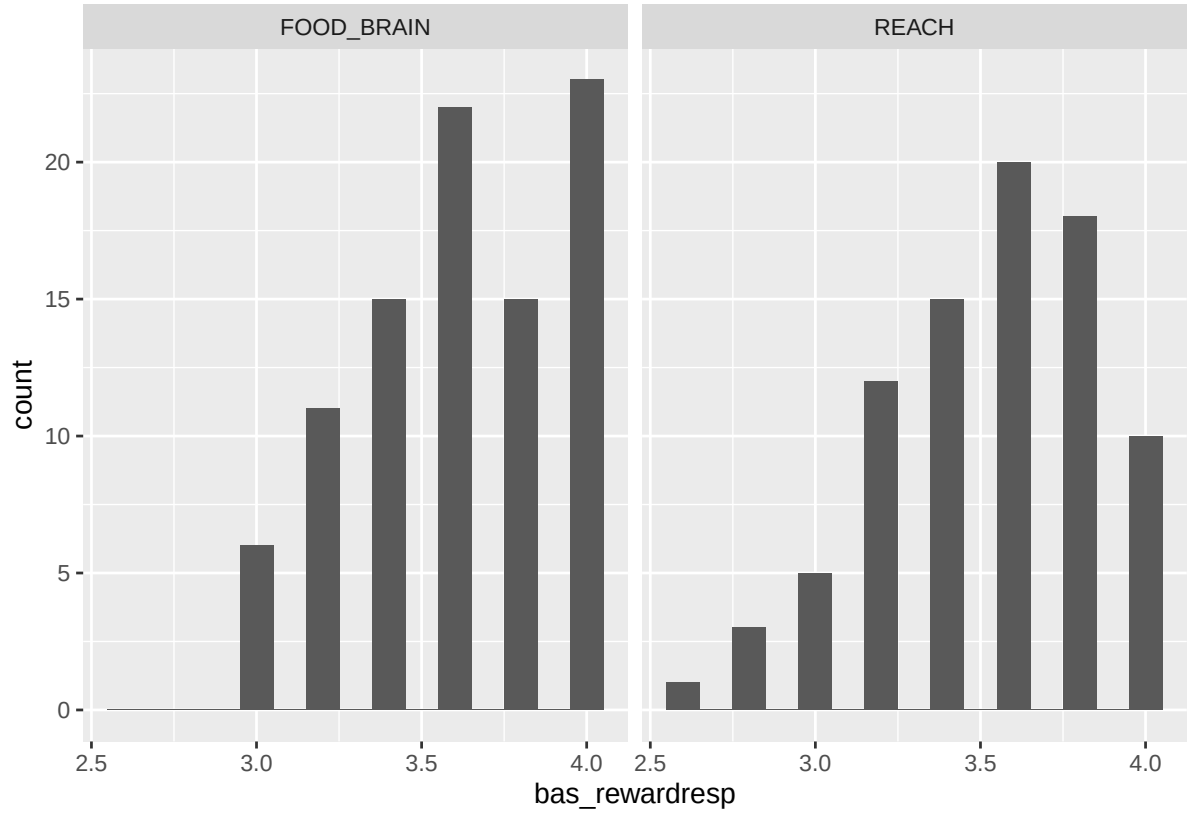
```
#Visualizing BAS reward responsive data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=bas_rewardresp)) +geom_boxplot() + geom_jitter(height = 
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
## Removed 3 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

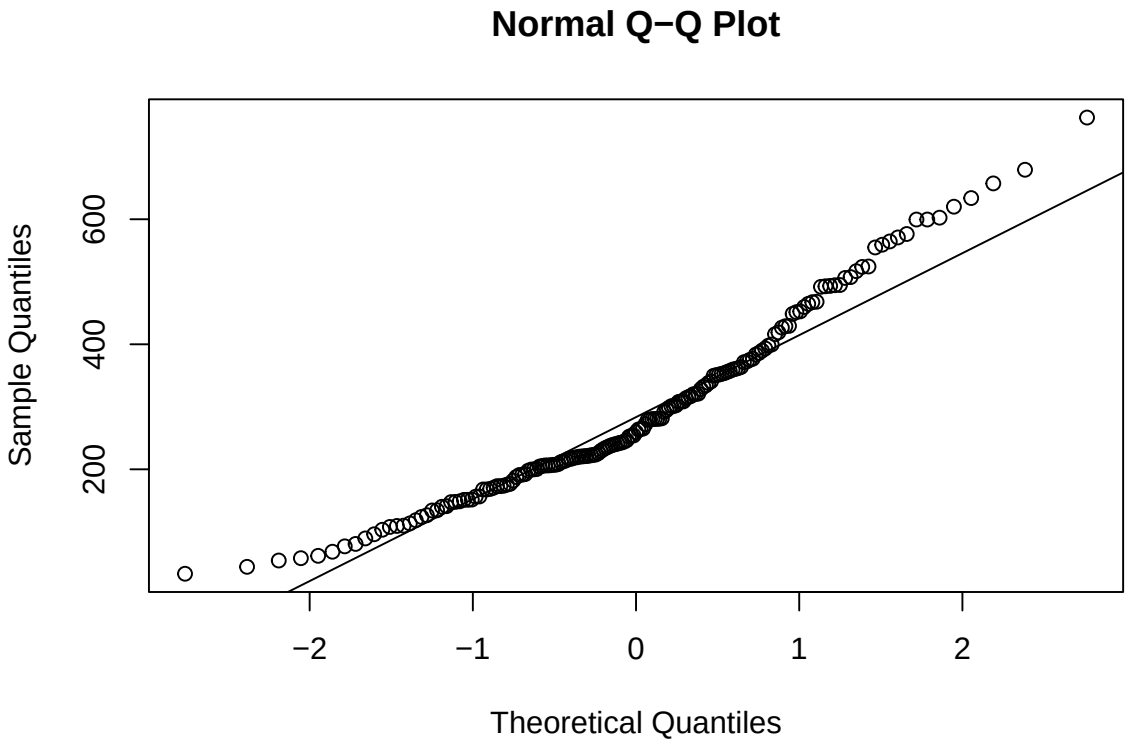



```
ggplot(thesis_data,aes(bas_rewardresp))+geom_histogram(bins=15)+ facet_grid(.~Study)
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```
# For variable Meal consumed in grams
qqnorm(thesis_data$meal_grams_consumed)
qqline(thesis_data$meal_grams_consumed)
```



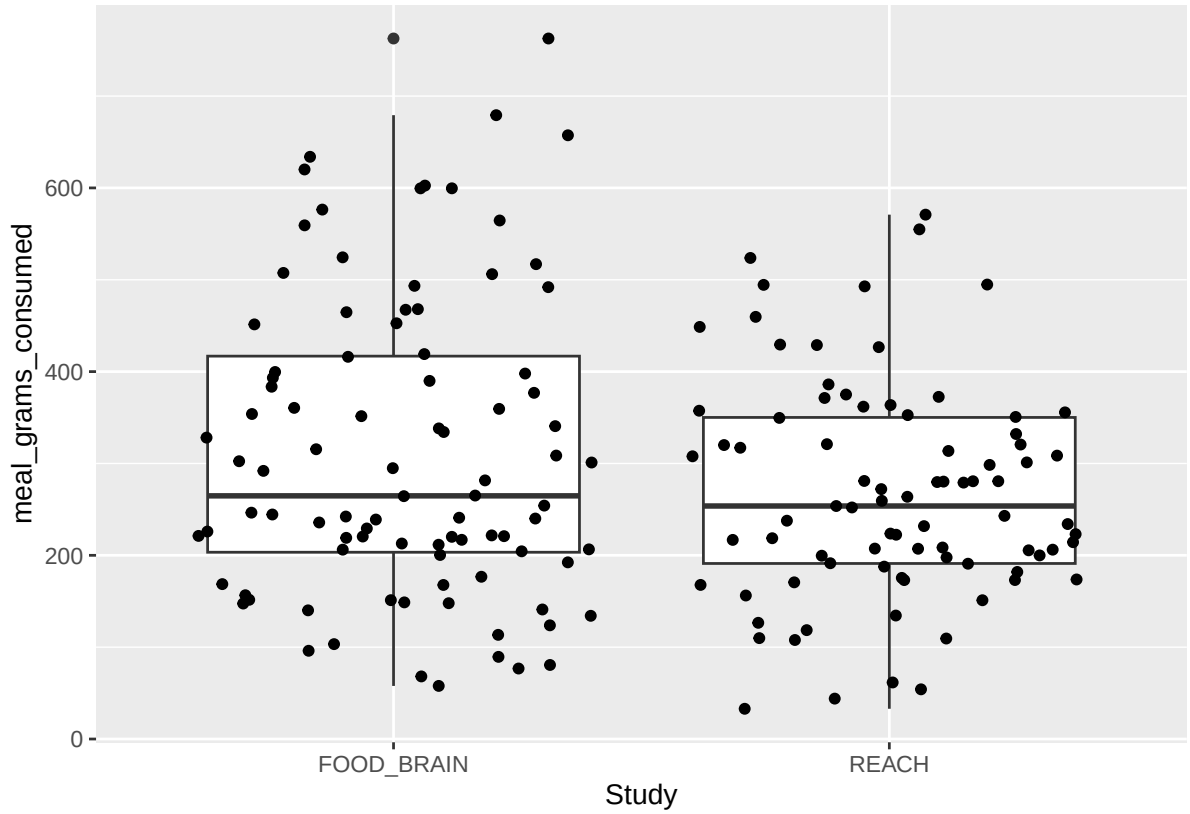
```r
shapiro.test(thesis_data$meal_grams_consumed) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$meal_grams_consumed
## W = 0.95722, p-value = 3.579e-05
```

```r
#Visualizing Meal consumed in grams data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=meal_grams_consumed)) + geom_boxplot() + geom_jitter(hei
```

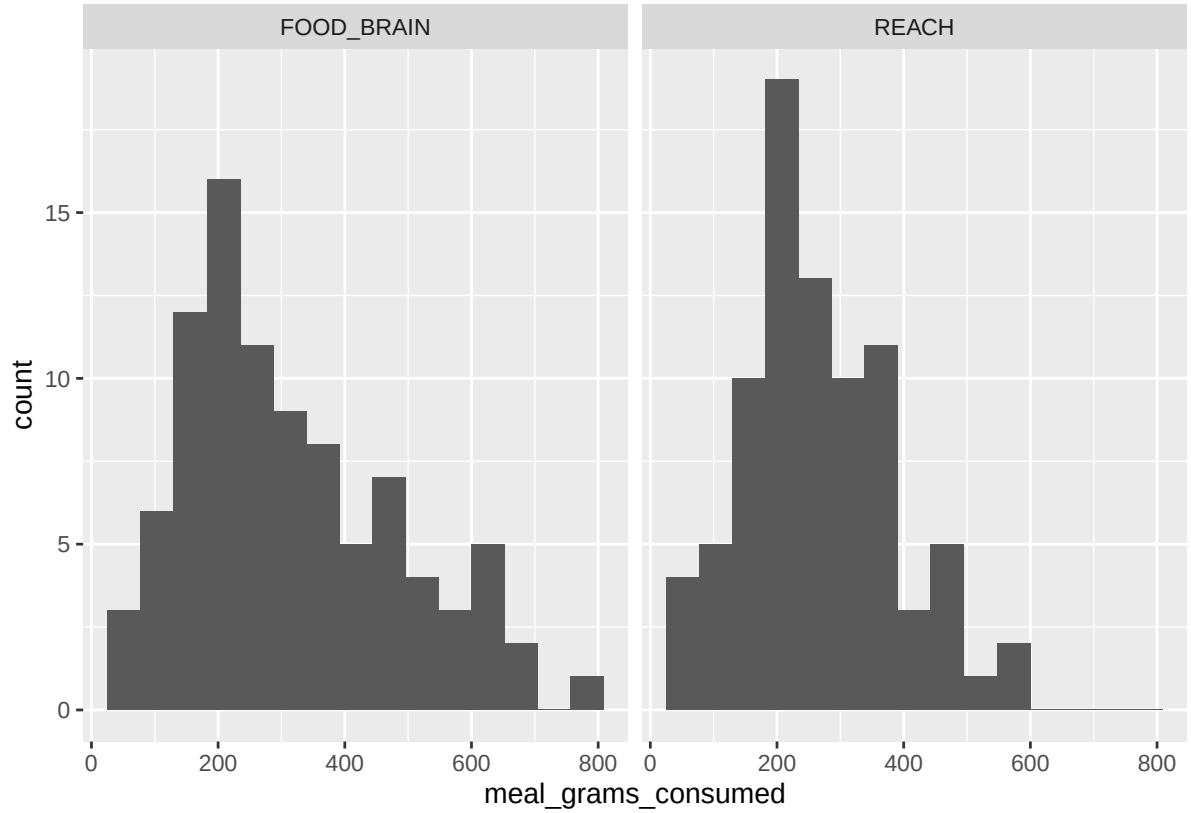
```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
```

```
## Warning: Removed 4 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

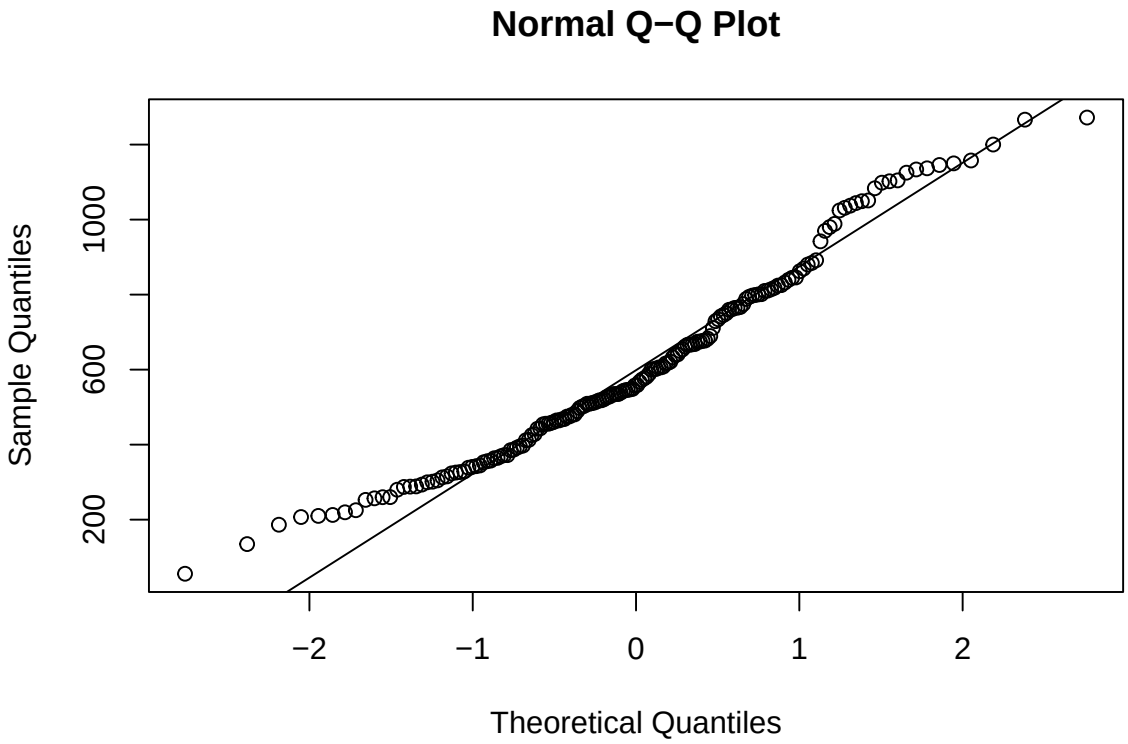



```r
ggplot(thesis_data,aes(meal_grams_consumed))+geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```
# For variable Meal consumed in kcal
qqnorm(thesis_data$meal_kcal_consumed)
qqline(thesis_data$meal_kcal_consumed)
```



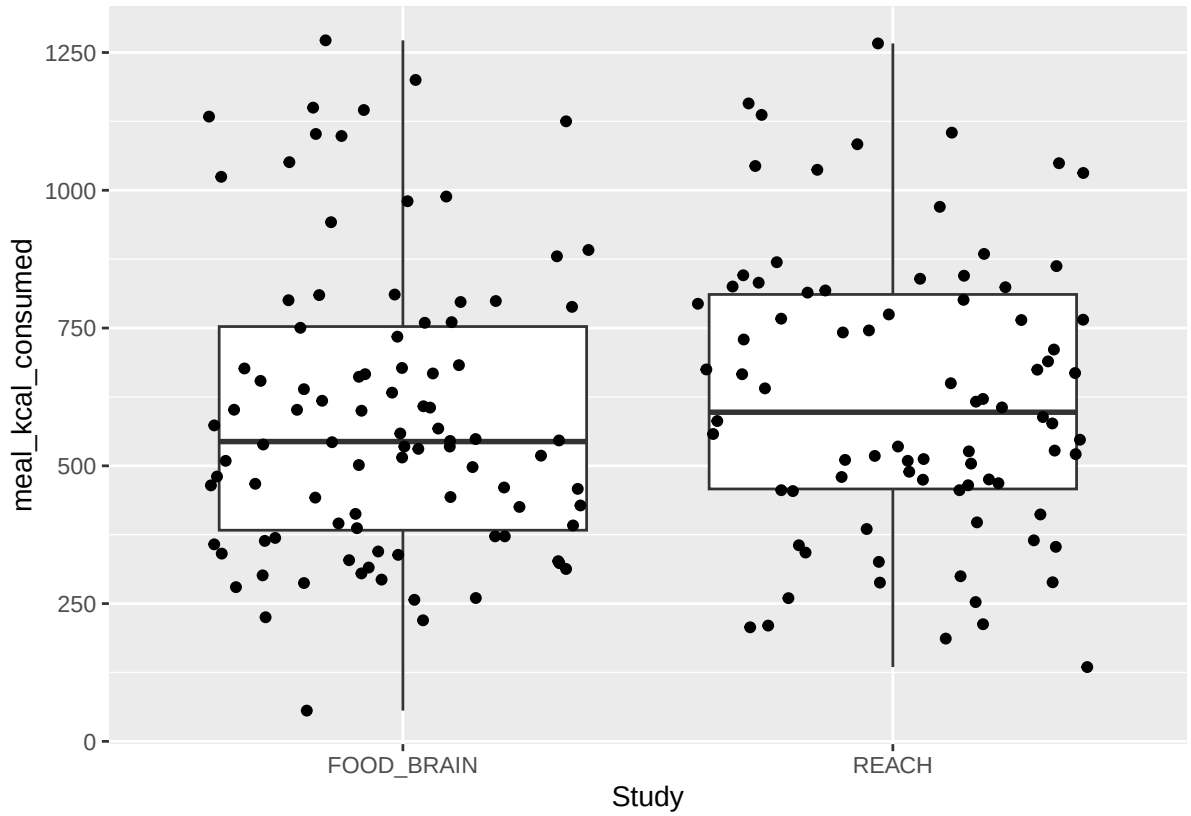
```
shapiro.test(thesis_data$meal_kcal_consumed) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$meal_kcal_consumed
## W = 0.96846, p-value = 0.0005531
```

```
#Visualizing Meal consumed in kcal data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=meal_kcal_consumed)) + geom_boxplot() + geom_jitter(heigh
```

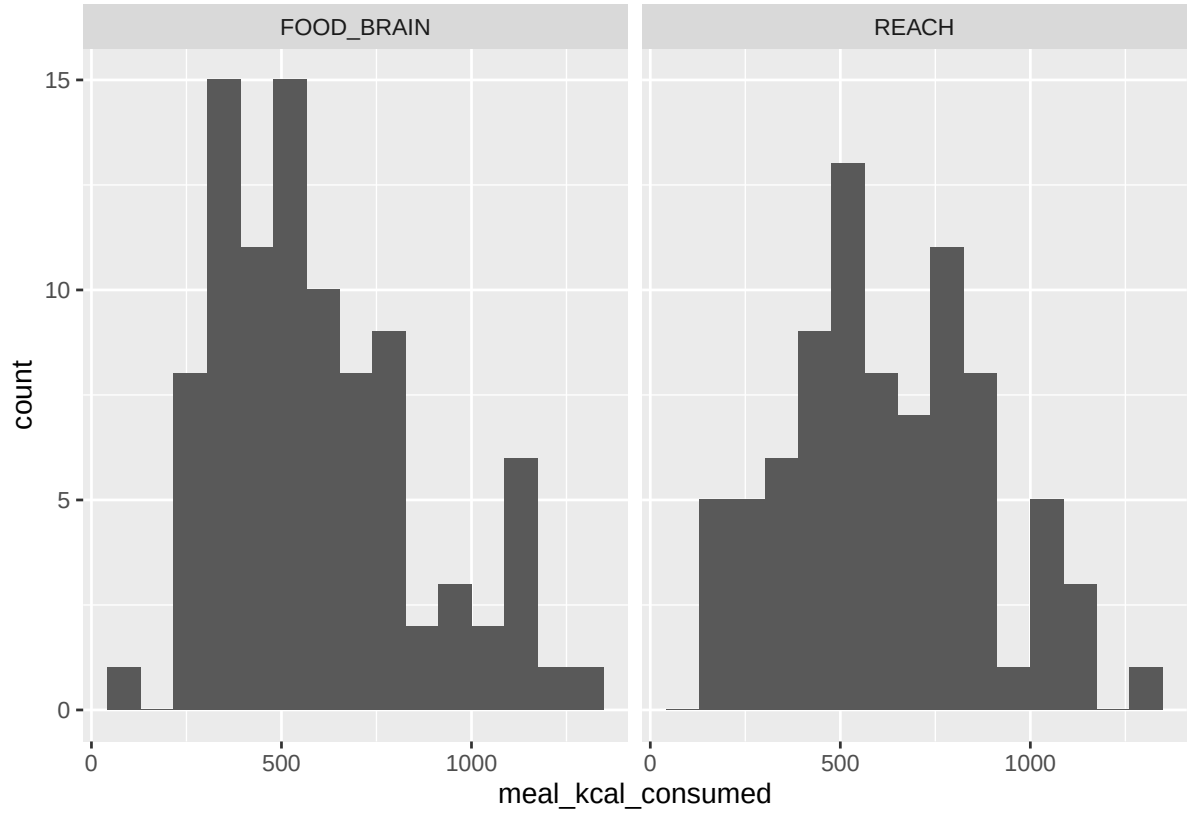
```
## Warning: Removed 5 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
```

```
## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

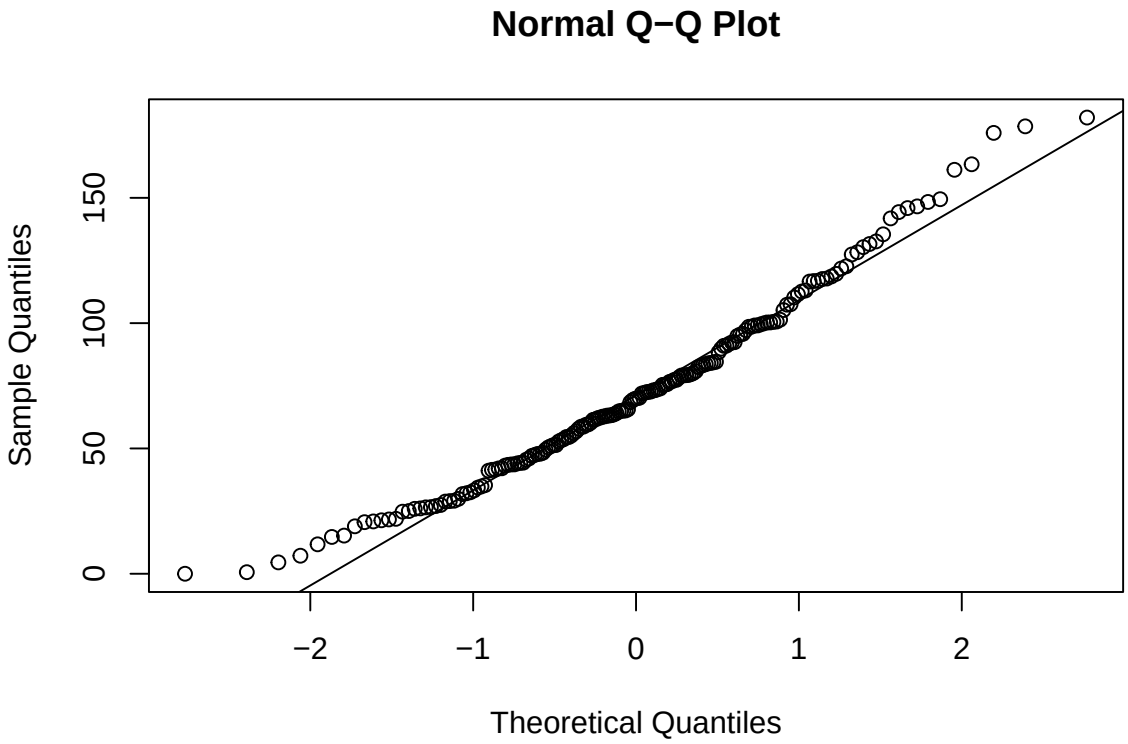



```
ggplot(thesis_data,aes(meal_kcal_consumed))+geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 5 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```
# For variable EAH consumed in grams
qqnorm(thesis_data$eah_grams_consumed_foodonly)
qqline(thesis_data$eah_grams_consumed_foodonly)
```



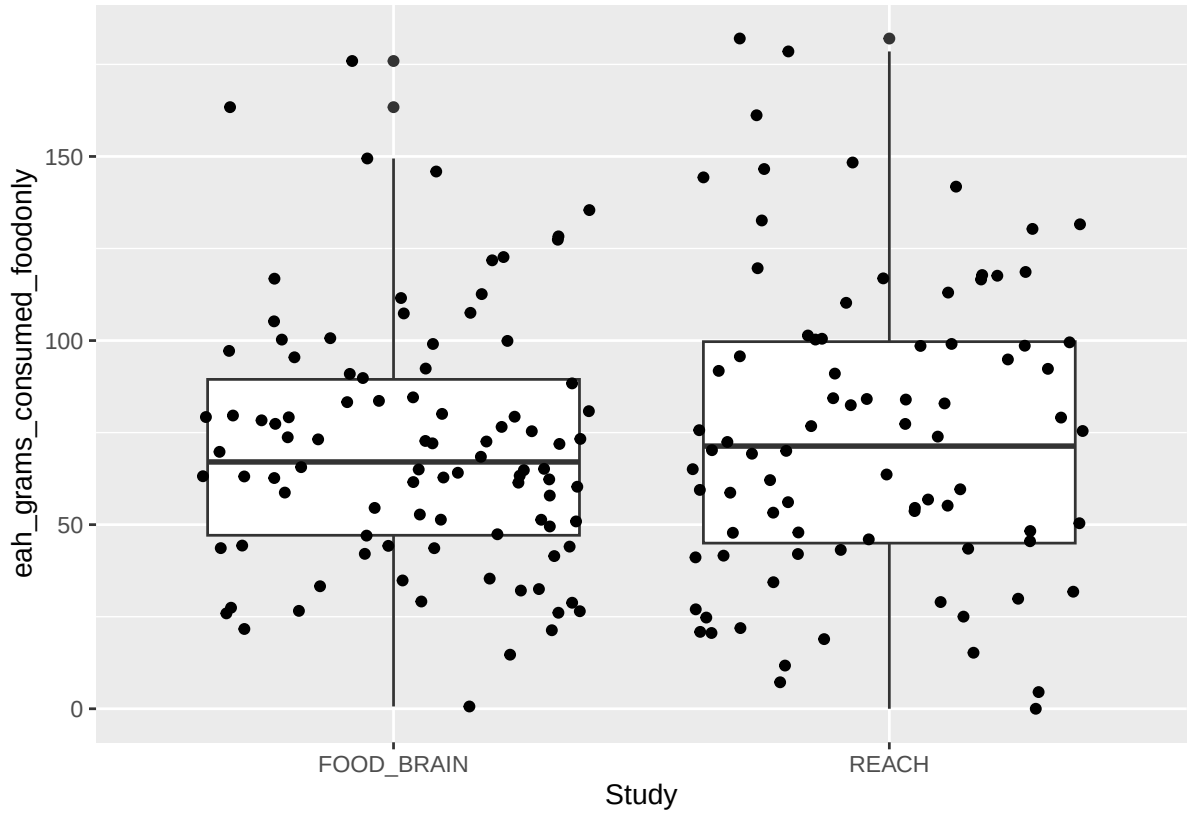
```
shapiro.test(thesis_data$eah_grams_consumed_foodonly) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$eah_grams_consumed_foodonly
## W = 0.97611, p-value = 0.003732
```

```
#Visualizing EAH consumed in grams data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=eah_grams_consumed_foodonly)) +geom_boxplot() + geom_jitt
```

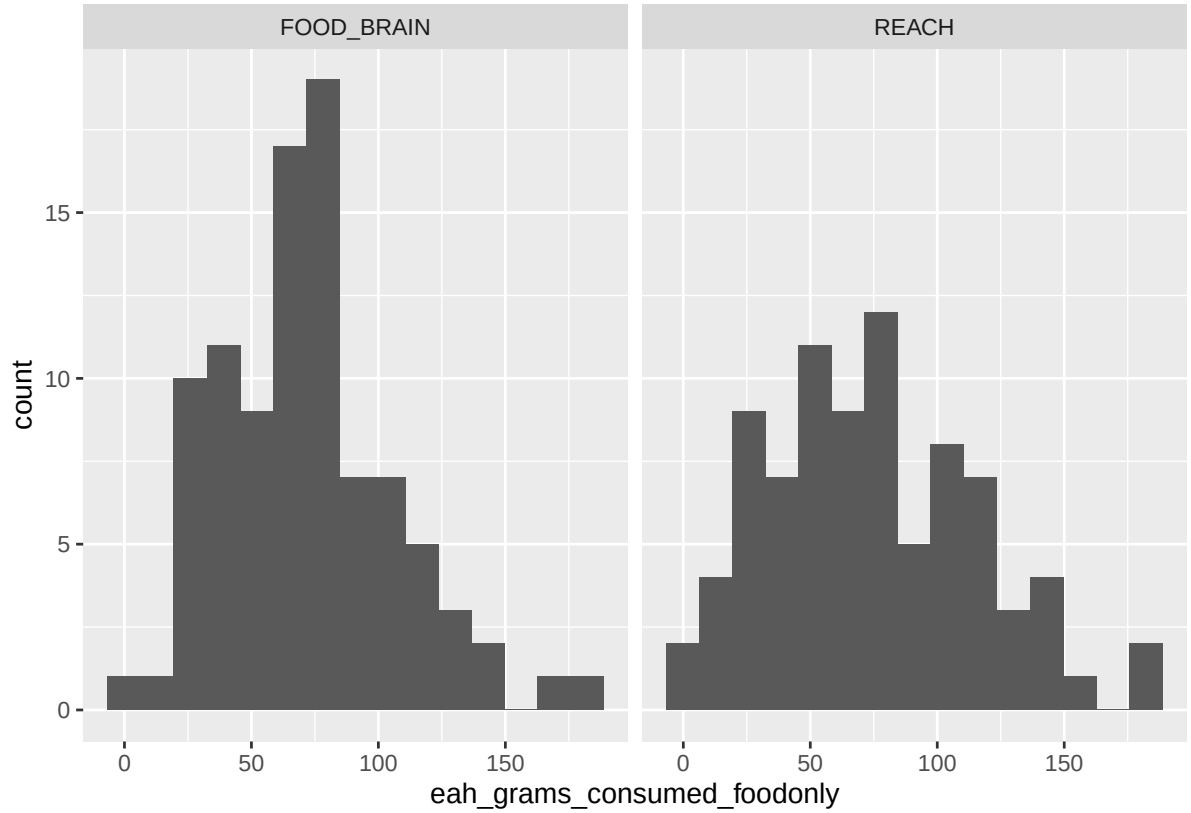
```
## Warning: Removed 1 row containing non-finite outside the scale range
## (‘stat_boxplot()‘).
```

```
## Warning: Removed 1 row containing missing values or values outside the scale range
## (‘geom_point()‘).
```

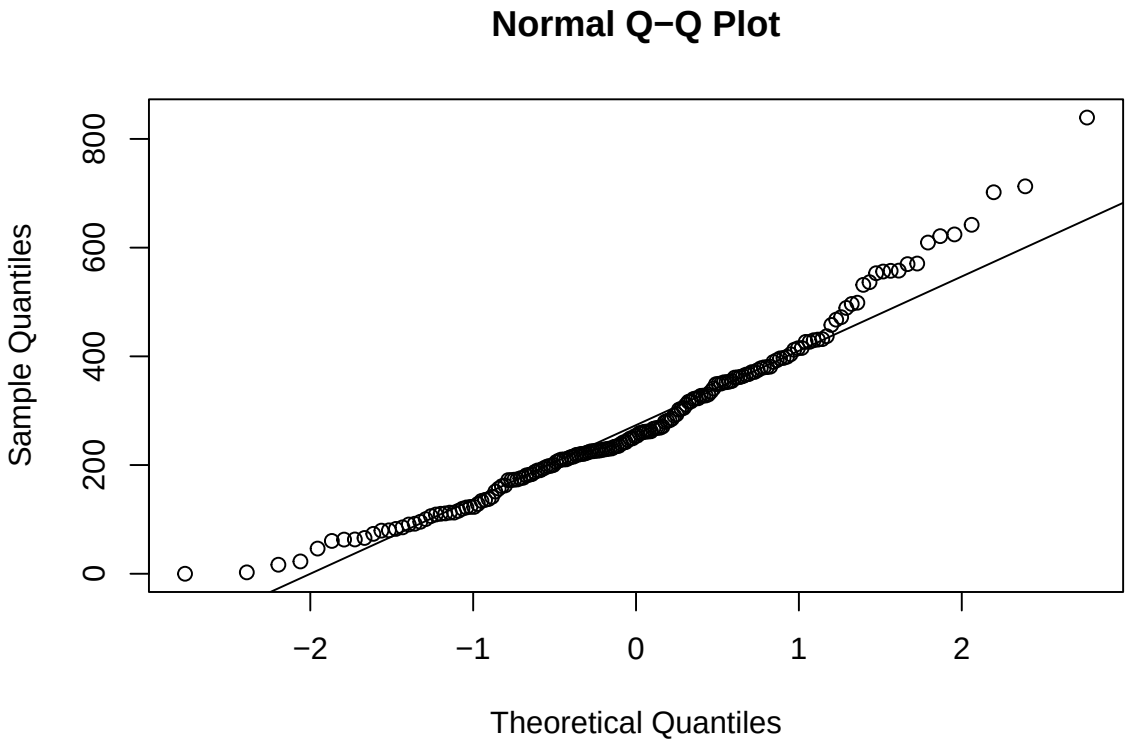



```
ggplot(thesis_data,aes(eah_grams_consumed_foodonly))+geom_histogram(bins=15)+facet_grid(.~St
```

```
## Warning: Removed 1 row containing non-finite outside the scale range
## (‘stat_bin()‘).
```




```
# For variable EAH consumed in kcal
qqnorm(thesis_data$eah_kcal_consumed)
qqline(thesis_data$eah_kcal_consumed)
```

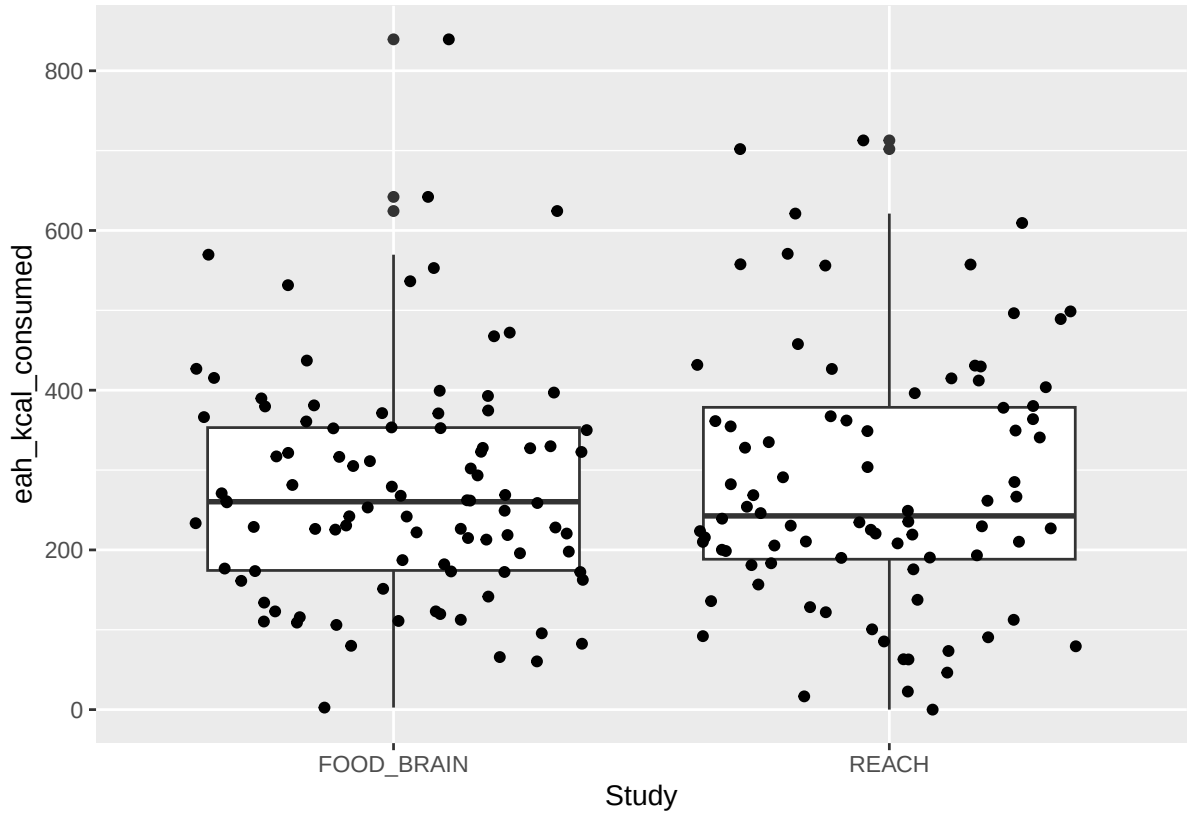


```r
shapiro.test(thesis_data$eah_kcal_consumed) #not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$eah_kcal_consumed
## W = 0.96228, p-value = 9.95e-05
```

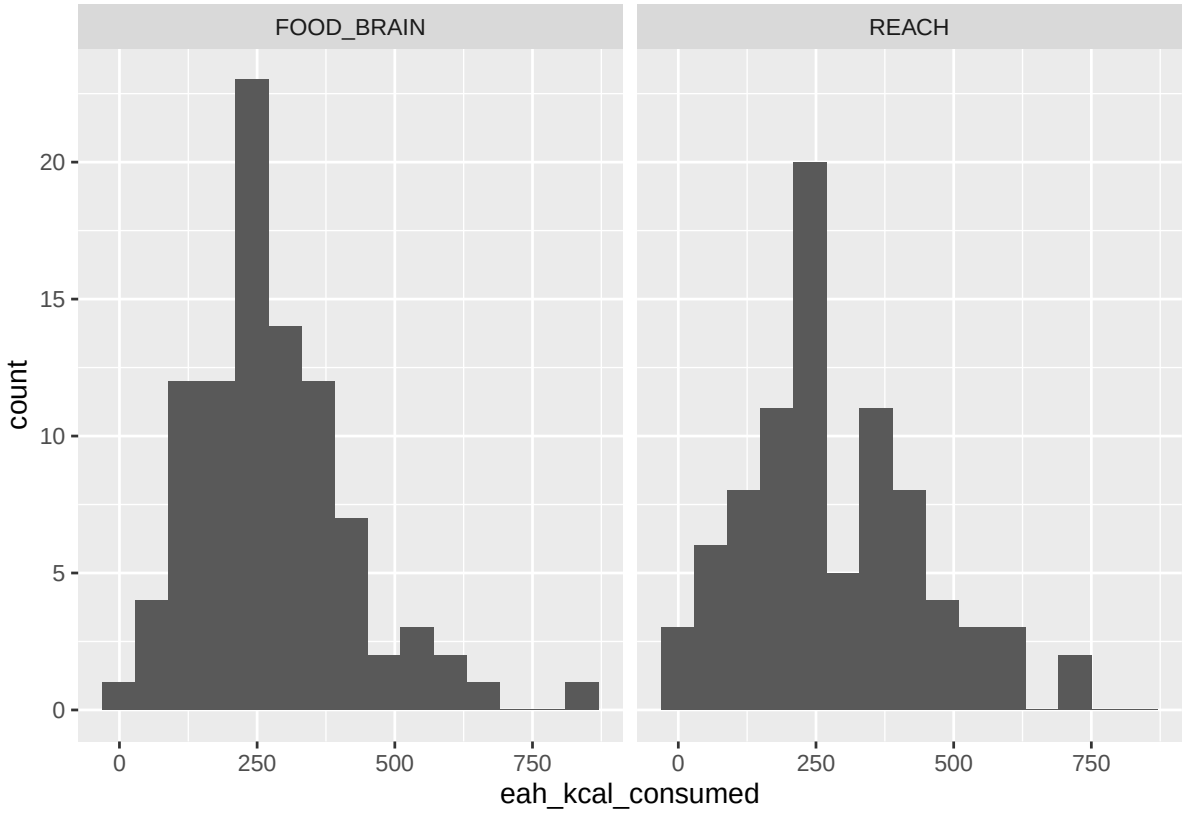
```r
#Visualizing EAH consumed in kcal data by Study, boxplot and histogram
ggplot(thesis_data, aes(x=Study, y=eah_kcal_consumed)) + geom_boxplot() + geom_jitter(height
```

```
## Warning: Removed 1 row containing non-finite outside the scale range (‘stat_boxplot()‘).
## Removed 1 row containing missing values or values outside the scale range
## (‘geom_point()‘).
```




```r
ggplot(thesis_data,aes(eah_kcal_consumed))+geom_histogram(bins=15)+facet_grid(.~Study)
```

```
## Warning: Removed 1 row containing non-finite outside the scale range
## (‘stat_bin()‘).
```



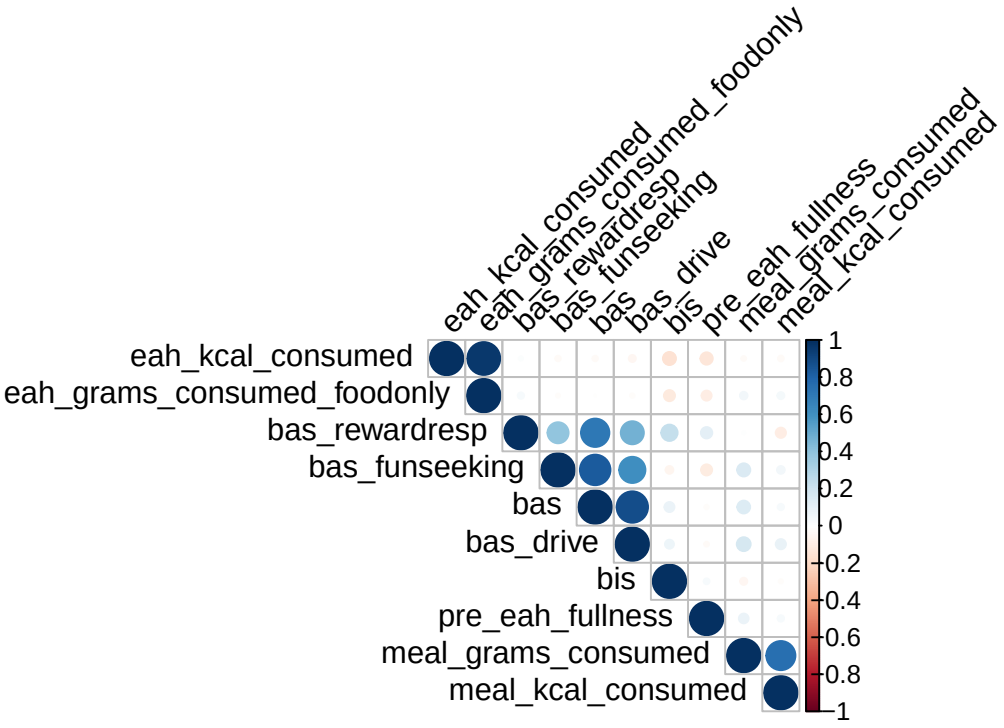
While some of the variables didn't pass the shapiro normality test but after looking at the qqplots of these variables we can consider them as normal.

3.Corrplots

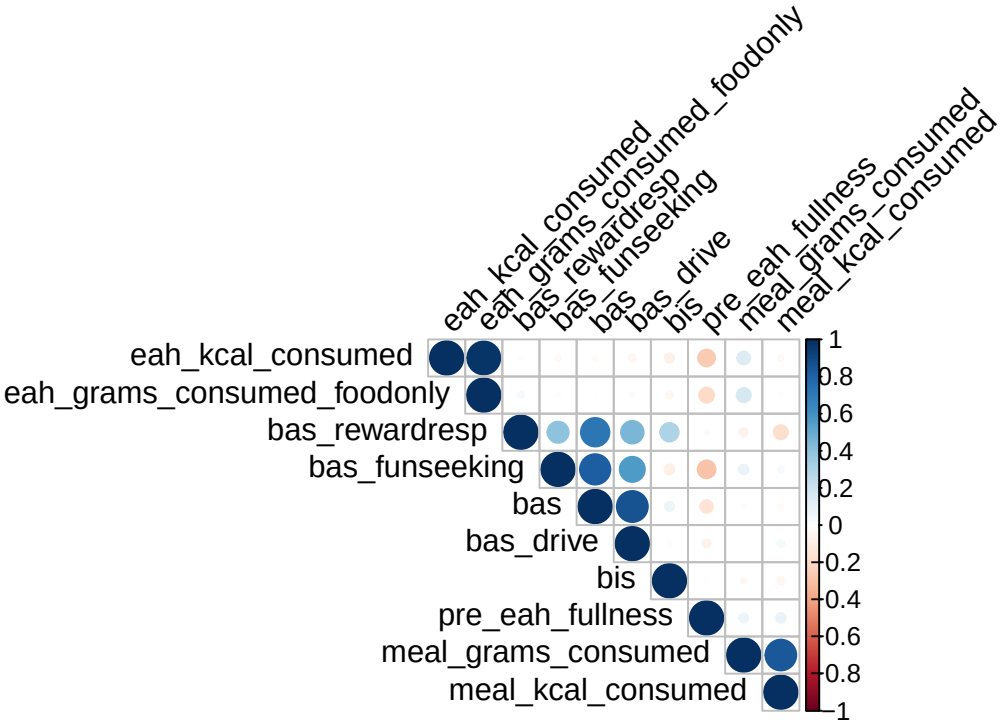
```
library(corrplot)
```

```
## corrplot 0.95 loaded
```

```
cor_all <- cor(thesis_data[c("bis", "bas","bas_funseeking","bas_drive", "bas_rewardresp", "
                             "meal_kcal_consumed","eah_kcal_consumed", "eah_grams_consumed_

cor_reach <- cor(thesis_data[thesis_data$Study == "REACH", c("bis", "bas","bas_funseeking","

cor_fb <- cor(thesis_data[thesis_data$Study == "FOOD_BRAIN", c("bis", "bas","bas_funseeking"


corrplot(cor_all, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
```




```
corrplot(cor_reach, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
```



```
corrplot(cor_fb, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
```


```
# 1. Relationship between BIS and EAH

## BIS is not associated with EAH gram intake
cor.test(thesis_data$bis, thesis_data$eah_grams_consumed_foodonly,
         use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bis and thesis_data$eah_grams_consumed_foodonly
## t = -1.4532, df = 172, p-value = 0.148
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.25472716  0.03928264
## sample estimates:
##        cor
## -0.1101308
```

```
## BIS is associated with EAH kcal intake
cor.test(thesis_data$bis, thesis_data$eah_kcal_consumed,
         use = "pairwise.complete.obs")
```

```
##
```

```
##  Pearson's product-moment correlation
##
## data:  thesis_data$bis and thesis_data$eah_kcal_consumed
## t = -2.0264, df = 172, p-value = 0.04427
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.294774354 -0.004022544
## sample estimates:
##       cor
## -0.152701
```

```
#2. Relationship between BAS and EAH

## BAS is not associated with EAH gram intake
cor.test(thesis_data$bis, thesis_data$eah_grams_consumed_foodonly,
         use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bis and thesis_data$eah_grams_consumed_foodonly
## t = -1.4532, df = 172, p-value = 0.148
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.25472716  0.03928264
## sample estimates:
##        cor
## -0.1101308
```

```
## BAS is not associated with EAH kcal intake
cor.test(thesis_data$bas, thesis_data$eah_kcal_consumed,
         use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas and thesis_data$eah_kcal_consumed
## t = -0.34611, df = 173, p-value = 0.7297
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1739694  0.1225161
## sample estimates:
##         cor
## -0.02630509
```

```
#3. Relationship between BAS funseeking and EAH

## BAS funseeking is not associated with EAH gram intake
cor.test(thesis_data$bas_funseeking,
         thesis_data$eah_grams_consumed_foodonly, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_funseeking and thesis_data$eah_grams_consumed_foodonly
## t = -0.18597, df = 173, p-value = 0.8527
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1621409  0.1344873
## sample estimates:
##         cor
## -0.01413783
```

```
## BAS funseeking is not associated with EAH kcal intake
cor.test(thesis_data$bas_funseeking,
         thesis_data$eah_kcal_consumed, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_funseeking and thesis_data$eah_kcal_consumed
## t = -0.34928, df = 173, p-value = 0.7273
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1742029  0.1222788
## sample estimates:
##        cor
## -0.0265458
```

```
#4. Relationship between BAS drive and EAH

## BAS drive is not associated with EAH gram intake
cor.test(thesis_data$bas_drive,
         thesis_data$eah_grams_consumed_foodonly, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_drive and thesis_data$eah_grams_consumed_foodonly
## t = -0.23044, df = 173, p-value = 0.818
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1654303  0.1311669
## sample estimates:
##         cor
## -0.01751707
```

```
## BAS drive is not associated with EAH kcal intake
cor.test(thesis_data$bas_drive,
         thesis_data$eah_kcal_consumed, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_drive and thesis_data$eah_kcal_consumed
## t = -0.58045, df = 173, p-value = 0.5624
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1911803  0.1049419
## sample estimates:
##         cor
## -0.04408754
```

```
#5. Relationship between BAS reward responsive and EAH

## BAS reward responsive is not associated with EAH gram intake
cor.test(thesis_data$bas_rewardresp,
         thesis_data$eah_grams_consumed_foodonly, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_rewardresp and thesis_data$eah_grams_consumed_foodonly
## t = 0.47405, df = 173, p-value = 0.6361
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1129282  0.1833816
## sample estimates:
##        cor
## 0.03601829
```

```
## BAS reward responsive is not associated with EAH kcal intake
cor.test(thesis_data$bas_rewardresp,
         thesis_data$eah_kcal_consumed, use = "pairwise.complete.obs")
```

```
##
##  Pearson's product-moment correlation
##
## data:  thesis_data$bas_rewardresp and thesis_data$eah_kcal_consumed
## t = 0.2106, df = 173, p-value = 0.8334
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1326488  0.1639631
## sample estimates:
##        cor
## 0.01600938
```

Based on the correlations and corr plots we can see that `bis` is negativley related with `eah_kcal_consumed`

4. Conducting levene's test on `bis` and `eah_kcal_consumed` by Study and then t-test on `bis` and `eah_kcal_consumed` to see if there is study effect.

```r
library(car)
```

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

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

```r
#For bis
leveneTest(
bis~as.factor(Study), data=thesis_data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0027 0.9584
##       173
```

```r
#For eah_kcal_consumed
leveneTest(
eah_kcal_consumed~as.factor(Study), data=thesis_data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.5361 0.2169
##       176
```

```r
#Assumptions for homegenity in variances are met

#Conducting indepedent t-test on bis to see study effect
t.test(thesis_data[thesis_data$Study == "REACH",]$bis,
       thesis_data[thesis_data$Study  == "FOOD_BRAIN",]$bis,
       alternative = "two.sided", var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data:  thesis_data[thesis_data$Study == "REACH", ]$bis and thesis_data[thesis_data$Study
## t = 3.6665, df = 173, p-value = 0.000327
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1057088 0.3522326
## sample estimates:
## mean of x mean of y
##   2.97619   2.74722
```

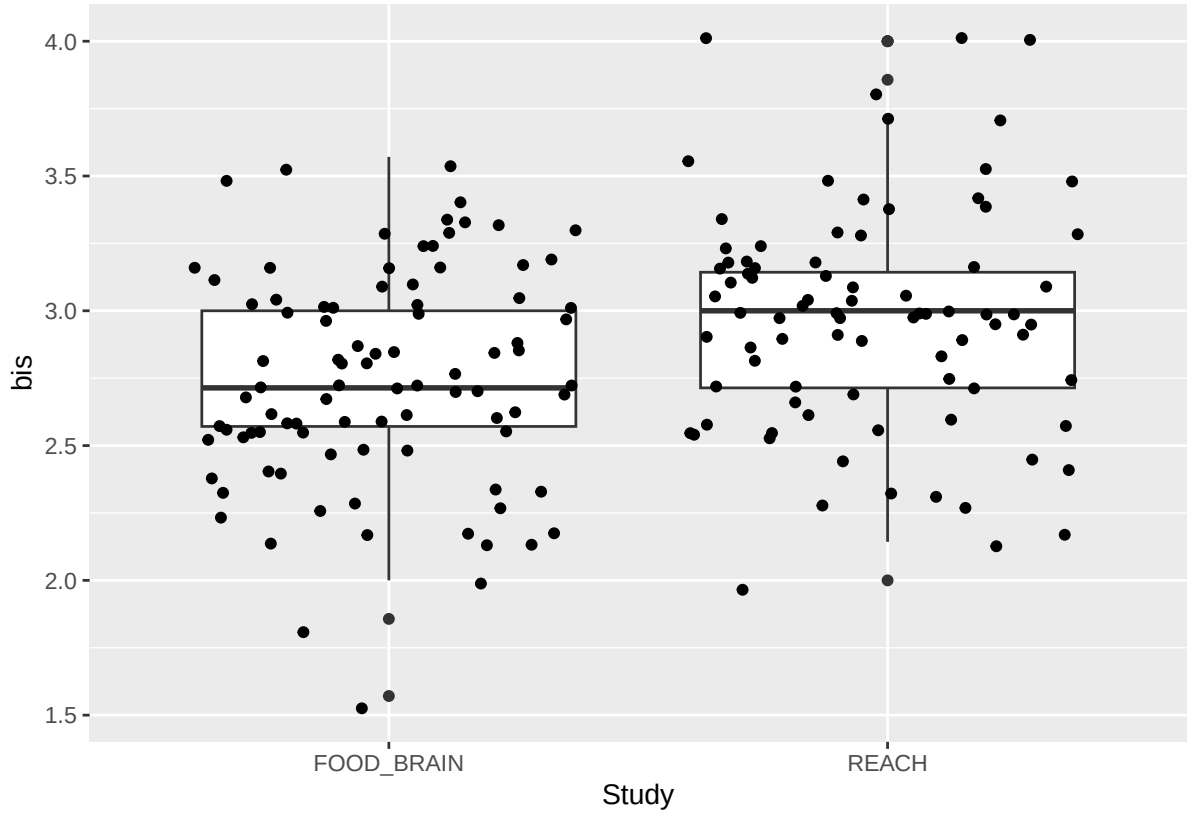
```r
#Conducting indepedent t-test on bis to see study effect
t.test(thesis_data[thesis_data$Study == "REACH",]$eah_kcal_consumed, thesis_data[thesis_data
       alternative = "two.sided", var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data:  thesis_data[thesis_data$Study == "REACH", ]$eah_kcal_consumed and thesis_data[thes
## t = 0.23976, df = 176, p-value = 0.8108
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -39.40483  50.30346
## sample estimates:
## mean of x mean of y
##  282.5406  277.0913
```

```r
#Visualizing
ggplot(thesis_data, aes(x=Study, y=bis)) +
geom_boxplot() +
geom_jitter(height = NULL)
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_boxplot()`).
```

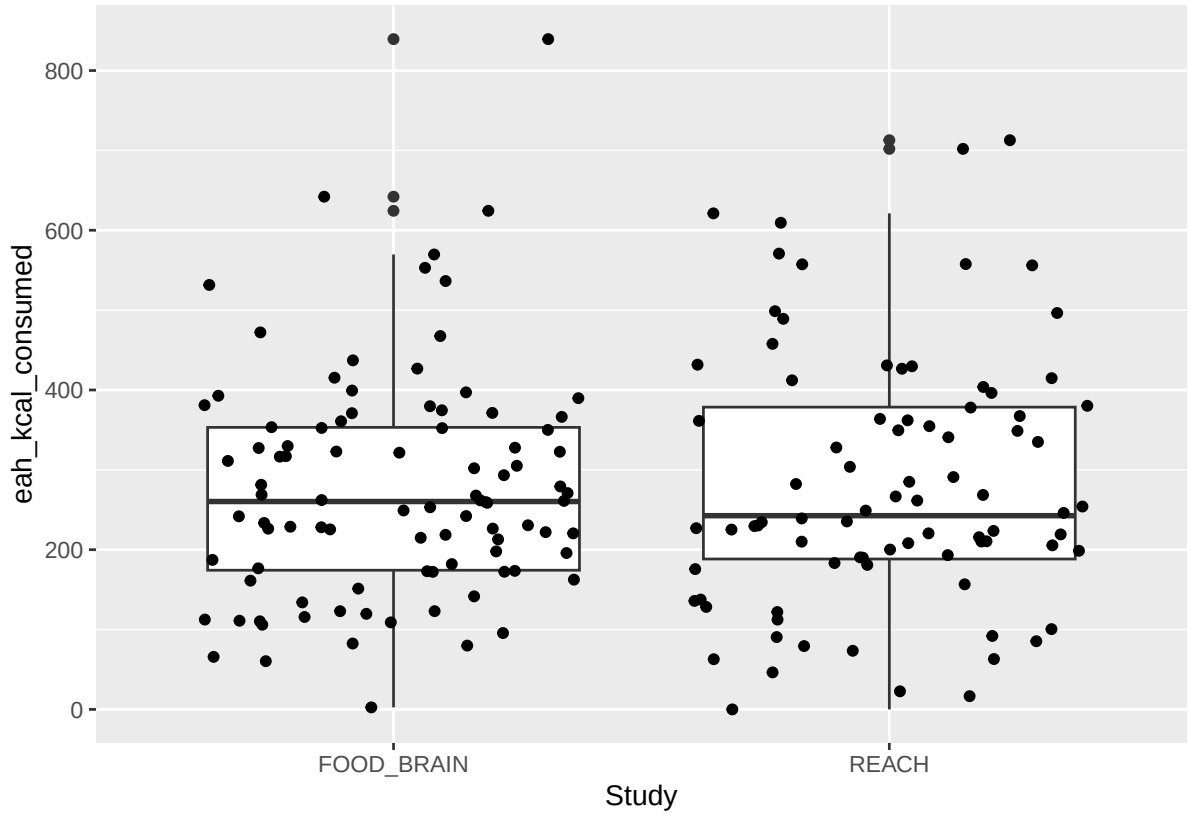
```
## Warning: Removed 4 rows containing missing values or values outside the scale range
## (`geom_point()`).
```



```
ggplot(thesis_data, aes(x=Study, y=eah_kcal_consumed)) +
  geom_boxplot() +
  geom_jitter(height = NULL)
```

```
## Warning: Removed 1 row containing non-finite outside the scale range
## (‘stat_boxplot()‘).
```

```
## Warning: Removed 1 row containing missing values or values outside the scale range
## (‘geom_point()‘).
```




```
thesis_data$Age.in.years
```

```
##   [1] 8.30 9.60 9.80 7.30 8.50 8.80 8.10 8.00 7.60 9.40 7.70 7.60 7.80 7.30 9.60
##  [16] 9.10 8.20 8.80 8.50 8.40 9.20 7.40 9.70 8.20 7.70 8.70 8.10 7.60 8.80 7.70
##  [31] 9.90 8.50 8.90 9.50 7.50 7.30 8.00 8.40 8.60 7.20 8.80 8.80 7.70 7.70   NA
##  [46] 9.30 7.70 7.80 9.80 7.10 7.30 8.20 7.70 8.00 7.60 8.70 8.10 8.30 7.20 9.20
##  [61] 9.60 9.50 7.20 9.40 8.20 7.30 8.60 8.80 8.80 9.90 7.30 8.30 8.00 8.40 7.20
##  [76] 9.20 8.90 7.40 7.80 8.50 9.20 7.10 9.80 7.70 8.84 7.46 7.07 7.38 7.82 7.03
##  [91] 8.65 7.18 7.68 7.00 7.48 8.22 7.67 7.39 7.18 7.77 8.81 7.68 7.79 8.32 7.25
## [106] 7.26 8.12 7.47 7.06 7.22 7.25 8.66 8.99 7.40 7.36 7.47 7.53 7.02 8.81 8.48
## [121] 8.14 7.34 7.86 8.92 8.26 7.79 8.47 8.33 7.05 8.91 7.17 8.24 7.33 7.41 7.24
## [136] 7.86 8.30 8.50 7.53 7.73 7.97 8.50 8.41 8.41 8.58 8.32 7.86 7.23 7.17 8.44
## [151] 8.71 8.61 7.44 8.51 8.07 7.33 7.26 7.33 7.42 7.80 8.44 8.63 7.36 8.51 7.84
## [166] 7.14 8.30 8.79 8.91 7.25 7.99 8.16 7.22 7.03 7.93 7.04 7.51 8.96 7.58
```

Based on these results, BIS scores are higher in REACH study and EAH consumption in kcal was similar in both the studies.

5. Linear regressions predicting EAH with covariates [sex + child bmi + age in years+ pre eah fullness, income] (no interactions) – no effects

```
model1 <- lm(eah_kcal_consumed ~ bis + Sex + Age.in.years + Child.BMI
             + Income + pre_eah_fullness, data = thesis_data)
summary(model1)
```

```
##
## Call:
## lm(formula = eah_kcal_consumed ~ bis + Sex + Age.in.years + Child.BMI +
##     Income + pre_eah_fullness, data = thesis_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -323.69 -104.78  -21.01   86.86  510.66
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -45.4120   202.0066  -0.225   0.8224
## bis                     -59.3086    28.3446  -2.092   0.0380 *
## SexMale                  23.8666    23.8026   1.003   0.3175
## Age.in.years             38.7347    17.2203   2.249   0.0259 *
## Child.BMI                 7.4366     8.2491   0.902   0.3687
## Income>$100,000         110.8061   108.2938   1.023   0.3078
## Income$20,000-$35,000    99.4185   125.0848   0.795   0.4279
## Income$36,000-$50,000   162.0122   115.3090   1.405   0.1620
## Income$51,000-$75,000   110.9349   110.5712   1.003   0.3172
## Income$76,000-$100,000   90.7284   109.3554   0.830   0.4080
## pre_eah_fullness         -0.6637     0.3435  -1.932   0.0551 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 149.8 on 159 degrees of freedom
##   (9 observations deleted due to missingness)
## Multiple R-squared:  0.1077, Adjusted R-squared:  0.0516
## F-statistic: 1.919 on 10 and 159 DF,  p-value: 0.04608
```

Based on the summary of the model of this multiple regression model we can see that higher BIS scores predicts a lower food intake in kcal (B=-60, p=0.04) in EAH paradigm.

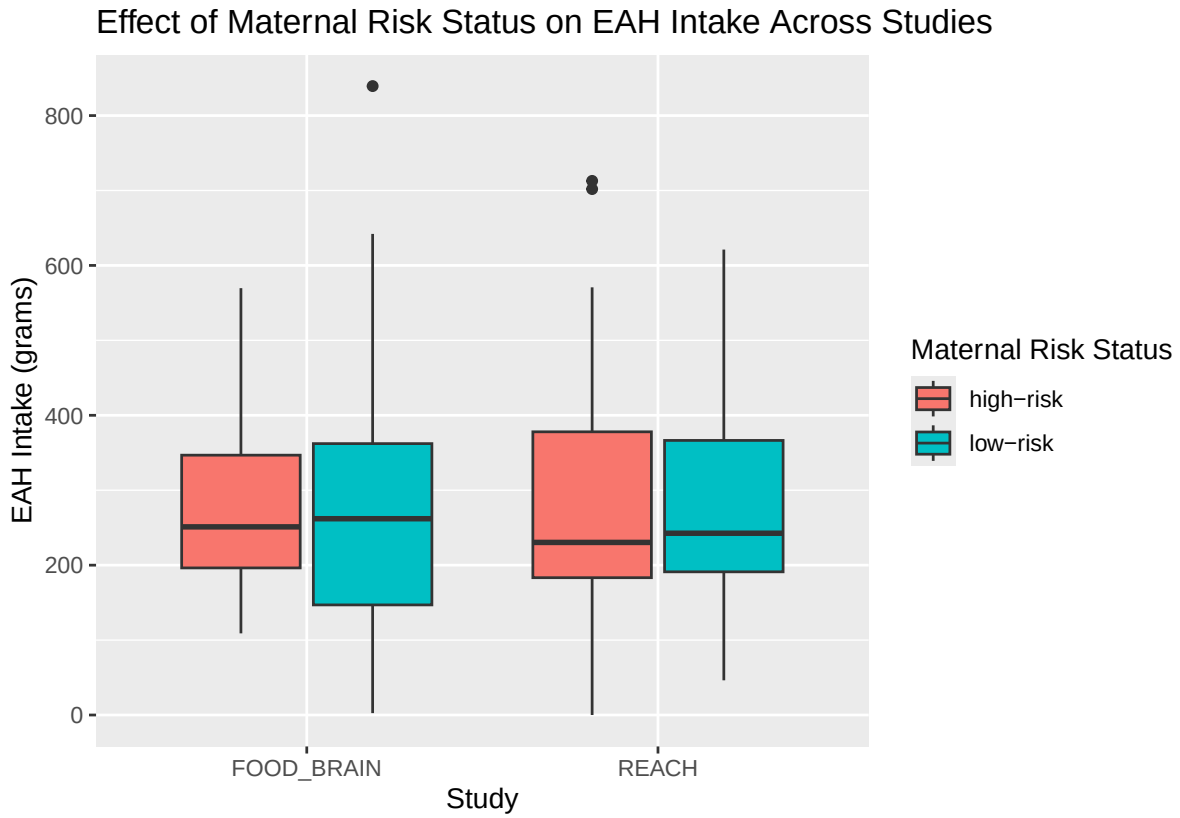
AIM 2: Does maternal risk status moderates the relationship between BIS, BAS and EAH

```
#Conducting 2 way ANOVA to see the effect of maternal risk status on EAH in kcal across both

thesis_data$Maternal.risk.status <- as.factor(thesis_data$Maternal.risk.status)
thesis_data$Study <- as.factor(thesis_data$Study)

anova_model <- aov(eah_kcal_consumed ~ Maternal.risk.status * Study, data = thesis_data)
summary(anova_model)
```

```
##                              Df  Sum Sq Mean Sq F value Pr(>F)
## Maternal.risk.status          1     702     702   0.030  0.862
## Study                         1     530     530   0.023  0.880
## Maternal.risk.status:Study    1     655     655   0.028  0.867
## Residuals                   173 4009072   23174
## 2 observations deleted due to missingness
```

```
#Visualization
maternal_data <- thesis_data %>% filter(!is.na(Study), !is.na(Maternal.risk.status))
library(ggplot2)
ggplot(maternal_data, aes(x = Study, y = eah_kcal_consumed, fill = Maternal.risk.status)) +
  geom_boxplot() +
  labs(title = "Effect of Maternal Risk Status on EAH Intake Across Studies",
       x = "Study",
       y = "EAH Intake (grams)",
       fill = "Maternal Risk Status")
```

```
## Warning: Removed 1 row containing non-finite outside the scale range
## (`stat_boxplot()`).
```



There wasn't any main effect of maternal risk status (p=0.87) and study(p=0.89) on EAH intake. Moreover, there wasn't any interaction effect between maternal risk status and study on EAH intake (p=0.87). Hence we can conclude that effect of maternal risk status on EAH paradigm was consistent in both the studies.

```
#Conducting moderation analysis adjusting for covariates
lm_eah_kcal_risk <- lm(eah_kcal_consumed ~ bis*Maternal.risk.status + pre_eah_fullness + Stu

summary(lm_eah_kcal_risk)
```

```
##
## Call:
## lm(formula = eah_kcal_consumed ~ bis * Maternal.risk.status +
##     pre_eah_fullness + Study + Child.BMI + Age.in.years + Sex +
##     Income, data = thesis_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -324.31  -93.64  -22.07   79.93  464.74
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    -185.0340   222.3309  -0.832   0.4066
## bis                               5.2541    39.8523   0.132   0.8953
## Maternal.risk.statuslow-risk    362.4266   158.3605   2.289   0.0235 *
## pre_eah_fullness                 -0.7023     0.3444  -2.039   0.0431 *
## StudyREACH                       -9.8158    25.7839  -0.381   0.7040
```

```
## Child.BMI                              6.6367     8.5817   0.773   0.4405
## Age.in.years                          41.6538    17.7052   2.353   0.0199 *
## SexMale                               26.8206    23.7586   1.129   0.2607
## Income>$100,000                       66.6211   109.1398   0.610   0.5425
## Income$20,000-$35,000                 46.2477   125.7886   0.368   0.7136
## Income$36,000-$50,000                102.8750   116.4163   0.884   0.3782
## Income$51,000-$75,000                 62.6119   111.2272   0.563   0.5743
## Income$76,000-$100,000                40.9441   110.2610   0.371   0.7109
## bis:Maternal.risk.statuslow-risk -131.0926    54.3772  -2.411   0.0171 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 148.3 on 155 degrees of freedom
##   (10 observations deleted due to missingness)
## Multiple R-squared:  0.1424, Adjusted R-squared:  0.07048
## F-statistic:  1.98 on 13 and 155 DF,  p-value: 0.02573
```

After adjusting for sex, child age, child bmi, parent income, Pre EAH fullness scores and study, we conducted moderation analysis. The results revealed a significant interaction between BIS_total and maternal risk status but only for children with low-risk of obesity (B= -131.1, p=0.02), indicating that children at low risk for obesity, a 1 unit increase in BIS corresponds to 131 less kcal consumed during EAH , while children at high risk for obesity, the association between BIS and EAH is not significant.

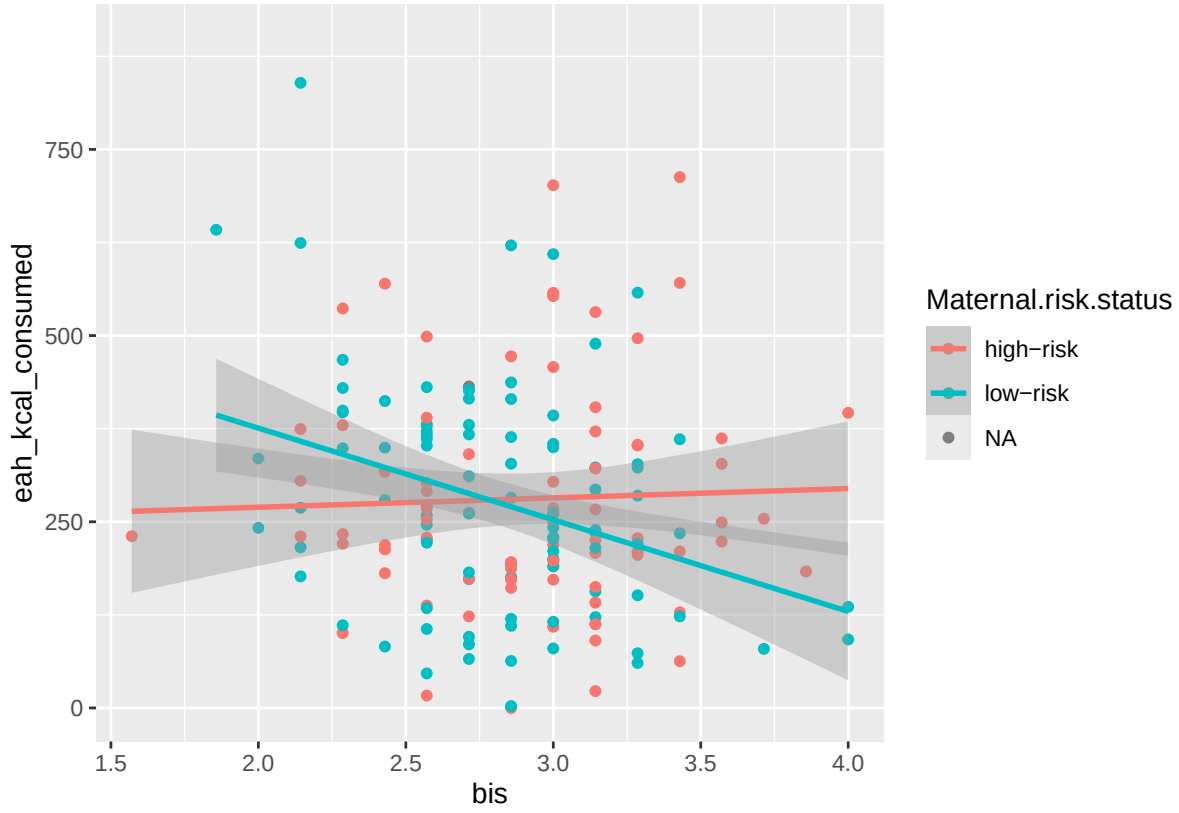
Making plots

```
# remove rows with missing values for model variables -- will make it easier to save predic
MISSING <- is.na(thesis_data$eah_kcal_consumed) |
           is.na(thesis_data$bis) |
           is.na(thesis_data$pre_eah_fullness) |
           is.na(thesis_data$Study) |
           is.na(thesis_data$Child.BMI) |
           is.na(thesis_data$Age.in.years) |
          is.na(thesis_data$Sex) | is.na(thesis_data$Maternal.risk.status)

thesis_data_no_na <- subset(thesis_data,
                      subset = !MISSING)

#Visualizations
# plot kcal (raw values)
ggplot(thesis_data, aes(x = bis, y = eah_kcal_consumed, color = factor(Maternal.risk.status)
  geom_point() +
  geom_smooth(method = "lm", se = TRUE, aes(group = Maternal.risk.status)) +
  labs(x = "bis", y = "eah_kcal_consumed", color = "Maternal.risk.status") + ylim(0, 900)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

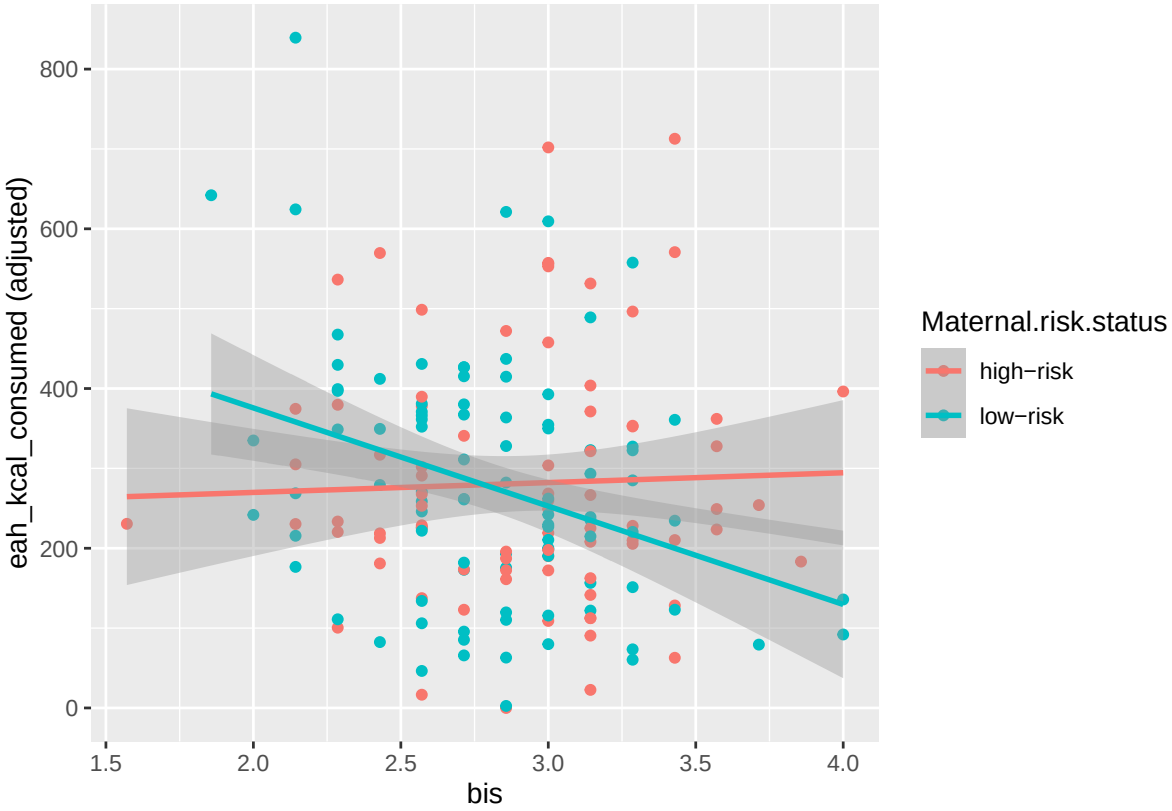
```
## Warning: Removed 5 rows containing non-finite outside the scale range
## (`stat_smooth()`).
```

```
## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_point()`).
```




```
#3
ggplot(thesis_data_no_na, aes(x = bis, y = eah_kcal_consumed, color = factor(Maternal.risk.s
  geom_point() +
  geom_smooth(method = "lm", se = TRUE, aes(group = Maternal.risk.status)) +
  labs(x = "bis", y = "eah_kcal_consumed (adjusted)", color = "Maternal.risk.status")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```


800
600
400
200
0
eah_kcal_consumed (adjusted)
1.5
2.0
2.5
3.0
3.5
4.0
bis
Maternal.risk.status
high−risk
low−risk