

Thesis Analysis

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Contents

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

```
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

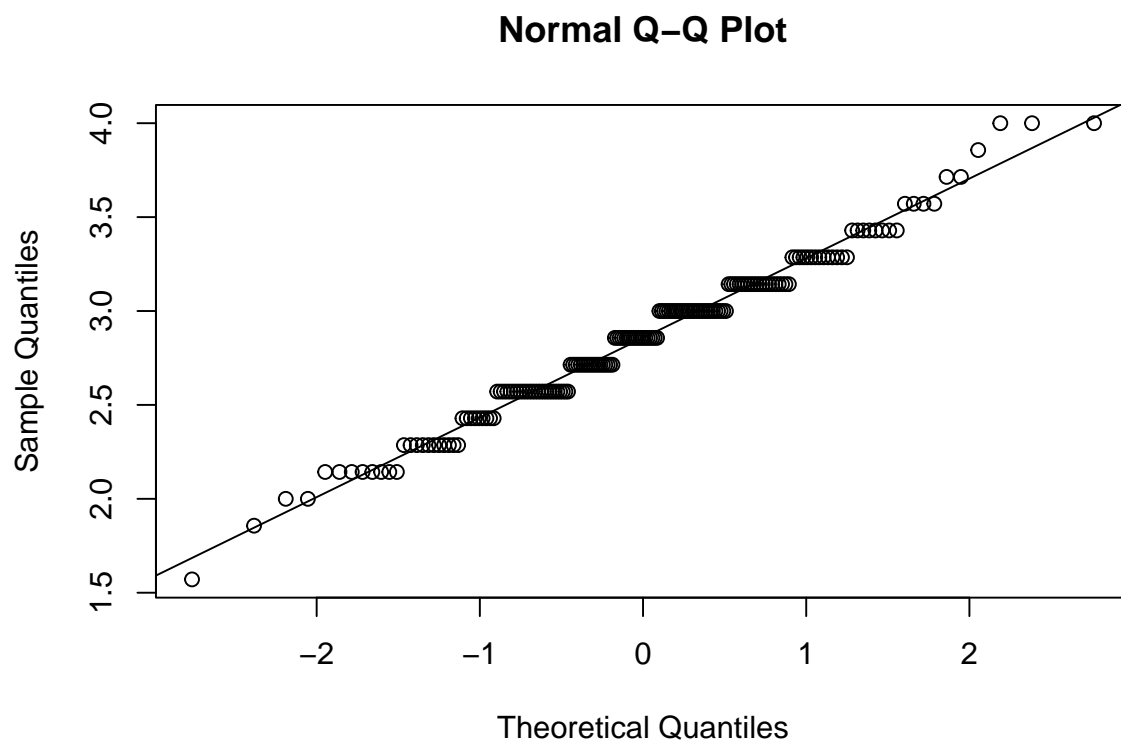
```
thesis_data<-read.csv("~/Desktop/Rhea MS thesis/MS_thesis/data/thesis_data.csv")
```

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

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



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

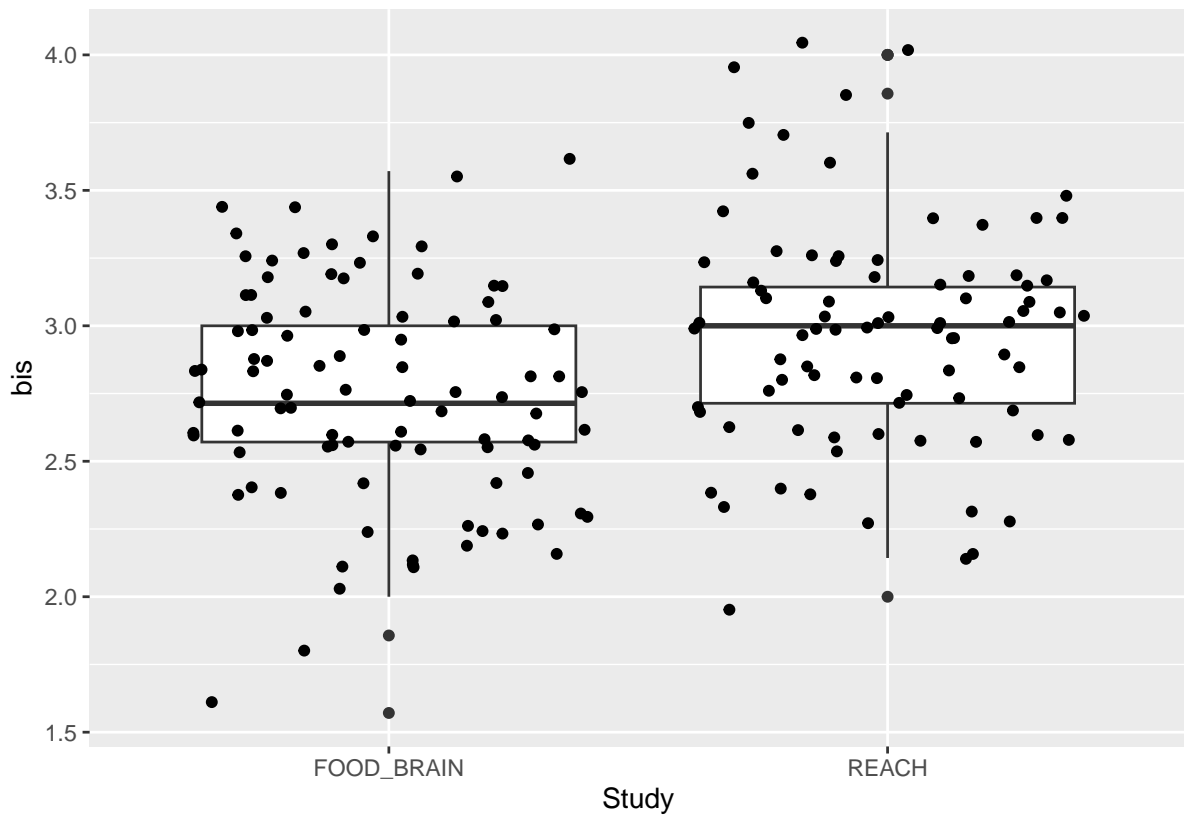
```
##
##  Shapiro-Wilk normality test
##
## data:  thesis_data$bis
## W = 0.98488, p-value = 0.05538
```

```
#Visualizing BIS data by Study, boxplot and histogram
```

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

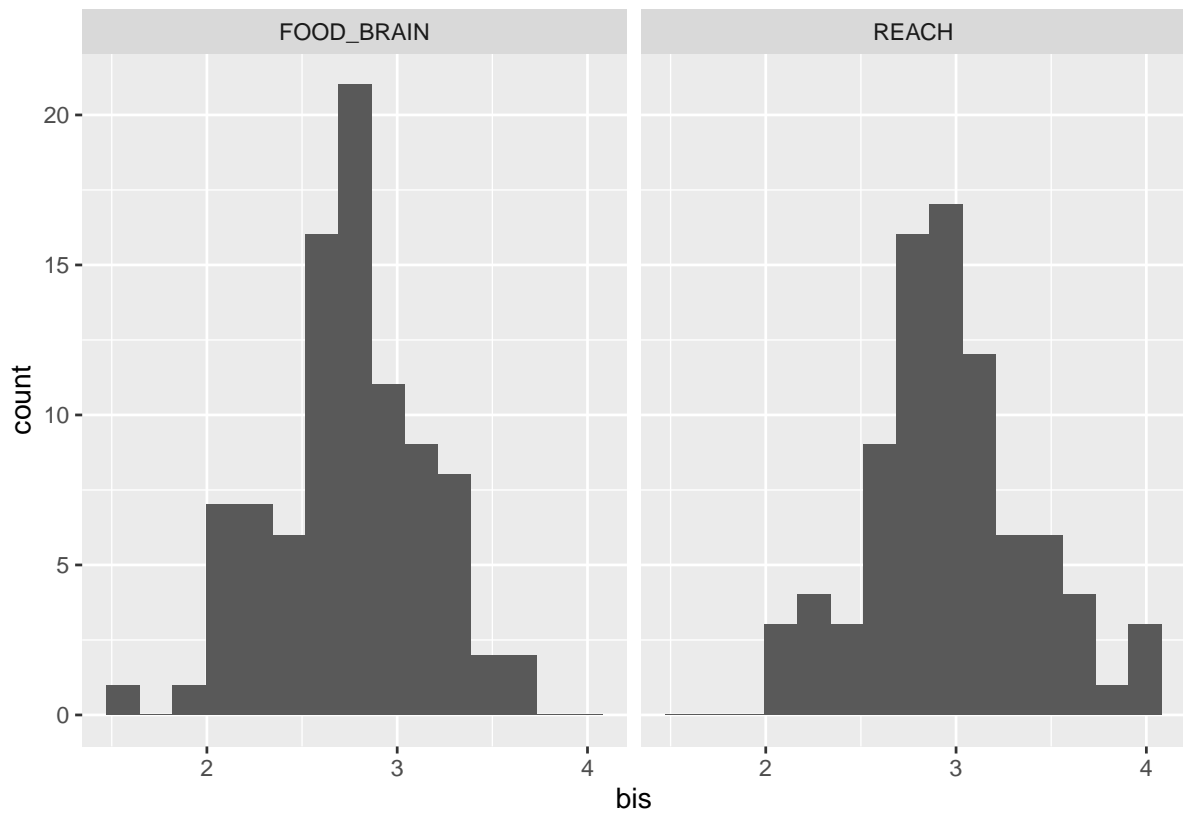
```
## Warning: Removed 4 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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



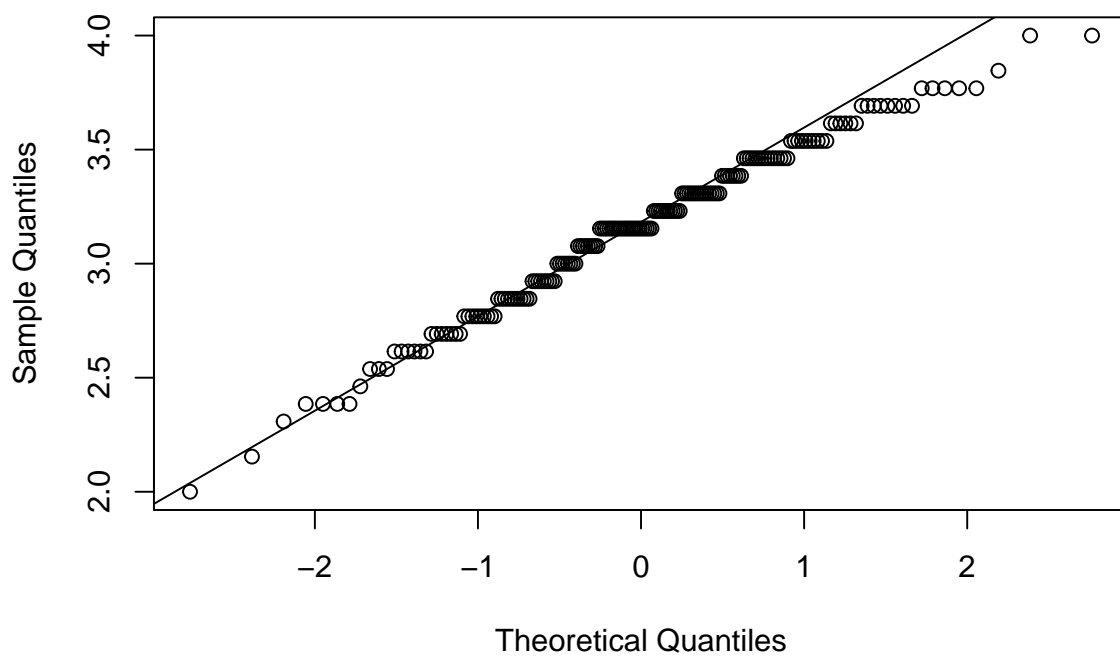
```
ggplot(thesis_data,aes(bis))+ geom_histogram(bins=15)+facet_grid(.~Study)
```

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



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

Normal Q-Q Plot



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

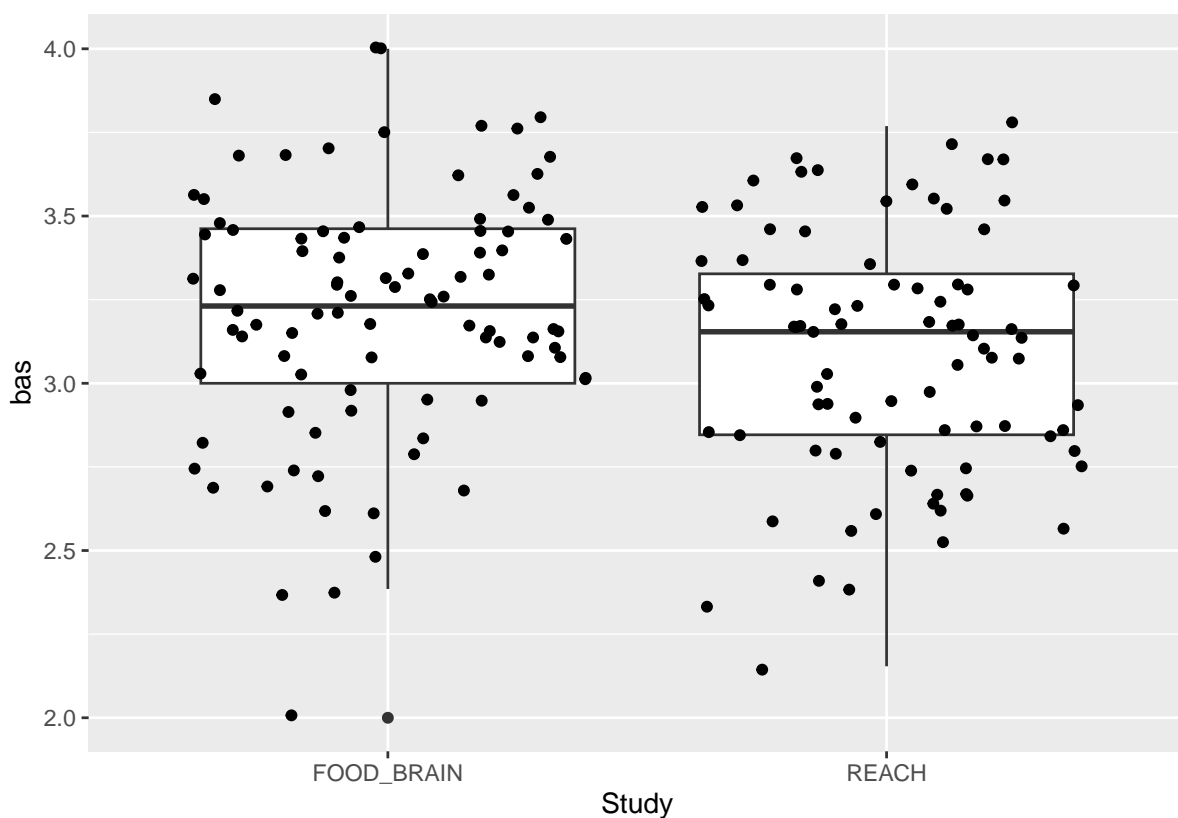
```
##
## Shapiro-Wilk normality test
##
## data:  thesis_data$bas
## W = 0.986, p-value = 0.07642
```

```
#Visualizing BAS data by Study, boxplot and histogram
```

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

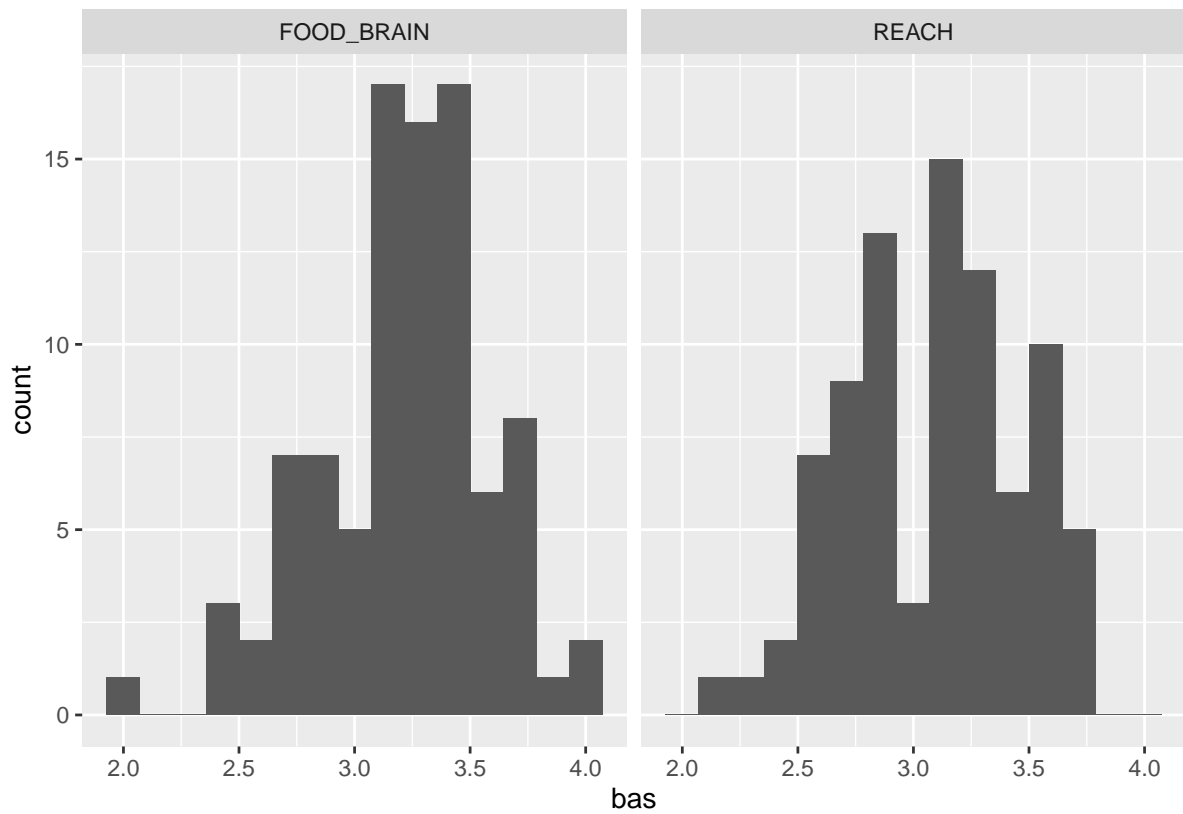
```
## Warning: Removed 3 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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



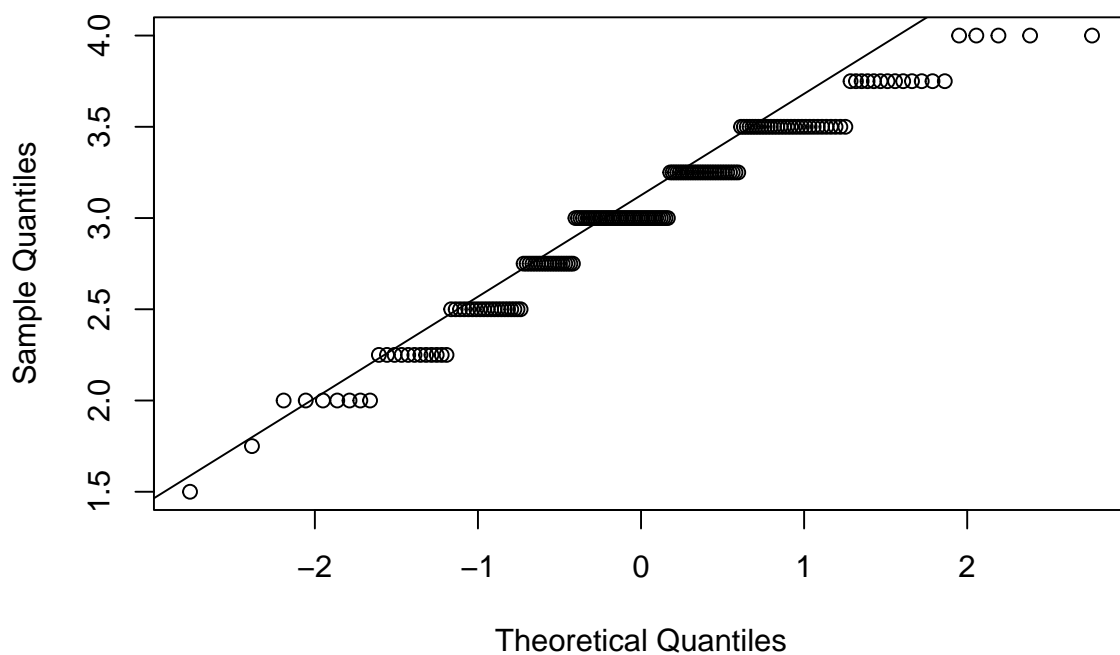
```
ggplot(thesis_data, aes(bas)) + geom_histogram(bins=15) + facet_grid(.~Study)
```

```
## 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)
```

Normal Q-Q Plot



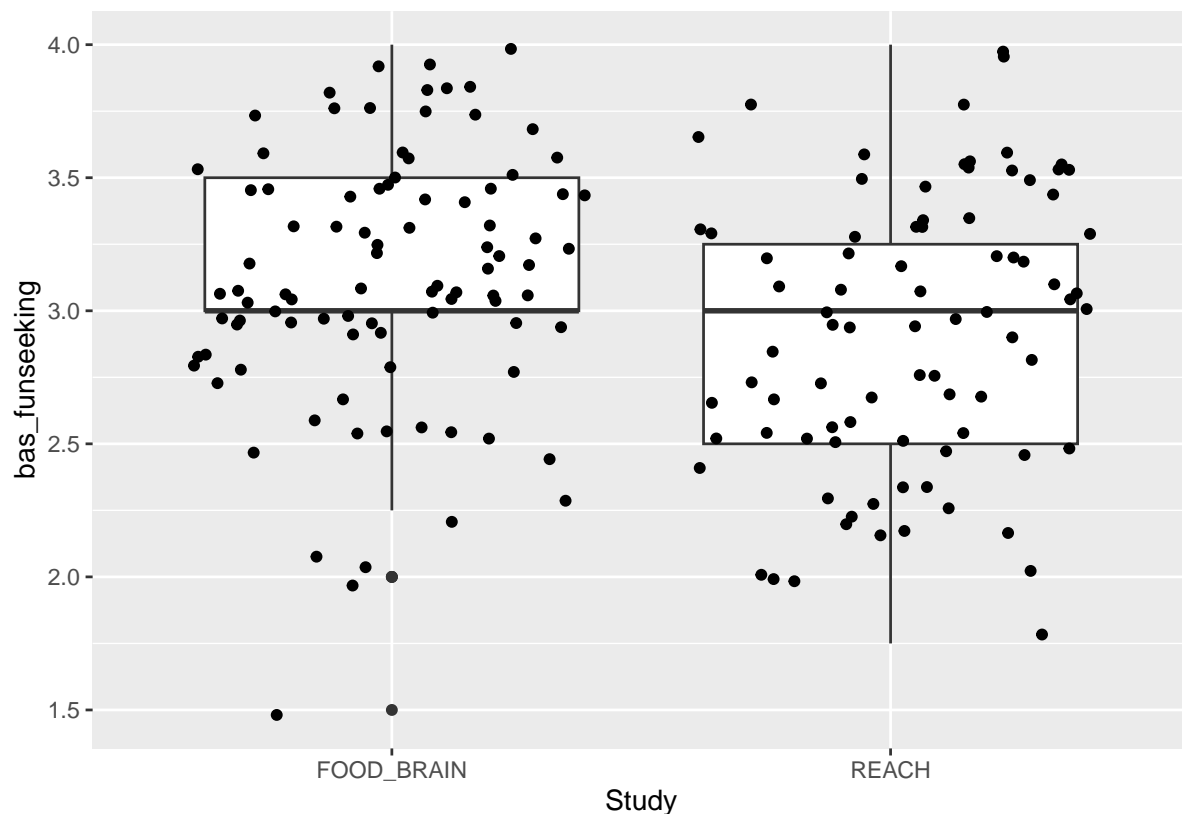
```
shapiro.test(thesis_data$bas_funseeking) #not normal
```

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

```
#Visualizing BAS funseeking data by Study, boxplot and histogram
```

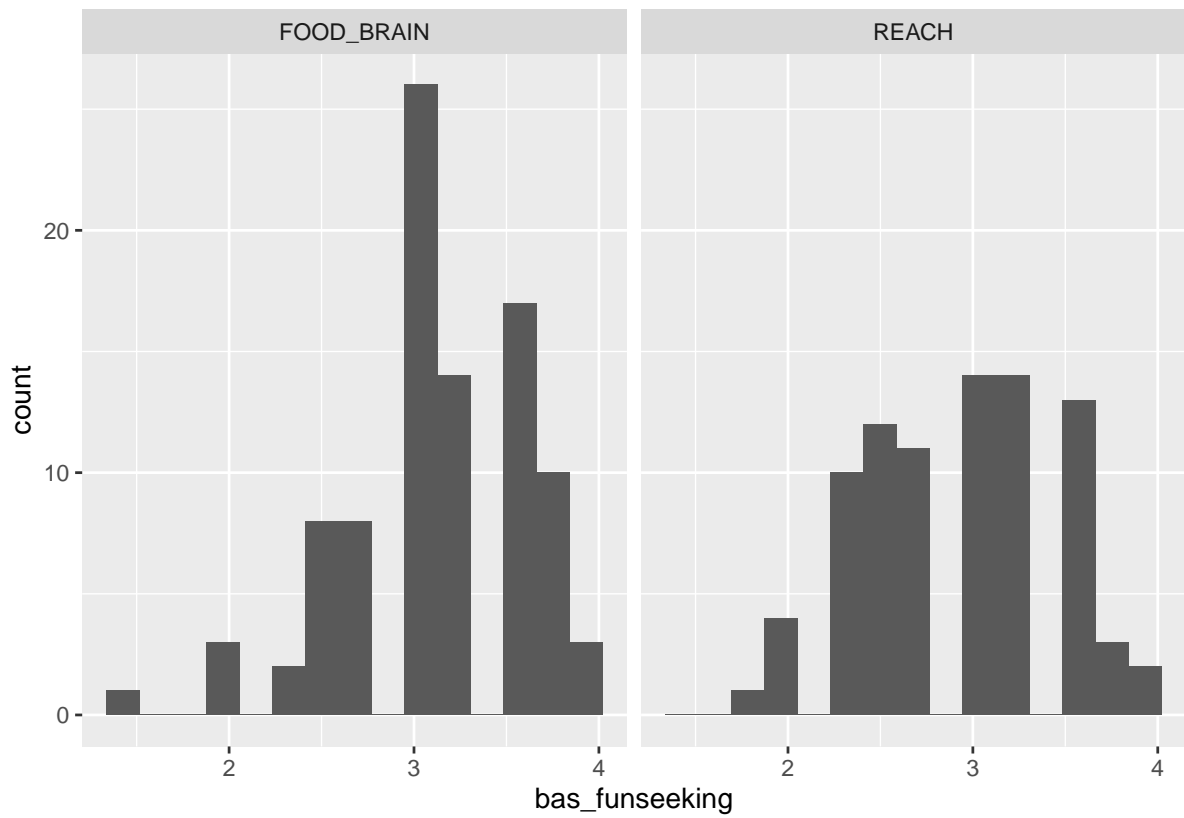
```
ggplot(thesis_data, aes(x=Study, y=bas_funseeking)) +geom_boxplot() +geom_jitter(height = 0.5)
```

```
## 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()').
```



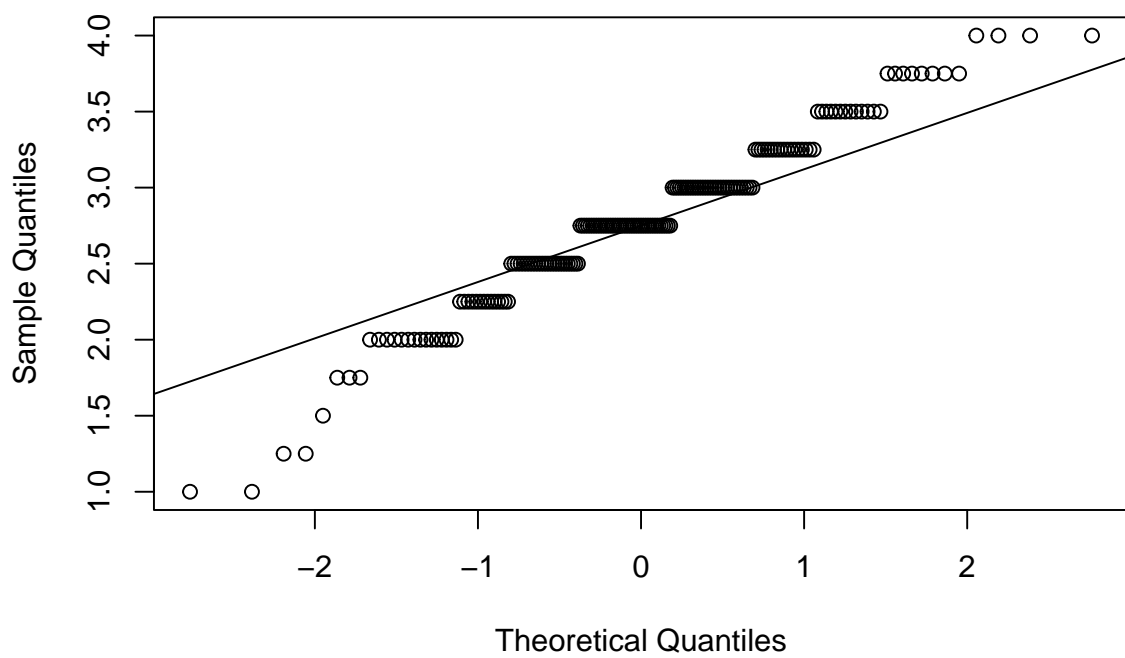
```
ggplot(thesis_data, aes(bas_funseeking)) +geom_histogram(bins=15) +facet_grid(.~Study)
```

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



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

Normal Q–Q Plot



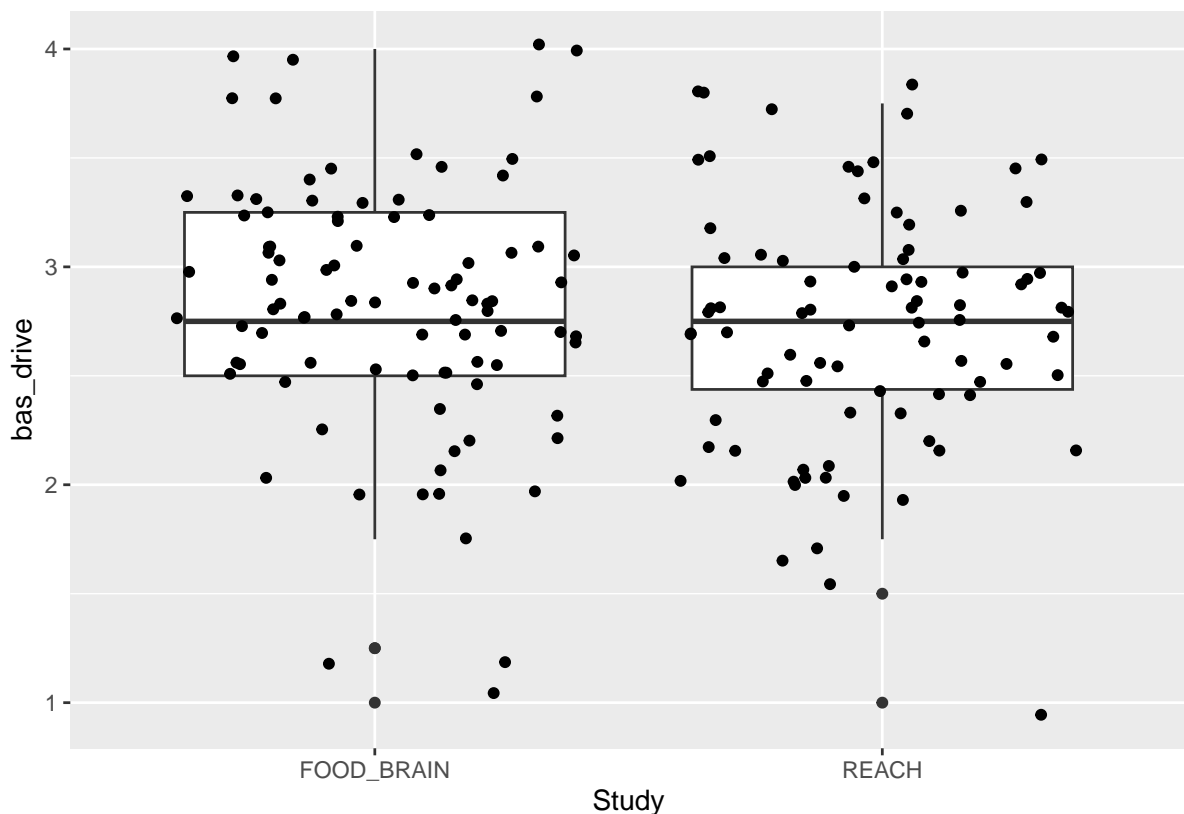

```
shapiro.test(thesis_data$bas_drive) #not normal
```

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

```
#Visualizing BAS drive data by Study, boxplot and histogram
```

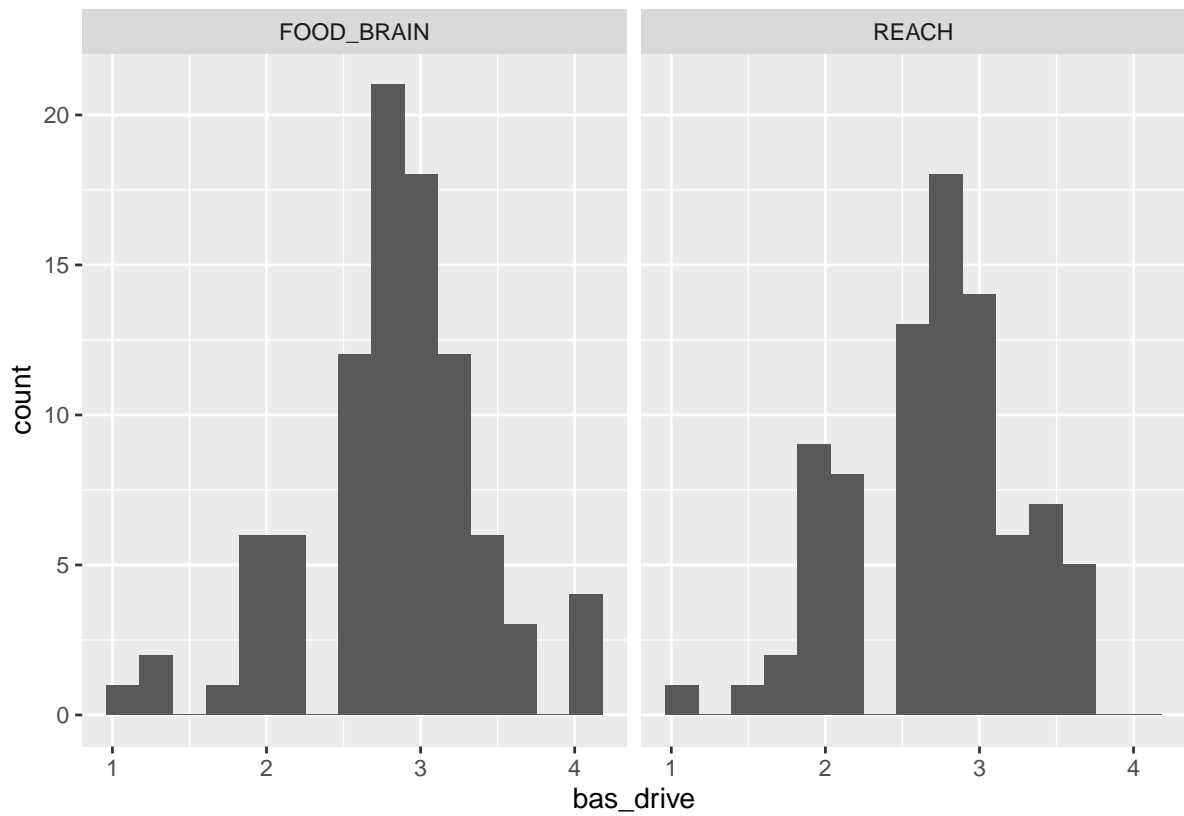
```
ggplot(thesis_data, aes(x=Study, y=bas_drive)) + geom_boxplot() + geom_jitter(height = NULL,
```

```
## 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()').
```



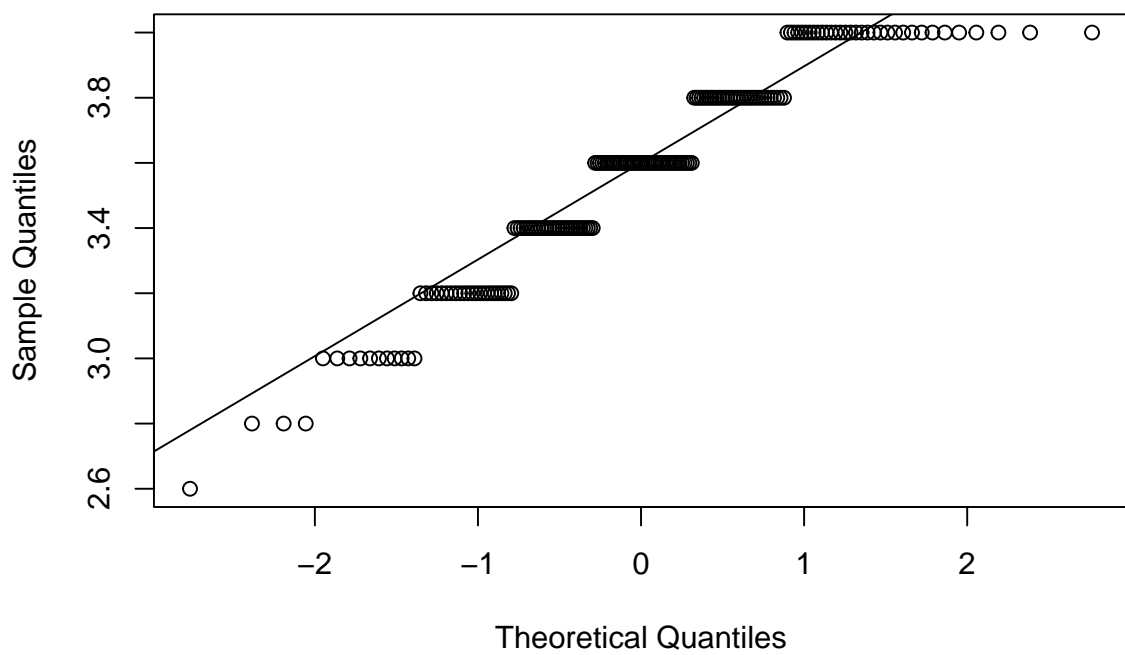
```
ggplot(thesis_data, aes(bas_drive)) + geom_histogram(bins=15) + facet_grid(.~Study)
```

```
## 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)
```

Normal Q-Q Plot



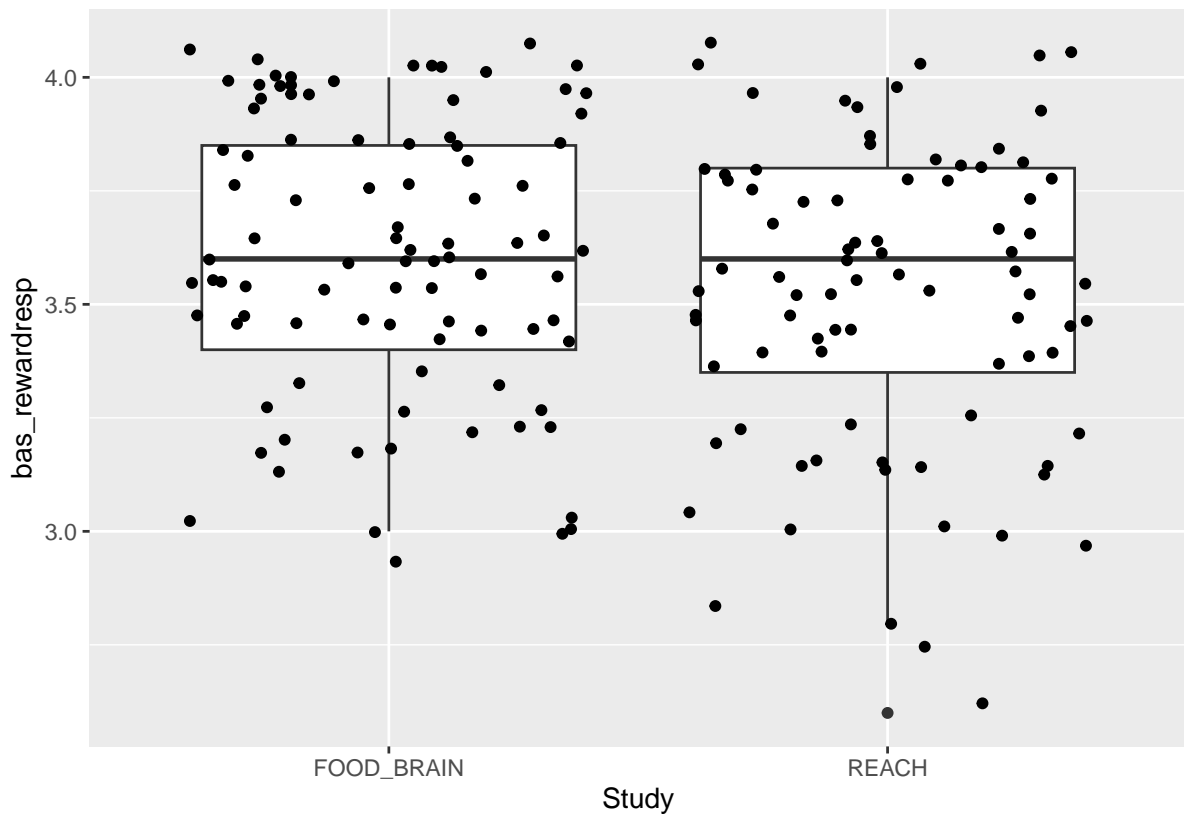
```
shapiro.test(thesis_data$bas_rewardresp) #not normal
```

```
##
## 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
```

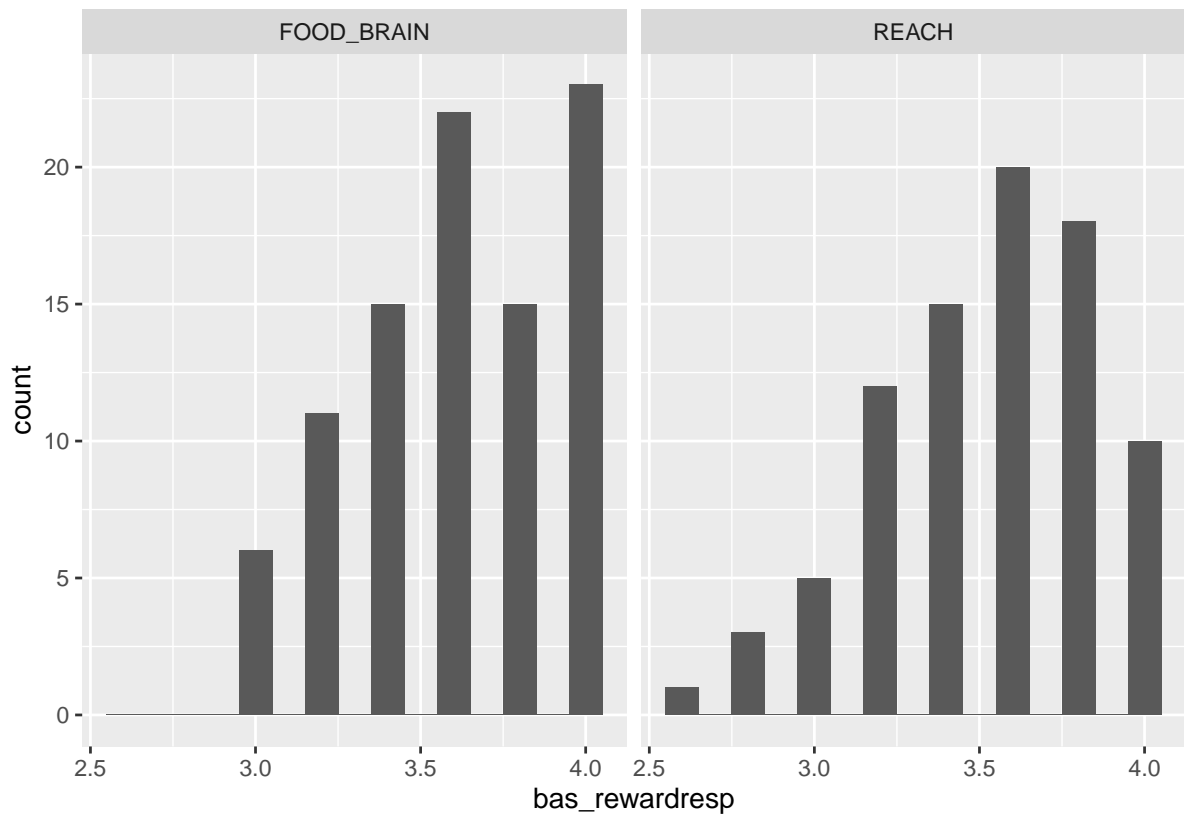
```
ggplot(thesis_data, aes(x=Study, y=bas_rewardresp)) +geom_boxplot() + geom_jitter(height = 1)
```

```
## 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()').
```



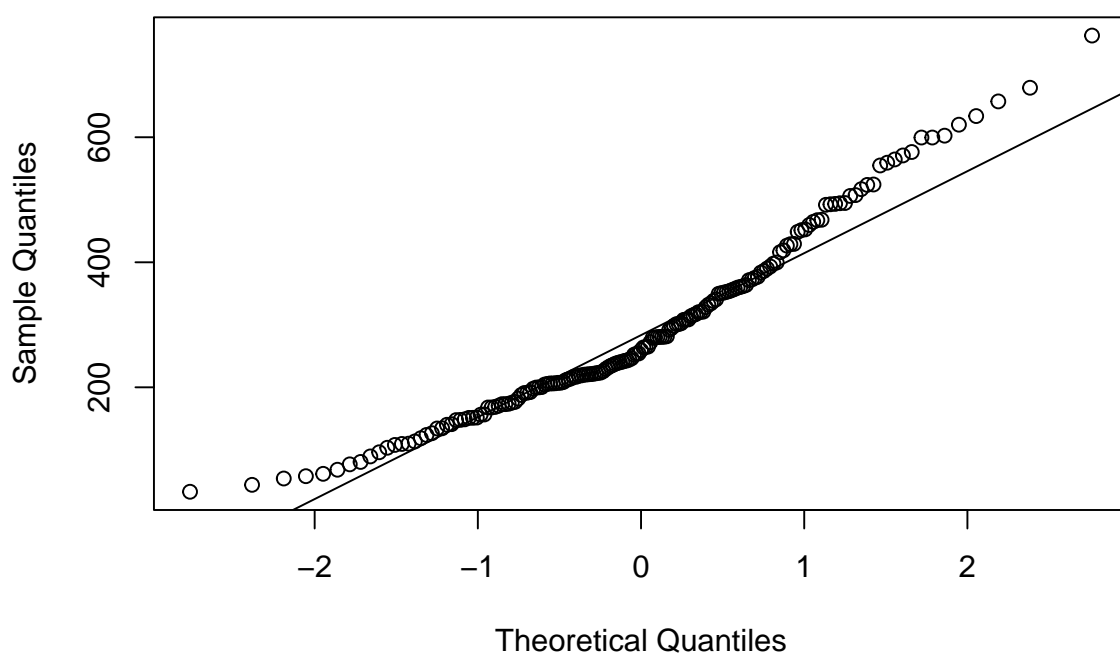
```
ggplot(thesis_data, aes(bas_rewardresp)) +geom_histogram(bins=15) + facet_grid(.~Study)
```

```
## 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)
```

Normal Q–Q Plot



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

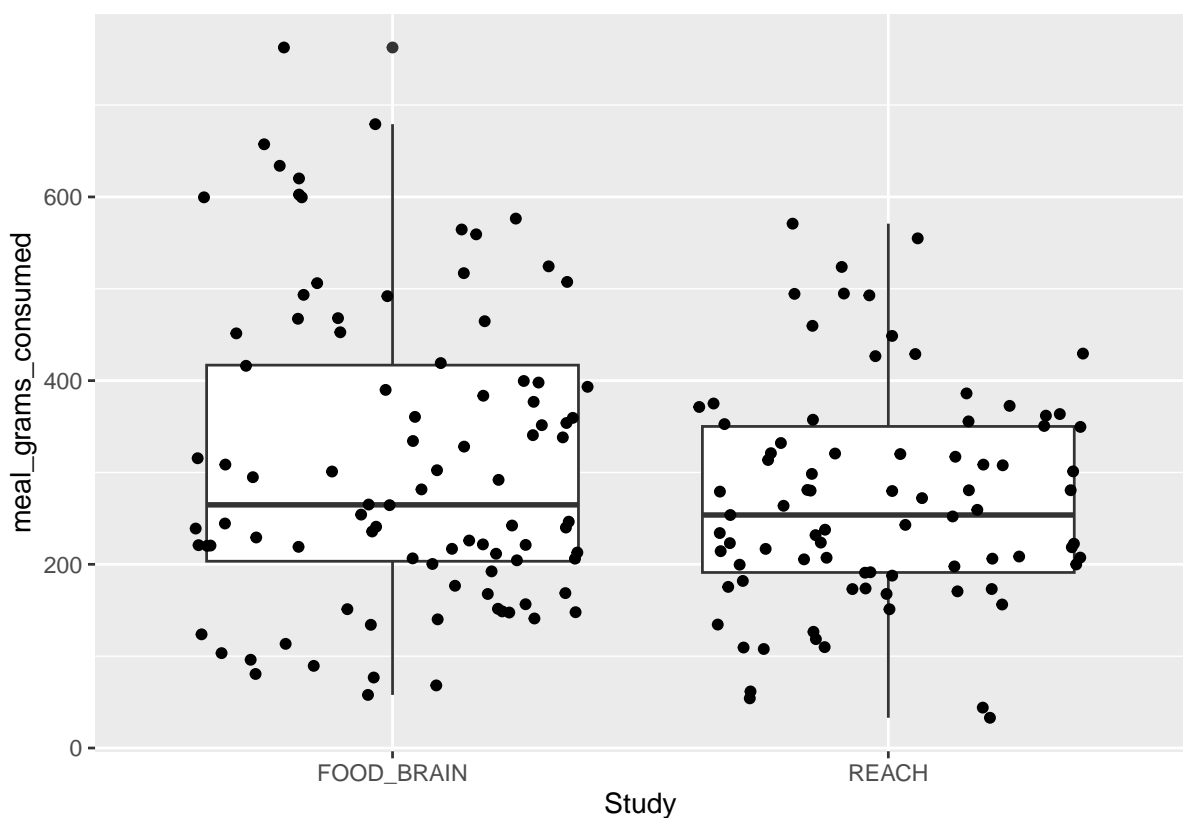
```
##
## Shapiro-Wilk normality test
##
## data:  thesis_data$meal_grams_consumed
## W = 0.95722, p-value = 3.579e-05
```

```
#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
```

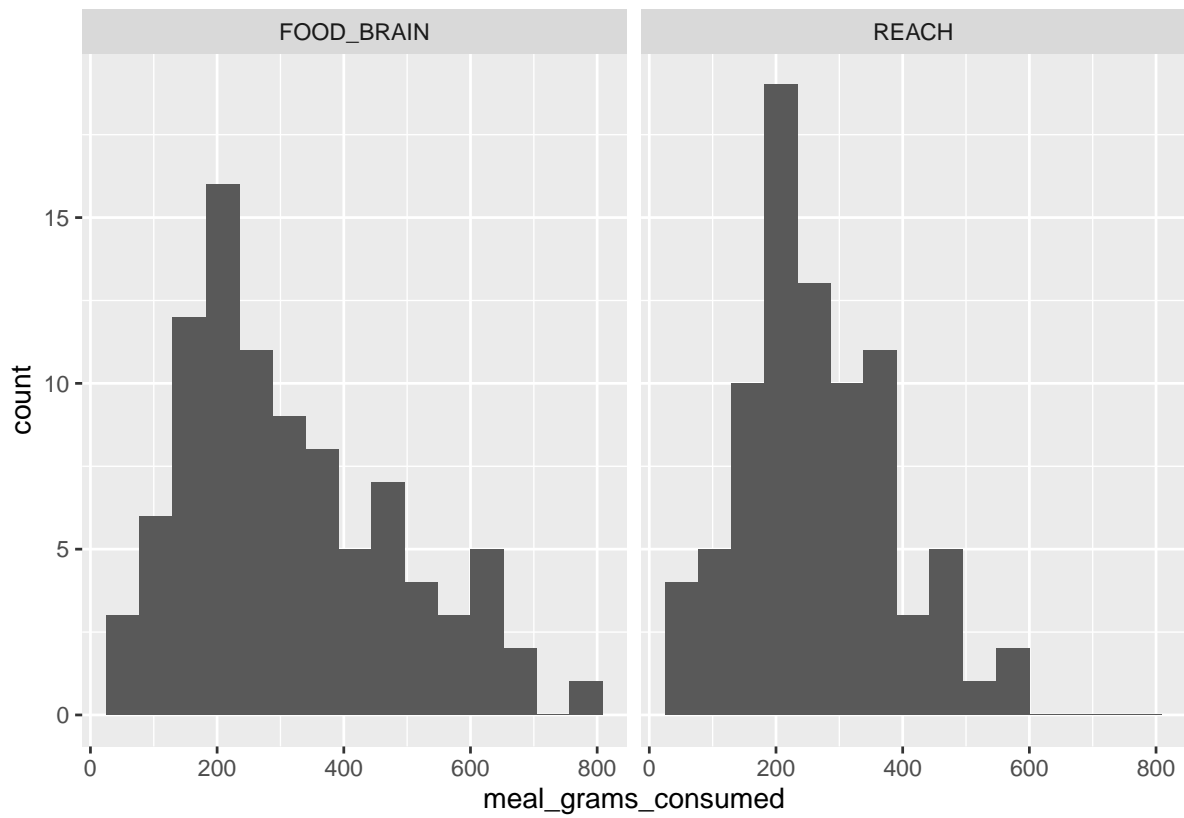
```
## Warning: Removed 4 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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



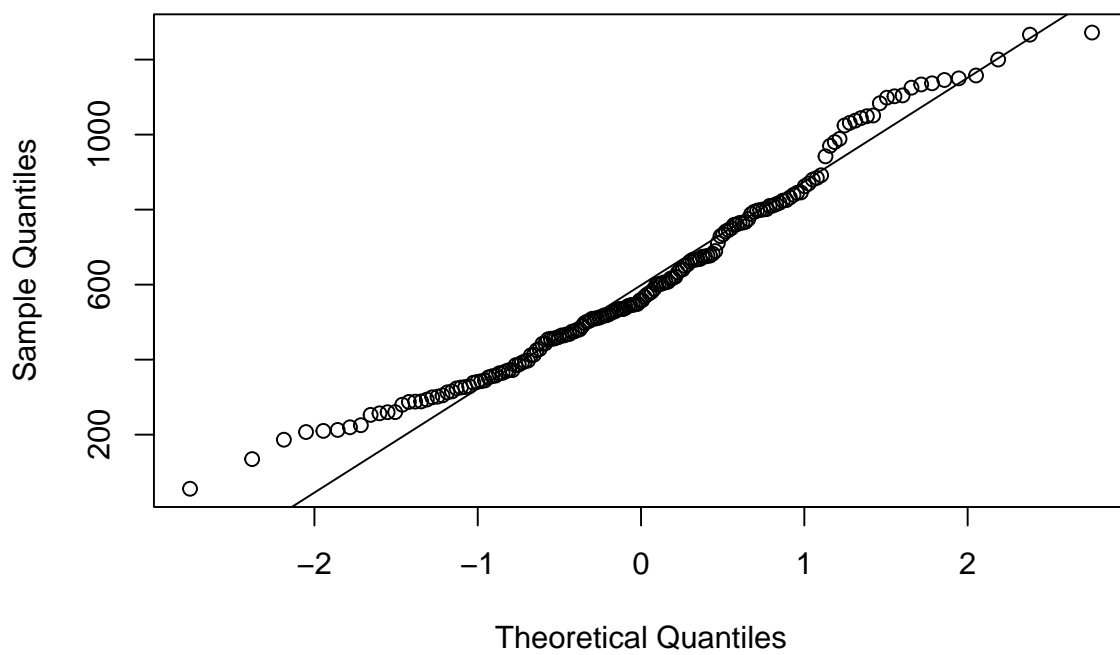
```
ggplot(thesis_data, aes(meal_grams_consumed)) + geom_histogram(bins=15) + facet_grid(.~Study)
```

```
## 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)
```

Normal Q–Q Plot



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

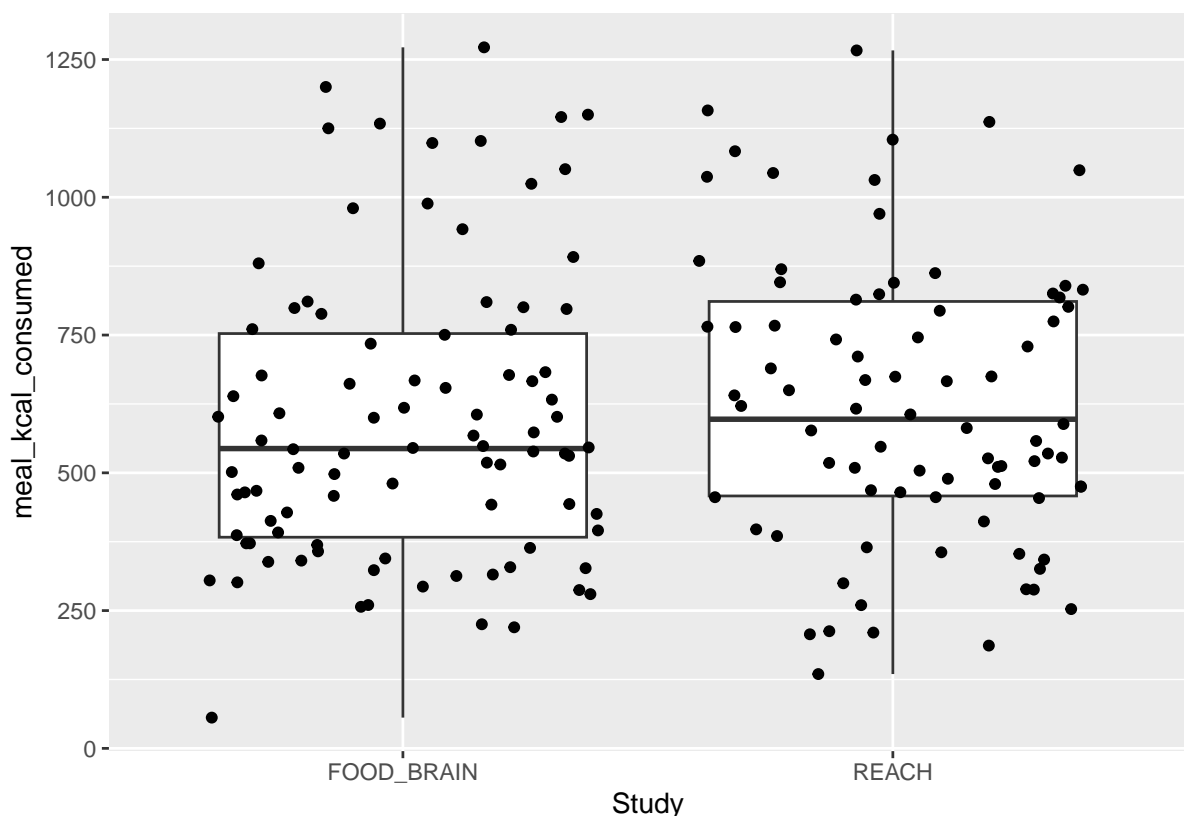
```
##
## Shapiro-Wilk normality test
##
## data:  thesis_data$meal_kcal_consumed
## W = 0.96846, p-value = 0.0005531
```

```
#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(height=0.5)
```

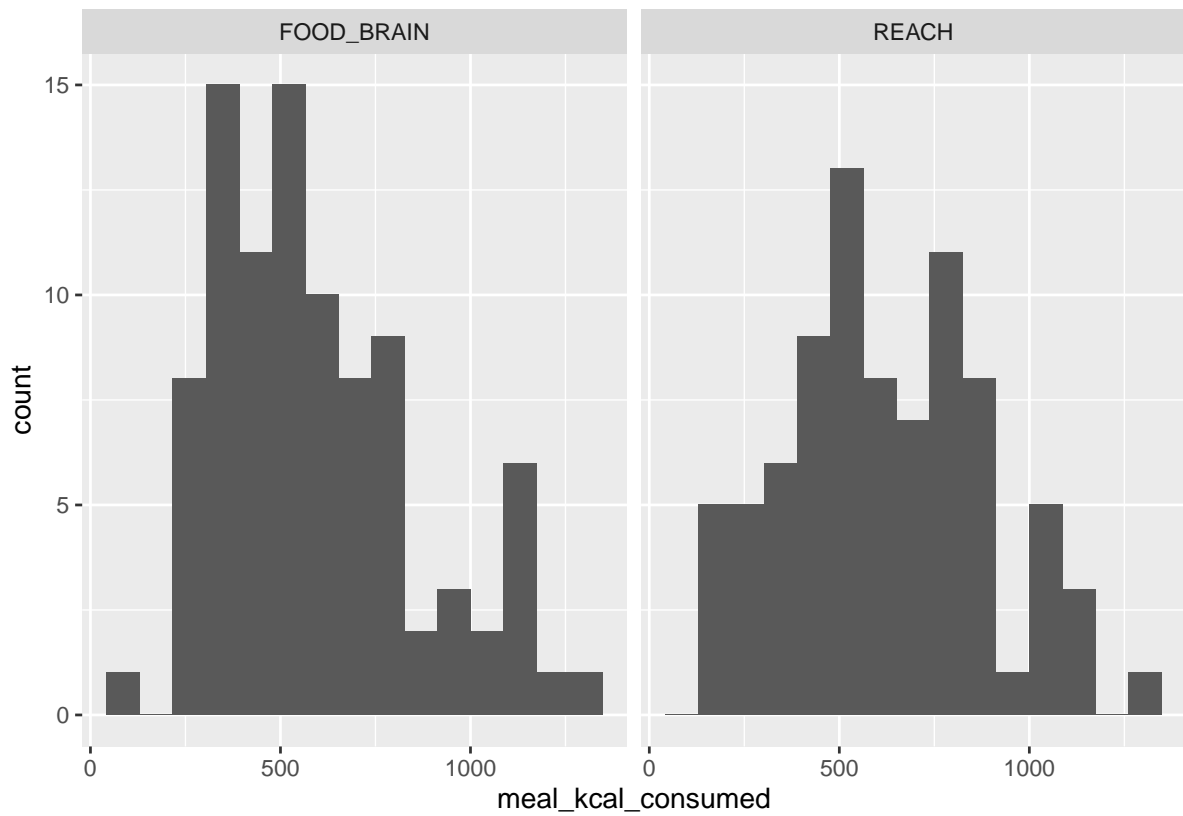
```
## Warning: Removed 5 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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



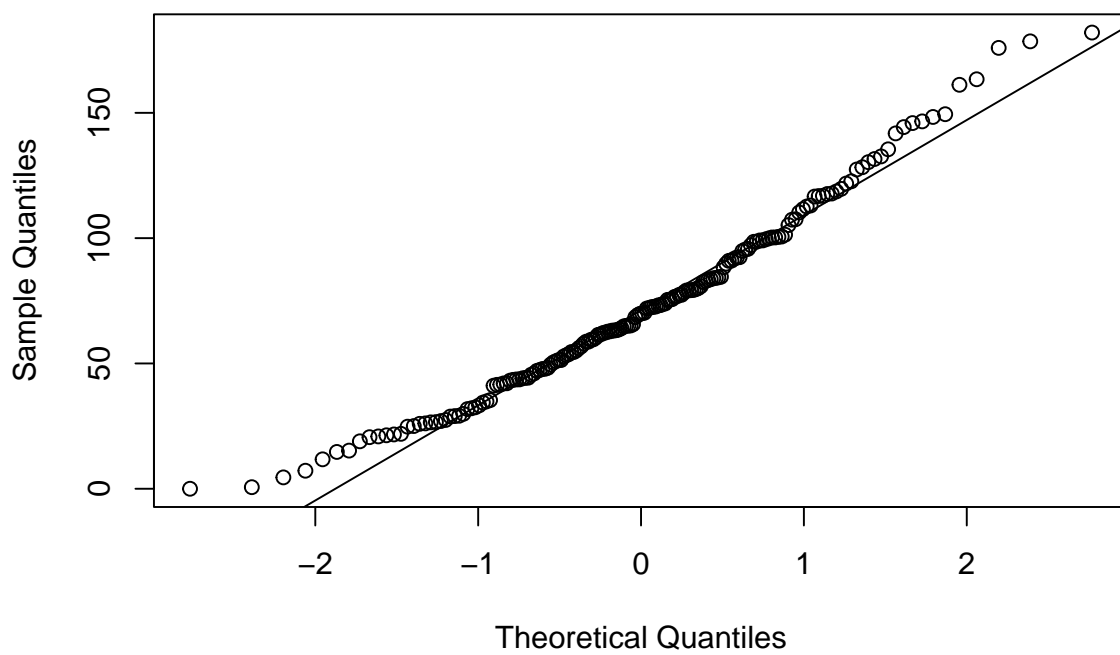
```
ggplot(thesis_data, aes(meal_kcal_consumed)) + geom_histogram(bins=15) + facet_grid(.~Study)
```

```
## 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)
```

Normal Q–Q Plot




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

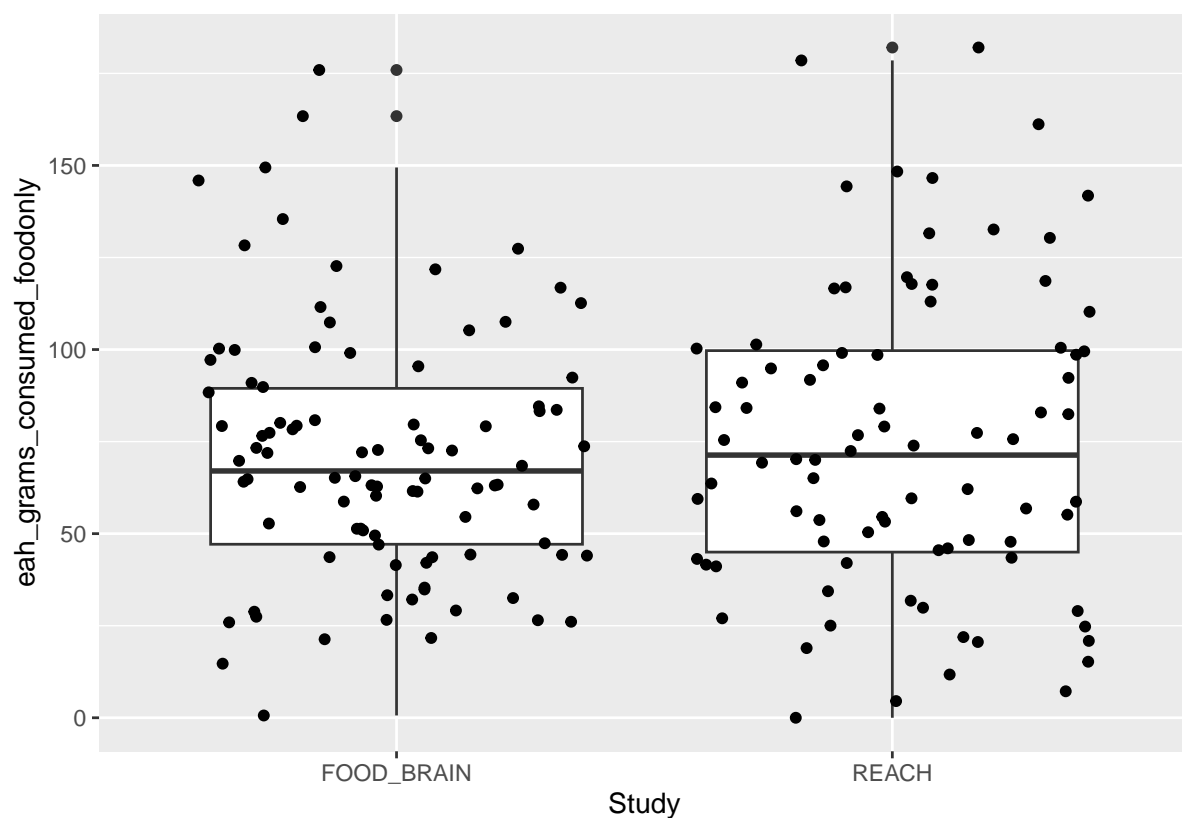
```
##
## Shapiro-Wilk normality test
##
## data:  thesis_data$eah_grams_consumed_foodonly
## W = 0.97611, p-value = 0.003732
```

```
#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_jitter
```

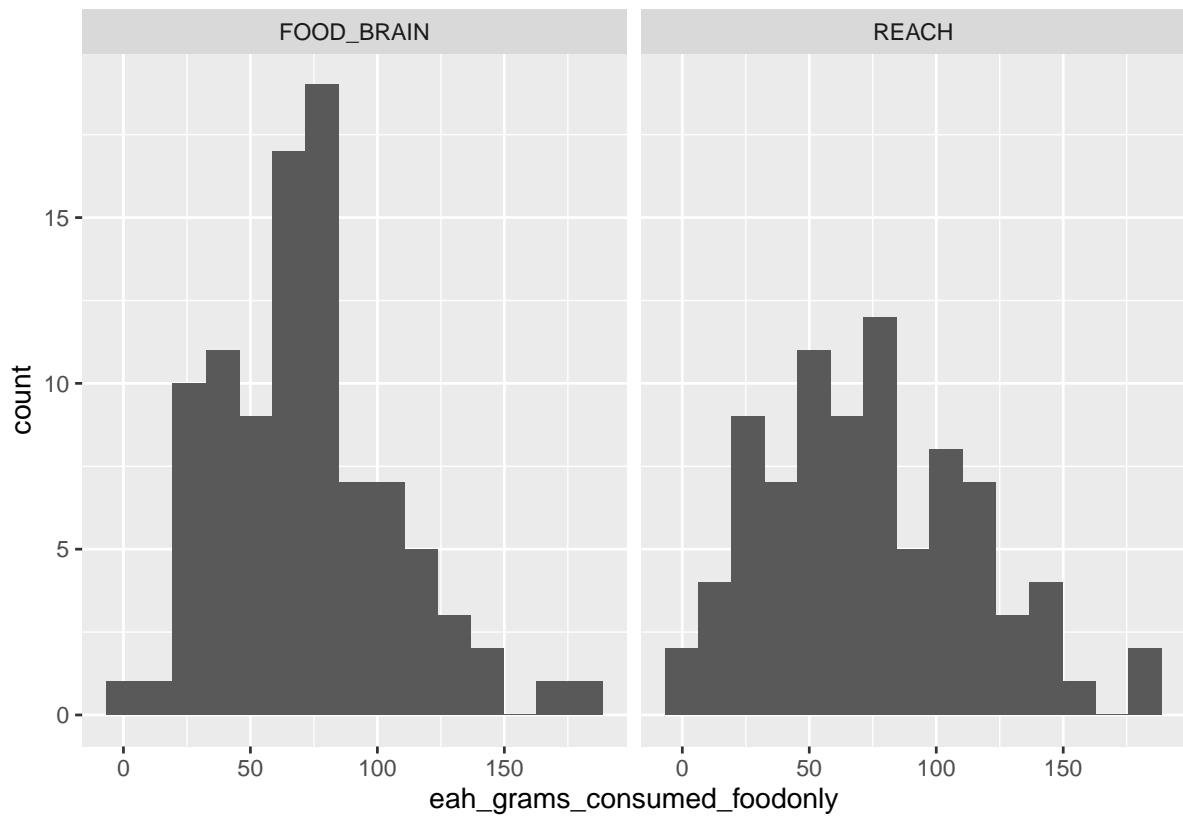
```
## Warning: Removed 1 row containing non-finite outside the scale range
## ('stat_boxplot()').
```

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



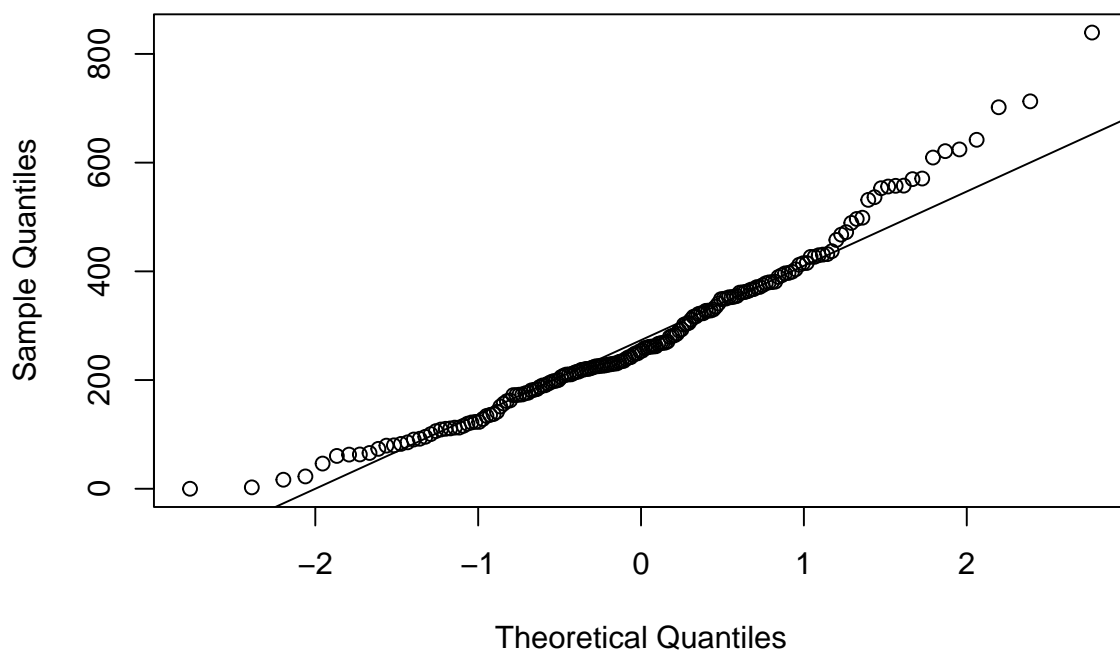
```
ggplot(thesis_data, aes(eah_grams_consumed_foodonly)) +geom_histogram(bins=15) +facet_grid(.~S
```

```
## 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)
```

Normal Q-Q Plot



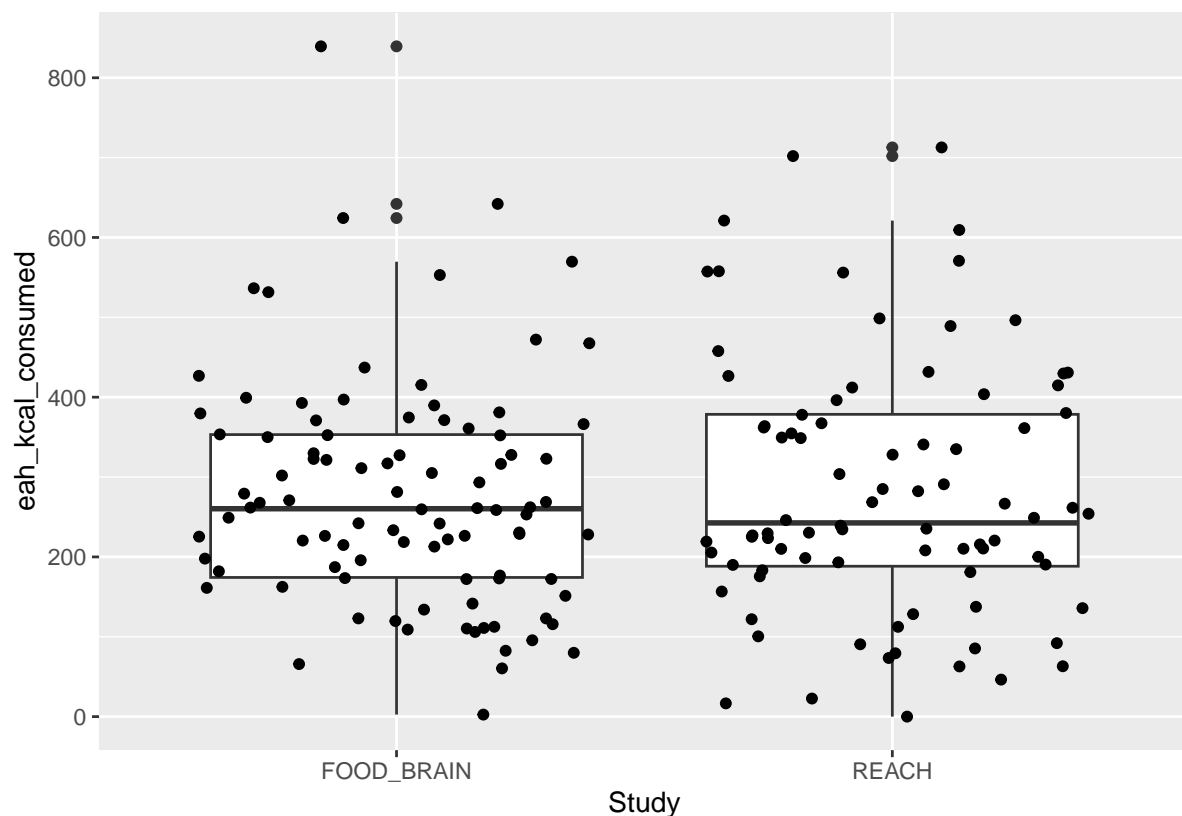
```
shapiro.test(thesis_data$eah_kcal_consumed) #not normal
```

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

```
#Visualizing EAH consumed in kcal data by Study, boxplot and histogram
```

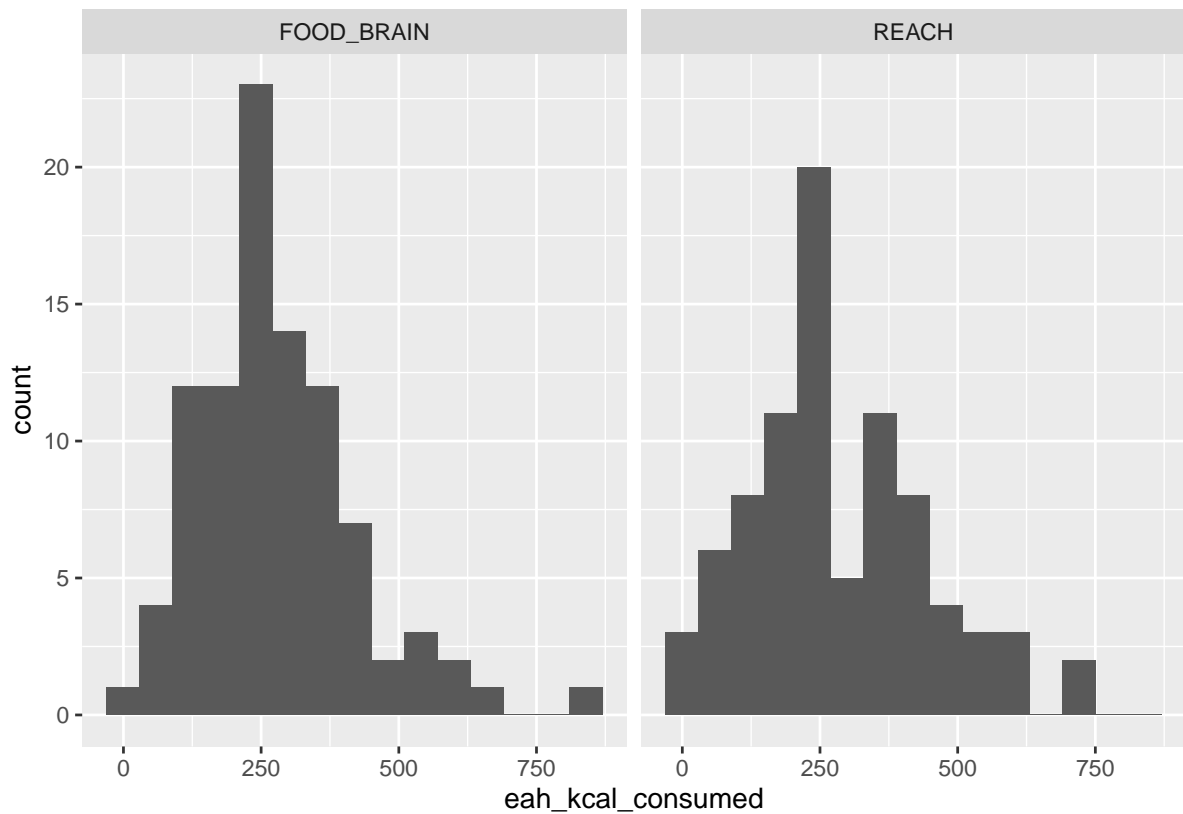
```
ggplot(thesis_data, aes(x=Study, y=eah_kcal_consumed)) + geom_boxplot() + geom_jitter(height=
```

```
## 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()').
```



```
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. Corrpplots between the interested variables

```
library(corrplot)
```

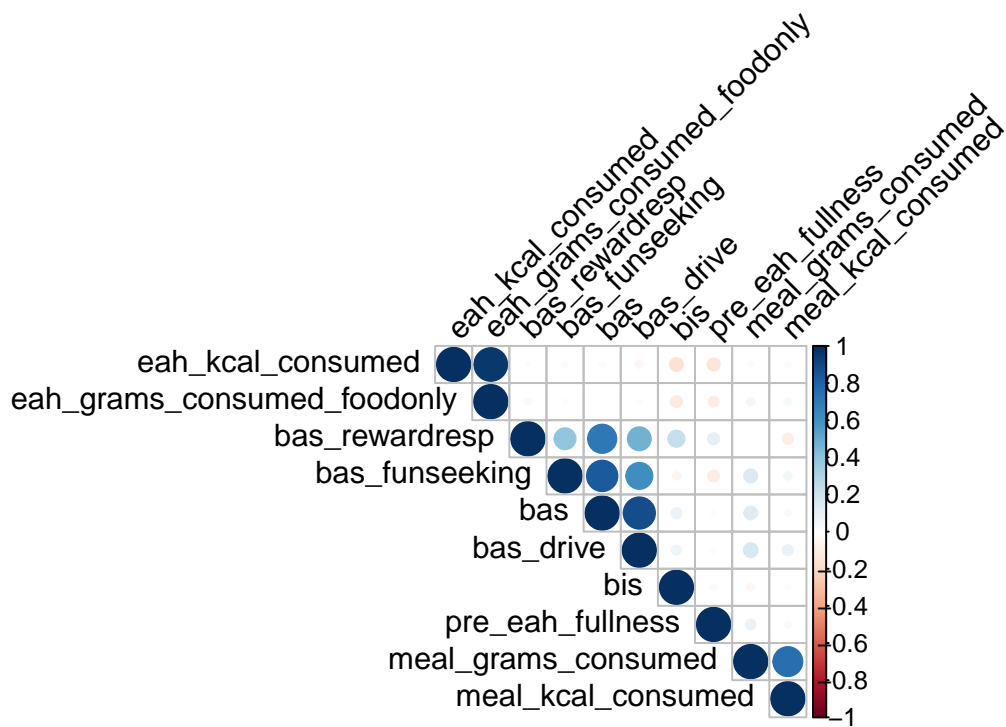
```
## corrplot 0.95 loaded
```

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

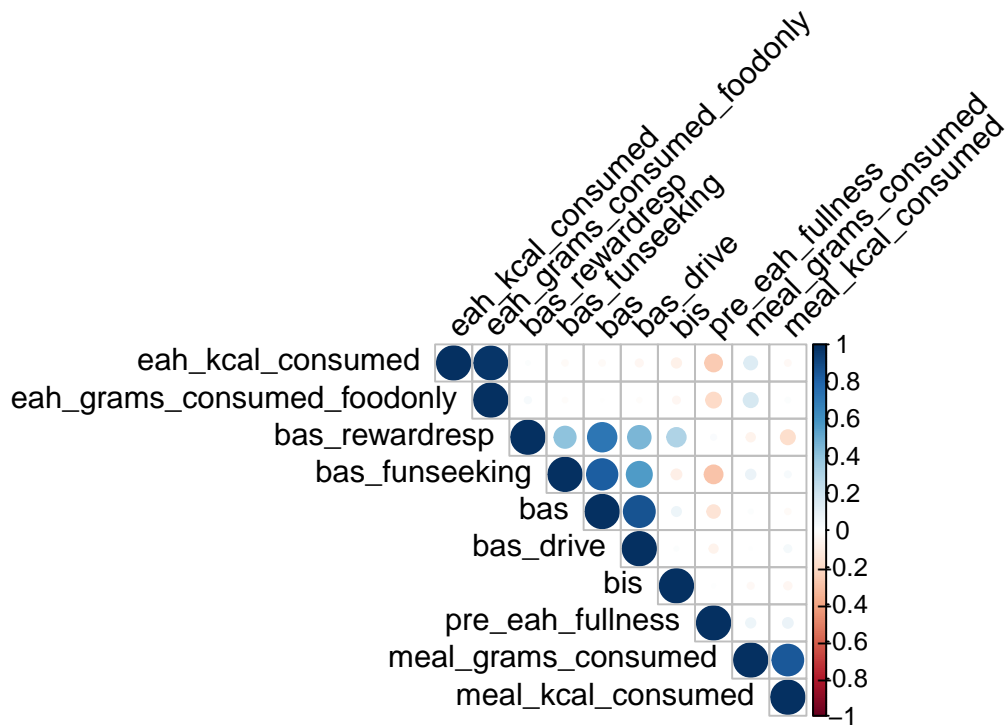
cor_reach <- cor(thesis_data[thesis_data$Study == "REACH", c("bis", "bas", "bas_funseeking",

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)
```



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

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.

```
library(car)
```

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

```
##
```

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

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

```
##
```

```
## recode
```

```
##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
```

```
#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
```

```
#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$Study == "FOOD_BRAIN", ]$bis  
## 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
```

```
#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$Study == "FOOD_BRAIN",]$eah_kcal_consumed,  
alternative = "two.sided", var.equal = TRUE)
```

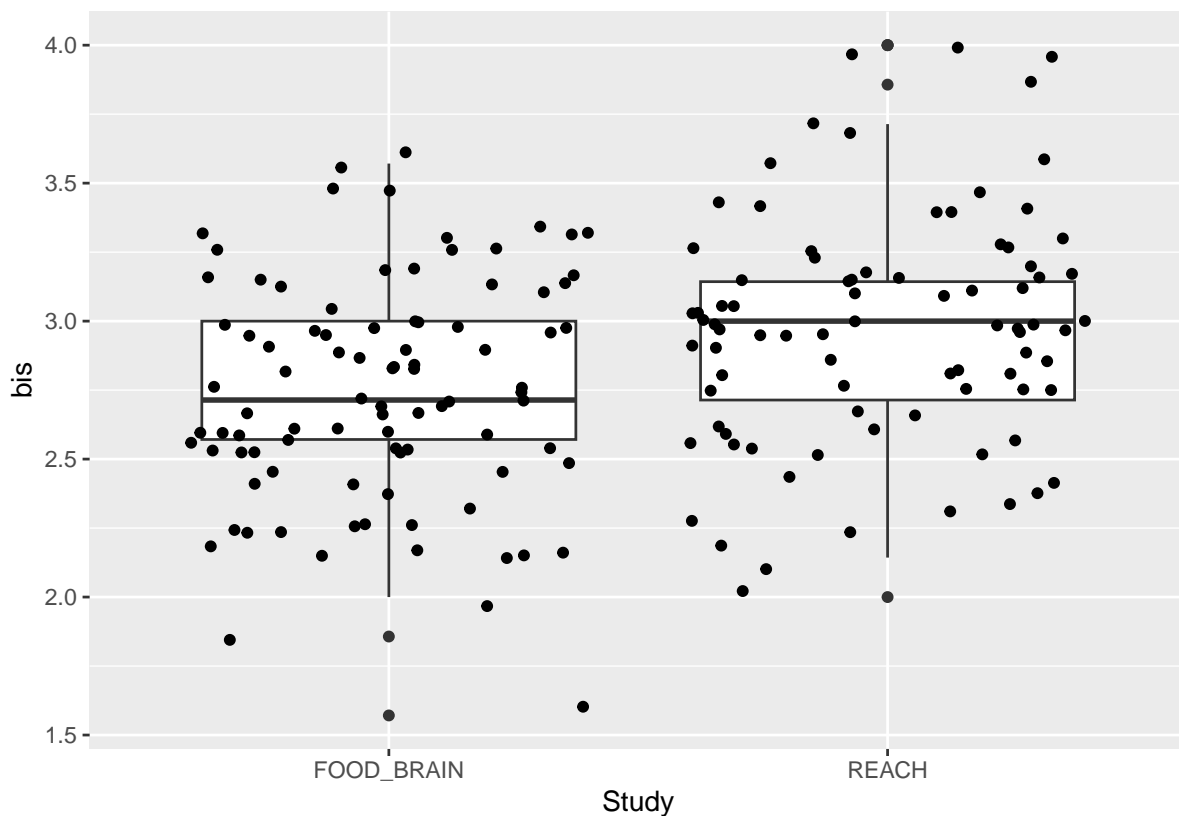
```
##  
## Two Sample t-test  
##  
## data: thesis_data[thesis_data$Study == "REACH", ]$eah_kcal_consumed and thesis_data[thesis_data$Study == "FOOD_BRAIN", ]$eah_kcal_consumed  
## t = 0.23976, df = 176, p-value = 0.8108  
## alternative hypothesis: true difference in means is not equal to 0  
##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

```
#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()').
```

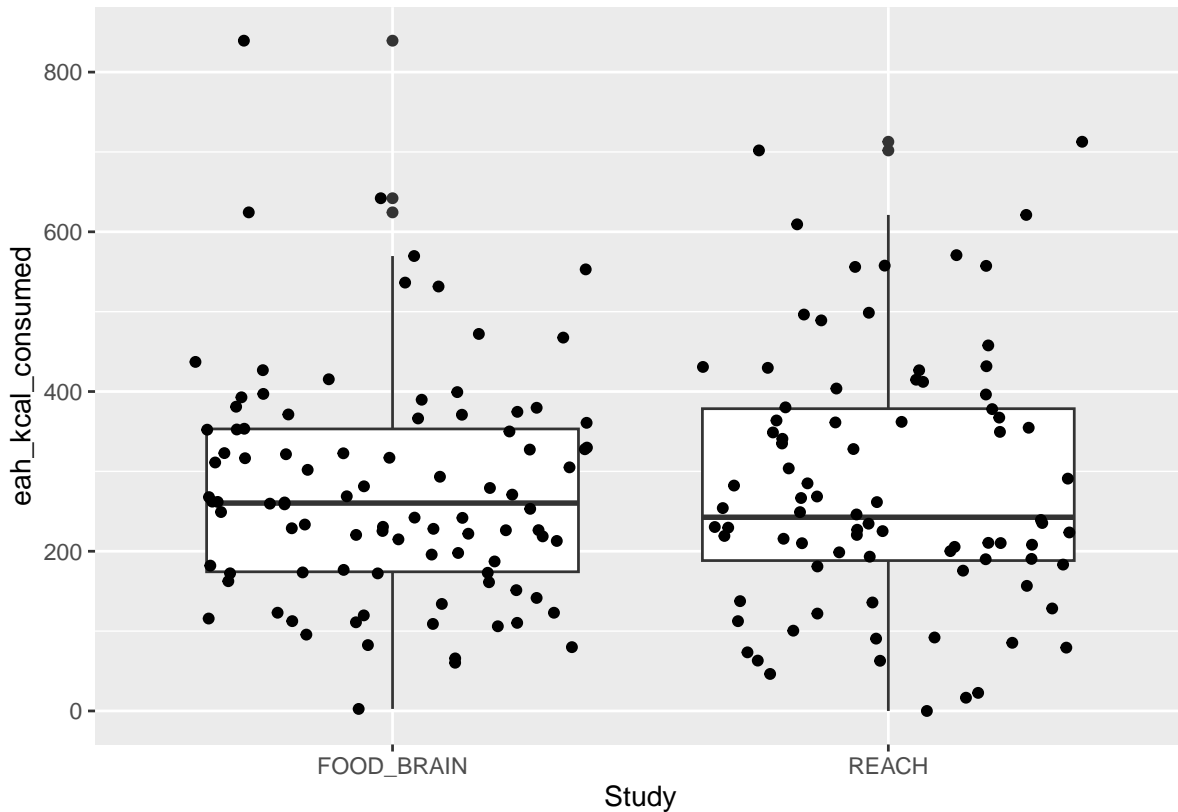
```
## Warning: Removed 4 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
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)
```

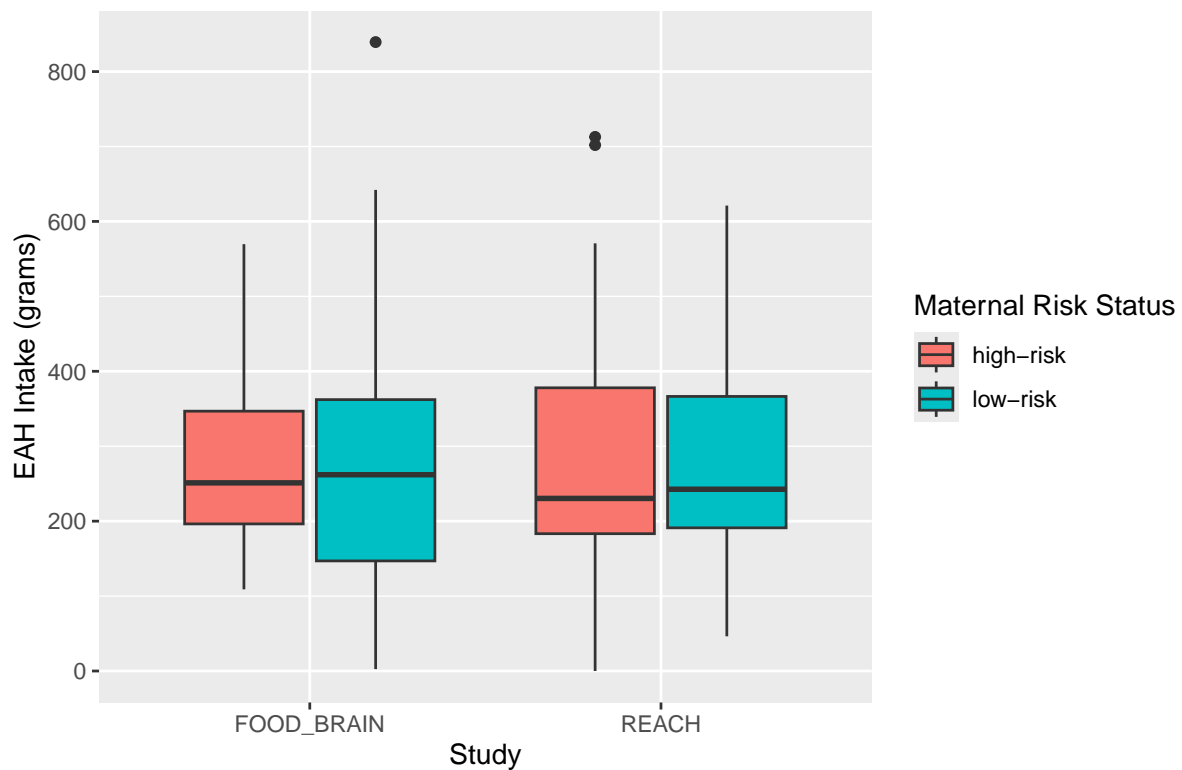
```
##              Df  Sum Sq Mean Sq F value Pr(>F)
## Maternal.risk.status      1      702      702  0.030  0.862
## Study                     1      530      530  0.023  0.880
## Maternal.risk.status:Study 1      655      655  0.028  0.867
## Residuals                173 4009072  23174
## 2 observations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

Effect of Maternal Risk Status on EAH Intake Across Studies



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 + Study)
```

```
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)

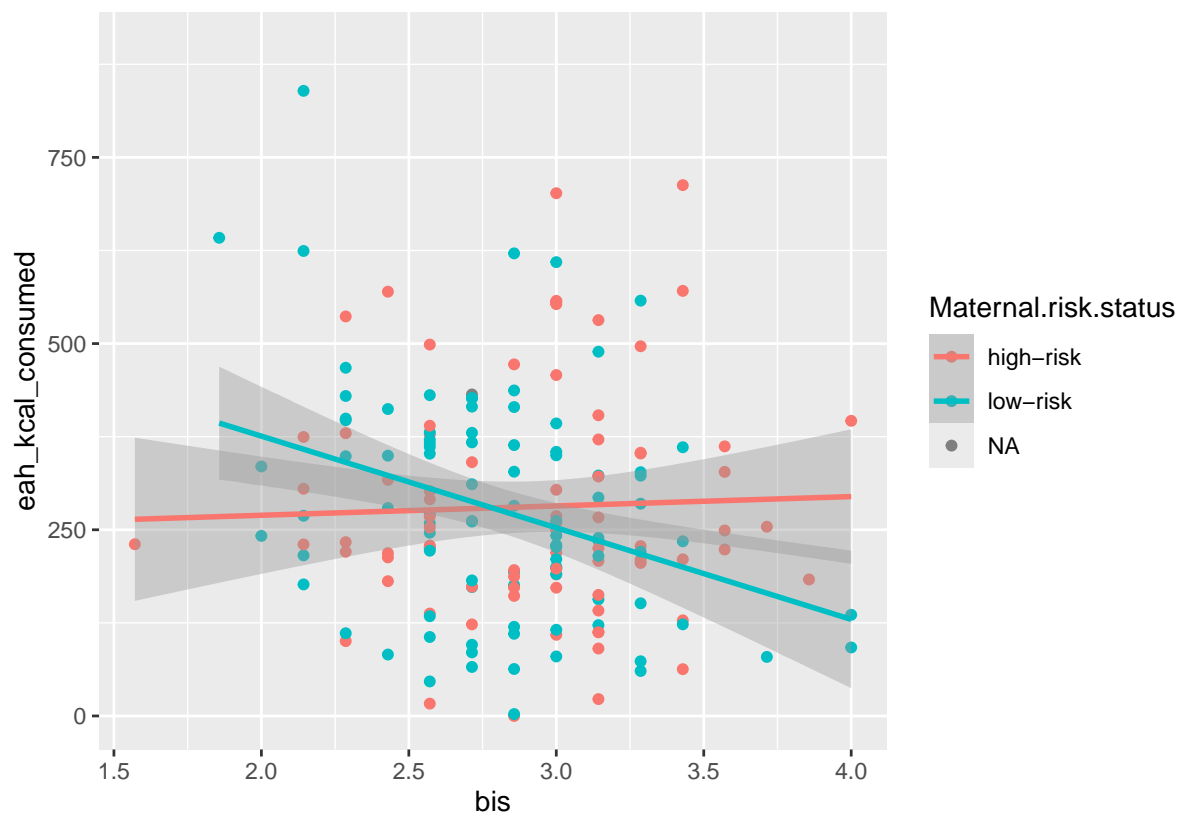
thesis_data_no_na <- subset(thesis_data,
  subset = !MISSING)

#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.status))) +
  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'

