

Lab sheet 5: Introduction to statistics

I have used codes from the book Dalgaard (2008) for this lab.

Descriptive statistics

```
x <- rnorm(50)
mean(x)

## [1] 0.2879942

sd(x)

## [1] 0.9741027

var(x)

## [1] 0.948876

median(x)

## [1] 0.4431678

quantile(x)

##          0%          25%          50%          75%         100%
## -2.1752971 -0.3625079  0.4431678  0.9609244  1.8387456

pvec <- seq(0,1,0.1)
pvec

## [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0

quantile(x,pvec)

##          0%          10%          20%          30%          40%
## -2.1752971 -0.9870185 -0.5175594 -0.1879778  0.2555013
##          50%          60%          70%          80%          90%
##  0.4431678  0.6864961  0.7929217  1.0217611  1.5129560
##          100%
##  1.8387456

data()
head(Nile)

## [1] 1120 1160  963 1210 1160 1160

summary(Nile)

##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  456.0  798.5   893.5   919.4 1032.5  1370.0

library('ISwR')
attach(juul)
names(juul)

## [1] "age"      "menarche" "sex"      "igf1"     "tanner"
```

```
## [6] "testvol"
mean(igf1)

## [1] NA
mean(igf1,na.rm=T)

## [1] 340.168
summary(igf1)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's
##      25.0  202.2   313.5   340.2  462.8   915.0     321

summary(juul)

##      age      menarche      sex      igf1
## Min.   : 0.170    No :369    M   :621    Min.   : 25.0
## 1st Qu.: 9.053    Yes:335    F   :713    1st Qu.:202.2
## Median :12.560    NA's:635    NA's: 5     Median :313.5
## Mean   :15.095                                     Mean   :340.2
## 3rd Qu.:16.855                                     3rd Qu.:462.8
## Max.   :83.000                                     Max.   :915.0
## NA's   :5                                           NA's   :321
## tanner      testvol
## I   :515    Min.   : 1.000
## II  :103    1st Qu.: 1.000
## III : 72    Median : 3.000
## IV  : 81    Mean   : 7.896
## V   :328    3rd Qu.:15.000
## NA's:240    Max.   :30.000
##              NA's   :859

detach(juul)

juul$sex <- factor(juul$sex,labels=c("M","F"))
juul$menarche <- factor(juul$menarche,labels=c("No","Yes"))
juul$tanner <- factor(juul$tanner,labels=c("I","II","III","IV","V"))
attach(juul)
summary(juul)

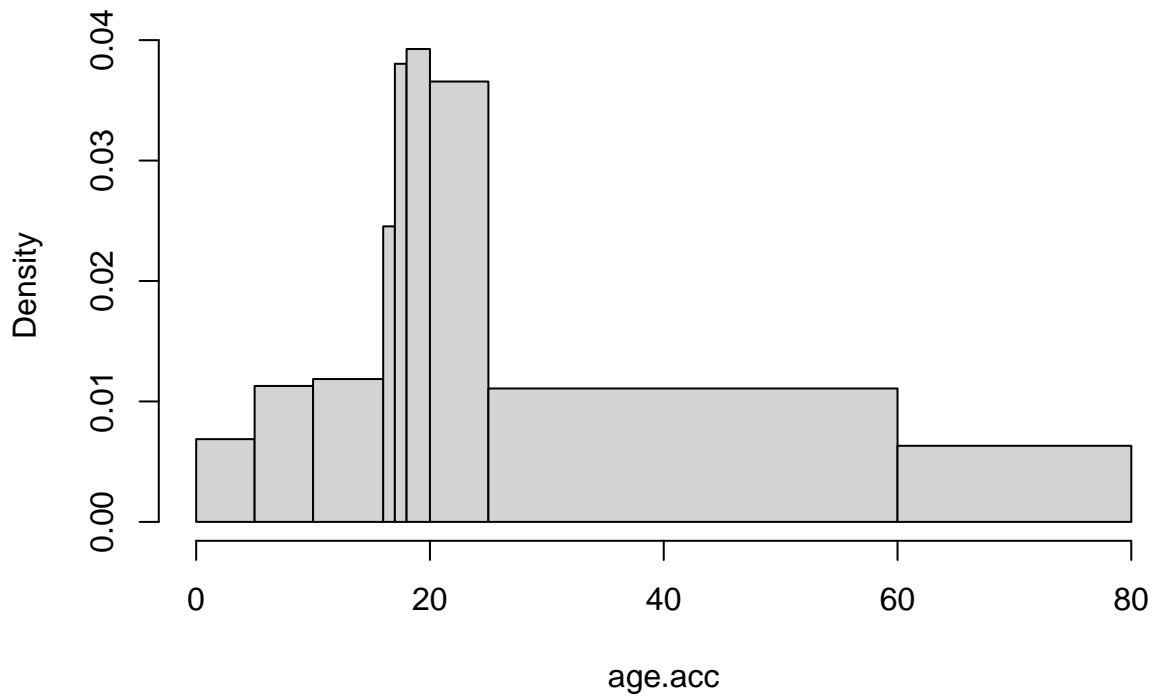
##      age      menarche      sex      igf1
## Min.   : 0.170    No :369    M   :621    Min.   : 25.0
## 1st Qu.: 9.053    Yes:335    F   :713    1st Qu.:202.2
## Median :12.560    NA's:635    NA's: 5     Median :313.5
## Mean   :15.095                                     Mean   :340.2
## 3rd Qu.:16.855                                     3rd Qu.:462.8
## Max.   :83.000                                     Max.   :915.0
## NA's   :5                                           NA's   :321
## tanner      testvol
## I   :515    Min.   : 1.000
## II  :103    1st Qu.: 1.000
## III : 72    Median : 3.000
## IV  : 81    Mean   : 7.896
## V   :328    3rd Qu.:15.000
## NA's:240    Max.   :30.000
##              NA's   :859
```

```
juul <- transform(juul,sex=factor(sex,labels=c("M","F")),
  menarche=factor(menarche,labels=c("No","Yes")),
  tanner=factor(tanner,labels=c("I","II","III","IV","V")))
```

Graphics for single data

```
mid.age <- c(2.5,7.5,13,16.5,17.5,19,22.5,44.5,70.5)
acc.count <- c(28,46,58,20,31,64,149,316,103)
age.acc <- rep(mid.age,acc.count)
brk <- c(0,5,10,16,17,18,20,25,60,80)
hist(age.acc,breaks=brk)
```

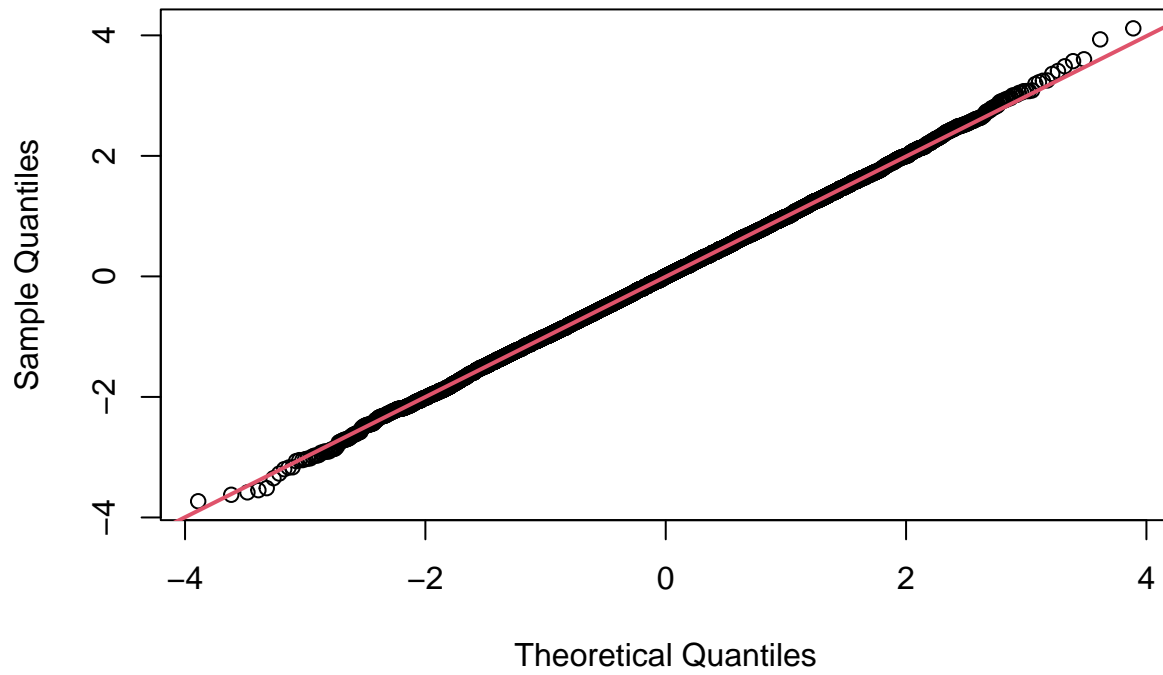
Histogram of age.acc



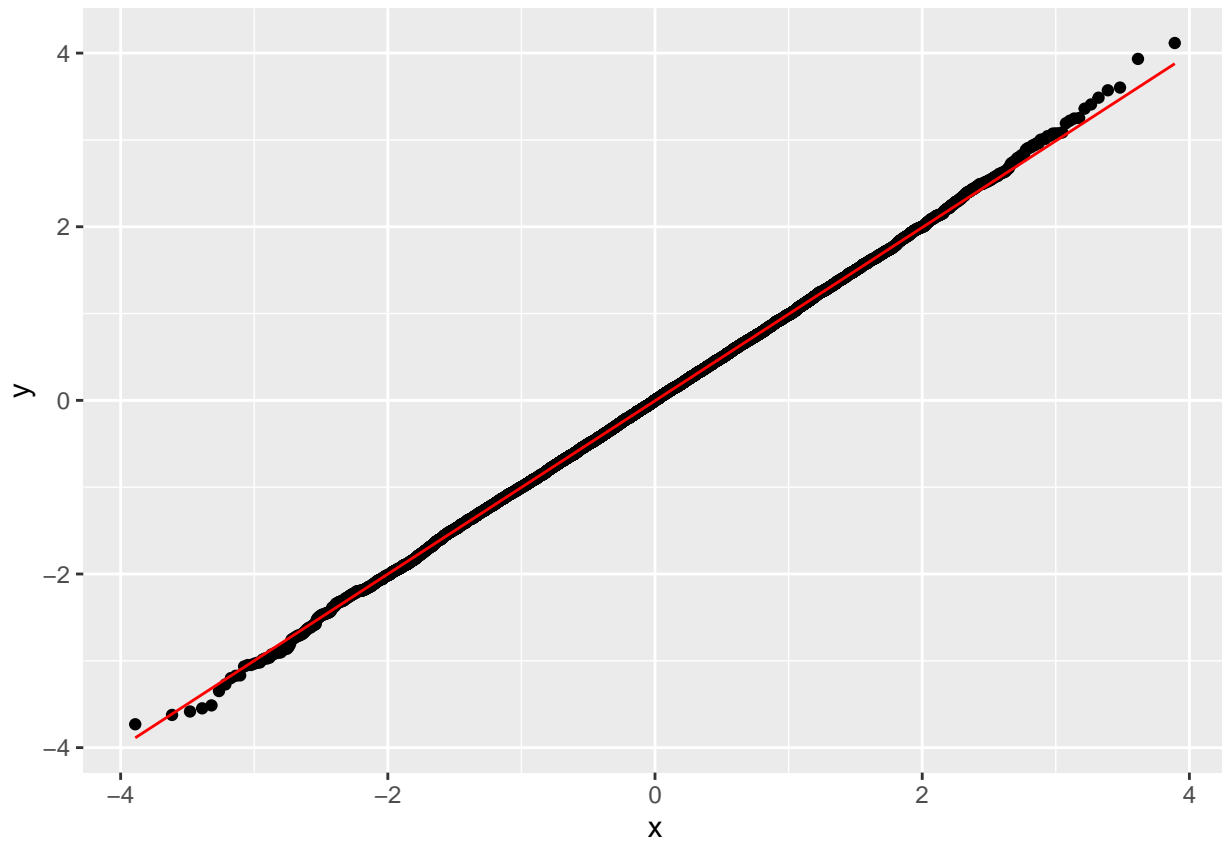
Q-Q plot

```
x <- rnorm(10000)
qqnorm(x)
qqline(x, col = 2,lwd=2)
```

Normal Q-Q Plot

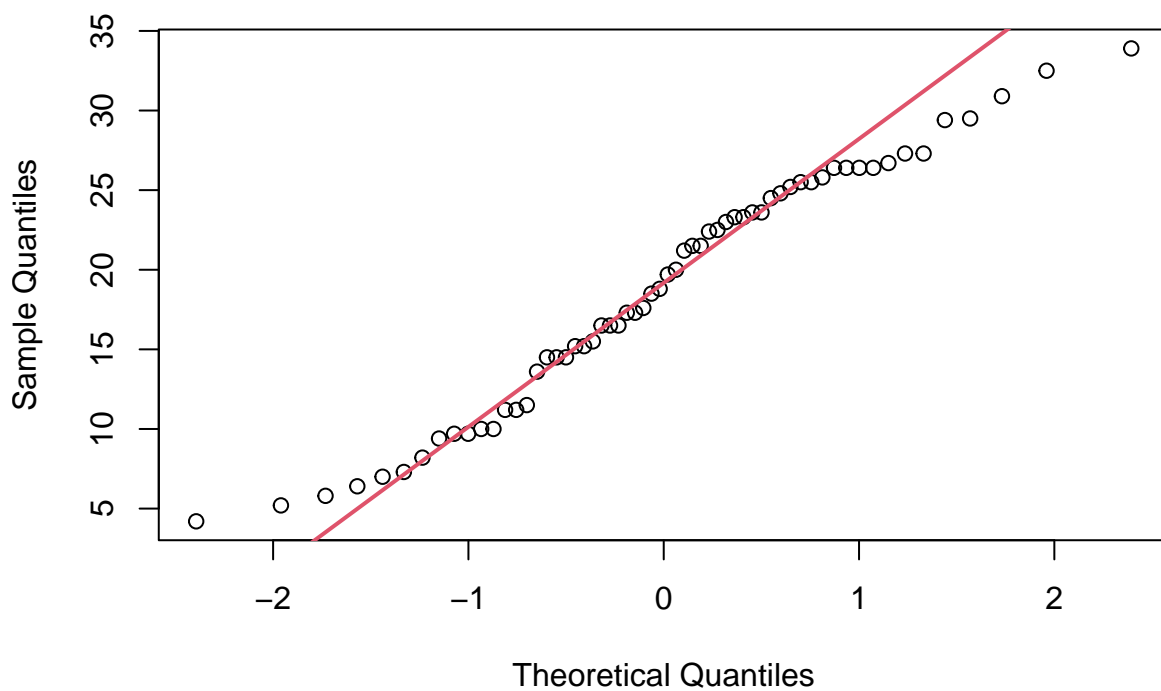


```
library(ggplot2)
data <- data.frame(x)
ggplot(data, aes(sample = x)) +
  stat_qq() +
  stat_qq_line(col = "red")
```



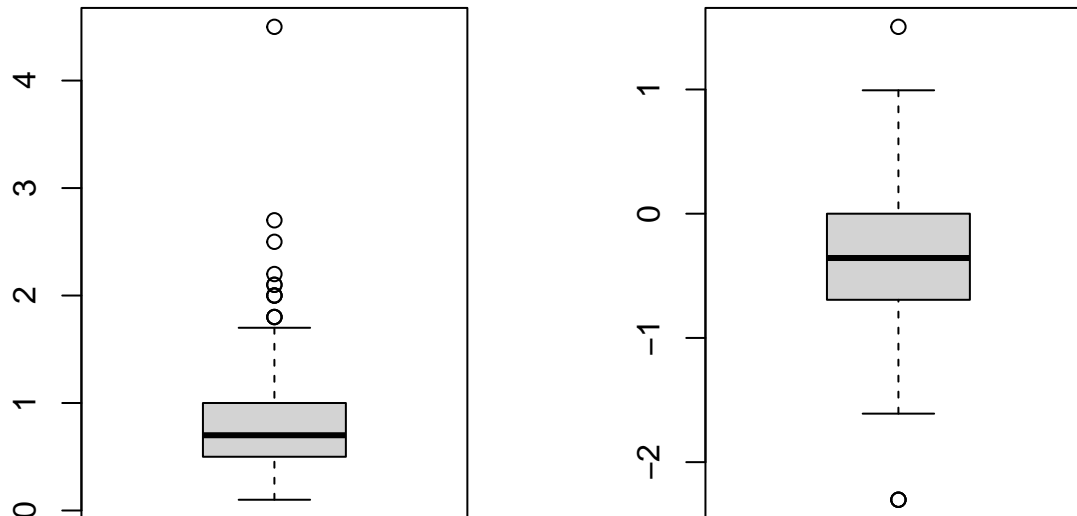
```
sample_data <- ToothGrowth
qqnorm(sample_data$len)
qqline(sample_data$len, col = 2, lwd = 2)
```

Normal Q-Q Plot



Box plot

```
par(mfrow=c(1,2))
boxplot(IgM)
boxplot(log(IgM))
```



```
par(mfrow=c(1,1))
```

Summary statistics by group

```
xbar <- tapply(igf1, tanner, mean, na.rm=T)
s <- tapply(igf1, tanner, sd, na.rm=T)
n <- tapply(igf1, tanner, length)
cbind(mean=xbar, std.dev=s, n=n)
```

```
##      mean  std.dev  n
## I    207.4727  90.27237 515
## II   352.6714 122.59332 103
## III  483.2222 152.28664  72
## IV   513.0172 119.09594  81
## V    465.3344 134.41867 328
```

```
aggregate(juul[c("age","igf1")], juul["sex"], mean, na.rm=T)
```

```
##   sex    age    igf1
## 1  M 15.38436 310.8866
## 2  F 14.84363 368.1006
```

```
by(juul, juul["sex"], summary)
```

```
## sex: M
##   age    menarche  sex    igf1    tanner
## Min.   : 0.17    No : 0  M:621  Min.   : 29.0    I   :291
## 1st Qu.: 8.85    Yes: 0  F:  0  1st Qu.:176.0   II  : 55
## Median :12.38    NA's:621           Median :280.0   III : 34
## Mean   :15.38                      Mean   :310.9    IV  : 41
## 3rd Qu.:16.77                      3rd Qu.:430.2   V   :124
## Max.   :83.00                      Max.   :915.0   NA's: 76
##                                     NA's   :145
##   testvol
```

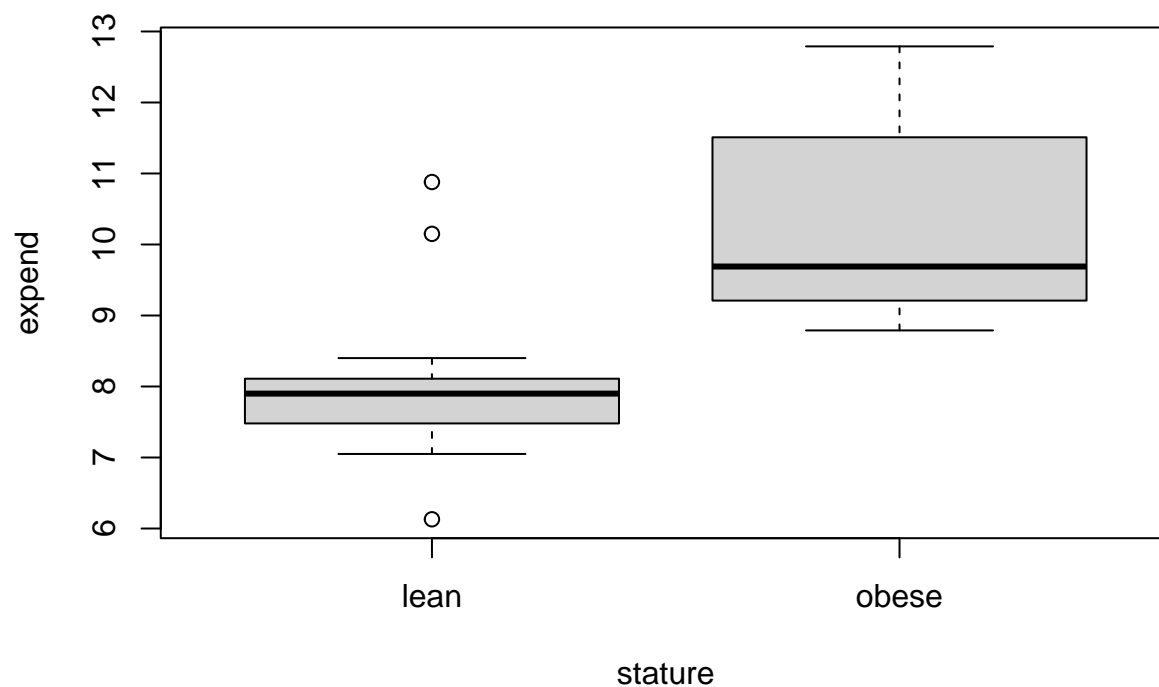
```
## Min.    : 1.000
## 1st Qu.: 1.000
## Median : 3.000
## Mean    : 7.896
## 3rd Qu.:15.000
## Max.    :30.000
## NA's    :141
## -----
## sex: F
##      age      menarche  sex      igf1      tanner
## Min.    : 0.25   No :369   M: 0   Min.    : 25.0   I    :224
## 1st Qu.: 9.30   Yes :335  F:713  1st Qu.:233.0  II   : 48
## Median :12.80   NA's: 9      Median :352.0  III  : 38
## Mean    :14.84      Mean    :368.1  IV   : 40
## 3rd Qu.:16.93      3rd Qu.:483.0  V    :204
## Max.    :75.12      Max.    :914.0  NA's:159
##                      NA's    :176
##      testvol
## Min.    : NA
## 1st Qu.: NA
## Median : NA
## Mean    :NaN
## 3rd Qu.: NA
## Max.    : NA
## NA's    :713
```

Graphics for grouped data

```
attach(energy)
expnd.lean <- expnd[stature=="lean"]
expnd.obese <- expnd[stature=="obese"]
par(mfrow=c(2,1))
hist(expnd.lean,breaks=10,xlim=c(5,13),ylim=c(0,4),col="white")
hist(expnd.obese,breaks=10,xlim=c(5,13),ylim=c(0,4),col="grey")
```



```
par(mfrow=c(1,1))
boxplot(expend ~ stature)
```



Tables

```
caff.marital <- matrix(c(652,1537,598,242,36,46,38,21,218,327,106,67),
                        nrow=3,byrow=T)
colnames(caff.marital) <- c("0","1-150","151-300", ">300")
```



```
rownames(caff.marital) <- c("Married","Prev.married","Single")
caff.marital
```

```
##           0 1-150 151-300 >300
## Married   652 1537    598 242
## Prev.married 36  46     38  21
## Single    218 327    106  67
```

```
names(dimnames(caff.marital)) <- c("marital","consumption")
caff.marital
```

```
##           consumption
## marital      0 1-150 151-300 >300
## Married      652 1537    598 242
## Prev.married 36  46     38  21
## Single       218 327    106  67
```

```
as.data.frame(as.table(caff.marital))
```

```
##      marital consumption Freq
## 1      Married           0 652
## 2 Prev.married           0  36
## 3      Single            0 218
## 4      Married       1-150 1537
## 5 Prev.married       1-150  46
## 6      Single       1-150 327
## 7      Married     151-300 598
## 8 Prev.married     151-300  38
## 9      Single     151-300 106
## 10     Married           >300 242
## 11 Prev.married           >300  21
## 12     Single           >300  67
```

```
table(menarche,tanner)
```

```
##           tanner
## menarche  I  II III  IV  V
## No      221 43 32 14  2
## Yes       1  1  5 26 202
```

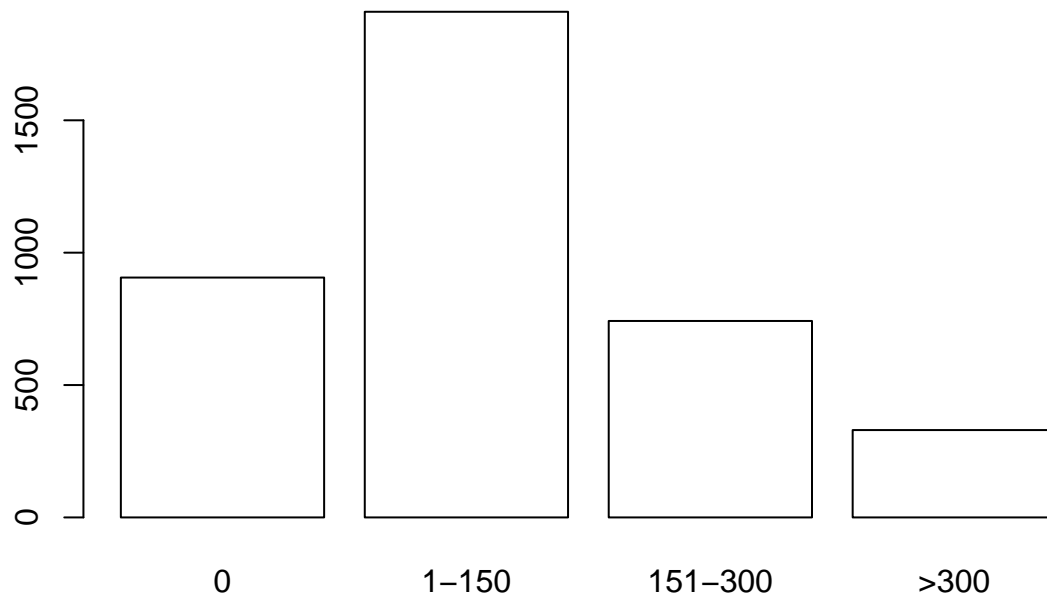
```
xtabs(~ tanner + sex, data=juul)
```

```
##           sex
## tanner  M  F
## I      291 224
## II     55  48
## III    34  38
## IV     41  40
## V     124 204
```

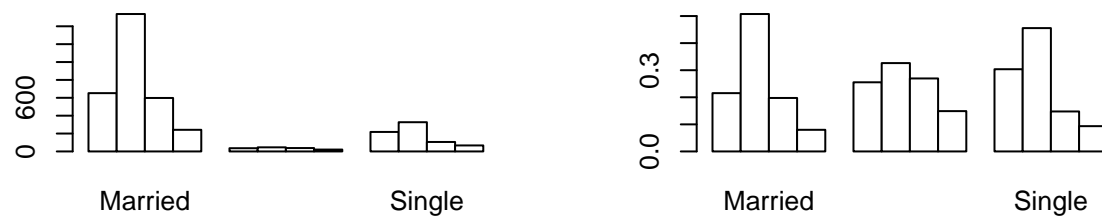
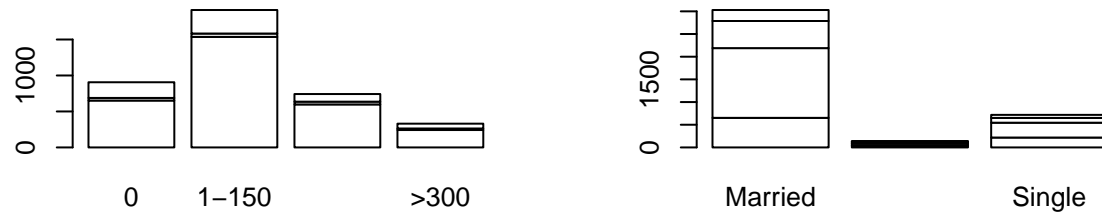
```
total.caff <- margin.table(caff.marital,2)
total.caff
```

```
## consumption
##      0 1-150 151-300 >300
## 906 1910 742 330
```

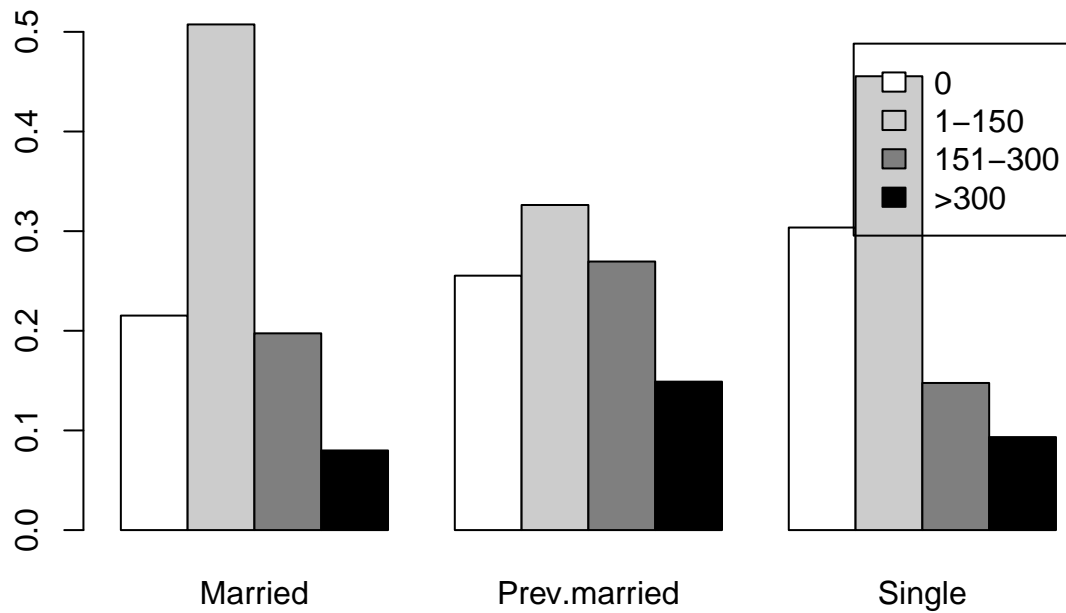
```
barplot(total.caff, col="white")
```



```
par(mfrow=c(2,2))
barplot(caff.marital, col="white")
barplot(t(caff.marital), col="white")
barplot(t(caff.marital), col="white", beside=T)
barplot(prop.table(t(caff.marital),2), col="white", beside=T)
```



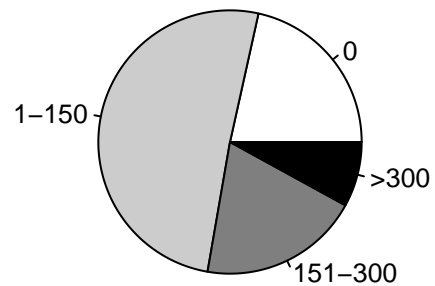
```
par(mfrow=c(1,1))
barplot(prop.table(t(caff.marital),2),beside=T,
        legend.text=colnames(caff.marital),
        col=c("white","grey80","grey50","black"))
```



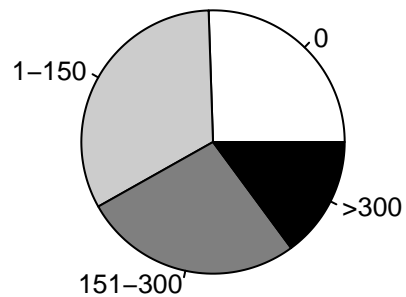
Piecharts

```
opar <- par(mfrow=c(2,2),mex=0.8, mar=c(1,1,2,1))
slices <- c("white","grey80","grey50","black")
pie(caff.marital["Married",], main="Married", col=slices)
pie(caff.marital["Prev.married",],
    main="Previously married", col=slices)
pie(caff.marital["Single",], main="Single", col=slices)
par(opar)
```

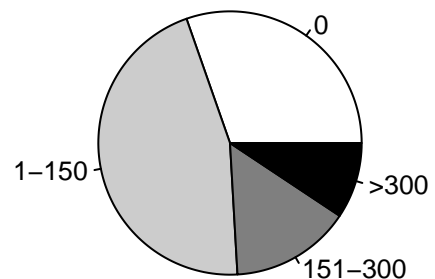
Married



Previously married



Single



References

Dalgaard, Peter. 2008. *Introductory Statistics with R*. Springer New York. <https://doi.org/10.1007/978-0-387-79054-1>.