Descriptive Statistics

Partially adapted from tableone's vignette

6/15/2021

Descriptive Statistics

- First analytical task to understand the data and begin to see patterns
- Numerical and graphical description of the data
- Today we'll (mostly) focus on univariate summary statistics (i.e. one variable at time)
- We'll discuss bivariate summary statistics (i.e. two variables at a time) next week

Mayo Clinic's PBC data

- Mayo Clinic trial in primary biliary cirrhosis (PBC) of the liver
- Conducted between 1974 and 1984.
- Placebo controlled trial of the drug D-penicillamine.
- First 424 PBC patients
- First 312 cases in the data set participated in the randomized trial and contain largely complete data.
- Additional 106 subjects did not participate in the clinical trial but consented to have data collected

```
setwd("~/LA's best")
pbc = read.csv('pbc.csv')
dim(pbc) #How many observations (rows) and how many variables (columns)
```

```
## [1] 418  20
```

Mayo Clinic's PBC data

Categorical variables:

- id
- status: 0=alive, 1=liver transplant, 2=dead
- trt: 1 = D-penicillamine, 2=placebo
- sex: 0=male, 1=female
- presence of ascites: 0=no 1=yes
- presence of hepatomegaly: 0=no 1=yes
- presence of spiders 0=no 1=yes
- presence of edema: 0=no edema and no diuretic therapy for edema; .5 = edema present without diuretics, or edema resolved by diuretics; 1 = edema despite diuretic therapy
- histologic stage of disease

Mayo Clinic's PBC data

Quantitative variables:

- number of days between registration and the earlier of death, transplantion, or study analysis time in July, 1986
- age in days
- serum bilirubin in mg/dl
- serum cholesterol in mg/dl
- albumin in gm/dl
- urine copper in ug/day
- alkaline phosphatase in U/liter
- SGOT (Serum glutamic oxaloacetic transaminase) in U/ml
- triglycerides in mg/dl
- platelets per cubic ml/1000
- prothrombin time in seconds

Mayo Clinic's PBC data

```
summary(pbc)
```

```
##        id              time          status            trt
##  Min.   :  1.0   Min.   :  41   Min.   :0.0000   Min.   :1.000
##  1st Qu.:105.2   1st Qu.:1093   1st Qu.:0.0000   1st Qu.:1.000
##  Median :209.5   Median :1730   Median :0.0000   Median :1.000
##  Mean   :209.5   Mean   :1918   Mean   :0.8301   Mean   :1.494
##  3rd Qu.:313.8   3rd Qu.:2614   3rd Qu.:2.0000   3rd Qu.:2.000
##  Max.   :418.0   Max.   :4795   Max.   :2.0000   Max.   :2.000
##                                                  NA's   :106
##       age            sex               ascites            hepato
##  Min.   :26.28   Length:418         Min.   :0.00000   Min.   :0.0000
##  1st Qu.:42.83   Class :character   1st Qu.:0.00000   1st Qu.:0.0000
##  Median :51.00   Mode  :character   Median :0.00000   Median :1.0000
##  Mean   :50.74                      Mean   :0.07692   Mean   :0.5128
##  3rd Qu.:58.24                      3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :78.44                      Max.   :1.00000   Max.   :1.0000
##                                     NA's   :106       NA's   :106
##     spiders           edema            bili              chol
##  Min.   :0.0000   Min.   :0.0000   Min.   : 0.300   Min.   : 120.0
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.: 0.800   1st Qu.: 249.5
##  Median :0.0000   Median :0.0000   Median : 1.400   Median : 309.5
##  Mean   :0.2885   Mean   :0.1005   Mean   : 3.221   Mean   : 369.5
##  3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.: 3.400   3rd Qu.: 400.0
##  Max.   :1.0000   Max.   :1.0000   Max.   :28.000   Max.   :1775.0
##  NA's   :106                                        NA's   :134
##     albumin          copper          alk.phos            ast
##  Min.   :1.960   Min.   :  4.00   Min.   :  289.0   Min.   : 26.35
##  1st Qu.:3.243   1st Qu.: 41.25   1st Qu.:  871.5   1st Qu.: 80.60
##  Median :3.530   Median : 73.00   Median : 1259.0   Median :114.70
##  Mean   :3.497   Mean   : 97.65   Mean   : 1982.7   Mean   :122.56
##  3rd Qu.:3.770   3rd Qu.:123.00   3rd Qu.: 1980.0   3rd Qu.:151.90
##  Max.   :4.640   Max.   :588.00   Max.   :13862.4   Max.   :457.25
```

Mayo Clinic's PBC data

```
head(pbc)
```

```
##   id time status trt      age sex ascites hepato spiders edema bili chol
## 1  1  400      2   1 58.76523   f       1      1       1   1.0 14.5  261
## 2  2 4500      0   1 56.44627   f       0      1       1   0.0  1.1  302
## 3  3 1012      2   1 70.07255   m       0      0       0   0.5  1.4  176
## 4  4 1925      2   1 54.74059   f       0      1       1   0.5  1.8  244
## 5  5 1504      1   2 38.10541   f       0      1       1   0.0  3.4  279
## 6  6 2503      2   2 66.25873   f       0      1       0   0.0  0.8  248
##   albumin copper alk.phos    ast trig platelet protime stage
## 1    2.60    156   1718.0 137.95  172      190    12.2     4
## 2    4.14     54   7394.8 113.52   88      221    10.6     3
## 3    3.48    210    516.0  96.10   55      151    12.0     4
## 4    2.54     64   6121.8  60.63   92      183    10.3     4
## 5    3.53    143    671.0 113.15   72      136    10.9     3
## 6    3.98     50    944.0  93.00   63       NA    11.0     3
```

```
pbc$sex = factor(pbc$sex, levels = c('m', 'f'), labels = c('M', 'F'))
pbc$trt = factor(pbc$trt, levels = c(1,2), labels = c('D-penicillamine', 'placebo'))
pbc$status = factor(pbc$status, levels = c(0,1,2), labels = c('alive', 'liver transplant', 'dead'))
```

Mayo Clinic's PBC data

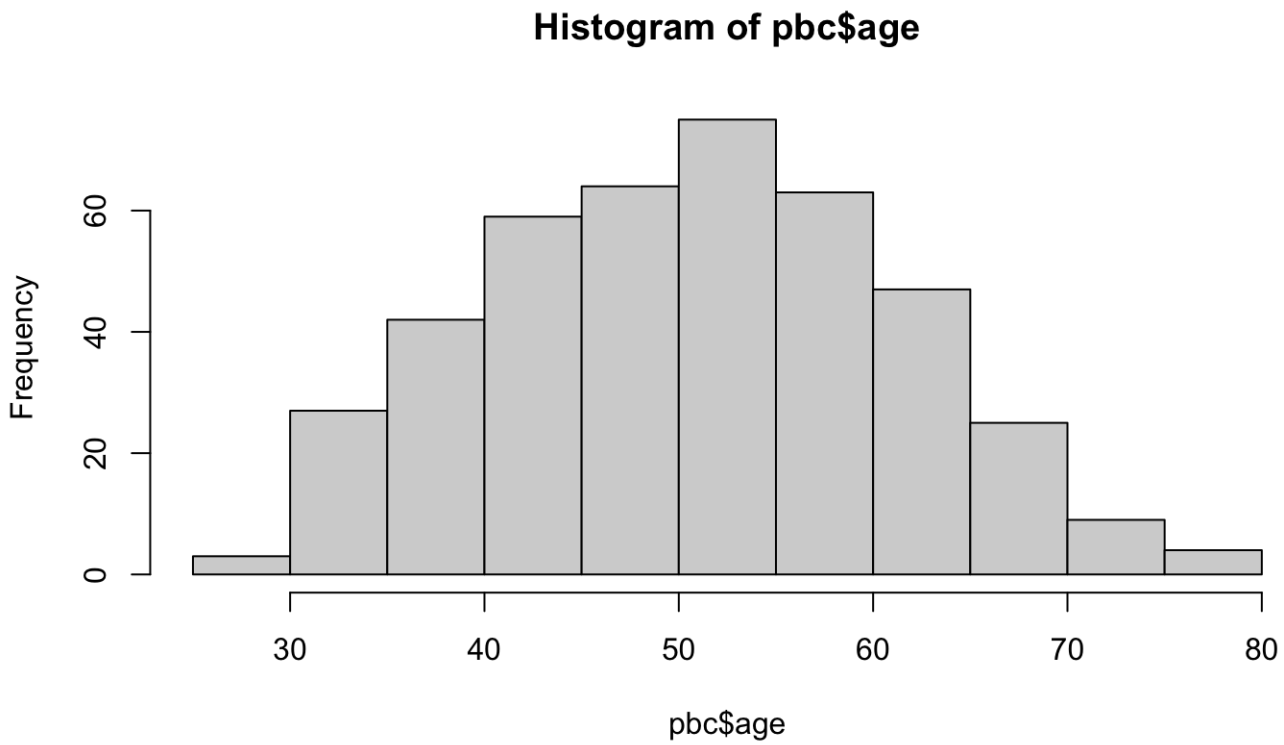
```
str(pbc)
```

```
## 'data.frame':    418 obs. of  20 variables:
##  $ id      : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ time    : int  400 4500 1012 1925 1504 2503 1832 2466 2400 51 ...
##  $ status  : Factor w/ 3 levels "alive","liver transplant",..: 3 1 3 3 2 3 1 3 3 3 ...
##  $ trt     : Factor w/ 2 levels "D-penicillamine",..: 1 1 1 1 2 2 2 2 1 2 ...
##  $ age     : num  58.8 56.4 70.1 54.7 38.1 ...
##  $ sex     : Factor w/ 2 levels "M","F": 2 2 1 2 2 2 2 2 2 2 ...
##  $ ascites : int  1 0 0 0 0 0 0 0 0 1 ...
##  $ hepato  : int  1 1 0 1 1 1 1 0 0 0 ...
##  $ spiders : int  1 1 0 1 1 0 0 0 1 1 ...
##  $ edema   : num  1 0 0.5 0.5 0 0 0 0 0 1 ...
##  $ bili    : num  14.5 1.1 1.4 1.8 3.4 0.8 1 0.3 3.2 12.6 ...
##  $ chol    : int  261 302 176 244 279 248 322 280 562 200 ...
##  $ albumin : num  2.6 4.14 3.48 2.54 3.53 3.98 4.09 4 3.08 2.74 ...
##  $ copper  : int  156 54 210 64 143 50 52 52 79 140 ...
##  $ alk.phos: num  1718 7395 516 6122 671 ...
##  $ ast     : num  137.9 113.5 96.1 60.6 113.2 ...
##  $ trig    : int  172 88 55 92 72 63 213 189 88 143 ...
##  $ platelet: int  190 221 151 183 136 NA 204 373 251 302 ...
##  $ protime : num  12.2 10.6 12 10.3 10.9 11 9.7 11 11 11.5 ...
##  $ stage   : int  4 3 4 4 3 3 3 3 2 4 ...
```

Histograms

Histogram: univariate graphical summary for a quantitative/continuous variable

```
hist(pbc$age)
```



Descriptive stats for quantitative variables

Measures of location: mean, mode, median, first quartile, third quartile, minimum, maximum

```
mean(pbc$age)
```

```
## [1] 50.74155
```

```
median(pbc$age)
```

```
## [1] 51.00068
```

```
min(pbc['age'])
```

```
## [1] 26.27789
```

```
max(pbc[, 5])    # Not recommended to subset by column number
```

```
## [1] 78.43943
```

Descriptive stats for quantitative variables

Measures of dispersion: variance, standard deviation, interquantile range (IQR)

```
var(pbc$age)
```

```
## [1] 109.1443
```

```
sd(pbc$age)
```

```
## [1] 10.44721
```

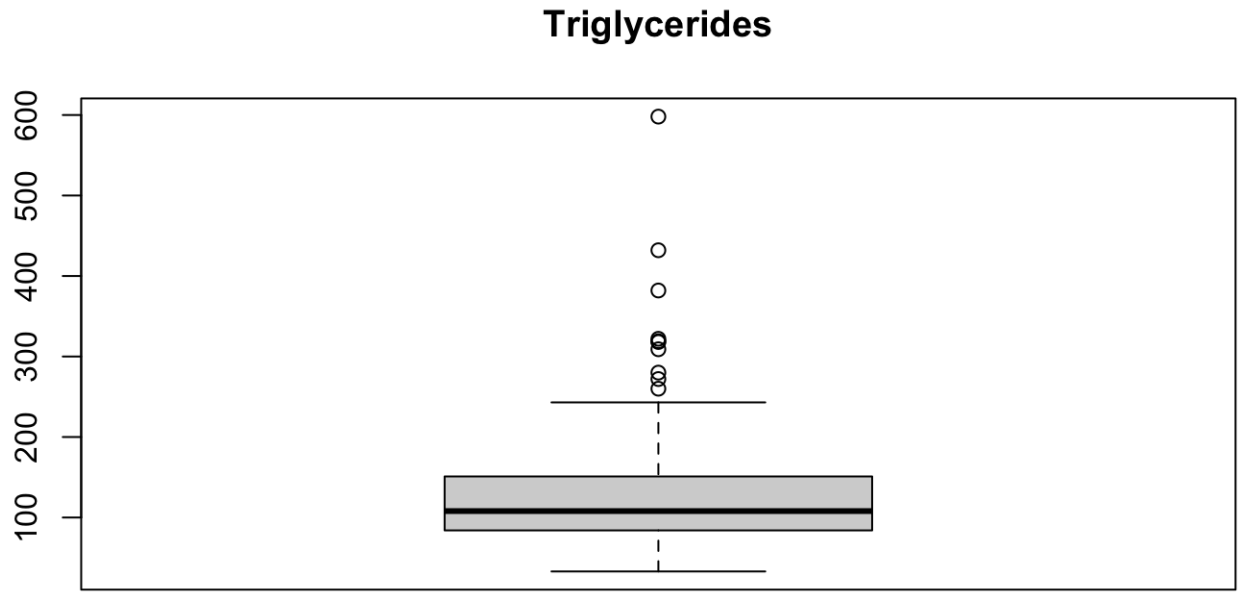
```
IQR(pbc[,'age'])
```

```
## [1] 15.40862
```

Boxplots

Boxplots combines key summary stats (median, quartiles, IQR) into a summary plot

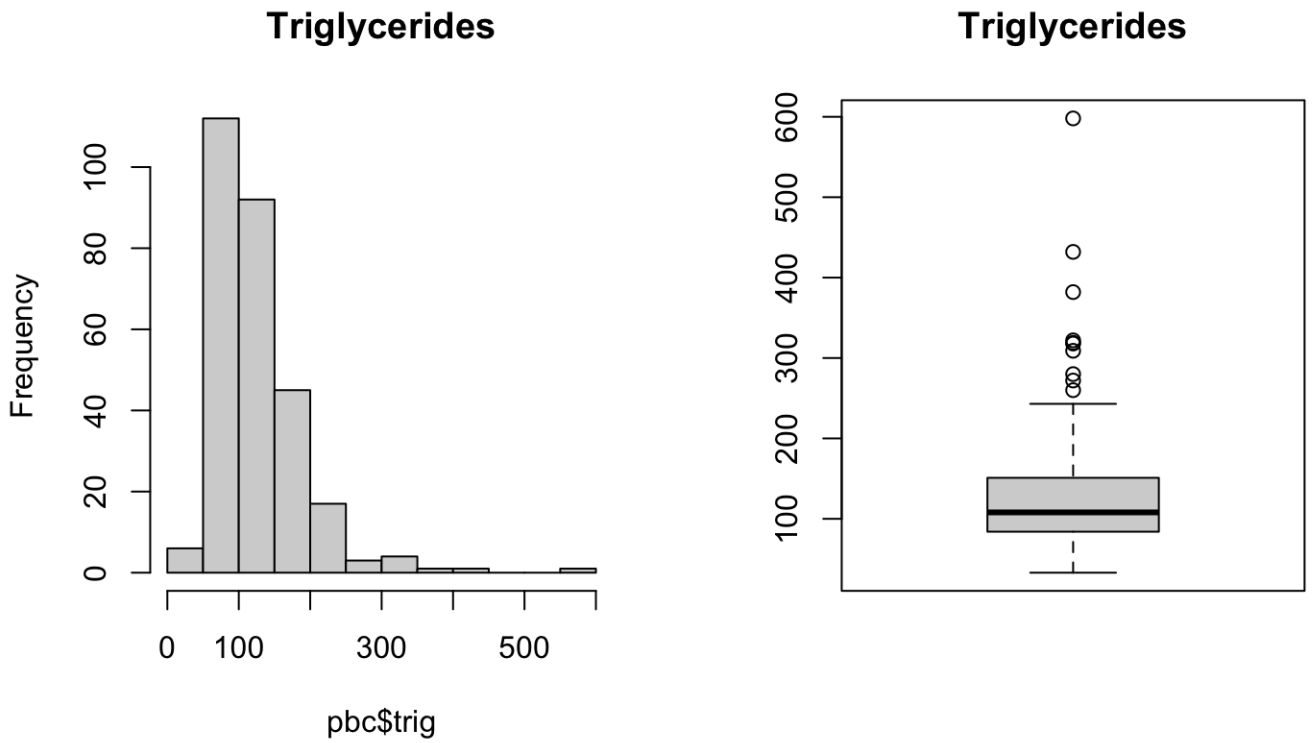
```
boxplot(pbc$trig, main = 'Triglycerides')
```



Is Triglycerides skewed left or right?

Histogram and boxplot on same plot

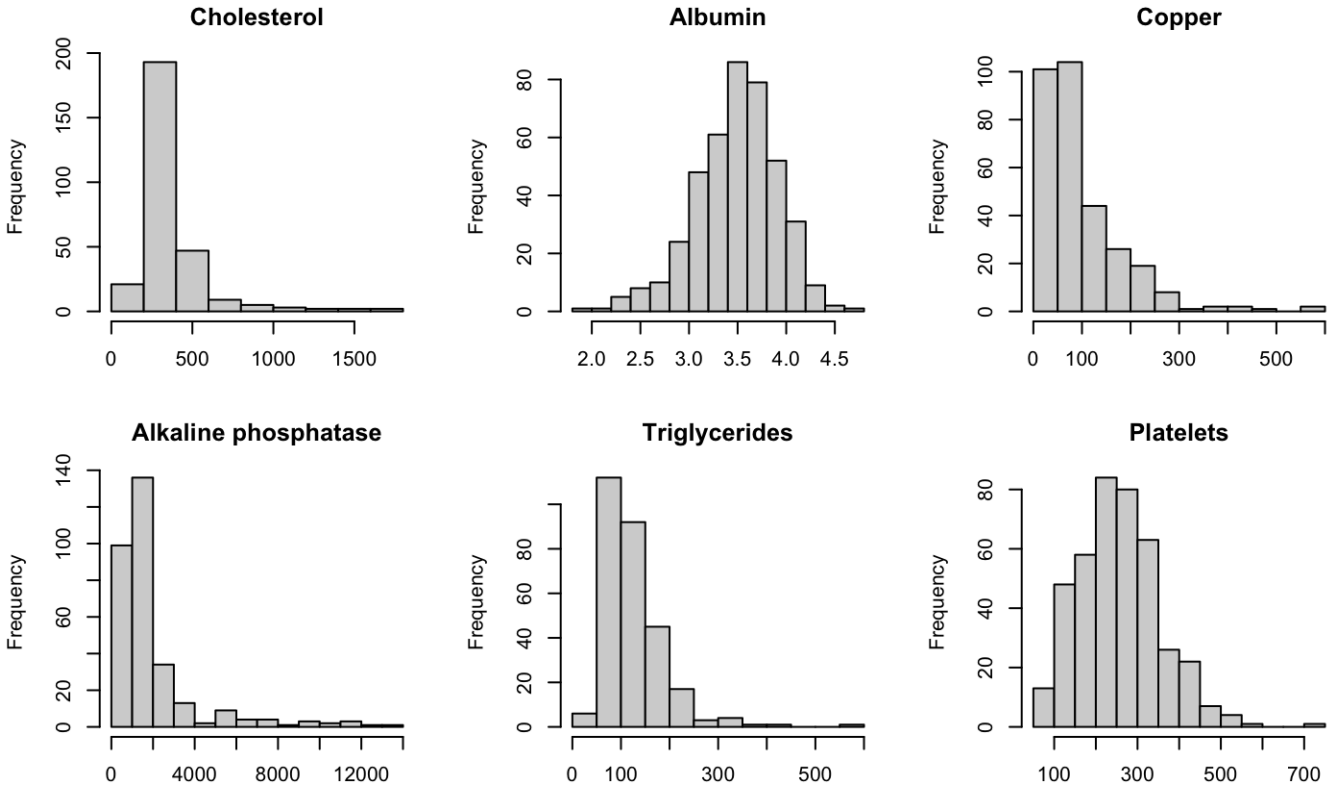
```
par(mfrow = c(1, 2))
hist(pbc$trig, main='Triglycerides')
boxplot(pbc$trig, main = 'Triglycerides')
```



Multiple Histograms

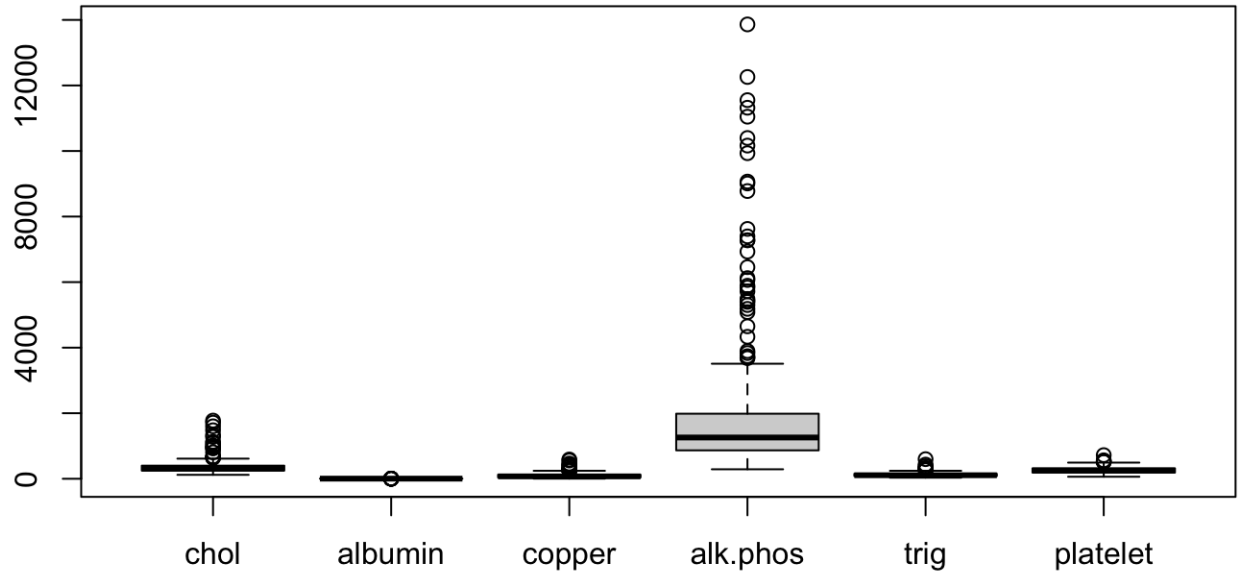
```
par(mfrow = c(2, 3))

hist(pbc$chol, main='Cholesterol')
hist(pbc$albumin, main='Albumin')
hist(pbc$copper, main='Copper')
hist(pbc$alk.phos, main='Alkaline phosphatase')
hist(pbc$trig, main='Triglycerides')
hist(pbc$platelet, main='Platelets')
```

Multiple Histograms

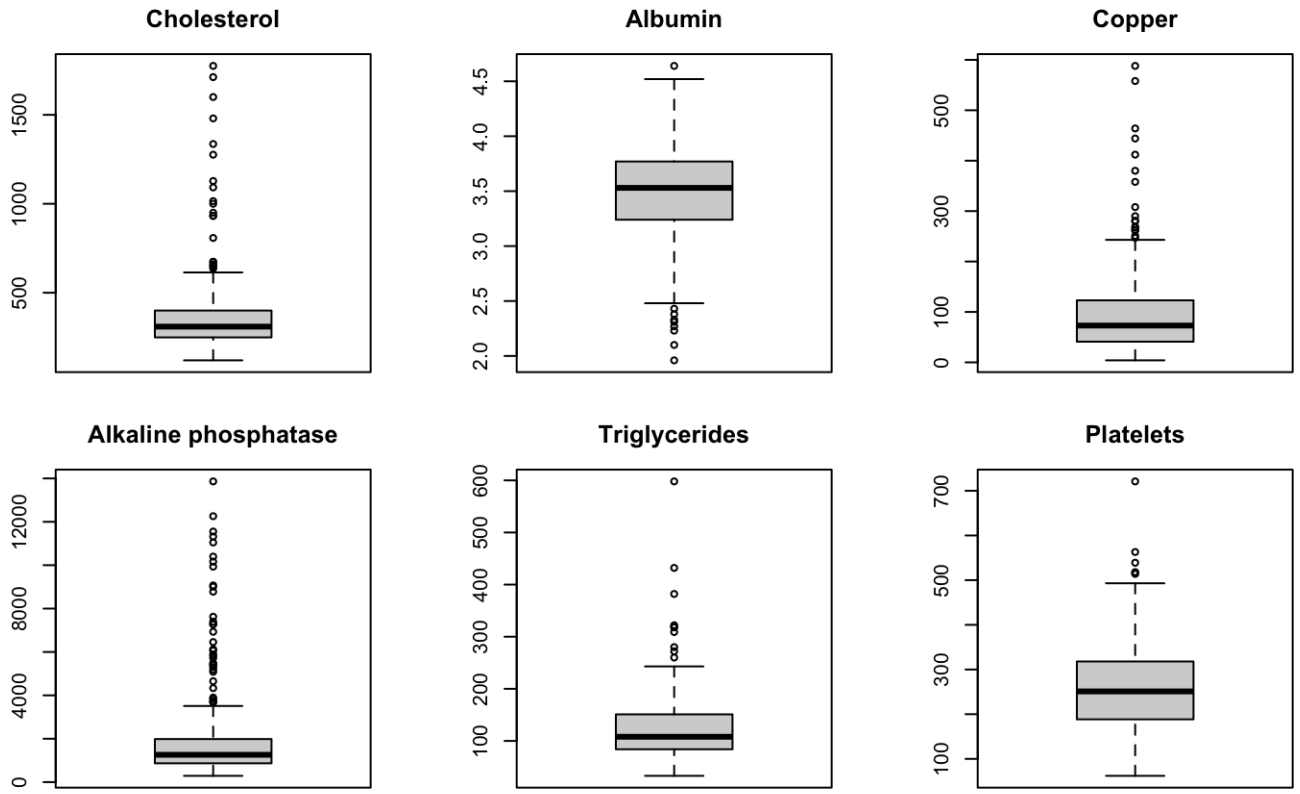


Multiple boxplots (Version 1)

```
boxplot(pbc[, c("chol", "albumin", "copper", "alk.phos", "trig", "platelet")])
```



Multiple boxplots (Version 2)



Descriptive stats for categorical variables

Numerical summary: Counts and proportion/percent per category

```
table(pbc$stage)
```

```
##
##   1   2   3   4
##  21  92 155 144
```

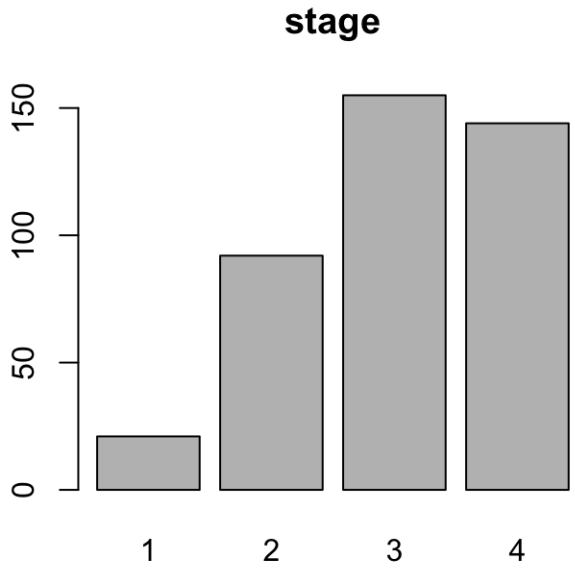
```
prop.table(table(pbc$stage))
```

```
##
##          1          2          3          4
## 0.05097087 0.22330097 0.37621359 0.34951456
```

Descriptive stats for categorical variables

Graphical summary: Barplot

```
barplot(table(pbc$stage), main = 'stage')
```



Package tableone

```
library(tableone)
```

- Makes it easy to construct table of baseline characteristics
- Commonly found in biomedical research papers as ‘Table 1’.
- Can summarize continuous and categorical variables on same table.
- Categorical variables can be summarized as counts and/or percentages.
- Continuous variables can be summarized by means and standard deviations
- or by medians and interquartile ranges.

Table 1 example

Table 1. Baseline Characteristics of the Patients.*

Variable	Rhythm-Control Group (N=682)	Rate-Control Group (N=694)
Male sex (%)	78	85
Age (yr)	66±11	67±11
Body-mass index†	27.8±5.4	28.0±5.1
Nonwhite race (%)‡	16	13
NYHA class III or IV (%)		
At baseline	32	31
During previous 6 mo	76	76
Predominant cardiac diagnosis (%)§		
Coronary artery disease	48	48
Valvular heart disease	5	5
Nonischemic cardiomyopathy	36	39
Congenital heart disease	1	1
Hypertensive heart disease	10	7
Coexisting conditions (%)		
Hypertension	49	46
Diabetes	22	20
Previous stroke or transient ischemic attack	11	8

From Roy et al. Rhythm Control versus Rate Control for Atrial Fibrillation and Heart Failure. NEJM (2008)

Single group summary

- Simplest use is for summarizing whole dataset.
- You can just feed in the data frame to the function CreateTableOne().

```
CreateTableOne(data = pbc)
```

Single group summary

```
##
##                        Overall
##   n                        418
##   id (mean (SD))         209.50 (120.81)
##   time (mean (SD))      1917.78 (1104.67)
##   status (%)
##      alive                 232 (55.5)
##      liver transplant       25 ( 6.0)
##      dead                  161 (38.5)
##   trt = placebo (%)        154 (49.4)
##   age (mean (SD))         50.74 (10.45)
##   sex = F (%)              374 (89.5)
##   ascites (mean (SD))      0.08 (0.27)
##   hepato (mean (SD))       0.51 (0.50)
##   spiders (mean (SD))      0.29 (0.45)
##   edema (mean (SD))        0.10 (0.25)
##   bili (mean (SD))         3.22 (4.41)
##   chol (mean (SD))       369.51 (231.94)
##   albumin (mean (SD))      3.50 (0.42)
##   copper (mean (SD))      97.65 (85.61)
##   alk.phos (mean (SD)) 1982.66 (2140.39)
##   ast (mean (SD))        122.56 (56.70)
##   trig (mean (SD))       124.70 (65.15)
##   platelet (mean (SD))   257.02 (98.33)
##   protime (mean (SD))     10.73 (1.02)
##   stage (mean (SD))        3.02 (0.88)
```

Subset of variables

Can specify a subset of variables to summarize using the vars argument (e.g. exclude id variable)

```
## Get variables' names
names(pbc)
```

```
##  [1] "id"       "time"     "status"   "trt"      "age"      "sex"
##  [7] "ascites"  "hepato"   "spiders"  "edema"    "bili"     "chol"
## [13] "albumin"  "copper"   "alk.phos" "ast"      "trig"     "platelet"
## [19] "protime"  "stage"
```

```
## Vector of variables to summarize
myVars <- c("status", "trt", "age", "sex", "ascites",
            "albumin", "copper", "stage")
```

```
CreateTableOne(data = pbc, vars = myVars)
```

Subset of variables

```
##
##                       Overall
##   n                     418
##   status (%)
##      alive              232 (55.5)
##      liver transplant    25 ( 6.0)
##      dead               161 (38.5)
##   trt = placebo (%)     154 (49.4)
##   age (mean (SD))     50.74 (10.45)
##   sex = F (%)           374 (89.5)
##   ascites (mean (SD))  0.08 (0.27)
##   albumin (mean (SD))  3.50 (0.42)
##   copper (mean (SD))  97.65 (85.61)
##   stage (mean (SD))    3.02 (0.88)
```

Categorical variables

- Some categorical variables are coded numerically in the dataframe (e.g. ascites, hepato)
- Need to either transform to factors as we did above for trt, sex and status
- or use factorVars argument to transform them on-the-fly.

```
catVars <- c("ascites", "stage")
```

Categorical variables

- Binary categorical variables are summarized as counts and percentages of the second level
- For 3+ category variable all levels are summarized
- Percentages are calculated after excluding missing values.

```
tab2 = CreateTableOne(vars = myVars, data = pbc, factorVars = catVars)
```

```
tab2
```

Categorical variables

```
##
##                        Overall
##   n                      418
##   status (%)
##      alive               232 (55.5)
##      liver transplant     25 ( 6.0)
##      dead                161 (38.5)
##   trt = placebo (%)      154 (49.4)
##   age (mean (SD))      50.74 (10.45)
##   sex = F (%)            374 (89.5)
##   ascites = 1 (%)         24 ( 7.7)
##   albumin (mean (SD))   3.50 (0.42)
##   copper (mean (SD))   97.65 (85.61)
##   stage (%)
##      1                    21 ( 5.1)
##      2                    92 (22.3)
##      3                   155 (37.6)
##      4                   144 (35.0)
```

Showing all categories

```
print(tab2, showAllLevels = TRUE)
```

```
##
##                      level            Overall
##   n                                     418
##   status (%)         alive              232 (55.5)
##                      liver transplant    25 ( 6.0)
##                      dead               161 (38.5)
##   trt (%)            D-penicillamine    158 (50.6)
##                      placebo            154 (49.4)
##   age (mean (SD))                     50.74 (10.45)
##   sex (%)            M                   44 (10.5)
##                      F                  374 (89.5)
##   ascites (%)        0                  288 (92.3)
##                      1                   24 ( 7.7)
##   albumin (mean (SD))                  3.50 (0.42)
##   copper (mean (SD))                  97.65 (85.61)
##   stage (%)          1                   21 ( 5.1)
##                      2                   92 (22.3)
##                      3                  155 (37.6)
##                      4                  144 (35.0)
```

Recoding ascites

```
pbc$ascites = factor(pbc$ascites, levels = c(0,1), labels = c('No', 'Yes'))
tab2 = CreateTableOne(vars = myVars, data = pbc, factorVars = catVars)
print(tab2, showAllLevels = TRUE)
```

```
##
##                       level            Overall
##   n                                      418
##   status (%)          alive              232 (55.5)
##                       liver transplant    25 ( 6.0)
##                       dead               161 (38.5)
##   trt (%)             D-penicillamine    158 (50.6)
##                       placebo            154 (49.4)
##   age (mean (SD))                      50.74 (10.45)
##   sex (%)             M                   44 (10.5)
##                       F                  374 (89.5)
##   ascites (%)         No                 288 (92.3)
##                       Yes                 24 ( 7.7)
##   albumin (mean (SD))                    3.50 (0.42)
##   copper (mean (SD))                   97.65 (85.61)
##   stage (%)           1                   21 ( 5.1)
##                       2                   92 (22.3)
##                       3                  155 (37.6)
##                       4                  144 (35.0)
```

Detailed information on missing values

```
summary(tab2$ContTable)
```

```
## strata: Overall
##           n miss p.miss mean    sd median  p25   p75 min   max   skew  kurt
## age     418    0      0 50.7 10.45   51.0 42.8  58.2  26  78.4  0.087 -0.62
## albumin 418    0      0  3.5  0.42    3.5  3.2   3.8   2   4.6 -0.468  0.57
## copper  418  108     26 97.6 85.61   73.0 41.2 123.0   4 588.0  2.304  7.62
```

Detailed information on missing values

```
summary(tab2$CatTable)
```

```
## strata: Overall
##      var   n miss p.miss            level freq percent cum.percent
##   status 418    0    0.0            alive  232    55.5        55.5
##                          liver transplant   25     6.0        61.5
##                                     dead  161    38.5       100.0
##
##      trt 418  106   25.4  D-penicillamine  158    50.6        50.6
##                                  placebo  154    49.4       100.0
##
##      sex 418    0    0.0                M   44    10.5        10.5
##                                         F  374    89.5       100.0
##
##  ascites 418  106   25.4               No  288    92.3        92.3
##                                        Yes   24     7.7       100.0
##
##    stage 418    6    1.4                1   21     5.1         5.1
##                                         2   92    22.3        27.4
##                                         3  155    37.6        65.0
##                                         4  144    35.0       100.0
##
```

Summarizing nonnormal variables

- albumin, and copper are negatively and positively skewed respectively
- Age is symmetric, bell-shaped, normal looking
- Skewed distributions are not well summarized by mean and sd
- Use median and IQR for skewed/nonnormal variables

```
skewed <- c("albumin","copper")
```

```
print(tab2, nonnormal = skewed)
```

Summarizing skewed variables

```
##
##                          Overall
##   n                        418
##   status (%)
##      alive                 232 (55.5)
##      liver transplant       25 ( 6.0)
##      dead                  161 (38.5)
##   trt = placebo (%)        154 (49.4)
##   age (mean (SD))        50.74 (10.45)
##   sex = F (%)              374 (89.5)
##   ascites = Yes (%)         24 ( 7.7)
##   albumin (median [IQR])  3.53 [3.24, 3.77]
##   copper (median [IQR])  73.00 [41.25, 123.00]
##   stage (%)
##      1                      21 ( 5.1)
##      2                      92 (22.3)
##      3                     155 (37.6)
##      4                     144 (35.0)
```

Fine tuning

Check out ?print.TableOne for the list of options (partial list below):

catDigits: Number of digits to print for proportions. Default 1.

contDigits: Number of digits to print for continuous variables. Default 2.

quote:
Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.

missing: Whether to show missing data information.

explain:
Whether to add explanation to the variable names, i.e., (%) is added to the variable names when percentage is shown.

Stratified table

We may want to summarize by levels of a categorical variable (e.g., treatment)

```
myVars = myVars <- c("status",  "age", "sex", "ascites", "albumin", "copper", "stage")
tab3 <- CreateTableOne(vars = myVars, strata = "trt" , data = pbc, factorVars = catVars)
```

```
print(tab3, nonnormal = skewed, formatOptions = list(big.mark = ","))
```

Stratified table

```
##                         Stratified by trt
##                          D-penicillamine       placebo               p
##   n                        158                   154
##   status (%)                                                          0.894
##      alive                  83 (52.5)             85 (55.2)
##      liver transplant       10 ( 6.3)              9 ( 5.8)
##      dead                   65 (41.1)             60 (39.0)
##   age (mean (SD))          51.42 (11.01)         48.58 (9.96)          0.018
##   sex = F (%)              137 (86.7)            139 (90.3)            0.421
##   ascites = Yes (%)         14 ( 8.9)             10 ( 6.5)            0.567
##   albumin (median [IQR])  3.56 [3.21, 3.83]     3.54 [3.34, 3.78]     0.950
##   copper (median [IQR])  73.00 [40.00, 121.00] 73.00 [43.00, 139.00]  0.717
##   stage (%)                                                           0.201
##      1                      12 ( 7.6)              4 ( 2.6)
##      2                      35 (22.2)             32 (20.8)
##      3                      56 (35.4)             64 (41.6)
##      4                      55 (34.8)             54 (35.1)
##                         Stratified by trt
##                          test
##   n
##   status (%)
##      alive
##      liver transplant
##      dead
##   age (mean (SD))
##   sex = F (%)
##   ascites = Yes (%)
##   albumin (median [IQR]) nonnorm
##   copper (median [IQR])  nonnorm
##   stage (%)
##      1
##      2
##      3
##      4
```

Exporting table to csv

```
tab3Mat <- print(tab3, nonnormal = skewed, exact = "stage", quote = FALSE,
                 noSpaces = TRUE, printToggle = FALSE)

write.csv(tab3Mat, file = "myTable1.csv")
```