# Introduction to Fundemental Statitsics in R

### Overall Goal

- Create a Table 1 with corresponding plots

### Learning objectives:

- Descriptive statistics (mean, median, variance)
- t-tests, Wilcoxon rank sum
- ANOVA, Kruskal Wallis
- Chi-square tests
- Correlations, heat map
- Plots: density plot, box plot, histogram, heat map

### Commenting

- Use # signs to comment.
- Anything to the right of a # is ignored by R.
- Helpful to comment code.

### Libraries

- We will use the boot package.

```
# Use the commented command below if you do not have boot installed
# install.packages("boot")
library(boot)

# Use the commented command below if you do not have table1 installed
#install.packages("table1")
library(table1)

#install.packages("corrplot")
library(corrplot)
```

### Dataset

- Load datasets using read.table, read.csv, fread (big datasets), etc
- Make sure you are in the right directory. Either use the path to load the data or pick the working directory where the data is stored (Session-Set Working directory -> or Choose directory or Misc-> change working directory)
- Example:

```
# d1<-read.table("/Users/path/datasetname.txt", sep="\t",header=T, na.strings="")
```

- Can store and load data as rdata but may be cumbersome, but allows for more complex data formats

### Melanoma dataset

- ?melanoma
- Andersen, P.K., Borgan, O., Gill, R.D. and Keiding, N. (1993) Statistical Models Based on Counting Processes. Springer-Verlag.

The data consist of measurements made on patients with malignant melanoma.

- Each patient had their tumour removed by surgery at the Department of Plastic Surgery, University Hospital of Odense, Denmark during the period 1962 to 1977.
- Surgery consisted of complete removal of the tumour together with about 2.5cm of surrounding skin.
- Among the measurements taken were the thickness of the tumour and whether it was ulcerated or not. These are thought to be important prognostic variables in that patients with a thick and/or ulcerated tumour have an increased chance of death from melanoma.
- Patients were followed until the end of 1977.

This data frame contains the following columns:

- time: Survival time in days since the operation, possibly censored.
- status: The patients status at the end of the study. 1 indicates that they had died from melanoma, 2 indicates that they were still alive and 3 indicates that they had died from causes unrelated to their melanoma.
- sex: The patients sex; 1=male, 0=female.
- age: Age in years at the time of the operation.
- year: Year of operation.
- thickness: Tumour thickness in mm.
- ulcer: Indicator of ulceration; 1=present, 0=absent.

What information would we need?

- Number/percent of subjects with each status
- Mean/var of age and thickness by status or median/range
- Maybe test is mean age differs by status (t-test/ANOVA)
- Number/percent for sex and ulcer by status
- Maybe test is status differs by sex (chi-square test)
- Consider if age is associated with sex (correlation)

First, examine the dataset.

```r
# create a melanoma2 dataset based on melanoma (alternative: melanoma2 = melanoma)
melanoma2 <- melanoma

# dimensions of melanoma2 matrix
dim(melanoma2)
```

```
## [1] 205   7
```

```r
# Check if there is missing data
# melanoma2<-na.omit(melanoma2) #creates data set without missing values
dim(na.omit(melanoma2))
```

```
## [1] 205   7
```

```
# view first 3 rows
melanoma2[1:3,]
```

```
##   time status sex age year thickness ulcer
## 1   10      3   1  76 1972      6.76     1
## 2   30      3   1  56 1968      0.65     0
## 3   35      2   1  41 1977      1.34     0
```

```
# view first 3 rows and first 2 columns
melanoma2[1:3,1:2]
```

```
##   time status
## 1   10      3
## 2   30      3
## 3   35      2
```

```
# column names of variables
colnames(melanoma2)
```

```
## [1] "time"      "status"    "sex"       "age"       "year"      "thickness"
## [7] "ulcer"
```

```
# Use $ for a given variable or melanoma2[,"age"]
melanoma2$age
```

```
##   [1] 76 56 41 71 52 28 77 60 49 68 53 64 68 63 14 72 46 72 95 54 89 25 37 43 68
##  [26] 67 86 56 16 42 65 52 58 60 68 75 19 66 56 46 58 74 65 64 27 73 56 63 69 77
##  [51] 80 76 65 61 26 57 45 31 36 46 43 68 57 57 55 58 20 67 44 59 32 83 55 15 58
##  [76] 47 54 55 38 41 56 48 44 70 40 53 65 54 71 49 55 69 83 60 40 77 35 46 34 69
## [101] 60 84 66 56 75 36 52 58 39 68 71 52 55 66 35 44 72 58 54 33 45 62 72 51 77
## [126] 43 65 63 60 50 40 67 69 74 49 47 42 54 72 45 67 48 34 44 31 42 24 58 78 62
## [151] 70 35 61 54 29 64 47 62 32 49 25 49 64 36 58 37 54 61 31 61 60 43 68  4 60
## [176] 50 20 54 29 56 60 46 42 34 56 12 21 46 49 35 42 47 69 52 52 30 22 55 26 19
## [201] 29 40 42 50 41
```

- Determine the number of subjects

```
# How many subjects?
nrow(melanoma2)
```

```
## [1] 205
```

```
# How many subjects with status 1: died from melanoma? Percent?
nrow(melanoma2[melanoma2$status==1,])
```

```
## [1] 57
```

```
nrow(melanoma2[melanoma2$status==1,])/nrow(melanoma2)
```

```
## [1] 0.2780488
```

```
# How many subjects with status 2: alive? Percent?
length(melanoma2$status[melanoma2$status==2])
```

```
## [1] 134
```

```
length(melanoma2$status[melanoma2$status==2])/length(melanoma2$status)
```

```
## [1] 0.6536585
```

```
# How many subjects with status 3 and did not have missing data?
nrow(melanoma2[melanoma2$status==3 & !is.na(melanoma2$status),])
```

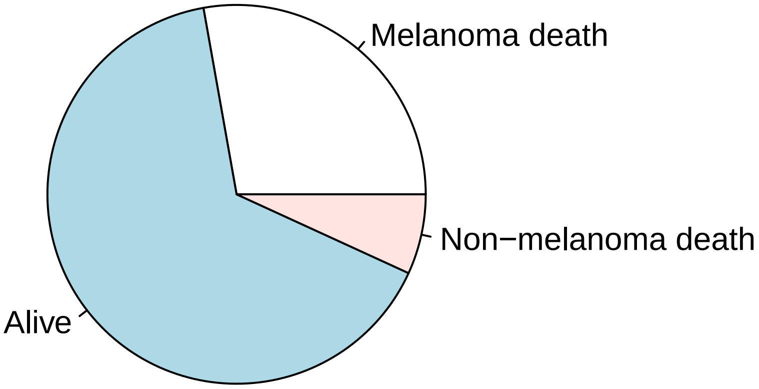
```
## [1] 14
```

```
#View status as a piechart
x<-c(nrow(melanoma2[melanoma2$status==1,]),nrow(melanoma2[melanoma2$status==2,]),
        nrow(melanoma2[melanoma2$status==3,]))
x
```

```
## [1]  57 134  14
```

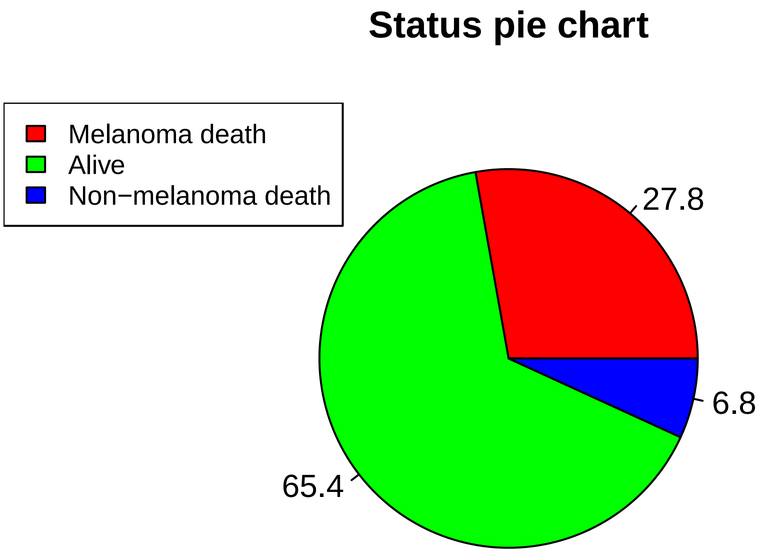
```
labels=c("Melanoma death","Alive","Non-melanoma death")

#regular pie chart
pie(x,labels)
```



```
# pie chart with percents
piepercent<- round(100*x/sum(x), 1)

pie(x, labels = piepercent, main = "Status pie chart",col = rainbow(length(x)))
legend("topleft", c("Melanoma death","Alive","Non-melanoma death"), cex = 0.8,
   fill = rainbow(length(x)))
```



### Mean, standard deviation, variance, median

- Consider age. What is the average age?

```
# mean for age overall or sum(melanoma2$age)/length(melanoma2$age)
mean(melanoma2$age)
```

```
## [1] 52.46341
```

```
#mean age if there where missing values in dataset
mean(melanoma2$age,na.rm=T)
```

```
## [1] 52.46341
```

```
# round mean age to 1 decimal place
round(mean(melanoma2$age),1)
```

```
## [1] 52.5
```

```
# mean age for status 1: died from melanoma
mean(melanoma2$age[melanoma2$status==1])
```

```
## [1] 55.08772
```

```
# mean age for status 2: alive
mean(melanoma2$age[melanoma2$status==2])
```

```
## [1] 50.00746
```

```
# mean age for status 3: died not from melanoma
mean(melanoma2$age[melanoma2$status==3])
```

```
## [1] 65.28571
```

- What is the variance and standard deviation?

```
# sd for age overall
sd(melanoma2$age)
```

```
## [1] 16.67171
```

```
# sd for age if there where missing values in dataset
sd(melanoma2$age,na.rm=T)
```

```
## [1] 16.67171
```

```
# variance for age overall
sd(melanoma2$age)^2
```

```
## [1] 277.946
```

```
var(melanoma2$age)
```

```
## [1] 277.946
```

```
# variance for age by status
round(c(var(melanoma2$age[melanoma2$status==1]),var(melanoma2$age[melanoma2$status==2]),
        var(melanoma2$age[melanoma2$status==3])),1)
```

```
## [1] 320.7 253.3 118.8
```

- What is the median and range for age?

```
# median for age overall
median(melanoma2$age)
```

```
## [1] 54
```

```
# minimum age
min(melanoma2$age)
```

```
## [1] 4
```

```
#maximum age
max(melanoma2$age)
```

```
## [1] 95
```

```
#range
range(melanoma2$age)
```

```
## [1]  4 95
```

```
# create new variables
AgeStatus1<-melanoma2$age[melanoma2$status==1]
AgeStatus2<-melanoma2$age[melanoma2$status==2]
AgeStatus3<-melanoma2$age[melanoma2$status==3]

#median age by status
c(median(AgeStatus1),median(AgeStatus2),median(AgeStatus3))
```

```
## [1] 56 52 65
```

```
#matrix of ranges
matRange<-matrix(c(range(AgeStatus1),range(AgeStatus2),range(AgeStatus3)),nrow=2,ncol=3)
colnames(matRange)<-c("Status1","Status2","Status3")
rownames(matRange)<-c("min","max")
matRange
```

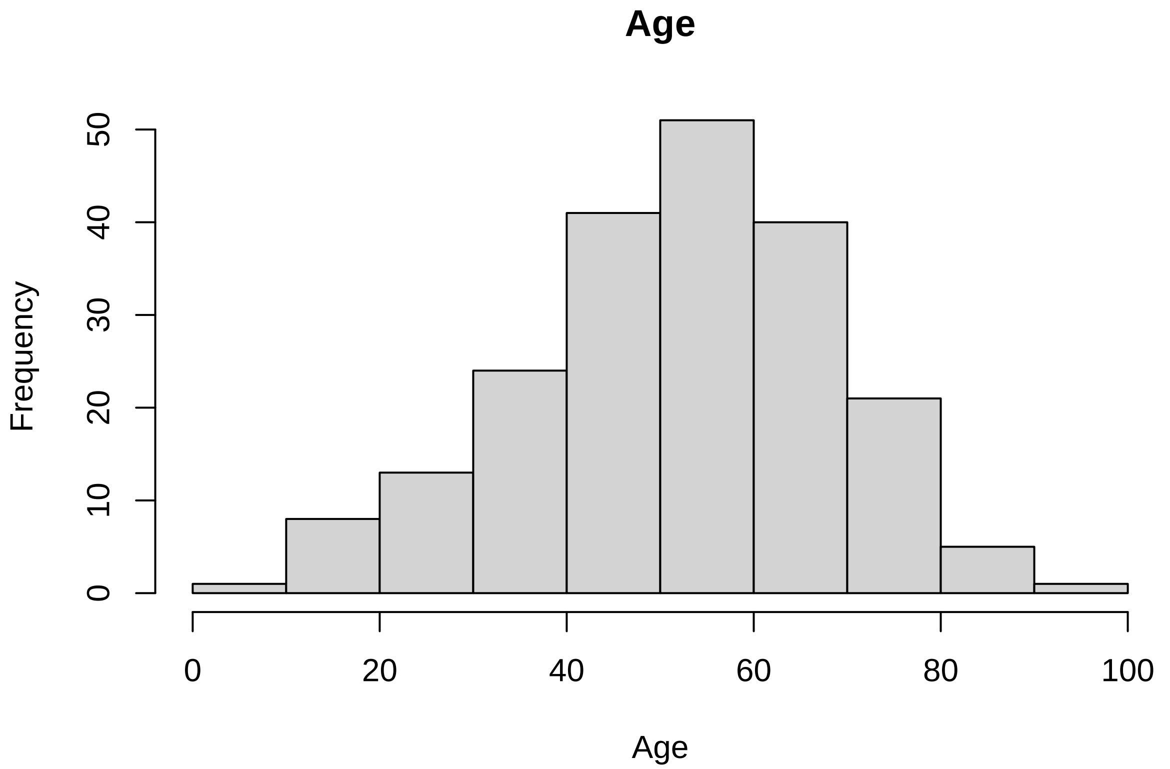
```
##     Status1 Status2 Status3
## min      14       4      49
## max      95      84      86
```

```
range(AgeStatus1)
```

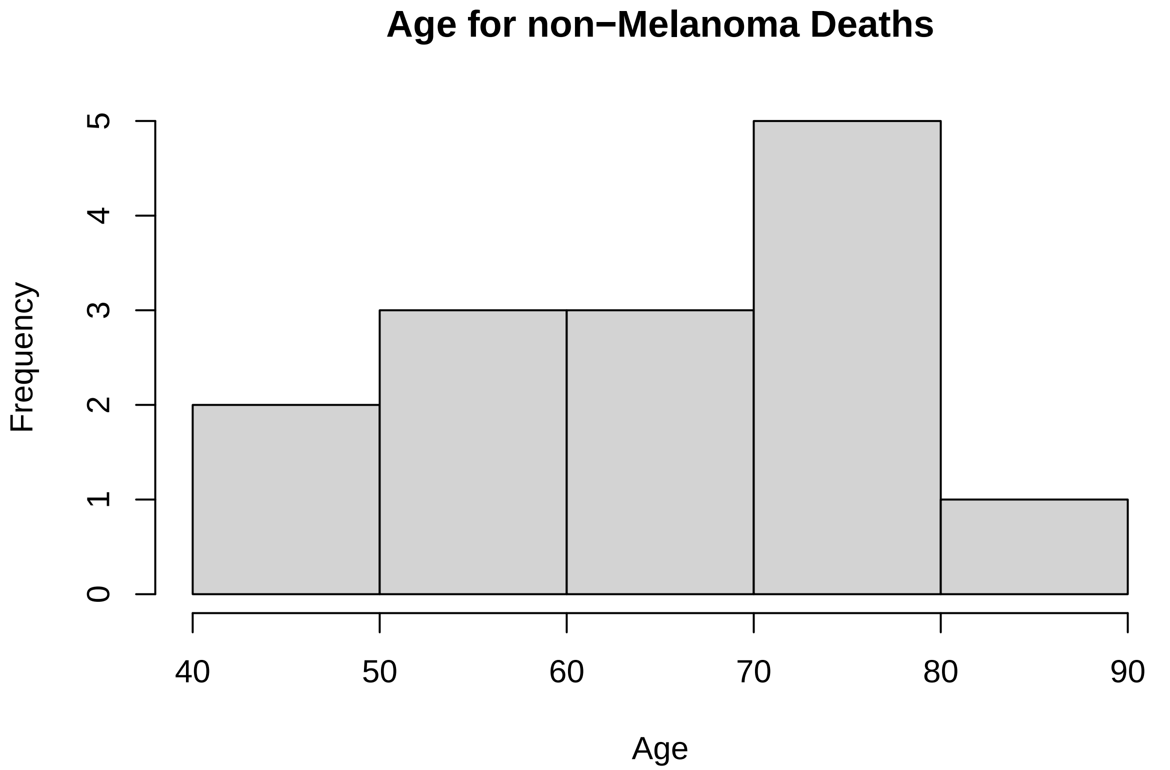
```
## [1] 14 95
```

- Should we be using medians or means? Check normality (Kolmogorov–Smirnov or Shapiro–Wilk test)

```
hist(melanoma2$age,main="Age",xlab="Age")
```

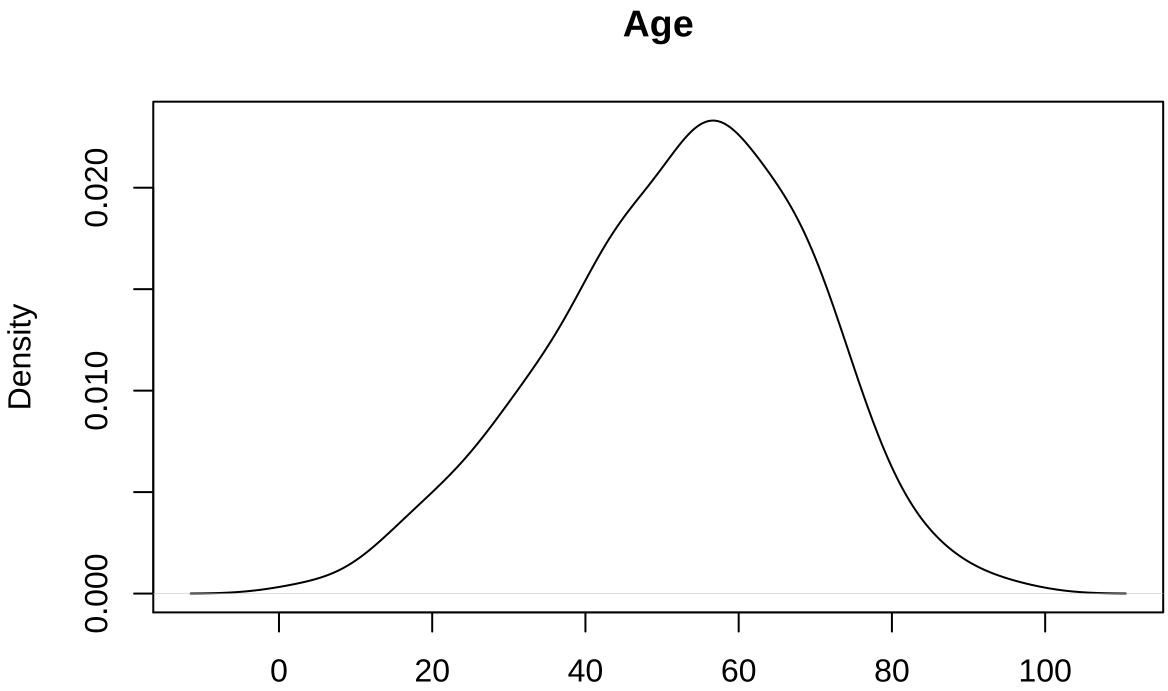


```
hist(melanoma2$age[melanoma2$status==3],main="Age for non-Melanoma Deaths",xlab="Age")
```

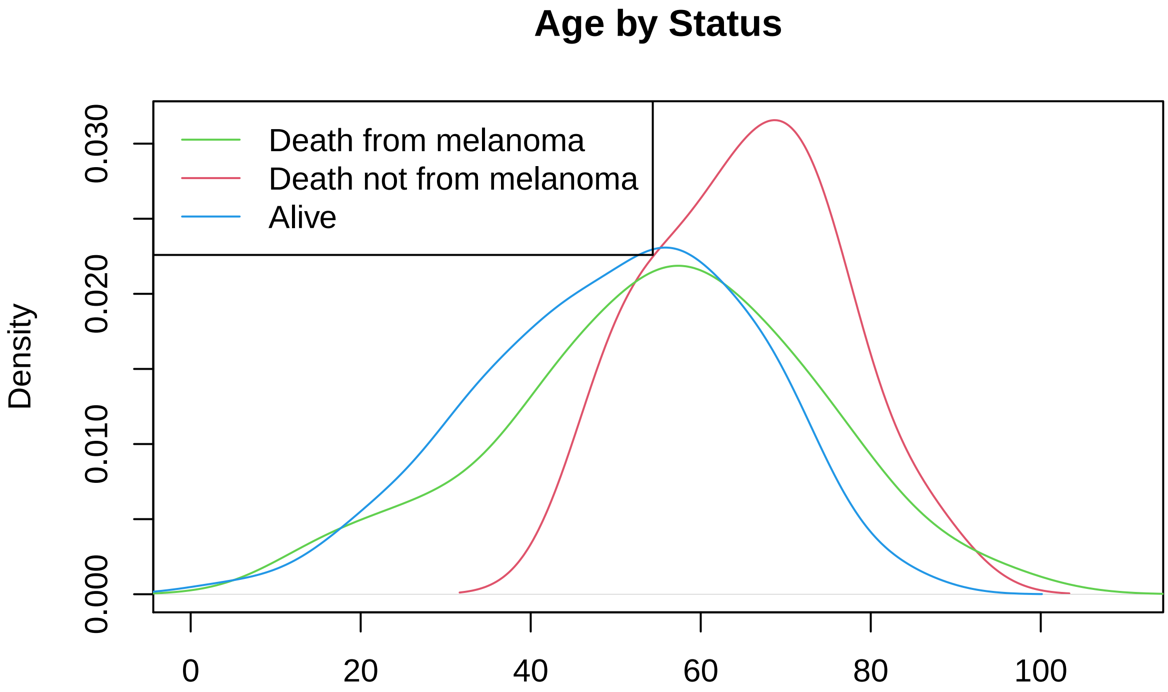


- Density plots (status samples size= 57,134,14)

```
#plot density for age overall
plot(density(melanoma2$age),main="Age",xlab="")
```

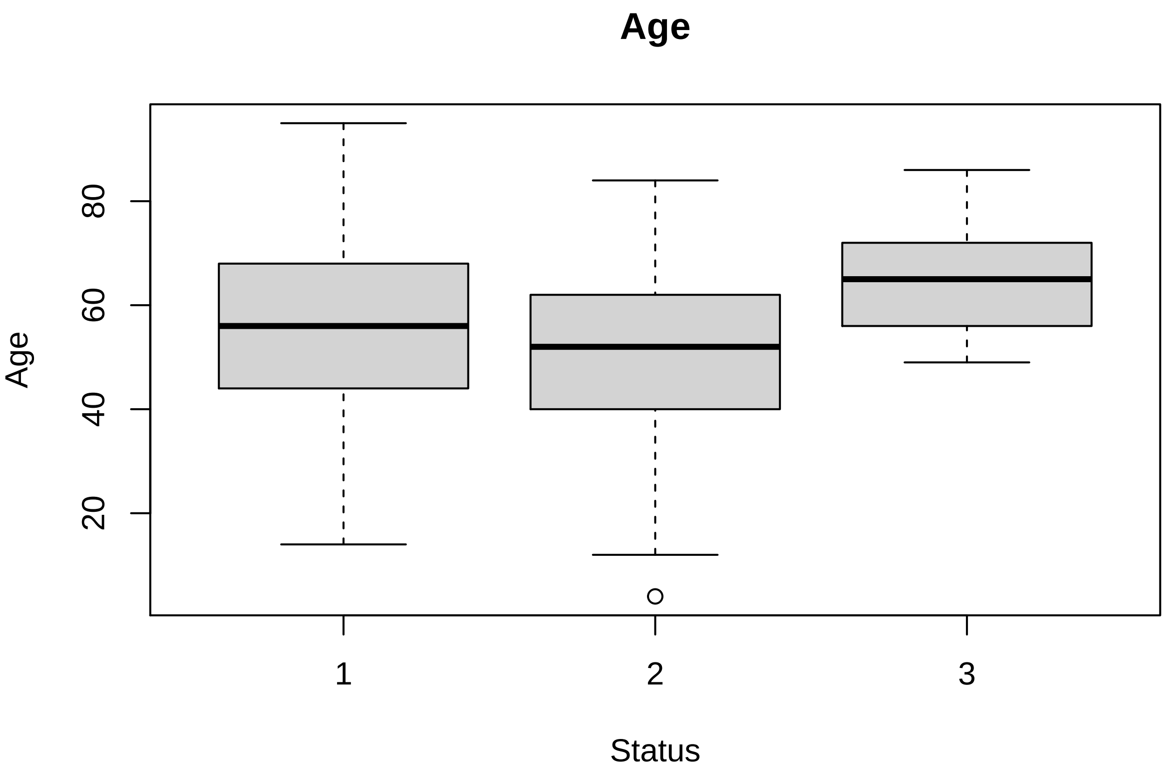


```
#plot density for age by status
plot(density(melanoma2$age[melanoma2$status==3]),main="Age by Status",xlab="",xlim=c(0,110),col=2)
lines(density(melanoma2$age[melanoma2$status==1]),col=3)
lines(density(melanoma2$age[melanoma2$status==2]),col=4)
legend("topleft",c("Death from melanoma","Death not from melanoma","Alive"),col=c(3,2,4),lwd=1)
```



- Boxplot

```
boxplot(age~status,data=melanoma2, main="Age",
   xlab="Status", ylab="Age")
```



**t-tests and Wilcoxon rank sum test**

- Does the average age differ by status 1 and 2?
- Which test to use? t-test assumes normality. t-test with equal variance or unequal?

```
# t test
t.test(melanoma2$age[melanoma2$status==1],melanoma2$age[melanoma2$status==2],
       alternative = "two.sided",paired = FALSE, var.equal = FALSE)
```

```
##
##  Welch Two Sample t-test
##
## data:  melanoma2$age[melanoma2$status == 1] and melanoma2$age[melanoma2$status == 2]
## t = 1.853, df = 95.424, p-value = 0.06698
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.3623352 10.5228485
## sample estimates:
## mean of x mean of y
##  55.08772  50.00746
```

- p-value=0.07. Average age does not significantly differ for subjects who died by melanoma versus subjects who were still alive.

- Wilcoxon rank sum test may be approriate if normality assumption is not met or samlple size is small. Used to test if the median differs in the 2 groups.

```
#Wilcoxon rank sum exact test (signed rank for paired =True)
wilcox.test(melanoma2$age[melanoma2$status==1],melanoma2$age[melanoma2$status==2],
            alternative = "two.sided",paired = FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  melanoma2$age[melanoma2$status == 1] and melanoma2$age[melanoma2$status == 2]
## W = 4458.5, p-value = 0.06749
## alternative hypothesis: true location shift is not equal to 0
```

### ANOVA and Kruskall-Wallis

- Does the average age differ by status?
- ANOVA assumes normality and vairance equal in all 3 groups.

```
#ANOVA
oneway.test(age ~ status,data = melanoma2,var.equal = TRUE)
```

```
##
##  One-way analysis of means
##
## data:  age and status
## F = 6.6498, num df = 2, denom df = 202, p-value = 0.001596
```

```
#Kruskall-Wallis
kruskal.test(age ~ status,data = melanoma2)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  age by status
## Kruskal-Wallis chi-squared = 13.028, df = 2, p-value = 0.001483
```

- p-value = 0.00159. The average age differs by status for at least 2 groups.

### Chi-square tests

- Is sex associated with status? Yes, p-value = 0.03.

```
table(melanoma2$sex, melanoma2$status)
```

```
##
##       1  2  3
##    0 28 91  7
##    1 29 43  7
```

```
chisq.test(melanoma2$sex, melanoma2$status)
```

```
##
##  Pearson's Chi-squared test
##
## data:  melanoma2$sex and melanoma2$status
## X-squared = 6.793, df = 2, p-value = 0.03349
```

### Correlations

- Is age correlated with sex?

```
cor(melanoma2$sex,melanoma2$age)
```

```
## [1] 0.06833741
```

```
# Test correlation (pearson, could use method = "spearman")
cor.test(melanoma2$sex,melanoma2$age,alternative = "two.sided",method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  melanoma2$sex and melanoma2$age
## t = 0.97594, df = 203, p-value = 0.3303
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.06934701  0.20346704
## sample estimates:
##        cor
## 0.06833741
```

- Age is note significantly correlated with sex (p-value=0.33).
- Plots for correlation. Need one of the traits to be continuous.

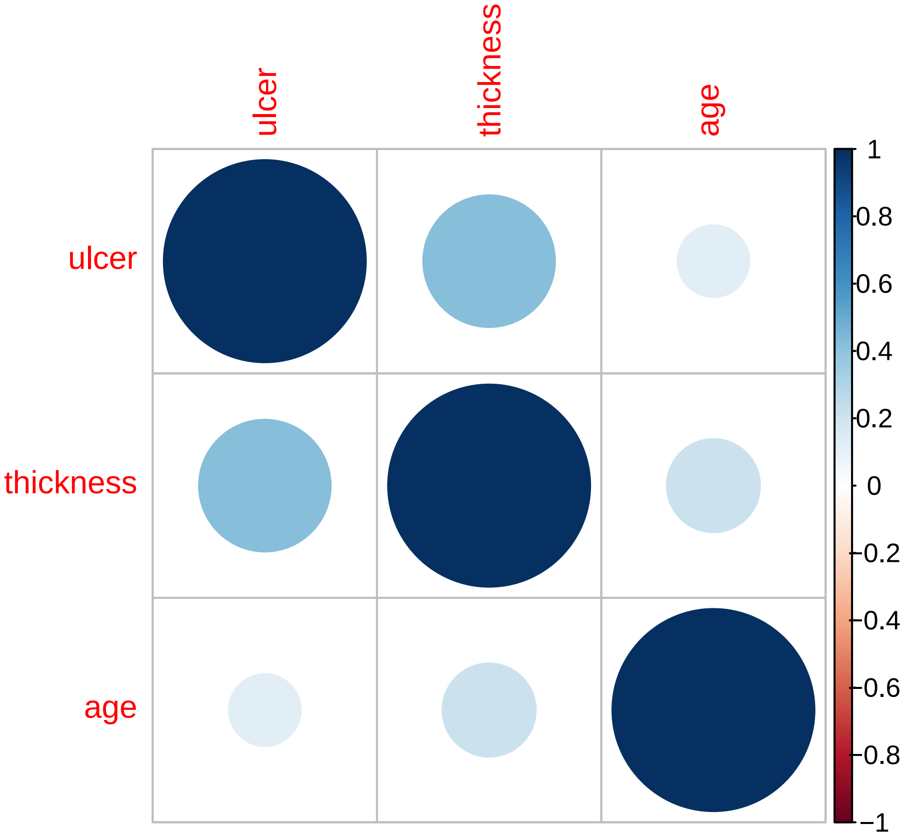
```
#https://cran.r-project.org/web/packages/corrplot/vignettes/corrplot-intro.html

# Create new matrix with only age, thickness, ulcer
melanoma3<-melanoma2[,c("age","thickness","ulcer")]

# Check
melanoma3[1:5,]
```

```
##   age thickness ulcer
## 1  76      6.76     1
## 2  56      0.65     0
## 3  41      1.34     0
## 4  71      2.90     0
## 5  52     12.08     1
```

```
# Plot correlation
M = cor(melanoma3)
corrplot(M, order = 'AOE')
```


ulcer
thickness
age
ulcer
thickness
age
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

### Existing packages

```
# https://cran.r-project.org/web/packages/table1/vignettes/table1-examples.html

# change status variable to text
melanoma2$status <-
   factor(melanoma2$status,
          levels=c(2,1,3),
          labels=c("Alive", # Reference
                   "Melanoma death",
                   "Non-melanoma death"))
melanoma2[1:5,]
```

```
##   time             status sex age year thickness ulcer
## 1   10 Non-melanoma death   1  76 1972      6.76     1
## 2   30 Non-melanoma death   1  56 1968      0.65     0
## 3   35              Alive   1  41 1977      1.34     0
## 4   99 Non-melanoma death   0  71 1968      2.90     0
## 5  185     Melanoma death   1  52 1965     12.08     1
```

```
 table1(~ factor(sex) + age + factor(ulcer) + thickness | status, data=melanoma2)
```

| | Alive | Melanoma death | Non-melanoma death | Overall |
|---|---|---|---|---|
| | (N=134) | (N=57) | (N=14) | (N=205) |
| factor(sex) | | | | |
| 0 | 91 (67.9%) | 28 (49.1%) | 7 (50.0%) | 126 (61.5%) |
| 1 | 43 (32.1%) | 29 (50.9%) | 7 (50.0%) | 79 (38.5%) |
| age | | | | |
| Mean (SD) | 50.0 (15.9) | 55.1 (17.9) | 65.3 (10.9) | 52.5 (16.7) |
| Median [Min, Max] | 52.0 [4.00, 84.0] | 56.0 [14.0, 95.0] | 65.0 [49.0, 86.0] | 54.0 [4.00, 95.0] |
| factor(ulcer) | | | | |
| 0 | 92 (68.7%) | 16 (28.1%) | 7 (50.0%) | 115 (56.1%) |
| 1 | 42 (31.3%) | 41 (71.9%) | 7 (50.0%) | 90 (43.9%) |
| thickness | | | | |
| Mean (SD) | 2.24 (2.33) | 4.31 (3.57) | 3.72 (3.63) | 2.92 (2.96) |
| Median [Min, Max] | 1.36 [0.100, 12.9] | 3.54 [0.320, 17.4] | 2.26 [0.160, 12.6] | 1.94 [0.100, 17.4] |

### R resources

- Harvard Catalyst or other free Harvard courses https://online-learning.harvard.edu/subject/r
- There are online courses through coursera https://www.coursera.org/learn/r-programming
- Software carpentry offers really fun 2 day workshops. You can check when there is one in Boston and make sure to sign up right away because they fill up quickly https://software-carpentry.org/workshops/