

# BST02: Using R for Statistics in Medical Research

## Part B: Basic use of R

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## In this Section

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- ▶ Using R
- ▶ In practice examples
- ▶ Basics in R
- ▶ Common R objects
- ▶ Importing data and saving your work
- ▶ Data transformation
- ▶ Data exploration
- ▶ Data visualization
- ▶ Indexing/Subsetting

Lots of practising

# Using R

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- ▶ R is a command-based procedural language
  - ▶ write and execute commands
  - ▶ use and define functions
- ▶ You may write the commands in the R console (Windows) or in a shell (Linux)

**You will become more familiar with the syntax as you use it**

## Using R (cont'd)

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- ▶ Strongly advisable to use a suitable text editor - Some available options:
  - ▶ RWinEdt (for Windows; you also need WinEdt installed)
  - ▶ Tinn-R (for Windows; <http://sciviews.org/Tinn-R/>)
  - ▶ Rkward (for Linux)
  - ▶ Emacs (w. ESS, all platforms)
  - ▶ Visual Studio (for Windows)
  - ▶ Rstudio (all major platforms; <http://www.rstudio.org/>)
  - ▶ for more check <https://r-dir.com/blog/2013/01/list-of-r-editors.html>

## Using R (cont'd)

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- ▶ For this course: Rstudio (<http://www.rstudio.org/>)
  - ▶ free
  - ▶ works fine in Windows, MacOS and Linux
  - ▶ helpful with errors

## Using R (cont'd)

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- ▶ Can I use R without Rstudio?
- ▶ Can I use Rstudio without R?

## Practical Examples

---

► Package **survival** - pbc data set

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.76523	f	14.5	261
2	4500	0	1	56.44627	f	1.1	302
3	1012	2	1	70.07255	m	1.4	176
4	1925	2	1	54.74059	f	1.8	244
5	1504	1	2	38.10541	f	3.4	279

## Practical Examples (cont'd)

---

- ▶ **id**: case number
- ▶ **time**: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
- ▶ **status**: status at endpoint, 0/1/2 for censored, transplant, dead
- ▶ **trt**: 1/2/NA for D-penicillmain, placebo, not randomised
- ▶ **age**: in years
- ▶ **sex**: m/f
- ▶ **bili**: serum bilirunbin (mg/dl)
- ▶ **chol**: serum cholesterol (mg/dl)

More details:

<https://stat.ethz.ch/R-manual/R-devel/library/survival/html/pbc.html>



## Practical Examples (cont'd)

---

- What is a **scalar**/vector/matrix

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.76523	f	14.5	261
2	4500	0	1	56.44627	f	1.1	302
3	1012	2	1	<b>70.07255</b>	m	1.4	176
4	1925	2	1	54.74059	f	1.8	244
5	1504	1	2	38.10541	f	3.4	279

## Practical Examples (cont'd)

---

- What is a scalar/**vector**/matrix

id	time	<b>status</b>	trt	age	sex	bili	chol
1	400	<b>2</b>	1	58.76523	f	14.5	261
2	4500	<b>0</b>	1	56.44627	f	1.1	302
3	1012	<b>2</b>	1	70.07255	m	1.4	176
4	1925	<b>2</b>	1	54.74059	f	1.8	244
5	1504	<b>1</b>	2	38.10541	f	3.4	279

## Practical Examples (cont'd)

---

- What is a scalar/**vector**/matrix

id	<b>time</b>	status	trt	age	sex	bili	chol
1	<b>400</b>	2	1	58.76523	f	14.5	261
2	<b>4500</b>	0	1	56.44627	f	1.1	302
3	<b>1012</b>	2	1	70.07255	m	1.4	176
4	<b>1925</b>	2	1	54.74059	f	1.8	244
5	<b>1504</b>	1	2	38.10541	f	3.4	279

## Practical Examples (cont'd)

---

- What is a scalar/vector/**matrix**

id	<b>time</b>	<b>status</b>	trt	age	sex	bili	chol
1	<b>400</b>	<b>2</b>	1	58.76523	f	14.5	261
2	<b>4500</b>	<b>0</b>	1	56.44627	f	1.1	302
3	<b>1012</b>	<b>2</b>	1	70.07255	m	1.4	176
4	<b>1925</b>	<b>2</b>	1	54.74059	f	1.8	244
5	<b>1504</b>	<b>1</b>	2	38.10541	f	3.4	279

## Practical Examples (cont'd)

- What is a scalar/vector/**matrix**

id	time	status	trt	age	sex	<b>bili</b>	<b>chol</b>
1	400	2	1	58.76523	f	<b>14.5</b>	<b>261</b>
2	4500	0	1	56.44627	f	<b>1.1</b>	<b>302</b>
3	1012	2	1	70.07255	m	<b>1.4</b>	<b>176</b>
4	1925	2	1	54.74059	f	<b>1.8</b>	<b>244</b>
5	1504	1	2	38.10541	f	<b>3.4</b>	<b>279</b>

## Practical Examples (cont'd)

---

- ▶ Common questions
  - ▶ What is the average age?
  - ▶ What is the average serum bilirubin?
  - ▶ What is the average serum cholesterol?
  - ▶ What is the percentage of females?
  - ▶ How many missing values do we have for serum cholesterol?

**All these questions can be answered using R!**

# Basics in R

---

- ▶ Elementary commands: **expressions** and **assignments**
- ▶ An **expression** given as command is evaluated printed and discarded
- ▶ An **assignment** evaluates an expression and passes the value to a variable - the result is not automatically printed

## Basics in R (cont'd)

---

Expression is given as a command,

```
103473
```

```
[1] 103473
```

- ▶ However, it cannot be viewed again unless the command is rerun.



## Basics in R (cont'd)

---

Expression is given as a command,

```
103473
```

```
[1] 103473
```

- ▶ However, it cannot be viewed again unless the command is rerun.

In order to store information, the expression should assign the command

```
x <- 103473
```

```
x
```

```
[1] 103473
```

## Basics in R (cont'd)

---

### You can use R as a calculator!

- ▶ Basic arithmetics

`+, -, *, /, ^`

```
y <- 103473 + 100000  
y
```

```
[1] 203473
```

- ▶ Complicated arithmetics

## Basics in R (cont'd)

---

### Tips:

- ▶ R is case sensitive, e.g.,
  - ▶ **"sex"** is different than **"Sex"**
- ▶ Commands are separated by a semi-colon or by a newline
- ▶ Comments can be put anywhere, starting with a hashmark **#**: everything to the end of the line is a comment
- ▶ Assign a value to an object by **<-** or **=**

## Basics in R (cont'd)

---

- ▶ Missing values
  - ▶ are coded as **NA** (i.e., not available) **is.na()**
- ▶ Infinity
  - ▶ is coded as **Inf** (plus infinity) or **-Inf** (minus infinity) **is.finite()**
- ▶ Not a number
  - ▶ is coded as **NaN** (Not a Number). Example:

```
0/0
```

```
[1] NaN
```

## Basics in R (cont'd)

---

### Demos

▶ Basic R **R** **html**

## Common R Objects

---

- There are different kinds of variables

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.77	f	14.5	261
2	4500	0	1	56.45	f	1.1	302
3	1012	2	1	70.07	m	1.4	176
4	1925	2	1	54.74	f	1.8	244
5	1504	1	2	38.11	f	3.4	279

## Common R Objects (cont'd)

---

- ▶ in R Everything (data, results, ...) is an object
- ▶ In order to list the created objects use the following functions

```
objects()  
ls()
```

## Common R Objects (cont'd)

---

- ▶ in R Everything (data, results, ...) is an object
- ▶ In order to list the created objects use the following functions

```
objects()  
ls()
```

- ▶ In order to remove objects

```
rm(...)  
rm(list=ls(all=TRUE))
```



## Common R Objects (cont'd)

- To investigate a specific object (e.g. pbc)

```
str(pbc[,c("id", "time", "status", "trt", "age", "sex", "bili", "chol")])
```

```
'data.frame':  418 obs. of  8 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  : int  2 0 2 2 1 2 0 2 2 2 ...
 $ trt     : int  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 ...
 $ 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 ...
```

## Common R Objects (cont'd)

---

The simplest data structures are:

- ▶ **numeric** : quantitative data
- ▶ **character** : qualitative data
- ▶ **integer** : whole numbers
- ▶ **logical** : TRUE or FALSE
- ▶ **factors** : qualitative data (ordered)

To find out what type of object you have, you can use the following function

```
mode(pbc$age)
```

```
[1] "numeric"
```

## Common R Objects (cont'd)

---

- ▶ Every object in R has a class
  - ▶ **Vectors** have the same type of elements with the same length (one dimension)
  - ▶ **Matrices** have the same type of elements with the same length (two dimensions)
  - ▶ **Data.frames** have elements of different type with the same length (two dimensions)
  - ▶ **Lists** have elements of different type and length (any dimension)

## Common R Objects (cont'd)

---

- Differences between **vector**, matrix, data.frame and list

```
pbcc[1:6, c("age")]
```

```
[1] 58.76523 56.44627 70.07255 54.74059 38.10541 66.25873
```

## Common R Objects (cont'd)

---

- Differences between vector, **matrix**, data.frame and list

```
pbmc[1:6, c("age", "bili", "chol")]
```

	age	bili	chol
1	58.76523	14.5	261
2	56.44627	1.1	302
3	70.07255	1.4	176
4	54.74059	1.8	244
5	38.10541	3.4	279
6	66.25873	0.8	248

## Common R Objects (cont'd)

---

- Differences between vector, matrix, **data.frame** and list

```
pbmc[1:6, c("id", "sex", "bili", "chol")]
```

	id	sex	bili	chol
1	1	f	14.5	261
2	2	f	1.1	302
3	3	m	1.4	176
4	4	f	1.8	244
5	5	f	3.4	279
6	6	f	0.8	248

## Common R Objects (cont'd)

- Differences between vector, matrix, data.frame and **list**

```
list(pbc[1:6, c("sex")], pbc[1:2, c("sex", "bili")], pbc$age[1:4])
```

```
[[1]]
```

```
[1] f f m f f f
```

```
Levels: m f
```

```
[[2]]
```

```
sex bili
```

```
1    f 14.5
```

```
2    f  1.1
```

```
[[3]]
```

```
[1] 58.76523 56.44627 70.07255 54.74059
```

## Common R Objects (cont'd)

---

### Create a vector

```
vec <- c(1, 2, 3, 4, 5)
vec
```

```
[1] 1 2 3 4 5
```

```
vec <- c(1:5)
vec
```

```
[1] 1 2 3 4 5
```



## Common R Objects (cont'd)

---

### Create a matrix

```
vec <- c(1, 2, 3, 4, 5, 6)
mat <- matrix(vec, 3, 3)
mat
```

	[,1]	[,2]	[,3]
[1,]	1	4	1
[2,]	2	5	2
[3,]	3	6	3

# Common R Objects (cont'd)

## Create a matrix

```
vec <- c(1, 2, 3, 4, 5, 6)
mat <- matrix(vec, 3, 3)
mat
```

	[,1]	[,2]	[,3]
[1,]	1	4	1
[2,]	2	5	2
[3,]	3	6	3

```
vec <- c(1, 2, 3, 4, 5, 6)
mat <- matrix(vec, 3, 3,
              byrow = TRUE)
mat
```

	[,1]	[,2]	[,3]
[1,]	1	2	3
[2,]	4	5	6
[3,]	1	2	3

## Common R Objects (cont'd)

---

### Create a data frame

```
dtf <- data.frame(pbc$sex, pbc$age)
dtf[1:3,]
```

	pbcc.sex	pbcc.age
1	f	58.76523
2	f	56.44627
3	m	70.07255

# Common R Objects (cont'd)

## Create a data frame

```
dtf <- data.frame(pbc$sex, pbc$age)
dtf[1:3,]
```

	pbcc.sex	pbcc.age
1	f	58.76523
2	f	56.44627
3	m	70.07255

```
dtf <- data.frame(Gender = pbc$sex,
                  Age = pbc$age)
dtf[1:3,]
```

	Gender	Age
1	f	58.76523
2	f	56.44627
3	m	70.07255

## Common R Objects (cont'd)

---

### Create a list

```
list1 <- list(vec = c(1:5), mat = pbc[1:2, c("age", "sex")])  
list1
```

```
$vec
```

```
[1] 1 2 3 4 5
```

```
$mat
```

	age	sex
1	58.76523	f
2	56.44627	f

## Common R Objects (cont'd)

---

### Demos

▶ Common R Objects [R](#) [html](#)

# Importing Data and Saving your Work

---

- ▶ function: **read.table()**, **read.csv()** and its variants
  - ▶ note: use forward slashes or double backward slashes in the file names, e.g.,  
"C:/Documents and Settings/User/Data/file.txt" or  
"C:\\Documents and Settings\\User\\Data\\file.txt"
- ▶ Specialized functions for importing data from other programs
  - ▶ package: **foreign**, function: **read.spss()**, **read.dta()**
  - ▶ package: **Hmisc**, function: **sas.get()**
  - ▶ package: **readxl**, function: **read\_excel()**
  - ▶ package: **haven**, function: **read\_spss()**
  - ▶ etc

## Importing Data and Saving your Work (cont'd)

---

### Tips:

- ▶ Short names are preferred over longer names
- ▶ Try to avoid using names that contain symbols
- ▶ Avoid spaces in names
- ▶ Remove any comments in your data set
- ▶ Make sure that any missing values in your data set are indicated with the same value (or no value)



## Importing Data and Saving your Work (cont'd)

---

- ▶ **save()**
  - ▶ can be used to save a list of R objects
  - ▶ a binary file with all the objects available in your last R session
- ▶ You can load your saved R objects using **load()**
  - ▶ be careful about overwriting
- ▶ Using **saveRDS** and **readRDS** you can save and read a single R object
  - ▶ The result has to be assigned to a variable
- ▶ Specialized functions for exporting data to other programs
  - ▶ function: **write.table()**, **write.csv()**
  - ▶ package: **foreign**, function: **write.spss()**, **write.dta()**
  - ▶ etc

## Importing Data and Saving your Work (cont'd)

---

### Demos

- ▶ Importing and Saving **R**  
**html**

# Data Transformation

---

**You will never receive the perfect data set!**

- ▶ **Round** continuous variables
- ▶ Convert **numeric** variables to **factors**
- ▶ Compute **new variables**
  - ▶ transform variables
- ▶ Data sets of **wide**  $\iff$  **long** format

## Data Transformation (cont'd)

- **Round** continuous variables

```
DF <- format(pbc[,c("id", "time", "status", "trt", "age",  
                    "sex", "bili", "chol")], digits = 2)  
head(DF)
```

	id	time	status	trt	age	sex	bili	chol
1	1	400	2	1	59	f	14.5	261
2	2	4500	0	1	56	f	1.1	302
3	3	1012	2	1	70	m	1.4	176
4	4	1925	2	1	55	f	1.8	244
5	5	1504	1	2	38	f	3.4	279
6	6	2503	2	2	66	f	0.8	248

## Data Transformation (cont'd)

- Convert **numeric** variables to **factors**

```
DF <- pbc[,c("id", "time", "status", "trt", "age",  
            "sex", "bili", "chol")]  
DF$trt <- factor(DF$trt, levels = c(1, 2),  
                labels = c("D-penicillmain", "placebo"))  
head(DF)
```

	id	time	status	trt	age	sex	bili	chol
1	1	400	2	D-penicillmain	58.76523	f	14.5	261
2	2	4500	0	D-penicillmain	56.44627	f	1.1	302
3	3	1012	2	D-penicillmain	70.07255	m	1.4	176
4	4	1925	2	D-penicillmain	54.74059	f	1.8	244
5	5	1504	1	placebo	38.10541	f	3.4	279
6	6	2503	2	placebo	66.25873	f	0.8	248

## Data Transformation (cont'd)

- ▶ Compute **new variables**
  - ▶ transform variables

```
DF <- pbc[,c("id", "time", "status", "trt", "age",  
            "sex", "bili", "chol")]  
DF$time <- DF$time/30  
DF$time_years <- DF$time/12  
head(DF)
```

	id	time	status	trt	age	sex	bili	chol	time_years
1	1	13.33333	2	1	58.76523	f	14.5	261	1.111111
2	2	150.00000	0	1	56.44627	f	1.1	302	12.500000
3	3	33.73333	2	1	70.07255	m	1.4	176	2.811111
4	4	64.16667	2	1	54.74059	f	1.8	244	5.347222
5	5	50.13333	1	2	38.10541	f	3.4	279	4.177778
6	6	83.43333	2	2	66.25873	f	0.8	248	6.952778

## Data Transformation (cont'd)

- Data sets of **wide**  $\iff$  long format

```
head(pbc[,c("id", "time", "status", "trt", "age",  
            "sex", "bili", "chol")])
```

	id	time	status	trt	age	sex	bili	chol
1	1	400	2	1	58.76523	f	14.5	261
2	2	4500	0	1	56.44627	f	1.1	302
3	3	1012	2	1	70.07255	m	1.4	176
4	4	1925	2	1	54.74059	f	1.8	244
5	5	1504	1	2	38.10541	f	3.4	279
6	6	2503	2	2	66.25873	f	0.8	248

## Data Transformation (cont'd)

- Data sets of wide  $\iff$  **long** format

```
head(pbcseq[, c("id", "futime", "status", "trt", "age", "day",  
               "sex", "bili", "chol")])
```

	id	futime	status	trt	age	day	sex	bili	chol
1	1	400	2	1	58.76523	0	f	14.5	261
2	1	400	2	1	58.76523	192	f	21.3	NA
3	2	5169	0	1	56.44627	0	f	1.1	302
4	2	5169	0	1	56.44627	182	f	0.8	NA
5	2	5169	0	1	56.44627	365	f	1.0	NA
6	2	5169	0	1	56.44627	768	f	1.9	NA



## Data Transformation (cont'd)

---

### Demos

▶ Data Transformation [R](#) [html](#)

# Data Exploration

---

- ▶ Common questions
  - ▶ What is the mean and sd for age?
  - ▶ What is the mean and sd for time?
  - ▶ What is the median and interquartile range for age?
  - ▶ What is the percentage of placebo patients?
  - ▶ What is the percentage of females?
  - ▶ What is the mean and sd for age in males?
  - ▶ What is the mean and sd for baseline serum bilirubin?
  - ▶ What is the percentage of missings in serum bilirubin?

**All these questions can be answered using R!**

## Data Exploration (cont'd)

---

- ▶ **Hints**

- ▶ Check functions: **mean(...)**, **sd(...)**, **percent(...)**, **median(...)**, **IQR(...)**

## Data Exploration (cont'd)

---

### Demos

► Data Exploration **R** **html**

# Data Visualization

---

- ▶ It is important to investigate each variable in our data set using plots
  - ▶ Descriptive statistics for continuous and categorical variables
  - ▶ Distributions of variables
  - ▶ Distributions of variables per group
  - ▶ Extreme values
  - ▶ Linear/nonlinear evolutions

## Data Visualization (cont'd)

---

- ▶ R has very powerful graphics capabilities
- ▶ Some good references are
  - ▶ Murrell, P. (2005) R Graphics. Boca Raton: Chapman & Hall/CRC.
  - ▶ Sarkar, D. (2008) Lattice Multivariate Data Visualization with R. New York: Springer-Verlag.

## Data Visualization (cont'd)

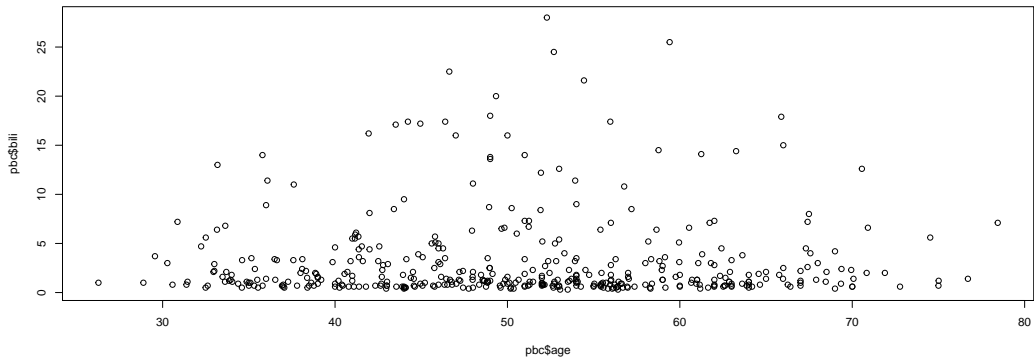
---

- ▶ Traditional graphics system
  - ▶ package **graphics**
- ▶ Trellis graphics system
  - ▶ package **lattice** (which is based on package grid)
- ▶ Grammar of Graphics implementation (i.e., Wilkinson, L. (1999) The Grammar of Graphics. New York: Springer-Verlag)
  - ▶ packages **ggplot** & **ggplot2**

# Data Visualization (cont'd)

Continuous variables

```
plot(pbc$age, pbc$bili)
```





## Data Visualization (cont'd)

---

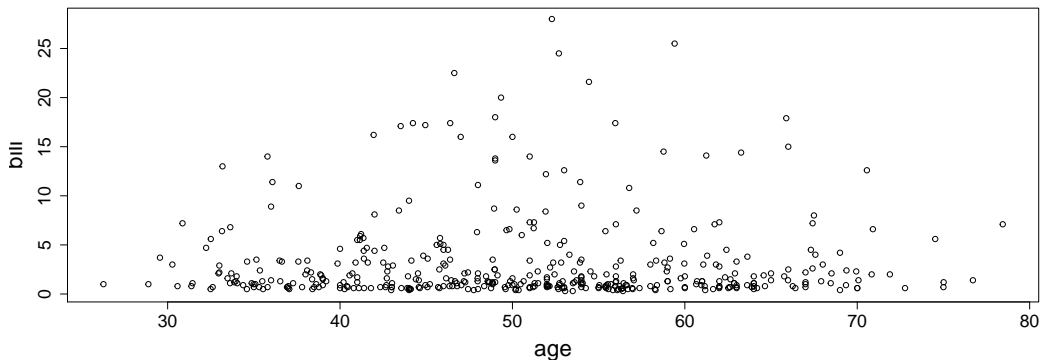
### Important plotting functions

- ▶ **plot()**: scatter plot (and others)
- ▶ **barplot()**: bar plots
- ▶ **boxplot()**: box-and-whisker plots
- ▶ **dotchart()**: dot plots
- ▶ **hist()**: histograms
- ▶ **pie()**: pie charts
- ▶ **qqnorm()**, **qqline()**, **qqplot()**: distribution plots
- ▶ **pairs()**: for multivariate data

# Data Visualization (cont'd)

Continuous variables

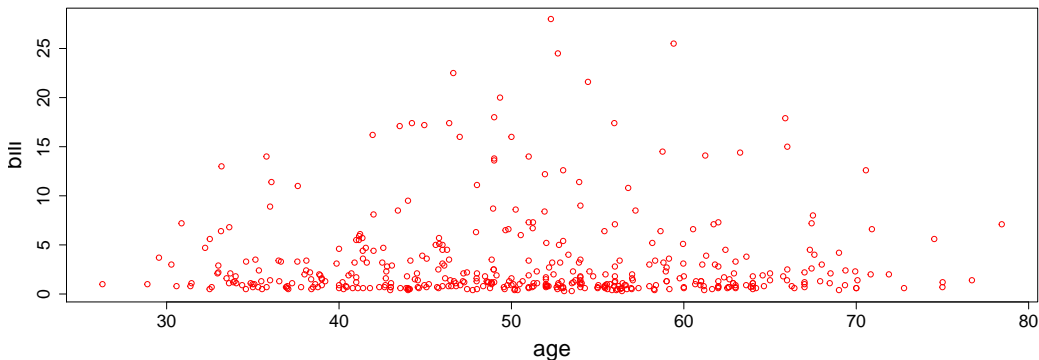
```
plot(pbc$age, pbc$bili, xlab = "age", ylab = "bili",  
     cex.lab = 1.9, cex.axis = 1.5)
```



# Data Visualization (cont'd)

Continuous variables

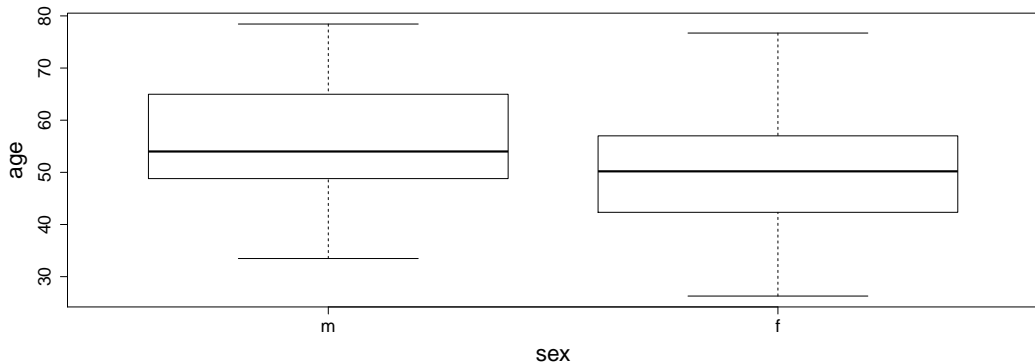
```
plot(pbc$age, pbc$bili, xlab = "age", ylab = "bili",  
     cex.lab = 1.9, cex.axis = 1.5, col = "red")
```



## Data Visualization (cont'd)

Continuous variables per group

```
boxplot(pbc$age ~ pbc$sex, xlab = "sex", ylab = "age",  
        cex.lab = 1.9, cex.axis = 1.5)
```



## Data Visualization (cont'd)

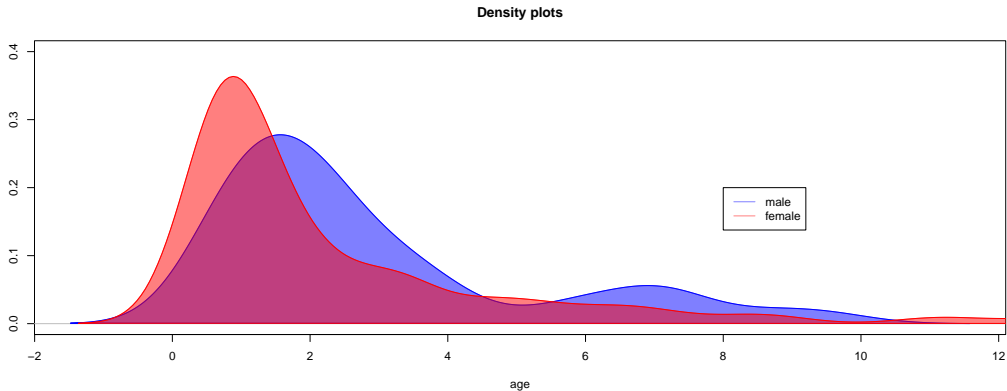
---

Continuous variables per group

```
pbm_male_bili <- pbm$bili[pbm$sex == "m"]
pbm_female_bili <- pbm$bili[pbm$sex == "f"]
plot(density(pbm_male_bili), col = rgb(0,0,1,0.5),
     main = "Density plots", xlab = "age", ylab = "")
polygon(density(pbm_male_bili), col = rgb(0,0,1,0.5),
       border = "blue")
lines(density(pbm_female_bili), col = rgb(1,0,0,0.5))
polygon(density(pbm_female_bili), col = rgb(1,0,0,0.5),
       border = "red")
legend(8,0.2, c("male", "female"),
      col = c(rgb(0,0,1,0.5), rgb(1,0,0,0.5)), lty = 1)
```

# Data Visualization (cont'd)

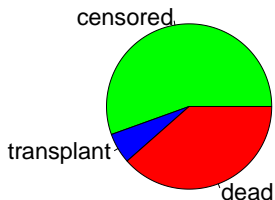
## Continuous variables per group



## Data Visualization (cont'd)

Categorical variables

```
pbcs$status <- factor(pbc$status, levels = c(0, 1, 2),  
                      labels = c("censored", "transplant", "dead"))  
pie(prop.table(table(pbc$status)),  
    col = c("green", "blue", "red"), cex = 2)
```



## Data Visualization (cont'd)

---

### Demos

▶ Data Visualization [R](#) [html](#)



# Useful Summary: Data manipulation

---

## Common R objects

- ▶ `c()`
- ▶ `matrix()`
- ▶ `data.frame()`
- ▶ `list()`
- ▶ `cbind(), rbind()`

## Transformation

- ▶ `factor()`
- ▶ `reshape()`
- ▶ `order()`
- ▶ `complete.cases()`

## Exploration

- ▶ `is.na()`
- ▶ `dim()`
- ▶ `mean(), sd()`
- ▶ `median(), IQR()`
- ▶ `percent()`

## Visualization

- ▶ `plot(), legend()`
- ▶ `hist()`
- ▶ `barchart()`
- ▶ `boxplot()`
- ▶ `par()`
- ▶ `xyplot()`

## Import/Save/Present

- ▶ `head()`
- ▶ `save(), saveRDS()`
- ▶ `load(), readRDS()`
- ▶ `read.csv(),`  
`write.csv(),`  
`read.xlsx(),`  
`write.xlsx(),`  
`read.table(),`  
`write.table()`

## Other

- ▶ `install.packages()`
- ▶ `library(), getwd()`
- ▶ `ls(), objects()`

# Indexing/Subsetting

---

- ▶ When transforming and analyzing data we often need to select specific observations or variables
  - ▶ Examples: Select ...
    - ▶ the 3rd element for vector age
    - ▶ the 3rd column of the pbc data set
    - ▶ the sex of the 10th patient
    - ▶ the baseline details of the 5th patient
    - ▶ the serum cholesterol for all males
    - ▶ the age for male patients or patients that have serum bilirubin more than 3
    - ▶ the first measurement per patient

## Indexing/Subsetting (cont'd)

---

- ▶ This can be done using square bracket (**[ ]**) notation and indices.
- ▶ Three basic types
  - ▶ position indexing
  - ▶ logical indexing
  - ▶ name indexing

# Indexing/Subsetting (cont'd)

## Indexing with vector

- For position indexing, use a **positive** value to select an element

```
x <- c(6:17)
```

```
x
```

```
[1] 6 7 8 9 10 11 12 13 14 15 16 17
```

```
x[2]
```

```
[1] 7
```

- Use multiple positive values to select multiple elements

```
x[c(2,3,4)]
```

```
[1] 7 8 9
```

## Indexing/Subsetting (cont'd)

### Indexing with `vector`

- For position indexing, use duplicated **positive** values to select the same elements

```
x <- c(6:17)
x
```

```
[1]  6  7  8  9 10 11 12 13 14 15 16 17
```

```
x[c(2,2,2)]
```

```
[1] 7 7 7
```

# Indexing/Subsetting (cont'd)

## Indexing with `vector`

- For position indexing, use a **negative** value to remove an element

```
x <- c(6:17)
```

```
x
```

```
[1]  6  7  8  9 10 11 12 13 14 15 16 17
```

```
x[-5]
```

```
[1]  6  7  8  9 11 12 13 14 15 16 17
```

- **Positive and negative indices cannot be combined**

## Indexing/Subsetting (cont'd)

---

### Indexing with vector

- Use logical index of the same length to select elements where the value is **TRUE**

```
x <- c(6:10)
y <- c(TRUE, FALSE, FALSE, FALSE, FALSE)
x[y]
```

```
[1] 6
```

# Indexing/Subsetting (cont'd)

## Indexing with vector

- Use logical indexing in combination with conditions

```
x <- c(6:10)
x[x > 7]
```

```
[1] 8 9 10
```

```
x[x > 7 & x > 9]
```

```
[1] 10
```

```
x[x > 7 | x > 9]
```

```
[1] 8 9 10
```



## Indexing/Subsetting (cont'd)

---

### Indexing with vector

- For name/character indexing, use the name of the element

```
x <- c(foo=5, bar=4, one=7, two=12, three=2)
x[c('foo', 'one')]
```

```
foo one
  5   7
```

- Use the function `names` to obtain the names

# Indexing/Subsetting (cont'd)

---

## Indexing with `matrix`

- ▶ Indexing matrices are similar to indexing vectors but with double index
  - ▶ The first position denotes the rows `["index", ]`
  - ▶ The first position denotes the columns `[, "index"]`

# Indexing/Subsetting (cont'd)

## Indexing with `matrix`

- ▶ Indexing matrices are similar to indexing vectors but with double index
  - ▶ The first position denotes the rows `["index", ]`
  - ▶ The second position denotes the columns `[, "index"]`
- ▶ Use position indexing as:

```
mat <- matrix(1:6, 3, 3)
```

```
mat
```

	[,1]	[,2]	[,3]
[1,]	1	4	1
[2,]	2	5	2
[3,]	3	6	3

```
mat[2, 2]
```

# Indexing/Subsetting (cont'd)

## Indexing with `matrix`

- ▶ When we leave a position blank all elements are selected

```
mat <- matrix(1:6, 3, 3)
mat
```

	[,1]	[,2]	[,3]
[1,]	1	4	1
[2,]	2	5	2
[3,]	3	6	3

```
mat[2, ]
```

```
[1] 2 5 2
```

# Indexing/Subsetting (cont'd)

---

## Indexing with `data.frame`

- ▶ When using a single index the data frame acts like a list of variables

```
DF <- data.frame(x = 1:4,  
                 y = c(35, 23, 14, 45))
```

DF

	x	y
1	1	35
2	2	23
3	3	14
4	4	45

# Indexing/Subsetting (cont'd)

## Indexing with `data.frame`

- ▶ When using a single index the data frame acts like a list of variables

```
DF <- data.frame(x = 1:4,  
                 y = c(35, 23, 14, 45))
```

DF

	x	y
1	1	35
2	2	23
3	3	14
4	4	45

- ▶ Use position indexing as:

```
DF[2]
```

	y
1	35
2	23
3	14
4	45

## Indexing/Subsetting (cont'd)

---

### Indexing with `data.frame`

- ▶ `$` provides a convenient notation to extract an element by name

```
head(pbc$time)
```

```
[1] 400 4500 1012 1925 1504 2503
```

# Indexing/Subsetting (cont'd)

---

## Indexing with `data.frame`

- ▶ When using a double index, indexing works like a matrix

```
DF <- data.frame(x = 1:3,  
                 y = c(35, 23, 14))
```

DF

	x	y
1	1	35
2	2	23
3	3	14



# Indexing/Subsetting (cont'd)

## Indexing with `data.frame`

- ▶ When using a double index, indexing works like a matrix

```
DF <- data.frame(x = 1:3,  
                 y = c(35, 23, 14))
```

DF

	x	y
1	1	35
2	2	23
3	3	14

- ▶ Use position indexing

```
DF[2, 2]
```

```
[1] 23
```

- ▶ Use logical indexing

```
DF[DF$y < 30, 2]
```

```
[1] 23 14
```

# Indexing/Subsetting (cont'd)

## Indexing with `data.frame`

- Combine logical and position indexing in data frame

```
pbcDF <- data.frame(pbc)
head(pbc[pbc$sex == "m", 1:7])
```

	id	time	status	trt	age	sex	ascites
3	3	1012	dead	1	70.07255	m	0
14	14	1217	dead	2	56.22177	m	1
21	21	3445	censored	2	64.18891	m	0
24	24	4079	dead	1	44.52019	m	0
48	48	4427	censored	2	49.13621	m	0
52	52	2386	dead	1	50.54073	m	0

# Indexing/Subsetting (cont'd)

## Indexing with `data.frame`

- Combine logical and position indexing in data frame

```
pbcDF <- data.frame(pbc)
head(pbc[pbc$age > 30 | pbc$sex == "f", 1:7])
```

	id	time	status	trt	age	sex	ascites
1	1	400	dead	1	58.76523	f	1
2	2	4500	censored	1	56.44627	f	0
3	3	1012	dead	1	70.07255	m	0
4	4	1925	dead	1	54.74059	f	0
5	5	1504	transplant	2	38.10541	f	0
6	6	2503	dead	2	66.25873	f	0

# Indexing/Subsetting (cont'd)

## Indexing with `data.frame`

- Combine logical and position indexing in data frame

```
pbcDF <- data.frame(pbc)
head(pbc[pbc$age > 30 & pbc$sex == "f", 1:7])
```

	id	time	status	trt	age	sex	ascites
1	1	400	dead	1	58.76523	f	1
2	2	4500	censored	1	56.44627	f	0
4	4	1925	dead	1	54.74059	f	0
5	5	1504	transplant	2	38.10541	f	0
6	6	2503	dead	2	66.25873	f	0
7	7	1832	censored	2	55.53457	f	0

# Indexing/Subsetting (cont'd)

## Indexing with `list`

- ▶ Lists can be subsetted in the same way as vectors using single brackets - Note that the output is a list
- ▶ Use position indexing

```
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))  
mylist[2]
```

```
$z  
[1] "m" "f" "f"
```

# Indexing/Subsetting (cont'd)

---

## Indexing with `list`

- ▶ Double square brackets can be also used - Note that the output is a vector
- ▶ Use position indexing

```
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))  
mylist[[2]]
```

```
[1] "m" "f" "f"
```

# Indexing/Subsetting (cont'd)

## Indexing with `list`

- ▶ `$` provides a convenient notation to extract an element by name -  
Note that the output is a vector

```
mylist <- list(y = c(14, 45), z = c("m", "f", "f"))  
mylist
```

```
$y  
[1] 14 45
```

```
$z  
[1] "m" "f" "f"
```

```
mylist$y
```


```
[1] 14 45
```

## Indexing/Subsetting (cont'd)

---

- ▶ Use the following webpage to further investigate indexing and subsetting  
<https://emcbiostatistics.shinyapps.io/indexing/>

### Demos

- ▶ Shiny app indexing subsetting 

In order to run the app you will need to install the packages:

- ▶ `survival`
- ▶ `shiny`



# Useful Summary: Indexing/Subsetting

---

## Vectors

- ▶ `[]`
- ▶ `[""]`

## Matrices

- ▶ `[,]`

## Data frames

- ▶ `[,]`
- ▶ `[[]]`
- ▶ `$`

## Lists

- ▶ `[]`
- ▶ `[[]]`
- ▶ `$`

## Useful Summary: Indexing/Subsetting (cont'd)

---

### Demos

- ▶ Indexing Subsetting [R](#) [html](#)

### Practicals

- ▶ Basic Use R [html](#)