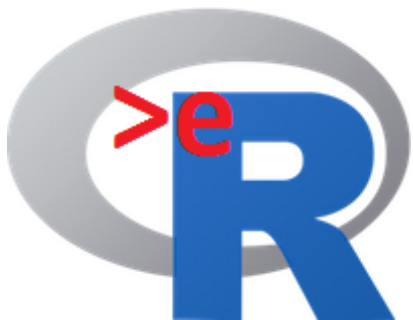




This course was developed as a part of the VLIR-UOS Cross-Cutting projects:

- Statistics: 2011-2016, 2017.
- Statistics: 2017.
- Statistics for development : 2018-2020.



The >eR-Biostat initiative  
Making R based education materials in  
statistics accessible for all

## An introduction to R: Short Version (2017)

### Part 2: basic programming

Developed by

Dan Lin (Hasselt University) and Ziv Shkedy (Hasselt University)

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ER-BioStat



<https://github.com/eR-Biostat>

Email: [erbiostat@gmail.com](mailto:erbiostat@gmail.com)



@erbiostat

# Overview

1. Basic programming in R: objects in R
2. Reading external datasets
3. Programming in R: a for loop
4. Programming in R: user functions
5. Application of a for loop: bootstrap.

# **Chapter 1**

## **Basic programming Objects in R**

# Simple objects

Assign the value of 5 to  
the R object x



```
> x <- 5
```

```
> x
```

```
[1] 5
```

```
> x^2
```

```
[1] 25
```

```
> x + 6
```

```
[1] 11
```

# Vectors

A function in R that creates a vector: **c()**

```
> x<-c("A","A","A","A","B","B","B","B")
> x
[1] "A" "A" "A" "A" "B" "B" "B" "B"
```

```
> y<-c(10,11,9,15,3,5,7,2)
> y
[1] 10 11 9 15 3 5 7 2
```

```
> y[1] —————> The first element in the vector y
```

```
[1] 10
```

```
> y[2] —————> The second element in the vector y
```

```
[1] 11
```

# Index vectors

```
y[ x=="A" ]
```

All the elements in y  
for which x=A

```
> ya<-y[ x=="A" ]  
> ya  
[1] 10 11 9 15
```

```
> yb<-y[ x=="B" ]  
> yb  
[1] 3 5 7 2
```

```
> tapply(y,x,mean)  
      A      B  
11.25  4.25
```

# Data frames

A data structure  
which contains more  
than 1 object.

Objects can be  
numeric objects and  
character objects

```
> z<-data.frame(x,y)
```

```
> z
```

	x	y
1	A	10
2	A	11
3	A	9
4	A	15
5	B	3
6	B	5
7	B	7
8	B	2



# The \$

The object x in z

```
> z$x
```

```
[1] A A A A B B B B
```

```
Levels: A B
```

```
> z$y
```

```
[1] 10 11 9 15 3 5 7 2
```

# Matrix

```
> w<-c(1,2,40,2,3,9,200,4,6000)
> matw<-matrix(w,3,3)
> matw
```

	[,1]	[,2]	[,3]
[1,]	1	2	200
[2,]	2	3	4
[3,]	40	9	6000

# Rows and columns

$X_{ij}=x[i,j]$

```
> w1<-matw[1,]  
> w2<-matw[,2]  
> w1  
[1]    1    2 200  
> w2  
[1]  2  3  9
```

# The matrix reloaded

```
> matw+10
```

	[,1]	[,2]	[,3]
[1,]	11	12	210
[2,]	12	13	14
[3,]	50	19	6010

```
>
```

[1]	1	3	6000
-----	---	---	------

# The inverse matrix

```
> solve(matw)
```

	[,1]	[,2]	[,3]
[1,]	-0.687854189	0.39056517	0.0226680962
[2,]	0.453361924	0.07658141	-0.0151631184
[3,]	0.003905652	-0.00271864	0.0000382907

```
> solve(matw)%*%(matw)
```

	[ ,1]	[ ,2]	[ ,3]
[1, ]	1.0000000e+00	9.714451e-17	1.998401e-15
[2, ]	5.551115e-17	1.0000000e+00	-8.104628e-15
[3, ]	4.336809e-19	-4.336809e-19	1.0000000e+00

# Example: data frame

```
> x<-c(25,36,21)  
> gender<-c("M","M","F")  
> data.frame(x,gender)
```

	x	gender
1	25	M
2	36	M
3	21	F

# Example: an R object of a data frame

```
> x<-c(25,36,21)
> gender<-c("M","M","F")
> xdat<-data.frame(x,gender)
> xdat
  x gender
1 25      M
2 36      M
3 21      F
> xdat$gender
[1] M M F
Levels: F M
```

# Practical session

- Create the folowig data frame:

A	100
B	99
C	105
D	35
E	0
F	250



# **Chapter 2**

## **Reading external datasets**

## Read an external file (**text file**)

```
> spwh3<-read.table('c:\\projects\\wseda\\spwh3.txt',  
                    header=FALSE,na.strings="NA", dec=".")
```

```
> dim(spwh3)  
[1] 60 4
```

```
> spwh3<-data.frame(spwh3)  
> names(spwh3)<-c("id","y","x1","gender")
```

## Read an external file (**csv file**)

```
> gsw.ts <- read.csv("C:/projects/NBA/GSW_TS.csv",header =  
FALSE,sep =";")
```

# The data

```
> spwh3
```

	id	y	x1	gender
1	1	10.111368	1	0
2	2	9.948930	1	0
3	3	10.322560	1	0
4	4	10.241052	1	0
5	5	9.911427	1	0
6	6	9.357969	1	0
7	7	10.649141	1	0
8	8	10.150197	1	0
9	9	9.403218	1	0
10	10	8.027072	1	0
11	11	20.020056	1	1

## The sleep data in R

```
> sleep
```

	extra	group	ID
1	0.7	1	1
2	-1.6	1	2
3	-0.2	1	3
4	-1.2	1	4
5	-0.1	1	5
.	.	.	.
14	0.1	2	4
15	-0.1	2	5
16	4.4	2	6
17	5.5	2	7
18	1.6	2	8
19	4.6	2	9
20	3.4	2	10

# Two samples t-test

```
> y1<-spwh3$y[spwh3$gender==0]  
> y2<-spwh3$y[spwh3$gender==1]  
> t.test(y1,y2)
```

Welch Two Sample t-test

data: y1 and y2

t = -9.1428, df = 58, p-value = 7.715e-13

alternative hypothesis: true difference in means is not  
equal to 0

95 percent confidence interval:

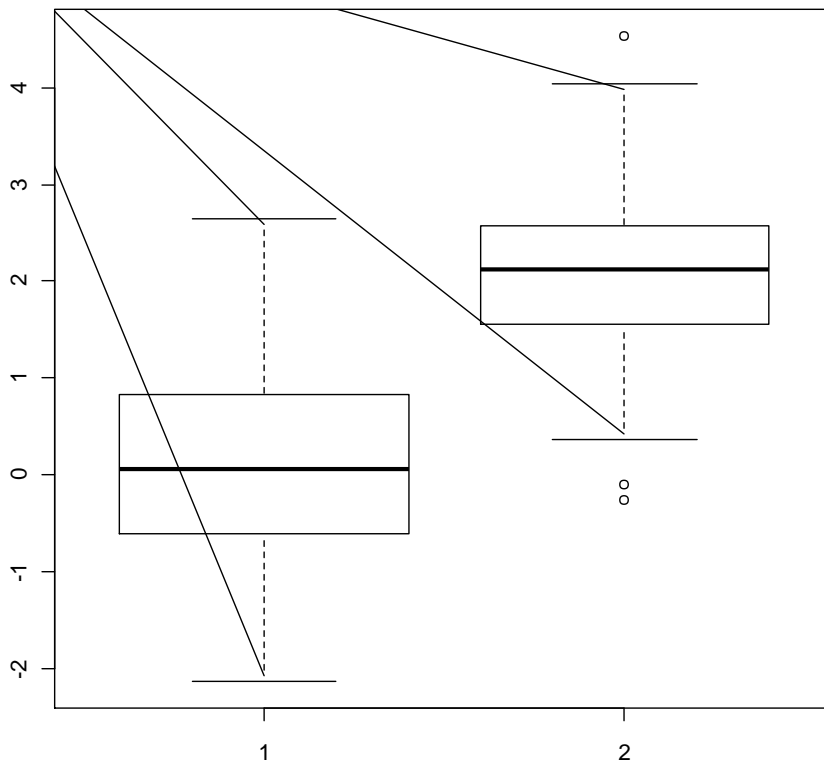
-12.229889 -7.836547

sample estimates:

mean of x mean of y

14.99933 25.03254

# Two samples t-test



```
> y1<-rnorm(100,0,1)  
> y2<-rnorm(57,2,1)  
> boxplot(y1,y2)
```

# Two samples t-test

```
> t.test(y1,y2)
```

Welch Two Sample t-test

data: y1 and y2

t = -14.2203, df = 126.176, p-value < 2.2e-16

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-2.290641 -1.730980

sample estimates:

mean of x mean of y

-0.0063866 2.0044240

# R object for the output

```
> t.t<-t.test(y1,y2)
```

```
> summary(t.t)
```

	Length	Class	Mode
statistic	1	-none-	numeric
parameter	1	-none-	numeric
p.value	1	-none-	numeric
conf.int	2	-none-	numeric
estimate	2	-none-	numeric
null.value	1	-none-	numeric
alternative	1	-none-	character
method	1	-none-	character
data.name	1	-none-	character



# R object for the output

```
> t.t
```

```
Welch Two Sample t-test
```

```
data: y1 and y2
```

```
t = -14.2203, df = 126.176, p-value < 2.2e-16
```

```
alternative hypothesis: true difference in means is not  
equal to 0
```

```
95 percent confidence interval:
```

```
-2.290641 -1.730980
```

```
sample estimates:
```

```
mean of x mean of y
```

```
-0.0063866 2.0044240
```

```
> t.t$p.value
```

```
[1] 5.570543e-28
```

```
> t.t$statistic
```

```
t
```

```
-14.22034
```

# Practical session

- Create the following text file:

A	100
B	99
C	105
D	35
E	0
F	250

and read it to R as an external file

# **Chapter 3**

## **Programming I: A for loop**

## A for loop


```
for(i in 1:B)  
{
```

*Here you ask from R to do the same  
thing B times.....*

```
}
```

# Generate 1000 samples from $N(2,1)$

A random sample from  $N(2,1)$ .  
Sample size=10.


$$X_i \sim N(\mu=2, \sigma=1)$$

```
> x<-rnorm(10,2,1)
```

```
> x
```

```
[1] 2.1531462 2.4426189 0.8080064 1.4051178 1.9392356 0.6466574  
[7] 0.7519918 -0.1097367 2.3338487 3.7598694
```

```
> x<-rnorm(10,2,1)
```

```
> x
```

```
[1] 2.9694328 1.1065506 1.5612572 0.3904008 1.6890423 3.7319756 0.9026146  
[8] 1.7763012 2.4356002 0.9643299
```

```
> x<-rnorm(10,2,1)
```

```
> x
```

```
[1] 2.1888795 2.6353313 2.7131707 1.2311123 2.8258664 0.8101126 2.1533630  
[8] 2.9126222 0.4085356 1.5586004
```

```
> mean(x)
```

```
[1] 1.943759
```

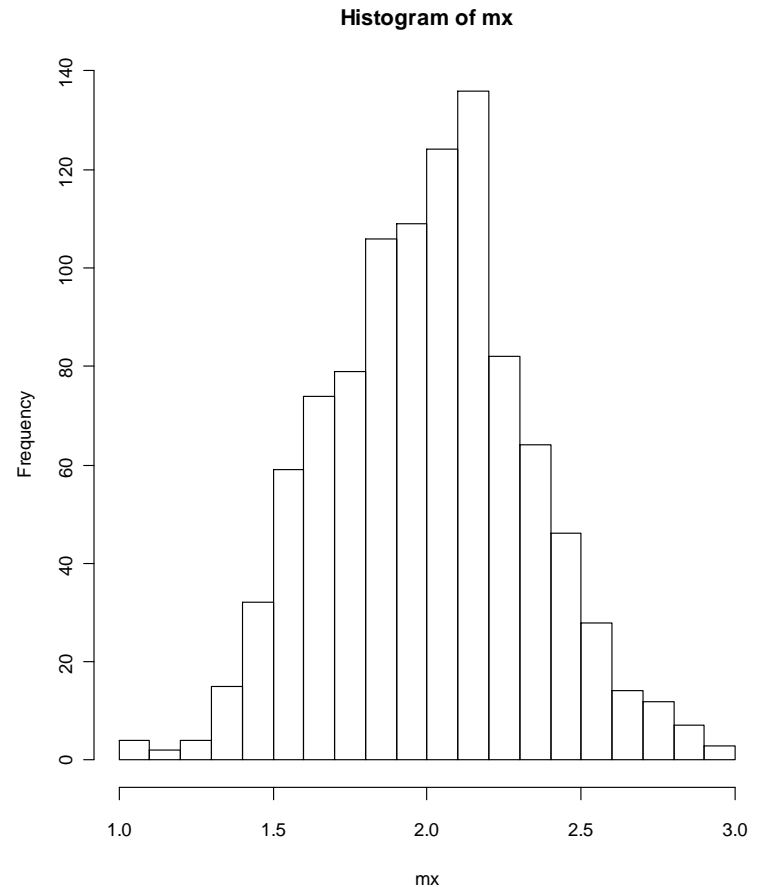
# Generate 1000 samples from $N(2,1)$

mx: A vector of 1000 numbers

```
> mx <- c(1:1000)
> for(i in 1:1000)
+ {
+   x <- rnorm(10, 2, 1)
+   mx[i] <- mean(x)
+ }
> hist(mx, nclass=25)
```

A random sample from  $N(2,1)$ .  
Sample size=10.

Repeat this 1000 times



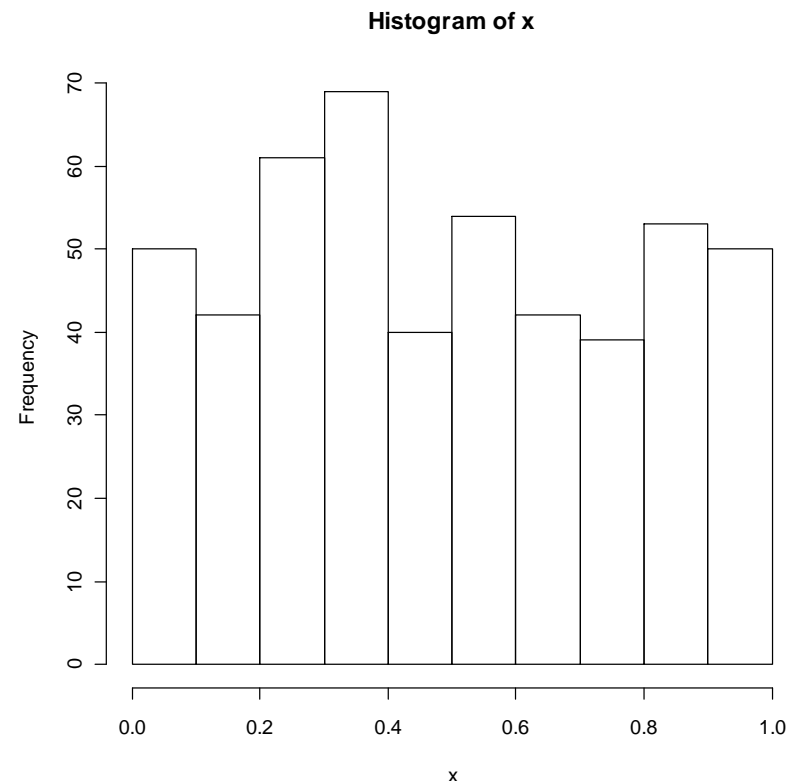
# Example: distribution of the minimum in uniform distribution

- Generate 1000 samples ( $n=50$ ) from  $U(0,1)$ .
- Calculate the minimum of each sample.
- Estimate the density of the minimum.

# Example: distribution of the minimum in uniform distribution

- Generate 1000 samples ( $n=50$ ) from  $U(0,1)$ .
- Calculate the minimum of each sample.

```
> x<-runif(500,0,1)
> hist(x)
> min(x)
[1] 0.004631357
```





# Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

```
for(i in 1:B)  
{
```

Generate 1000 samples ( $n=50$ ) from  $U(0,1)$ .  
Calculate the minimum of each sample.

```
}
```

# Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

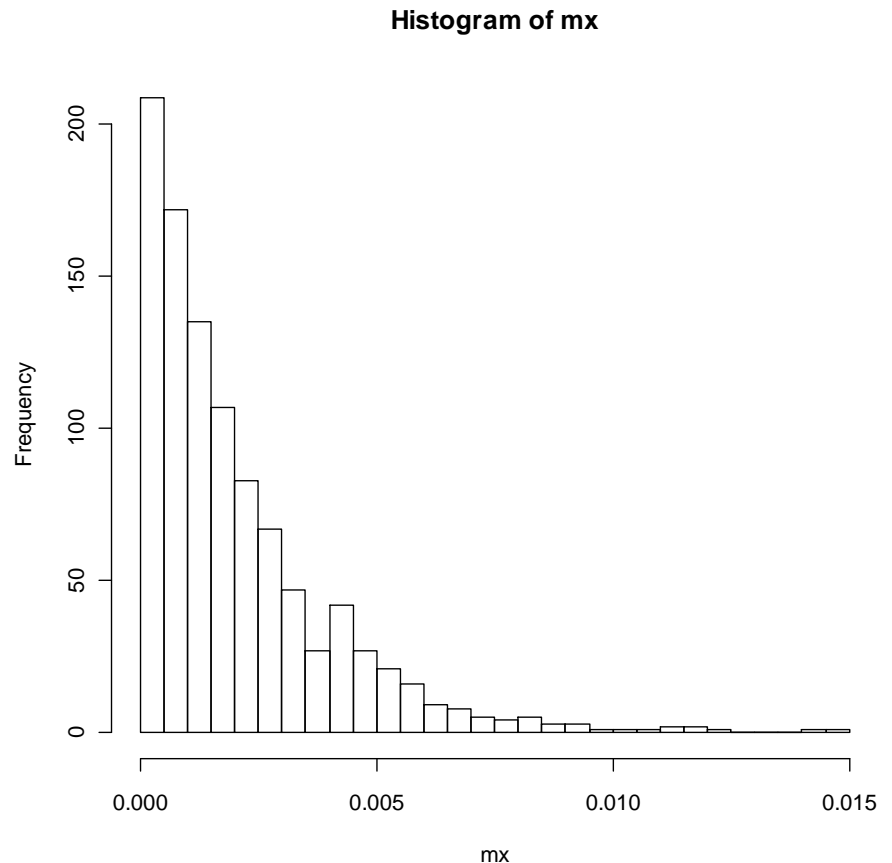
```
for(i in 1:B)
{
  Generate 1000 samples (n=50) from U(0,1).
  Calculate the minimum of each sample.
}
```

```
> mx<-c(1:1000)
> for(i in 1:1000)
+ {
+   x<-runif(500,0,1)
+   mx[i]<-min(x)
+ }
```

# Example: distribution of the minimum in uniform distribution

- Estimate the density of the minimum.

```
> mx<-c(1:1000)
> for(i in 1:1000)
+ {
+ x<-runif(500,0,1)
+ mx[i]<-min(x)
+ }
>hist(mx)
```



# Practical session

- Make a for loop that print your name 500 times.

# **Chapter 4**

## **Programming in R II: User functions**

Generate a random sample of size 1000  
from  $N(0,3)$

```
> x<-rnorm(1000,0,3)
```

```
> mean(x)
```

```
[1] 0.3080260
```

```
> median(x)
```

```
[1] 0.4176008
```

```
> quantile(x)
```

0%	25%	50%	75%	100%
-5.9877043	-1.7844439	0.4176008	1.5712923	8.5930491

## A user function: general form

```
function name<-function(x)  
{
```

*R commands (what do you want that the function will do for you.....)*

```
}
```

# A user function: general form

```
function name<-function(x)
{
}
}
```

Input: a sample

Output:

- Descriptive statistics:  
mean, median, quantiles
- Graphical output:  
histogram

R functions for the output:

```
mean()
median()
quantile(x)
hist()
```



# A user function: general form

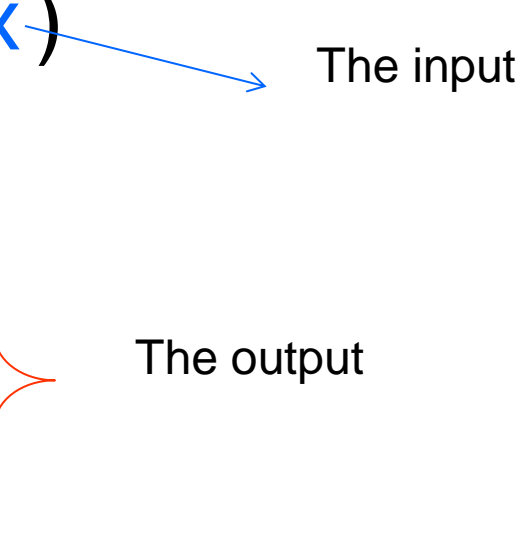
A small program to produce the output:

```
mean.x<-mean(x)  
med.x<-median(x)  
quantile(x)  
hist(x)
```

See slide 39.

## A user function: example

```
fch20<-function(x)
{
mean.x<-mean(x)
med.x<-median(x)
q.x<-quantile(x)
hist(x)
return(mean.x,med.x,q.x)
}
```



The input

The output

The diagram illustrates the function's flow. A blue arrow points from the parameter 'x' in the function definition to the text 'The input'. A red bracket groups the four lines of code that calculate statistical measures (mean, median, quantile, and histogram) and point to the text 'The output'.

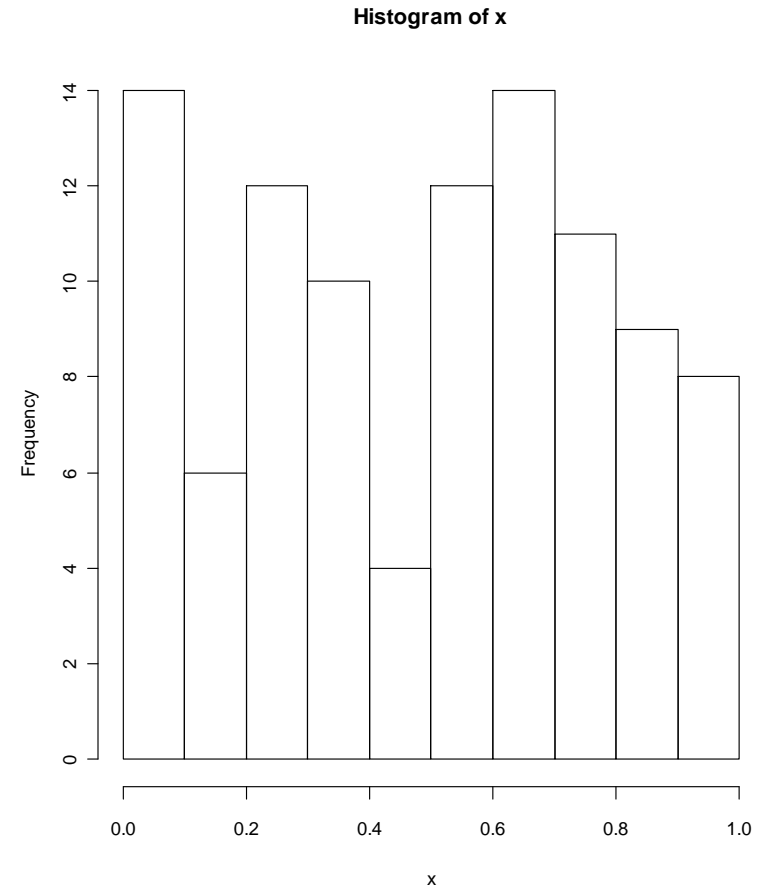
# A user function: output

```
> z<-runif(100,0,1)
> fch20(z)
$mean.x
[1] 0.4947539

$med.x
[1] 0.5291341

$q.x
      0%      25%
50% 0.01240262 0.24212404
      0.52913405 0.72482479
      0.98413912

Warning message:
In return(mean.x, med.x, q.x) :
  multi-argument returns are deprecated
>
```



# Practical session

- Write a function which receive a numerical vector as an input and calculate the mean of the vector.

# **Chapter 5:**

## **Application : the for loop**

**The bootstrap estimate of the standard error for the mean**

# The observed data

A sample of 10 observations:

```
> x <- c(11.201, 10.035, 11.118, 9.055, 9.434, 9.663, 10.403, 11.662, 9.285, 8.84)
> mean(x)
[1] 10.0696
```

We wish to estimate the standard error of the sample mean

$$S.E(\bar{x}) = \frac{\sigma_F}{\sqrt{n}}$$

# Parametric and nonparametric bootstrap

## nonparametric bootstrap

$$F \rightarrow (x_1, x_2, \dots, x_n)$$

We resample from  
the empirical  
distribution

## parametric bootstrap

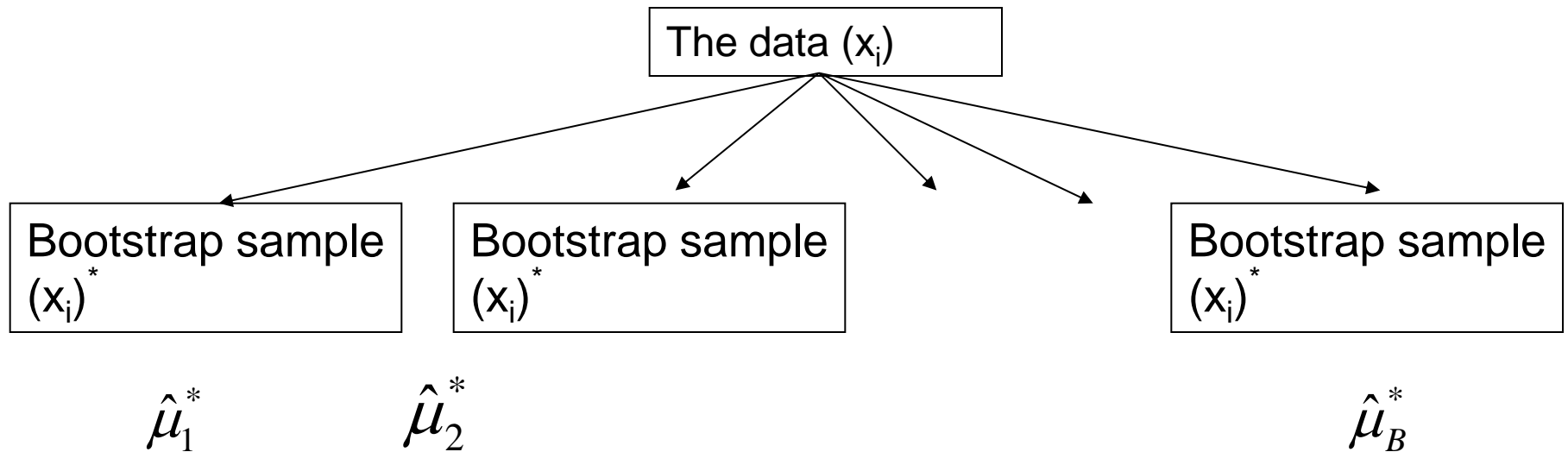
We assume a parametric  
model for  $F$

$$F(\theta)$$

We resample from

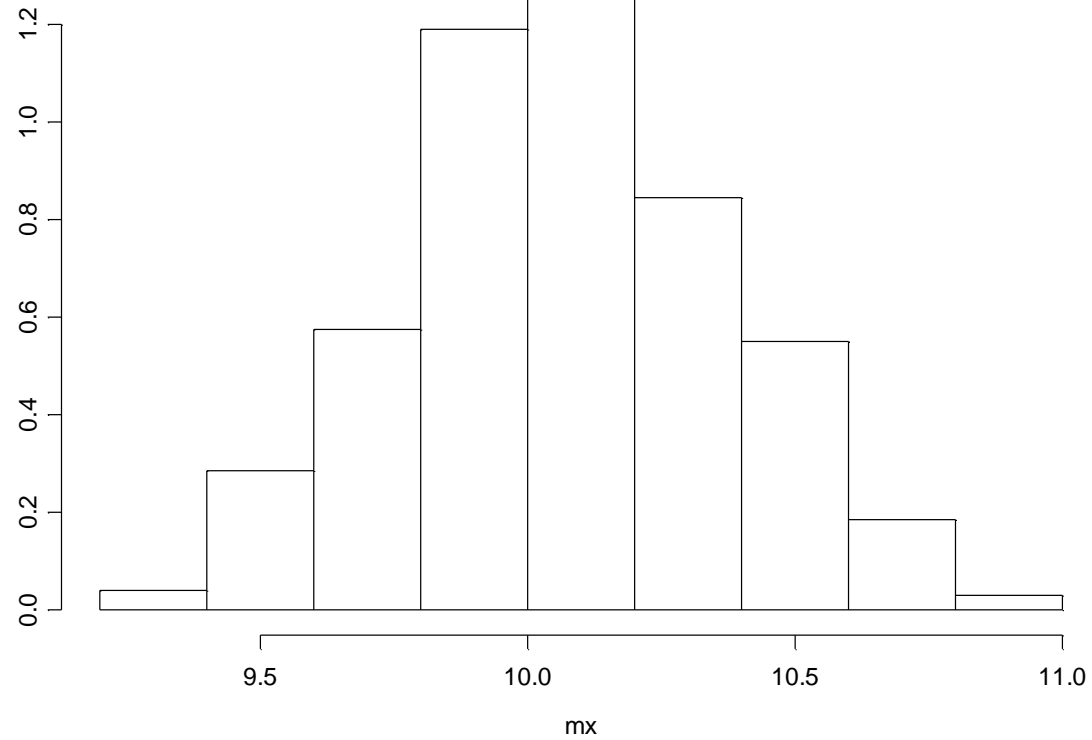
$$F(\hat{\theta})$$

# Nonparametric bootstrap

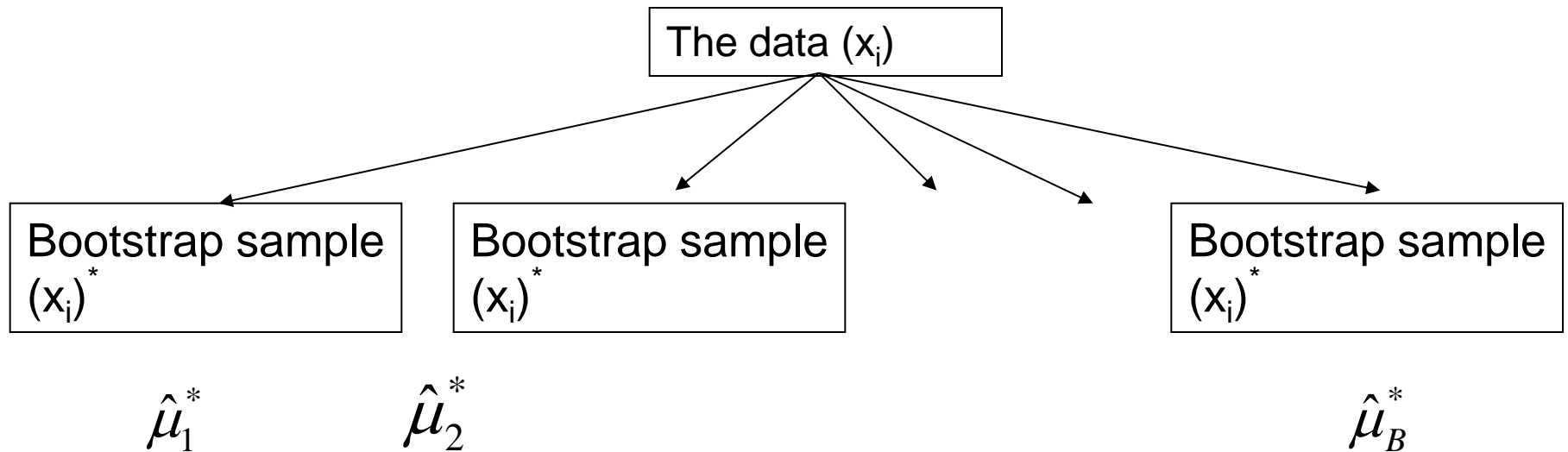




# Nonparametric bootstrap



# Nonparametric bootstrap



$$S.E.(\hat{\mu}) = \left\{ \frac{1}{B-1} \sum_{b=1}^B (\hat{\mu}_b^* - \hat{\mu}^*)^2 \right\}^{0.5}$$

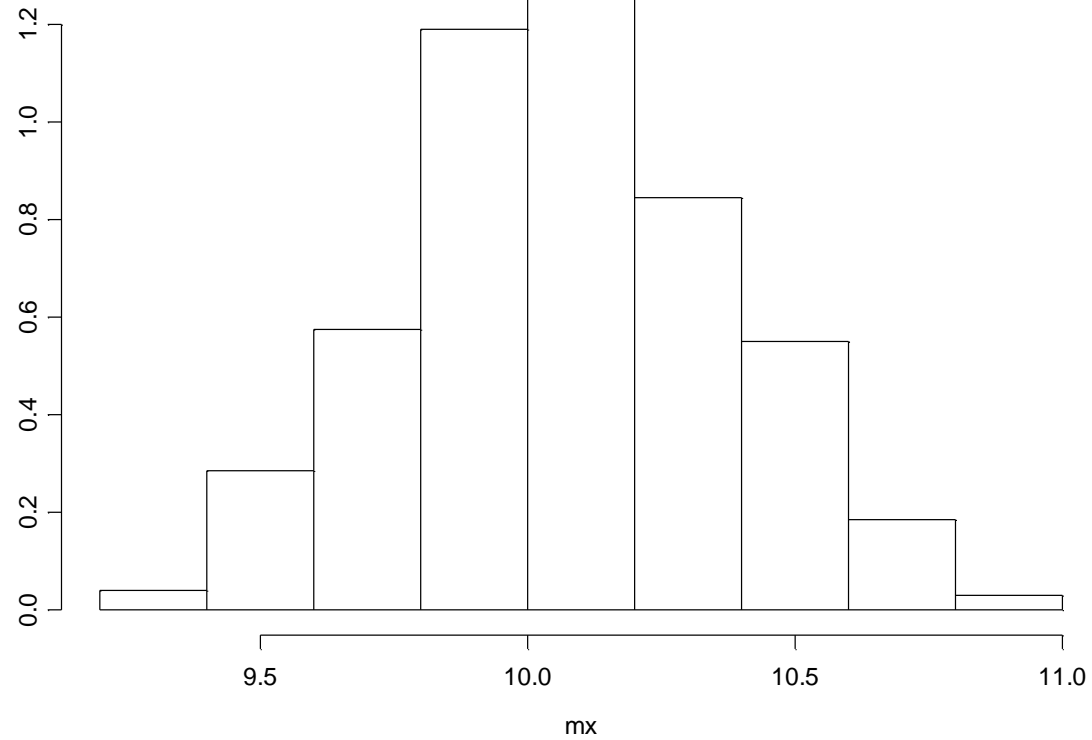
## R code

```
> var(mx)
[1] 0.09357364
```

The estimated  
standard error 0.093

```
n<-length(x)
B<-1000
mx<-c(1:B)
for(i in 1:B){
  cat(i)
  boot.i<-sample(x,n,replace=T)
  mx[i]<-mean(boot.i)
}
```

# Nonparametric bootstrap



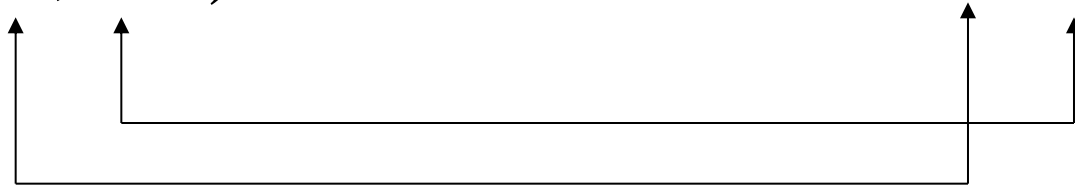
# Parametric bootstrap

We assume a parametric model for  $F$

We estimate  $F$  by

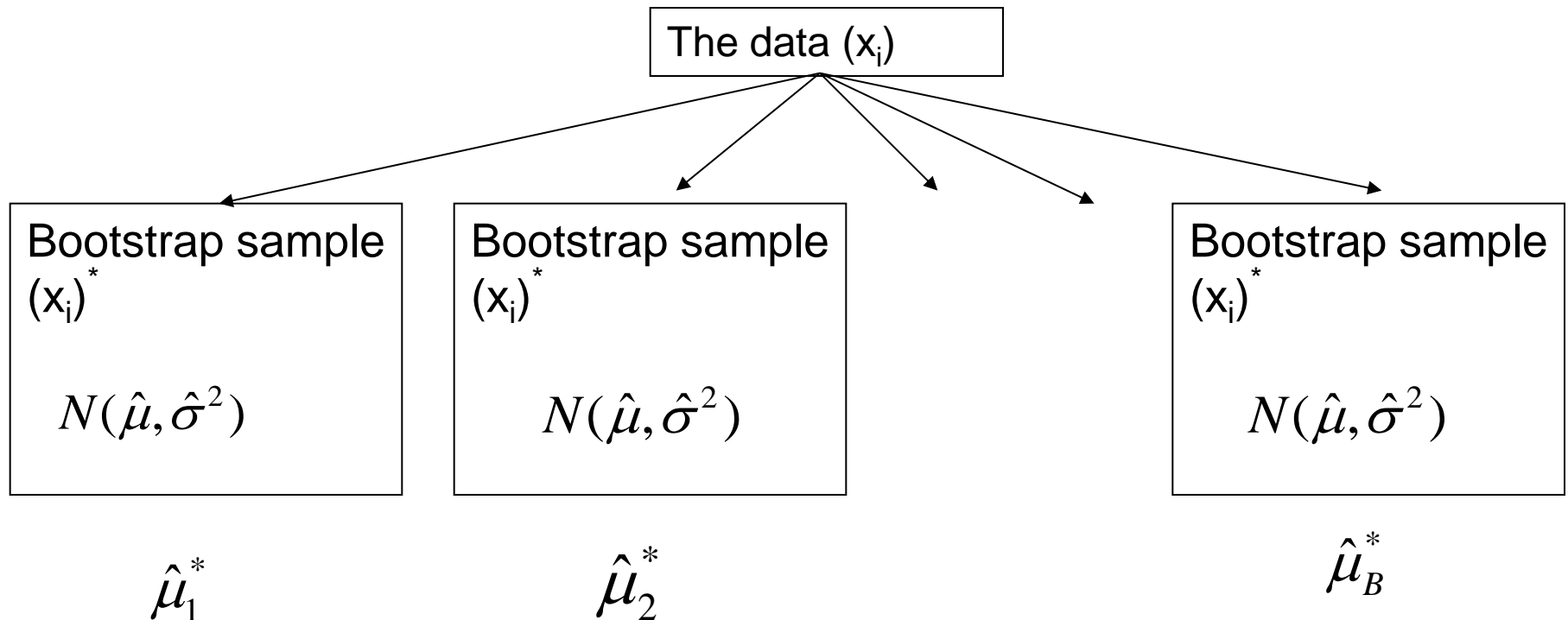
$$F = N(\mu, \sigma^2)$$

$$\hat{F} = N(\hat{\mu}, \hat{\sigma}^2)$$



We replace the unknown parameters in  $F$  with their plug-in estimates

# Parametric bootstrap



$$S.E.(\hat{\mu}) = \left\{ \frac{1}{B+1} \sum_{b=1}^B (\hat{\mu}_b^* - \hat{\mu}^*)^2 \right\}^{0.5}$$

## R code

```
> var(mx)
[1] 0.1007613
```

Bootstrap estimate for the  
standard error for the mean

```
B<-1000
MLx<-mean(x)
Varx<-var(x)
mx<-c(1:B)
for(i in 1:B){
  cat(i)
  boot.i<-rnorm(n,MLx,sqrt(Varx))
  mx[i]<-mean(boot.i)
}
```

# Parametric bootstrap

