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R Insight 2018

Xavier Thibert-Plante ¹

October 23, 2018

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What you won't learn today

- Statistics
- ► Experimental design

- ► Basic usage of high level programming
- ► Tool to learn more on your own

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What R is not going to do for you

- Not useful to enter data
- Will not tell you if you are using the right statistical test

- Perform statistical test
- ▶ Plot figures

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- Install Anaconda
- > sudo apt-get install libcurl4-openssl-dev libssl-dev
- > sudo R
- ► Inside R
 - > update.packages()
 - > install.packages(c('repr', 'IRdisplay', 'evaluate', 'crayon', 'pbdZMQ', 'devtools', 'uuid', 'digest'))

devtools::install_github('IRkernel/IRkerneMath) operation

 \triangleright > q()

Introduction

This page can take up to 30 minutes of computation

Installing R

► Start R without the sudo from a terminal, then inside R

```
> IRkernel::installspec()
```

- \triangleright > q()
- ➤ You can now start you jupyter notebook (in a virtual environment if you like)

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Installing R



localhost:8889/tree#

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- > q()
- or
 > quit()

You can save your session (variables and function and continue later)

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R graphical interface

- R is a command line interface, your mouse is useless here.
 - ► Advantage: batch files
 - Inconvenient: when you don't know what to type you feel pretty lonely

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Matrix operation

Conclusion

- One value
 - > a <- 1 equivalent to a=1

> 1 -> a

- ► A vector
 - > b < -c(1,2,3)

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Complusion

▶ One value

$$> b < -c(1,2,3)$$

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Matrix operation

Conclusion

One value

$$> b <-c(1,2,3)$$

Vector

- > a <- array(NA, dim=10)</pre>
- > a[4] < -5
- Matrix
 - > b <- matrix(NA,ncol=10,nrow=30)</pre>
 - > b[30,3]<-1

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Help

RTFM

- > help(array)
- > help(matrix)

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Matrix operation

- Sequence vector
 - > a<-array(seq(1,10,2))
- Random vector
 - > a<-array(rnorm(10,mean=15,sd=3)</pre>
- ► Sequence matrix
 - > b<-matrix(seq(1,20),ncol=2,nrow=10</pre>
- Random matrix
 - > b<-matrix(runif(21),ncol=3,nrow=7</pre>

One variable nanipulations

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- Random matrix
 - > b<-matrix(runif(21),ncol=3,nrow=7)</pre>

Simple arithmetic operations

>	a+a	>	a*k
>	a+5	>	b*k
>	1+b	>	a-a
>	5*a	>	a-5
>	a*a	>	a/2

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Structure

x is a matrix with column and lines

```
x[,1] # refers to the first column x[,2] # refers to the second column x[1,] # refers to the first line
```

► x[line,column]

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Read the data

Go to my github

- https://github.com/xavierthibertplante/r_crash_course
- Pull

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Matrix operation

Modifying the database

- ► Remove special character (#\$%&?+=-)
- ► Make sure that the first line is the title of the column without space ("colOne" vs "col one")
- ► Save as csv (Coma Separated Variable)

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Aatrix operation

Entering your data

- ► Use excel spreadsheet
- Save as csv (coma separated variable)
- Look at the csv file in a text editor, such as Notepac
- One column must have only one type of cell: number except for the first one, sometime.

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Load the data

- ► Open R
 - > x<-read.csv("hendryEtAl.csv")</pre>
- ▶ We can now play with the database with the variable :

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► x[line,column]

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Sanity check

▶ Number of line in the data before and after loading

- > length(x[,1])
- ▶ Number of column:
 - > length(x[1,])

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Sanity check

▶ Number of line in the data before and after loading

$$>$$
 length(x[,1])

Number of column:

$$>$$
 length(x[1,])

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Column name

Syntax: <variableName>\$<columnName>

- > x\$Years instead of
- > x[,18]
- Note that it is case sensitive
 - > x\$years will not work

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Matrix operation

Column name

► Syntax: <variableName>\$<columnName>

> x\$Years

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Your data set in R

First line: column name (no space or special character in the name)

- ► Each column is of one type
- ► Save as "csv"
- ► Look at your file in a text editor (note the separation ";" or "," and the decimal point "." or ",")
- Adapt the option of read.csv function
 > help(read.csv)
- Load your data
 yourName<-read.csv("fileName.csv")</pre>
- ► Test length and names of columns

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Conclusion

- Reload the database
 - > x<-read.csv("hendryEtAl.csv")</pre>
- ► Histogram of the Haldanes
 - > hist(x\$Haldanes)
- ► Change number of bars
 - > hist(x\$Haldanes,breaks=100
- Customize the position of the bars
 - > hist(...,

breaks=seq(from=-1.2, to=0.8, by=0.1)

> x<-read.csv("hendryEtAl.csv")</pre>

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- ► Customize the position of the bars
 - > hist(...,
 breaks=seq(from=-1.2,to=0.8,by=0.1))

One variable manipulations

Simple plot

- ► Change the color of the bars
 - > hist(...,col=2)
- ► Change the color of the borders
 - > hist(....border=3)

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Matrix operation

► Shapiro-Wilk normality test

> shapiro.test(x\$Haldanes)

► Kolmogorov-Smirnov test

> ks.test(x\$Haldanes, "pnorm",
 mean=mean(x\$Haldanes, na.rm=T),
 sd=sd(x\$Haldanes, na.rm=T))

► Give numbers, not its meaning

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Function

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► Import a new database

> mydata<-read.csv("fruits.csv")</pre>

- Extract the information
 - > str(mydata)
 - > help(aggregate)
 - > aggregate(mydata\$Fruit, list(mydata\$State), mean)
 - > aggregate(mydata\$Fruit,

list(State=mydata\$State), mean)

> aggregate(x=mydata\$Fruit,
by=list(State=mydata\$State), FUN=mean

NOT

> aggregate(mydata\$Fruit, mydata\$State,
mean)

> help(aggregate)

Tables

- Import a new database
 - > mydata<-read.csv("fruits.csv")</pre>
- Extract the information
 - > str(mydata)
 - help(aggregate)
 - > aggregate (mydata\$Fruit, list(mydata\$State), mean)

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- > aggregate(x=mydata\$Fruit,
 by=list(State=mydata\$State), FUN=mean)
 NOT
- > aggregate(mydata\$Fruit, mydata\$State,
 mean)
- > help(aggregate)

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Import a new database

> mydata<-read.csv("fruits.csv")

Extract the information

- > str(mydata)
- > help(aggregate)
- > aggregate (mydata\$Fruit, list(mydata\$State), mean)
- > aggregate(mydata\$Fruit,
- list(State=mydata\$State), mean)
- > aggregate(x=mydata\$Fruit,
 by=list(State=mydata\$State), FUN=mean)

NOT

- > aggregate(mydata\$Fruit, mydata\$State,
 mean)
- > help(aggregate

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Import a new database

> mydata<-read.csv("fruits.csv")</pre>

Extract the information

> str(mydata)

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> aggregate (mydata\$Fruit, list(mydata\$State), mean)

> aggregate(mydata\$Fruit,

list(State=mydata\$State), mean)

> aggregate(x=mydata\$Fruit,
by=ligt(\$tato=mydata\$Stato)

by=list(State=mydata\$State), FUN=mean)

NOT

> aggregate(mydata\$Fruit, mydata\$State,
mean)

> help(aggregate

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► Import a new database

> mydata<-read.csv("fruits.csv")</pre>

Extract the information

> str(mydata)

> help(aggregate)

> aggregate (mydata\$Fruit, list(mydata\$State), mean)

> aggregate(mydata\$Fruit,

list(State=mydata\$State), mean)

> aggregate(x=mydata\$Fruit, by=list(State=mydata\$State), FUN=mean)

NOT

> aggregate(mydata\$Fruit, mydata\$State,
mean)

> help(aggregate)

Summary

Data

```
> n.fruit <- aggregate(mydata$Fruit,</p>
list(State=mydata$State), length)
> mean.fruit <- aggregate(mydata$Fruit,</pre>
list(State=mydata$State), mean)
> sd.fruit <- aggregate(mydata$Fruit,</pre>
list(State=mydata$State), sd)
```

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Tables

```
> n.fruit <- aggregate(mydata$Fruit,
list(State=mydata$State), length)
> mean.fruit <- aggregate(mydata$Fruit,
list(State=mydata$State), mean)
> sd.fruit <- aggregate(mydata$Fruit,
list(State=mydata$State), sd)</pre>
```

▶ Built the table

```
> summary.table <- cbind(n.fruit[,2],
mean.fruit[,2], sd.fruit[,2])
> summary.table
```

Add names

```
> dimnames(summary.table) <-
list(n.fruit[,1], c("n", "mean", "SD"))</pre>
```

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Data

```
> n.fruit <- aggregate(mydata$Fruit,</p>
list(State=mydata$State), length)
> mean.fruit <- aggregate(mydata$Fruit,</pre>
list(State=mydata$State), mean)
> sd.fruit <- aggregate(mydata$Fruit,</pre>
list(State=mydata$State), sd)
```

▶ Built the table

```
> summary.table <- cbind(n.fruit[,2],</pre>
mean.fruit[,2], sd.fruit[,2])
> summary.table
```

Add names

```
> dimnames(summary.table) <-</pre>
list(n.fruit[,1], c("n", "mean", "SD"))
```

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- Import a new database
 - > mydata<-read.csv("gain.csv")</pre>
- Extract the information
 - > str(mydata)
 - > aggregate(mydata\$growth,
 list(mydata\$experiment, mydata\$food)
 mean)
- Another table format
 - > mean.growth<-tapply(mydata\$growth,
 list(mydata\$experiment, mydata\$food),
 mean)</pre>

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- Import a new database
 - > mydata<-read.csv("gain.csv")</pre>
- Extract the information
 - > str(mydata)
 - > aggregate(mydata\$growth,
 list(mydata\$experiment,mydata\$food),
 mean)
- ► Another table format
 - > mean.growth<-tapply(mydata\$growth, list(mydata\$experiment,mydata\$food), mean)

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Conclusion

► Import a new database

> mydata<-read.csv("fruits.csv")

- Extract the information
- Data

```
> n.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), length)
> mean.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), mean)
> sd.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), sd)</pre>
```

- ► Barplot > barplot (mean.fruit)
- May be better
 - > help(barplot)

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Import a new database

> mydata<-read.csv("fruits.csv")

- ► Extract the information
- Data

```
> n.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), length)
> mean.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), mean)
> sd.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), sd)</pre>
```

- ► Barplot > barplot (mean.fruit)
- ► May be better
 - > help(barplot)

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► Import a new database

> mydata<-read.csv("fruits.csv")</pre>

- ► Extract the information
- Data

```
> n.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), length)
> mean.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), mean)
> sd.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), sd)</pre>
```

- ► Barplot > barplot (mean.fruit)
- May be better
 - > help(barplot)

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Conclusion

► Import a new database

> mydata<-read.csv("fruits.csv")

- Extract the information
- Data

```
> n.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), length)
> mean.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), mean)
> sd.fruit <- tapply(mydata$Fruit,
list(State=mydata$State), sd)</pre>
```

- ► Barplot > barplot (mean.fruit)
- May be better
 - > help(barplot)

► Add names on the axes

```
> barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
```

Add error bars

```
> mids<-barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
> arrows(mids,mean.fruit+sd.fruit
mids, mean.fruit - sd.fruit)
```

► Almost

> help(arrows)

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Add names on the axes

```
> barplot (mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
```

Add error bars

```
> mids<-barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
vlim=c(0,100)
> arrows(mids, mean.fruit+sd.fruit,
mids, mean.fruit - sd.fruit)
```

Add names on the axes

```
> barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
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Add error bars

```
> mids<-barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
> arrows(mids, mean.fruit+sd.fruit,
mids, mean.fruit - sd.fruit)
```

Almost

> help(arrows)

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```
> mids<-barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
> arrows(mids,mean.fruit+sd.fruit,
mids, mean.fruit - sd.fruit,
angle=90, code=3)
> text(mids,5, paste("N = ", n.fruit))
```

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```
> mids<-barplot(mean.fruit,
xlab="Treatement",
ylab="Fruit production",
ylim=c(0,100))
> arrows(mids, mean.fruit+sd.fruit,
mids, mean.fruit - sd.fruit,
angle=90, code=3)
> text(mids,5, paste("N = ", n.fruit))
```

More complex

- > myData<-read.csv("gain.csv")</pre>
- > mean.growth<-tapply(myData\$growth,
 list(myData\$experiment,myData\$food),
 mean)</pre>
- > sd.growth<-tapply(myData\$growth, list(myData\$experiment,myData\$food), sd)
- > n.growth<-tapply(myData\$growth,
 list(myData\$experiment,myData\$food),
 length)</pre>
- > barplot(mean.growth)
 Almost

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More complex

- > myData<-read.csv("gain.csv")</pre>
- > mean.growth<-tapply(myData\$growth, list(myData\$experiment,myData\$food), mean)
- > sd.growth<-tapply(myData\$growth, list(myData\$experiment,myData\$food), sd)
- > n.growth<-tapply(myData\$growth,
 list(myData\$experiment,myData\$food),
 length)</pre>
- > barplot(mean.growth)
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More complex

```
> myData<-read.csv("gain.csv")</pre>
 mean.growth<-tapply(myData$growth,
list (myData$experiment, myData$food),
mean)
  sd.growth<-tapply(myData$growth,
list (myData$experiment, myData$food),
sd)
```

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```
> myData<-read.csv("gain.csv")</pre>
> mean.growth<-tapply(myData$growth,</pre>
list (myData$experiment, myData$food),
mean)
> sd.growth<-tapply(myData$growth,
list (myData$experiment, myData$food),
sd)
> n.growth<-tapply(myData$growth,</p>
list (myData$experiment, myData$food),
length)
```

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```
> myData<-read.csv("gain.csv")</pre>
> mean.growth<-tapply(myData$growth,</pre>
list (myData$experiment, myData$food),
mean)
> sd.growth<-tapply(myData$growth,</p>
list (myData$experiment, myData$food),
sd)
> n.growth<-tapply(myData$growth,</p>
list (myData$experiment, myData$food),
length)
> barplot (mean.growth)
```

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More complex

```
> myData<-read.csv("gain.csv")</pre>
> mean.growth<-tapply(myData$growth,</pre>
list (myData$experiment, myData$food),
mean)
> sd.growth<-tapply(myData$growth,</p>
list (myData$experiment, myData$food),
sd)
> n.growth<-tapply(myData$growth,</p>
list (myData$experiment, myData$food),
length)
> barplot (mean.growth)
Almost
```

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Plus complexe

```
> mids<- barplot(mean.growth,beside=T,</pre>
xlab="Food type",
vlab="Gain",
vlim=c(0,35),
col=grey(c(0,0.3,0.6,1)))
```

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Plus complexe

```
> mids<- barplot(mean.growth,beside=T,</pre>
xlab="Food type",
vlab="Gain",
vlim=c(0,35),
col=grey(c(0,0.3,0.6,1)))
> arrows (mids, mean.growth+sd.growth,
mids, mean.growth-sd.growth,
angle=90, code=3, length=0.1)
```

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```
> mids<- barplot(mean.growth,beside=T,</pre>
xlab="Food type",
vlab="Gain",
vlim=c(0,35),
col=grey(c(0,0.3,0.6,1)))
> arrows (mids, mean.growth+sd.growth,
mids, mean.growth-sd.growth,
angle=90, code=3, length=0.1)
> text(mids, 2, paste(n.growth),
col=c("white", rep("black",3)))
```

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```
> mids<- barplot(mean.growth,beside=T,</pre>
xlab="Food type",
vlab="Gain",
vlim=c(0,35),
col=grey(c(0,0.3,0.6,1)))
> arrows (mids, mean.growth+sd.growth,
mids, mean.growth-sd.growth,
angle=90, code=3, length=0.1)
> text(mids, 2, paste(n.growth),
col=c("white", rep("black",3)))
> legend("topleft",
legend=rownames (mean.growth),
fill=grey(c(0,0.3,0.6,1)))
```

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Simple graph

```
> plot(mydata$Root, mydata$Fruit)
```

```
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production")
```

> plot(mydata\$Root, mydata\$Fruit
 xlab="Root size",
 ylab="Fruit production",
 pch=21,bg="grey",cex=2.0)

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Simple graph

```
> plot(mydata$Root, mydata$Fruit)
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production")
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg="grey",cex=2.0)
Intact versus eaten
```

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Simple graph

```
> plot(mydata$Root, mydata$Fruit)
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production")
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg="grey",cex=2.0)
Intact versus eaten
```

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Simple graph

```
> plot(mydata$Root, mydata$Fruit)
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production")
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg="grey",cex=2.0)
Intact versus eaten
```

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```
> clr<-ifelse(mydata$State == "Eaten",
"Green","Blue")</pre>
```

```
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg=clr,cex=2.0)
```

```
> legend("topleft",
    legend=c("Eaten", "Intact"), pch=21,
    pt.bg=c("Green", "Blue"), pt.cex=2.0
```

```
> clr<-ifelse(mydata$State == "Eaten",
"Green","Blue")
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg=clr,cex=2.0)
> legend("topleft",
    legend=c("Eaten", "Intact"), pch=21,
```

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```
> clr<-ifelse(mydata$State == "Eaten",
"Green","Blue")
> plot(mydata$Root, mydata$Fruit,
    xlab="Root size",
    ylab="Fruit production",
    pch=21,bg=clr,cex=2.0)
> legend("topleft",
    legend=c("Eaten", "Intact"), pch=21,
    pt.bg=c("Green", "Blue"), pt.cex=2.0)
```

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► Title of the graph

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Size of the points

Axes size

Axes legend size

Axes range

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Modifications possibles sur un graphique.

- ► Title of the graph
 - > plot(..., main="Title")
- Axes name

- > plot(..., xlab="nameX",ylab="nameY")
- Size of the point
 - > plot(..., cex=2.0)
- Axes size
 - > plot(..., cex.lab=2.0
- Axes legend size
 - > plot(..., cex.axis=2.0)
- Axes range
 - > plot(..., xlim=c(0,100),ylim=c(0,2))

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Modifications possibles sur un graphique.

► Title of the graph

> plot(..., main="Title")

Axes name

Simple graph

> plot(..., xlab="nameX",ylab="nameY")

► Size of the points

> plot(..., cex=2.0)

Axes size

> plot(..., cex.lab=2.0)

Axes legend size

> plot(..., cex.axis=2.0)

Axes range

> plot(..., xlim=c(0,100),ylim=c(0,2))

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Modifications possibles sur un graphique.

- ► Title of the graph
 - > plot(..., main="Title")
- Axes name

- > plot(..., xlab="nameX",ylab="nameY")
- ► Size of the points
 - > plot(..., cex=2.0)
- Axes size
 - > plot(..., cex.lab=2.0)
- Axes legend size
 - > plot(..., cex.axis=2.0)
- Axes range
 - > plot(..., xlim=c(0,100),ylim=c(0,2))

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Modifications possibles sur un graphique.

- ► Title of the graph
 - > plot(..., main="Title")
- Axes name

- > plot(..., xlab="nameX",ylab="nameY")
- ► Size of the points
 - > plot(..., cex=2.0)
- Axes size
 - > plot(..., cex.lab=2.0)
- ► Axes legend size
 - > plot(..., cex.axis=2.0)
- Axes range
 - > plot(..., xlim=c(0,100),ylim=c(0,2))

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Modifications possibles sur un graphique.

- ► Title of the graph
 - > plot(..., main="Title")
- Axes name

- > plot(..., xlab="nameX",ylab="nameY")
- ► Size of the points
 - > plot(..., cex=2.0)
- Axes size
 - > plot(..., cex.lab=2.0)
- Axes legend size
 - > plot(..., cex.axis=2.0)
- Axes range
 - > plot(..., xlim=c(0,100), ylim=c(0,2))

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Add points to a graph

One point

- > points(x=50,y=0)
- ► Type of point
 - > points(...,pch=2
- Color of point
 - > points(..., col=2)
- Size of poin
 - > points(..., cex=2.0
- Many points
 - > points (x=c(1,2,3),y=c(1,2,3))

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Add points to a graph

One point

- > points(x=50,y=0)
- ► Type of point
 - > points(...,pch=2)
- Color of point
 - > points(..., col=2
- ► Size of point
 - > points(..., cex=2.0
- Many points
 - > points (x=c(1,2,3),y=c(1,2,3))

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Add points to a graph

One point

- > points(x=50,y=0)
- ► Type of point
 - > points(...,pch=2)
- Color of point
 - > points(..., col=2)
- ► Size of poin
 - > points(..., cex=2.0)
- Many points
 - > points(x=c(1,2,3),y=c(1,2,3))

One variable nanipulations

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Add points to a graph

One point

- > points(x=50,y=0)
- ► Type of point
 - > points(...,pch=2)
- Color of point
 - > points(..., col=2)
- ► Size of point
 - > points(..., cex=2.0)
- Many points
 - > points (x=c(1,2,3),y=c(1,2,3))

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Add points to a graph

One point

- > points(x=50,y=0)
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Add line to a graph

- ightharpoonup One line between (x1,y1) and (x2,y2)
 - > lines(x=c(x1,x2),y=c(y1,y2))
- ► Line type
 - > lines(..., lty=2)
- ► Ligne color
 - > lines(..., col=2
- ► Ligne size
 - > lines(..., lwd=2.0)
- ► Many lines together
 - > lines(x=c(x1,x2,x3),y=c(y1,y2,y3))

Add line to a graph

- ightharpoonup One line between (x1,y1) and (x2,y2)
 - > lines(x=c(x1,x2),y=c(y1,y2))
- ► Line type
 - > lines(..., lty=2)
- Ligne color
 - > lines(..., col=2)
- ► Ligne size
 - > lines(..., lwd=2.0)
- Many lines together
 - > lines(x=c(x1,x2,x3),y=c(y1,y2,y3))

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 - > lines(x=c(x1,x2,x3),y=c(y1,y2,y3))

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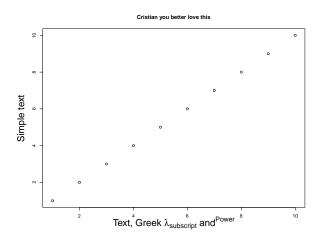
Add line to a graph

Simple graph

- \blacktriangleright One line between (x1,y1) and (x2,y2)
 - > lines(x=c(x1,x2),y=c(y1,y2))
- ► Line type
 - > lines(..., lty=2)
- ► Ligne color
 - > lines(..., col=2)
- ► Ligne size
 - > lines(..., lwd=2.0)
- Many lines together
 - > lines(x=c(x1,x2,x3),y=c(y1,y2,y3))

Two variables manipulations

Simple graph



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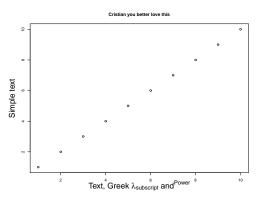
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```
> plot(1:10, xlab=expression(paste(
"Text, Greek ", lambda[subscript]," ",
and^ {Power})), ylab="Simple text",
main="Cristian you better love this")
```

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- ► Lazy : click file-> save as -> jpeg
- ► More efficien
 - > jpeg("fileName.jpg"
 - > plot(...
 - > dev.off()
- ► More option with command line
 - > help(jpeg)

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- ► Lazy : click file-> save as -> jpeg
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 - > plot(...)
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- ► Lazy : click file-> save as -> jpeg
- ► More efficient
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 - > plot(...)
 - > dev.off()
- ► More option with command line
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- Format
 - postscript
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 - jpeg
 - png
 - bmp
 - ► tiff
- Options
 - Size (width, height)
 - ► Compression (quality)
 - ▶ Pointsize (pointsize)

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Variables

> help(save)

> save(x,y,z,file="saveXYZ.RData"

> save.image(file="workspace.RData")

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Matrix operation

- > help(save)
- > save(x,y,z,file="saveXYZ.RData")

The whole workspace

> save.image(file="workspace.RData")

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Matrix operation

```
> help(save)
```

> save(x,y,z,file="saveXYZ.RData")

The whole workspace

> save.image(file="workspace.RData")

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Matrix operation

Get the infomation back

```
> load("saveXYZ.RData")
```

> load("workspace.RData")

What was loaded

> 1s()

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Get the infomation back

```
> load("saveXYZ.RData")
```

> load("workspace.RData")

What was loaded

> ls(

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Get the infomation back

```
> load("saveXYZ.RData")
```

> load("workspace.RData")

What was loaded

> ls()

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onclusion

► Haldane function of generation length?

- ► Syntax: x\$Haldanes ~x\$GLength
 - > lm(x\$Haldanes ~x\$GLength)
 or
 - > my.lm<-lm(x\$Haldanes ~x\$GLength)</pre>
- ▶ More information
 - > summary(lm(x\$Haldanes ~x\$GLength))
 or
 - > summary(my.lm)

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One variable manipulations

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- ► Haldane function of generation length?
- ► Syntax: x\$Haldanes ~x\$GLength
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- > my.lm<-lm(x\$Haldanes ~x\$GLength)
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 or
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Linear regression

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latrix operation

- Extract the information from the model
 - > attributes(my.lm)
- Residuals
 - > my.lm\$residuals
- Predicted value
 - > my.lm\$coefficients

Linear regression

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latrix operation

- Extract the information from the model
 - > attributes(my.lm)
- Residuals
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Linear regression

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- Extract the information from the model
 - > attributes(my.lm)
- Residuals
 - > my.lm\$residuals
- Predicted values
 - > my.lm\$coefficients

Linear Regression

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- Matrix operation
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- Extract more information from the model
 - > my.summ.lm<-summary(my.lm)</pre>
 - > attributes(my.summ.lm)
- R^2
 - > my.summ.lm\$r.squared
- ► F-statistics
 - > my.summ.lm\$fstatistic

Linear Regression

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- Extract more information from the model
 - > my.summ.lm<-summary(my.lm)</pre>
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- $ightharpoonup R^2$
 - > my.summ.lm\$r.squared
- ► F-statistics
 - > my.summ.lm\$fstatistic

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- $ightharpoonup R^2$
 - > my.summ.lm\$r.squared
- ► F-statistics
 - > my.summ.lm\$fstatistic

Linear models

How it looks like?

> plot(x\$Haldanes ~x\$GLength)

This is equivalent to

> plot(x\$GLength,x\$Haldanes)

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How it looks like?

```
> plot(x$Haldanes ~x$GLength)
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This is equivalent to

> plot(x\$GLength,x\$Haldanes)

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Linear models

► Absolute values of Haldanes function of generation

- length?
 > lm(x\$HaldanesAbs ~x\$GLength)
- ► More information
 - > summary(lm(x\$HaldanesAbs ~x\$GLength)

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► Absolute values of Haldanes function of generation length?

- > lm(x\$HaldanesAbs ~x\$GLength)
- ► More information:
 - > summary(lm(x\$HaldanesAbs ~x\$GLength))

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Data

► Two factor

> m1<- x\$HaldanesAbs ~x\$GLength+x\$Years

► Interaction term

> m2<- x\$HaldanesAbs ~x\$GLength:x\$Years

► Two factor + interaction term

> m3<- x\$HaldanesAbs ~x\$GLength*x\$Years equivalent to:

> m3<- x\$HaldanesAbs ~x\$GLength +
x\$Years + x\$GLength:x\$Years</pre>

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Two factor

> m1<- x\$HaldanesAbs ~x\$GLength+x\$Years

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equivalent to:</pre>

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x\$Years + x\$GLength:x\$Years</pre>

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▶ Two factor

> m1<- x\$HaldanesAbs ~x\$GLength+x\$Years</pre>

► Interaction term

> m2<- x\$HaldanesAbs ~x\$GLength:x\$Years

► Two factor + interaction term:

> m3<- x\$HaldanesAbs ~x\$GLength*x\$Years
equivalent to:</pre>

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x\$Years + x\$GLength:x\$Years</pre>

- ▶ Look at the file anova.txt in a text editor
- Read a table
 - > z<-read.table("anova.txt")</pre>
- ► Give names to the column
 - > names(z) <- c("response", "category", "replicat", "coVar")
- ► Shortcut to column name
 - > attach(z)
 - > response
 - > detach(z)
 - > response
 - > attach(z)

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http://www.agr.kuleuven.ac.be/vakken/statisticsbyR/ANOVAbyRr/ANCOVAinR.htm

- ► Look at the file anova.txt in a text editor
- Read a table
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ANOVA

ANOVA

Setup

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ANOVA

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Nominal term

- ► Everything is considered numeric as default
- ▶ Define the categorie RDexp: nomina
 - > category<-factor(category</pre>

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Nominal term

- Everything is considered numeric as default
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First steps

- ▶ Write the model
 - > mod1<-response ~category</pre>
- Take a look at the model
 - > boxplot (mod1)
- Linear model of the data
 - > mod1.lm < -lm (mod1)
- ► Vizualize the mode
 - > plot (mod1.lm)
- ▶ Get the information out of the model
 - > summary(mod1.lm
- ▶ Perform the ANOVA
 - > anova(mod1.lm)

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First steps

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- ▶ Perform the ANOVA
 - > anova(mod1.lm

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- ► Get the information out of the model
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 - > anova(mod1.lm

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 - > mod1.lm < -lm (mod1)
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 - > plot (mod1.lm)
- Get the information out of the model
 - > summary (mod1.lm)
- ► Perform the ANOVA
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First steps

- Write the model
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- Take a look at the model
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 - > plot (mod1.lm)
- ▶ Get the information out of the model
 - > summary (mod1.lm)
- ► Perform the ANOVA
 - > anova(mod1.lm)

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Models

- ► Sanity check:
 - > is.factor(category)
- Look at the data
 - > plot(response
 - ~coVar,pch=as.numeric(category)
- ► Everything in common:
 - > ResE<-response ~coVar
- Common slope, different intercept:
 - > ResCD<-response ~category+ coVar
- Full model:
 - > ResFull<-response ~category+ coVar +
 category:coVar</pre>

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Matrix operation

- ► Sanity check:
 - > is.factor(category)
- ► Look at the data:
 - > plot(response
 - ~coVar,pch=as.numeric(category))
- Everything in common:
 - > ResE<-response ~coVar
- Common slope, different intercept:
 - > ResCD<-response ~category+ coVar
- ► Full model
 - > ResFull<-response ~category+ coVar +
 category:coVar</pre>

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 - > is.factor(category)
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Models

► Linear model

- > ResE.lm<-lm(ResE)</pre>
- > ResCD.lm<-lm(ResCD)</pre>
- > ResFull.lm<-lm(ResFull)</pre>
- ► Look at the models
 - > plot (ResE.lm)
 - > plot(ResCD.lm)
 - > plot(ResFull.lm

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Models

► Linear model

- > ResE.lm<-lm(ResE)</pre>
- > ResCD.lm<-lm(ResCD)</pre>
- > ResFull.lm<-lm(ResFull)</pre>

► Look at the models

- > plot (ResE.lm)
- > plot(ResCD.lm)
- > plot(ResFull.lm)

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Analysis

Get the infomation from the models:

- summary(ResE.lm)
- summary(ResCD.lm)
- summary(ResFull.lm)

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Get the infomation from the models:

- > summary(ResE.lm)
- > summary(ResCD.lm)
- > summary(ResFull.lm)

ANCOVA

- > anova(ResE.lm, ResFull.lm)
- > anova(ResE.lm, ResCD.lm, ResFull.lm)

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Matrix aparation

Useful command

Verify the hypothesis of equal variance within group

- > tapply(response, category, var, na.rm=TRUE)
- ▶ Verify the hypothesis of normality in a group
 - > tapply(response, category, function(x) shapiro.test(x))

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Matrix operation

Loops:

while

- Conditions if
- ► No help

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Loops: for while

- Conditions:
- ▶ No help

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Loops: for while

- Conditions:
- ► No help!

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Loops

```
> for (dummyVariable in array) {
>    operation
> }
or
> while (condition) {
>    operation
>    change the condition
>  }
```

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```
Loop example
```

Fibonacci

```
> x < - array(1, dim=10)
> for (i in seq(3,length(x))) {
     x[i] < -x[i-1] + x[i-2]
>
> }
or
> x <- array(1, dim=10)
> i < -3
> while (i <= length(x)) {
     x[i] < -x[i-1] + x[i-2]
> i<-i+1
```

Condition

```
> if (condition) {
>    operation 1
> } else {
>    operation 2
> }
```

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List of conditions

> Greater

>= Greater or equal

< Smaller

<= Smaller or equal

== Equal

! = Not equal

& And

Or

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Condition example

```
> if (x>0) {
>    x<-x+1
> } else {
>    x<-x-1
> }
```

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- ▶ Logistic equation: $x_{t+1} = r \times x_t(1 x_t)$)
- Run simulation of 1000 generations
- ► Set your initial population size
- ► Try different r values between 3 and 4
- ▶ Plot the time serie

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- ▶ Logistic equation: $x_{t+1} = r \times x_t(1 x_t)$)
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- Logistic equation: $x_{t+1} = r \times x_t(1 x_t)$
- ► Run simulation of 1000 generations
- ► Set your initial population size
- ► Try different r values between 3 and 4
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Logistic equation: $x_{t+1} = r \times x_t(1 - x_t)$

- ► Run simulation of 1000 generations
- ► Set your initial population size
- ► Try different r values between 3 and 4
- ▶ Plot the time serie

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Chaos solution

```
> x<-array(dim=1000)
> x[1]=0.5
> r<-3.7
> for (t in 2:length(x)){
> x[t]<-r*x[t-1]*(1-x[t-1])
> }
```

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Chaos solution

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> x[1]=0.5
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> for (t in 2:length(x)){
> x[t]<-r*x[t-1]*(1-x[t-1]);
> }
```

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Chaos solution

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> x[1]=0.5
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> for (t in 2:length(x)){
> x[t]<-r*x[t-1]*(1-x[t-1])
> }
```

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Your first function

You want to be able to change you parameter faster: write a function

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Before

```
> x<-array(dim=1000)
> x[1]=0.5
> r<-3.7
> for (t in 2:length(x)){
> x[t]<-r*x[t-1]*(1-x[t-1])
> }
```

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Callign your function

- > chaos (1000, 3.5, 0.5)
- > c<-chaos (1000, 3.5, 0.5)
- > plot(c)
- > plot (chaos (1000, 3.5, 0.5))

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General

All procedure that you will repeat more than once: do a function of it

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Create a vector

- > V1 <- as.vector(seq(1,10))
- > V2 <- as.vector(rnorm(10))</pre>

Matrix operation

Matrix operation

- Create a vector
 - > V1 <- as.vector(seq(1,10))
 - > V2 <- as.vector(rnorm(10))</pre>
- Scalar product
 - > V3<- V1 * V2

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Matrix operation

- Create a vector
 - > V1 <- as.vector(seq(1,10))</pre>
 - > V2 <- as.vector(rnorm(10))</pre>
- Scalar product
 - > V3<- V1 * V2
- ► Vectorial product ((1 x n) * (n x 1))
 - > s1<- t(V1) %*% V2
- External vectoriel product ((n x 1) * (1 x n))
 - > M1<- V1 %*% t(V2)

Matrix operation

- Create a vector
 - > V1 <- as.vector(seq(1,10))
- > V2 <- as.vector(rnorm(10))</pre>
- Scalar product
 - > V3<- V1 * V2
- ► Vectorial product ((1 x n) * (n x 1))
- > s1<- t(V1) %*% V2
- External vectoriel product ((n x 1) * (1 x n))
 - > M1<- V1 %*% t(V2)

One variable manipulation

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Matrix operation

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Building a matrix from vectors
 Line by line M1<-rbind (V1, V2)
 Column by column M2<-cbind (V1, V2)

▶ Building matrix element by element (column major)

matrix(c(1,2,3,4,5,6),ncol=3,nrow=2)

$$\left(\begin{array}{rrr}1&3&5\\2&4&6\end{array}\right)$$

> M4 <-

matrix(c(1,2,3,4,5,6),ncol=2,nrow=3)

$$\left(\begin{array}{cc}
1 & 4 \\
2 & 5 \\
3 & 6
\end{array}\right)$$

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Matrix operation

-Complication

▶ Building a matrix from vectors Line by line M1<-rbind (V1, V2) Column by column M2<-cbind (V1, V2)</p>

▶ Building matrix element by element (column major)

(135)

$$\left(\begin{array}{rrr}1 & 3 & 5\\2 & 4 & 6\end{array}\right)$$

matrix(c(1,2,3,4,5,6),ncol=2,nrow=3)

$$\left(\begin{array}{cc}
1 & 4 \\
2 & 5 \\
3 & 6
\end{array}\right)$$

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Matrix operation

Conclusion

Multiply matrix by a vector

$$\left(\begin{array}{rrr}1 & 3 & 5\\2 & 4 & 6\end{array}\right)\left(\begin{array}{r}7\\8\\9\end{array}\right)$$

> M1 <- matrix(c(1,2,3,4,5,6), ncol=3, nrow=2)

> V1 <- as.vector(c(7,8,9))

> M1 %*% V1

NOT: > V1 %*% M1

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Multiply matrix by matrix

$$\left(\begin{array}{rrr} 1 & 3 & 5 \\ 2 & 4 & 6 \end{array}\right) \left(\begin{array}{rrr} 7 & 10 \\ 8 & 11 \\ 9 & 12 \end{array}\right)$$

> M1 <- matrix(c(1,2,3,4,5,6), ncol=3, nrow=2) > M2 <- matrix(c(7,8,9,10,11,12), ncol=2, nrow=3) > M1 %*% M2 and not the opposite: > M2 %*% M1 Proportion of population at equilibrium (Leslie matrix)

$$T = \left(\begin{array}{ccc} 0 & 0.63 & 0.702 \\ 0.7 & 0 & 0 \\ 0 & 0.2 & 0 \end{array}\right) P = \left(\begin{array}{c} 1 \\ 0 \\ 0 \end{array}\right)$$

$$P_1 = TP$$

$$P_2 = TP_1$$

$$P_3 = TP_2$$

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► Eigenvalue and eigenvector

$$\left(\begin{array}{ccc}
0 & 0.63 & 0.702 \\
0.7 & 0 & 0 \\
0 & 0.2 & 0
\end{array}\right)$$

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Inverse, eigenvalue and diagonal

$$\left(\begin{array}{ccc}
0 & 0.63 & 0.702 \\
0.7 & 0 & 0 \\
0 & 0.2 & 0
\end{array}\right)$$

> diag(M1)

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Conclusion

► RTFM

help(functionName) and
help.search("what your looking for")

- Text editors are your best compagnions
 - Verify the format of your data csv and others
 - ► To write down the command BEFORE you put them in the R console
- ➤ You will NEVER screw up your data in R if you load them from a file

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Acknowledgement

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► Thanks you!