R

Insight 2018

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Introduction

What you won't learn today

- Statistics
- Experimental design

What you will learn today

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

Introduction

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

What R is going to do for you

- Perform statistical test
- Plot figures

Introduction

Installing R

- 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/IRkernel')`
  - `> q()`

This page can take up to 30 minutes of computation

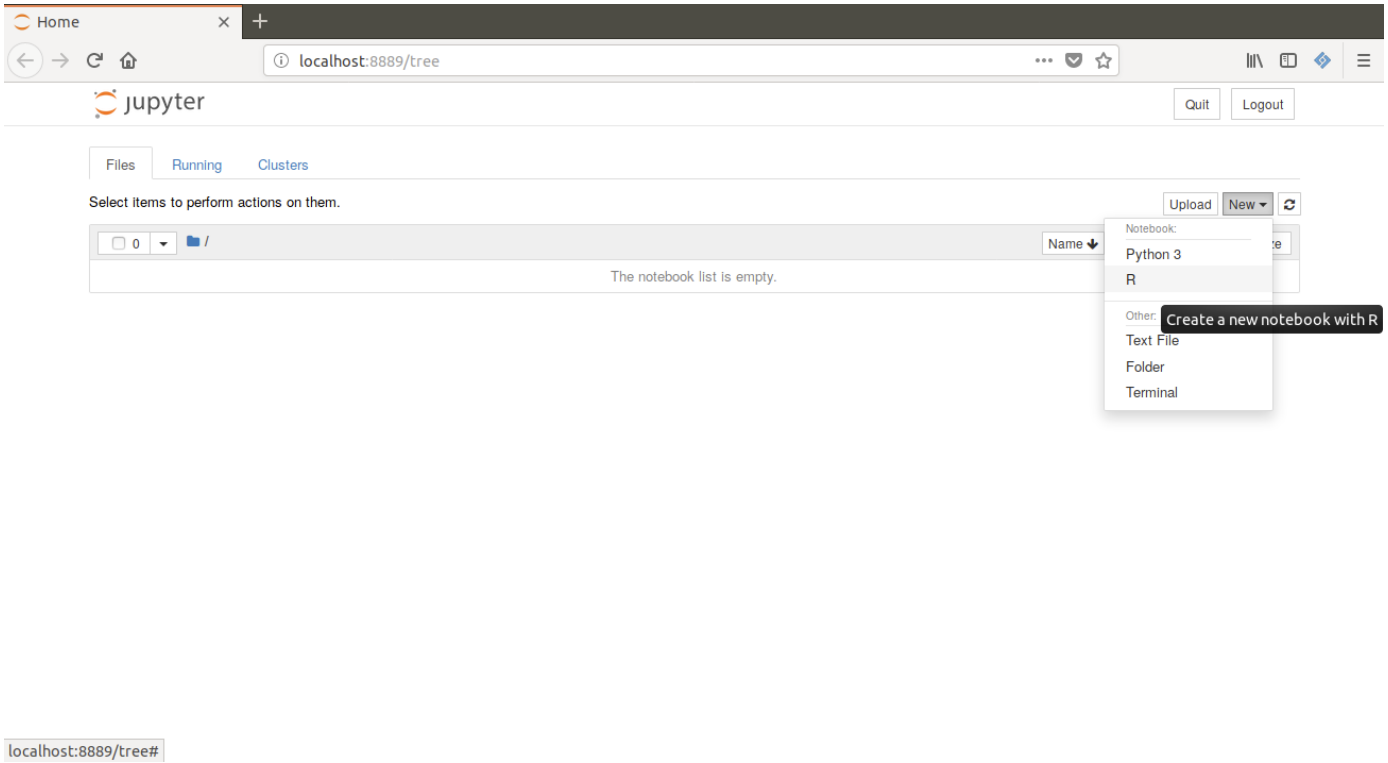
Introduction

Installing R

- Start R without the sudo from a terminal, then inside R
  - `> IRkernel::installspec()`
  - `> q()`
- You can now start you jupyter notebook (in a virtual environment if you like)

Introduction

Installing R



Introduction

Quit

```
> q()
```

or

```
> quit()
```

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

Introduction

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

Variables

- One value

  ```
  > a <- 1
  ```

  equivalent to a=1

  ```
  > 1 -> a
  ```

- A vector

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

Variables

Empty

- Vector

```
> a <- array(NA,dim=10)
> a[4] <- 5
```

- Matrix

```
> b <- matrix(NA,ncol=10,nrow=30)
> b[30,3]<-1
```

Variables

Help

RTFM

```
> help(array)
> help(matrix)
```

Variables

Generating vector and matrix

- Sequence vector

```
> a<-array(seq(1,10,2))
```

- Random vector

```
> a<-array(rnorm(10,mean=15,sd=3))
```

- Sequence matrix

```
> b<-matrix(seq(1,20),ncol=2,nrow=10)
```

- Random matrix

```
> b<-matrix(runif(21),ncol=3,nrow=7)
```

Variables

Simple arithmetic operations

```
> a+a
> a+5
> 1+b
> 5*a
> a*a
```

```
> a*b
> b*b
> a-a
> a-5
> a/2
```

Variables

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]

Data

Read the data

Go to my github

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

Data

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)

Data

Entering your data

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

Data

Load the data

- Open R

```
> x<-read.csv("hendryEtAl.csv")
```

- We can now play with the database with the variable x

Data

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]

Data

Sanity check

- Number of line in the data before and after loading

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

- Number of column:

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

Data

Column name

- Syntax: <variableName>$<columnName>

  ```
  > x$Years
  ```

  instead of

  ```
  > x[,18]
  ```

- Note that it is case sensitive:

  ```
  > x$years
  ```

  will not work

Data

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")`
- Test length and names of columns

One variable manipulations

Simple plot

- Reload the database

```
> x<-read.csv("hendryEtAl.csv")
```

- 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))
```

One variable manipulations

Simple plot

- Change the color of the bars

  ```
  > hist(...,col=2)
  ```

- Change the color of the borders

  ```
  > hist(...,border=3)
  ```

One variable manipulations

Test of normality

- 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

Tables

- 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)
```

Tables

Summary

- Data

```
> 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)
```

- 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"))
```

Tables

More complex

- Import a new database

```
> mydata<-read.csv("gain.csv")
```

- 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)
```

Barplot

- 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)
```

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

```
> help(barplot)
```

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)
```

Barplot

```
> 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))
```

Barplot

More complex

```
> myData<-read.csv("gain.csv")
> 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)
> barplot(mean.growth)
```

Almost

Barplot

Plus complexe

```
> mids<- barplot(mean.growth,beside=T,
xlab="Food type",
ylab="Gain",
ylim=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)))
```

Two variables manipulations

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

Two variables manipulations

Simple graph

```
> 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)
```

Two variables manipulations

Simple graph

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))
```

Two variables manipulations

Simple graph

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))
```

Two variables manipulations

Simple graph

Add line to a graph

- 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

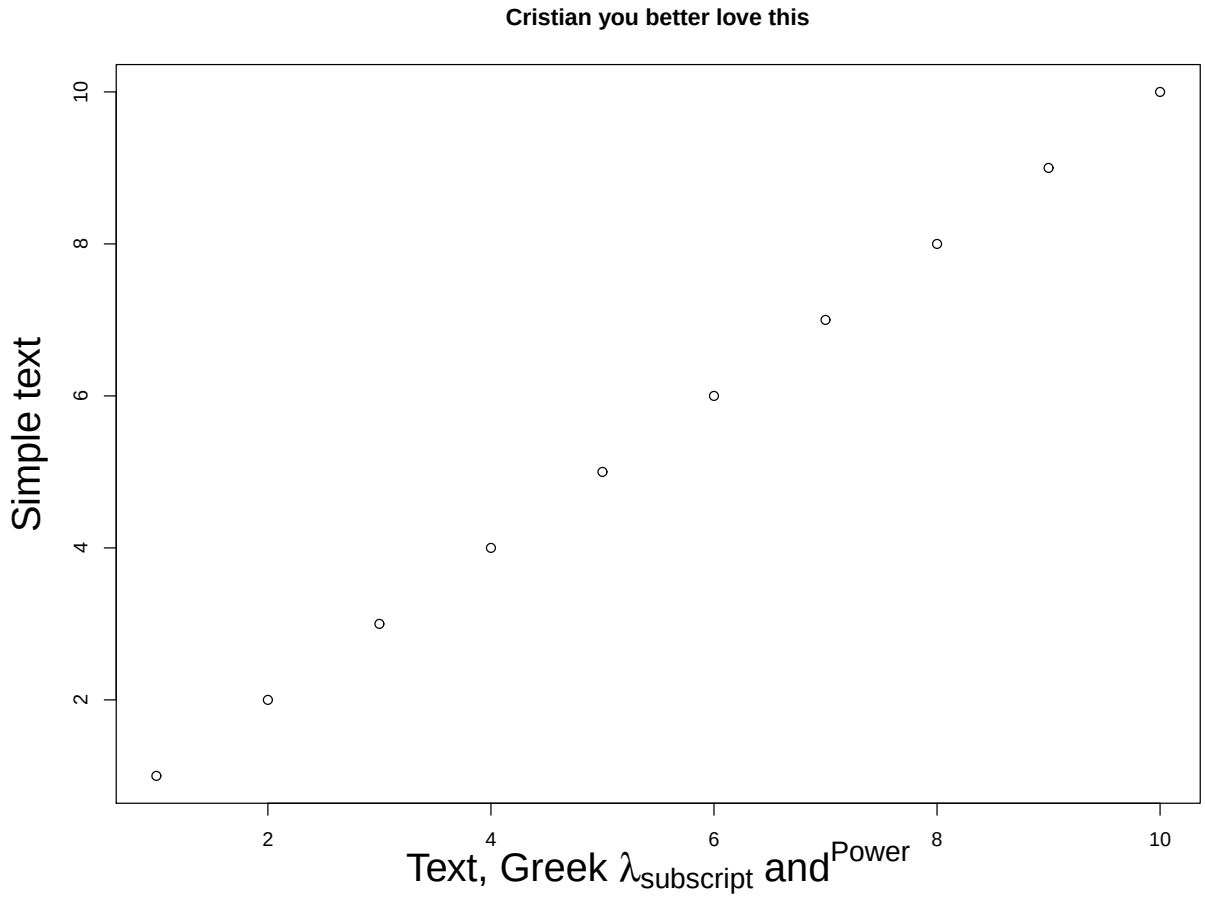
```
> lines(..., lwd=2.0)
```

- Many lines together

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

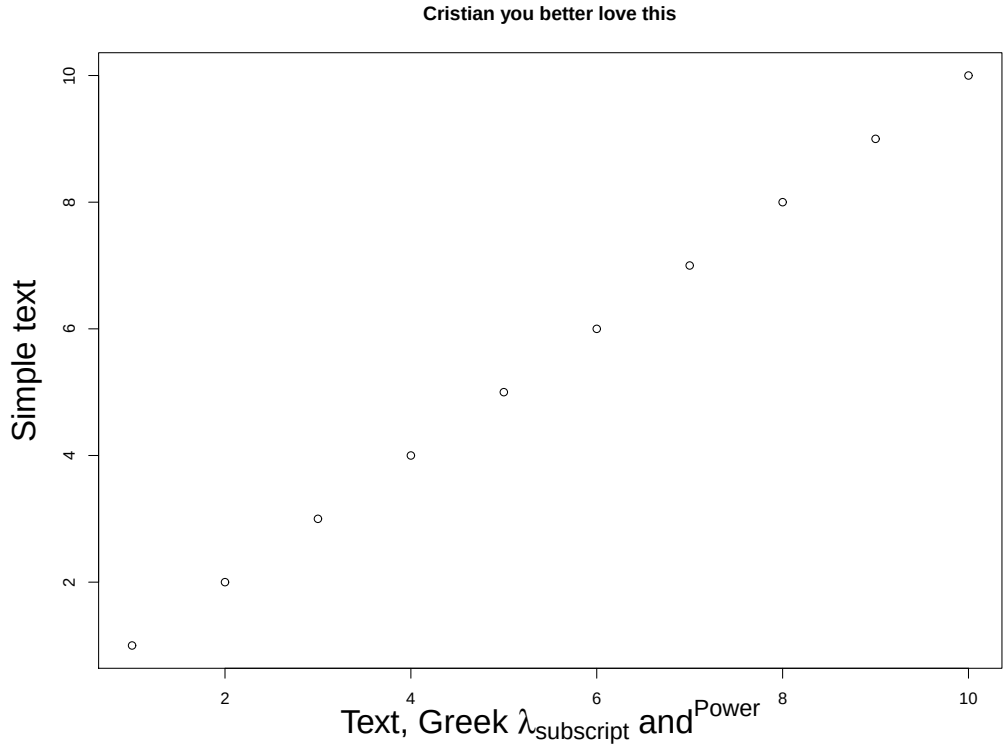
Two variables manipulations

Simple graph



Two variables manipulations

Simple graph




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

Save information

Figures

- Lazy : click file-> save as -> jpeg
- More efficient

```
> jpeg("fileName.jpg")
> plot(...)
> dev.off()
```

- More option with command line

```
> help(jpeg)
```

Save information

Figures

- Format
  - postscript
  - pdf
  - jpeg
  - png
  - bmp
  - tiff
- Options
  - Size (`width, height`)
  - Compression (`quality`)
  - Pointsize (`pointsize`)

Save information

Variables

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

The whole workspace

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

Save information

Get the infomation back

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

What was loaded

```
> ls()
```

Linear models

- Haldane function of generation length?
- Syntax: `x$Haldanes ~x$GLength`

  ```
  > lm(x$Haldanes ~x$GLength)
  ```

  or

  ```
  > my.lm<-lm(x$Haldanes ~x$GLength)
  ```

- More information:

  ```
  > summary(lm(x$Haldanes ~x$GLength))
  ```

  or

  ```
  > summary(my.lm)
  ```

Linear regression

- Extract the information from the model

  ```
  > attributes(my.lm)
  ```

- Residuals

  ```
  > my.lm$residuals
  ```

- Predicted values

  ```
  > my.lm$coefficients
  ```

Linear Regression

- Extract more information from the model

```
> my.summ.lm<-summary(my.lm)
> attributes(my.summ.lm)
```

- 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)
```

Linear models

- Absolute values of Haldanes function of generation length?

```
> lm(x$HaldanesAbs ~x$GLength)
```

- More information:

```
> summary(lm(x$HaldanesAbs ~x$GLength))
```

Linear models

More factor

- 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
```

ANOVA

Setup

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

```
> z<-read.table("anova.txt")
```

- Give names to the column

```
> names(z) <- c("response", "category",
"replicat", "coVar")
```

- Shortcut to column name

```
> attach(z)
> response
> detach(z)
> response
> attach(z)
```

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

ANOVA

Nominal term

- Everything is considered numeric as default
- Define the categorie RDexp: nominal

```
> category<-factor(category)
```

ANOVA

First steps

- Write the model

  ```
  > mod1<-response ~category
  ```

- Take a look at the model

  ```
  > boxplot(mod1)
  ```

- Linear model of the data

  ```
  > mod1.lm<-lm(mod1)
  ```

- Vizualize the model

  ```
  > plot(mod1.lm)
  ```

- Get the information out of the model

  ```
  > summary(mod1.lm)
  ```

- Perform the ANOVA

  ```
  > anova(mod1.lm)
  ```

ANCOVA

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
```

ANCOVA

Models

- Linear model

```
> ResE.lm<-lm(ResE)
> ResCD.lm<-lm(ResCD)
> ResFull.lm<-lm(ResFull)
```

- Look at the models

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

ANCOVA

Analysis

- Get the infomarion 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)
```

ANCOVA

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))
```

Simple Programming

- Loops:
  for
  while
- Conditions:
  if
- No help!

Simple Programming

Loops

```
> for (dummyVariable in array){
>     operation
> }
```

or

```
> while (condition){
>     operation
>     change the condition
> }
```

Simple Programming

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
> }
```

Simple Programming

Condition

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

Simple Programming

List of conditions

>	Greater
>=	Greater or equal
<	Smaller
<=	Smaller or equal
==	Equal
!=	Not equal
&	And
|	Or

Simple Programming

Condition example

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

Simple Programming

Your first program: chaos

- 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

Simple Programming

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])
> }
```

Functions

Your first function

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

Functions

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])
> }
```

Functions

After

```
> chaos <- function(time,r,popS){
>     x<-array(dim=time)
>     x[1]=popS
>     for (t in 2:length(x)){
>         x[t]<-r*x[t-1]*(1-x[t-1])
>     }
>     return(x)
> }
```

Functions

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))
```

Functions

General

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

Matrix operation

- Create a vector

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

- 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

- 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)

```
> M3 <-
matrix(c(1,2,3,4,5,6),ncol=3,nrow=2)
```

$$\begin{pmatrix} 1 & 3 & 5 \\ 2 & 4 & 6 \end{pmatrix}$$

```
> M4 <-
matrix(c(1,2,3,4,5,6),ncol=2,nrow=3)
```

$$\begin{pmatrix} 1 & 4 \\ 2 & 5 \\ 3 & 6 \end{pmatrix}$$

Matrix operation

- Multiply matrix by a vector

$$\begin{pmatrix} 1 & 3 & 5 \\ 2 & 4 & 6 \end{pmatrix} \begin{pmatrix} 7 \\ 8 \\ 9 \end{pmatrix}$$

- ```
  > 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`
  ```

Matrix operation

- Multiply matrix by matrix

$$\begin{pmatrix} 1 & 3 & 5 \\ 2 & 4 & 6 \end{pmatrix} \begin{pmatrix} 7 & 10 \\ 8 & 11 \\ 9 & 12 \end{pmatrix}$$

- `> 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`

Matrix operation

Exercise

- Proportion of population at equilibrium (Leslie matrix)

$$T = \begin{pmatrix} 0 & 0.63 & 0.702 \\ 0.7 & 0 & 0 \\ 0 & 0.2 & 0 \end{pmatrix} P = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}$$

- $$P_1 = TP$$

$$P_2 = TP_1$$

$$P_3 = TP_2$$

Matrix operation

- Eigenvalue and eigenvector

$$\begin{pmatrix} 0 & 0.63 & 0.702 \\ 0.7 & 0 & 0 \\ 0 & 0.2 & 0 \end{pmatrix}$$

- ```
  > M1 <-
  matrix(c(0,0.7,0,0.63,0,0.2,0.702,0,0),
  ncol=3, nrow=3)
  > eigen(M1)
  ```
  ```

Matrix operation

- Inverse, eigenvalue and diagonal

$$\begin{pmatrix} 0 & 0.63 & 0.702 \\ 0.7 & 0 & 0 \\ 0 & 0.2 & 0 \end{pmatrix}$$

- ```
  > M1 <-
  matrix(c(0,0.7,0,0.63,0,0.2,0.702,0,0),
  ncol=3, nrow=3)
  > solve(M1)
  > M1 %*% solve(M1)
  > det(M1)
  > diag(M1)
  ```
  ```

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

Acknowledgement

- Thanks you!