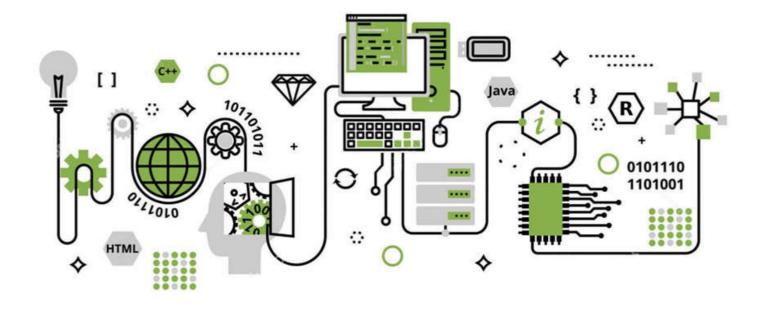
NBIS SciLifeLab



Introduction To R

Introduction to Bioinformatics

Roy Francis | 19-Sep-2018

Contents NBIS SciLifeLab

- Getting Started
- Variables & Operators
- Data Types
- Datatype Conversion
- Functions
- Control Structures
- R Packages
- Base Graphics
- Grid Graphics
- Input/Output
- Help & Learning R

Topics

NBIS SciLifeLab

- Familiarise with R & RStudio environment
- Running code, scripting, sourcing script
- Variables and operators
- Data types & datatype conversion
- Creating and running functions
- Base and grid graphics
- Input & output from R

NBIS SciLifeLab

What? Why R?

- R is a language and environment for statistical computing and graphics.
- Command line interface

Pros

- Data analysis
- Statistics
- High quality graphics
- Huge number of packages
- R is popular
- Reproducible research
- RStudio IDE
- FREE! Open source

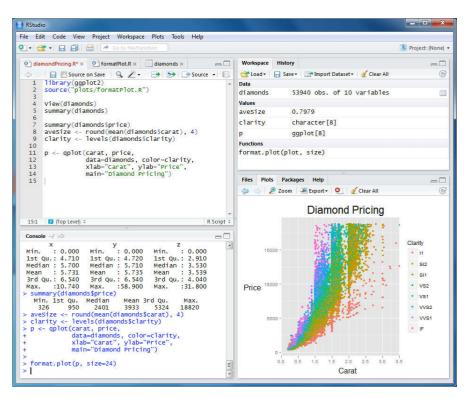
Cons

- Steep learning curve
- Not elegant/consistent
- Slow



Getting Started | Installation

- Install R from r-project.org.
- Install Rtools from https://cran.r-project.org/bin/
- Install RStudio IDE
- Code editor, highlighting, navigation, projects, version control, package building, debugger, profiler



Getting Started | Interaction

NBIS SciLifeLab

- Execute commands directly in Console
- Ready console shows
- Console shows + when waiting for information
- Press Esc to escape from + to >
- Save commands by writing scripts
- Run lines using Ctrl + Enter
- Run entire script using Ctrl + Shift + Enter

NBIS SciLifeLab

Variables & Operators

Assign variables using <- or =

```
x <- 4
x = 4
x
```

Arithmetic operators

```
x <- 4; y <- 2;

x + y # add
x - y # subtract
x * y # multiply
x / y # divide
x %% y # modulus
x ^ y # power</pre>
```

```
## [1] 6
## [1] 2
## [1] 8
## [1] 0
## [1] 16
```

Logical operators return TRUE or FALSE

```
x == y # equal to?
x != y # not equal to?
x > y # greater than?
x < y # less than?
x >= y # greater than or equal to?
x <= y # less than or equal to?</pre>
```

```
## [1] FALSE
## [1] TRUE
## [1] FALSE
```

```
T | F # OR
T & F # AND
```

```
## [1] TRUE
## [1] FALSE
```

• any(), all for logical vectors

Variables & Operators

NBIS SciLifeLab

• The function paste() concatenates strings

```
z <- "Look!"
z1 <- "Cat"
paste(z,z1)

## [1] "Look! Cat"</pre>
```

- Avoid conflicting variable names like c, t etc
- Variable names cannot start with a number
- print() function
- newline character

```
dimension homogenous heterogenous
## 1 1D Atomic vector List
## 2 2D Matrix Dataframe
## 3 nD Array
 • Use typeof() to find type of a variable
x \leftarrow 4; typeof(x)
## [1] "double"
y <- "this"; typeof(y)</pre>
## [1] "character"
mode(x); class(x)
str(x); structure(x)
## [1] "numeric"
## [1] "numeric"
## num 4
## [1] 4
```

• Explicit handling of missing data as NA and undefined data as NULL (NA vs NULL)

Data Type | Basic

Mode

```
mode(1.0)
mode(1L)
mode("hello")
mode(factor(1))
mode(T)

## [1] "numeric"
## [1] "character"
## [1] "numeric"
## [1] "logical"
```

Type

```
typeof(1.0)
typeof(1L)
typeof("hello")
typeof(factor(1))
typeof(T)
```

```
## [1] "double"

## [1] "integer"

## [1] "character"

## [1] "integer"

## [1] "logical"
```

Data Type | Vector | Create

- Vector stores multiple values
- Concatenate variables, values and vectors using the function c()

```
x <- c(2,3,4,5,6)
y <- c("a","c","d","e")
x
y
```

```
## [1] 2 3 4 5 6
## [1] "a" "c" "d" "e"
```

Few different ways to create vectors.

```
c(2,3,5,6)
2:8
seq(2,5,by=0.5)
rep(1:3,times=2)
```

```
## [1] 2 3 5 6
## [1] 2 3 4 5 6 7 8
## [1] 2.0 2.5 3.0 3.5 4.0 4.5 5.0
## [1] 1 2 3 1 2 3
```

NBIS SciLifeLab

Data Type | Vector | Access

• Access vectors using the [] operator.

```
x[1]; y[3]

## [1] 2
## [1] "d"
```

• Function c() to specify multiple positions.

```
x[c(1,3)]
## [1] 2 4
```

Vectorised operation

```
x <- c(2,3,4,5); y <- c(9,8,7,6)
x+y
z <- c("a","an","a","a"); k <- c("boy","apple","girl","mess")
paste(z,k)</pre>
```

```
## [1] 11 11 11 11
## [1] "a boy" "an apple" "a girl" "a mess"
```

Data Type | Vector

Verify data type

```
x \leftarrow c(2,3,4,5)
z <- c("a", "an", "a", "a")
mode(x)
mode(z)
str(x)
str(z)
## [1] "numeric"
## [1] "character"
## num [1:4] 2 3 4 5
## chr [1:4] "a" "an" "a" "a"
is.atomic(x)
is.numeric(x)
is.character(z)
## [1] TRUE
## [1] TRUE
## [1] TRUE
```

Data Type | Factor

Factors store categorical data

```
x <- factor(c("a","b","c","c"))
class(x)
str(x)</pre>
```

```
## [1] "factor"
## Factor w/ 3 levels "a","b","c": 1 2 2 3 3
```

• Factor x has 3 categories (3 levels)

```
levels(x)
```

```
## [1] "a" "b" "c"
```

• Verify if an R object is a factor

```
is.factor(x)
```

```
## [1] TRUE
```

Data Type | Matrix | Create

• Create a matrix from vector

```
x <- matrix(c(2,3,4,5,6,7))
x</pre>
```

```
## [,1]
## [1,] 2
## [2,] 3
## [3,] 4
## [4,] 5
## [5,] 6
## [6,] 7
```

Matrix has rows and columns

```
dim(x) # dimensions
nrow(x) # number of rows
ncol(x) # number of columns
```

```
## [1] 6 1
## [1] 6
## [1] 1
```

Specify rows and columns

```
## [,1] [,2]
## [1,] 2 3
## [2,] 4 5
## [3,] 6 7
```

str(x)

```
## num [1:3, 1:2] 2 4 6 3 5 7
```

• Verify if an R object is a matrix

```
is.matrix(x)
```

Data Type | Matrix | Access

• Access matrix using [] operator as [row, col]

```
x[2,2]
## [1] 5
```

• Get whole row/col using [row,] or [,col]

```
x[1,]
x[,2]
## [1] 2 3
## [1] 3 5 7
```

• Use drop=FALSE to retain a matrix as [row,col,drop=FALSE]

```
x[1,,drop=F]
x[,2,drop=F]
```

```
## [,1] [,2]

## [1,] 2 3

## [,1]

## [1,] 3

## [2,] 5

## [3,] 7
```

NBIS SciLifeLab

Data Type | Matrix | Label

• Add row/column names

Access using labels

```
x["b",]
x[,"p"]
```

```
## k p
## 4 5
## a b c
## 3 5 7
```

Data Type | List

• Create using list()

```
## [[1]]
## [1] 2 3 4 5
##
## [[2]]
## [1] "a" "b" "c" "d"
##
## [[3]]
## [1] a a b
## Levels: a b
##
## [[4]]
## [,1] [,2]
## [1,] 3 5
## [2,] 2 6
## [3,] 3 7
```

```
typeof(x); class(x);
```

```
## [1] "list"
## [1] "list"
```

Access lists using [] and [[]]

```
x[1]
```

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

• Lists are recursive

```
x <- list(list(list())))
str(x)</pre>
```

```
## List of 1
## $:List of 1
## ..$:List of 1
## ...$: List()
```

Data Type | data.frame | Create

```
dfr \leftarrow data.frame(x = 1:3, y = c("a", "b", "c"))
dfr
## X Y
## 1 1 a
## 2 2 b
## 3 3 c
str(dfr)
## 'data.frame': 3 obs. of 2 variables:
## $ x: int 1 2 3
## $ v: Factor w/ 3 Levels "a", "b", "c": 1 2 3
 • Use <a href="stringsAsFactors=FALSE">stringsAsFactors=FALSE</a> to avoid auto factor conversion
```

```
dfr <- data.frame(x = 1:3, y = c("a", "b", "c"), stringsAsFactors = F)</pre>
str(dfr)
is.data.frame(dfr)
```

```
## 'data.frame': 3 obs. of 2 variables:
## $ x: int 1 2 3
## $ y: chr "a" "b" "c"
## [1] TRUE
```

Data Type | data.frame | Access

NBIS SciLifeLab

• Access using [] or \$ operator

```
dfr$x
dfr$y

## [1] 1 2 3
## [1] "a" "b" "c"
```

- head() / tail() functions show first/last six lines
- Subset a data.frame using subset()

```
subset(dfr,dfr$y=="a")
```

```
## x y
## 1 1 a
```

```
x <- c(1,2,3); str(x)

## num [1:3] 1 2 3
```

Convert to character

```
y <- as.character(x); str(y)
## chr [1:3] "1" "2" "3"</pre>
```

• Character coerced (if possible) to number

```
x <- c("1","2","hello"); str(x)

## chr [1:3] "1" "2" "hello"

str(as.numeric(x))

## num [1:3] 1 2 NA</pre>
```

• Few other conversion functions

```
as.matrix(), as.data.frame(), as.integer(), as.Date()
```

```
# generate 10 random numbers between 1 and 200
x <- sample(x=1:200,10); x;</pre>
## [1] 189 21 117 182 90 47 165 164 150 124
sum(x) # sum
mean(x) # mean
median(x) # median
min(x) # min
log(x) # log
exp(x) # exponent
sqrt(x) # square-root
round(x) # round
sort(x) # sort
## [1] 1249
## [1] 124.9
## [1] 137
## [1] 21
   [1] 5.241747 3.044522 4.762174 5.204007 4.499810 3.850148 5.105945
   [8] 5.099866 5.010635 4.820282
   [1] 1.206861e+82 1.318816e+09 6.493134e+50 1.100514e+79 1.220403e+39
   [6] 2.581313e+20 4.556061e+71 1.676081e+71 1.393710e+65 7.120586e+53
   [1] 13.747727 4.582576 10.816654 13.490738 9.486833 6.855655 12.845233
   [8] 12.806248 12.247449 11.135529
   [1] 189 21 117 182 90 47 165 164 150 124
##
   [1] 21 47 90 117 124 150 164 165 182 189
```

```
a <- "sunny"; b <- "day"

paste(a,b) # join
grep("sun",a) # find a pattern
nchar("sunny") # number of characters
toupper("sunny") # to uppercase
tolower("SUNNY") # to lowercase
sub("sun", "fun", "sunny") # replace pattern
substr("sunny", start=1, stop=3) # substring</pre>
```

```
## [1] "sunny day"
## [1] 1
## [1] 5
## [1] "SUNNY"
## [1] "sunny"
## [1] "funny"
## [1] "sun"
```

Functions | Custom

```
a <- 1:6; b <- 8:10

d <- a*b
e <- log(d)
f <- sqrt(e)
f</pre>
```

[1] 1.442027 1.700109 1.844234 1.861649 1.951067 2.023449

Custom function definition

```
my_function <- function(a,b){
  d <- a*b
  e <- log(d)
  f <- sqrt(e)
  return(f)
}</pre>
```

• Re-use function

```
my_function(a=2:4,b=6:8)
## [1] 1.576359 1.744856 1.861649
```

• Function names must not start with number

Control Structure | if

Conditional statements using if()

```
a <- 2; b <- 5;
if(a < b) print(paste(a, "is smaller than", b))
## [1] "2 is smaller than 5"</pre>
```

• Use else for alternative output

```
if(a < b) {
  print(paste(a,"is smaller than",b))
}else{
  print(paste(b,"is smaller than",a))
}</pre>
```

```
## [1] "2 is smaller than 5"
```

• Chain if else statements

```
grade <- "B"

if(grade == "A"){
  print("Grade is Excellent!")
}else if(grade == "B"){
  print("Grade is Good.")
} else if (grade == "C") {
  print("Grade is Alright.")
}</pre>
```

```
## [1] "Grade is Good."
```

Control Structure | for

• Use for() loop for known iterations

```
for (i in 1:5){
  print(i)
}

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

• Use while() loop for unknown number of iterations

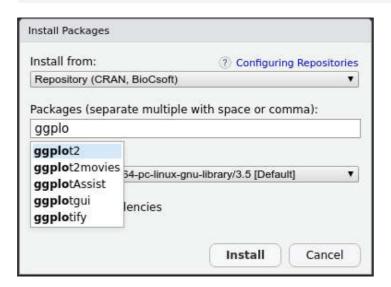
```
i <- 1
while(i < 5){
  print(i)
  i <- i+1
}</pre>
```

```
## [1] 1
## [1] 2
## [1] 3
## [1] 4
```

R Packages

- CRAN (The Comprehensive R Archive Network)
- Bioconductor for Biology/Bioinformatics/NGS packages
- Use install.packages()

install.packages("ggplot2",dependencies=TRUE)



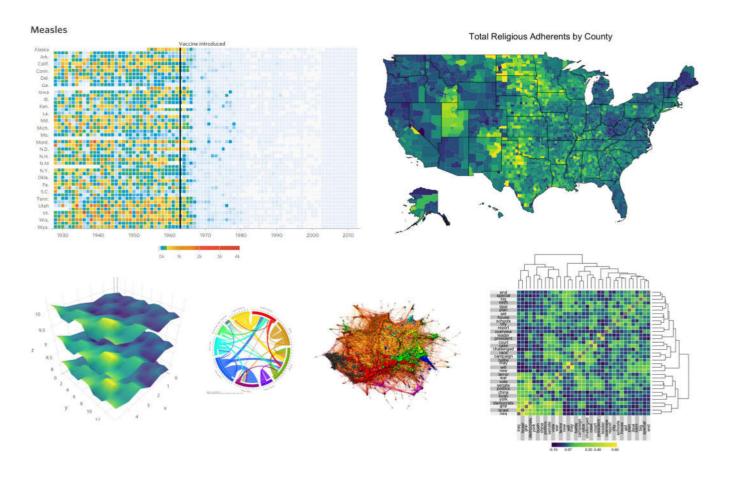
• For local packages, use type="source"

```
install.packages(path="./dir/package.zip",type="source")
```

• Use install_github() from package devtools to install from GitHub

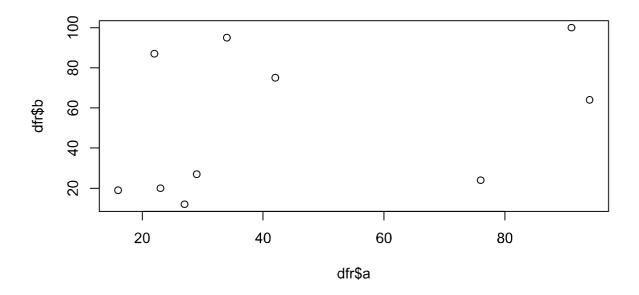
Graphics

NBIS SciLifeLab



Graphics | Base

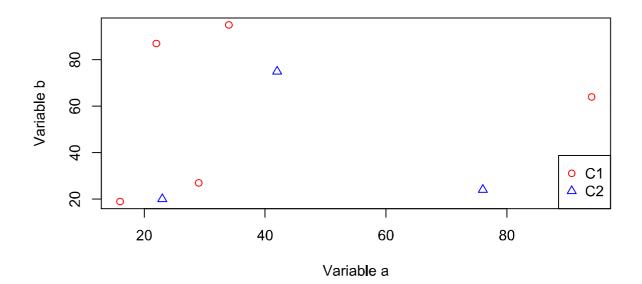
```
dfr <- data.frame(a=sample(1:100,10),b=sample(1:100,10))
plot(dfr$a,dfr$b)</pre>
```



• Add axes labels etc

```
plot(dfr$a,dfr$b,xlab="Variable a",ylab="Variable b")
plot(dfr$a,dfr$b,xlab="Variable a",ylab="Variable b",type="b")
```

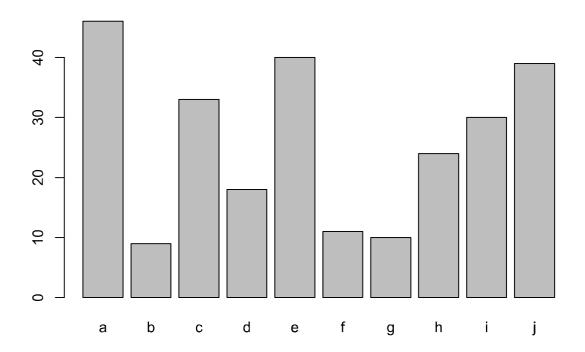
Graphics | Base



Graphics | Base

• Barplot

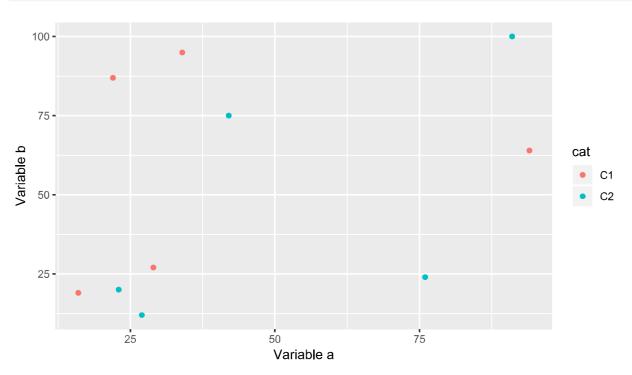
```
ldr <- data.frame(a=letters[1:10],b=sample(1:50,10))
barplot(ldr$b,names.arg=ldr$a)</pre>
```



Graphics | ggplot2

```
library(ggplot2)

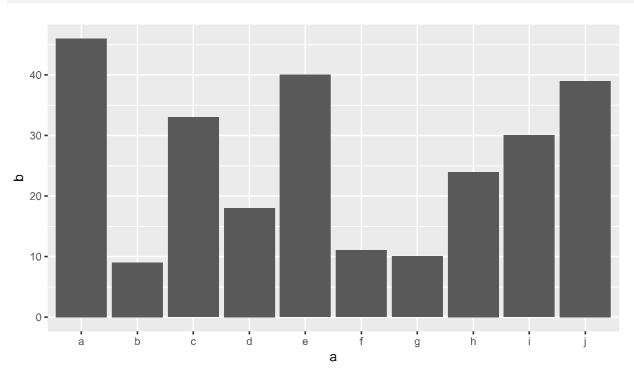
ggplot(dfr,aes(x=a,y=b,colour=cat))+
  geom_point()+
  labs(x="Variable a",y="Variable b")
```



Graphics | ggplot2

• Barplot

```
ggplot(ldr,aes(x=a,y=b))+
  geom_bar(stat="identity")
```



Input/Output | Text

quotes around strings.

```
dfr <- read.table("iris.txt",header=TRUE,stringsAsFactors=F)</pre>
head(dfr)
    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##
## 1 5.1
                    3.5
                         1.4 0.2 setosa
## 2 4.9 3.0 1.4 0.2 setosa
## 3 4.7 3.2 1.3 0.2 setosa
## 4 4.6 3.1 1.5 0.2 setosa
                          1.4 0.2 setosa
## 5 5.0 3.6
                          1.7 0.4 setosa
## 6 5.4
                    3.9
str(dfr)
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species : chr "setosa" "setosa" "setosa" "setosa" ...
dfr1 <- dfr[dfr$Species == "setosa",]</pre>
write.table(dfr1,"iris-setosa.txt",sep="\t",row.names=F,quote=F)
sep="\t" sets tab delimiter, row.names=F avoids printing rownames, quote=F avoids
```

NBIS SciLifeLab

Input/Output | Image

Create data

```
dfr <- data.frame(a=sample(1:100,10),b=sample(1:100,10))</pre>
```

• Base plot

```
png(filename="plot-base.png")
plot(dfr$a,dfr$b)
dev.off()
```

• ggplot method 1

```
p <- ggplot(dfr,aes(a,b)) + geom_point()

png(filename="plot-ggplot-1.png")
print(p)
dev.off()</pre>
```

• ggplot method 2

```
ggsave(filename="plot-ggplot-2.png",plot=p)
```

Help

NBIS SciLifeLab

- Use **?function** to get function documentation
- Use ??name to search for a function
- Use args(function) to get the arguments to a function
- Go to the package CRAN page/webpage for vignettes
- R bloggers: Great blog to follow to keep updated with the latest in the R world as well as tutorials.
- Stackoverflow: Online community to find solutions to your problems.



There are lots of resources for getting help in R.

Tutorials

- Introduction to R: Tutorial by Datacamp with excellent tutorials.
- R programming tutorial: Youtube video tutorial by Derek Banas.
- R for data science Data science tutorial by Hadley wickham.
- Data carpentry Data carpentry R workshop (Medium-Advanced)

Reference

- R Cookbook: General purpose reference.
- Quick R: General purpose reference.
- Awesome R: Curated list of useful R packages.
- RStudio cheatsheets: Useful cheatsheets.
- Advanced R by Hadley Wickham (Medium-Advanced)

Links

• Tutorialspoint List: Good list of resources.



Useful packages

These are some useful packages when starting with data analysis in R.

- dplyr, tidyr: Data manipulation
- ggplot2: Data visualisation
- stringr: String manipulation
- lubridate: Date/time manipulation
- rmarkdown: Reproducible research and report generation





Thank you

Built on: # 19-Sep-2018 at () 11:09:42. Graphics from freepik.com