Seminario III: R/Bioconductor

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Agosto - Diciembre, 2009

Reviewing how to use R

Welcome

Basic R intro

Finding help

R objects and structures

Reading files into R

Basic R plots

Reviewing how to use R

Flow control

Exercises

And so it begins

- First 32hr Bioconductor only course at LCG
- BioC2009 as an inspiration source
- All the material in English and Spanish
- Classes in English: Bioc and OCW
- Assistants: Alejandro, José and Víctor
- Official course page:
  `http://www.lcg.unam.mx/~lcollado/B/`
- Remember to ask for help through the forum

Course syllabus

- Objectives
- Project: search for Bioconductor papers.
- A Sample Class
- Evaluation
- *Tentative* class calendar

Course info

- The course is meant as a Bioconductor overview.
- Several Bioconductor experts looked at the syllabus and gave us pointers!
- The calendar is directly linked to *Bioinformatics and Statistics I* course. `Biostrings` case.
- Trying to get an expert to visit us :)

Video recording

- This course is LCG's pilot for a complete OpenCourseWare course.
- All classes will be recorded: thanks to the UATI group!
- So, English at all times
- One week lag

R background

- R is an open-source implementation of the S language: Becker, Wilks and Chambers. S-PLUS is a private one.
- Created by Ross Ihaka and Robert Gentleman[1]
- It's an interpreted language and *lives* on the interpretation moment.
- Useful as a programming environment: plots, statistics, packages such as the biological (genomic) ones from Bioconductor.
- Six month release cycle: stable and devel versions.
- R is multi-plataform: Windows, Linux/Unix and Mac.
- R Core and the Comprehensive R Archive Network (CRAN) `http://cran.r-project.org`

[1] He also created the Bioconductor project

Installing R

- For Windows and Mac, basically download the base binary from CRAN, double click on it and follow the instructions.
  - Windows stable and Mac stable releases.
- For Linux/Unix, it will depend on the flavor you have. Say you have Ubuntu, then you need to follow these instructions to get the latest stable version as `sudo apt-get install r-base` is generally not updated to the latest version.
- For this course you'll need the R devel version which currently is named 2.10.0devel and Bioconductor release 2.5.
  - Installed on Montealban (Windows) and will soon be installed on the Solaris servers.

A basic R session

- We highly recommend you to use Emacs or XEmacs for your R work. At the very least use a text editor and copy paste your commands[2].
- Either type R on your terminal or double click on the R icon. Basic info shows up.
- You can simply use R as a calculator, so type in some commands :)

```
> 2 + 3 * 5
```

```
[1] 17
```

```
> 2^3
```

```
[1] 8
```

A basic R session

```
> 6/3
[1] 2
> sqrt(pi)
[1] 1.772454
> exp(log(5))
[1] 5
```

- You can insert comments into your code by using the # symbol.
- Quit by using the q or quit function.

```
> q("no")
```

[2] In windows you can use the R GUI script editor and run commands by using CTRL + R.

Workspace and history

Sometimes you need to interrupt your work, so saving your R objects, history and/or session is useful.

- You can save and load objects by specifying the objects, path and file name into a .Rda file.

```
> save(object1, object2, file = file.path("folder",
+     "file.Rda"))
> load(file = file.path("folder",
+     "file.Rda"))
```

- To view your recent commands use the history function. You can save and load your history using savehistory and loadhistory.

Workspace and history

```
> history()
> savehistory(file = file.path("folder",
+     "file.Rhistory"))
> loadhistory(file = file.path("folder",
+     "file.Rhistory"))
```

- You can save your session into a `.Rdata` file by specifying so when quitting or by using the save.image function and use load to reload it.

```
> q(save = "yes")
> save.image(file = file.path("folder",
+     "file.Rdata"))
> load(file = file.path("folder",
+     "file.Rdata"))
```

Workspace and history

- While working, you might need to change your working directory or view what's in there. Functions such as getwd, setwd, list.files() and dir() will be most helpful.

R help

There are a lot of ways to get help in R. I mention some below.

- The most basic help function is simply, help. I generally use its shorcut: ?

```
> help(quit)
> `?`(q)
```

- Another great help tool is to start the help browser by using help.start. During the same session, the help pages will open in your browser.

```
> help.start()
```

- I also use the apropos and args quite frequently. The first one lists all the functions whose name includes your query and the second one lists the arguments of a function.

```
> apropos("history")
```

R help

```
[1] "history"     "loadhistory"
[3] "savehistory"
```

```
> args(savehistory)
```

```
function (file = ".Rhistory")
NULL
```

- If you want to search on the R web site, you can use RSiteSearch. For example:

```
> RSiteSearch("help")
```

- For a specific package, you can also view some basic information using the following syntaxis. Try it out with the package stats.

```
> library(help = packagename)
```

R help

- Another excellent tool is to use the R mailing list `https://stat.ethz.ch/mailman/listinfo/r-help`
- Spend some time reading the *posting guide*. Using the function sessionInfo is very important here.

```
> sessionInfo()

R version 2.10.0 Under development (unstable) (2009-07-
i686-pc-linux-gnu

locale:
 [1] LC_CTYPE=en_US.UTF-8
 [2] LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8
 [4] LC_COLLATE=en_US.UTF-8
```

R help

```
 [5] LC_MONETARY=C
 [6] LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8
 [8] LC_NAME=C
 [9] LC_ADDRESS=C
[10] LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8
[12] LC_IDENTIFICATION=C

attached base packages:
[1] stats     graphics  grDevices
[4] utils     datasets  methods
[7] base
```

Objects

- Everything in R is an object and they can be named with numbers, letters, period and underscore[3].
- Assigning a value to a variable[4], is done with the <- operator or alternatively with =. However, a best practice is to use = only inside functions and argument definitions.
- Any object has a *class* such as `integer` and can have *attributes* which you can attach and manipulate by using the attr function. To view them use the attributes function.

```
> x <- 1:10
> names(x) <- letters[1:10]
> attributes(x)
```

Objects

```
$names
 [1] "a" "b" "c" "d" "e" "f" "g" "h" "i"
[10] "j"
```

- As for the functions, they can have different *methods* and R supports two object oriented-programming systems OOP (S3 and S4) but we won't get into them.

[3] It can't start with the last two

[4] Which creates an object

Vectors

- It's the most basic data structure in R. You can create one by using the most used R function... c

```
> x <- c("hola", seq(0, 25, by = 5),
+     TRUE)
> x
```

```
[1] "hola" "0"    "5"    "10"   "15"
[6] "20"   "25"   "TRUE"
```

- What is the class of the object x?
- *Atomic vectors* contain all values of the same type such as integers, doubles, logicals or character strings.

Vectors

```
> y <- c(NA, sample(rep(c(TRUE, FALSE),
+     10), 4))
> y
[1]    NA  TRUE  TRUE FALSE FALSE
```

- Is `y` an atomic vector?

A curious parenthesis

- Type[5] the following code:

```
> a <- sqrt(2)
> a * a == 2
> a * a - 2
```

- What do you notice?

[5] The R code is available on the official course website

Factors

- They are useful for when you have data that can be categorized. For example, kids, adults and elderly people.

```
> f <- sample(c("kid", "adult", "elderly"),
+     10, replace = T)
> f <- factor(f)
> f

 [1] elderly adult   kid     adult
 [5] adult   kid     kid     adult
 [9] elderly kid
Levels: adult elderly kid
```

- You can also create ordered factors by using the ordered function.

Lists

- It's a vector-like object that can hold different types of data including other R objects.

```
> x <- list(name = "Leonardo", age = 22,
+       x = c(TRUE, FALSE, NA))
> x

$name
[1] "Leonardo"

$age
[1] 22

$x
[1]  TRUE FALSE    NA
```

Lists

```
> names(x)
[1] "name" "age"  "x"
> x$age
[1] 22
> x[[3]]
[1]  TRUE FALSE    NA
> y <- "name"
> x[[y]]
[1] "Leonardo"
```

Data frames and matrices

- You can define a *matrix* by using the matrix funcion or by changing the dimensions of a vector with dim. All the values have to be of the same type.

```
> x <- 1:4
> dim(x) <- c(2, 2)
> x[, 2]
```

```
[1] 3 4
```

- *Data frames* are rectangular just like matrices but every column (variable) can hold different types of data.

```
> students <- data.frame(age = 18:21,
+     height = 170:173, passed = c(TRUE,
+         FALSE, TRUE, TRUE))
> students
```

Data frames and matrices

	age	height	passed
1	18	170	TRUE
2	19	171	FALSE
3	20	172	TRUE
4	21	173	TRUE

Basis

- The two basic functions for reading files into R are scan and read.table. For example, read.csv is analog to a type of `read.table`.Check their help files for more details.
- Lets read the `stats.txt` file which contains information on several contigs.

```
> contigs <- read.table(file = file.path("../../data",
+     "stats.txt"), header = T)
```

- The above line works fine for me, but my file path is different from yours.[6] We can solve this simply by reading the file from the web :)

```
> contigs <- read.table(file = file.path("http://www.lcg.unam.mx/~lcollado/
+     "stats.txt"), header = T)
```

[6] We use the file.path function to be plataform independent

Exploring your object

- Once we have read a file, there are some functions which can help us explore our new object.
- Try them out :)

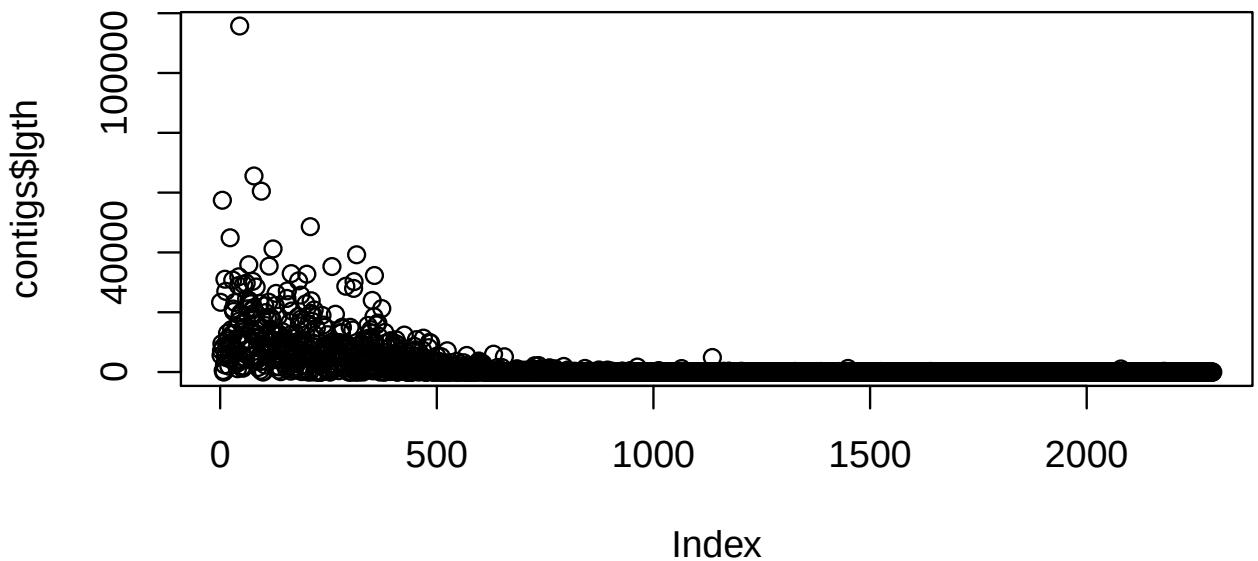
```
> class(contigs)
> object.size(contigs)
> names(contigs)
> head(contigs)
> tail(contigs)
> dim(contigs)
> summary(contigs$lgth)
```

Basis

- R is quite strong for plotting data fast.
- Some plotting functions start a new graphic while others plot on top of a previous graph.
- Most arguments are passed as ... You can learn more about graphical parameters with `?par`
- `http://www.harding.edu/fmccown/R/` is quite useful for beginner tips.
- Plots are a *crucial* part of doing Exploratory Data Analysis

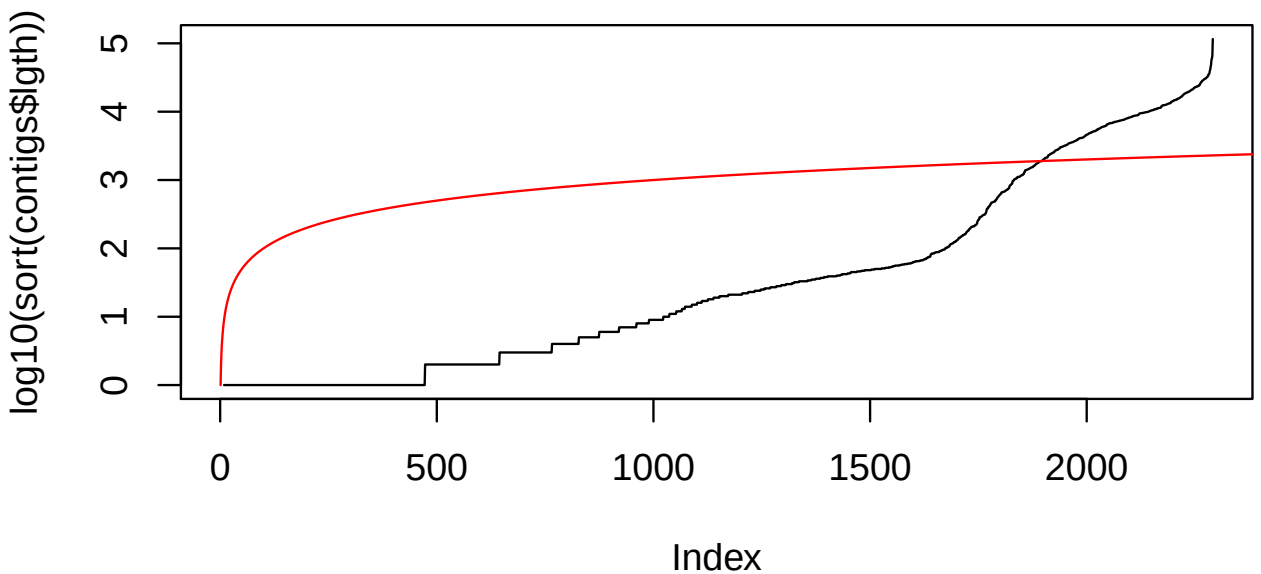
Plot

```
> plot(contigs$lgth)
```



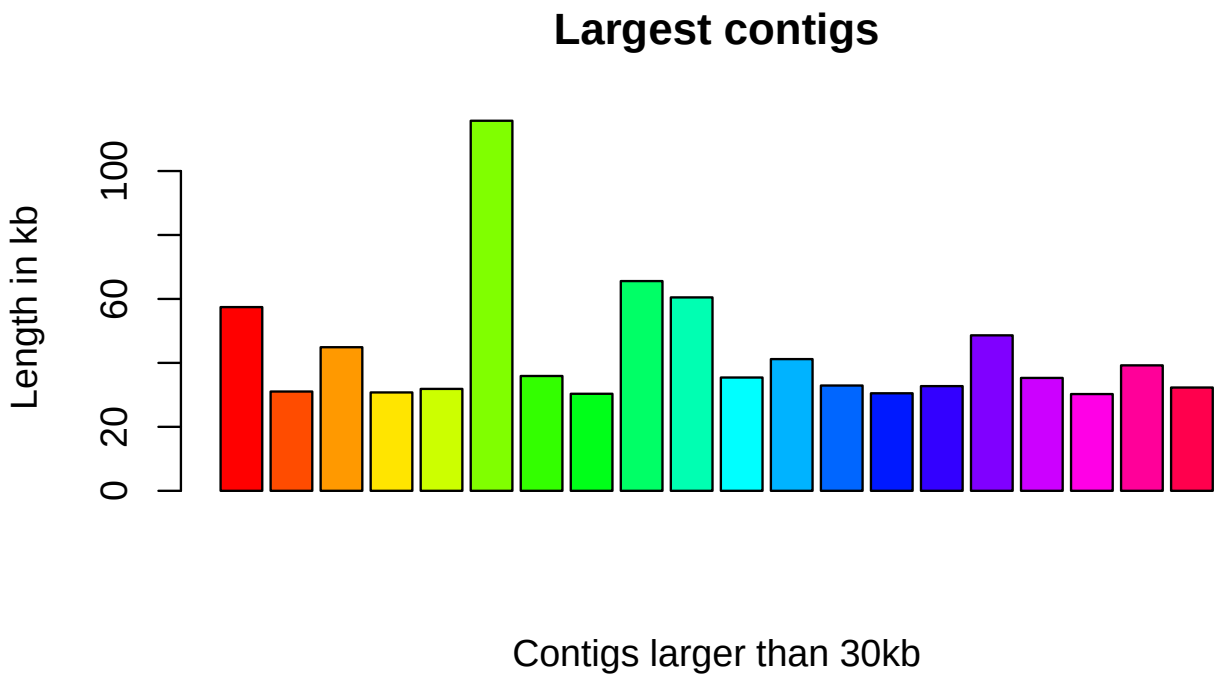
Lines

```
> plot(log10(sort(contigs$lgth)),
+      type = "l")
> lines(log10(1:length(contigs$lgth)^2),
+      col = "red")
```



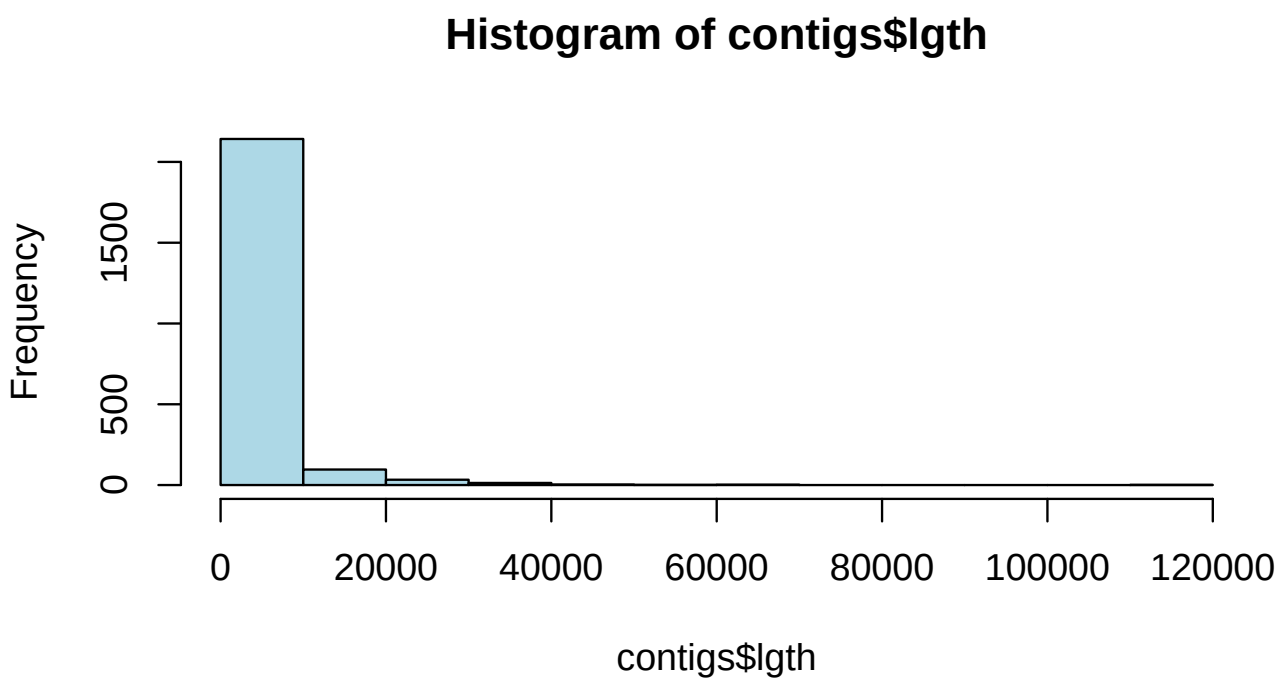
Barplot

```
> barplot(contigs$lgth[contigs$lgth >
+     30000]/1000, col = rainbow(length(contigs$lgth[contigs$lgth >
+     30000])), xlab = "Contigs larger than 30kb",
+     ylab = "Length in kb", main = "Largest contigs")
```



Basic histogram

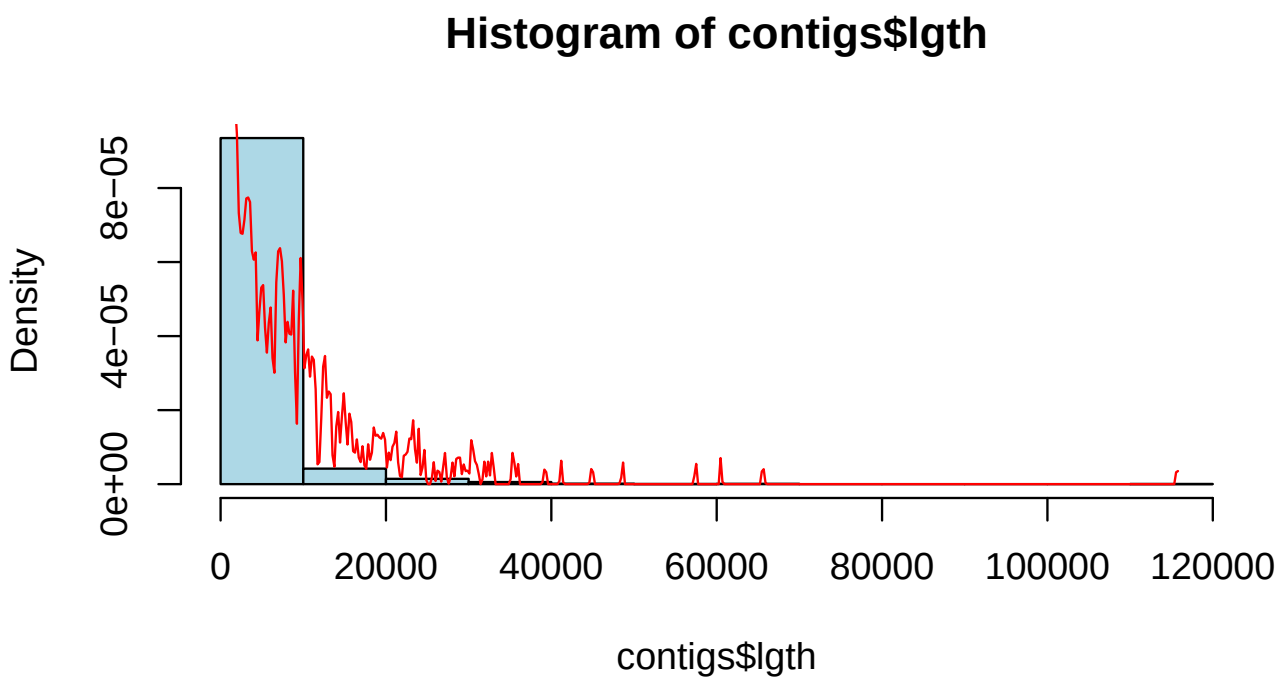
```
> hist(contigs$lgth, col = "lightblue")
```



Plotting the density

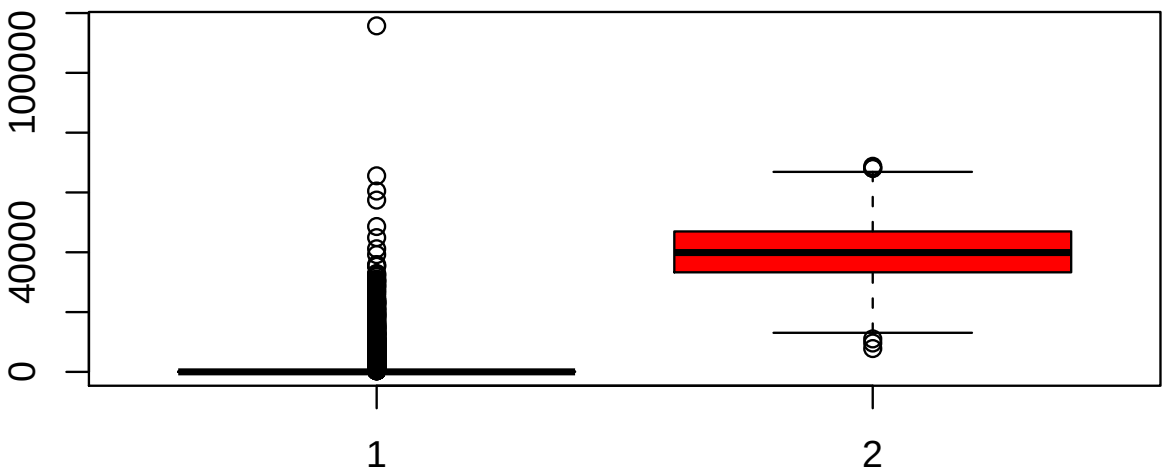
```
> hist(contigs$lgth, col = "lightblue",
+      prob = T)
> lines(density(contigs$lgth), col = "red")
```

Plotting the density



Graphical view of the summary

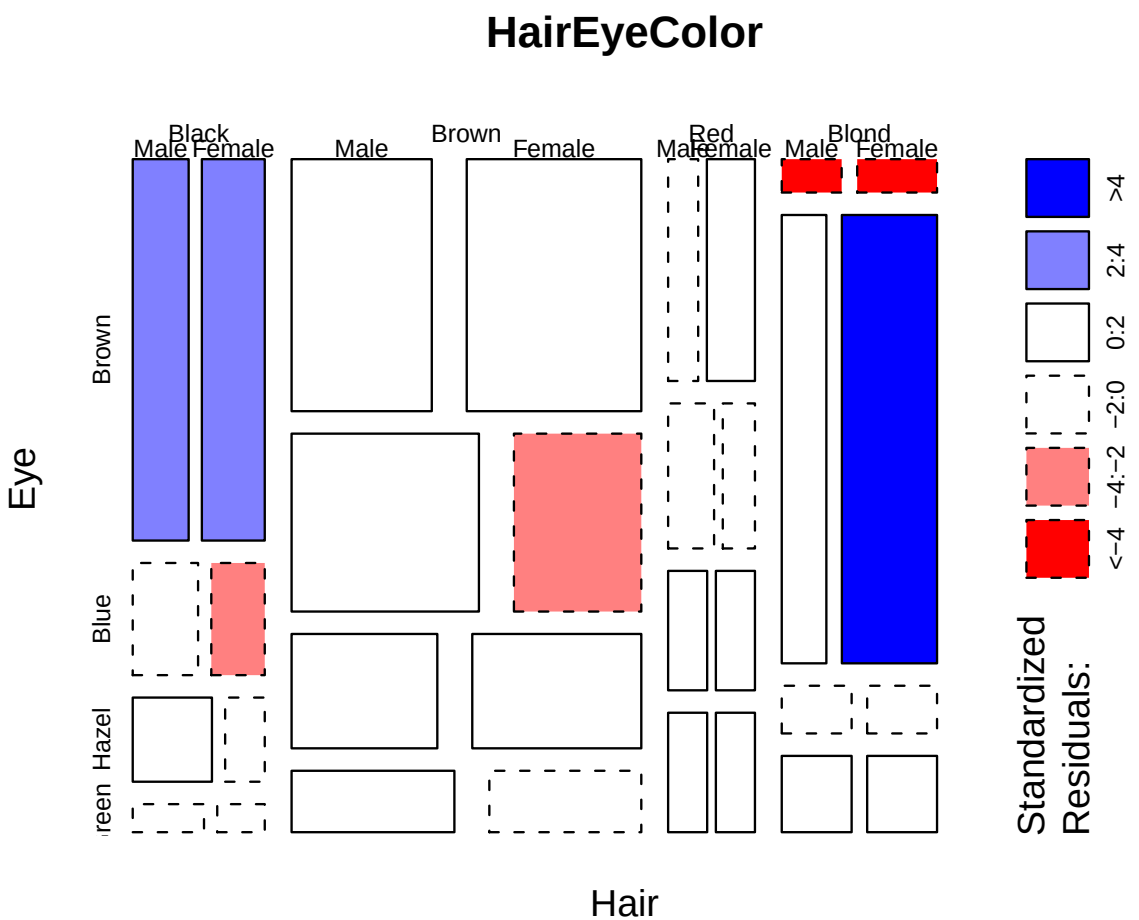
```
> boxplot(contigs$lgth, rnorm(1000,
+     40000, 10000), col = c("lightblue",
+     "red"))
```



Great for table with 3 dims

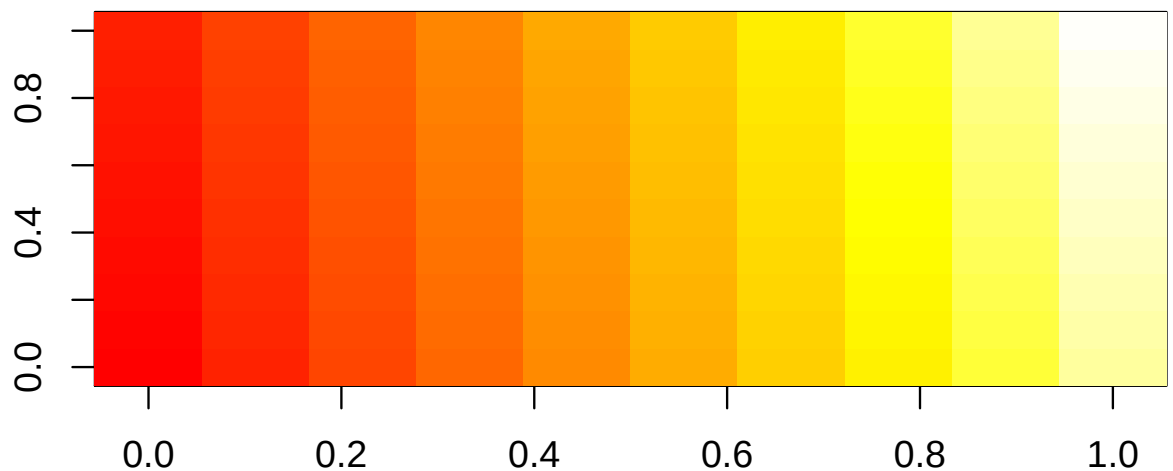
```
> mosaicplot(HairEyeColor, shade = TRUE)
```

Great for table with 3 dims



Helps visualize your matrix

```
> x <- matrix(1:100, 10, 10, byrow = T)
> image(x, col = heat.colors(100))
```



Exporting images

- You can always export your images into PDF or PNG files.

```
> pdf(file = "file.pdf", onefile = T)
> plot("some data")
> dev.off()
> png(file = "image.png")
> plot("some data")
> dev.off()
```

Two options

- While is quite easy to use: `while (cond) expr`

```
> x <- NULL
> while (length(x) < 10) {
+     x <- c(x, runif(1))
+ }
```

- What is the length of the `x` object? Now lets use repeat with break.
- With `while` and `repeat` be careful to avoid infinite loops!

Two options

```
> x <- 1
> repeat {
+     x <- x + 2
+     print(x)
+     if (x > 10)
+         break
+ }
```

```
[1] 3
[1] 5
[1] 7
[1] 9
[1] 11
```

An alternative

- The most widely used form of iteration is the for cycle: `for (var in seq) expr`

```
> for (i in seq_len(3)) print(i)

[1] 1
[1] 2
[1] 3

> for (i in letters[4:6]) print(i)

[1] "d"
[1] "e"
[1] "f"
```

- Using `seq_len` is recommended versus using `1:length(object)`

An alternative

- As you might want to use conditionals if, ifelse and switch could be of your interest.

Basis

- Its quite easy to write your own R functions using function.
- While it can take several arguments as input, it only returns one object which can be a vector.
- The object returned is either the last one to be evaluated or the one specified with return.
- Say you use an argument x inside a function, this one will not be related to a variable x outside the function.[7]

```
> x <- 5
> y <- function(x) rnorm(x)
> y(2)
[1] -1.1001290 -0.4363984
> x
[1] 5
```

[7] For more curious users, look for guides on environments

A neat family

- Their main utility is to *apply* a function to all the elements of an object. Say all the columns of a matrix.
- In most cases, the return value is simplified and in others its an argument.
- Its easier for someone to understand a code with apply functions than `for` loops.

```
> mat <- matrix(rnorm(100), 10, 10)
> apply(mat, 1, sum)
```

```
 [1] -3.3583902  0.8250018  3.9749494
 [4]  0.8761072 -2.6867082 -0.5183255
 [7] -1.2522203  0.4885079 -0.5388356
[10] -0.2917741
```

A neat family

- Keep in mind that some R functions are way faster than using apply, such as rowMeans.

```
> apply(mat, 1, sum) == rowSums(mat)
```

```
 [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [8] TRUE TRUE TRUE
```

- Some packages implement new apply functions, but here are the common ones:
  - apply Useful for matrices and data.frames
  - lapply Its the list version
  - sapply Simplest one to use (lists and vectors)

```
> x <- list(rnorm(100), runif(100),
+     rlnorm(100))
> sapply(x, quantile)
```

A neat family

```
            [,1]       [,2]       [,3]
0%   -2.7540348 0.03099712  0.1231390
25%  -0.7164680 0.31074536  0.5880255
50%   0.1520818 0.54236418  0.9720055
75%   0.8725263 0.71203283  2.2368822
100%  2.3792556 0.99192278 11.6742964
```

- `tapply` Uses a vector and a factor, great for grouped data

```
> x <- data.frame(info = rnorm(10),
+     group = as.factor(sample(1:3,
+         10, replace = T)))
> tapply(x$info, x$group, mean)
```

```
         1          2          3
-0.2252659  0.7718850 -0.6408342
```

- `eapply` For environments and the curious ones

A neat family

- `mapply` Multivariate version of `sapply`

```
> mapply(rep, 1:4, 4:1)
[[1]]
[1] 1 1 1 1

[[2]]
[1] 2 2 2

[[3]]
[1] 3 3

[[4]]
[1] 4
```

- `rapply` Recursive version of `lapply`

- You might find this site useful: advanced_function_r.htm

or homework :P

- Please go to the official course site and complete the first exercise file.
- Homework specifications are available on the `Course Syllabus`.
  - For this homework only hand in a portable `.R` file with comments. Next week we'll learn about `Sweave` and *vignette* files.