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of Immunobiology, Freiburg

Introduction to R

http://www.r-project.org/

Thomas Manke

Start and Stop

Start	> R
Stop	> q()

From R to Linux

1. Try the following R commands and understand their output

   - err=system("pwd")
   - pwd=getwd()
   - rf=list.files("/")
   - nd=setwd("~")
   - hf=list.files(".")

Getting help

?, ??	> ?matrix
examples	> example(rnorm)
web	http://www.r-project.org/ http://www.bioconductor.org/ http://epicenter/courses/2010.11.11_linux/materials/
Mailing lists	e.g. r-help@r-project.org
Packages	> vignette("affy")

When seeking help from the community, it is a good idea to send also the output of
> sessionInfo()

A better pocket calculator

- 2+2
- 2^2
- sin(pi/2)
- sqrt(2)
- factorial(20)
- 1+exp(-1i*pi)

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Data and Data Types

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Assignments and Removal

- x=2
- y<-2
- 2->z
- rm(z)
- ls()
- rm(list=ls())
- ls()

Conversions

- x=2
- typeof(x)
- as.character(x)
- as.logical(x)

R-objects are made from atomic elements:
logical, numeric, character, complex

Creating a vector

```
> x = c(1,2,3,4,5,6,7,8,9,10)
> x = seq(1,10,by=1)
> x = 1:10
```

What is the difference between a=1:10-1 and b=1:(10-1) ?

Create a reversed vector (10,9,…,1)

“letters” and “LETTERS” are predefined vectors.
Of which type? Give an interpretation of >as.logical(LETTERS)

Naming vector elements

Vector elements can be named for convenience.

- x=c(a=1,b=2); str(x)
- X = 1:100; str(X)
- names(X)=letters; str(X)
- X[1]
- X["a"]
- names(X)[100]="This is the end"
- Y=as.characters(X); str(Y)

Combining vectors

- x=c(1,2,3); y=c(2,2,2);
- x>y # comparsion
- x+y # addition
- x*y # element-wise multiplication
- x %*% y # scalar-product

Vector elements are recycled

Vector Mystic

Execute the following and try to understand

- 1:8 + c(10,20)
- x=1:100; i=30:70; x[i]; x[-i]
- x[x %% 2 == 0]

Matrices

Definition:

- M=1:100; str(M); dim(M)
- dim(M)=c(20,5); str(M); dim(M)
- M=matrix(1:100,ncol=5)
- M=matrix(1:110,nrow=20)

Matrices

Access:

- M[20,1]; M[1,20]
- M[c(1,2),]; M[,c(1,4)]
- M[25]

Query:

> dim(M); nrow(M); ncol(M)

Matrices

Manipulation:

- t(M)
- cbind(M,1:5)
- rbind(M,1:5)

Naming:

- rownames(M)=letters[1:nrow(M)]
- colnames(M)=LETTERS[1:ncol(M)]

Data Frames

Definition:

- D=data.frame(x=1:9,l=letters[1:9], b=1:9<5)
- str(D)

Access:

- D[,1]; D$x

Data frames are generalized matrices where different columns can have different types.

Lists

Definition:

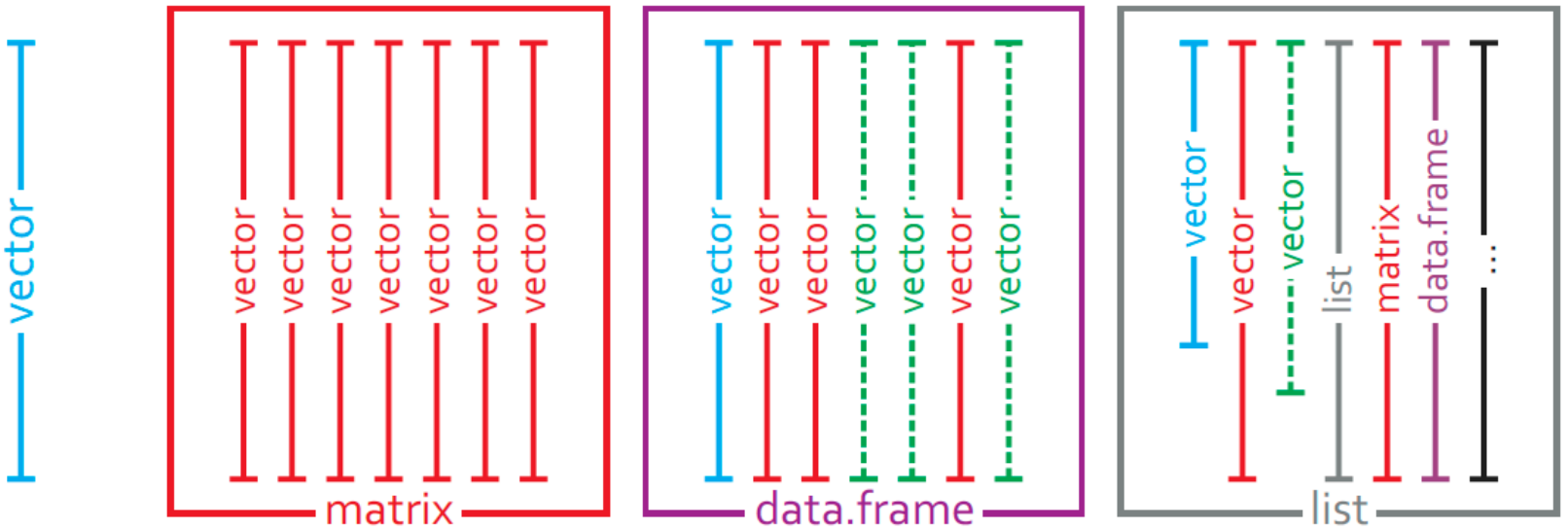
- L=list(x=1:9,l=letters[1:3], b=1:20<10)
- str(L)

Access:

- L[,1]; L[1], L$x
- str(L[c(2,3)]), str(L[[1]])

Lists are generalized data frame where different columns can have different length.

Summary: Data Types



Data type	single	single	multiple	multiple
elements	atomic	atomic	vector	any
subsets	X[i] X[“a”]	M[i,j] M[“row”,”col”]	D[i,j] D$”colname”	L[[i]] L$”colname”

i and j can be index vectors!

from Michael Stadler (FMI)

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Thomas Manke

Information on objects

Available objects	➢ls() ➢objects()
Information on objects	➢typeof(x) ➢class(x) ➢length(x) ➢str(x)

R has precompiles data sets that are suitable for exploration > data()

Exercises

Vectors and matrices. Create the following:

1. Create a vector v1 with number 1 to 200 in steps of 2.
2. Create a vector v2 with 100 with alternating TRUE/FALSE
3. Convert vector v1 into a 10x10 matrix M
4. Name the rows of M (a,b,..j) and the columns (A,B,…J)
5. Take the transpose of M

Data frames and lists. Create

1. a data frame D with column V that takes the vector v1 and logical vector which labels whether v1 is smaller or bigger than 100
2. A list L of four elements (a=v1, b=v2, c=M, d=D)

Access. Try and understand those three commands

which(L[[2]]); sum(L[[3]]["a",]); L[[4]]$v1

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Data Descriptions

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Creating synthetic data

Sample from normal distribution

- X=rnorm(100,mean=2,sd=0.1)
- X
- plot(X)

R supports many different distributions.
Try to find some of them ?r<tab>

Plots

- X=1:100
- Y=X+rnorm(100,mean=0,sd=1)
- plot(X,Y)

The plot command is very customizable (labels, titles, etc). See ?plot for details.

Descriptive statistics

values	➢max(x) ➢mean(x) ➢var(x) ➢sd(x) ➢median(x) ➢summary(x)
plots	➢hist(x) ➢stem(x) ➢boxplot(x) ➢plot(density(x))

Exercise

- x=rnorm(300,mean=c(1,2,1),sd=c(0.1,0.1,1))

Of what type is x, how many elements does it have?

- v=sum((x-mean(x))^2)/(length(x)-1)

Identify all functions in this expression.

What is being calculated?

What is the maximum/minimum element of x?

Show the summary statistics?

What is the mean and standard variation

What is the distribution of X?

Generate a boxplot of X and try to customize it.

Histograms

>Hist(x); Hist(x,breaks=100); hist(x,breaks=100,prob=TRUE)

>lines(density(x),col="red")

- hist(x[seq(1,300,3)],xlim=c(0.5,2.5),30)
- hist(x[seq(2,300,3)],xlim=c(0.5,2.5),30,add=TRUE,col="red")

Replace title and the x-label with your favorite words.

Plot the histogram of a Poisson distribution with mean=16

Overlay it with the density plot of a normal distribution with mean=16 and standard deviation=4

Efficency with Data Frames

skipped

Generate a factor

- F=rep(letters[1:3],100)

Generate data frame

- D=data.frame(X=x,F=f)
- summary(D)
- tapply(DX, DF, mean)

  Describe the effect of this function.

- boxplot(D$X ~ D$F, col=c("red","green","blue"))

Converting Data Frames

skipped

- L=tapply(DX, DF, c)

  What does this function do?

  What data type is L?
- A=cbind(a=L$a,b=L$b,c=L$c)

  What data type is A and what is its dimension?

More images

- A=cbind(a=rnorm(100,1,0.1), b=rnorm(100,2,0.1), c=rnorm(100,1,1))
- image(A)
- image(t(A), axes=FALSE)

Use ?image to find out how to change the colours.

What is the default? Try with 100 topo.colors.

Correlations

- plot(A[,1],A[,3])
- cor(A[,1],A[,3])
- pairs(A)
- cor(A)

Dendrograms

- A = cbind(A, d=A[,1]+rnorm(100,0,0.2))
- pairs(A)
- cor(A)
- d=dist(t(A)); plot(hclust(d))

See ?dist and ?hclust to find out about other possible definitions of distance and clustering methods

Correlations

Plot is not sufficient for dense data

- n=10000
- x1=matrix(rnorm(n), ncol=2)
- x2=matrix(rnorm(n, mean=4, sd=1.2), ncol=2)
- x=rbind(x1,x2)
- smoothScatter(x)

Heatmaps

- heatmap
- heatmap(A)
- heatmap(A,labRow="",scale="none")

As with all plot commands, there are many ways to customize heatmaps. There is even a separate package "heatmap.2"

Saving images

- jpeg(“heatmap.jpg”)
- heatmap(A,labRow=“”,scale=“none”)
- dev.off() # close device

The device “jpeg” can be customized.
See ?jpeg for details.

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Retrieving external data

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Reading files

R-files (objects)	> load(file)
tables	> read.tables(file, … options …)
scan	> scan(files, … options …)

There are many different ways to read data. Try

- ?read<tab>

The reality of I/O

Getting data into R can be difficult and time-consuming.

Therefore:
Keep you data files simple and structured!!!

A real-world example

Loading ChIP-chip data (yeast; Harbinson et al. 2004)

Repeat the steps below and watch out for errors

1. D= read.table("ChIP-chip.tab")
2. D= read.table("ChIP-chip.tab", skip=1)
3. D= read.table("ChIP-chip.tab", skip=1, header=TRUE)
4. D= read.table("ChIP-chip.tab", skip=1, header=TRUE, sep="\t")
5. D= read.table("ChIP-chip.tab", skip=1, header=TRUE, sep="\t", comment.char="")
6. D= read.table("ChIP-chip.tab", skip=1, header=TRUE, sep="\t", comment.char="", quote="\"")
7. D= read.table("ChIP-chip.tab", skip=1, header=TRUE, sep="\t", comment.char="", quote="\"",nrows=6229)

Saving files and data

R-files (objects)	> save(objects, file)
tables	> write.tables(object,file, … options …)

There are many different ways to write data. Try

- ?write<tab>
- ?save<tab>

Binary R-files are a very compact, convenient and efficient way to share results and data

Loading and saving

- rm(list=ls()) # clear all objects
- load(url("http://epicenter/courses/2010.11.11_linux/data/ChIP-chip.Rdata"))

Which objects were loaded? Of which type?
Display their structure.
Interprete the output of summary(D)
Create a scatter plot for D$FHL1_YPD and D$RAP1_YPD

Convert data frame to matrix

- A = as.matrix(cbind(D[,4:207]))
- rownames(A)=D$X

Save objects

- save(D,A,file="mydata.Rdata")

Removing missing values

Undefined or missing values is a common problem with real data. The can be identified using is.na()

What is the output of x=is.na(D$FHL1_YPD)?
What is !x ? What is which(x)?
Compare D$FHL1_YPD[x] and D$FHL1_YPD[!x]

Repeat the above for y=is.na(D$RAP1_YPD).

Given an interpretation of

- I = intersect(which(x), which(y))
- U= union(which(x),which(y))

Thresholding

Convert matrix A into binary matrix B

- A[is.na(A)]=1
- B = A<1e-3

Create a contingency matrix of FHL1 and RAP1

- table(B[,"FHL1_YPD"],B[,"RAP1_YPD"])

Question: is this overlap large?

Venn Diagrams

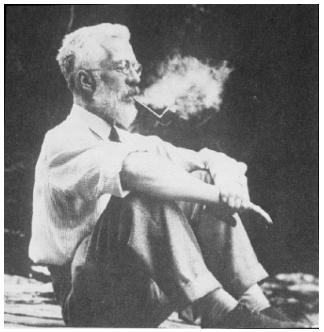
- library(gplots)
- t=1E-3
- L=list(FHL1=which(D$FHL1_YPD<t),
  RAP1=which(D$RAP1_YPD<t),
  MCM1=which(D$MCM1_YPD<t))
- venn(L)

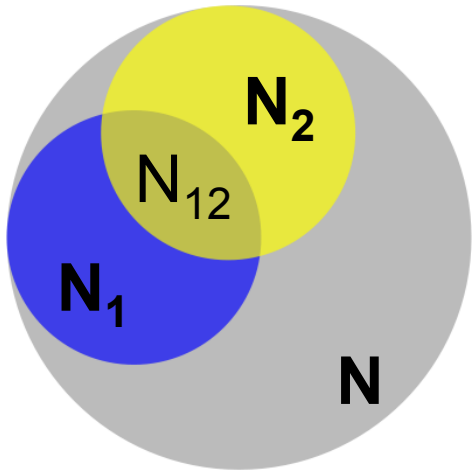
Compare the plot with the contingency table.

Fisher Exact Test

	+	-	
+	a	b	N_1
-	c	d	
	N_2		N

2x2 table





Venn diagram

Probability that overlap > N_{12}

➢ phyper(q=N_{12}-1,m=N_2,n=N-N_2,k=N_1,lower.tail=FALSE)

Is the overlap between FHL1 and RAP1 significant?

The final exercise

- rm(list=ls()) # clear all objects
- load(url("http://epicenter/courses/2010.11.11_linux/data/expression.Rdata"))

Which objects were loaded? Of which type?
Display their structure.

Create a data subset for the top 100 genes

Create an image of the data.

Create a heatmap of the same.

Not covered

- Bioconductor (biobase package)
- Scripts and logical control
- User-defined functions
- Plot-configurations and parameters
- Distribution function
- String functions and regular expression
- Matrix algebra, inversions, etc …
- models