Introduction to R

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Areas of interest: genetic variation, splicing, next gen sequencing methods, personalized medicine, machine learning, pharmacogenomics

Collaboratory Website

http://collaboratory.lifesci.ucla.edu/

Workshop 3: Introduction to R

- **Day1**
  - Introduction to R
    - Installation, configuration, basic concepts, syntax and usage
- **Day 2**
  - Data Analysis
    - Visualization methods
    - Statistical methods
- **Day 3**
  - Scripting, batch mode
  - Packages, Bioconductor (DEseq, etc)

Workshop 3: Introduction to R

- **Day 1**
  - What is R? Why use it?
  - Getting up and running
    - Installation, configuration issues
    - overview of R interface
    - GUIs for working with R
  - Your first R session
  - Basic concepts
    - Starting and stopping an R session
    - finding help/documentation
    - Data structures
    - Getting data in and out of R
    - Basic analysis

Workshop 3: Introduction to R

- **Day 2**
  - Statistical methods
    - Probability distributions
    - Random number generation
    - Common tests
      - Fisher's exact test, chi square, qvalue, etc…
  - Visualization
    - Plotting functions
    - Customizing plots
    - Saving plots for publication

Workshop 3: Introduction to R

- **Day 3**
  - Automating or scripting R
    - Batch mode
  - Packages that extend R
    - Installation
    - Documentation (Vignettes)
    - Useful packages
  - Bioconductor
    - Extending R for the life sciences
    - Useful bioconductor packages
    - Some basic bioC concepts
    - Bioconductor demo

Dropbox

- In the drop box folder are:
  - course powerpoint
  - sample scripts
  - exercises
- Please DO NOT make changes to these files because they will affect EVERYONE!
- INSTEAD, copy them to a directory on your computer
- Let me know if you need to be invited to the dropbox folder

What is R?

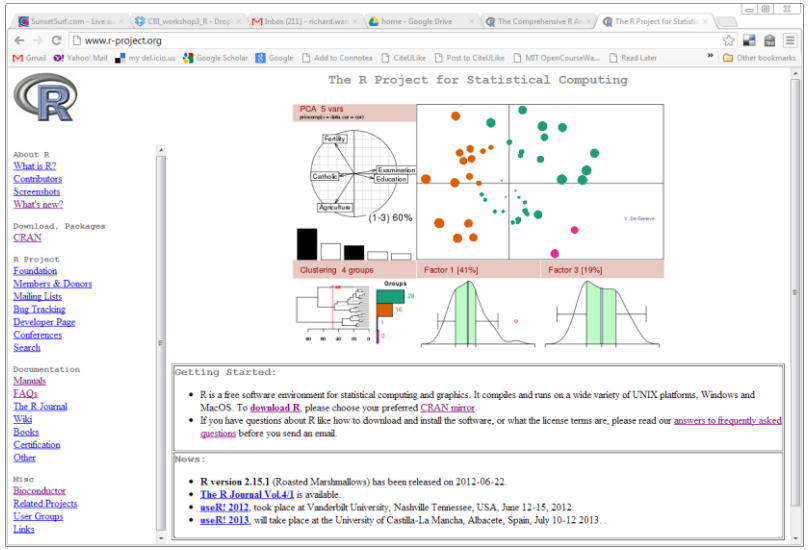
- A glorified calculator
- Statistical tables
- Visualization tool
- Programming language and environment

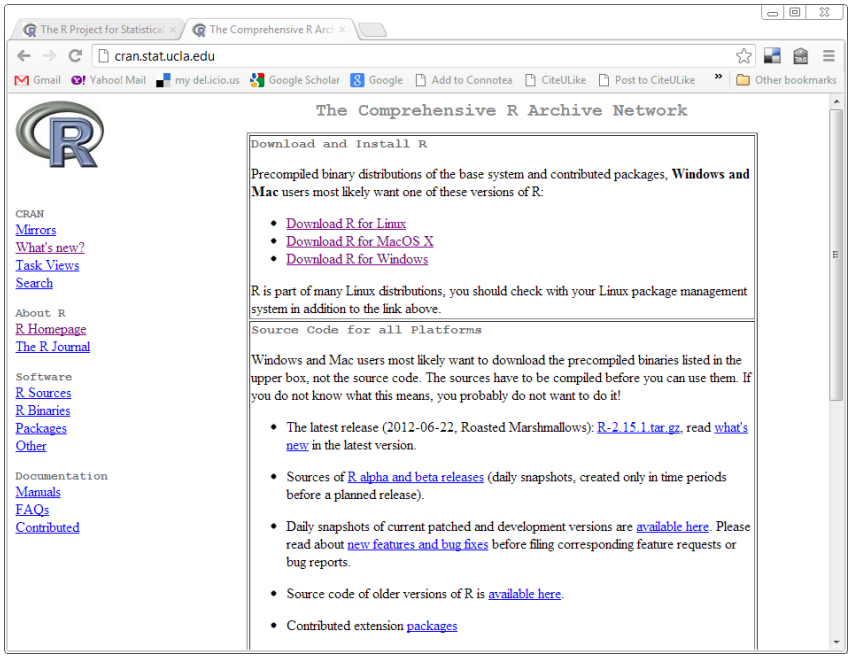
Why R?

- Many tools STATA, SPSS, Matlab, Excel…
- Advantages
  - powerful
  - up to date with latest algorithms (packages, Bioconductor)
  - strong community of users
  - lingua franca of statistics community
  - it's free
- Disadvantages
  - steep learning curve, but can be useful quickly
  - not pretty
  - can be memory intensive

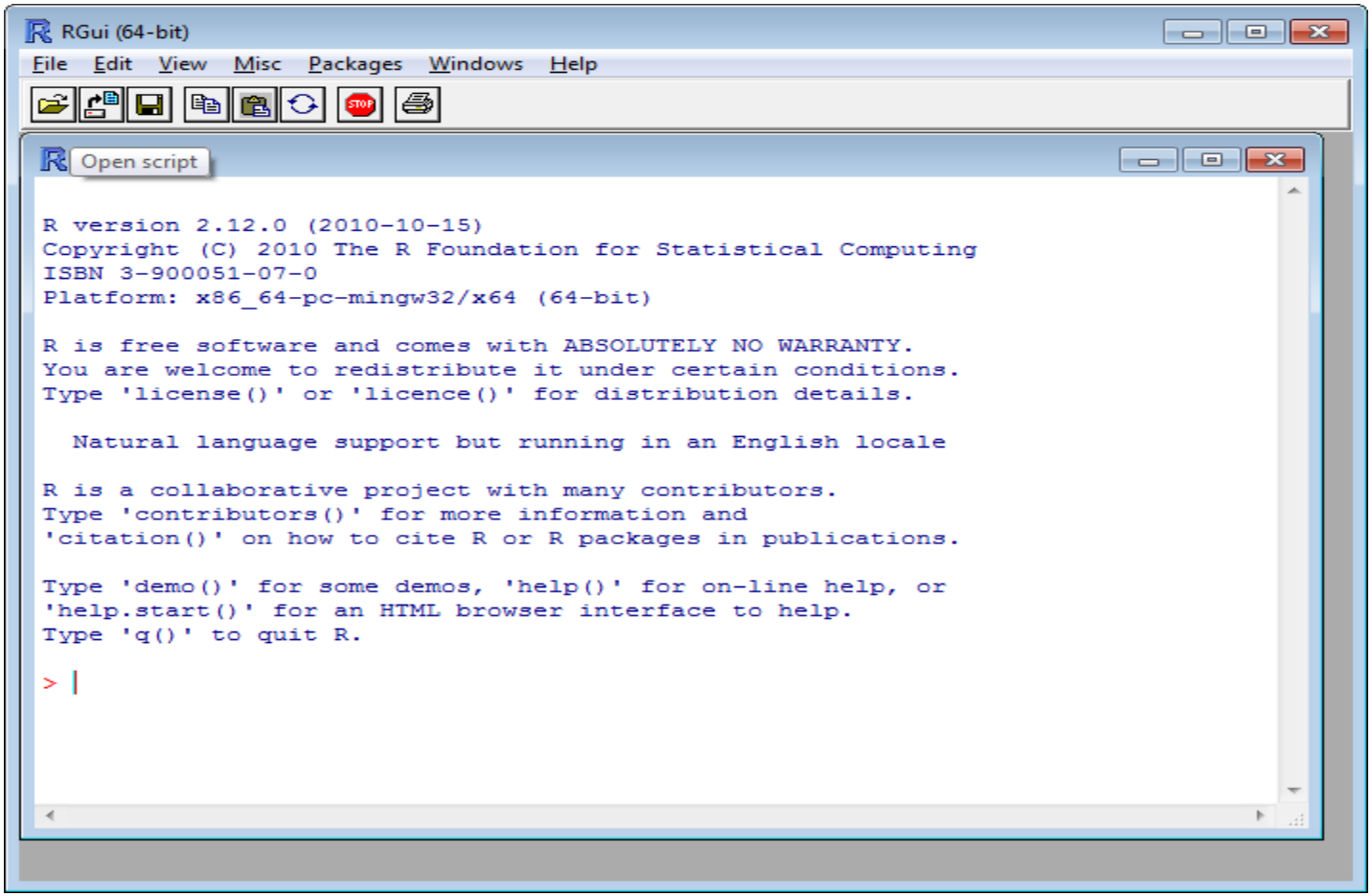
Where to download R?

- Use http://r-project.org or a CRAN mirror (http://cran.stat.ucla.edu)



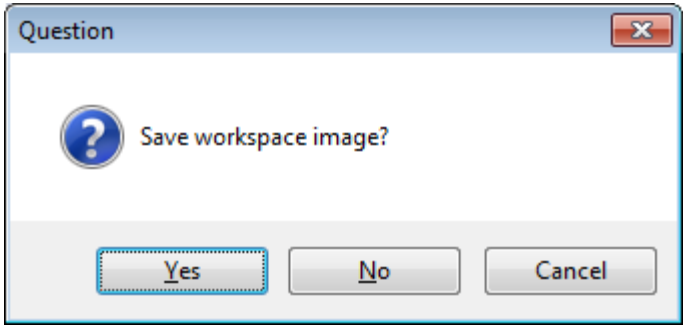


Starting Up…


RGui (64-bit)
File Edit View Misc Packages Windows Help
Open script
R version 2.12.0 (2010-10-15)
Copyright (C) 2010 The R Foundation for Statistical Computing
ISBN 3-900051-07-0
Platform: x86_64-pc-mingw32/x64 (64-bit)
R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.
Natural language support but running in an English locale
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
>

Stopping

- To end your session
  - Close window or q()
- What does this mean?

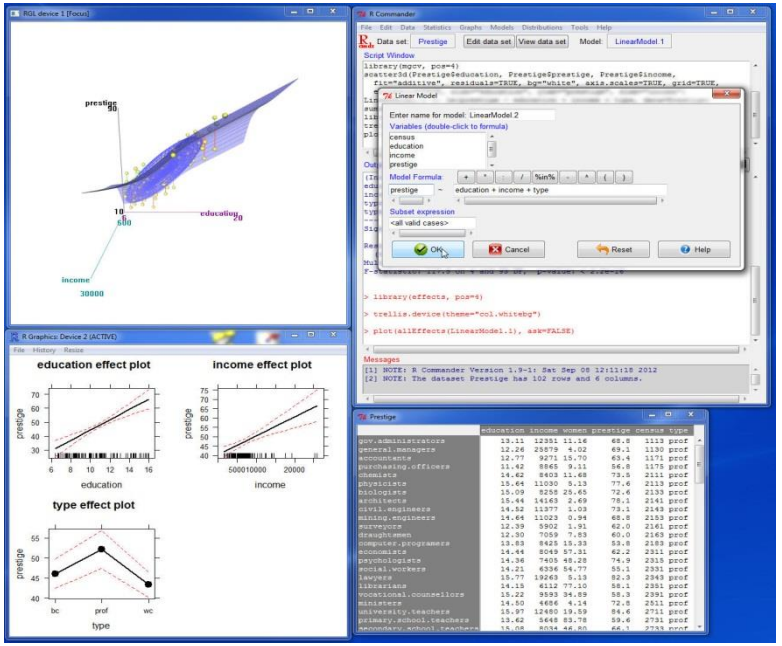


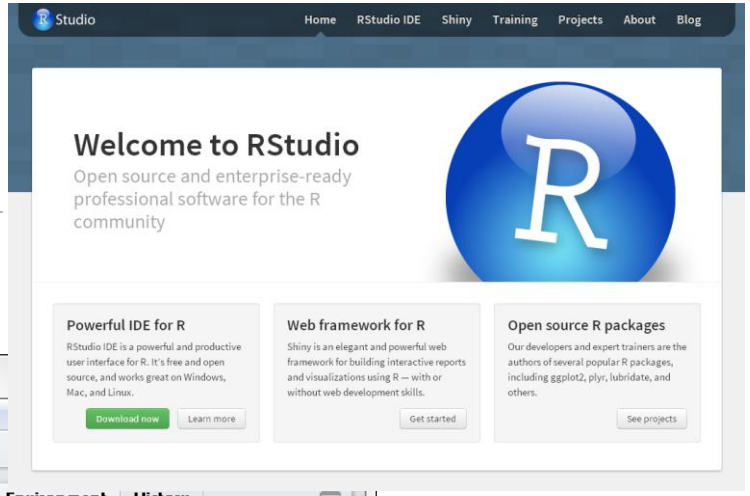
  - It saves everything you created (variables, etc) into a (hidden) file in the current directory usually named .Rdata

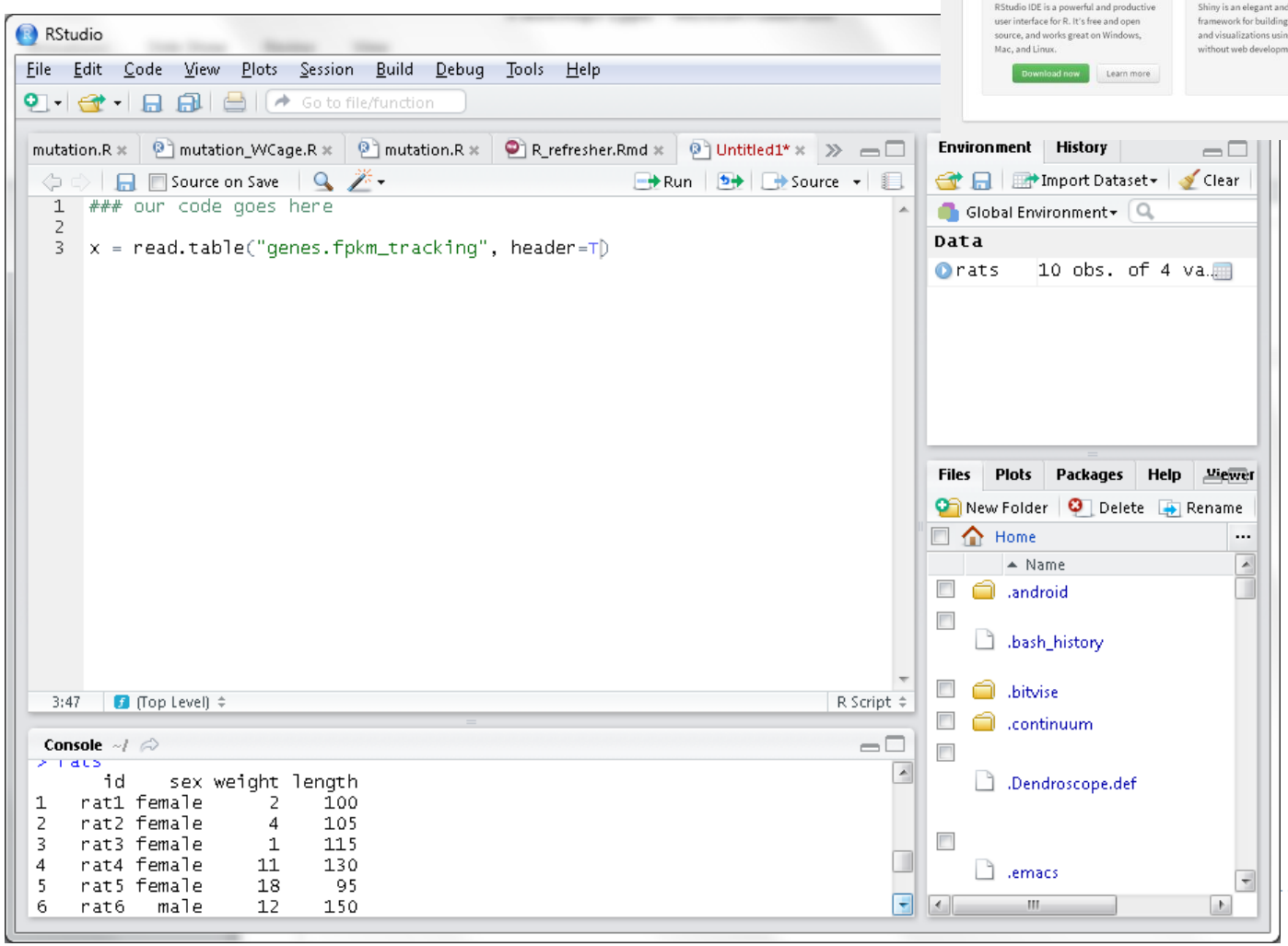
GUIs and IDEs

- R interface is pretty sparse
- Some alternatives:

	Win	Mac	Linux
RStudio	x	x	?
Rcommander	x	x	x
Tinn-R	x		
JGR	x	x	x
RKWard	x		x
Emacs/ESS	x	x	x
Vi	x	x	x
notepad	x	x	x




Studio
Home
RStudio IDE
Shiny
Training
Projects
About
Blog
Welcome to RStudio
Open source and enterprise-ready professional software for the R community
R
Powerful IDE for R
RStudio IDE is a powerful and productive user interface for R. It's free and open source, and works great on Windows, Mac, and Linux.
Download now
Learn more
Web framework for R
Shiny is an elegant and powerful web framework for building interactive reports and visualizations using R — with or without web development skills.
Get started
Open source R packages
Our developers and expert trainers are the authors of several popular R packages, including ggplot2, plyr, lubridate, and others.
See projects


RStudio
File Edit Code View Plots Session Build Debug Tools Help
Go to file/function
mutation.R
mutation_WCage.R
mutation.R
R_refresher.Rmd
Untitled1*
Source on Save
Run
Source
1 ### our code goes here
2
3 x = read.table("genes.fpkm_tracking", header=T)
3:47
(Top Level)
R Script
Console ~/
> rats
id sex weight length
1 rat1 female 2 100
2 rat2 female 4 105
3 rat3 female 1 115
4 rat4 female 11 130
5 rat5 female 18 95
6 rat6 male 12 150
Environment
History
Import Dataset
Clear
Global Environment
Data
rats 10 obs. of 4 va...
Files
Plots
Packages
Help
Viewer
New Folder
Delete
Rename
Home
Name
.android
.bash_history
.bitvise
.continuum
.Dendroscope.def
.emacs

It's like unix

- Many of the commands are similar to command line unix tools (cat, ls, grep, …)
- but in R, everything is a function so **()** is important!
  - cat()
  - ls()
- What happens if you forget the parentheses?
  - try it!

Finding help

```
> help("data.frame")
> ?data.frame
> help.search("chisquare")
> apropos("mean")
 [1] "colMeans"         "kmeans"           "mean"             "mean.data.frame"
 [5] "mean.Date"        "mean.default"     "mean.difftime"    "mean.POSIXct"
 [9] "mean.POSIXlt"     "rowMeans"         "weighted.mean"
```

Advice for learning R

- There are no easy ways to learn R except by
  1. Typing examples in yourself! It makes a difference (muscle memory, syntax)
  2. Persisting!
  3. Iterating!
- Steep learning curve, but with a few commands it can be useful quickly
- Try things out – you will not break your data!

A few things

- comments start with a hash tag (#) and are ignored by R. Great way to make notes!
- The prompt ">" is where you type commands, statements

```
> a = 1
```

- "+" is a continuation character; if your statement is not complete, R prompts you to finish it:

```
> a =
+ 3
> a
[1] 3
```

- Typing the variable name gives you its contents

```
> a
[1] 3
```

- Case matters! **A** is not the same as **a**

```
> A
Error: object 'A' not found
```

- Typing a function name without parens () gives the source code

If you get stuck …

- To interrupt
  - MAC: <CMD> <Option> <.> or <ESC>
  - PC/Linux: Ctrl-C
- Or push the red stop sign button
- Most useful when you accidentally start a loop or a very long running function

Getting around

- R starts in a particular directory, usually the one where R is located

```
# print the current working directory
getwd()
# set the current working directory
setwd("/home/rwang/project1")
# show the files in your current directory
dir()
```

- Create a directory for your project
  - good way to organize

Try it out

```
# genes.fpkm_tracking output of cufflinks
# it is tab delimited with a header line
# what happens if we say header=F?
x = read.table("genes.fpkm_tracking", header=T)
ls()
# what do the numbers in dim() mean?
dim(x)
names(x)
head(x)
class(x)
sum(x[,11] > 100)
sum(x$q1_FPKM > 100)
# try changing the axis limits "ylim" and printing character "pch"
plot(x[,11], x[,14], xlim=c(0, 10), ylim=c(0,20), xlab="exp", main="my
experiment", pch=2)
# try chaning the number of breaks
hist(x[,11], col="red", breaks=100)
cor.test(x[,11], x[,14])
newx = x[ x$status=="OK", ]
ls()
```

Indexing

- let's create a vector

```
a = c(1,2,3,4)
a[2] # gives 2, indexing in R start with 1 not 0!
a[1:3]
```

- create a matrix

```
m = matrix(c(1,2,3,4,5,6),  nrow=2, ncol=3)
m[,1]
[1] 1 2
m[,2] = 30
```

- logical indexing

```
x = 1:10
x > 5
[1] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
x[ x > 5]
[1]  6  7  8  9 10
```

Basic data structures in R

- vectors
- factors
- matrices and arrays
- lists
- environments
- data frames
- functions

Vectors

- Basically arrays

```
> v = 100
> v <- 100
> c(1,2,3)
> 1:3
> rep(1:2, 3)
> vector(mode="numeric", length=5)
```

- Vector Arithmetic

```
> 1 + 1:3
[1] 2 3 4
> 1:2 + 1:3 #what happens?
```

Vector Arithmetic

- Vector Arithmetic

```
> 1:2 + 1:3 #what happens? - ERROR!
> 1:2 + 1:10
[1]  2  4  4  6  6  8  8 10 10 12
```

- Vector indexing (1-based)

```
> b = 1:2 + 1:10
> b[1]
```

- Vector length

```
> length(b)
```

Factors

- Categorical variables
- not the same as character class

```
> col = c("red", "green", "red", "yellow", "red")
> class(col)
[1] "character"
> col.f = factor(col)
[1]  red       green    red       yellow  red
Levels:  green  red  yellow
> levels(col.f) = c("green", "red", "blue")
> col.f
[1] red   green red   blue  red
Levels: green red blue
> table(col.f)
col.f
green   red  blue
    1     3     1
```

Matrices

- Grid of numbers. Must be numeric!

```
>  x  <-  matrix(1:10,  nrow=2)
>  dim(x)
[1]  2  5
>  x
[,1]  [,2]  [,3]  [,4]  [,5]
[1,]       1       3       5       7       9
[2,]       2       4       6       8      10
>  as.vector(x)
[1]    1    2    3    4    5    6    7    8    9  10
> dim(x)
[1] 2 5

# hint: x[2,4] means get element from row 2, col 4
```

Data frames

- the most useful data structure
- data frames hold data like a spreadsheet
  - observations are rows
  - covariates are columns
- like matrices, they can be subsetted and indexed with two subscripts

Data frames

```
> df  =  data.frame(type=rep(c("case",  "control"),  c(2,  3)),
time=rexp(5))
>  df
      type       time
1     case  1.1745712
2     case  1.1691266
3  control  0.8227643
4  control  0.1301390
5  control  1.0581316
>  df$time
[1]  1.1745712  1.1691266  0.8227643
[4]  0.1301390  1.0581316
> df["time"]
```

Data frames

```
# let's update row names
>  names(df)
[1]  "type"  "time"
>  rn  <-  paste("id",  1:5,  sep="")
>  rownames(df)  <-  rn
>  df[1:2,  ]
     type  time
id1  case  1.174571
id2  case  1.169127
# update column names
> names(df) = c("var1", "var2")
> df[1:2,]
    var1 var2
id1 case 0.1653743
id2 case 0.4509330
```

Data type conversions

- Many problems are due to unexpected data types
  - eg. using a factor in place of a character string
- to convert from one data type to another, try

```
as.vector()
as.character()
as.data.frame()
as.numeric()
as.matrix()
```

- to determine what data type your variable is, try

```
class(variable)
```

Functions

- you can define your own functions

```
> square = function(x) {
+                 x*x
+                    }
> square(10)
[1] 100

> square(1:4)
[1]    1    4    9  16
```

- R functions take can take named and default parameters

```
say = function(word="hi", repeats=3) {
  cat( rep(word, repeats), "\n")
}
say()
say(word="hola", repeats=1)
say(repeats=2)
```

Reading in data

- A very common operation

```
> x = read.table("myfile.txt")
```

- Several variants: read.csv(), read.delim()

```
> x = read.table("myfile.txt", header=T, skip=1)
```

- this reads a delimited file into a data.frame object
- every line of the file must have the same number of elements!
  - sometimes you can fix things eg read.table("myfile.txt", sep="\t")
- entire file read into memory, so this can be slow but optimizations possible

Reading the help

```
read.table(file, header = FALSE, sep = "", quote = "\"'",
           dec = ".", row.names, col.names,
           as.is = !stringsAsFactors,
           na.strings = "NA", colClasses = NA, nrows = -1,
           skip = 0, check.names = TRUE, fill = !blank.lines.skip,
           strip.white = FALSE, blank.lines.skip = TRUE,
           comment.char = "#",
           allowEscapes = FALSE, flush = FALSE,
           stringsAsFactors = default.stringsAsFactors(),
           fileEncoding = "", encoding = "unknown")

read.csv(file, header = TRUE, sep = ",", quote="\"", dec=".",
         fill = TRUE, comment.char="", ...)

read.csv2(file, header = TRUE, sep = ";", quote="\"", dec=",",
          fill = TRUE, comment.char="", ...)

read.delim(file, header = TRUE, sep = "\t", quote="\"", dec=".",
           fill = TRUE, comment.char="", ...)

read.delim2(file, header = TRUE, sep = "\t", quote="\"", dec=",",
            fill = TRUE, comment.char="", ...)
```

Writing data

- Writing data to a file is pretty simple
- Some odd defaults need to be commonly overridden

```
write.table(x, file="file_name.txt", quote=F, sep="\t",
row.names=F, col.names=T)
```

- Other variants write.csv()

Saving and loading session

- all objects in your workspace can be saved to a file that can be read again on the next startup
- save() or save.image()
- the file is usually called .RData in your current directory
- load() will load an .RData file
- GUI might have these options

Some useful commands

- show a recent history of commands you typed
  - history()
- customizing your R
  - .Rprofile is a file found in your home directory where you can set defaults, define some commonly used functions, etc
- rm() – remove an object from workspace
- ls() – list the objects in your workspace
- cbind(array1, array2) – combine columns
- rbind(array1, array2) – combine rows
- t() – transpose a vector, matrix or data frame
- sessionInfo() – info about your settings

Match

- match returns a vector of the positions of (first) matches of its first argument in its second.

```
> df1 = read.table("df1.txt", header=T)
> df2 = read.table("df2.txt", header=T)
> match(df2$id, df1$id)
[1]  1  4  8  9 NA NA

# alternate syntax
> df2[,1] %in% df1[,1]
[1]  TRUE  TRUE  TRUE  TRUE FALSE FALSE
```

Merge

- Merge two data frames that have a common identifier

```
df1 = read.table("df1.txt", header=T)
df2 = read.table("df2.txt", header=T)
both = merge(df1, df2, by.x=1, by.y=1)
new = merge(df1, df2, by.x=1, by.y=1, all.x=T)
```

which

- which helps you find the index of an element

```
> a = 1:10
> which(a < 5)
[1] 1 2 3 4
> a[which(a < 5)]
[1] 1 2 3 4
> ids = which(a < 5)
[1] 1 2 3 4
> a[ids]
```

Special values

- NA (Not available)
  - sometimes data shows up as 'NA'
  - usually due to
    - missing data
    - conversion
  - **not** the same as zero (0) !
  - test with is.na(x)
- NaN (not a number)
  - 0/0
  - is.nan()
- Inf (infinite) or -Inf
  - 10/0
  - test with is.finite(x) or is.infinite(x)

NA/NAN/INF

```
#Test if any NaN
  sum(is.nan(df1[,1]))
#Test if any INF
  sum(is.finite(df1$id))
#Test if any NA's
  sum(is.na(df2))
#Find the col/row with the NA
res = is.na(df2)
> colSums(res)
    id    age weight
     0      0      1
> rowSums(res)
[1] 0 0 0 1 0 0
```

Logical operators

- Useful for chaining operations
  - | (OR), & (AND), ! (NOT)
    - for instance, you want values greater than 10 or less than 5

```
df[ df[,1] > 10 | df[,1] < 5]
df[ !is.na(df[,1])]
df[ df[,2] == "gene" & df[,1] > 10]
```

- == is the equal operator (not =, which assigns)

Flow control

- If statements for branching

```
if (x == 3){
    doSomething()
} else {
    doSomethingElse()
}
```

- loops
  - slow in R

```
a = seq(1,10)
for(i in 1:length(a)){
cat(a[i], "\n")
}
```

Apply

- R operations are usually vectorized, so loops are avoided.
- Loops are quite slow in R

```
mat = matrix(seq(1,10), 2)
# how to get rowwise or columnwise mean?
# could use a loop, but you have to specify dimension
# margin 1 = row, 2 = cols
apply(mat, 1, mean)
apply(mat, 2, mean)
```

Sorting

- Sorting returns an array in sorted order

```
> b = c(1,9,8,2,4,6)
> sort(b, decreasing=F)
```

- Ordering returns a vector of array indicies that puts the vector in a particular order
  - more useful for sorting data frames

```
> b = c(1,9,8,2,4,6)
b.order = order(b, decreasing=F)
> b.order
[1] 1 4 5 6 3 2
> b[b.order]
[1] 1 2 4 6 8 9
```

Reading in a script

- Suppose you've written a R script that processes your data
- source() will read it in as if you typed it and execute all commands listed in the file
- source("R_script_file.R")

Additional resources

- Many resources but sometimes difficult to access
  - R-bloggers.com
  - R-project.org – FAQ and manuals
  - bioconductor.org
  - UCLA ATS (http://www.ats.ucla.edu/stat/r/)
  - Quick R http://www.statmethods.net/index.html
  - http://onertipaday.blogspot.com/
  - http://wiki.stdout.org/rcookbook/
  - http://gettinggeneticsdone.blogspot.com/
  - manuals.bioinformatics.ucr.edu/workshops
- Help sites
  - stackoverflow.com
  - nabble.com
  - google
- Good free books
  - An Introduction to R (on r-project.org)
  - Using R

Additional resources

- Courses
  - Coursera
    - https://class.coursera.org/rprog-002
  - EdX.org
    - https://www.edx.org/course/harvardx/harvardx-ph525x-data-analysis-genomics-1401#.U0xFnvldW_g
  - Stanford Class
    - https://class.stanford.edu/courses/HumanitiesScience/StatLearning/Winter2014/about
  - Google YouTube
    - https://www.youtube.com/watch?v=iffR3fWv4xw&list=PLOU2XLYxmsIK9qQfztXeybpHvru-TrqAP
  - Bioconductor
    - http://www.bioconductor.org/help/events/

Shortcuts

- To interrupt
  - MAC: <CMD> <Option> <.> or <ESC>
  - PC/Linux: Ctrl-C

- sessionInfo()
  - this displays details about your environment, what packages are loaded, etc… useful for debugging

History

- 10/12/12
  - fixed smart quotes
  - fixed for loop example
- 7/9/13
  - rownames(df) instead of names(df)
  - Comment out t.test() example