



Introduction to R

วิชา การค้นพบองค์ความรู้และการทำเหมืองข้อมูลชั้นสูง

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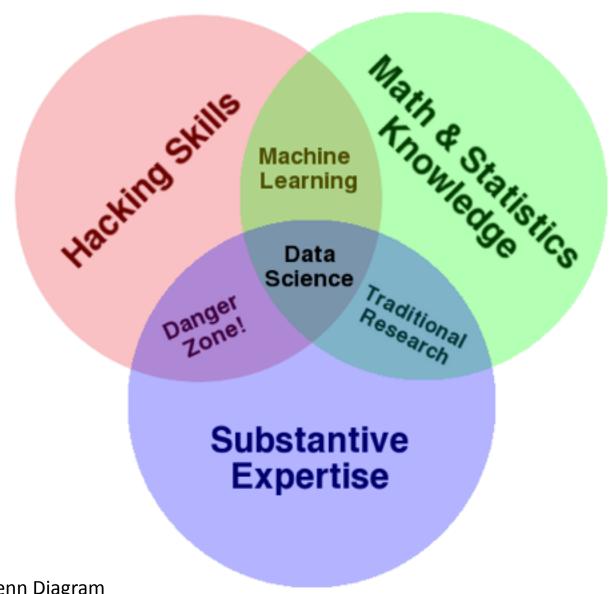
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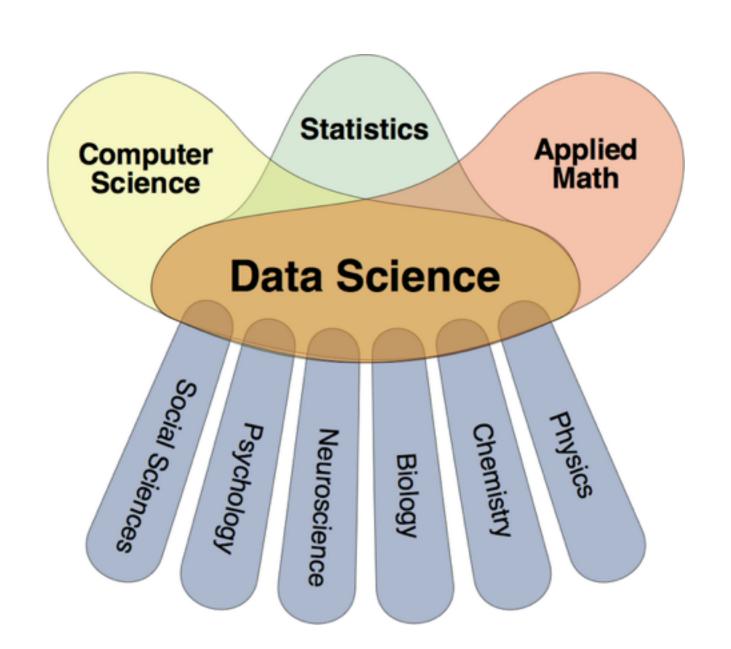


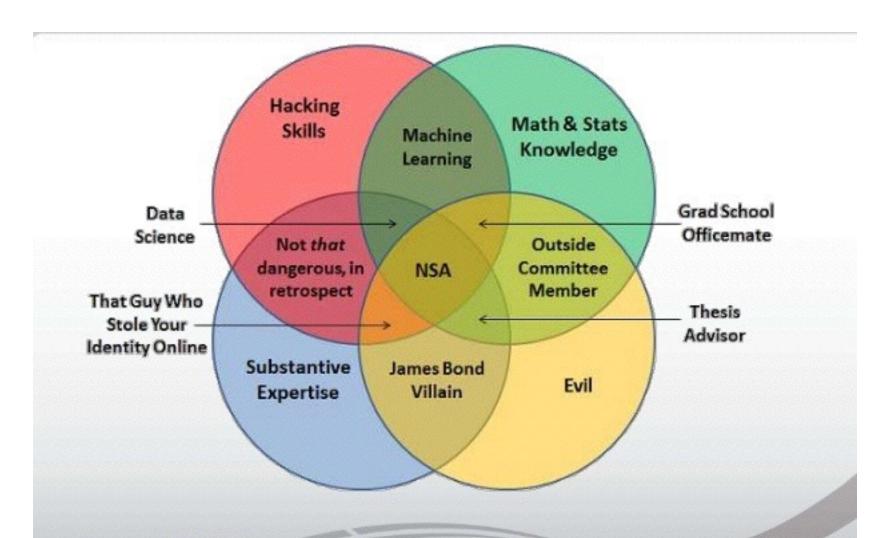
Slide and Sample Data

https://github.com/vkrit/chula_datamining

The beginner's perspective







http://joelgrus.com/2013/06/09/post-prism-data-science-venn-diagram

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What is R?

- R is a system for statistical computation and graphics.
- It is heavily influenced by the S language
- R was initially written by Ross Ihaka and Robert Gentleman at the Department of Statistics of the University of Auckland in Auckland, New Zealand.
- The "R Core Team" maintain the source code for the software and release regular updates

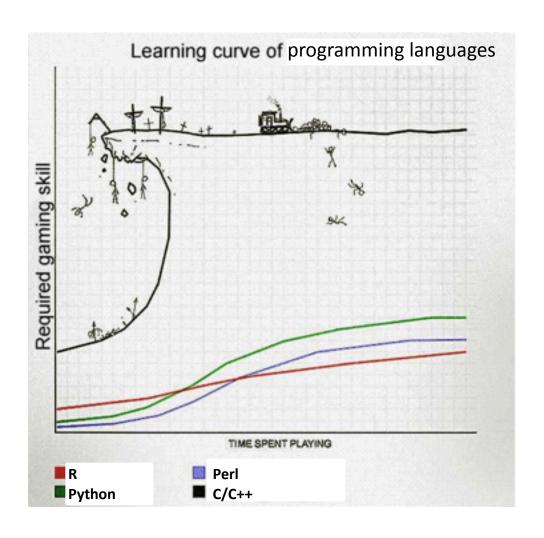
What is R?

- In addition, the R project is added to by many of its users, who write source code for many different types of analytical procedures
- Everything from analytical chemistry to epidemiology to linguistics
- Currently 4,045 different user--written libraries available

Why use R?

- R is Open-Source Software
- Many built-in functions and installable packages that will cover nearly every possible need
- R is an interpreted language
 - Code doesn't have to be compiled
- Interactive console makes testing and debugging easy
- Cons to using R
 - Slower than compiled languages
 - Can have runtime errors

Why use R?



Tools



R www.r-project.org

The engine*



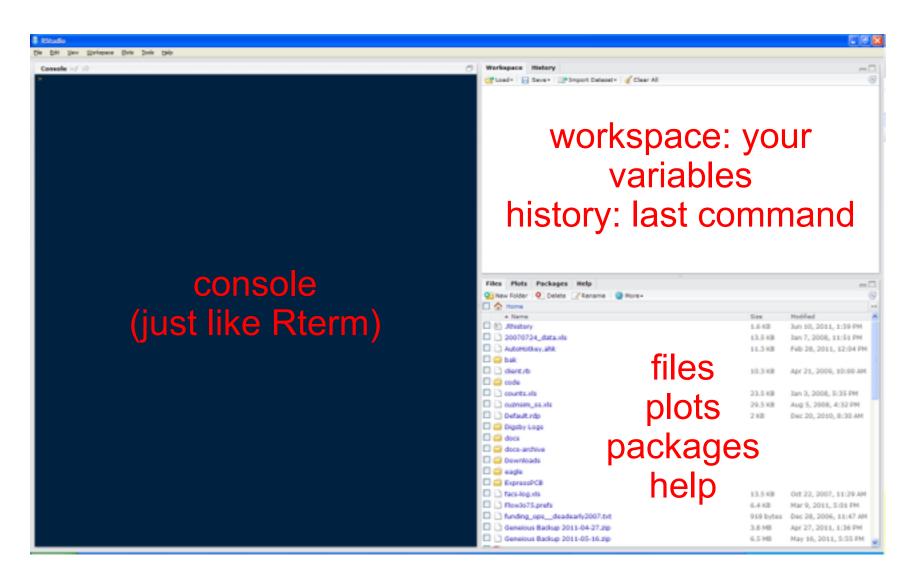
RStudio www.rstudio.org

The pretty face**

* Many alternatives exist. Smallest learning curve.

** A few alternatives exist. This happens to be the easiest at the moment.

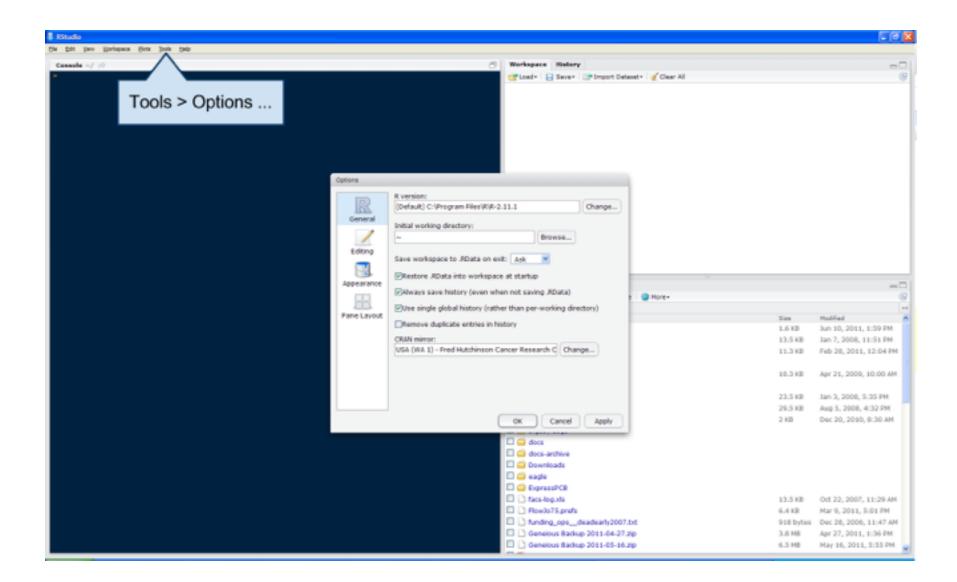
Introducing RStudio



RStudio Features

- Code completion
- Command history search
- Command history to R script / file
- Function extraction from Rscript
- Sweave support

Configuring RStudio



Choosing a CRAN Mirror

 CRAN mirrors contain the R packages that can extend the functionality of R

 Choose a mirror located close to you as that will most likely give you the fastest downloads

Choosing Repositories

- Repositories host the packages
 - CRAN, CRANextra, BioCsoft, BioCann, BioCexp,
 BioCext, Omegahat, R-Forge and rforge.net

Use this code to set your repositories

```
setRepositories()
```

setRepositories()

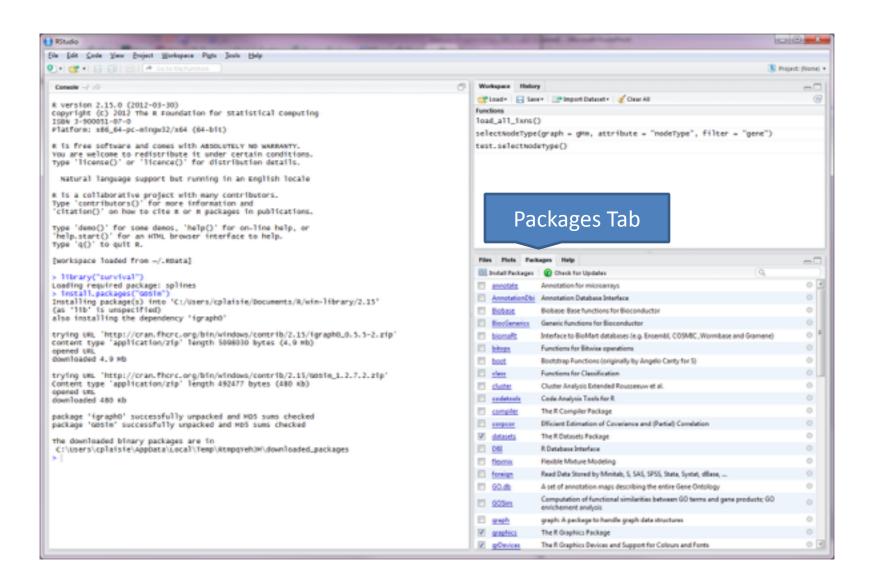
```
> setRepositories()
--- Please select repositories for use in this session ---

1: + CRAN
2: + CRAN (extras)
3: BioC software
4: BioC annotation
5: BioC experiment
6: BioC extra
7: Omegahat
8: R-Forge
9: rforge.net

Enter one or more numbers separated by spaces, or an empty line to cancel

1:
```

Packages Tab



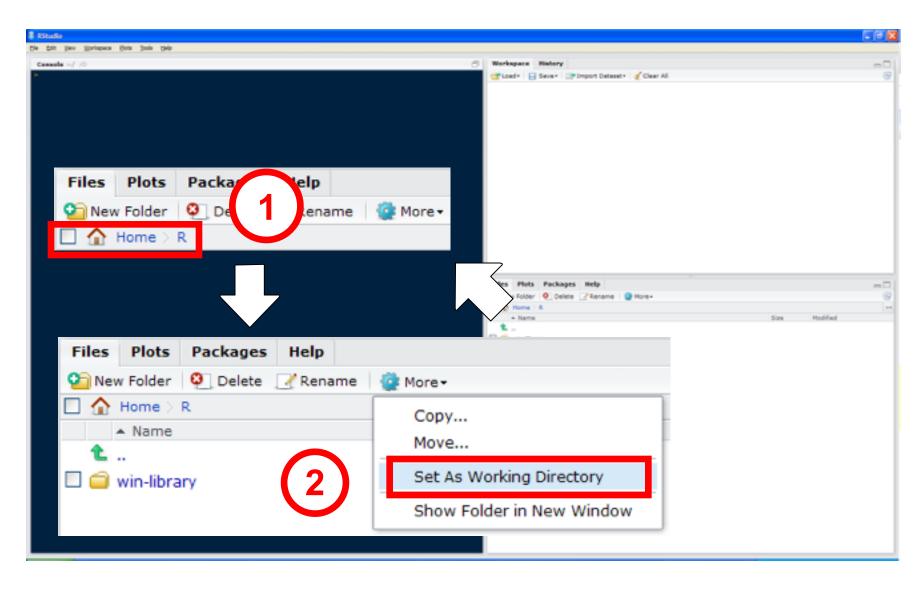
How do Packages Work?

Packages tab lets you see what packages are installed

- A package must be loaded before you can use it
 - In Rstudio this is accomplished by clicking the checkbox next to the package name in the package tab

We will be using different packages throughout this tutorial

Working Directory



Ready to Code!

 The working directory is where RStudio will look first for scripts

 Keeping everything in a self contained directory helps organize code and analyses

Check you current working directory with

```
getwd()
```

R as a Calculator

```
RStudio
 Edit View Workspace Plots Tools Help
Source
Console ≈/ Ø
                                                                       -0
> c(1+1,1-1,1*1,1/1)
[1] 2 0 1 1
> c(1&1,1|1,1&&1,1||1,1==1,1!=1)
[1] TRUE TRUE TRUE TRUE FALSE
                                                                                 Plots I
                                                                            win-library
```

Basic Math / Basic Logic

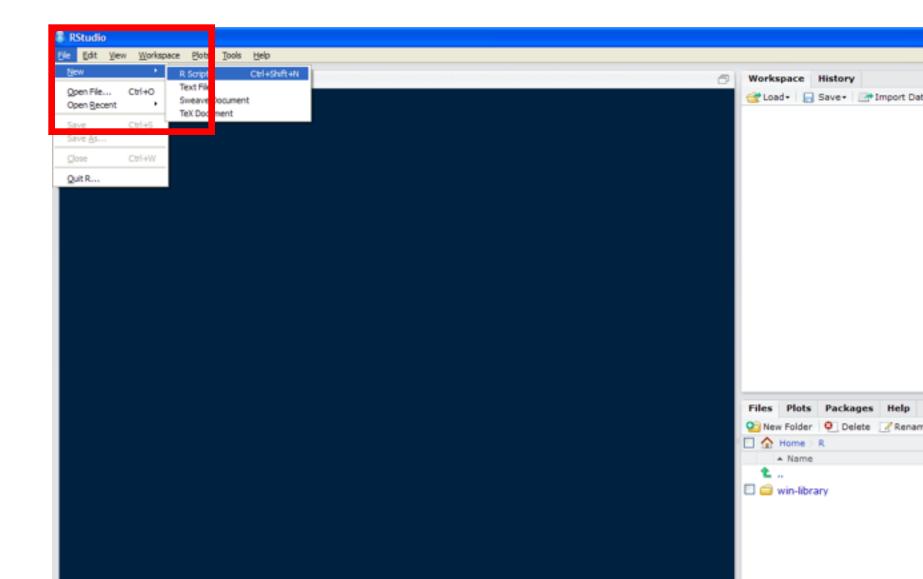
- + addition
- subtraction
- * multiplication
- / division
- % modulus (remainder)
- ^ to the power

?Arithmetic

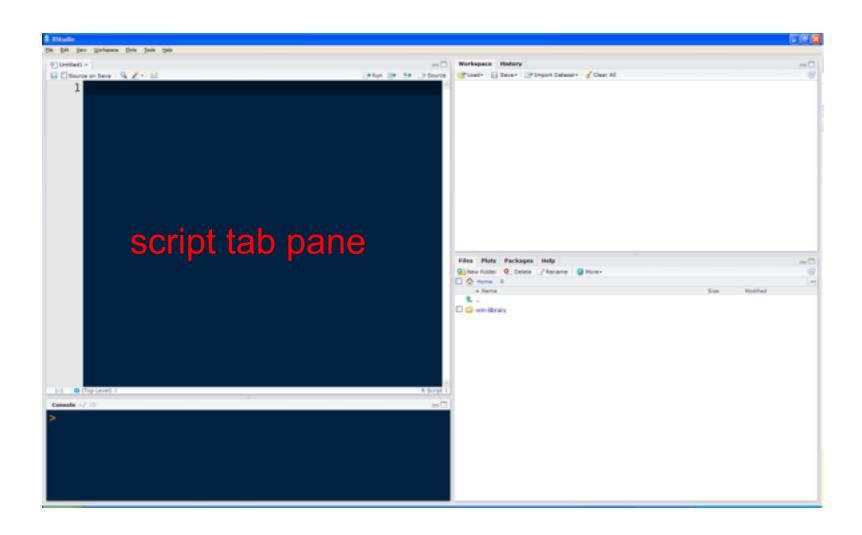
- ! NOT
- & bitwise AND
- | bitwise OR
- && short circuit AND
- || short circuit OR
- == equality
- != NOT equality

?Logic

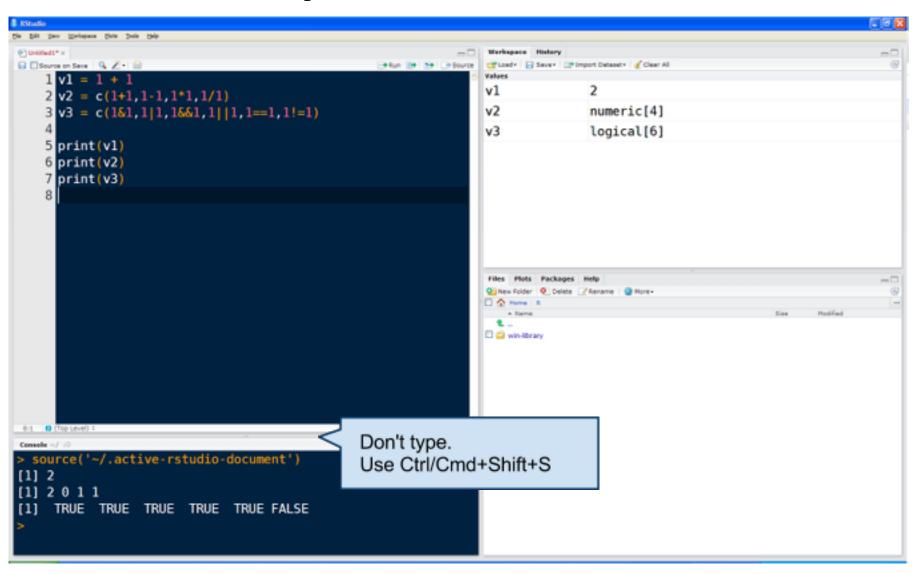
Make New R Script

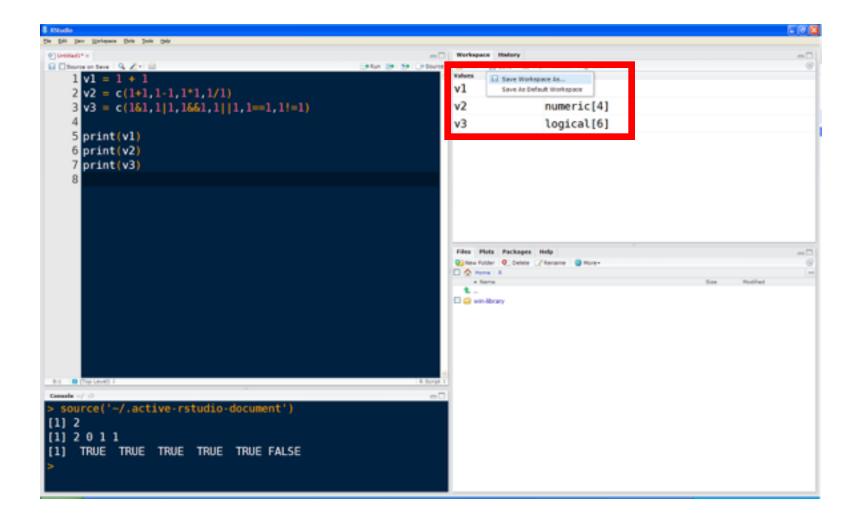


Make New R Script



Run Script Loaded in RStudio





Saving Your Workspace

 In R you can save your entire workspace, variables and all in its current state

 Then you can reload this at a later time or can provide this to collaborators

Workspace data files are saved with the extension '.Rdata'

Getting Help

- Inside of R
 - Simplify make a fake dataset
 - help(<function name>)
 - Help.start()
 - ?<function name>
 - ??<search term>
- On the web
 - <u>www.rseek.org</u> and R only search engine
 - CRAN
 - Google topic with CRAN

Creating Variables

- Named containers for data
- Names can be anything you like except for 'special' words
 - if else repeat while function for in next break
 - TRUE FALSE NULL Inf NaN NA NA_integer_ NA_real_ NA_complex_ NA_character_
- Better if names describe what the stored data is Creating / Setting variables is a matter of equality:

```
var = somedata
var <- somedata</pre>
```

Difference between = and <-

- The operators <- and = assign into the environment in which they are evaluated.
- The operator <- can be used anywhere, whereas the operator = is only allowed at the top level (e.g., in the complete expression typed at the command prompt) or as one of the subexpressions in a braced list of expressions.

```
matrix(1,nrow=2)
matrix(1,nrow<-2)</pre>
```

Data Types in R

- R's atomic data type is the vector
 - numeric
 - floating point
 - integer
 - logical
 - character
- functions
- lists
 - let you combine other data types

R as calculator

$$> pi * 2^3 - sqrt(4)$$

> factorial(4)

Reading and Getting Data into R

Combine Command

```
    c(1, 2, 3, 4)
    c(item1, item2, item3, item4)
    c("item1", "item2", "item3")
```

Scan Command

```
    our.data = scan()
    scan(what = 'character')
    data5 = scan(sep = ',', what = 'char')
    data6 = scan(file = 'data.txt')
```

Working Directory

- ➤ getwd()
- >> setwd('pathname')

Reading Bigger Data Files

- ➤read.csv()
- > read.csv(file, sep = ',', header = TRUE, row.names)
- >= fw = read.csv(file.choose())
- my.ssv = read.table(file.choose(), header = TRUE)
- my.tsv = read.delim(file.choose())
- >my.tsv = read.csv(file.choose(), sep = '\t')
- >my.tsv = read.table(file.choose(), header = TRUE,
 sep = '\t')

Convert between number and text data

- > cut2 = as.character(cut)
- >cut3 = as.factor(cut2)
- \rightarrow data7i = as.integer(data7)
- >>data7n = as.numeric(data7i)

Data Frames

• 2 Dimensional Objects, it has rows and columns. R treats the columns as separate samples or variables, rows represent the replicates or observations.

```
> grass species cut
1 12 mow
2 15 mow
3 17 mow
4 11 mow
5 15 mow
6 8 unmow
7 9 unmow
9 9 unmow
```

Matrix Objects

 A matrix is a two-dimensional data object. At first glance a matrix looks just like a data frame:

> bird					
	Garden	Hedgerow	Parkland	Pasture	Woodland
Blackbird	47	10	40	2	2
Chaffinch	19	3	5	0	2
Great Tit	50	0	10	7	0
House Sparrow	46	16	8	4	0
Robin	9	3	0	0	2
Song Thrush	4	0	6	0	0

Structure of Objects

- >str()
- ➤ To Examine the structure of an object

- >>class()
- ➤ Tell you the class of object

Saving Data Files to Disk

- save()
- ➤ save(list, file = 'filename')
- > save(bf, bf.lm, bf.beta, file = 'desktop/ butterly.rdata')
- ➤ save(list = ls(pattern ='^bf'), file = 'desktop/ butterfly.rdata')
- ➤ save(list = ls(all=TRUE), file='filename')
- ➤ save.image(file='filename')

Reading Data Files from Disk

- load(file='filename.Rdata')
- load(file=file.choose())

Save Data to disk as text files

write(x, file="data", sep=".")

Save Data Frame or Matrix

 write.table(mydata, file='filename', row.names=TRUE, sep=' ', col.names=TRUE)

Selecting and displaying parts of a vector

COMMAND	RESULT		
data1[1]	Shows the first item in the vector.		
data1[3]	Shows the third item.		
data1[1:3]	Shows the first to the third items.		
data1[-1]	Shows all except the first item.		
data1[c(1, 3, 4, 8)]	Shows the items listed in the $c()$ part.		
data1[data1 > 3]	Shows all items greater than 3.		
data1[data1 5 data1 > 7]	Shows items less than 5 or greater than 7.		

Sorting and rearranging a vector

- >>sort()
- ➤sort(unmow, decreasing =TRUE)

Get an Index using order()

> order(unmow)

Logical Values from a vector

- data1 = c(3, 5, 7, 3, 2, 6)
- which(data1 == 6)

- Quicklooks
- head(mf)
- head(mf, n = 3)

Give simple Stat

summary(bird.m)

Rotating Data Tables

• fw.t = t(fw)

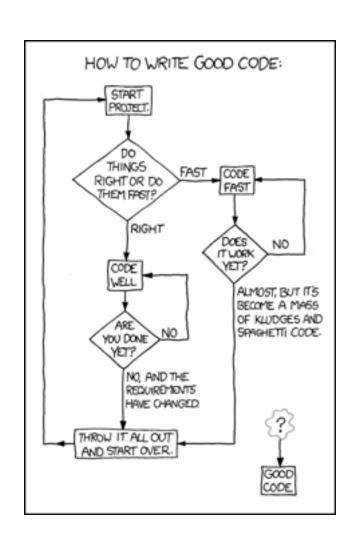
Making Data Frames

My.frame = data.frame(item1, item2, item3)

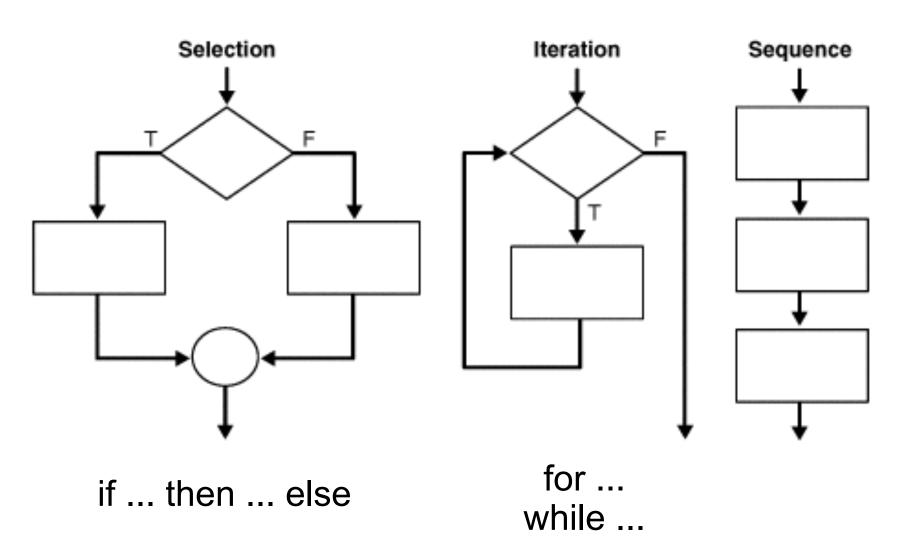
Making Matrix Objects

cmat = cbind(sampl1, sampl2)

Coding



Programmatic Structure



For Loop

- Repeats a line or lines (known as a block) of code until:
 - (for loop) a count limit is reached

```
for (i in 1:10) {
    ... code ...
}
```

- the above loop runs 10 times
- '{' and '}' enclose code looped
- the variable i updated in the loop to values in the sequence 1:10

A Simple For Loop

```
# P-values from our analysis
p.values = c(0.1, 0.05, 0.003, 0.4, 0.9)
# A vector to store the negative log p-values
neglog10.p.values = 1:5
# Transform the p-values
for(p in 1:length(p.values)) {
 neglog10.p.values[p] = -log10(p.values[p])
```

While Loop

- Repeats a line or lines (known as a block) of code until:
 - (while loop) a logical condition is reached

```
while (stop != TRUE) {
   ... code ...
}
```

- the above loop runs until code sets
- stop = TRUE
- warning: if not properly written while loops can run infinitely

A Simple While Loop

```
# Numbers from our analysis
v1 = c(21, 22, 53, 74, 85, 96, 97, 58, 49, 30, 85)
# Iterator
i = 1
# Look for first instance of 85
while(v1[i] != 85) {
      i = i + 1
# Print out where we found it
print(paste('v1[',i,'] = 85',sep=''))
```

Functions

- Bits of code that do one thing and (preferrably) do it well
- Functions break up your code into more manageable and reusable parts
- Defining (e.g. in a script):

```
fun = function(arguments) {
    ... code ...
}
```

Calling:

```
party = fun(food, beer, folks)
```

A Simple Function

```
fn1 <- function(N) {
    for(i in as.numeric(1:N)) {
        y <- i*i
fn2 <- function(N) {
    i = 1
    while(i <= N) {</pre>
        y <- i*i
        i <- i + 1
system.time(fn1(60000))
system.time(fn2(60000))
```

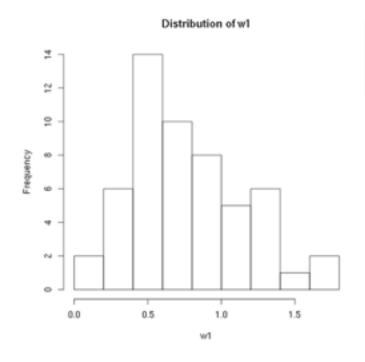
Basic Plots

```
> w1 <- read.csv(file="w1.dat",sep=",",head=TRUE)</pre>
> names(w1)
[1] "vals"
> tree <- read.csv(file="trees91.csv",sep=",",head=TRUE)</pre>
> names(tree)
 [1] "C"
              "N"
                       "CHBR"
                                "REP"
                                         "LFBM"
                                                  "STBM"
                                                           "RTBM"
                                                                    "LFNCC"
 [9] "STNCC" "RTNCC" "LFBCC" "STBCC" "RTBCC" "LFCACC" "STCACC" "RTCACC"
[17] "LFKCC" "STKCC" "RTKCC" "LFMGCC" "STMGCC" "RTMGCC" "LFPCC" "STPCC"
[25] "RTPCC" "LFSCC" "STSCC" "RTSCC"
```

- > stripchart(w1\$vals,vertical=TRUE)
 > stripchart(w1\$vals,vertical=TRUE,method="jitter")

Histogram

- > hist(w1\$vals)
- > hist(w1\$vals,main="Distribution of w1",xlab="w1")



> title('Leaf BioMass in High CO2 Environment', xlab='BioMass of Leaves')

Boxplot

```
> boxplot(w1$vals)
```

Scatter Plot

```
> plot(tree$STBM, tree$LFBM)
> cor(tree$STBM, tree$LFBM)
[1] 0.911595
```

Vignettes

- Some packages have vignettes
 - A vignettes is an example of how to run the code and a lot of additional text explaining a lot more that you may want to know
- List all available vignettes:

```
vignette()
```

Display the vignette as a pdf by executing

```
vignette('<topic>')
```

To play with the vignette code

```
vig = vignette('<topic>')
edit(vig)
```

More tutorial

- http://swirlstats.com/
- http://cran.r-project.org/doc/manuals/Rintro.html