



BIMM 143
Data analysis with R
Lecture 4
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UC San Diego
<http://thegrantlab.org/bimm143>

Today's Learning Goals

- Familiarity with R's basic **syntax**.
- Familiarity with major R **data structures**.
- Understand the basics of using **functions**.
- Be able to use R to **read** comma-separated value (csv) formatted files ready for subsequent analysis.
- Appreciate how you can use R **scripts** to aid with reproducibility.



What is R?

R is a freely distributed and widely used programming **language** and **environment** for statistical computing, data analysis and graphics.

R provides an unparalleled interactive environment for data analysis.

It is script-based (*i.e.* driven by computer code) and not GUI-based (point and click with menus).



```
R console R
R version 3.2.2 (2015-08-14) -- "Fire Safety"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (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.
```

<http://cran.r-project.org>

The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, Windows and Mac users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2018-07-02, Feather Spray) [R-3.5.1.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.

```
4. sandbox (R)
pico: sandbox> R

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Type 'q()' to quit R.

> ← This is the R prompt
```

```
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'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Type "R" in your terminal

This is the R prompt: Type q() to quit!

What R is NOT

- A performance optimized software library for incorporation into your own C/C++ etc. programs.
- A molecular graphics program with a slick GUI.
- Backed by a commercial guarantee or license.
- Microsoft Excel!

What about Excel?

- Data manipulation is easy
- Can see what is happening
- **But:** graphics are poor
- Looping is hard
- Limited statistical capabilities
- Inflexible and irreproducible
- There are many many things Excel just cannot do!



Use the right tool!

54 Christie Bahlai @cbahlai · 2h
 Weekly plug for scripted analyses:

Coauthor: "Can you change x,y,z about the analysis?"
 Me [not crying]: "Yes." [changes 2 lines of code]

RETWEETS 11 FAVORITES 7

Rule of thumb: Every analysis you do on a dataset will have to be redone 10–15 times before publication. Plan accordingly!

Why use R?

Productivity
Flexibility
Designed for data analysis

R is designed specifically for data analysis

- Large friendly user and developer community.
- As of Jan 6th 2019 there are 13,645 add on **R packages** on **CRAN** and 1,649 on **Bioconductor** - much more on these later!
- Virtually every statistical technique is either already built into R, or available as a free package.
- Unparalleled data analysis environment for **high-throughput genomic data**.

Modularity	Core R functions are modular and work well with others
Interactivity	R offers an unparalleled exploratory data analysis environment
Infrastructure	Access to existing tools and cutting-edge statistical and graphical methods
Support	Extensive documentation and tutorials available online for R
R Philosophy	Encourages open standards and reproducibility

Modularity	Core R functions are modular and work well with others
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Modularity

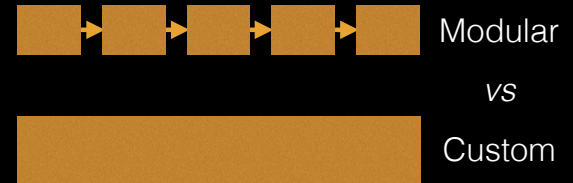
R was designed to allow users to interactively build complex workflows by interfacing smaller **'modular' functions** together.

get.seq() → hmmer() → pdbaln() → pdbfit() → pca() → plot()

An alternative approach is to write a **single complex program** that takes raw data as input, and after hours of data processing, outputs publication figures and a final table of results.

All-in-one custom 'Monster' program

Which would you prefer and why?



Advantages/Disadvantages

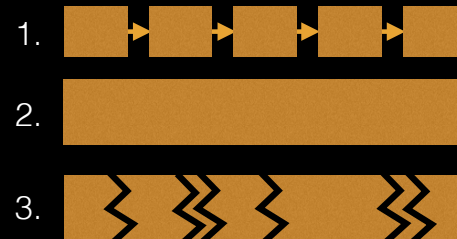
The 'monster approach' is **customized to a particular project** but results in **massive, fragile** and difficult to modify (therefore **inflexible, untransferable, and error prone**) code.

With **modular workflows**, it's easier to:

- **Spot errors** and figure out where they're occurring by inspecting intermediate results.
- **Experiment** with alternative methods by swapping out components.
- **Tackle novel problems** by remixing existing modular tools.

'Scripting' approach

Another common approach to bioinformatics data analysis is to write individual scripts in Perl/ Python/ Awk/ C etc. to carry out each subsequent step of an analysis



This can offer many advantages but can be challenging to make robustly modular and interactive.

Interactivity & exploratory data analysis

Learning R will give you the freedom to explore and experiment with your data.

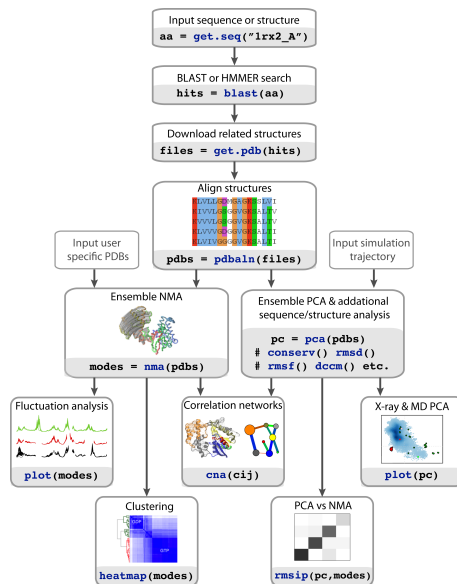
“Data analysis, like experimentation, must be considered as a highly interactive, iterative process, whose actual steps are selected segments of a stabbily branching, tree-like pattern of possible actions”. [J. W. Tukey]

Interactivity & exploratory data analysis

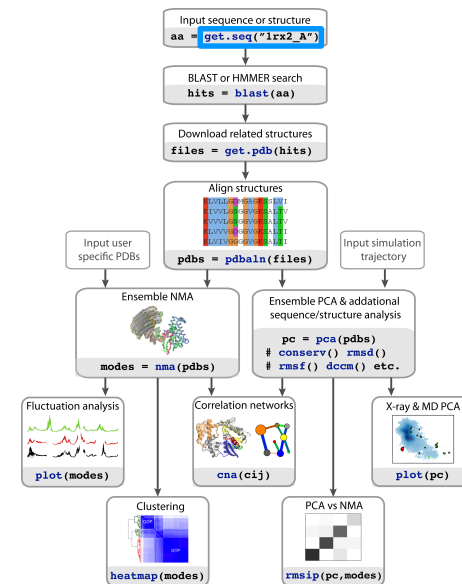
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Bioinformatics data is intrinsically **high dimensional** and frequently ‘messy’ requiring **exploratory data analysis** to find patterns - both those that indicate interesting biological signals or suggest potential problems.



R Features = functions()



How do we use R?

Two main ways to use R

```
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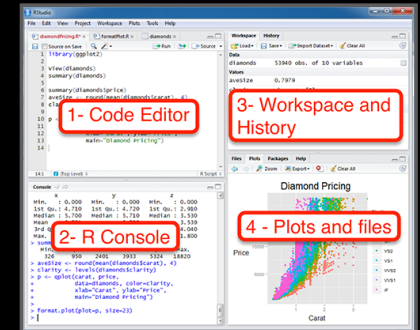
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> |
```

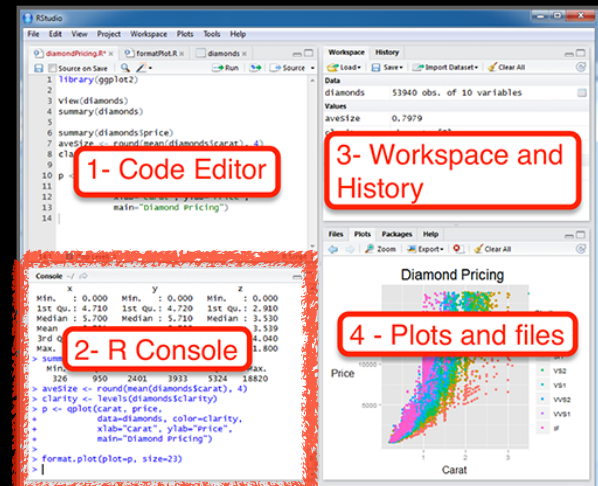
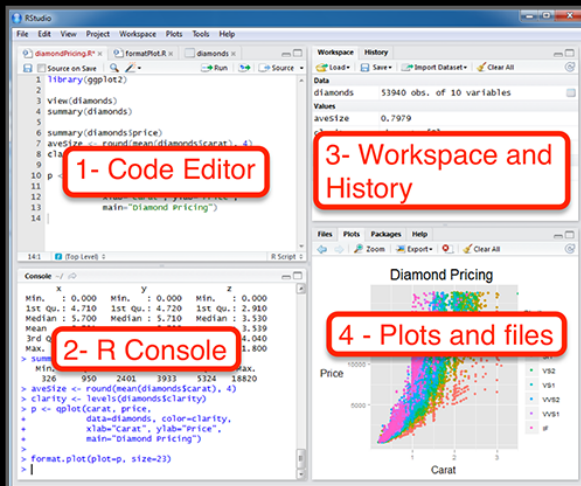


1. Terminal

2. RStudio

We will use RStudio today

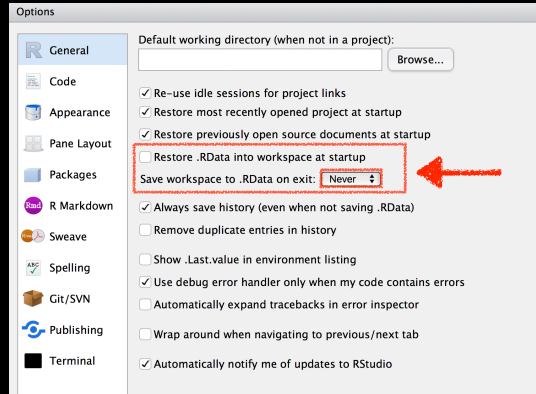
Lets get started...



Tools > Global Options

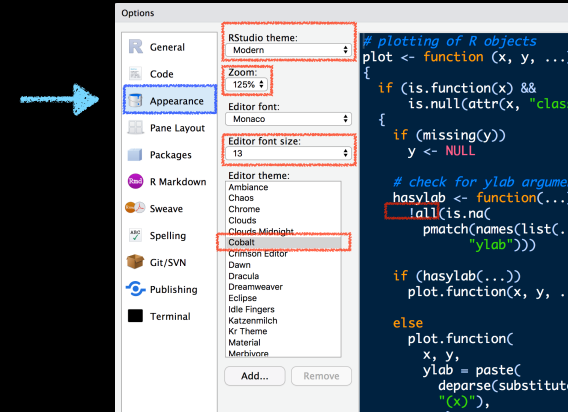
Do it Yourself!

- We will **NOT** save our workspace...



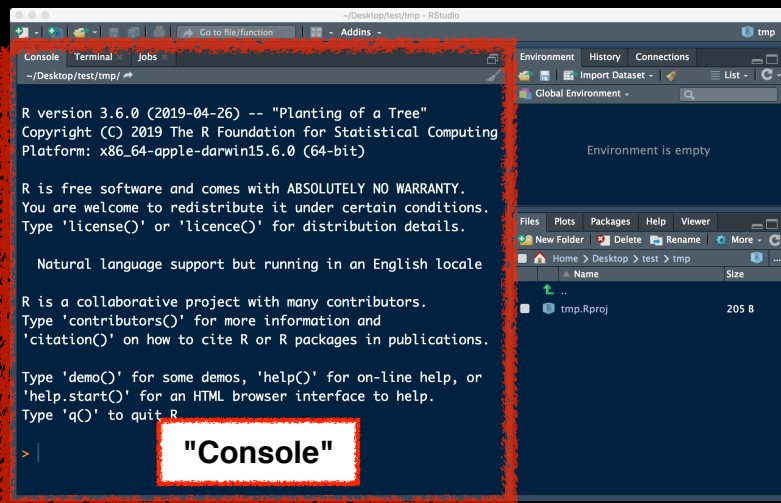
Tools > Global Options

- [Optional] Change to dark **Appearance** and increase font size, etc. ..



Lets get started...

Do it Yourself!

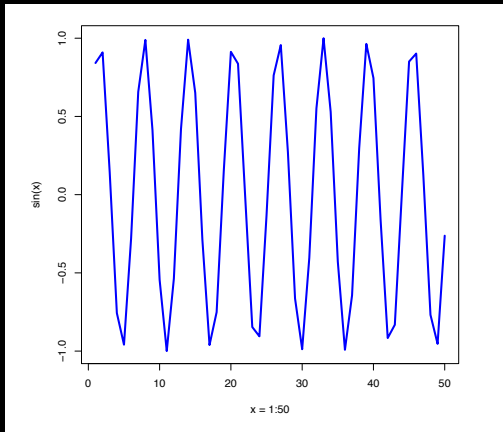


Some simple R commands

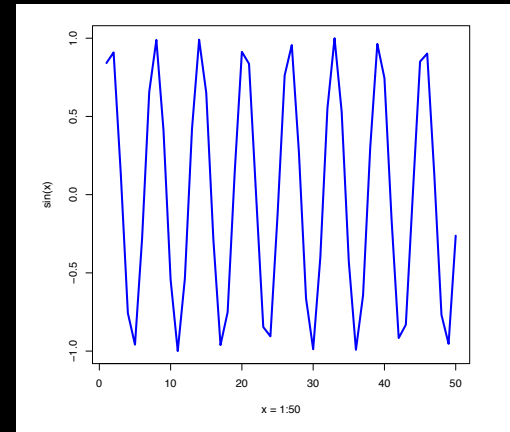
Do it Yourself!

- R prompt, don't type this!
- `>` `2+2`
[1] 4 **Result of the command**
 - `>` `3^2`
[1] 9
 - `>` `sqrt(25)`
[1] 5
 - `>` `2*(1+1)`
[1] 4
 - `>` `2*1+1` **Order of precedence**
[1] 3
 - `>` `exp(1)`
[1] 2.718282
 - `>` `log(2.718282)`
[1] 1
 - `>` `log(10, base=10)` **Optional argument**
[1] 1
 - `>` `log(10, base = 10)` **Incomplete command**
[1] 1
 - `>` `x=1:50`
`>` `plot(x, sin(x))`

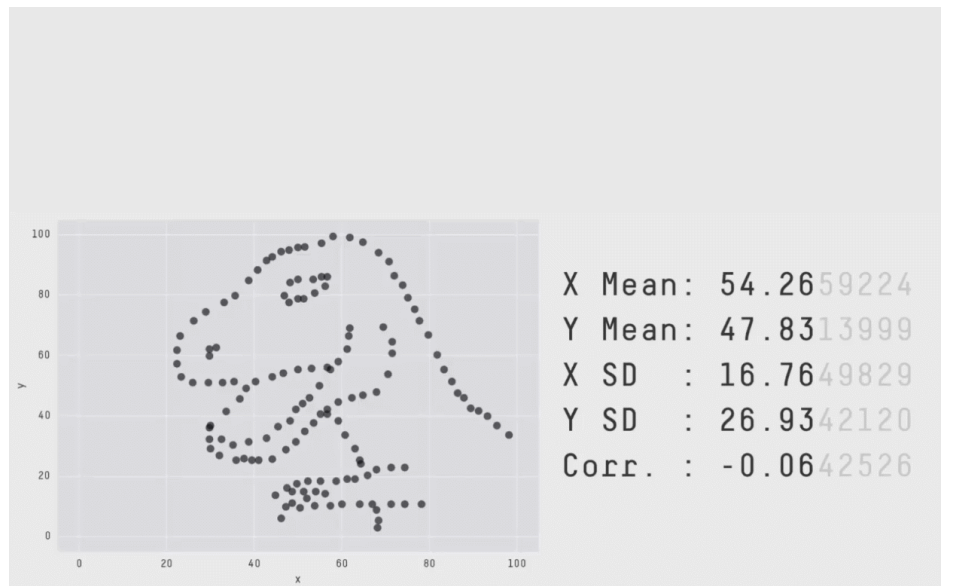
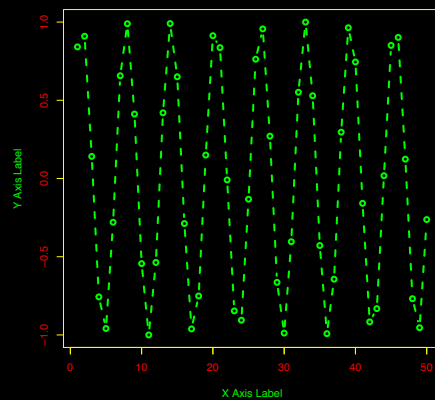
Does your plot look like this?



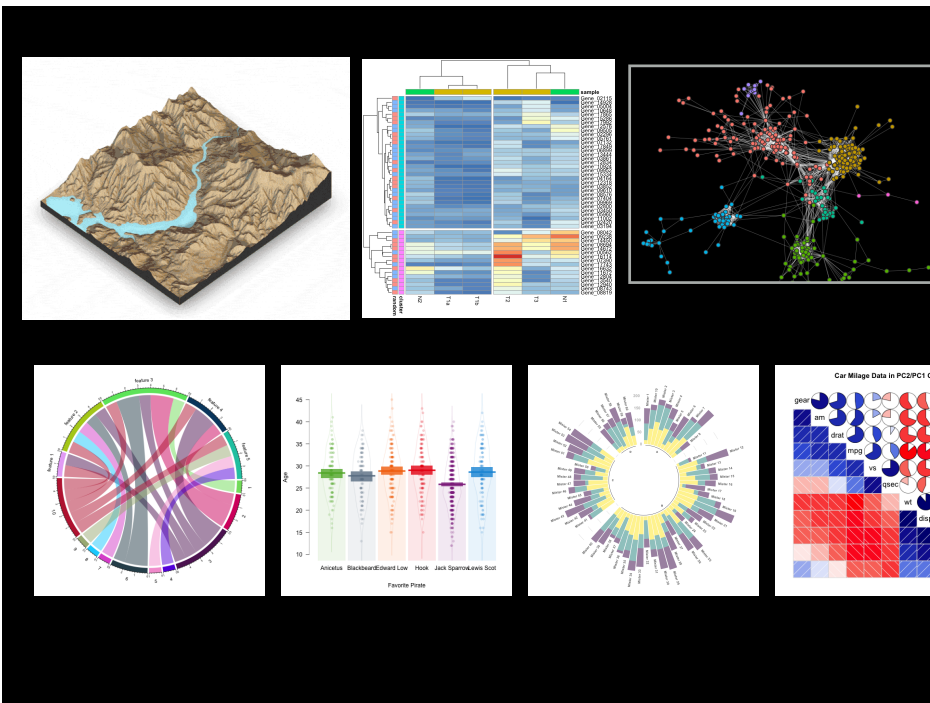
```
plot(x, sin(x), typ="l", col="blue", lwd=3, xlab="x = 1:50")
```



Options: `?plot` `?plot.default`



Key point: You need to visualize your data!



Error Messages

Sometimes the commands you enter will generate errors. Common beginner examples include:

- Incomplete brackets or quotes *e.g.*

```
((4+8)*20 <enter>
```

+

This returns a + here, which means you need to enter the remaining bracket - R is waiting for you to finish your input. Press **<ESC>** to abandon this line if you don't want to fix it.
- Not separating arguments by commas *e.g.*

```
plot(1:10 col="red")
```
- Typos including miss-spelling functions and using wrong type of brackets *e.g.*

```
exp{4}
```

Do it Yourself!

Your turn!

https://bioboot.github.io/bimm143_W20/class-material/04_rintro/

If you have done the introductory DataCamp course then feel free to jump to section #3 *Object Assignment*

Topics Covered:

Calling Functions
Getting help in R
Vectors and vectorization
Workspace and working directory
RStudio projects

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Vectors

- Vectors are the most basic data structure in R
- All elements of a vector must be the same type

```
dbl_var <- c(1, 2.5, 4.5)  
log_var <- c(TRUE, FALSE, T, F)  
chr_var <- c("these are", "some", "strings")
```

- When you attempt to combine different types they will be coerced to the most flexible type.

```
var <- c(1, "G", "4", 0.05, TRUE)
```

Names

- You can name a vector in several ways:
 - When creating it: `x <- c(a = 1, b = 2, c = 3)`
 - By modifying an existing vector in place:

```
x <- 1:3; names(x) <- c("a", "b", "c")
```

- You can then use the names to access a subset of vector elements:

```
x [ c("b", "a") ]
```

Why is this useful?

- Because if you know the name (i.e. your label) then you don't have to remember which element of a vector the data you are after was stored in. Consider this *fictional* example:

```
> grades <- c(alice=80, barry=99, chandra=60, chris=100)
> grades["barry"]
barry
 99
> which.max(grades)
chris
 4
> sort(grades)
chandra alice barry chris
 60    80    99    100
```

R has many data structures

These include:

- **vector**
- **data frame**
- **list**
- **matrix**
- **factors**

data.frame

- **data.frame** is the *de facto* data structure for most **tabular data** and what we use for statistics and plotting with **ggplot2** - more on this later!
- Arguably the most important R data structure
- Data frames can have additional attributes such as **rownames()** and **colnames()**, which can be useful for annotating data, with things like **subject_id** or **sample_id**

data.frame continued...

Do it Yourself!

- Created with the function **data.frame()**

```
dat <- data.frame(id = letters[1:10], x = 1:10, y = 11:20)
```

- Or more commonly when reading delimited files (*i.e.* **importing data**) with the functions **read.csv()**, **read.table()**, **read_xlsx()** *etc...*

```
dep <- read.csv2("http://bio3d.uib.no/data/pdb_deposition2.csv")
```

- R Studio can do this for you via:
File > Import Dataset > From CSV...

Useful **data.frame** Functions

- **head()** -and **tail()** shows first 6 rows and last 6 rows respectively
- **dim()** - returns the dimensions (i.e. number of rows and columns)
- **nrow()** and **ncol()** returns the number of rows and columns separately.
- **rownames()** and **colnames()**- shows the names attribute for rows and columns
- **str()** - returns the structure including name, type and preview of data in each column

Key Points

- R's basic data types are **logical**, **character**, **numeric**, integer and complex.
- R's basic data structures include **vectors**, lists, **data frames**, matrices and factors.
- Objects may have attributes, such as **name**, **dimension**, and **class**.

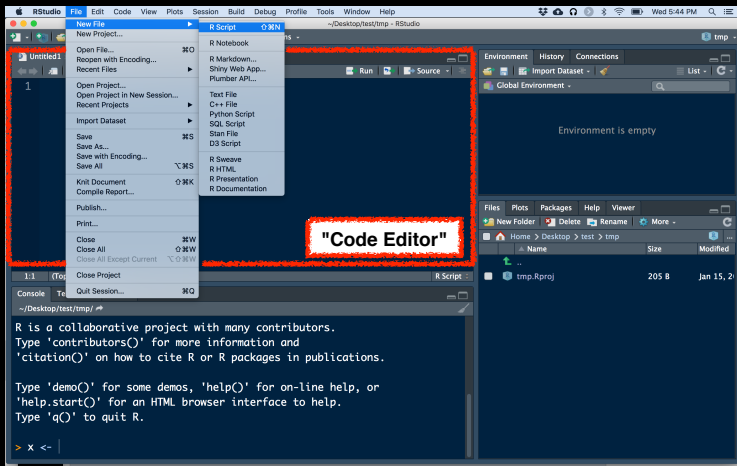
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Side-note: Use the code editor for R scripts



R scripts

- A simple text file with your R commands (e.g. lecture04.r) that contains your R code for one complete analysis
- **Scientific method:** complete record of your analysis
- **Reproducible:** rerunning your code is easy for you or someone else
- In RStudio, select code and type `<ctrl+enter>` to run the code in the R console
- **Key point:** Save your R script!

Side-note: RStudio shortcuts

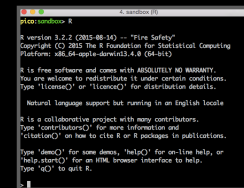
Sends current line or selection to console (faster to type: `command/ctrl+enter`)

Sends entire file to console

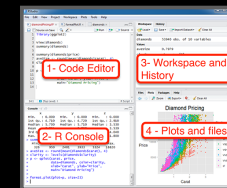
Re-send the lines of code you last ran to the console (useful after edits)

Other RStudio shortcuts!
Up/Down arrows (recall cmds)
Ctrl + 2 (move cursor to console)
Ctrl + 1 (move cursor to editor)

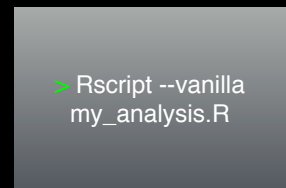
Rscript: Third way to use R



1. Terminal



2. RStudio



3. Rscript

From the command line!

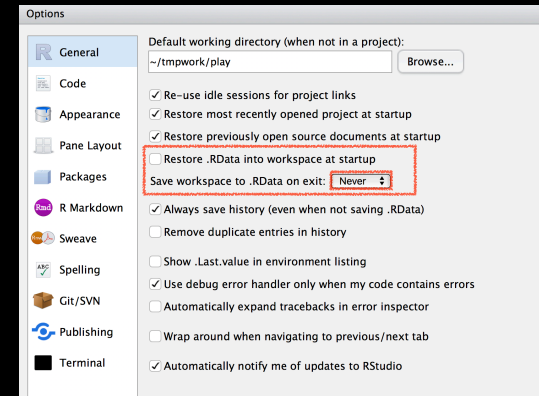
`> Rscript --vanilla my_analysis.R`
`# or within R: source("my_analysis.R")`

R workspaces

- When you close RStudio, **SAVE YOUR .R SCRIPT**
- You can also save data and variables in an R workspace, but this is generally not recommended
- Exception: working with an enormous dataset
- Better to start with a clean, empty workspace so that past analyses don't interfere with current analyses
- `rm(list = ls())` clears out your workspace or broom icon
- You should be able to reproduce everything from your R script, so **save your R script, don't save your workspace!**

R workspaces

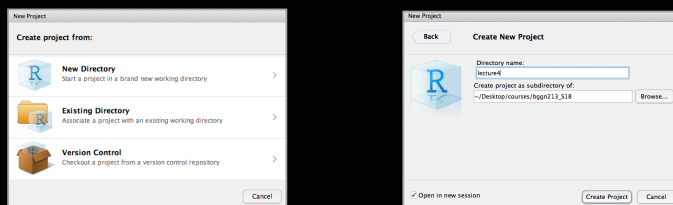
- Set **Tools > Global Options**



RStudio Projects

- We will use a new RStudio **project** for each new class going forward.

File > New Project > New Directory > New Project...



- These projects will help keep us **organized** and divide our work into multiple contexts, each with their own working directory, workspace, history, and source documents.

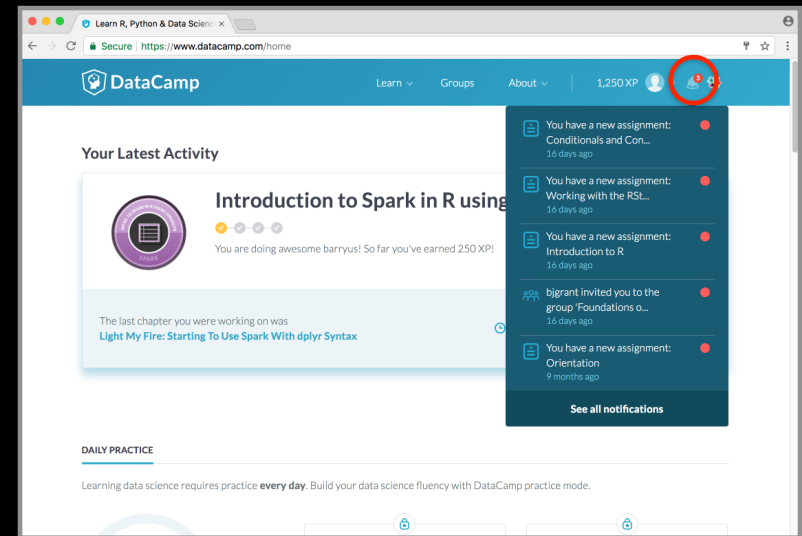
Learning Resources

- **TryR**. An excellent interactive online R tutorial for beginners.
< <http://tryr.codeschool.com/> >
- **RStudio**. A well designed reference card for RStudio.
< <https://help.github.com/categories/bootcamp/> >
- **DataCamp**. Online tutorials using R in your browser.
< <https://www.datacamp.com/> >
- **R for Data Science**. A new O'Reilly book that will teach you how to do data science with R, by Garrett Grolemund and Hadley Wickham.
< <http://r4ds.had.co.nz/> >

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< <https://www.datacamp.com/> >
- **R for Data Science**. A new O'Reilly book that will teach you how to do data science with R, by Garrett Grolemund and Hadley Wickham.
< <http://r4ds.had.co.nz/> >

< <https://www.datacamp.com/> >



Final Knowledge Check!

- What is R and why should we use it?
- Familiarity with R's basic syntax.
- Familiarity with major R data structures namely *vectors* and *data.frames* (with more on *lists* and *matrices* next day).
- Understand the basics of using functions (arguments, vectorization and re-cycling).
- Be able to use R to read and parse comma-separated (.csv) formatted files ready for subsequent analysis.
- Appreciate how you can use R scripts to aid with reproducibility.

Reference Slides:

Optional!

<http://swcarpentry.github.io/r-novice-inflammation/>

Sections: 1, 11 & 12 only!

Optional Exercise

Optional!

Use R to do the following. Create a new script to save your work and code up the following four equations:

$$1 + 2(3 + 4)$$

$$\ln(4^3+3^{2+1})$$

$$\sqrt{(4+3)(2+1)}$$

$$\left(\frac{1+2}{3+4}\right)^2$$

Help from within R

- Getting help for a function

> `help("log")`

> `?log`

- Searching across packages

> `help.search("logarithm")`

- Finding all functions of a particular type

> `apropos("log")`

```
[7] "as.logical" "as.logical.factor" "dlogis" "is.logical"
```

```
[13] "log" "log10" "log1p" "log2" "logLik" "logb"
```

```
[19] "logical" "loglin" "plogis" "print.logLik" "qlogis" "rlogis"
```

-Or use google

(e.g. "[r log function](#)") to find online docs

?log

R: Logarithms and Exponentials Find in Topic R Documentation

Logarithms and Exponentials

Description What the function does in general terms

`log` computes logarithms, by default natural logarithms. `log10` computes common (i.e., base 10) logarithms, and `log2` computes binary (i.e., base 2) logarithms. The general form `log(x, base)` computes logarithms with base `base`.

`log1p(x)` computes $\log(1+x)$ accurately also for $|x| \ll 1$ (and less accurately when x is approximately -1).

`exp` computes the exponential function.

`expm1(x)` computes $\exp(x) - 1$ accurately also for $|x| \ll 1$.

Usage How to use the function

```
log(x, base = exp(1))
logb(x, base = exp(2))
log10(x)
log2(x)
```

```
log1p(x)
```

```
exp(x)
```

```
expm1(x)
```

Arguments What does the function need

`x` a numeric or complex vector.
`base` a positive or complex number: the base with respect to which logarithms are computed. Defaults to $e = \exp(1)$.

Details

All except `logb` are generic functions: methods can be defined for them individually or via the `Math` group generic.

`log10` and `log2` are only convenience wrappers, but logs to bases 10 and 2 (whether computed via `log` or the wrappers) will be computed more efficiently and accurately where supported by the OS. Methods can be set for them individually (and otherwise methods for `log` will be used).

`logb` is a wrapper for `log` for compatibility with S. If (S3 or S4) methods are set for `log` they will be dispatched. Do not set S4 methods on `logb` itself.

All except `log` are [primitive](#) functions.

Value What does the function return

A vector of the same length as `x`, containing the transformed values. `log(0)` gives $-\text{Inf}$, and `log(x)` for negative values of `x` is NaN . `exp(-Inf)` is 0.

For complex inputs to the log functions, the value is a complex number with imaginary part in the range $[-\pi, \pi]$, which end of the range is used might be platform-specific.

S4 methods

`exp`, `expm1`, `log`, `log10`, `log2` and `log1p` are S4 generic and are members of the `Math` group generic.

Note that this means that the S4 generic for `log` has a signature with only one argument, `x`, but that `base` can be passed to methods (but will not be used for method selection). On the other hand, if you only set a method for the `Math` group generic then `base` argument of `log` will be ignored for your class.

Source

`log1p` and `expm1` may be taken from the operating system, but if not available there are based on the Fortran subroutines `dlnr1` by W. Fullerton of Los Alamos Scientific Laboratory (see <http://www.netlib.org/slatec/fnlib/dlnr1>) and (for small `x`) a single Newton step for the solution of `log1p(y) = x` respectively.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (for `log`, `log10` and `exp`.)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (for `logb`.)

See Also Discover other related functions

[Trig](#), [sqrt](#), [Arithmetic](#)

Examples Sample code showing how it works

```
log(exp(3))
log10(1e7) # = 7
x <- 10~(1+2*1:9)
cbind(x, log(1+x), log1p(x), exp(x)-1, expm1(x))
```

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