

BIMM 143

More on R functions and packages

Lecture 7

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<http://thegrantlab.org/bimm143>

Office hour check-in!

Recap From Last Time:

- Covered data input with the `read.table()` family of functions including `read.csv()`, `read.delim()` etc. and how to set the ***header*** and ***sep*** arguments appropriately.
- Covered the **When**, **Why**, **What** and **How** of writing your own R functions.
 - **When**: When you find yourself doing the same thing 3 or more times with repetitive code consider writing a function.
 - **Why**:
 1. Makes the purpose of the code more clear
 2. Reduces mistakes from copy/paste
 3. Makes updating your code easier
 4. Reduces code duplication and facilitates re-use.

Recap...

- **How**: Follow a step-by-step procedure to go from working code snippet to refined and tested function.
 1. Start with a simple problem and write a working snippet of code.
 2. Rewrite for clarity and to reduce duplication
 3. Turn into an initial function
 4. Test on small well defined input
 5. Report on potential problem by failing early and loudly!

Recap...

→ **How:** Follow a step-by-step procedure to go from working code snippet to refined and tested function.

1. Start with a simple problem and write a working snippet of code.

2. Rewrite for clarity and to reduce duplication

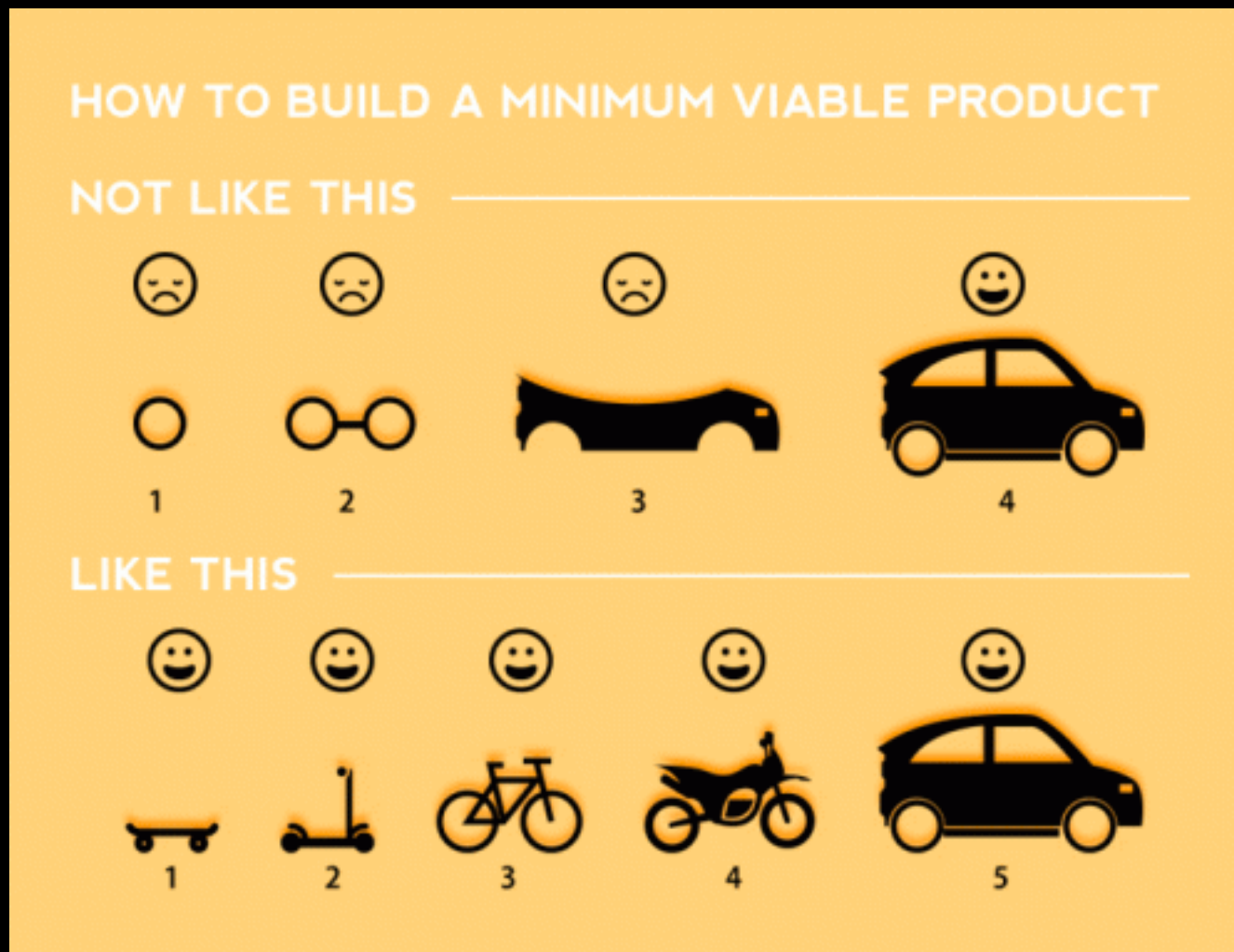
3. Turn into an initial function

4. Test on small well defined input

5. Report on potential problem by failing early and loudly!

Recap...

1. Start with a simple problem and write a working snippet of code.



Build that skateboard before you build the car.

A limited but functional thing is very useful and keeps the spirits high.

[Image credit: Spotify development team]

[[MPA link](#)]

Back by popular demand

**More examples of how to
write your own functions!**

What is a function

```
1      name.of.function <- function(2      arg1, arg2) {  
      statements  
      3      return(something)  
      }
```

1 **Name** (can be *almost* anything you want)

2 **Arguments** (i.e. input to your function)

3 **Body** (where the work gets done)

Revisit our first example function from last day...

```
source("http://tinyurl.com/rescale-R")
```

```
rescale <- function(x, na.rm=TRUE, plot=FALSE, ...) {  
  if(na.rm) {  
    rng <- range(x, na.rm=na.rm)  
  } else {  
    rng <- range(x)  
  }  
  
  answer <- (x - rng[1]) / (rng[2] - rng[1])  
  
  if(plot) { plot(answer, ...) }  
  return(answer)  
}
```

```
# Test fail  
rescale( c(1,10,"string") )
```

The functions `warning()` and `stop()`

- The functions `warning()` and `stop()` are used inside functions to handle and report on unexpected situations
- They both print a user defined message (which you supply as a character input argument to the `warning()` and `stop()` functions).
- However, `warning()` will keep on going with running the function body code whereas `stop()` will terminate the action of the function.
- A common idiom is to use `stop("some message")` to report on unexpected input type or other problem early in a function, i.e. **fail early and loudly!**

```
rescale2 <- function(x, na.rm=TRUE, plot=FALSE, ...) {  
  if( !is.numeric(x) ) {  
    stop("Input x should be numeric", call.=FALSE)  
  }  
  
  rng <- range(x, na.rm=TRUE)  
  
  answer <- (x - rng[1]) / (rng[2] - rng[1])  
  
  if(plot) {  
    plot(answer, ...)  
  }  
  return(answer)  
}
```

```
source("http://tinyurl.com/rescale-R")
```

```
rescale2 <- function(x, na.rm=TRUE, plot=FALSE, ...) {  
  if( !is.numeric(x) ) {  
    stop("Input x should be numeric", call.=FALSE)  
  }  
  
  rng <- range(x, na.rm=TRUE)  
  
  answer <- (x - rng[1]) / (rng[2] - rng[1])  
  
  if(plot) {  
    plot(answer, ...)  
  }  
  return(answer)  
}
```

```
source("http://tinyurl.com/rescale-R")
```

Suggested steps for writing your functions

1. Start with a simple problem and get a working snippet of code
2. Rewrite to use temporary variables (e.g. x, y, df, m etc.)
3. Rewrite for clarity and to reduce calculation duplication
4. Turn into an initial function with clear useful names
5. Test on small well defined input and (subsets of) real input
6. Report on potential problem by failing early and loudly!
7. Refine and polish

Side-Note: What makes a good function?

- Correct
- Understandable (remember that functions are for humans and computers)
- Correct + Understandable = **Obviously correct**
- Use sensible names throughout. What does this code do?

```
baz <- foo(df, v=0)  
df2 < replace_missing(df, value=0)
```

- Good names make code understandable with minimal context. You should strive for self-explanatory names

More examples

- We want to write a function, called `both_na()`, that counts how many positions in two input vectors, `x` and `y`, both have a missing value

```
# Should we start like this?  
  
both_na <- function(x, y) {  
  # something goes here?  
}
```

No! Always start with a simple definition of the problem

- We should start by solving a simple example problem first where we know the answer.

```
# Lets define an example x and y
x <- c( 1, 2, NA, 3, NA)
y <- c(NA, 3, NA, 3, 4)
```

- Here the answer should be **1** as only the third position has NA in both **x** and **y** and **is.na()** and **sum()** functions

Get a **working snippet** of code first that is close to what we want

```
# Lets define an example x and y
x <- c( 1, 2, NA, 3, NA)
y <- c(NA, 3, NA, 3, 4)
```

```
# use the is.na() and sum() functions
is.na(x)
[1] FALSE FALSE TRUE FALSE TRUE
```

```
sum( is.na(x) )
[1] 2
```

```
# Putting together!
sum( is.na(x) & is.na(y) )
[1] 1
```

Then rewrite your snippet as a *first* function

```
# Lets define an example x and y
x <- c( 1, 2, NA, 3, NA)
y <- c(NA, 3, NA, 3, 4)
```

```
# Our working snippet
sum( is.na(x) & is.na(y) )
```

```
# No further simplification necessary
both_na <- function(x, y) {
  sum( is.na(x) & is.na(y) )
}
```


Test on various inputs (a.k.a. **eejit proofing**)

- We have a function that works in at least one situation, but we should probably check it works in others.

```
x <- c(NA, NA, NA)
y1 <- c( 1, NA, NA)
y2 <- c( 1, NA, NA, NA)
```

```
both_na(x, y1)
[1] 2
```

```
# What will this return?
both_na(x, y2)
```


Report on potential problem by **failing early and loudly!**

- The generic warning with recycling behavior of the last example may not be what you want as it could be easily missed especially in scripts.

```
both_na2 <- function(x, y) {  
  
  if(length(x) != length(y)) {  
    stop("Input x and y should be the same length")  
  }  
  
  sum( is.na(x) & is.na(y) )  
}
```

Refine and polish: Make our function more useful by returning more information

```
both_na3 <- function(x, y) {  
  
  if(length(x) != length(y)) {  
    stop("Input x and y should be vectors of the same length")  
  }  
  
  na.in.both <- ( is.na(x) & is.na(y) )  
  na.number  <- sum(na.in.both)  
  na.which   <- which(na.in.both)  
  
  message("Found ", na.number, " NA's at position(s):",  
          paste(na.which, collapse=" ", " ") )  
  
  return( list(number=na.number, which=na.which) )  
}
```

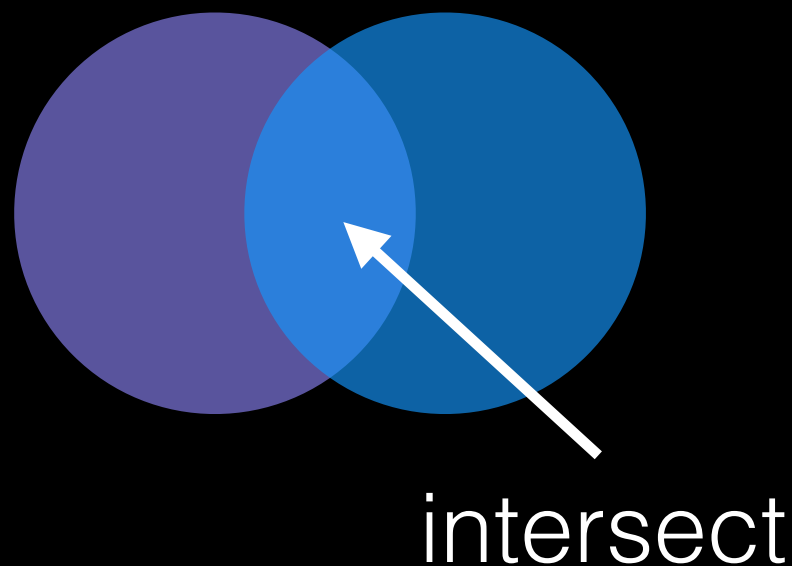


Re-cap: Steps for function writing

1. Start with a simple problem and get a working snippet of code
2. Rewrite to use temporary variables
3. Rewrite for clarity and to reduce calculation duplication
4. Turn into an initial function
5. Test on small well defined input and (subsets of) real input
6. Report on potential problem by failing early and loudly!
7. Refine and polish,
8. Document and comment within the code on your reasoning.

One last example

Find common genes in two data sets and return their associated data (from each data set)



Follow along!

```
# source("http://tinyurl.com/rescale-R")

# Start with a simple version of the problem
df1 <- data.frame(IDs=c("gene1", "gene2", "gene3"),
                  exp=c(2,1,1),
                  stringsAsFactors=FALSE)

df2 <- data.frame(IDs=c("gene2", "gene4", "gene3", "gene5"),
                  exp=c(-2, NA, 1, 2),
                  stringsAsFactors=FALSE)

# Simplify further to single vectors
x <- df1$IDs
Y <- df2$IDs

# Now what do we do?
```

```
source("http://tinyurl.com/rescale-R")
```

Follow along!

```
# source("http://tinyurl.com/rescale-R")

# Simplify problem
df1 <- data.frame(IDs=c("gene1", "gene2", "gene3"),
                  exp=c(2,1,1),
                  stringsAsFactors=FALSE)

df2 <- data.frame(IDs=c("gene2", "gene4", "gene3", "gene5"),
                  exp=c(-2, NA, 1, 2),
                  stringsAsFactors=FALSE)

x <- df1$IDs
y <- df2$IDs

# Search for existing functionality to get us started...
??intersect

intersect(x, y)
[1] "gene2" "gene3"
```

```
# Close but not useful for returning indices yet.
```

```
intersect(x, y)
```

```
[1] "gene2" "gene3"
```

```
# Back to the documentation to find something more useful
```

```
??intersect
```

Follow along!

Follow along!

```
# Close but not useful for returning indices yet.
```

```
intersect(x, y)
```

```
[1] "gene2" "gene3"
```

```
# Back to the documentation to find something more useful
```

```
? "%in%"
```

```
# This looks like a more useful starting point - indices!
```

```
x %in% y
```

```
[1] FALSE TRUE TRUE
```

Follow along!

```
# Close but not useful for returning indices yet.
intersect(x, y)
[1] "gene2" "gene3"

# Back to the documentation to find something more useful
?"%in%"

# This looks like a more useful starting point - indices!
x %in% y
[1] FALSE TRUE TRUE

x[x %in% y]
[1] "gene2" "gene3"

y[ y %in% x ]
[1] "gene2" "gene3"

# We can now cbind() these these results to yield intersect
```


Follow along!

```
# Putting together
```

```
cbind( x[ x %in% y ], y[ y %in% x ] )
```

```
      [,1]      [,2]
```

```
[1,] "gene2" "gene2"
```

```
[2,] "gene3" "gene3"
```

```
# Make it into a first function
```

Follow along!

```
# Putting together
```

```
cbind( x[ x %in% y ], y[ y %in% x ] )
```

```
      [,1]      [,2]  
[1,] "gene2"  "gene2"  
[2,] "gene3"  "gene3"
```

```
# Make it into a first function
```

```
gene_intersect <- function(x, y) {  
  cbind( x[ x %in% y ], y[ y %in% x ] )  
}
```

```
# Looks good so far but we need to work with data frames
```

```
gene_intersect(x, y)  
      [,1]      [,2]  
[1,] "gene2"  "gene2"  
[2,] "gene3"  "gene3"
```

Follow along!

```
# Previous function for vector input
gene_intersect <- function(x, y) {
  cbind( x[ x %in% y ], y[ y %in% x ] )
}

# Lets change to take input data frames
gene_intersect2 <- function(df1, df2) {
  cbind( df1[ df1$IDs %in% df2$IDs, ],
         df2[ df2$IDs %in% df1$IDs, "exp" ] )
}

# Correct but yucky format for 2nd colnames
gene_intersect2(df1, df2)
  IDs exp df2[df2$IDs %in% df1$IDs, "exp"]
2 gene2  1 -2
3 gene3  1  1
```

Follow along!

```
# Our input $IDs column name may change so lets add flexibility
# By allowing user to specify the gene containing column name

# Experiment first to make sure things are as we expect
gene.colname="IDs"
df1[,gene.colname]
[1] "gene1" "gene2" "gene3"

# Next step: Add df1[,gene.colname] etc to our current function.
```

Follow along!

```
# Looks complicated - simplify for human consumption!
```

```
gene_intersect3 <- function(df1, df2, gene.colname="IDs") {  
  cbind( df1[ df1[,gene.colname] %in% df2[,gene.colname], ],  
        exp2=df2[ df2[,gene.colname] %in% df1[,gene.colname], "exp"] )  
}
```

```
# Works but the function is not kind on the reader
```

```
gene_intersect3(df1, df2)
```

```
  IDs exp exp2  
2 gene2  1  -2  
3 gene3  1   1
```

```
# Looks much better
```

```
gene_intersect4 <- function(df1, df2, gene.colname="IDs") {  
  
  df1.name <- df1[,gene.colname]  
  df2.name <- df2[,gene.colname]  
  
  df1.inds <- df1.name %in% df2.name  
  df2.inds <- df2.name %in% df1.name  
  
  cbind( df1[ df1.inds, ],  
         exp2=df2[ df2.inds, "exp" ] )  
}
```

```
# Getting closer!
```

```
gene_intersect4(df1, df2)  
  IDs exp exp2  
2 gene2  1  -2  
3 gene3  1   1
```

```
# Test, break, fix, text again
```

```
df1 <- data.frame(IDs=c("gene1", "gene2", "gene3"),  
                  exp=c(2,1,1),  
                  stringsAsFactors=FALSE)
```

```
df3 <- data.frame(IDs=c("gene2", "gene2", "gene5", "gene5"),  
                  exp=c(-2, NA, 1, 2),  
                  stringsAsFactors=FALSE)
```

```
# Works but could do with more spit and polish!
```

```
gene_intersect4(df1, df3)
```

```
  IDs exp exp2  
1 gene2  1  -2  
2 gene2  1  NA
```

```
Warning message:
```

```
In data.frame(..., check.names = FALSE) :
```

```
  row names were found from a short variable and have been  
discarded
```

```
# Additional features we could add
# - Catch and stop when user inputs weird things
# - Use different colnames for matching in df1 and df2,
# - Match based on the content of multiple columns,
# - Optionally return rows not in df1 or not in df2 with NAs
# - Optionally sort results by matching column
# - etc...
```

```
merge(df1, df2, by="IDs")
```

```
  IDs exp.x exp.y
1 gene2    1   -2
2 gene3    1    1
```


For more details refer to
sections 2-5 in last days
handout!

<http://tinyurl.com/bimm143-L6>

Remember **Section 1B** (question 6) is your last days
homework (see also scoring rubric).

The **Sections 2** to **5** are there for your benefit.

R Highlight!

CRAN & Bioconductor

Major repositories for **R packages**
that extend R functionality

CRAN: Comprehensive R Archive Network

- CRAN is a network of mirrored servers around the world that administer and distribute R itself, R documentation and **R packages** (basically add on functionality!)
- There are currently ~11,700 packages on CRAN in the areas of finance, bioinformatics, machine learning, high performance computing, multivariate statistics, natural language processing, *etc. etc.*

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

Side-note: R packages come in all shapes and sizes



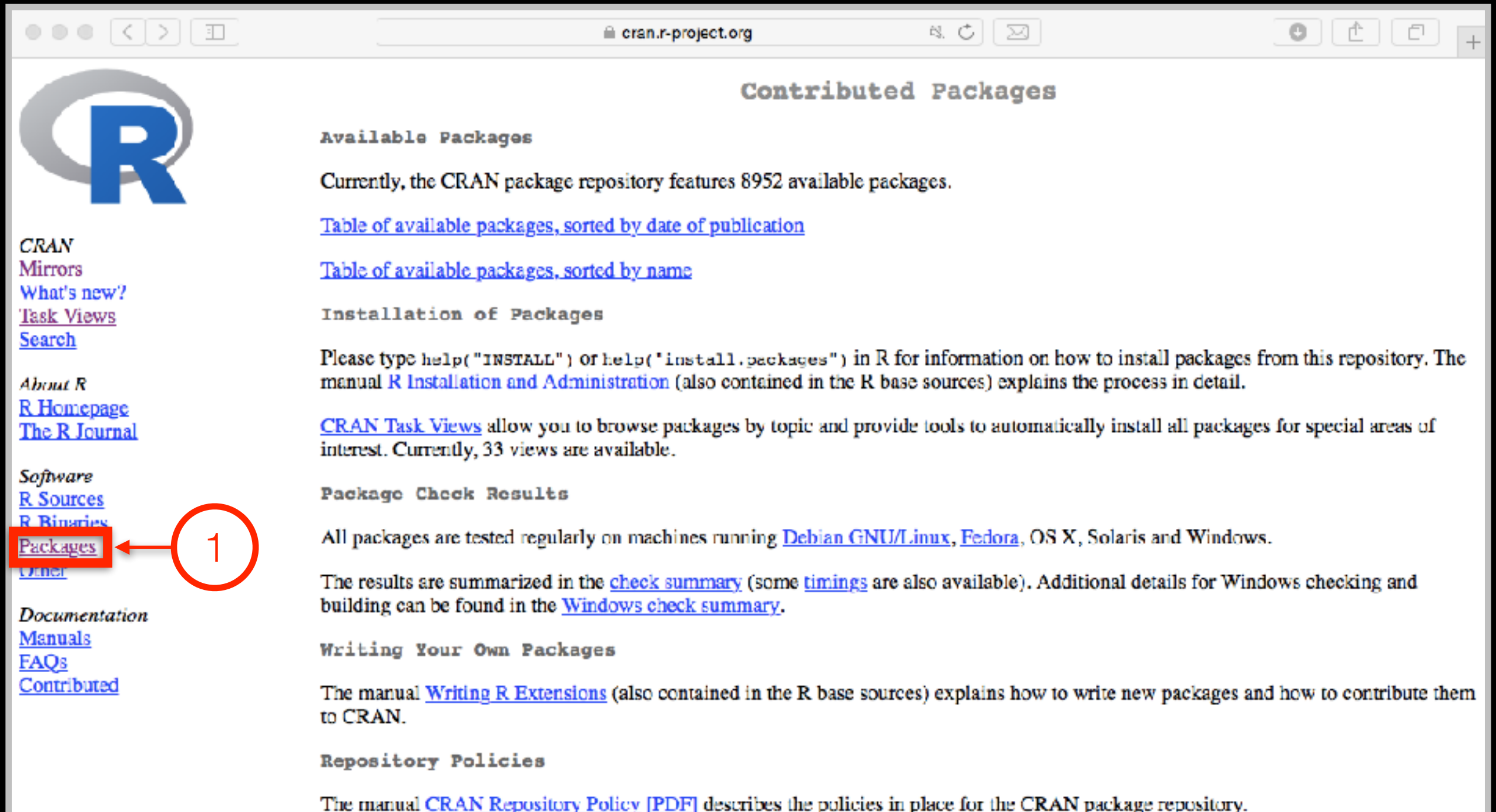
R packages can be of variable quality and often there are multiple packages with overlapping functionality.

Refer to relevant publications, package citations, update/maintenance history, documentation quality and your own tests!

“ The journal has sufficient experience with CRAN and Bioconductor resources to endorse their use by authors. We do not yet provide any endorsement for the suitability or usefulness of other solutions. ”

From: “Credit for Code”. *Nature Genetics* (2014), 46:1

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



Contributed Packages

Available Packages

Currently, the CRAN package repository features 8952 available packages.

[Table of available packages, sorted by date of publication](#)

[Table of available packages, sorted by name](#)

Installation of Packages

Please type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from this repository. The manual [R Installation and Administration](#) (also contained in the R base sources) explains the process in detail.

[CRAN Task Views](#) allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 33 views are available.

Package Check Results

All packages are tested regularly on machines running [Debian GNU/Linux](#), [Fedora](#), OS X, Solaris and Windows.

The results are summarized in the [check summary](#) (some [timings](#) are also available). Additional details for Windows checking and building can be found in the [Windows check summary](#).

Writing Your Own Packages

The manual [Writing R Extensions](#) (also contained in the R base sources) explains how to write new packages and how to contribute them to CRAN.

Repository Policies

The manual [CRAN Repository Policy \[PDF\]](#) describes the policies in place for the CRAN package repository.

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Installing a package

RStudio > Tools > Install Packages

```
> install.packages("bio3d")
```

```
> library("bio3d")
```

Bioconductor

R packages and utilities for working with
high-throughput genomic data

<http://bioconductor.org>



More pragmatic:

Bioconductor is a **software repository of R packages** with **some rules and guiding principles.**

Version 3.3 had 1211 software packages.

Bioconductor has
emphasized

Reproducible Research

since its start, and has been
an early adapter and driver
of tools to do this.

“Bioconductor: open software development for computational biology and bioinformatics”

Gentleman et al

Genome Biology 2004, 5:R80

“Orchestrating high-throughput genomic analysis with Bioconductor”

Huber et al

Nature Methods 2015, 12:115-121

Installing a bioconductor package

```
> source("https://bioconductor.org/biocLite.R")  
> biocLite()  
> biocLite("GenomicFeatures")
```

See: <http://www.bioconductor.org/install/>

Your Turn: Form a group of 3,
pick a package to explore and install,
Report back to the class.

Do it Yourself!

ggplot2, bio3d, rgl, rentrez, igraph,
blogdown, shiny, circlize,

Questions to answer:

- How does it extend R functionality? (i.e. What can you do with it that you could not do before?)
- How is it's documentation, vignettes, demos and web presence?
- Can you successfully follow a tutorial or vignette to get started quickly with the package?
- Can you find a GitHub or Bitbucket site for the the package with a regular heartbeat?

[Collaborative Google Doc Link](#)

Summary

- R is a powerful data programming language and environment for statistical computing, data analysis and graphics.
- Introduced R syntax and major R data structures
- Demonstrated using R for exploratory data analysis and graphics.
- Exposed you to the why, when, and how of writing your own R functions.
- Introduced CRAN and Bioconductor package repositories.

[\[Muddy Point Assessment Link\]](#)

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/> >