



BGGN 213
**More on R functions
and packages**
Lecture 7
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Office hour reminder!
Make use of free advice :-)

Recap From Last Time:

- Covered the **When**, **Why**, **What** and **How** of writing your own R functions.

...

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 - **When**: When you find yourself doing the same thing 3 or more times with repetitive code consider writing a function.

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Recap From Last Time:

- 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 From Last Time:

- Covered the **When**, **Why**, **What** and **How** of writing your own R functions.
- **What:** A function is defined with:
 1. A user selected **name**,
 2. A comma separated set of input **arguments**, and
 3. Regular R code for the **function body** including an optional output **return value** e.g.

```
fname <- function(arg1, arg2) { paste(arg1, arg2) }
```

Name Input arguments Function body

...

Recap From Last Time:

- **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. Then, and only then, turn into an initial function
 4. Test on small well defined input
 5. Report on potential problem by failing early and loudly!

...

Recap From Last Time:

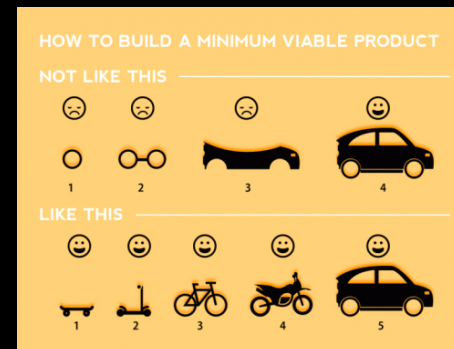
- **How:** Follow a step-by-step procedure to go from working code snippet to refined and tested function.

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

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(arg1, arg2) {  
2   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, ...) {  
  rng <- range(x, na.rm=na.rm)  
  
  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=na.rm)

  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=na.rm)

  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 inputs `x` and `y`.

Tip: Search for existing functionality to get us started...

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=", ") )

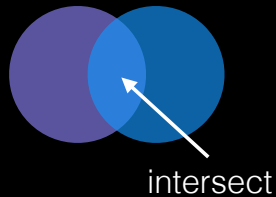
  return( list(number=na.number, which=na.which) )
}
```

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)



intersect

```
# 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"
```

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
??intersect
```

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
```

Follow along!

```
# 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, test 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!

https://bioboot.github.io/bggn213_S18/lectures/#6

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 ~12,530 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>

A screenshot of the CRAN website. The browser address bar shows 'cran.r-project.org'. The page title is 'Contributed Packages'. The main content area says 'Available Packages' and 'Currently, the CRAN package repository features 8952 available packages.' It lists several links: 'Table of available packages, sorted by date of publication', 'Table of available packages, sorted by name', 'Installation of Packages', 'Package Check Results', 'Writing Your Own Packages', and 'Repository Policies'. On the left sidebar, there is a navigation menu with 'Packages' highlighted in red and circled with a red '1'. Other items in the menu include 'About R', 'R Homepage', 'The R Journal', 'Software', 'R Sources', 'R Mirrors', 'Documentation', 'Manuals', 'FAQs', and 'Contributed'.

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 3.6 has 1,473 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

“Accessible, curated metagenomic data through
ExperimentHub”

Pasolli *et al.*

Nature Methods 2017, 14:1023–1024.

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.

[ggplot2](#), [bio3d](#), [rgl](#), [rentrez](#), [igraph](#),
[blogdown](#), [shiny](#), [msa](#), [phyloseq](#)

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 its 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](#)]

Do it Yourself!

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/> >