Introduction: Course Aims

This is a *first* course in R. We aim to cover:

- Reading in, summarizing & managing data

- Use of functions in R – doing jobs by programming, not by using drop-down menus (much)

- *Some* standard functions for statistical analysis – but minimal statistics in this module

- How to use other people’s code, how to get help, what to learn next

We assume no previous use of R, also non-extensive programming skills in other languages. If this is *not* your level, please consider switching to a later module.
Introduction: Resources

Most importantly, the class site is

http://faculty.washington.edu/kenrice/rintro

Contains (or will contain):

- PDF copies of slides (in color, and contains a few hyperlinks)
- All datasets needed for exercises
- Exercises for you to try
- Our solutions to exercises (later!)
- Links to other software, other courses, book, and places to get R help
- Links to a few helpful websites/email list archives

Of course, search engines will find much more than this, and can be a useful start, when tackling analyses with R.
Introduction: About Tim

- Associate Prof, UW Biostat
- A useR and an instructor
- Research in Genetic Epidemiology for Complex Human Traits
Introduction: About Ken

- Prof, UW Biostat
- Author of a few R packages, user, teacher
- Genetic/Genomic research in Cardiovascular Epidemiology

... and you?

(Briefly, who are you, what’s your genetics/infectious disease?)
Introduction: Course structure

10 sessions over 2.5 days

- Day 1; (Mostly RStudio) Data management, using functions
- Day 2; (Standard R) More about programming
- Day 2.5; More advanced ideas

Web page: http://faculty.washington.edu/kenrice/rintro/
Introduction: Session structure

What to expect in a typical session;

- 45 mins teaching (please interrupt!)
- 30 mins hands-on; please work in pairs
- 15 mins summary, discussion/extensions (interrupt again!)

There will also be one ‘take-home’ exercise, on Day 2; the final session will include in-depth discussion/evaluation.

Please note: the 2.5 day course moves quickly, and later material builds on earlier material. So, please interrupt!
1. Reading in data

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University of Washington

Seattle, July 2019
What is R?

R is a ‘programming environment for statistics and graphics’

- Does *basically* everything, can also be extended
- It’s the default when statisticians implement new methods
- Free, open-source

But;

- Steeper learning curve than e.g. Excel, Stata
- Command-line driven (programming, not drop-down menus)
- Gives only what you ask for!

To help with these difficulties, we will begin with RStudio, a graphical user interface (front-end) for R that is slightly more user-friendly than ‘Classic’ R’s GUI.

So *after* installing the latest version of R...
RStudio

In your favorite web browser, download from rstudio.com;

- Select & download the FREE installer for your system
- Default installation is fine
- Working in pairs *highly* recommended
RStudio

You should also install R - RStudio is a ‘front end’ to R itself. On first startup, RStudio should look like this; (up to version and Mac/PC differences)

If you’ve used it before, RStudio defaults to remembering what you were doing.
We’ll use the ‘Console’ window first – as a (fancy!) calculator

```r
> 2+2
[1] 4
> 2^5+7
[1] 39
> 2^(5+7)
[1] 4096
> exp(pi)-pi
[1] 19.9991
> log(20+pi)
[1] 3.141632
> 0.05/1E6 # a comment; note 1E6 = 1,000,000
[1] 5e-08
```

- All common math functions are available; parentheses (round brackets) work as per high school math
- Try to get used to bracket matching. A ‘+’ prompt means the line isn’t finished – hit Escape to get out, then try again.
R stores data (and everything else) as objects. New objects are created when we assign them values;

```r
> x <- 3
> y <- 2 # now check the Environment window
> x+y
[1] 5
```

Assigning new values to existing objects over-writes the old version – and be aware there is no Ctrl-Z ‘undo’;

```r
> y <- 17.4 # check the Environment window again
> x+y
[1] 20.4
```

- Anything after a hash (#) is ignored – e.g. comments
- Spaces don’t matter
- Capital letters do matter
RStudio: Reading in data

To import a dataset, follow pop-ups from the File tab;
RStudio: Reading in data

More on those options;

- **Name**: Name of the object that will store the whole dataset, when it’s read in
- **Heading**: Does the first row contain column names?
- **Row names**: are there names for each row?
- **Separator**: what’s between items on a single line?
- **na.strings**: How are missing values denoted?

The defaults are sensible, but R assumes you *know* what your data *should* look like – and whether it has named columns, numeric/character data, etc. No software is smart enough to cope with every format that might be used by you/your colleagues to store data.
RStudio: Reading in data

After successfully reading in the data;

- The environment now includes a mammals object – or whatever you called the data read from file
- A copy of the data can be examined in the Excel-like data viewer (below) – if it looks weird, find out why & fix it!

... we’ll return later, to `read.csv()` in the Console window
What's a good name for my new object?

- Something memorable (!) and not easily-confused with other objects, e.g. $x$ isn’t a good choice if you already have $x$
- Names must start with a letter or period ("."), after that any letter, number or period is okay
- Avoid other characters; they get interpreted as math ("-", "*") or are hard to read ("_") so should not be used in names
- Avoid names of existing functions – e.g. `summary`. Some one-letter choices (c, C, F, t, T and S) are already used by R as names of functions, it’s best to avoid these too
Operating on data

To operate on data, type commands in the Console window, just like our earlier calculator-style approach;

> str(mammals)
'data.frame': 62 obs. of 2 variables:
$ body: num 3.38 0.48 1.35 465 36.33 ...
$ brain: num 44.5 15.5 8.1 423 119.5 ...
> summary(mammals)

<table>
<thead>
<tr>
<th></th>
<th>body</th>
<th>brain</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min.</td>
<td>0.005</td>
<td>0.14</td>
</tr>
<tr>
<td>1st Qu.</td>
<td>0.600</td>
<td>4.25</td>
</tr>
<tr>
<td>Median</td>
<td>3.342</td>
<td>17.25</td>
</tr>
<tr>
<td>Mean</td>
<td>198.790</td>
<td>283.13</td>
</tr>
<tr>
<td>3rd Qu.</td>
<td>48.203</td>
<td>166.00</td>
</tr>
<tr>
<td>Max.</td>
<td>6654.000</td>
<td>5712.00</td>
</tr>
</tbody>
</table>

- `str()` tells us the structure of an object
- `summary()` summarizes the object

Can also use these commands on any object – e.g. the single numbers we created earlier (try it!)
Operating on data: columns

Individual columns in data frames are identified using the $ symbol – just seen in the \texttt{str()} output.

\begin{verbatim}
> mammals$brain
[1]  44.50  15.50   8.10  423.00  119.50  115.00  98.20   5.50  58.00
[10]  6.40   4.00   5.70   6.60   0.14   1.00  10.80  12.30   6.30
[19] 4603.00  0.30  419.00  655.00   3.50  115.00  25.60   5.00  17.50
[28]  680.00 406.00  325.00  12.30 1320.00  5712.00   3.90 179.00  56.00
[37]  17.00   1.00   0.40   0.25  12.50  490.00  12.10 175.00 157.00
[46]  440.00 179.50   2.40  81.00  21.00  39.20   1.90   1.20   3.00
[55]  0.33 180.00  25.00 169.00   2.60  11.40   2.50  50.40

> summary(mammals$brain)
      Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
   0.140   4.250  17.250   283.100  166.000  5712.000
\end{verbatim}

Think of $ as ‘apostrophe-S’, i.e. mammals’S brain.

Unlike many other statistical packages, R can handle \textit{multiple} datasets at the same time – helpful if your data are e.g. phenotypes & genotypes, or county & disease outbreak data. This isn’t possible without $, or \textit{some} equivalent syntax.
Operating on data: columns

New columns are created when you assign their values – here containing the brain weights in kilograms;

```r
> mammals$brainkg <- mammals$brain/1000
> str(mammals)
'data.frame': 62 obs. of 3 variables:
$ body : num 3.38 0.48 1.35 465 36.33 ...
$ brain : num 44.5 15.5 8.1 423 119.5 ...
$ brainkg: num 0.0445 0.0155 0.0081 0.423 0.1195 ...
> summary(mammals$brainkg)
     Min.  1st Qu.   Median      Mean  3rd Qu.     Max.  
0.00014 0.00425 0.01725 0.28313 0.16600 5.71200
```

- Assigning values to existing columns over-writes existing values – again, with no warning
- With e.g. `mammals$newcolumn <- 0`, the new column has every entry zero; R *recycles* this single value, for every entry
- It's unusual to delete columns... but if you *must*; `mammals$brainkg <- NULL`
Operating on data: columns

Some other functions useful for summarizing data frames, and their columns;

> names(mammals)
[1] "species" "body"   "brain"
> dim(mammals)       # dim is short for dimension
[1] 62   3
> length(mammals$body) # how many rows in our dataset?
[1] 62
> min(mammals$body)
[1] 0.005
> max(mammals$body)
[1] 6654
> range(mammals$body)
[1] 0.005 6654.000
> mean(mammals$brain)
[1] 283.1342
> sd(mammals$brain)   # sd is short for standard deviation
[1] 930.2789
> median(mammals$brain)
[1] 17.25
RStudio: the Script window

While fine for occasional use, entering every command ‘by hand’ is error-prone, and quickly gets tedious. A much better approach is to use a Script window – open one with Ctrl-Shift-N, or the drop-down menus;

- Opens a nice editor, enables saving code (.R extension)
- Run current line (or selected lines) with Ctrl-Enter, or Ctrl-R
RStudio: the Script window

An important notice: from now on, we assume you are using a script editor.

- First-time users tend to be reluctant to switch! – but it’s worth it, ask any experienced user
- Some code in slides may be formatted for cut-and-paste into scripts – it may not look exactly like what appears in the Console window
- Exercise ‘solutions’ given as .R files
- Scripts make it easy to run slightly modified code, without re-typing everything – remember to save them as you work
- Also remember the Escape key, if e.g. your bracket-matching goes wrong

For a very few jobs, e.g. changing directories, we’ll still use drop-down menus. But commands are available, for all tasks.
Operating on data: subsets

To identify general subsets – not just the columns selected by $ – R uses square brackets. Selecting individuals elements:

> mammals$brain[32] # 32nd element of mammals$brain
[1] 1320
> mammals$brain[32] # 32nd element of mammals$brain
[1] 1320
> row.names(mammals)[32]
[1] "Human"
> mammals$body[32]
[1] 62

Can also select entire columns or entire rows this way – and ‘blank’ entries indicate you want everything.

> mammals[32,2] # subtable with just 32nd row, 2nd column
[1] 1320

> mammals[32,]     # everything in the 32nd row
body  brain  brainkg
Human  62  1320  1.32

> sum(mammals[,3]) # sum of all the brains masses...
[1] 17.55432
Operating on data: subsets

Suppose we were interested in the brain weight (i.e. 2nd column) for mammals (i.e. rows) 14, 55, & 61. How to select these multiple elements?

```r
> mammals[c(14,55,61),1]
[1] 0.005 0.048 0.104 # check these against data view
```

But what is `c(14,55,61)`? It’s a *vector* of numbers – `c()` is for *combine*;

```r
> length(c(14,55,61))
[1] 3
> str(c(14,55,61))
  num [1:3] 14 55 61
```

We can select these rows and all the columns;

```r
> mammals[c(14,55,61),]
body   brain
Lesser short-tailed shrew 0.005 0.14
Musk shrew                0.048 0.33
Tree shrew                0.104 2.50
```
Operating on data: subsets

A very useful special form of vector;

```r
> 1:10
[1] 1 2 3 4 5 6 7 8 9 10
> 6:2
[1] 6 5 4 3 2
> -1:-3
[1] -1 -2 -3
```

R expects you to know this shorthand – see e.g. its use of 1:3 in the output from `str()`, on the previous slide. For a ‘rectangular’ selection of rows and columns;

```r
> mammals[20:22, 1:2]
            body brain
Big brown bat 0.023  0.3
Donkey      187.100 419.0
Horse       521.000 655.0
```

Negative values correspond to *dropping* those rows/columns;

```r
> mammals[-3:-62, 1:2]  # everything but the first two rows, & columns 1 and 2
            body brain
Arctic fox 3.385   44.5
Owl monkey 0.480   15.5
```
Operating on data: subsets

As well as storing numbers and character strings (like "Donkey", "Big brown bat") R can also store *logicals* – TRUE and FALSE.

To make a new vector, with elements that are TRUE if body mass is above 500kg and FALSE otherwise:

```r
> is.heavy <- mammals$body > 500
> table(is.heavy)  # another useful data summary command
is.heavy
           FALSE TRUE
      58      4
```

Which mammals were these? (And what were their masses?)

```r
> mammals[is.heavy,]  # just the rows for which is.heavy is TRUE
           body     brain
Asian elephant  2547    4603
Horse          521      655
Giraffe        529      680
African elephant 6654    5712
```

Use e.g. `mammals[is.heavy,2]` to combine TRUE/FALSE (rows) and numbers (columns)
Operating on data: subsets

One final method... for now! Instead of specifying columns of interest by number, or through vectors of TRUEs/FALSEs, we can also just give the names – as character strings, or vectors of character strings.

```r
> mammals[1:3, "body"]
[1] 3.385 0.480 1.350
> mammals[is.heavy,"body"]
[1] 2547 521 529 6654
```

– this is more typing than the other methods, but is much easier to debug/reuse. Neither is ‘right’ or ‘wrong’ – R is just flexible.
Quitting time (almost)

When you’re finished with RStudio;

- Ctrl-Q, or the drop-down menus, or entering q() at the command line all start the exit process
- You will be asked “Save workspace image to ~/.RData?”
  - No/Don’t Save: nothing is saved, and is not available when you re-start. *This is recommended*, because you will do different things in each session
  - Yes: Everything in memory is stored in R’s internal format (.Rdata) and will be available when you re-start RStudio
  - Cancel: don’t quit, go back
- Writing about what you did (output from a script) often takes much longer than re-running that script’s analyses – so often, a ‘commented’ script is all the R you need to store

To get rid of objects in your current session, use rm(), e.g. rm(is.heavy, mammals, x, y) ... or RStudio’s ‘broom’ button.
Summary

- In RStudio, read in data from the pop-up menu in the Environment window (or Tools menu)

- Data frames store data; can have many of these objects – and multiple other objects, too

- Identify vectors with $, subsets with square brackets

- Many useful summary functions are available, with sensible names

- Scripts are an important drudgery-avoidance tool!