SISG & SISMID

Module 3: Introduction to R

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University of Washington

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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
- Links to other software, other courses, book, and places to get R help
- Links to a few helpful websites/email list archives

Of course, any search engine will find much more than this, and can be useful first step in finding how to tackle a problem in R.

Introduction: About Tim

- Assistant Prof, UW Biostat
- A useR and an instructoR
- Research in Genetic Epidemiology for Complex Human Traits
- Spare time: teaching my 2 and 4 year old how to swim!

Introduction: About Ken

- Associate Prof, UW Biostat
- AuthoR of a few R packages, useR, teacheR
- Genetic/Genomic research in Cardiovascular Epidemiology
- Sings bass (July 17 & 18!)

... and you?

(who are you, what genetics/infectious disease you work on)

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 (interrupt again!)

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

1. Reading in data

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What is R?

R is a ‘programming environment for statistics and graphics’

- Does *basically* everything, can also be extended
- 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 front-end for R that is slightly more user-friendly than the default.

RStudio

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

- Select, download & install version for your (desktop) system
- Default installation is fine
- Working in pairs *highly* recommended

RStudio

We'll use the 'Console' window first – as a (fancy!) calculator

```
> 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.

RStudio

R stores data (and everything else) as *objects*. New objects are created when we *assign* them values;

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

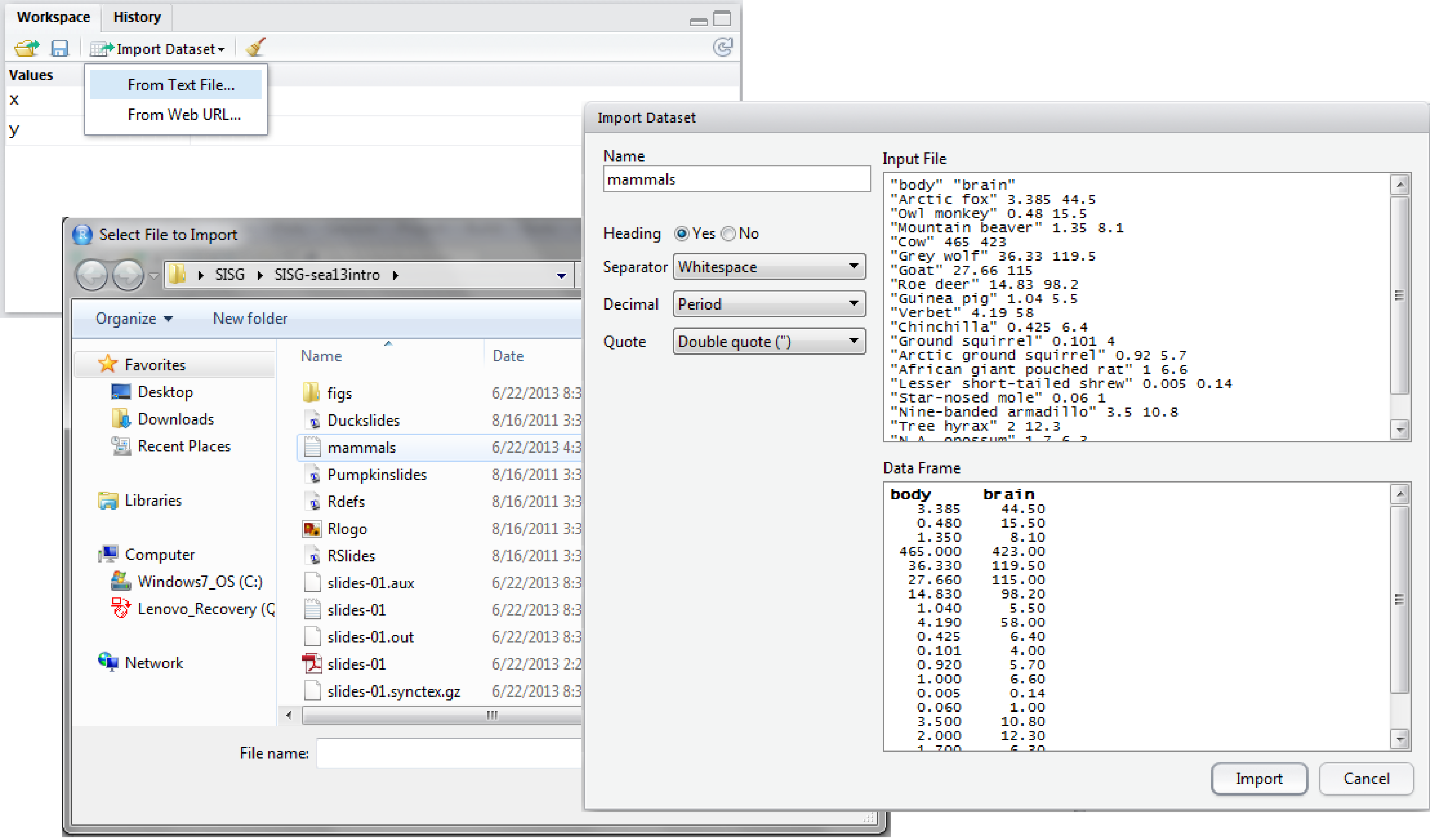
Assigning new values to existing objects over-writes the old version – and be aware there is no ‘undo’;

```
> y <- 17.4 # check the Workspace 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 Workspace tab;



Name: mammals

Heading ● Yes ○ No

Separator: Whitespace

Decimal: Period

Quote: Double quote (")

Input File

```
"body" "brain"
"Arctic fox" 3.385 44.5
"Owl monkey" 0.48 15.5
"Mountain beaver" 1.35 8.1
"Cow" 465 423
"Grey wolf" 36.33 119.5
"Goat" 27.66 115
"Roe deer" 14.83 98.2
"Guinea pig" 1.04 5.5
"Verbet" 4.19 58
"Chinchilla" 0.425 6.4
"Ground squirrel" 0.101 4
"Arctic ground squirrel" 0.92 5.7
"African giant pouched rat" 1 6.6
"Lesser short-tailed shrew" 0.005 0.14
"Star-nosed mole" 0.06 1
"Nine-banded armadillo" 3.5 10.8
"Tree hyrax" 2 12.3
```

Data Frame

```
body      brain
  3.385   44.50
  0.480   15.50
  1.350    8.10
465.000  423.00
 36.330  119.50
 27.660  115.00
 14.830   98.20
  1.040    5.50
  4.190   58.00
  0.425    6.40
  0.101    4.00
  0.920    5.70
  1.000    6.60
  0.005    0.14
  0.060    1.00
  3.500   10.80
  2.000   12.30
```

RStudio: Reading in data

More on those options;

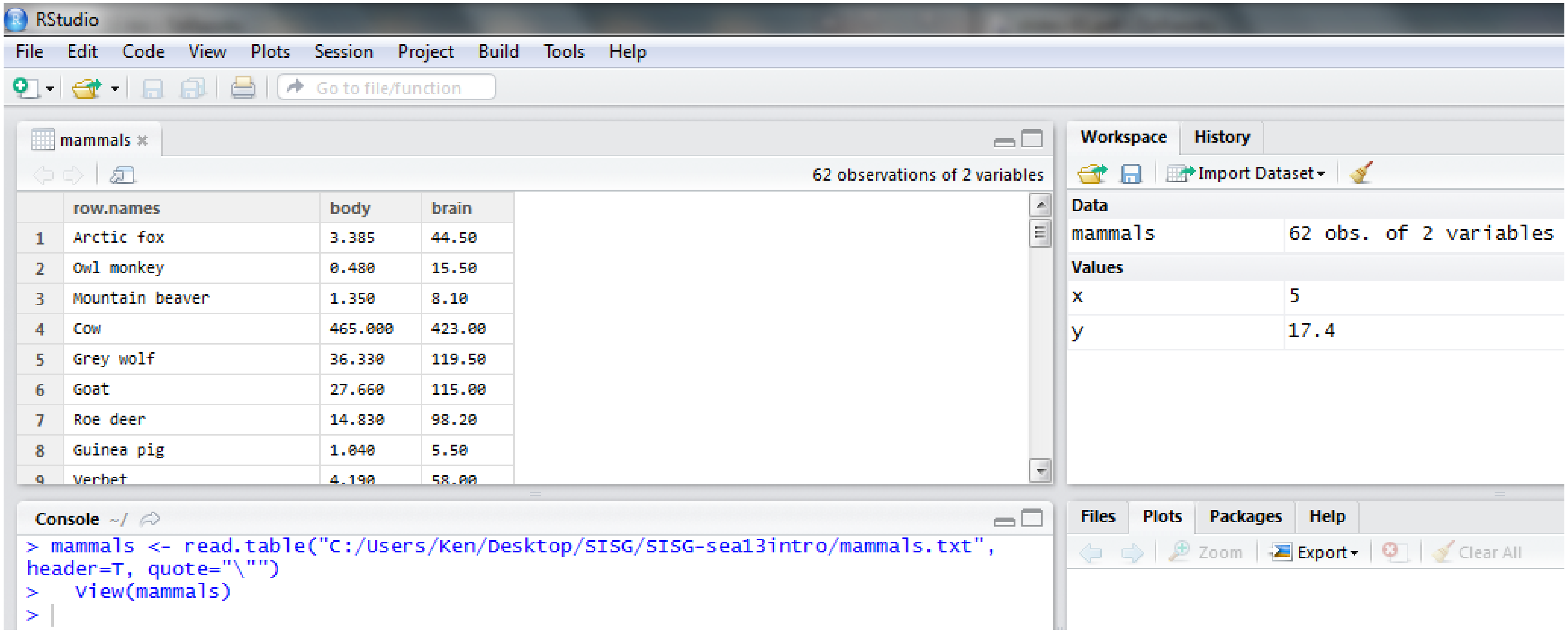
- **Name**: Name of the data frame object that will store the whole dataset
- **Separator**: what's between items on a single line?
- **Decimal**: Usually a period (".")
- **Quote**: Usually double – seldom critical

The defaults are sensible, but R assumes you *know* what your data *should* look like – and whether it has named columns, row names etc.

RStudio: Reading in data

After successfully reading in the data;

- The workspace 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!



62 observations of 2 variables

	row.names	body	brain
1	Arctic fox	3.385	44.50
2	Owl monkey	0.480	15.50
3	Mountain beaver	1.350	8.10
4	Cow	465.000	423.00
5	Grey wolf	36.330	119.50
6	Goat	27.660	115.00
7	Roe deer	14.830	98.20
8	Guinea pig	1.040	5.50
9	Vervet	4.190	58.00

Data

mammals	62 obs. of 2 variables

Values

x	5
y	17.4

```
> mammals <- read.table("C:/Users/Ken/Desktop/SISG/SISG-sea13intro/mammals.txt",
header=T, quote="\"")
>   View(mammals)
> |
```

… we'll return later, to **`read.table`** in the Console window

RStudio: Reading in data

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)
      body                brain
 Min.   :   0.005   Min.   :   0.14
 1st Qu.:   0.600   1st Qu.:   4.25
 Median :   3.150   Median :  17.25
 Mean   : 198.738   Mean   : 283.13
 3rd Qu.:  48.203   3rd Qu.: 166.00
 Max.   :6654.000   Max.   :5712.00
```

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

Can also use these commands on 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 `str()` output.

```
> 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.
   0.14    4.25   17.25  283.10  166.00 5712.00
```

Think of $ as 'apostrophe-S', i.e. `mammals`'S `brain`.

Unlike many other statistical packages, R can handle *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 some similar bits of syntax.

Operating on data: columns

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

```
> 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 0.28310 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`

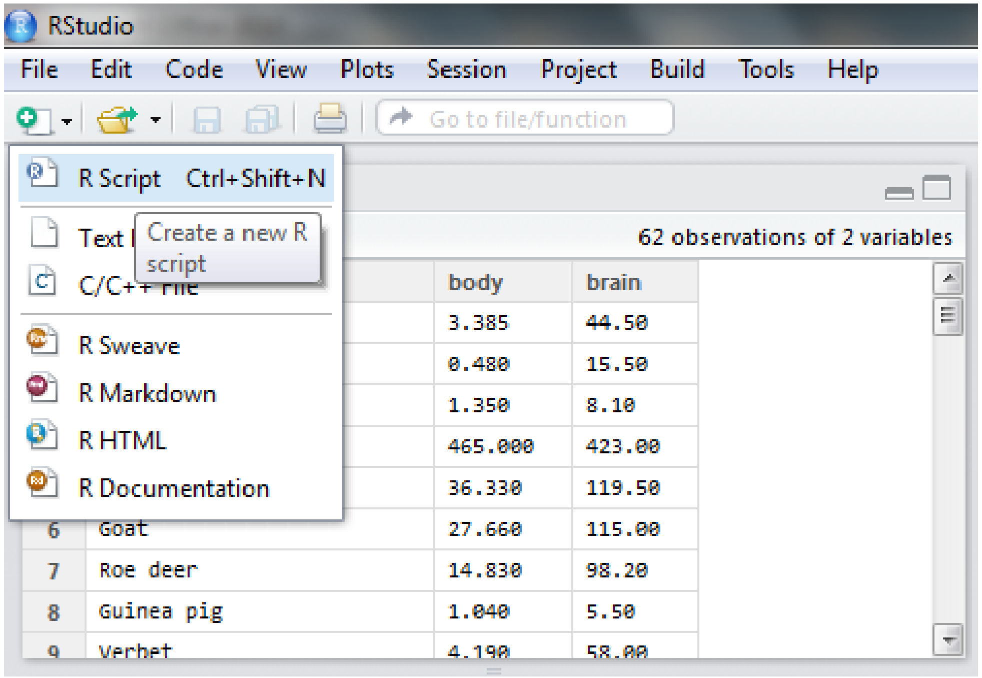
Operating on data: columns

Other functions useful for summarizing data frames, and their columns;

```
> names(mammals)
[1] "body"  "brain"
> dim(mammals)      # dim is short for dimension
[1] 62  2
> length(mammals$body)
[1] 62
> min(mammals$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$brain)
[1] 17.25
> median(mammals$br) # uses pattern-matching (but hard to debug later)
[1] 17.25
```

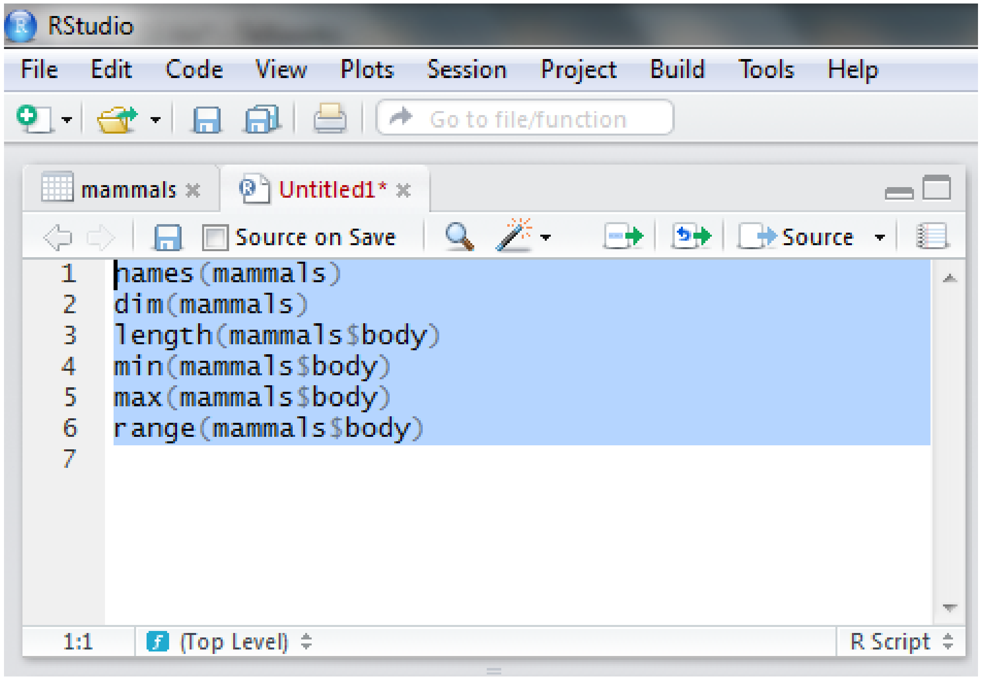
RStudio: the Script window

It's fine for occasional use, but 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;



62 observations of 2 variables

		body	brain
		3.385	44.50
		0.480	15.50
		1.350	8.10
		465.000	423.00
		36.330	119.50
6	Goat	27.660	115.00
7	Roe deer	14.830	98.20
8	Guinea pig	1.040	5.50
9	Vervet	4.190	58.00



```
names(mammals)
dim(mammals)
length(mammals$body)
min(mammals$body)
max(mammals$body)
range(mammals$body)
```

- 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, we will still use drop-down menus, e.g. changing directories – though commands *are* available.

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
> row.names(mammals)[32]
[1] "Human"
> mammals$body[32]
[1] 62
> mammals[32,2] # 32nd row, 2nd column
[1] 62
```

Selecting entire columns (again!) or entire rows, blank entries indicate you want everything.

```
> mammals[32,]     # everything in the 32nd row
      body brain
Human   62  1320
> sum(mammals[32,])
[1] 1382
```

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?

```
> 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*;

```
> 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;

```
> 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;

```
> 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 on the previous slide. For a 'rectangular' selection of rows and columns;

```
> 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;

```
> mammals[-3:-62, 1:2] # everything but the first two rows, & columns 1:2
            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;

```
> 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?)

```
> 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
> mammals[is.heavy,2]     # combining TRUE/FALSE (rows) and numbers (columns)
[1] 4603  655  680 5712
```

Operating on data: subsets

One final method... for now!

Instead of specifying rows/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.

```
> mammals[c("Cow","Goat","Human"),"body"]
[1] 465.00  27.66  62.00
> mammals[c("Cow","Goat","Human"),c("body","brain")]
        body brain
Cow   465.00   423
Goat   27.66   115
Human  62.00  1320
> mammals[c("Cow","Goat","Human"),2] # okay to mix & match
[1]  423  115 1320
```

– this is more typing than the other options, but much easier to debug/reuse.

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

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 pop-up menu in Workspace window
- Data frames store data; can have many of these objects, and others
- Identify vectors with $, subsets with square brackets
- Many useful summary functions are available, with sensible names
- Scripts are an important drudgery-avoidance tool!