Data Programming with R

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Lecture 10 - Debugging

Debugging

- Simple tips
- R's debugging tools
    - `browser`
- A simple example
- Other debugging tools
- Setting breakpoints
- Extended example

What is debugging?

- Debugging is the process of checking your code and finding and fixing mistakes.
- You will already have encountered many occasions where your R code does not work: you typed in something incorrect and need to change it. R will usually (try to) tell you what you have done wrong.
- Worse, sometimes your code works but does not give the answers you expected. You need to locate where the problem is in the code and fix it.
- You will often spend more time debugging code than writing it!
- In this lecture we will go through the different tools R & Rstudio have for checking and finding mistakes in R code.

Tips for debugging

- Put comments into your code as you go.
- Start small. Try some very simple test cases and avoid working with large data objects.
- Debug in a modular, top-down manner. Try to write a main function which isn't very long which calls other functions as it goes through. It's easier to debug and check small individual functions than one long huge one.
- Use anti-bugging. The `stop()` and `stopifnot()` functions will stop a function if it has a dodgy value in it:

```r
x <- 5
if(length(x) != 3) stop("x is supposed to be of length 3!")
```

```
## Error in eval(expr, envir, enclos): x is supposed to be of length 3!
```

```r
stopifnot(x < 0)
```

```
## Error in eval(expr, envir, enclos): x < 0 is not TRUE
```

Using debugging tools

- The simplest way of debugging is to simply insert `print` commands into your code to check that it is returning the correct values.
- This is an incredibly slow way to debug and can prove distracting as the `print` statements can contain bugs too.

- Instead R contains a very useful function, `browser`, which will allow you to explore the internals of a function whilst you are running it.

Using `browser`

- The `browser` function, when inserted into another function, allows you to explore the workspace inside the function as it is being run.
- When `browser` has been called, the R prompt changes from `>` to `Browse[d]>` where `d` is how many environments we are nested in.
- When in `browser` mode there are number of special commands:
  - `n` (for next): advances the program by one line
  - `c` (for continue): will execute the rest of the function and stop again if it hits the `browser` command (which might not happen). You can use Enter for this too.
  - `where`: will give you the stack trace (i.e. the functions that were called beforehand)
  - `Q`: will quit `browser` and go back to the location above where `browser` was called (usually back to the R command prompt).

Some notes about `browser`

- Whilst in `browser` mode you can execute any R command you like. It is usually desirable to explore the objects in the current workspace with commands like `print`, `plot`, `head`, etc.
- Be careful if you have objects named `n` or `c` as the `browser` commands will take priority over them. If you have an object named `n` use `print(n)` to see it.
- You can have multiple calls to `browser` in different functions. The prompt will tell you how 'nested' your current `browser` call is.
- In the next few slides we go through a simple example.

A simple debugging example

SC 1

- Debugging `neglikfun`

A simple wrong example

- Recall the likelihood example of lecture 6:

```r
neglikfun <- function(parameters) {
  beta0 <- parameters[1]
  beta1 <- parameters[2]
  daty0 <- y == 0
  daty1 <- y == 1
  loglikelihood <- sum(log(1 / (1 + exp(-beta0 - beta1*x[daty1])))) +
    sum(log( - (1 / (1 + exp(-beta0 - beta1*x[daty0])))))
    return(-loglikelihood)
  }
neglikfun(c(1,-0.1))
```

```
## [1] NaN
```

- We've made a mistake somewhere, but where?

Debugging the likelihood

- If we insert `browser()` just after the function definition and then run it we end up with:

```
neglikfun <- function(parameters) {
  browser()
  beta0 <- parameters[1]
  beta1 <- parameters[2]
  daty0 <- y == 0
  daty1 <- y == 1
  loglikelihood <- sum(log(1 / (1 + exp(-beta0 - beta1*x[daty1])))) +
    sum(log( - (1 / (1 + exp(-beta0 - beta1*x[daty0])))))
    return(-loglikelihood)
  }
neglikfun(c(1,-0.1))
```

Debugging the likelihood

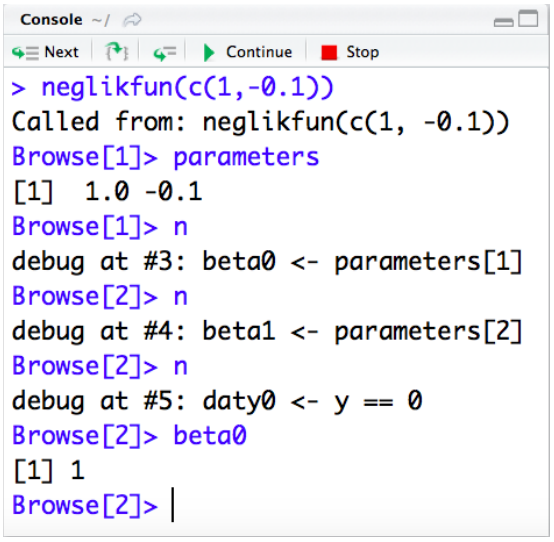
- We can now explore the R workspace to see what's available.
- It's usually a good idea to first check that the function arguments (here `parameters`) were called in correctly:

```
parameters
```

- That seems ok. If we hit `n` a few times we can check whether each line is coming up ok:

```
n
beta0
```

- Note that the line `browser` displays is the line that is about to be run.



```
> neglikfun(c(1,-0.1))
Called from: neglikfun(c(1, -0.1))
Browse[1]> parameters
[1]  1.0 -0.1
Browse[1]> n
debug at #3: beta0 <- parameters[1]
Browse[2]> n
debug at #4: beta1 <- parameters[2]
Browse[2]> n
debug at #5: daty0 <- y == 0
Browse[2]> beta0
[1] 1
Browse[2]>
```

Debugging the likelihood

- We should see that all the lines are working as expected, until we get to this one:

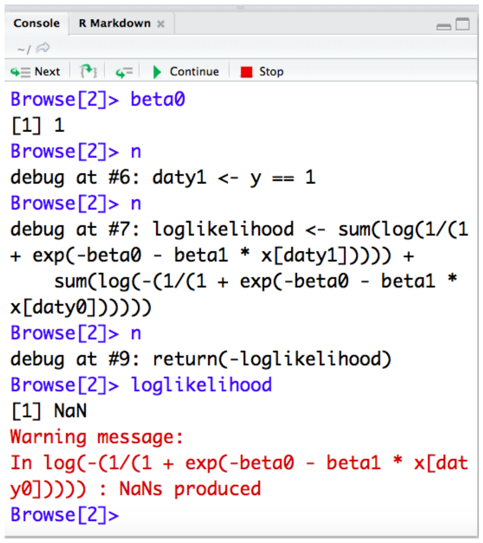
```
loglikelihood
```

- Somewhere in this line there is a mistake in. Let's check each bit:

```
sum(log(- (1/(1 + exp(-beta0 - beta1 * x[daty0])))))
```

- This sum is wrong, I have `log` of negative values - I've missed out a `1`!

```
sum(log(1 - (1/(1 + exp(-beta0 - beta1 * x[daty0])))))
```



```
Browse[2]> beta0
[1] 1
Browse[2]> n
debug at #6: daty1 <- y == 1
Browse[2]> n
debug at #7: loglikelihood <- sum(log(1/(1
+ exp(-beta0 - beta1 * x[daty1])))) +
    sum(log(-(1/(1 + exp(-beta0 - beta1 *
x[daty0])))))
Browse[2]> n
debug at #9: return(-loglikelihood)
Browse[2]> loglikelihood
[1] NaN
Warning message:
In log(-(1/(1 + exp(-beta0 - beta1 * x[dat
y0])))) : NaNs produced
Browse[2]>
```

- You can type `Q` to exit `browser`.

Other debugging tools

- Beyond `browser`
- `trace` and `untrace`
- `traceback`
- Setting breakpoints
- More advanced tools

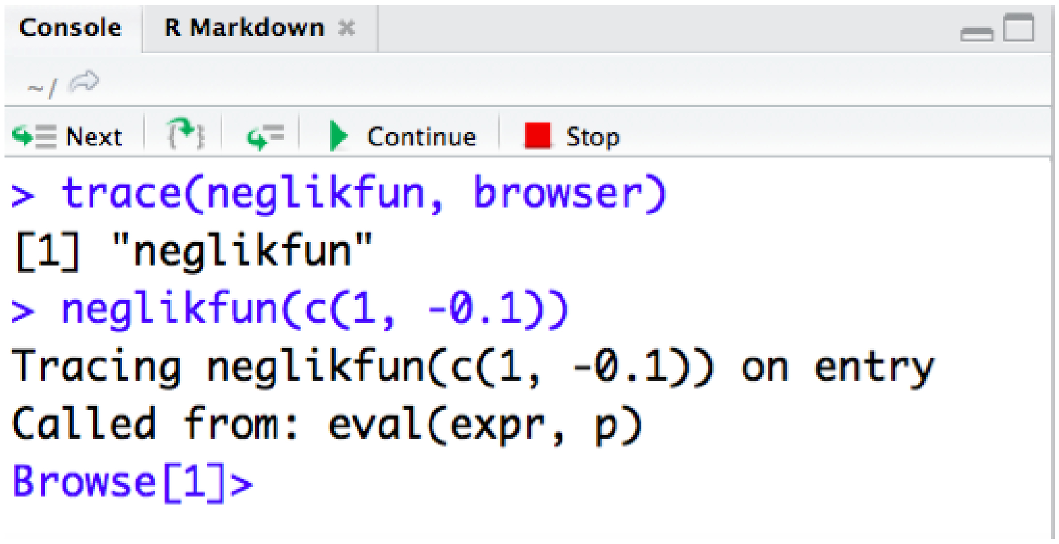
Beyond `browser`

- `browser` is more helpful than putting `print` commands everywhere, but it still involves fiddling around inside your functions.
- A slightly more elegant way of debugging involves calling `debug(neglikfun)` which will call `browser` every time you run the function. You can stop it by calling `undebug(neglikfun)`.
- If you think the bug is only small and you'll fix it immediately (optimistic!) you can run `debugonce(neglikfun)` which will only call `browser` the first time you run the function.
- If you're in a loop and only want to call `browser` once, say, at `i = 20`, you can use `if(i == 20) browser()`
- Remember to hit `Q` when you're finished with `browser`.

`trace` and `untrace`

- `trace` gives you the opportunity to call a function when you enter another function.
- The general syntax is `trace(f, t)` where `t` is the function you want to call (e.g. `browser`) and `f` is the function you want it to be called from.

```r
trace(neglikfun, browser)
neglikfun(c(1, -0.1))
```



```
> trace(neglikfun, browser)
[1] "neglikfun"
> neglikfun(c(1, -0.1))
Tracing neglikfun(c(1, -0.1)) on entry
Called from: eval(expr, p)
Browse[1]>
```

- Of course this is essentially what `debug` is doing, but with far more flexibility.
- We can remove the trace with `untrace(f)`.

`traceback` and `debugger`

- If your code has already crashed and you want to see where, try `traceback()`.
- This will tell you which function crashed and which functions were called before it.
- You can even more information if you have set `options(error = dump.frames)`.
- Once you've done this you can type `debugger()` after the crash and will be able to explore the environments of the different previous functions
- Another is `options(error = recover)` which automatically enters `debugger` when an error is encountered.
- Switch all this off with `options(error = NULL)`.

Setting breakpoints

- Usually, you would put `browser` at the beginning of your function, but often this is unhelpful, as you know the bug occurs later in the code.
- In such cases you might set a breakpoint at certain locations where you think things are about to go wrong. One way to do this is simply to put `browser` at these points.
- Another way is use the `setBreakpoint` function. This works as `setBreakpoint(filename, linenumber)` where `filename` is the name of the `.R` file which contains your function and `linenumber` is the line at which you want to call `browser`
- An example. Suppose you had a call to `browser` and were currently at line 12 of your file `work.R` and you wanted the next `browser` call at line 28. Instead of exiting the function and inserting `browser` there you can just type `setBreakpoint(work.R, 28)` and hit `c`.

Final notes about debugging tools

- Take a look at the Debug menu in RStudio which will allow you to step through code and add breakpoints easily. More information can be found at: https://support.rstudio.com/hc/en-us/articles/

205612627-Debugging-with-RStudio
- There is a package `debug` that includes many more advanced tools for debugging R code.
- If you're dealing with random numbers, use `set.seed(x)` where `x` is some fixed number (e.g. 123) at the start of your code/function so that the random simulations repeat every time you run the code.
- Don't forget the obvious - brackets! More often than not the reason it's not working is because brackets aren't matching.
- If you see any `warnings` don't ignore them - it usually means something went wrong.

Extended example

Debugging `findruns`

Debugging `findruns`.

- Recall our function for finding runs of ones (lecture 2). This is a slightly broken version:

```
findruns <- function(x, k){
  n <- length(x)
  runs <- NULL
  for(i in 1:(n - k)) {
    if(all(x[i:i+k-1] == 1)) runs <- c(runs, i)
    }
  return(runs)
}
```

- Can you spot where the bug(s) are?
- Suppose I had it stored in the file `findruns.R`. I can run:

```
source('findruns.R')
y <- c(1, 0, 0, 1, 1, 1, 0, 1, 1)
findruns(y, 2)
```

```
## [1] 3 4 5 7
```

- This is wrong!

Debugging `findruns`.

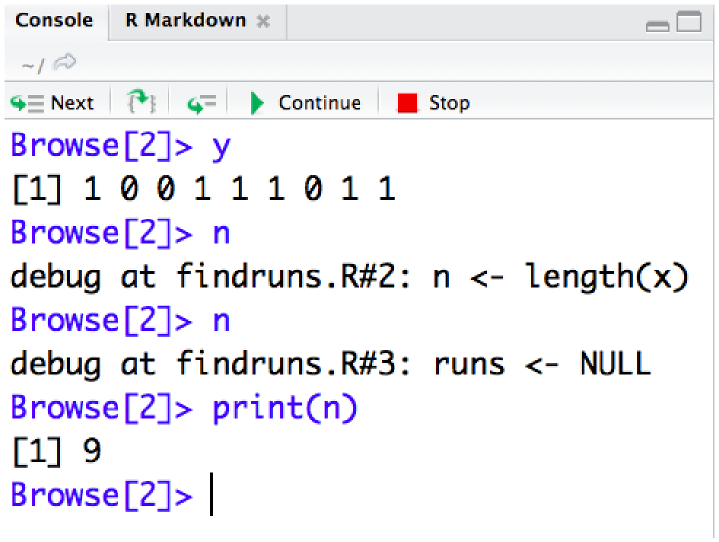
Let's try `debug`:

```
debug(findruns)
findruns(y, 2)
y
```

- That seems ok - it's read in `y`
- Step through a few more times:

```
n
n
print(n)
```

- Note `print(n)` rather than `n`. It seems to have got this correct…



```
Browse[2]> y
[1] 1 0 0 1 1 1 0 1 1
Browse[2]> n
debug at findruns.R#2: n <- length(x)
Browse[2]> n
debug at findruns.R#3: runs <- NULL
Browse[2]> print(n)
[1] 9
Browse[2]>
```

```
n
n
i
```

- Check here that it's selecting the right parts - on the first loop it should be `x[1:2]`

```
x[i:i + k - 1]
```

- No - wrong!

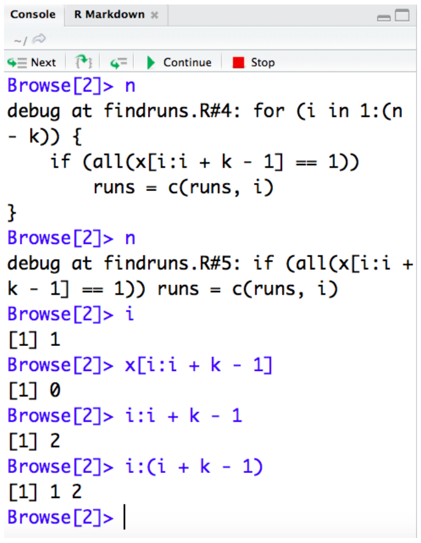
```
i:i + k - 1
```

```
## [1] 2
```

- We've missed a bracket - should be `i:(i+k-1)`!

```
i:(i + k - 1)
```

```
## [1] 1 2
```



```
Browse[2]> n
debug at findruns.R#4: for (i in 1:(n
- k)) {
    if (all(x[i:i + k - 1] == 1))
        runs = c(runs, i)
}
Browse[2]> n
debug at findruns.R#5: if (all(x[i:i +
k - 1] == 1)) runs = c(runs, i)
Browse[2]> i
[1] 1
Browse[2]> x[i:i + k - 1]
[1] 0
Browse[2]> i:i + k - 1
[1] 2
Browse[2]> i:(i + k - 1)
[1] 1 2
Browse[2]>
```

Did that fix it?

```r
findruns <- function(x, k){
  n <- length(x)
  runs <- NULL
  for(i in 1:(n - k)) {
    if(all(x[i:(i+k-1)] == 1)) runs <- c(runs, i)
  }
  return(runs)
}
```

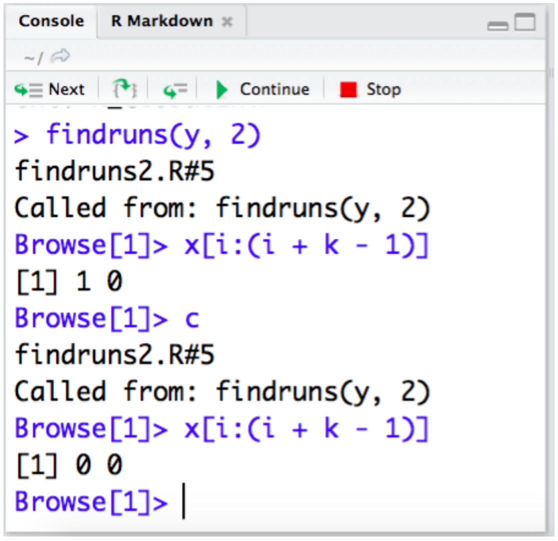
```r
source('findruns2.R')
findruns(y,2)
```

```
## [1] 4 5
```

- No! It should be 4, 5 and 8
- Let's set a breakpoint inside the loop (line 5):

```r
setBreakpoint('findruns2.R', 5)
findruns(y, 2)
x[i:(i + k - 1)]
c
x[i:(i + k - 1)]
```

- It seems to be reading in the right pairs of data - let's set a browser at `i = 8`.



```
> findruns(y, 2)
findruns2.R#5
Called from: findruns(y, 2)
Browse[1]> x[i:(i + k - 1)]
[1] 1 0
Browse[1]> c
findruns2.R#5
Called from: findruns(y, 2)
Browse[1]> x[i:(i + k - 1)]
[1] 0 0
Browse[1]>
```

Final steps

```r
findruns <- function(x, k){
  n <- length(x)
  runs <- NULL
  for(i in 1:(n - k)) {
    if(i == 8) browser()
    if(all(x[i:(i+k-1)] == 1)) runs <- c(runs, i)
  }
  return(runs)
}
```

```
source('findruns3.R')
findruns(y, 2)
```

```
## [1] 4 5
```

- Why isn't it entering `browser`?
- The upper limit of the loop is `n - k = 9 - 2 = 7`. It should be `8`.
- We need to change the loop from `i in 1:(n-k)` to `i in 1:(n-k+1)`

Final steps

```
findruns <- function(x, k){
  n <- length(x)
  runs <- NULL
  for(i in 1:(n - k + 1)) {
    if(all(x[i:(i+k-1)] == 1)) runs <- c(runs, i)
  }
  return(runs)
}
```

```
source('findruns4.R')
findruns(y, 2)
```

```
## [1] 4 5 8
```

- It works!

Lessons from this week

- You can solve many problems by structuring your code well in the first place - write small functions and lots of comments.
- Learn how to use `browser` - it makes debugging far easier.