# **Debugging R code**

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#### Overview

#### Using R's tools

- Call traceback() after error to print the sequence of calls that lead to the error.
- Use debug(faultyFunction) to register faultyFunction for debugging, so that browser() will be called on entry. In browser mode, the execution of an expression is interrupted and it is possible to inspect the environment (with ls()). Use undebug(faultyFunction) to revert to normal usage.
- Use trace() to insert code into functions, start the browser or recover() from error.
- Set options(error=recover) to get the call stack and browse in any of the function calls.
- RStudio has build-in debugging facilities.

Good reference: An Introduction to the Interactive Debugging Tools in Ra

Stojnic and Gatto (CSBC) Debugging November 3, 2014

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ahttp://www.biostat.jhsph.edu/~rpeng/docs/R-debug-tools.pdf

### Debugging example (1)

Let's walk through an example<sup>1</sup>. The buggy setp is:

```
e <- function(i) {
    x <- 1:4
    if (i < 5) x[1:2]
    else x[-1:2] # oops! x[-(1:2)]
}
f <- function() sapply(1:10, e)
g <- function() f()</pre>
```

<sup>&</sup>lt;sup>1</sup>credit Martin Morgan and Robert Gentleman

## Debugging example (2)

```
> g()
Error in x[-1:2] (from #3) : only 0 s may be mixed with negat:
> traceback()
5: FUN(1:10[[5L]], ...)
4: lapply(X = X, FUN = FUN, ...)
```

2: f() at #1

1: g()

3: sapply(1:10, e) at #1

#### Debugging example (3)

Using options(error=recover), we are given a list of frames to debug. Once inside a frame, one can view and modify variables.

```
Error in x[-1:2] (from #3) : only 0 s may be mixed with negat:
Enter a frame number, or 0 to exit

1: g()
2: #1: f()
3: #1: sapply(1:10, e)
4: lapply(X = X, FUN = FUN, ...)
5: FUN(1:10[[5]], ...)
```

Selection:

> g()

## Debugging example (4)

```
Selection: 5
[\ldots]
Browse[1] > ls()
[1] "i" "x"
Browse[1]> c
Enter a frame number, or 0 to exit
1: g()
2: #1: f()
3: #1: sapply(1:10, e)
4: lapply(X = X, FUN = FUN, ...)
5: FUN(1:10[[5]], ...)
Selection: 0
options(error = NULL)
```

### Using the debugger directly

```
> debug(e)
> g()
debugging in: FUN(1:10[[1L]], ...)
debug at #1: {
    x < -1:4
    if (i < 5)
        x[1:2]
    else x[-1:2]
}
Browse[2] > debug at #2: x <- 1:4
Browse[2]> Q
> undebug(e)
```

### Using trace

```
## Report whenever e invoked
trace(e)
## Evaluate arbitrary code whenever e invoked
trace(e, quote(cat("i am", i, "\n")))
## Another way to enter browser whenver e invoked
trace(e, browser)
## stop tracing
untrace(e)
```

## Calling with custom handlers (1)

The withCallingHandlers function allows to defined special behaviour in case of /unusual conditions/, including warnings and errors. In the example below, we start a browser in case of (obscure) warnings.

```
f <- function(x = 10) {
    lapply(seq_len(x), function(i) {
        ## make an example 2x2 contingency table
        d = matrix(sample(4:10, 4), nrow=2, ncol=2)
        ## will produce warning if there is a 5 or less
        ## in the contingency table
        chisq.test(d)
    })
}</pre>
```

# Calling with custom handlers (2)

```
set.seed(1)
f()
set.seed(1)
withCallingHandlers(f(), warning=function(e) recover())
```

#### **Exercise**

The readFasta2 function is similar to readFasta, but reads multiple sequences in a fasta file and returns a list of DnaSeq instances... at least, that's what it is supposed to do.

- ① Get readFasta2.R file with sequences:::debugme(), and try the function with the moreDnaSeqs.fasta file dir(system.file("extdata", package = "sequences"), full.names=TRUE).
- Prepare for debugging: debug(readFasta2).
- Oblige the property of the
- fix the function.

Hint: when debugging, use n (or an empty line) to advance to the next step, c to continue to the end of the current context (to the end of a loop for instance), where to print the stack trace of all active function calls and  $\mathbb Q$  to exit the browser.

Other hint: use ls(all.names=TRUE) to see all objects, also those that start with a '.'.