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 R*[a]

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[a]http://www.biostat.jhsph.edu/~rpeng/docs/R-debug-tools.pdf

Debugging example (1)

Let's walk through an example[1]. The buggy code 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()
```

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[1]credit Martin Morgan and Robert Gentleman

Debugging example (2)

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

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.

```
> g()
Error in x[-1:2] (from #3) : only 0 s may be mixed with negati

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:
```

Debugging example (4)

```
Selection: 5
[...]
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

```r
## 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)
```

```r
require("stats4")
## Debug S4 methods with signature argument
trace("plot", browser, exit = browser,
      signature = c("track", "missing"))
```

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.

```r
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)
    })
}
```

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).

2. Prepare for debugging: debug(readFasta2).

3. Debug!

4. 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 Q to exit the browser.

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