# Debugging the partools and parallel Packages

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I place huge importance on debugging, and indeed, once wrote a book on the topic (*The Art of Debugging with GDB*, *DDD*, and *Eclipse*, N. Matloff and P. Salzman, NSP, 2008). Accordingly, **partools** includes some debugging tools, which by the way apply not only to **partools** but to the **parallel** package in general. This vignette will introduce the usage of those tools.

## 1 Running Example

We'll use this simple file, **fg.R** as our example:

```
f <- function(x) {
    x <- x + 1
    y <- g(x)
    x^2 + y^2
}

g <- function(t) {
    if (t > 0) return(5)
    6
}
```

# 2 The Fundamental Principle of Debugging

Pete Salzman and I make this statement, early in our book on debugging:

Fixing a buggy program is a process of confirming, one by one, that the many things you *believe* to be true about the code actually *are* true. When you find that one of your assumptions is *not* true, you have found a clue to the location (if not the exact nature) of a bug.

In our code above, after executing

```
y \leftarrow g(x)
```

we may believe that **y** should be 5. But we should check that it really is 5. Eventually, we will find a case where our belief is wrong, and thus have a clue about the bug.

## 3 Quick and Dirty Method

The classic way to do the confirmation discussed in the last section is to add code, say that prints out the values of some key variables. This is not generally recommended, because the process of inserting such check code and later removing it is too distracting, making us lose our train of thought. It's much preferable to use a debugging aid, even a primitive one like R's **debug()**, than to insert print statements. We'll use **debug()** in the next section.

But even adding print statements, which we will do in this section, is not so easy as it sounds, because in **parallel** operations, we don't have terminal windows. A statement such as

```
cls <- makeCluster(2)</pre>
```

sets up 2 instantiations of R, but they are not attached to terminal windows, so we can't invoke debug()!

What we can do instead, of course, is insert code that writes confirmation messages to a file rather than to the sccreen. Even that is not so easy, because if all our cluster nodes write to the same file, we have chaos.

Instead, **partools** includes a function **dbsmsg()** that does print to a file, but with the file name having a suffix corresponding to the cluster node number. With a 2-node cluster, the file names would be **dbs.1** and **dbs.2**. We run the code, then check the files.

In the little example above, say, we add the call to **dbsmsg()** and get the code to the cluster nodes:

```
> source('fg.R')
> f
function(x) {
    x <- x + 1
    y <- g(x)
    dbsmsg(y)
    x^2 + y^2
}
> clusterExport(cls,c('f','g'))
```

Then run:

```
> clusterEvalQ(cls,f(8))
```

We then check the files **dbs.1** and **dbs.2** to see the value of y (both 5 in this simple example).

A similar, but somewhat more sophisticated method involves the function  $\mathbf{dbsdump}()$ . We add the call to, say,  $\mathbf{g}()$ , then run:

```
> clusterExport(cls,'g')
> clusterEvalQ(cls,f(8))
This creates one output file for each node. Let's use the one from node 2:
> load('last.dump.2.rda')
> debugger(last.dump.2)
Message: Available environments had calls:
1: parallel:::.slaveRSOCK()
2: slaveLoop(makeSOCKmaster(master, port, timeout, useXDR))
3: tryCatch({
    msg <- recvData(master)</pre>
    if (msg$type == "DONE") {
4: tryCatchList(expr, classes, parentenv, handlers)
5: tryCatchOne(expr, names, parentenv, handlers[[1]])
6: doTryCatch(return(expr), name, parentenv, handler)
7: tryCatch(do.call(msg$data$fun, msg$data$args, quote = TRUE), error = handle
8: tryCatchList(expr, classes, parentenv, handlers)
9: tryCatchOne(expr, names, parentenv, handlers[[1]])
10: doTryCatch(return(expr), name, parentenv, handler)
11: do.call(msg$data$fun, msg$data$args, quote = TRUE)
12: (function (expr, envir = parent.frame(), enclos = if (is.list(envir) || is.
13: eval(expr, envir, enclos)
14: f(8)
15: <tmp>#4: dbsdump()
16: eval(parse(text = cmd))
17: eval(expr, envir, enclos)
Enter an environment number, or 0 to exit Selection: 14
Browsing in the environment with call:
  f(8)
Called from: debugger.look(ind)
Browse[1] > x
Γ1 9
Browse[1]> y
[1] 5
Browse[1] > debug(g)
Browse[1] > g(x)
debugging in: g(x)
debug at <tmp>#1: {
    if (t > 0)
        return(5)
Browse[4]> t
Γ1 9
```

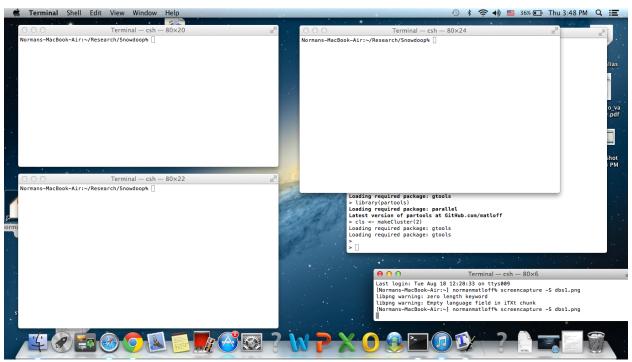
We checked the values of  $\mathbf{x}$  and  $\mathbf{y}$  in  $\mathbf{f}()$ , and then even made a call to  $\mathbf{g}()$ , checking things out there.

Again, this is an exceedingly simple example, but applying these ideas in a more realistic setting would involve the same actions.

## 4 Advanced Method

This method is suitable for more detailed debugging that requires single-stepping through code and so on. It is somewhat more involved, but actually very easy to use after doing it once. It requires a Unix-family system, such as a Mac or a Linux box, or Cygwin on Windows, because it make use of the **screen** utility. It allows you to debug your code with the ordinary R **debug()** facility, with one instantiation of the latter for each of your cluster nodes.

So, here is our initial screen setting:

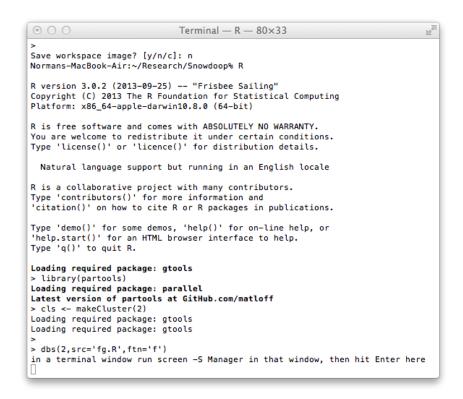


In preparation for running **debug()** on two cluster nodes, we have the two windows on the left. To run the "manager" node, from which **parallel** functions will be called such as

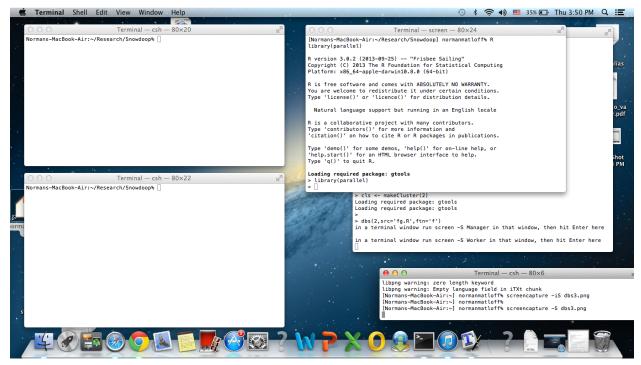
### > clusterEvalQ(cls,f(8))

we have another window on the top right. Under Linux, the creation of these windows can be done automatically.

We launch the debugging from the partially hidden window:



The call to **dbs()** sets up a **parallel** cluster **cls** with 2 nodes, and instructs those nodes to do **source('fg.R')** and **debug(f)**. It also instructs us, the user, to run **screen** in the manager window and in each cluster window, and it starts up R for us in the manager window:



Finally, **dbs()** runs R in the two cluster windows. Those instantiations of R are now waiting for commands.



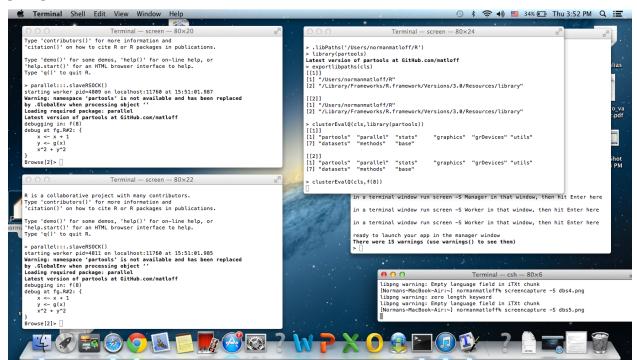
We can now run our **parallel** code normally. So, at the manager window, we type

#### > clusterEvalQ(cls,f(8))

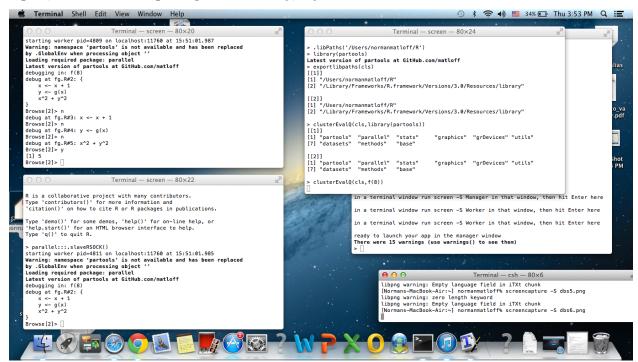
And voila!, we are in debug mode in the two cluster node windows, with the familiar

### Browse[]

#### prompt:



Again, we can then single-step etc. normally, say in the first cluster node window:



Last, when we are done with this debugging sequence, we can kill the **screen** invocations and so on, by calling **killdebug()**:

