Parallel processing with the RNetLogo Package

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Abstract

RNetLogo is a flexible interface for NetLogo to R. It opens various possiblities to connect agent-based models with advanced statistics. It opens the possiblity to use R as the starting point to design systematic experiments with agent-based models and perform parameter fittings and sensitivity analysis. Therefore, it can be necessary to perform repeated (independent) simulations which could be parallelized. Here, I present how such a parallelization can be done for the **RNetLogo** package. The techniques presented here can be used to run multiple simulations in parallel on a single computer with multiple processors or to spread multiple simulations to several processors in computer clusters/grids. Using the **parallel** package has a positive side effect: It enables you to start more than one NetLogo instance with GUI in parallel, which is not possible without parallelization.

Keywords: NetLogo, R, agent based modelling, abm, individual based modelling, ibm, parallelization.

1. Motivation

Since modern computers mostly have more than one processor and agent-based simulations are often complex and time consuming it is desireable to spread repeated simulations, for example for parameter fitting or sensitivity analysis, to multiple processors in parallel. Here, I will present one way of how it is possible to spread multiple NetLogo simulations controlled from R via the **RNetLogo** package to multiple processors.

2. Parallelization in R

R itself is not able to make use of multiple processors of a computer. But there are several R packages available, which enable the user to spread repeated processes to multiple processors. There is a CRAN Task View called "High-Performance and Parallel Computing with R" at http://cran.r-project.org/web/views/HighPerformanceComputing.html. Since R version 2.14.0 there is the **parallel** package included in every standard R installation. In the following I will present how to use this **parallel** package in conjunction with **RNetLogo**. Therefore, to follow the examples it requires that you have an R version >= 2.14.0 installed. There is a pdf file coming with the **parallel** packing giving a short introduction into the usage

of the package and the platform specific differences. You should always start by reading this document. A last note, before we start: The commands presented in the following have been tested on Windows and Linux operation systems only. If you have experiences with Mac OS please let me know.

3. Parallelize a simple process

The basic concept of the **parallel** package is to parallelize an apply (or lapply, sapply etc.) operation. This means that the process you want to parallelize has to be a process which is applied to an array, matrix, list, etc.

Let us start with a simple example without using **RNetLogo**. First, we define a simple function which calculates the square of an input number.

```
R> testfun1 <- function(x) {
+    return(x*x)
+  }
```

We can apply this simple function to a vector of values using `sapply` like this:

```
R> my.v1 <- 1:10
R> print(my.v1)
 [1]  1  2  3  4  5  6  7  8  9 10
R> my.v1.quad <- sapply(my.v1, testfun1)
R> print(my.v1.quad)
 [1]   1   4   9  16  25  36  49  64  81 100
```

The result is a vector with the squared values of the input vector, i.e. the function was applied sequentially to each element of the input vector.

One way to use the **parallel** package is to run the parallel version of the `sapply` function which is called `parSapply`.

Before we can use this function, we have to make/register a cluster, as you know from the manual of the **parallel** package. Therefore, we could, for example, detect the number of cores of our local computer and start a local cluster with this number of processors, as shown here:

```
R> # load the parallel package
R> library(parallel)
R> # detect the number of cores available
R> processors <- detectCores()
R> # create a cluster
R> cl <- makeCluster(processors)
```

Then, we can run our simple function on this cluster. At the end, we should always stop the cluster.

```
R> # call parallel sapply
R> my.v1.quad.par <- parSapply(cl, my.v1, testfun1)
R> print(my.v1.quad.par)
 [1]   1   4   9  16  25  36  49  64  81 100
R> # stop cluster
R> stopCluster(cl)
```

4. Parallelize RNetLogo

As you know from the **RNetLogo** manual, it requires an initialization using the `NLStart` and (maybe) `NLLoadModel` function. To parallelize **RNetLogo** we need this initialization to be done for every processor, because they are independent from each other (which is a very important property, because, for example, random processes in parallel simulations should not beeing influenced by each other).

Therefore, it makes sence to put the initialization, the simulation, and the quiting process into separate functions. These functions can look like the following (if you want to test these, don't forget to adapt the paths appropriate):

```
R> # the initialization function
R> prepro <- function(dummy, gui, nl.path, model.path) {
+    library(RNetLogo)
+    NLStart(nl.path, nl.version=5, gui=gui)
+    NLLoadModel(model.path)
+  }
R> # the simulation function
R> simfun <- function(x) {
+    NLCommand("print ",x)
+    NLCommand("set density", x)
+    NLCommand("setup")
+    NLCommand("go")
+    NLCommand("print count turtles")
+    ret <- data.frame(x, NLReport("count turtles"))
+    names(ret) <- c("x","turtles")
+    return(ret)
+  }
R> # the quit function
R> postpro <- function(x) {
+    NLQuit()
+  }
```

4.1. With Graphical User Interface (GUI)

Now, we have to start the cluster, run the initialization function in each processor, which will open as many NetLogo windows as we have processors.

Note, that this is also a nice way to run multiple NetLogo GUI instances in parallel, which is not possible within one R session without this parallelization.

```
R> # load the parallel package, if not already done
R> require(parallel)
R> # detect the number of cores available
R> processors <- detectCores()
R> # create cluster
R> cl <- makeCluster(processors)
R> # set variables for the start up process
R> # adapt path appropriate (or set an environment variable NETLOGO_PATH)
R> gui <- TRUE
R> nl.path <- Sys.getenv("NETLOGO_PATH", "C:/Program Files/NetLogo 5.0.3")
R> model.path <- "models/Sample Models/Earth Science/Fire.nlogo"
R> # load NetLogo in each processor/core
R> invisible(parLapply(cl, 1:processors, prepro, gui=gui,
+                       nl.path=nl.path, model.path=model.path))
```

After the initialization is done in all processors, we can run the simulation. Here, we will use the Fire model from NetLogo's Model Library. We will vary the density value from 1 to 20, i.e. we will run 20 independent simulations each with a different density value.

```
R> # create a vector with 20 density values
R> density <- 1:20
R> print(density)
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20


R> # run a simulation for each density value
R> # by calling parallel sapply
R> result.par <- parSapply(cl, density, simfun)


R> print(data.frame(t(result.par)))
    x turtles
1   1     252
2   2     261
3   3     261
4   4     264
5   5     261
6   6     265
7   7     269
8   8     269
9   9     277
10 10     276
11 11     273
```

```
12 12     284
13 13     279
14 14     289
15 15     282
16 16     289
17 17     302
18 18     296
19 19     300
20 20     294
```

At the end, we should stop all NetLogo instances and the cluster.

```
R> # Quit NetLogo in each processor/core
R> invisible(parLapply(cl, 1:processors, postpro))
R> # stop cluster
R> stopCluster(cl)
```

4.2. Headless

The same is possible with the headless mode, i.e. without the GUI. We just have to set the variable `gui` to `FALSE`.

It can look like this:

```
R> # run in headless mode
R> gui <- FALSE
R> # create cluster
R> cl <- makeCluster(processors)
R> # load NetLogo in each processor/core
R> invisible(parLapply(cl, 1:processors, prepro, gui=gui,
+                       nl.path=nl.path, model.path=model.path))


R> # create a vector with 20 density values
R> density <- 1:20
R> print(density)
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20


R> # run a simulation for each density value
R> # by calling parallel sapply
R> result.par <- parSapply(cl, density, simfun)


R> print(data.frame(t(result.par)))
```

```
    x turtles
1   1     253
2   2     256
3   3     259
4   4     258
5   5     268
6   6     267
7   7     272
8   8     272
9   9     278
10 10     278
11 11     280
12 12     281
13 13     276
14 14     284
15 15     290
16 16     295
17 17     296
18 18     295
19 19     300
20 20     289
```

```
R> # Quit NetLogo in each processor/core
R> invisible(parLapply(cl, 1:processors, postpro))
R> # stop cluster
R> stopCluster(cl)
```

5. Conclusion

We have seen one way of how it is possible to spread repeated and independent simulations to multiple processors using the **parallel** package. Therefore, **RNetLogo** can be efficiently used to perform parameter fittings and sensitivity analyses where large number of repeated simultions are required.

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