

# Parallel R

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Why **R**? The **R** language has a lot of advantages:

- Open Source.
- Cross-Platform.
- Free.
- Many basic tools.
- **R** extensions.
- Arguably fast with **R**-way style and well-implemented **R** distribution.

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*Solution:* [Parallel Execution](#). How exactly?

- Single-threaded: multiple CPU's (and cores).
- Memory-bound: spread data from one computer (master) to several computers (slaves).

The two types of parallelism:

- **Implicit** — the OS abstracts parallelism from the user.
- **Explicit** — user controls details of the process.

A **computer cluster** consists of a set of loosely or tightly connected computers that work together so that, in many respects, they can be viewed as a single system (Wiki).

**Master/slave** is a model of communication where one device or process has unidirectional control over one or more other devices (Wiki).

## **snow**

Explicit parallelism by using

*Usage:* clusters (works on Linux,  
Windows, Mac OS X).

*Solves:* Single-threaded, memory-bound.

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## **Hadoop**

**R** + Hadoop, RHIPE, Segue.

*“... R was not built in anticipation of the Big Data revolution. R was born in 1995. Disk space was expensive, RAM even more so, and this thing called The Internet was just getting its legs. Notions of “large-scale data analysis” and “high-performance computing” were reasonably rare. Outside of Wall Street firms and university research labs, there just wasn’t that much data to crunch.”*

— Q. Ethan McCallum and Stephen Weston “Parallel **R**”

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*General use case:* Main word is `cluster`, provides `explicit` parallelism.

*Examples:* Monte Carlo simulations, bootstrapping, cross validation, ensemble machine learning algorithms.

*Solves:* Single-threaded, memory-bound.

*Cool features:*

- Different transport mechanisms between Master and Slaves: Sockets, MPI (`rmpi`), NWS (`nws`), PVM (`rpvm`).
- Good support of RNG (`rsprng`, `rlecuyer`).

*Problems:* No communication between the workers (slaves).

## snow: quick look

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*Problems:* No communication between the workers (slaves).

*Warning:* The input arguments **must fit** into memory when calling **snow** function. Its up to the user to arrange high-performance distributed file systems.

*Start and stop clusters:* `makeCluster`, `stopCluster`.

*Low-level (cluster-level) functions:* `cluster*` — `clusterApply`, `clusterApplyLB`, `clusterEvalQ`, `clusterCall`, `clusterSplit`, etc.

*High-level functions:* `par[L,S,A,R,C]apply` — parallel versions of `apply` and related functions.

*(Uniform) RNG:* `L'Ecuyer` (package: `rlecuyer`),  
`SPRNG [deprecated]` (package: `rsprng`).

*Timing:* `snow.time(expr)` — very useful.



# Start and stop clusters

Basic way:

```
c1 <- makeCluster(8, type = "SOCK") # or you may use  
                                     # makeSOCKcluster(),  
                                     # makePVMcluster(), etc.  
stopCluster(c1)
```

First parameter is spec — specification. It is ssh-configurable unless you type "localhost":

```
c1 <- makeCluster(c("localhost", "localhost"), type = "SOCK")  
stopCluster(c1)
```

*Warning:* Be aware of computational costs of cluster setup.

All of them are `cluster*` and designed for computing *on* a cluster. Most interesting are as follows.

<code>clusterApply(cl, x, fun, ...)</code>	Jobs are being “recycled”.
<code>clusterApplyLB(cl, x, fun, ...)</code>	Load Balancing version of <code>clusterApply()</code> .
<code>clusterCall(cl, fun, ...)</code>	Calls a function <code>fun</code> with identical arguments ... on each node in the cluster <code>cl</code> and returns a list of the results.
<code>clusterEvalQ(cl, expr)</code>	Evaluates an expression <code>expr</code> on each node in the cluster <code>cl</code> ; implemented using <code>clusterCall()</code> .
<code>clusterMap(cl, fun, ...,   MoreArgs = NULL, RECYCLE = TRUE)</code>	Similar to <code>mapply</code> .

# Example, K-means

Basic one-core way:

```
library(MASS)
result <- kmeans(Boston, 4,
                 nstart=100)
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Before using snow it is easier to think  
\*apply-way:

```
results <- lapply(rep(25, 4),
                  function(nstart)
                    kmeans(Boston, 4, nstart=nstart)
                  )
i <- sapply(results,
            function(result)
              result$tot.withinss
            )
result <- results[[which.min(i)]]
```

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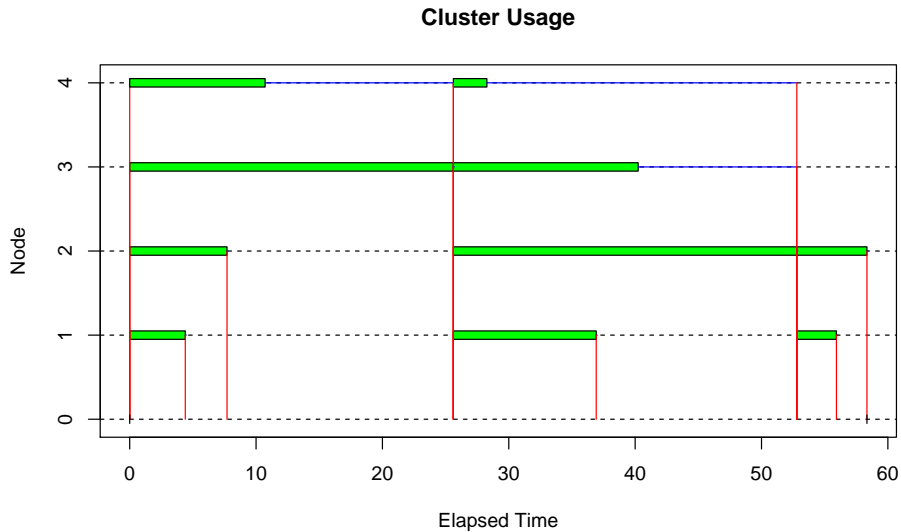
```
results <- lapply(rep(25, 4),
                  function(nstart)
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                  )
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            )
result <- results[[which.min(i)]]
```

Finally snow version.

```
ignore <-
  clusterEvalQ(cl, {library(MASS); NULL})
results <-
  clusterApply(cl, rep(25, 4),
              function(nstart)
                kmeans(Boston, 4, nstart=nstart)
              )
i <- sapply(results,
            function(result)
              result$tot.withinss
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```

`clusterApply()` uses a *robin-round* fashion for scheduling tasks for clusters. It means one time for every cluster. It could be not very wise to do that.

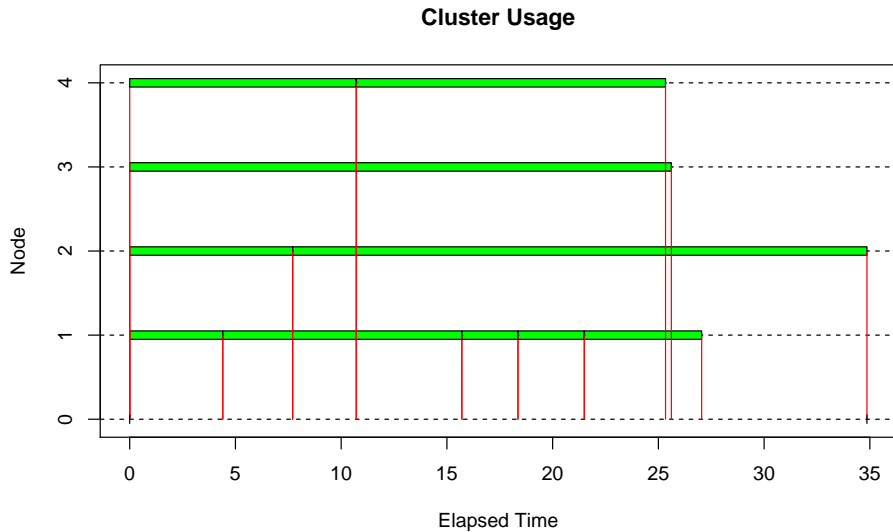
```
set.seed(123)
sleeptime <- abs(rnorm(10, 10, 10))
tm <- snow.time(clusterApply(cl, sleeptime, Sys.sleep))
```



So we waited for more than 50 seconds. A more efficient way would be pull the tasks to clusters when they are needed. This technique is called “load balancing”. Function `clusterApplyLB()` uses that technique.

```
set.seed(123)
sleeptime <- abs(rnorm(10, 10, 10))
tm <- snow.time(clusterApplyLB(cl, sleeptime, Sys.sleep))
```





So, here we waited for about 30 seconds. This is an improvement. The only wasted time was at the end.

<code>parLapply(cl, x, fun, ...)</code>	Parallel version of <code>lapply()</code> .
<code>parSapply(cl, X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)</code>	Parallel version of <code>sapply()</code> .
<code>parApply(cl, X, MARGIN, FUN, ...)</code>	Parallel version of <code>apply()</code> .
<code>parRapply(cl, x, fun, ...)</code>	Row <code>apply()</code> for matrix.
<code>parCapply(cl, x, fun, ...)</code>	Column <code>apply()</code> for matrix.

The most useful is `parLapply()` function. It is different from `clusterApply()` because it splits the task into “equal” tasks.

```
parLapply
```

```
## function (cl, x, fun, ...)  
## docall(c, clusterApply(cl, splitList(x, length(cl)), lapply,  
##     fun, ...))  
## <environment: namespace:snow>
```

where `splitList()` is an internal `snow` function.

## Example of comparison `clusterApply()` and `parLapply()`

`parLapply()` could be more efficient if you have more tasks than workers. Another situation — you send large arguments to `parLapply()`. Let's take a look at the example.

```
bigsleep <- function(sleeptime, mat) Sys.sleep(sleeptime)
bigmatrix <- matrix(0, 2000, 2000)
sleeptime <- rep(1, 100)
```

Firstly, let's try `clusterApply()`.

# Example of comparison `clusterApply()` and `parLapply()`



## Example of comparison `clusterApply()` and `parLapply()`

Definitely not highly efficient. Those gaps are due to I/O time. Ideally we should have 25 seconds... Let's give `parLapply()` a try.

# Example of comparison `clusterApply()` and `parLapply()`



# Load Balancing parLapply?



# Load Balancing parLapply?

Short answer: no, there is no such a function in snow package.  
Good news: it is possible to write your own.

There are 2 basic steps.

- 1 Configure your cluster workers to use a generator.

```
library(rlecuyer)
clusterSetupRNG(cl, type = 'RNGstream')

## [1] "RNGstream"
```

- 2 Be happy to generate your numbers.

```
unlist(clusterCall(cl, runif, 1))

## [1] 0.12701112 0.75958186 0.72850979 0.09570262
```

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## Multicore *[deprecated]* : quick look

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*General use case:* Main word is `fork` (thus no Windows support), provides `implicit` parallelism.

*Examples:* `lapply()` runs for ages on your Intel Core i999.

*Solves:* Single-threaded.

- No Windows support.
- No internal RNG support.
- Problems:*
  - Runs only on one computer.
  - Cannot be used with **R** GUI.
  - No internal Load Balancing, however, it can be imitated.

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*Problems:*

- Runs only on one computer.
- Cannot be used with **R** GUI.
- No internal Load Balancing, however, it can be imitated.

*Warning:* Jobs started by `multicore` share the same state (because of `fork`).

We will only consider *high-level* API and let *low-level* to be out-of-scope.

<code>mclapply()</code>	Parallel version of <code>lapply()</code> .
-------------------------	---

<code>mcmapply()</code>	Parallel version of <code>mapply()</code> .
-------------------------	---

<code>pvec()</code>	Somewhat an high-level analog of low-level <code>clusterSplit()</code> function.
---------------------	--

<code>parallel()</code> and <code>collect()</code>	<code>parallel()</code> creates a new process with <code>fork()</code> , evaluate expression in parallel and after that the result is retrieved by the <code>collect()</code> .
--	---



`mclapply()` is a parallel `lapply()`.

Syntax is as follows:

```
mclapply(X, FUN, ..., mc.preschedule = TRUE, mc.set.seed = TRUE,  
         mc.silent = FALSE, mc.cores = getOption("mc.cores"))
```

where

- 1 `mc.preschedule = TRUE` — how jobs are created for `X`.
- 2 `mc.set.seed = TRUE` — do you need to randomly seed slaves, or fork it?
- 3 `mc.silent = FALSE` — hide info from 'stdout' for all parallel forked processes. 'stderr' is not affected.
- 4 `mc.cores == getOption("mc.cores")` — number of **workers** (not cores, actually) to start.

Meaning:

- TRUE: divide data in `mc.cores-jobs` beforehand and fork it to `mc.cores-processes`.
- FALSE: for each piece of data construct a new job (up to `mc.cores`).

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## Rule of thumb: use

- TRUE: you don't need load balance (for instance, if there are lot's of values in the data).
- FALSE: the variance of job completion is very high (so, you need load balance).

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*General use case:* Main word is [mainstream](#),  
almost a wrapper of `snow` and `multicore` packages.

*Examples:* Anything above.

*Solves:* Single-threaded and (partially) memory-bound.

- Preinstalled into **R** since 2.14.0.
  - Full RNG support with no dependency on `rlecuyer` package.
- Cool features:*
- Almost nothing to learn (if you are still awake).
  - Can be easily used on any platform including Windows.
  - Highly compatible with `snow` and `multicore`.

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*Cool features:*

*Warning:* On Windows you can't use more than one machine.  
It also can be difficult to configure multiple Linux machines.

How many cores?

```
library(parallel)
mc.cores <- detectCores()
mc.cores

## [1] 8
```

*Warning:* It is important to take into account that you maybe have hyper-threading.

Unlike snow package no additional packages (like rlecuyer) are needed.

Fork (no Windows) way:

```
RNGkind("L'Ecuyer-CMRG")
unlist(mclapply(rep(1,4), runif))

## [1] 0.3768615 0.3824588 0.3845725 0.9092709
```

Cluster way:

```
detach("package:snow", character.only=TRUE)
library(parallel)
RNGkind("L'Ecuyer-CMRG")
cl <- makeCluster(2, type="PSOCK")
unlist(clusterCall(cl, function(x) runif(2)))

## [1] 0.3114024 0.9506436 0.6032429 0.8057068

stopCluster(cl)
```



## parallel RNG: reproducible results

Basic way to get reproducible results would be `mc.reset.stream()` — the parallel random number generator is reinitialized using the current seed on the master.

```
detach("package:snow", character.only=TRUE)
library(parallel)
RNGkind("L'Ecuyer-CMRG")
cl <- makeCluster(2, type="PSOCK")
clusterSetRNGStream(cl, 123)
unlist(clusterCall(cl, function(x) runif(2)))

## [1] 0.1663742 0.3898457 0.3411064 0.9712727

clusterSetRNGStream(cl, 123)
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stopCluster(cl)
```

Let's sum up the differences between modern parallel package and his predecessors.

`parallel > multicore`

- Prefix `mc` in `mcfork()`, `mcexit()`, `mckill()`, `mcpipeline()`, `mccollect()`, `mc.cores`.
- Different default value of `mc.cores` argument.
- New `mc.reset.stream()` function.

`parallel ≠ snow`

- New function `clusterSetRNGStream()` initializes parallel RNG.
- `snow.time()` function not included.
- `makeCluster()` supports additional types FORK.

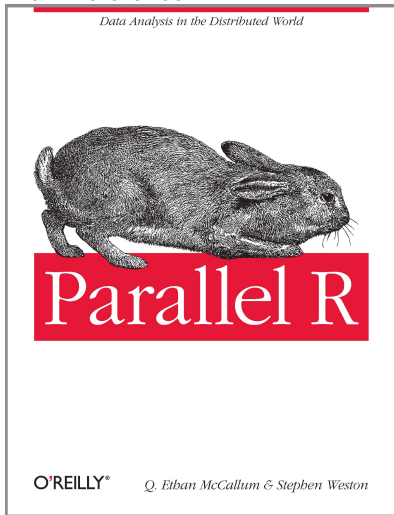
Also useful `detectCores()` is added.

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We covered 3 (2.5 really) packages: `snow`, `multicore`, `parallel`. What else?

- *Revolution Analytics* `foreach` package for iteration over a set of values.
- MapReduce via Java Hadoop: RHIPE (negotiator between you with your MapReduce functions and Hadoop).
- Segue for Amazon Elastic MapReduce lovers. Be aware of terminating clusters.
- `doRedis`.
- <http://cloudNumbers.com>
- **R** and GPUs: `gputools` etc.

## Main reference:



## Useful links:

- [Advanced R](#) by Hadley Wickham.
- [The R Inferno](#) by Patrick Burns.
- [R Packages](#) by Hadley Wickham.
- [Writing R Extensions](#).
- [Los Angeles R Users Group: Parallelization in R, Revisited](#) by Ryan R. Rosario.
- [Package parallel manual](#).