Parallel Computing with R

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Parallel Computing: Why?

- Getting results faster
  - Running in parallel **may** speed up the time to reach solution

Example: Moving 200 boxes by 1 person vs. 10 people

- Dealing with bigger data sets
  - Running in parallel **may** allow you to use more memory than that available on a single computer

Example: Moving a grand piano by 1 person vs. 10 people

Parallel Computing: How?

- Identify a group of workers
  - For sake of simplicity we will use worker/process/thread interchangeably
- Divide the workload into chunks
- Assign one chunk or a number of chunks to each worker
- Each worker processes its own assignment **in parallel** with other workers

Parallel Computing: Requirements

- Hardware: modern computers are equipped with more than one CPU core and are capable of processing workloads in parallel
  - Your laptop/desktop/workstation has many cores
  - HPC clusters is composed of many nodes (servers), each of which has many cores
- Software: many software packages are aware of parallel hardware and are capable of coordinating workload processing among workers

Parallel Computing: Requirements

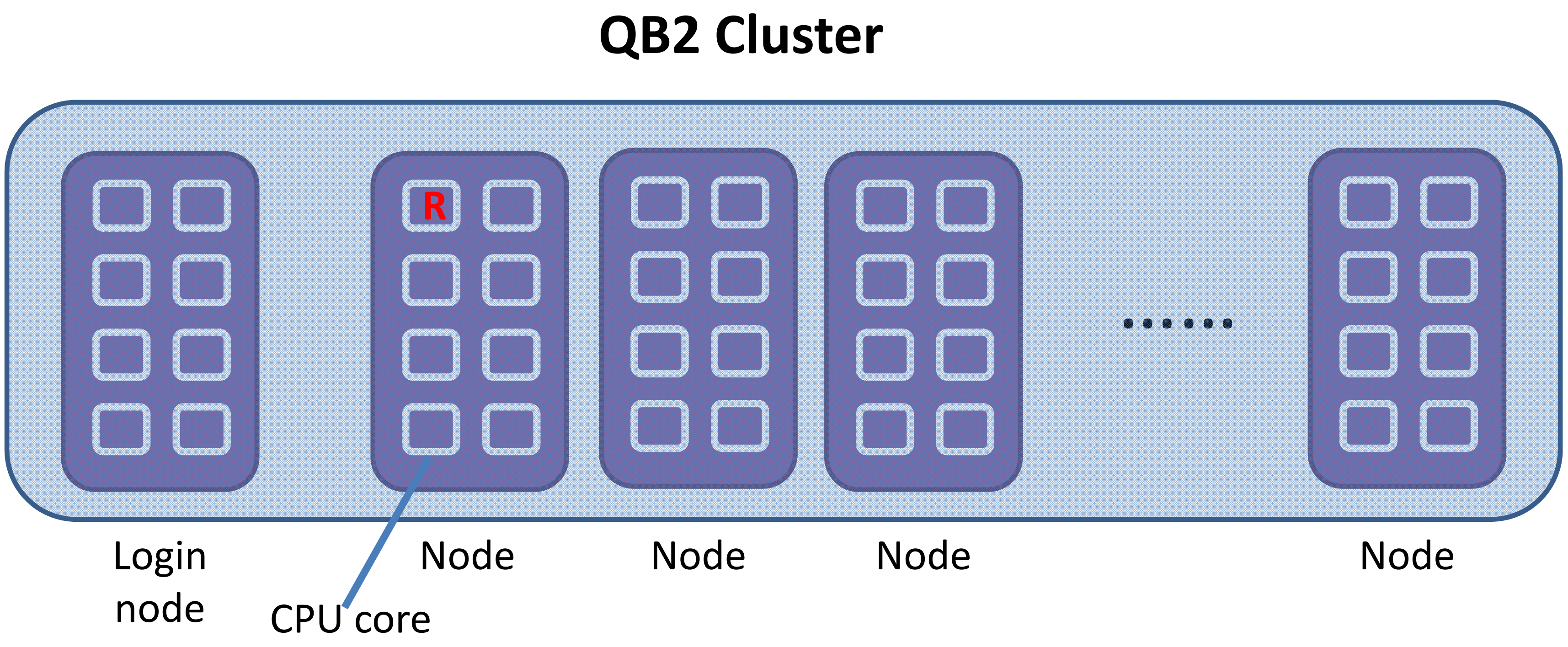
- Hardware: modern computers are equipped with more than one CPU core and are capable of processing workloads in parallel
  - Your laptop/desktop/workstation has many cores
  - HPC clusters is composed of many nodes (servers), each of which has many cores
- Base R is single-threaded, i.e. not parallel
  - Regardless how many cores are available, R can only use one of them

Parallel Computing: Requirements

- Hardware: modern computers are equipped with more than one CPU core and are capable of processing workloads in parallel
  - Your laptop/desktop/workstation has many cores
  - HPC clusters is composed of many nodes (servers), each of which has many cores
- Bas
  - R only u

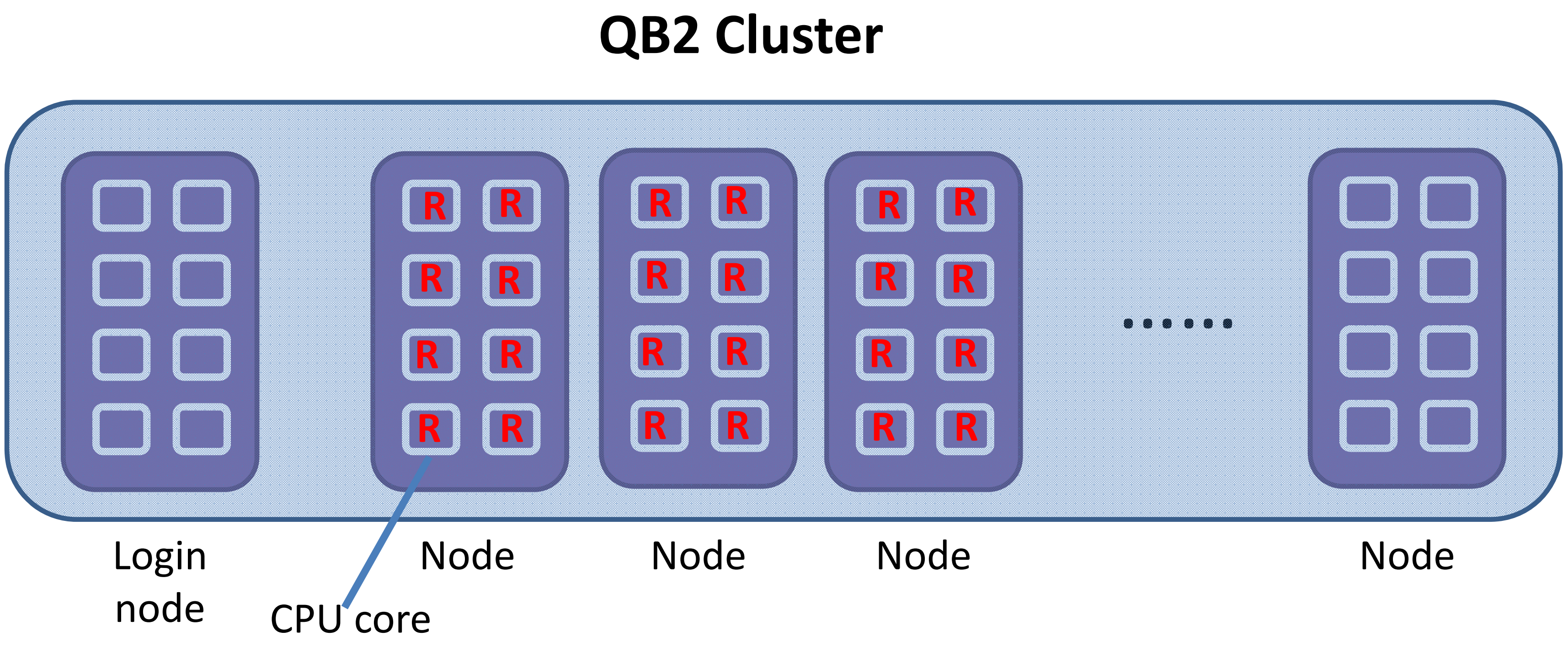
The goal of this training is to show how to use some R packages to achieve parallel processing

Where We Are with Base R



Cluster = multiple nodes (servers) x multiple cores per node

What We Want to Achieve



Cluster = multiple nodes (servers) x multiple cores per node

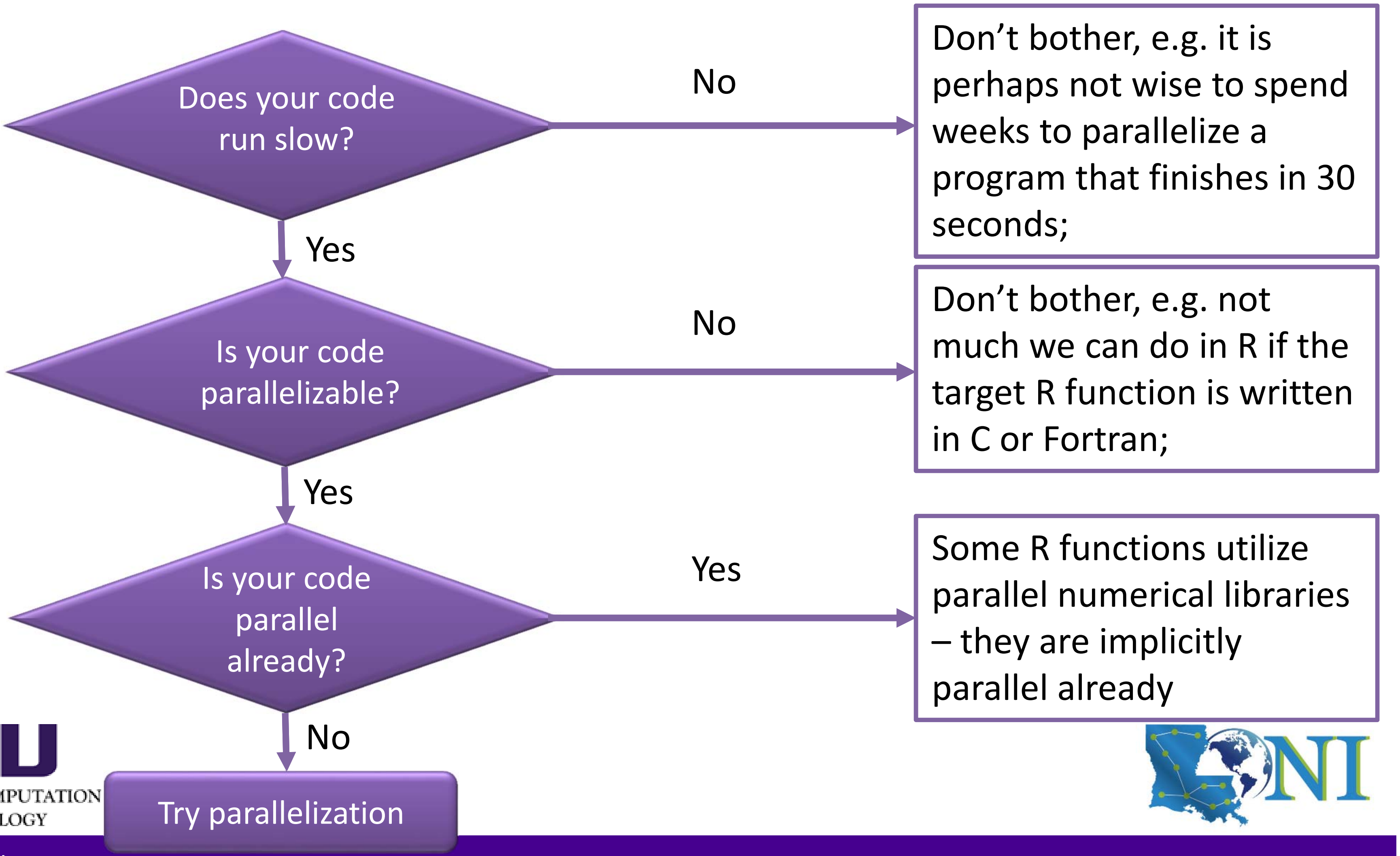
Parallel Computing: Caveats

- Using more workers does not always make your program run faster

Example: Moving 200 boxes by 200 people vs. 1,000 people

- **Efficiency** of parallel programs
  - Low efficiency means idle workers and vice versa
  - Defined as speedup divided by number of workers
    - 4 workers, 3x speedup, efficiency = 3/4 = 75%
    - 8 workers, 4x speedup, efficiency = 4/8 = 50%
  - Usually decrease with increasing number of workers

Is Parallel Computing for You?



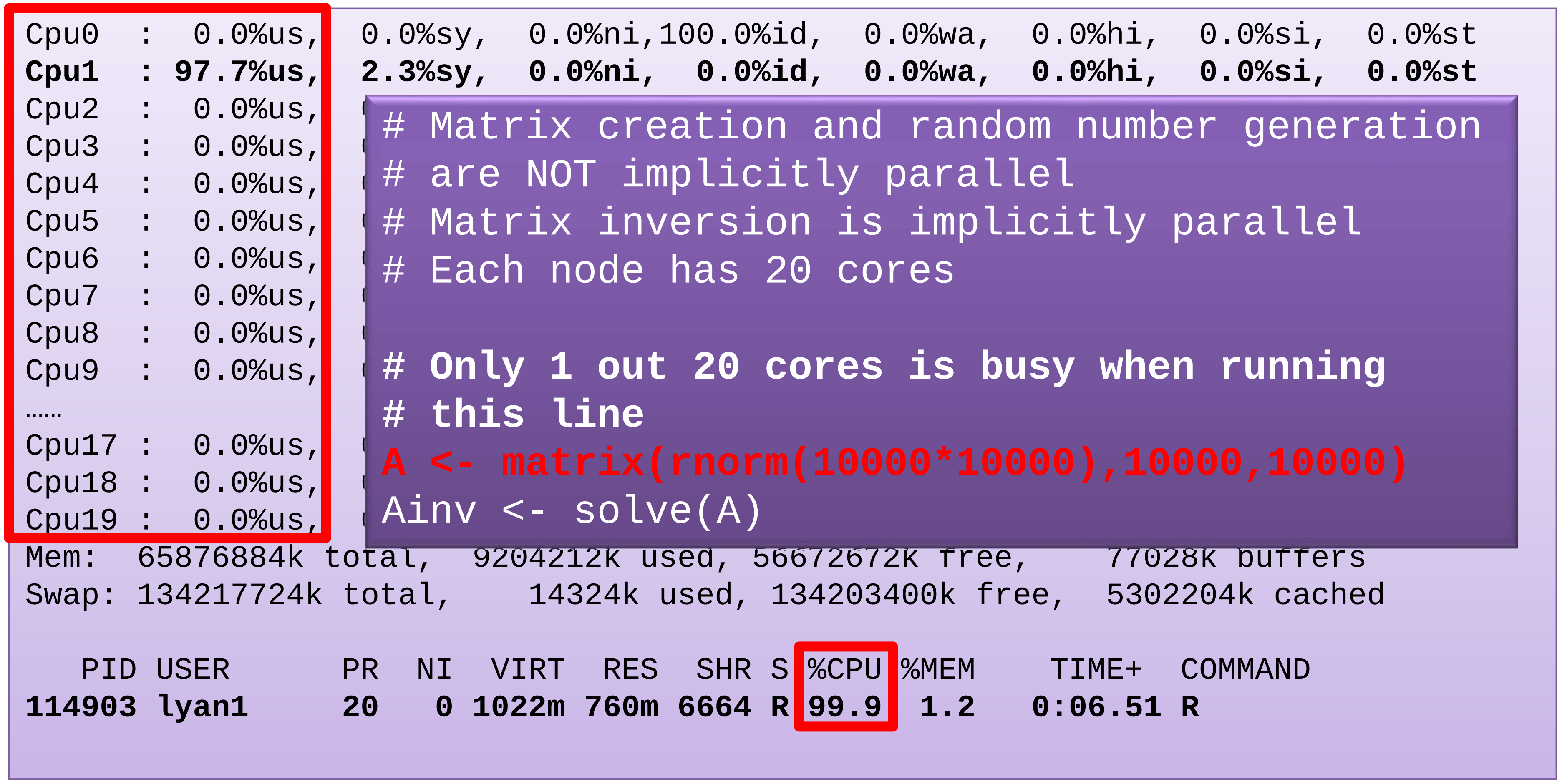
Don't bother, e.g. it is perhaps not wise to spend weeks to parallelize a program that finishes in 30 seconds;

Don't bother, e.g. not much we can do in R if the target R function is written in C or Fortran;

Some R functions utilize parallel numerical libraries – they are implicitly parallel already

Implicit Parallelization

- Some functions in R can call parallel numerical libraries
  - On LONI and LSU HPC clusters this is the multi-threaded Intel MKL library
  - Mostly linear algebraic and related functions
    - Example: linear regression, matrix decomposition, computing inverse and determinant of a matrix



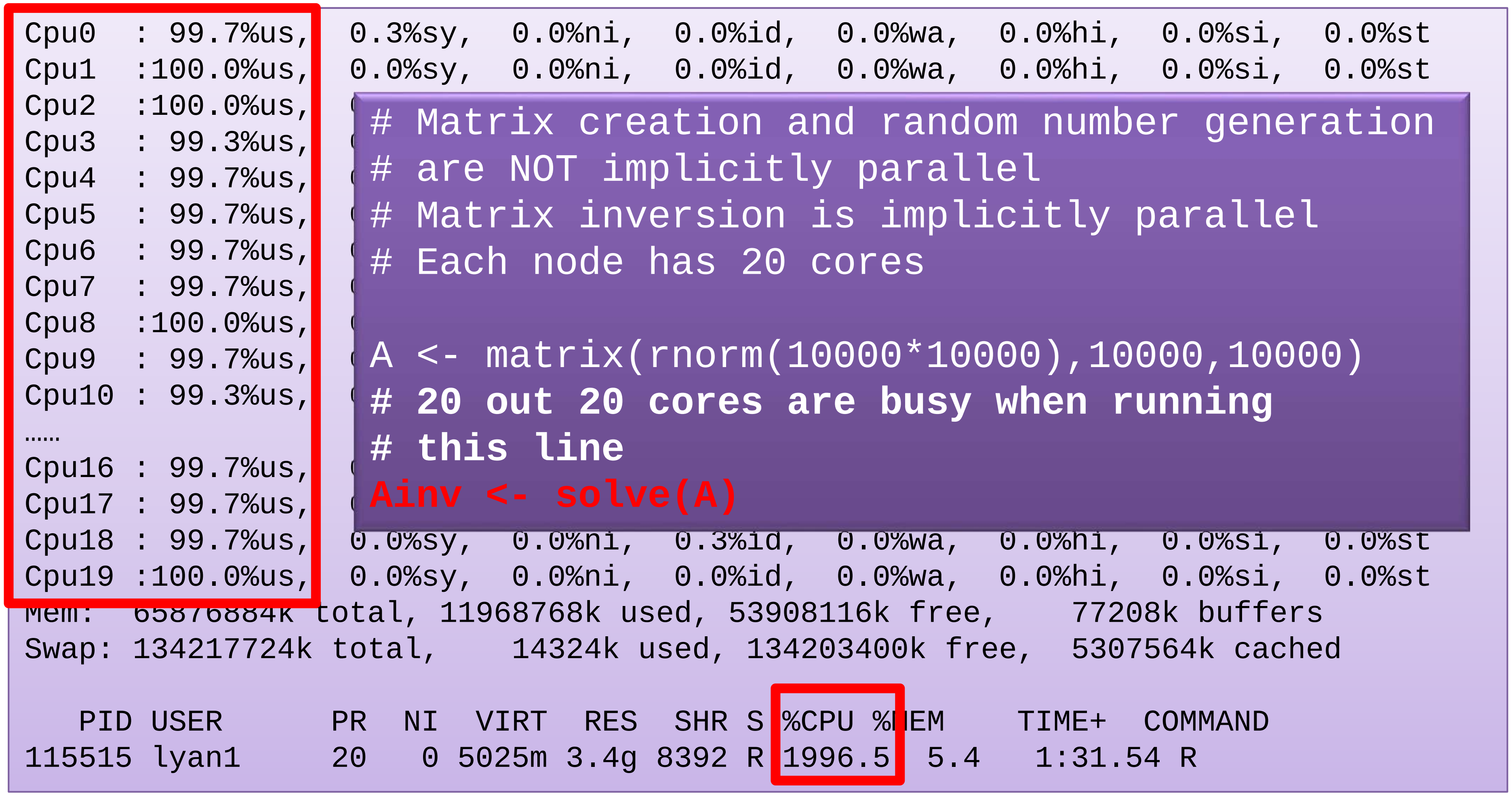
```
Cpu0  :  0.0%us,  0.0%sy,  0.0%ni,100.0%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Cpu1  : 97.7%us,  2.3%sy,  0.0%ni,  0.0%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Cpu2  :  0.0%us,
Cpu3  :  0.0%us,
Cpu4  :  0.0%us,
Cpu5  :  0.0%us,
Cpu6  :  0.0%us,
Cpu7  :  0.0%us,
Cpu8  :  0.0%us,
Cpu9  :  0.0%us,
……
Cpu17 :  0.0%us,
Cpu18 :  0.0%us,
Cpu19 :  0.0%us,
Mem:   65876884k total,  9204212k used, 56672672k free,    77028k buffers
Swap: 134217724k total,    14324k used, 134203400k free,  5302204k cached

   PID USER      PR  NI  VIRT  RES  SHR S %CPU %MEM    TIME+  COMMAND
114903 lyan1     20   0 1022m 760m 6664 R 99.9  1.2   0:06.51 R
```

```
# Matrix creation and random number generation
# are NOT implicitly parallel
# Matrix inversion is implicitly parallel
# Each node has 20 cores

# Only 1 out 20 cores is busy when running
# this line
A <- matrix(rnorm(10000*10000),10000,10000)
Ainv <- solve(A)
```

R running on one node of the QB2 cluster:
20 cores total, 1 busy, 19 idle



```
Cpu0  : 99.7%us,  0.3%sy,  0.0%ni,  0.0%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Cpu1  :100.0%us,  0.0%sy,  0.0%ni,  0.0%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Cpu2  :100.0%us,
Cpu3  : 99.3%us,
Cpu4  : 99.7%us,
Cpu5  : 99.7%us,
Cpu6  : 99.7%us,
Cpu7  : 99.7%us,
Cpu8  :100.0%us,
Cpu9  : 99.7%us,
Cpu10 : 99.3%us,
……
Cpu16 : 99.7%us,
Cpu17 : 99.7%us,
Cpu18 : 99.7%us,  0.0%sy,  0.0%ni,  0.3%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Cpu19 :100.0%us,  0.0%sy,  0.0%ni,  0.0%id,  0.0%wa,  0.0%hi,  0.0%si,  0.0%st
Mem:  65876884k total, 11968768k used, 53908116k free,    77208k buffers
Swap: 134217724k total,    14324k used, 134203400k free,  5307564k cached

   PID USER      PR  NI  VIRT  RES  SHR S %CPU %MEM    TIME+  COMMAND
115515 lyan1     20   0 5025m 3.4g 8392 R 1996.5  5.4   1:31.54 R
```

```
# Matrix creation and random number generation
# are NOT implicitly parallel
# Matrix inversion is implicitly parallel
# Each node has 20 cores

A <- matrix(rnorm(10000*10000),10000,10000)
# 20 out 20 cores are busy when running
# this line
Ainv <- solve(A)
```

R running on one node of the QB2 cluster:
20 cores total, 20 busy, 0 idle

Know Your R Program

- Before starting writing programs, you need to be able to answer these questions
  - How do I know the program runs faster after parallelization?
  - Which part of my code slows the execution down (the most)?
- First step in parallelization: performance analysis
  - Purpose: know which part takes how long, and locate the "hotspot" first
  - Two most frequent used methods in R
    - `system.time()`
    - `rprof()` and `summaryRprof()`

system.time()

```
## Output from system.time() function
## User: time spent in user-mode
## System: time spent in kernel (I/O etc.)
## Elapsed: wall clock time

## Usage: system.time(<code segment>)

system.time(
{
  A <- matrix(rnorm(10000*10000),10000,10000)
  Ainv <- solve(A)
})
   user  system elapsed
156.582   0.948  16.325
```

How much wall clock time it takes - perhaps the most important metric

system.time()

Code

```
[lyan1@qb032 R]$ cat inv_st.R

print("Matrix creation:")
system.time({
A <- matrix(rnorm(10000*10000),10000,10000)
})

print("Matrix inversion:")
system.time({
Ainv <- solve(A)
})
```

Measure the execution times of different functions

Output

```
[lyan1@qb032 R]$ Rscript inv_st.R

[1] "Matrix creation:"
   user  system elapsed
  7.437   0.278   7.711
[1] "Matrix inversion:"
   user  system elapsed
149.092   0.768   9.417
```

Note the huge discrepancy between “user” and “elapsed” – it is an indication of implicit parallelization

rprof() and summaryRprof()

Start profiling

End profiling

Print profiling result

```
[lyan1@qb032 R]$ cat inv_prof.R

Rprof()
A <- matrix(rnorm(10000*10000),10000,10000)
Ainv <- solve(A)
Rprof(NULL)
summaryRprof()
```

CENTER FOR COMPUTATION & TECHNOLOGY

rprof() and summaryRprof()

```
[lyan1@qb032 R]$ Rscript inv_prof.R

$by.self
                  self.time self.pct total.time total.pct
"solve.default"      153.36    95.09     153.58     95.23
".External"            6.68     4.14       6.68      4.14
"matrix"               1.02     0.63       7.70      4.77
"diag"                 0.22     0.14       0.22      0.14

$by.total
                  total.time total.pct self.time self.pct
"solve.default"       153.58     95.23    153.36    95.09
"solve"               153.58     95.23      0.00     0.00
"matrix"                7.70      4.77      1.02     0.63
".External"             6.68      4.14      6.68     4.14
"rnorm"                 6.68      4.14      0.00     0.00
"diag"                  0.22      0.14      0.22     0.14
```

How much time is spent in this function itself

How much time is spent in this function and the functions it calls

Writing Parallel R Code – `parallel` Package

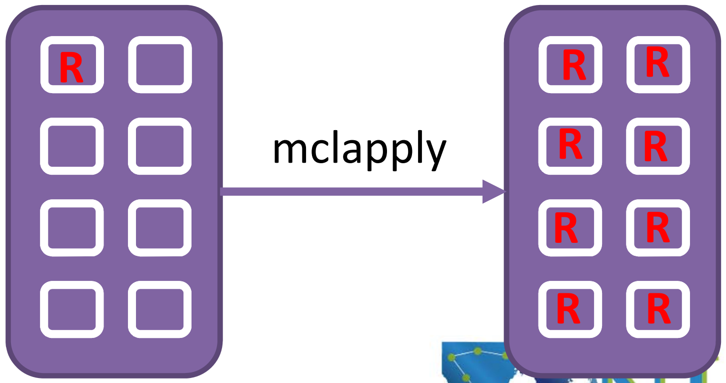
- Introduced in R 2.14.1
- Integrated previous `multicore` and `snow` packages
- Coarse-grained parallelization
  - Suit for the chunks of computation are unrelated and do not need to communicate
- Two ways of using `parallel` packages
  - `mc*apply` function
  - `for` loop with `%dopar%`
    - Need `foreach` and `doParallel` packages

Function `mclapply`

- Parallelized version of the `lapply` function
  - Similar syntax with mc.cores indicates how many cores/workers to use

```
mclapply(X, FUN, mc.cores = <number of cores>, …)
```

  - Return a list of the same length as X, each element of which is the result of applying ‘FUN’ to the corresponding element of X
- Can use all cores on one node
  - But not on multiple nodes



```
# Quadratic Equation: a*x^2 + b*x + c = 0
solve.quad.eq <- function(a, b, c)
{
 # Return solutions
 x.delta <- sqrt(b*b - 4*a*c)
 x1 <- (-b + x.delta)/(2*a)
 x2 <- (-b - x.delta)/(2*a)

 return(c(x1, x2))
}
```

Function solve.quad.eq
Input: three coefficients of a quadratic equation
Output: solutions of the quadratic equation

Create 10 million sets of randomly generated coefficients

```
len <- 1e7
a <- runif(len, -10, 10); b <- runif(len, -10, 10); c <- runif(len, -10, 10)
```

lapply function: call the solve.quad.eq function for each set of coefficients

```
#Serial: lapply
res1.s <- lapply(1:len, FUN = function(x) { solve.quad.eq(a[x], b[x], c[x])})
```

mclapply function: same arguments with one extra: mc.cores

```
#Parallel: mclapply with 4 cores
library(parallel)
res1.p <- mclapply(1:len,
                   FUN = function(x) { solve.quad.eq(a[x], b[x], c[x]) },
                   mc.cores = 4)
```

```
# Quadratic Equation: a*x^2 + b*x + c = 0
solve.quad.eq <- function(a, b, c)
{
 # Return solutions
 x.delta <- sqrt(b*b - 4*a*c)
 x1 <- (-b + x.delta)/(2*a)
```

Function solve.quad.eq

Input: three coefficients of a quadratic equation

```
> system.time(
+res1.s <- lapply(1:len, FUN = function(x) { solve.quad.eq(a[x], b[x], c[x])})
)
   user  system elapsed
358.878   0.375 359.046
> system.time(
+ res1.p <- mclapply(1:len,
+                    FUN = function(x) { solve.quad.eq(a[x], b[x], c[x]) },
+                    mc.cores = 4)
+ )
   user  system elapsed
 11.098   0.342  81.581
```

mclapply function: same arguments with one extra: mc.cores

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#Parallel: mclapply with 4 cores
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res1.p <- mclapply(1:len,
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CENTER FOR COMPUTATION & TECHNOLOGY

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358.878   0.375 359.046
> system.time(
+ res1.p <- mclapply(1:len,
+                     FUN = func
+                     mc.cores =
+ )
   user  system elapsed
 11.098   0.342  81.581
```

It's always a good idea to check the efficiency of a parallel program:

Speedup = 359.046/81.581 = 4.40

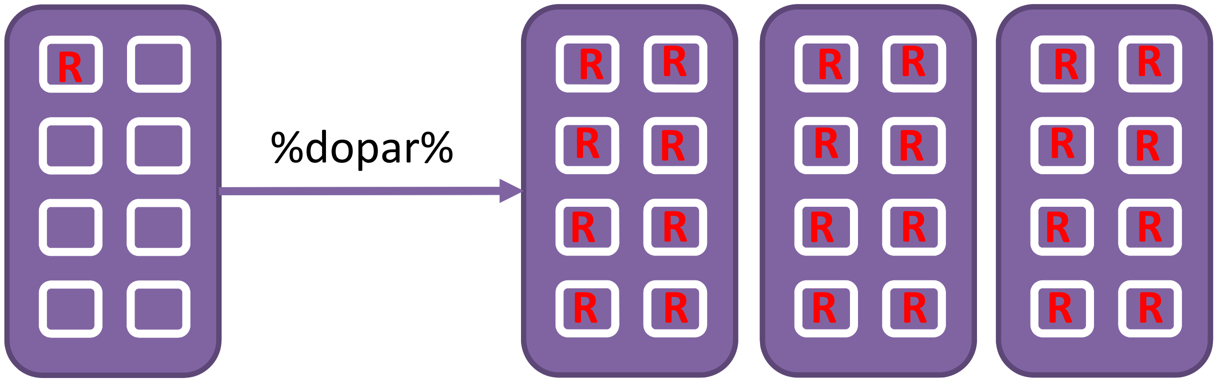
Efficiency = 4.40/4 = 110% (!)

```
#Parallel: mclapply with 4 cores
library(parallel)
res1.p <- mclapply(1:len,
                   FUN = function(x) { solve.quad.eq(a[x], b[x], c[x]) },
                   mc.cores = 4)
```

mclapply function: same arguments with one extra: mc.cores

%dopar%

- From `doParallel` package
  - On top of packages `parallel`, `foreach`, `iterator`
- Purpose: parallelize a `for` loop
- Can run on multiple nodes



`%dopar%`

- Steps
  - Create a cluster of workers (`makeCluster`)
  - Register the cluster (`registerDoParallel`)
  - Process the `for` loop in parallel (`foreach … %dopar%`)
  - Stop the cluster (`stopCluster`)

%dopar%: On A Single Node

```
# Workload:
# Create 1,000 random samples, each with
# 1,000,000 observations from a standard
# normal distribution, then take a
# summary for each sample.

iters <- 1000

# Sequential version
for (i in 1:iters) {
  to.ls <- rnorm(1e6)
  to.ls <- summary(to.ls)
}
```

```
# Parallel version with %dopar%

# Step 1: Create a cluster of 4 workers
cl <- makeCluster(4)

# Step 2: Register the cluster
registerDoParallel(cl)

# Step 3: Process the loop
ls <- foreach(icount(iters)) %dopar% {
  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)
}

# Step 4: Stop the cluster
stopCluster(cl)
```

%dopar%: On A Single Node

```
# Workload:
# Create 1,000 randor
# 1,000,000 observati
# normal distributior
summary for each samp

iters <- 1000

# Sequential version
for (i in 1:iters) {
  to.ls <- rnorm(1e6
  to.ls <- summary(tc
}
```

```
# Sequential
system.time(
for (i in 1:iters) {
  to.ls <- rnorm(1e6)
  to.ls <- summary(to.ls)
}
)
   user  system elapsed
 60.249   3.499  63.739

# Parallel with 4 cores
system.time({
cl <- makeCluster(4)
registerDoParallel(cl)
ls<-foreach(icount(iters)) %dopar% {
  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)
}
stopCluster(cl)
})
   user  system elapsed
  0.232   0.032  17.738
```

```
ith %dopar%

luster of 4 workers


he cluster
l)

e loop
ters)) %dopar% {

ls)


luster
```

%dopar%: One Single Node

```
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 60.249   3.499  63.739

# Parallel with 4 cores
system.time({
cl <- makeCluster(4)
registerDoParallel(cl)
ls<-foreach(icount(iters)) %dopar% {
  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)
}
stopCluster(cl)
})
   user   system elapsed
  0.232   0.032  17.738
```

```
ith %dopar%

luster of 4 workers

he cluster
l)

                                    {

ls)

luster
```

Speedup = 63.739/17.738 = 3.59

Efficiency = 3.59/4 = 90%

makeCluster()

- We specify how many workers to use
- On the same node:

```
cl <- makeCluster(<number of workers>)
```

- On multiple nodes:

```
cl <- makeCluster(<list of hostnames>)
```

  - Example: create 4 workers, 2 on `qb101` and 2 on `qb102`

```
cl <- makeCluster(c(“qb101”,”qb101”,”qb102”,”qb102”))
```

%dopar%: Multiple Nodes on QB2 Cluster

```
# Read all host names
hosts <-
as.vector(unique(read.table(Sys.getenv("PBS_NODEFILE"),stringsAsFactors=F))[,1])
# Count number of hosts
nh <- length(hosts)
# Use 4 workers
nc <- 4

# Make a cluster on multiple nodes
cl <- makeCluster(rep(hosts , each = nc/nh))

registerDoParallel(cl)

ls<-foreach(icount(iters)) %dopar% {

  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)

}

stopCluster(cl)
```

Get the host names of the nodes

Same steps for the rest of the code:
- Make a cluster
- Register the cluster
- Process loop with %dopar%
- Stop the cluster

Running Parallel R Codes

- Now we have a R code that can run in parallel
- So the next question is:
  - How do we know how many workers we should we run it with?
    - The more the better (faster)?

Running Parallel R Codes

- Now we have a R code that can run in parallel
- So the next question is:
  - How do we know how many workers we should we run it with?
    - The more the better (faster)?

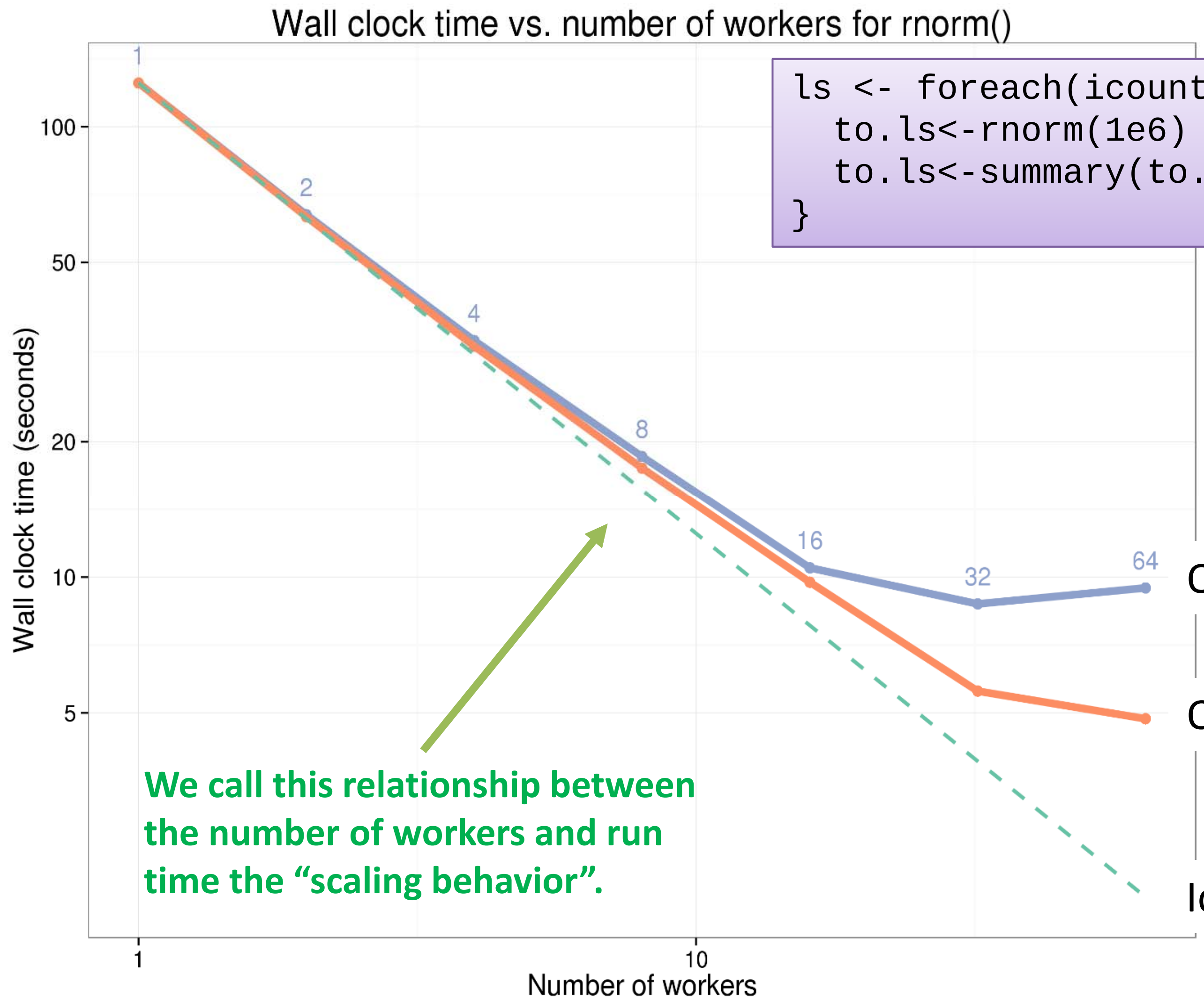
The answer is: scaling test (trial and error)

```
cl <- makePSOCKcluster(rep(hosts , each = clusterSize[i]/nh))
registerDoParallel(cl)

t <- system.time(
  ls <- foreach(icount(iters)) %dopar% {
    to.ls <- rnorm(1e6)
    to.ls <- summary(to.ls)
    }
)

stopCluster(cl)
```

Nothing is returned, so chunks of the workload are independent of each other



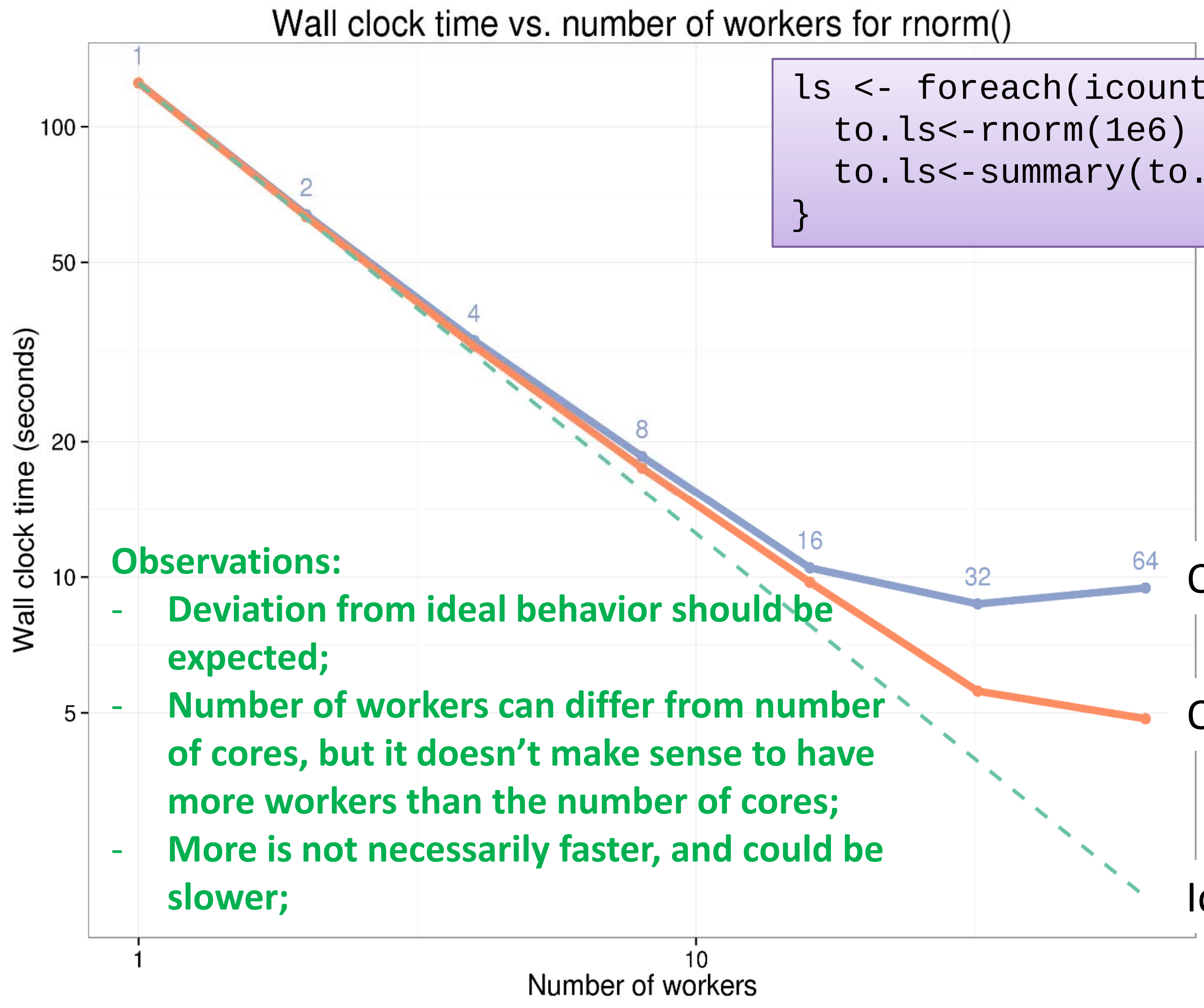
```
ls <- foreach(icount(iters)) %dopar% {
  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)
}
```

On one node (20 cores total)

On two nodes (40 cores total)

Ideal behavior

We call this relationship between the number of workers and run time the "scaling behavior".



```
ls <- foreach(icount(iters)) %dopar% {
  to.ls<-rnorm(1e6)
  to.ls<-summary(to.ls)
}
```

On one node (20 cores total)

On two nodes (40 cores total)

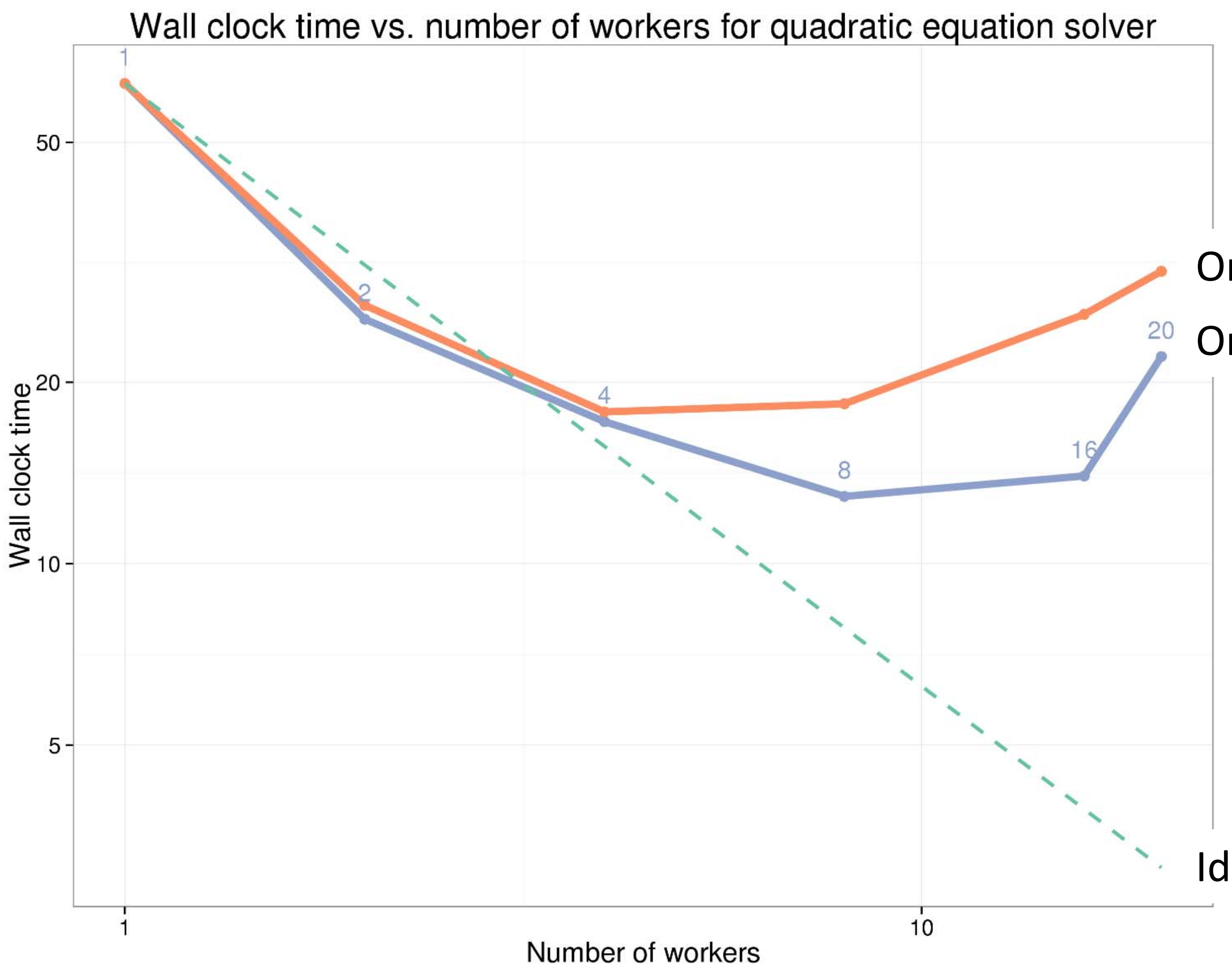
Ideal behavior

Observations:

- **Deviation from ideal behavior should be expected;**
- **Number of workers can differ from number of cores, but it doesn't make sense to have more workers than the number of cores;**
- **More is not necessarily faster, and could be slower;**

```
res2.p <- foreach(i=1:core, .combine='rbind') %dopar%
  {
    # local data for results
    res <- matrix(0, nrow=chunk.size, ncol=2)
    for(x in ((i-1)*chunk.size+1):(i*chunk.size)) {
       res[x - (i-1)*chunk.size,] <- solve.quad.eq(a[x], b[x], c[x])
    }
    # return local results
    res
  }
```

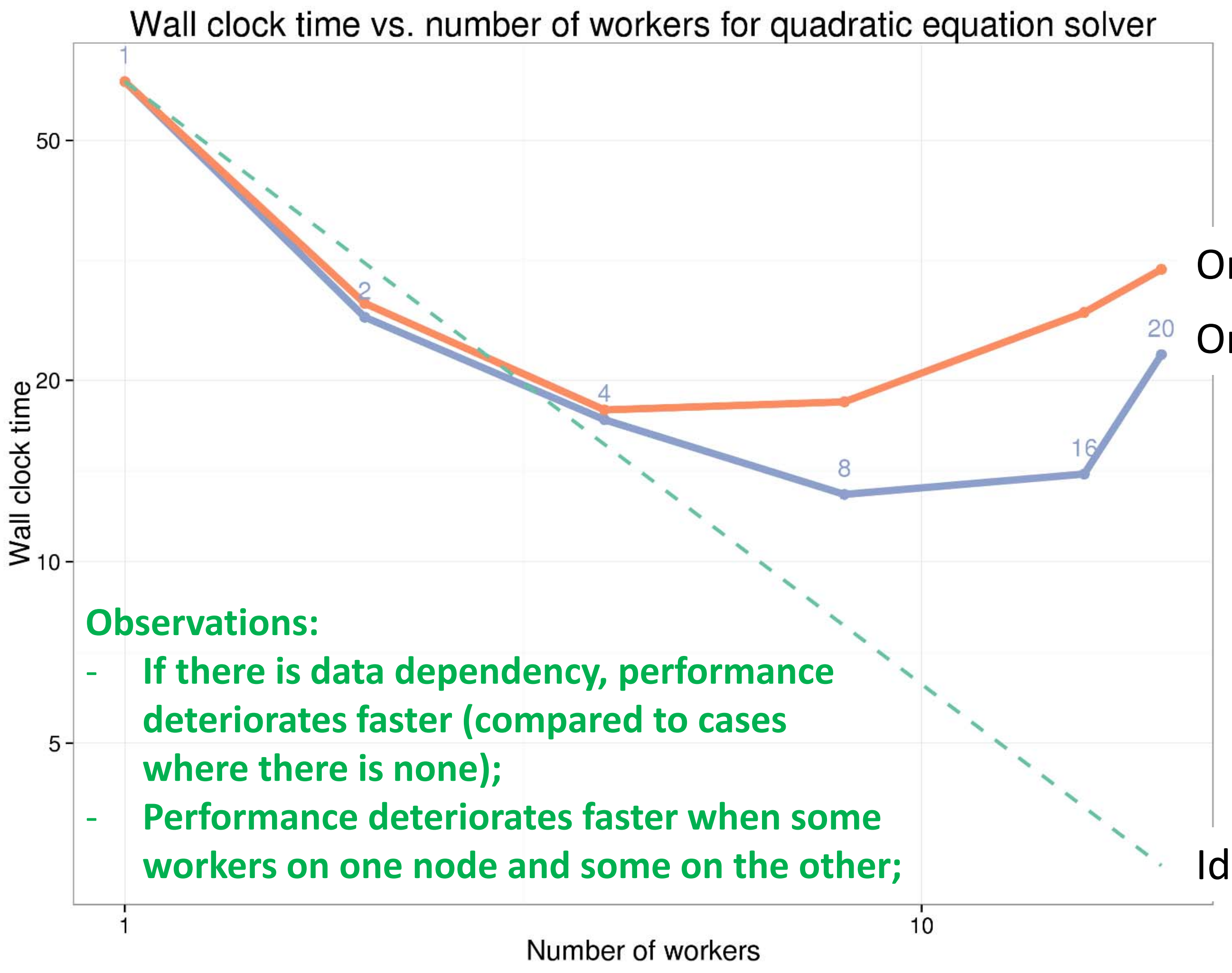
The results from each chunk are aggregated into "res2.p", so chunks of the workload are independent



On two nodes (40 cores total)

On one node (20 cores total)

Ideal behavior



On two nodes (40 cores total)

On one node (20 cores total)

Ideal behavior

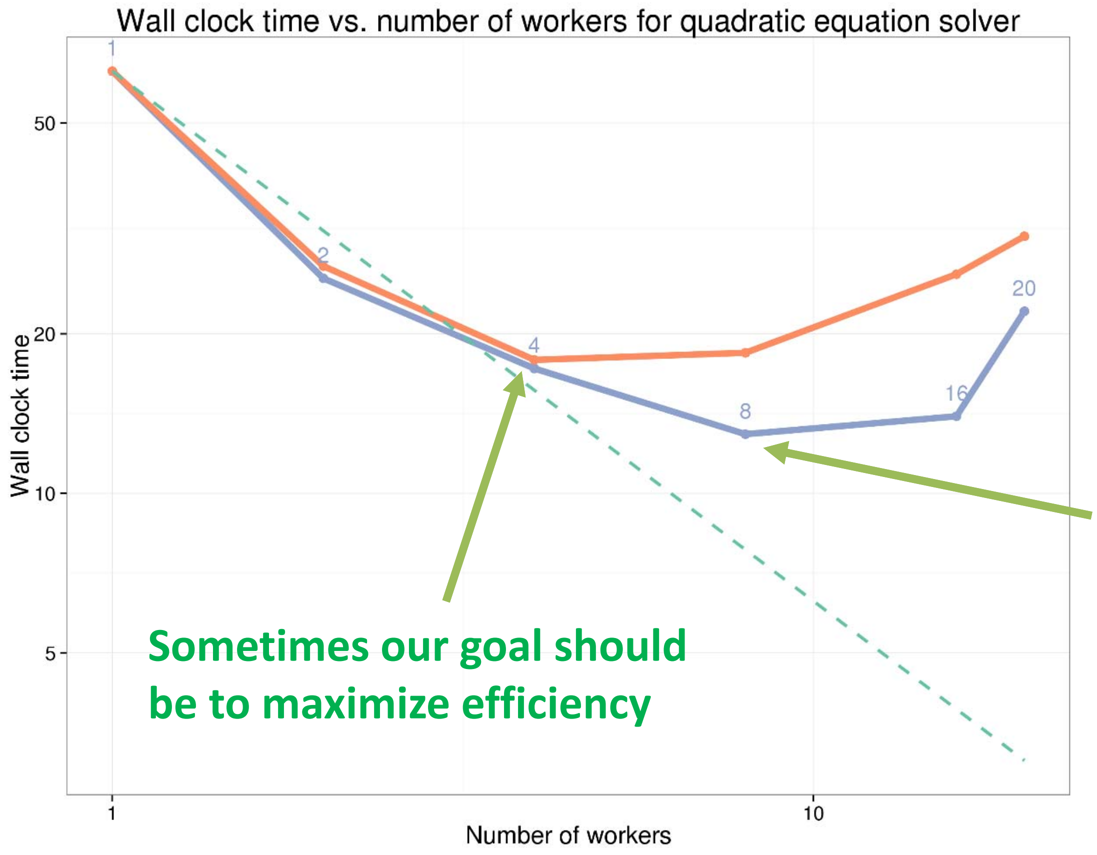
Observations:

- **If there is data dependency, performance deteriorates faster (compared to cases where there is none);**
- **Performance deteriorates faster when some workers on one node and some on the other;**

What we have learned about parallel (R) codes

- With increasing number of workers, efficiency decreases, and eventually adding more workers slows it down
- Best scaling behaviors are typically found with codes with no data dependency (we call it "embarrassingly parallel")
- With this in mind, when developing our codes, we should reduce data dependency as much as possible

How Many Workers to Use



Sometimes our goal should be to maximize efficiency

If there is no constraint, minimize the wall clock time

Summary:
Steps of Developing Parallel (R) Codes

- Step 1: Analyze performance
  - Find “hot spots” – parallelizable code segments that slow down the execution the most
- Step 2: Parallelize code segments
- Step 3: Run scaling tests
  - How do efficiency and run time change with increasing number of workers?
  - What are the optimal number of workers?
- Step 4: Is the code fast enough?
  - If yes, stop developing (for now) and move on to production runs;
  - If no, go back to step 1 and start another iteration.

Memory Management

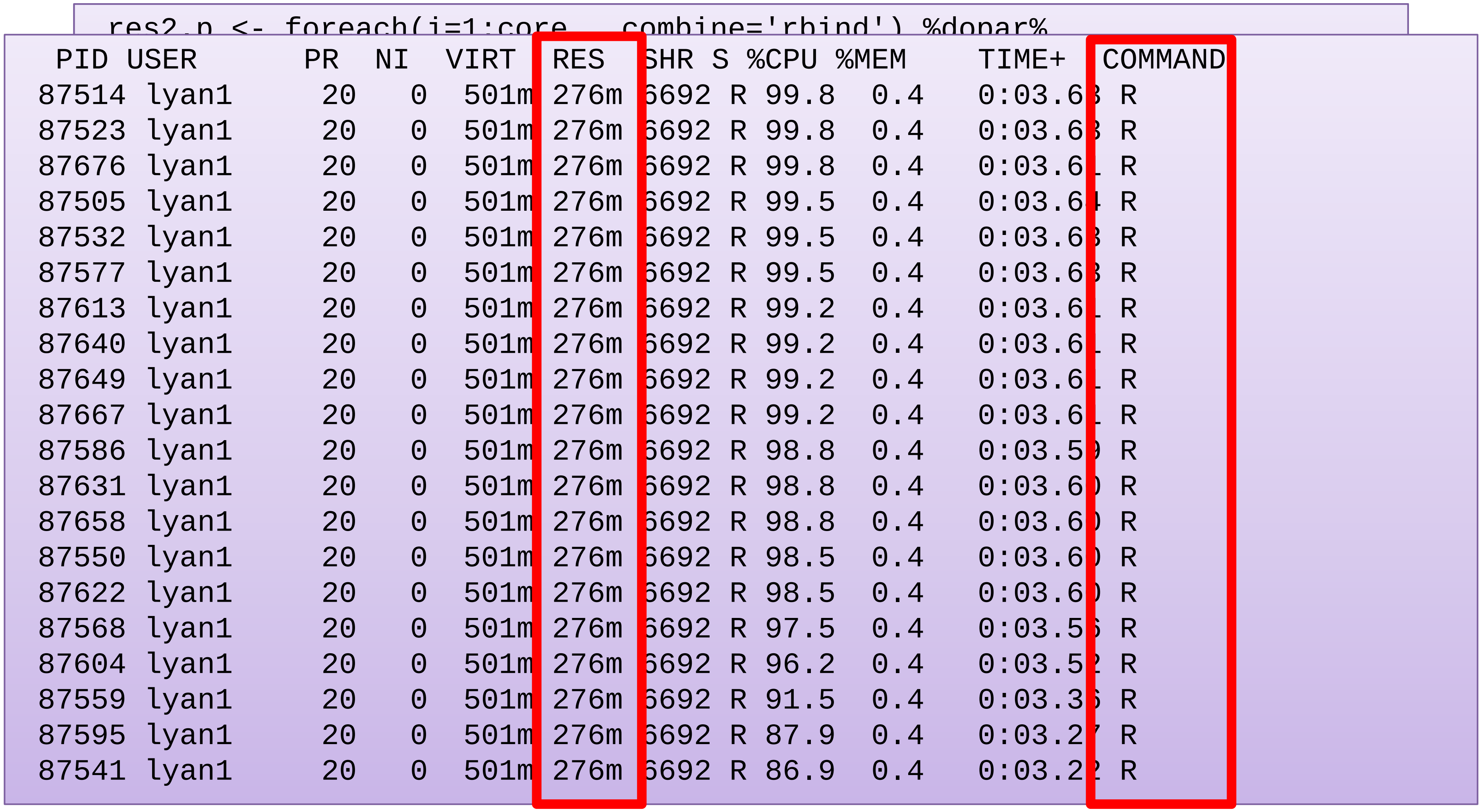
- Replica of data objects could be created for every worker
  - Memory usage would increase with the number of workers
- R does not necessarily clean them up even if you close the cluster
  - Need to monitor memory footprint closely
  - The `Rprof` function is capable of memory profiling as well

```
res2.p <- foreach(i=1:core, .combine='rbind') %dopar%
  {
    # local data for results
    res <- matrix(0, nrow=chunk.size, ncol=2)
    for(x in ((i-1)*chunk.size+1):(i*chunk.size)) {
       res[x - (i-1)*chunk.size,] <- solve.quad.eq(a[x], b[x], c[x])
    }
    # return local results
    res
  }
```

```
   PID USER      PR  NI  VIRT  RES  SHR S %CPU %MEM    TIME+  COMMAND
 87483 lyan1     20   0  539m 314m 6692 R 100.0  0.5   0:02.05 R
 87492 lyan1     20   0  539m 314m 6692 R 100.0  0.5   0:02.05 R
 87465 lyan1     20   0  539m 314m 6692 R  99.4  0.5   0:02.04 R
 87474 lyan1     20   0  539m 314m 6692 R  99.4  0.5   0:02.05 R
```

With 4 workers:

Memory = 314*4 = 1256 MB



```
res2.p <- foreach(i=1:core,  combine='rbind') %dopar%
```

```
  PID USER      PR  NI  VIRT  RES  SHR S %CPU %MEM    TIME+  COMMAND
87514 lyan1     20   0  501m 276m 6692 R 99.8  0.4   0:03.63 R
87523 lyan1     20   0  501m 276m 6692 R 99.8  0.4   0:03.63 R
87676 lyan1     20   0  501m 276m 6692 R 99.8  0.4   0:03.61 R
87505 lyan1     20   0  501m 276m 6692 R 99.5  0.4   0:03.64 R
87532 lyan1     20   0  501m 276m 6692 R 99.5  0.4   0:03.63 R
87577 lyan1     20   0  501m 276m 6692 R 99.5  0.4   0:03.63 R
87613 lyan1     20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87640 lyan1     20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87649 lyan1     20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87667 lyan1     20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87586 lyan1     20   0  501m 276m 6692 R 98.8  0.4   0:03.59 R
87631 lyan1     20   0  501m 276m 6692 R 98.8  0.4   0:03.60 R
87658 lyan1     20   0  501m 276m 6692 R 98.8  0.4   0:03.60 R
87550 lyan1     20   0  501m 276m 6692 R 98.5  0.4   0:03.60 R
87622 lyan1     20   0  501m 276m 6692 R 98.5  0.4   0:03.60 R
87568 lyan1     20   0  501m 276m 6692 R 97.5  0.4   0:03.56 R
87604 lyan1     20   0  501m 276m 6692 R 96.2  0.4   0:03.52 R
87559 lyan1     20   0  501m 276m 6692 R 91.5  0.4   0:03.36 R
87595 lyan1     20   0  501m 276m 6692 R 87.9  0.4   0:03.27 R
87541 lyan1     20   0  501m 276m 6692 R 86.9  0.4   0:03.22 R
```

With 20 workers:

Memory = 276*20 = 5520 MB

```
res2.p <- foreach(i=1:core   combine='rbind') %dopar%
```

```
  PID USER       PR  NI  VIRT  RES  SHR S %CPU %MEM    TIME+  COMMAND
87514 lyan1       20   0  501m 276m 6692 R 99.8  0.4   0:03.63 R
87523 lyan1       20   0  501m 276m 6692 R 99.8  0.4   0:03.63 R
87676 lyan1       20   0  501m 276m 6692 R 99.8  0.4   0:03.61 R
87505 lyan1       20   0  501m 276m 6692 R 99.5  0.4   0:03.64 R
87532 lyan1       20   0  501m 276m 6692 R 99.5  0.4   0:03.63 R
87577 lyan1       20   0  501m 276m 6692 R 99.5  0.4   0:03.63 R
87613 lyan1       20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87640 lyan1       20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87649 lyan1       20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87667 lyan1       20   0  501m 276m 6692 R 99.2  0.4   0:03.61 R
87586 lyan1       20   0  501m 276m 6692 R 98.8  0.4   0:03.59 R
87631 lyan1       20   0  501m 276m 6692 R 98.8  0.4   0:03.60 R
87658 lyan1       20   0  501m 276m 6692 R 98.8  0.4   0:03.60 R
87550 lyan1       20   0  501m 276m 6692 R 98.5  0.4   0:03.60 R
87622 lyan1       20   0  501m 276m 6692 R 98.5  0.4   0:03.60 R
87568 lyan1       20   0  501m
87604 lyan1       20   0  501m
87559 lyan1       20   0  501m
87595 lyan1       20   0  501m
87541 lyan1       20   0  501m 276m 6692 R 86.9  0.4   0:03.22 R
```

The memory footprint doesn't increase linearly with the number of workers, but quite close, so we need to monitor it closely when changing the number of workers.

With 20 workers:

Memory = 276*20 = 5520 MB

R with GPU

- GPU stands for **G**raphic **P**rocessing **U**nit
  - Originally designed to process graphic data
  - Can tremendously accelerate certain types of computation as well, e.g. matrix multiplications
  - All nodes on LONI QB2 cluster are equipped with two GPU's
- Package gpuR brings the processing power of GPU to R

Example: Matrix Multiplication on GPU

```
[lyan1@qb032 R]$ cat matmul_gpu.R
# Load necessary library
library(gpuR)

ORDER <- 8192

# On CPU
A <- matrix(rnorm(ORDER^2), nrow=ORDER)
B <- matrix(rnorm(ORDER^2), nrow=ORDER)
ctime <- system.time(C <- A %*% B)
print(paste("On CPU:",ctime["elapsed"],"seconds"))


# On GPU
vclA <- vclMatrix(rnorm(ORDER^2), nrow=ORDER, ncol=ORDER)
vclB <- vclMatrix(rnorm(ORDER^2), nrow=ORDER, ncol=ORDER)
gtime <- system.time(vclC <- vclA %*% vclB)
print(paste("On GPU:",gtime["elapsed"],"seconds"))

print(paste("The speedup is",ctime["elapsed"]/gtime["elapsed"]))
```

On CPU: Create matrix A and B, then multiply them

On GPU: Create matrix A and B (with a different function than on CPU), then multiply them

Example: Matrix Multiplication on GPU

```
[lyan1@qb072 R]$ Rscript matmul_gpu.R
Loading required package: methods
Number of platforms: 1
- platform: NVIDIA Corporation: OpenCL 1.2 CUDA 8.0.0
  - gpu index: 0
    - Tesla K20Xm
  - gpu index: 1
    - Tesla K20Xm
checked all devices
completed initialization
gpuR 1.2.1
Attaching package: ‘gpuR’
The following objects are masked from ‘pa

    colnames, svd

[1] "On CPU: 4.295 seconds"
[1] "On GPU: 0.0309999999999988 seconds"
[1] "The speedup is 138.54838709678"
```

Wow! Huge speedup! Especially so given the CPU results are obtained with 20 cores (implicitly parallel)

The Other Side of The Coin

```
[lyan1@qb072 R]$ cat matmul_gpu_overall.R
# Load necessary library
library(gpuR)

ORDER <- 8192

# On CPU
ctime <- system.time({
A <- matrix(rnorm(ORDER^2), nrow=ORDER)
B <- matrix(rnorm(ORDER^2), nrow=ORDER)
C <- A %*% B
})
print(paste("On CPU:",ctime["elapsed"],"seconds"))

# On GPU
gtime <- system.time({
vclA <- vclMatrix(rnorm(ORDER^2), nrow=ORDER, ncol=ORDER)
vclB <- vclMatrix(rnorm(ORDER^2), nrow=ORDER, ncol=ORDER)
vclC <- vclA %*% vclB
})
print(paste("On GPU:",gtime["elapsed"],"seconds"))

print(paste("The speedup is",ctime["elapsed"]/gtime["elapsed"]))
```

Same code with only one difference:
Now we are measuring the run time including matrix creation.

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The Other Side of The Coin

```
[lyan1@qb072 R]$ Rscript matmul_gpu_overall.R
Loading required package: methods
Number of platforms: 1
- platform: NVIDIA Corporation: OpenCL 1.2 CUDA 8.0.0
  - gpu index: 0
    - Tesla K20Xm
  - gpu index: 1
    - Tesla K20Xm
checked all devices
completed initialization
gpuR 1.2.1

Attaching package: ‘gpuR’

The following objects are mask

    colnames, svd

[1] "On CPU: 14.298 seconds"
[1] "On GPU: 13.897 seconds"
[1] "The speedup is 1.02885514859322"
```

This time, not impressive at all:
Matrix creation is not much work, but moving data to/from GPU takes a lot of time.
And again, wall clock time is what matters at the end of day.

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Deep Learning in R

- Since 2012, Deep Neural Network (DNN) has gained great popularity in applications such as
  - Image and pattern recognition
  - Natural language processing
- There are a few R packages that support DNN
  - MXNet (multiple nodes with GPU support)
  - H2o (multiple nodes)
  - Darch
  - Deepnet
  - Rpud

References

- ParallelR (www.parallelr.com)
  - Code: https://github.com/PatricZhao/ParallelR
- R Documentation for packages mentioned in this tutorial

Thank you!