Parallel Computing Practical

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Question 1

Use a `foreach` loop to repeat 100 times:

- generate a random sample from an exponential distribution with mean 1
- calculate mean and variance
- *row-bind* your results (`rbind`) (results = mean and variance).

```
library(doParallel)
```

```
Loading required package: foreach
```

```
Loading required package: iterators
```

```
Loading required package: parallel
```

```
cores <- detectCores() - 1  # Use available cores minus 1
cl <- makeCluster(cores)
registerDoParallel(cl)


result <- matrix(nrow=0, ncol = 2)

# Put "combine = rbind"
system.time({
  results <- foreach(i= 1:100,.combine = rbind) %dopar% {
    y <- rexp(100, rate = 1)
    x_bar <- mean(y)
    s_square <- var(y)
```

```
    cbind(x_bar, s_square)
  }
})
```

```
   user  system elapsed
   0.06    0.00    0.17
```

```
head(results)
```

```
         x_bar  s_square
[1,] 1.0211623 0.8559820
[2,] 1.0011973 0.9139009
[3,] 0.9637895 0.7791651
[4,] 1.0401809 1.1893508
[5,] 0.9897926 0.8440796
[6,] 1.1496366 1.4098015
```

Question 2

Use the `doParallel` package and `foreach` to bootstrap the median for the galaxies data (in library MASS).

If the `foreach` function needs access to data or a function from a certain package, this can be done by adding the `.packages='MASS'` (for example) argument.

How does processing time compare to that of serial processing? If each iteration's run time is small, relative to the amount of data that needs to be loaded and returned, parallel processing might not actually speed up the total run time. Bootstrapping is relatively small: draw a sample, calculate a statistic. It might only start making a difference if each chunk becomes large relatively to the overheads of data transfer. Experiment with this. Try doing 1000 bootstrap samples at a time instead of managing single bootstrap samples.

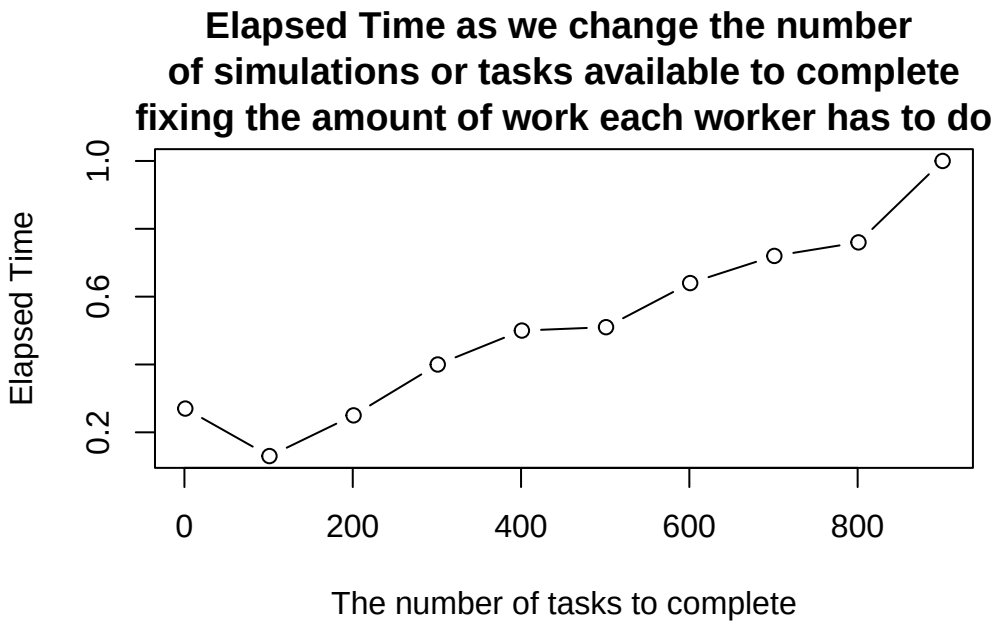
```
library(doParallel)
library(MASS)

cores <- detectCores() - 1  # Use available cores minus 1
cl <- makeCluster(cores)
registerDoParallel(cl)

bootstrap_median <- function(dat, N, B){
  medians <- foreach(i = 1:N, .packages = 'MASS', .combine = c) %dopar%   {
    bootstrap <- sample(B, size = length(dat), replace=TRUE)
    median(bootstrap)
  }
  return(medians)
}
```

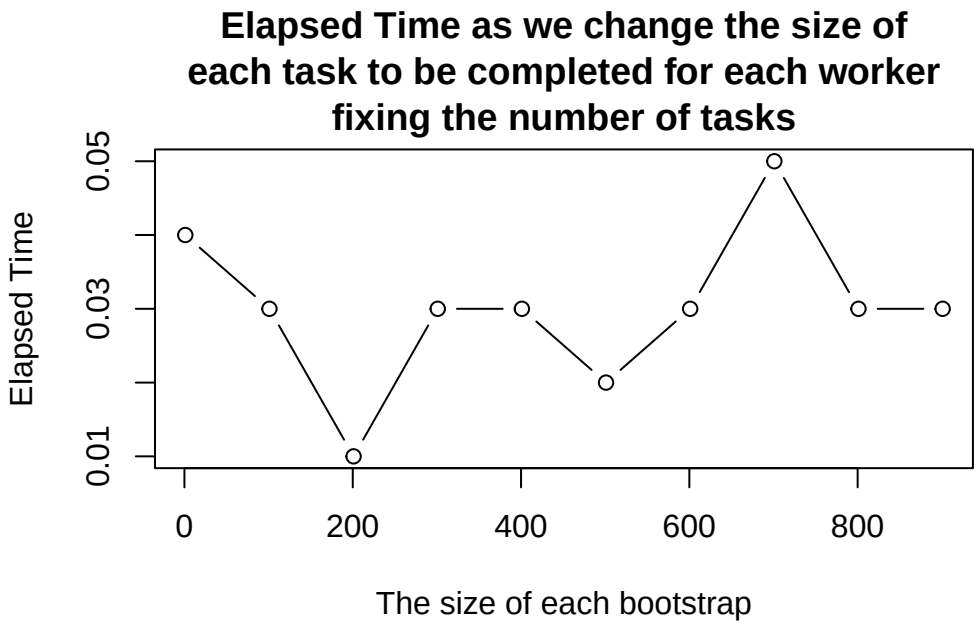
```
# Testing how the number of tasks affects run time
elapsed_time <- c()
i <- 1
for(j in seq(1, 1000, by = 100) ){
  elapsed_time[i] <- system.time({
    bootstrap_median(galaxies, j, length(galaxies))
    })["elapsed"]
  i <- i+1
}
plot(x=seq(1, 1000, by = 100), y =elapsed_time,
main = "Elapsed Time as we change the number
of simulations or tasks available to complete
fixing the amount of work each worker has to do",
```

```
     xlab = "The number of tasks to complete",
     ylab = "Elapsed Time", type = "b")
```



Interpretation: As we increase the number of tasks, the elapsed time increases i.e. runs slower. This means that the overhead costs of the parallelized code become more significant as the number of tasks grows

```
# Testing how the size of each tasks affects run time
elapsed_time <- c()
i <- 1
for(j in seq(1, 1000, by = 100) ){
  elapsed_time[i] <- system.time({
    bootstrap_median(galaxies, 10, j)
    })["elapsed"]
  i <- i+1
}
plot(x=seq(1, 1000, by = 100), y =elapsed_time,
main = "Elapsed Time as we change the size of
each task to be completed for each worker
fixing the number of tasks",
xlab = "The size of each bootstrap",
ylab = "Elapsed Time", type = "b")
```



Interpretation: As we increase the size of the tasks for each set of of workers, we see an initial decrease in elapsed time, however it increases later on due to overhead costs.

Question 3

Estimate coverage of a percentile bootstrap confidence interval for the following scenario: sample of size 50 from an exponential distribution with mean 1.

```
library(doParallel)

cores <- detectCores() - 1  # Use available cores minus 1
cl <- makeCluster(cores)
registerDoParallel(cl)

set.seed(123)

bootstrap_coverage <- function(B,N){
   true_mean <- 1 # for exponential distribution true mean is lamda / rate

  suppressWarnings(count <- foreach(i = 1:N, .combine="+") %dopar% {
    dat <- rexp(50, rate = 1)

    bootstrap_means <- replicate(B, mean(sample(dat,size=length(dat),replace = TRUE)))

    upper_ci <- as.numeric(quantile(bootstrap_means, 0.975))
    lower_ci <- as.numeric(quantile(bootstrap_means, 0.025))

    ifelse(true_mean > lower_ci & true_mean < upper_ci, 1, 0)
  })
  coverage <- count/N
  return(coverage)
}

B <- 50 # Number of bootstraps be task
N <- 10000 # Number of simulations
suppressWarnings(system.time(print(bootstrap_coverage( B, N))))
```

```
[1] 0.8903
```

```
   user  system elapsed
  12.22    1.78   24.03
```

```
# Coverage Probability (should be close to the 95%, our confidence interval )
```

Question 4

The package `iterators` provides several functions that can be used to create sequences for the `foreach` function. For example, the `irnorm` function creates an object that iterates over vectors of normally distributed random numbers. It is useful when you need to use random variables drawn from one distribution in an expression that is run in parallel.

In this exercise, use the `foreach` and `irnorm` functions to iterate over 3 vectors, each containing 5 random variables. Find the largest value in each vector, and print those largest values.

Before running the `foreach` function set the seed to 1234.

```
set.seed(1234)

cores <- detectCores() - 1  # Use available cores minus 1
cl <- makeCluster(cores)
registerDoParallel(cl)


# Use foreach to find the maximum in each vector
suppressWarnings(system.time(
max_values <- foreach(i = 1:3, .combine = c) %dopar% {
  library(iterators)
  it <- irnorm(1, count=5)
  max(nextElem(it))  # Find max value in each vector
}))
```

```
   user  system elapsed
   0.01    0.00    0.24
```

```
print(matrix(max_values))
```

```
           [,1]
[1,]  1.0551610
[2,] -0.9196660
[3,]  0.6529472
```

Question 5

Compare run time between `parLapply`, `foreach` and `replicate` for the above problem.

```
library(iterators)
library(doParallel)
set.seed(1234)

cores <- detectCores() - 1  # Use available cores minus 1
cl <- makeCluster(cores)
registerDoParallel(cl)

# Parallel Function
parallel_apply <-  function(i) {
  library(iterators)
  it <- irnorm(1, count=5)
  max(nextElem(it))
}

# Use foreach to find the maximum in each vector
foreach_func <- function(n){
  max_values <- foreach(i = 1:n, .combine = c) %dopar% {
  library(iterators)
  it <- irnorm(1, count=5)
  max(nextElem(it))
}}

# Use parLapply to find the maximum in each vector
parLapply_func <- function(n){
  max_values <- parLapply(cl, 1:n, parallel_apply)
}

# Use replicate to find the maximum in each vector
replicate_func <- function (n){
  max_values <- replicate(n,parallel_apply(i=n))
}
```

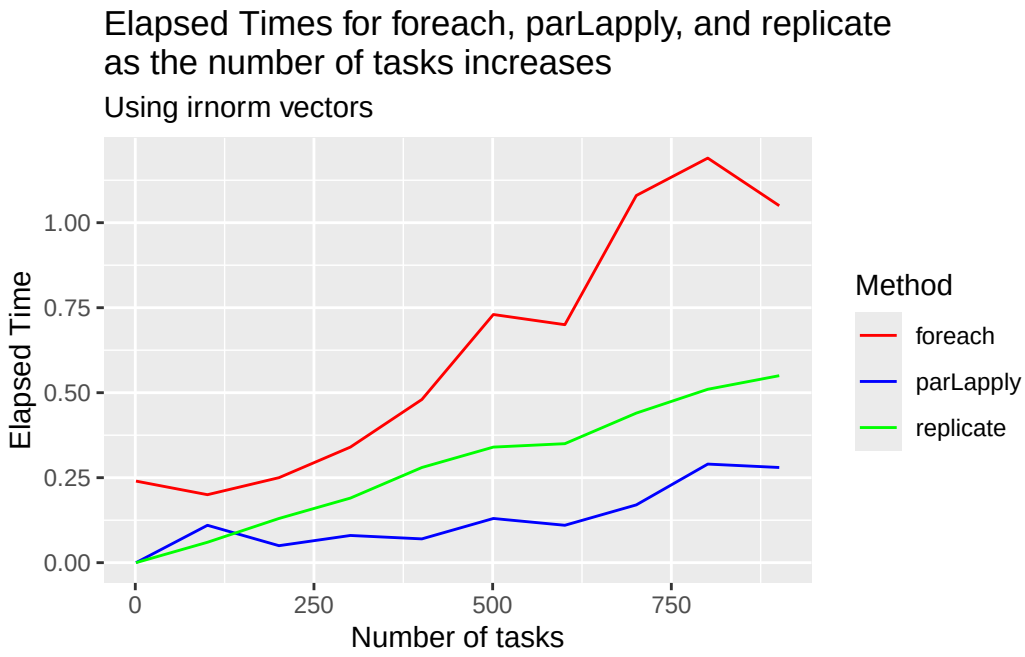
```
# Testing how the number tasks affects run time for each function
foreach_time <- c()
parLapply_time <- c()
replicate_time <- c()
```

```r
set.seed(1234)

x <- seq(1, 1000, by = 100)
i <- 1
for(n in x){
  foreach_time[i] <- system.time(foreach_func(n))["elapsed"]
  parLapply_time[i] <- system.time(parLapply_func(n))["elapsed"]
  replicate_time[i] <- system.time(replicate_func(n))["elapsed"]
  i <- i+1
}

df1 <- data.frame(x=x, y=foreach_time, Group = "foreach")
df2 <- data.frame(x=x, y=parLapply_time, Group = "parLapply")
df3 <- data.frame(x=x, y=replicate_time, Group = "replicate")
combined_df <- rbind(df1, df2, df3)

library(ggplot2)
ggplot(data = combined_df, aes(x = x, y = y, color = Group)) +
  geom_line() +
  labs(
    title = "Elapsed Times for foreach, parLapply, and replicate
as the number of tasks increases",
    subtitle = "Using irnorm vectors",
    x = "Number of tasks",
    y = "Elapsed Time",
    color = "Method"
  ) +
  scale_color_manual(
    values = c("foreach" = "Red", "parLapply" = "Blue", "replicate" = "Green")
    )
```



Interpretation: The foreach function is slower than both parLapply and replicate due to high parallelization overhead. While replicate is faster initially for small tasks, parLapply outperforms it as the number of tasks increases, thanks to better scalability and efficient workload distribution across cores. For large tasks, parLapply is the best choice, while replicate is more suitable for smaller, serial operations.