Parellel Computing in R
from `parallel` to `foreach` and `future`

Chao Cheng

School of Statistics and Management
Shanghai University of Finance and Economics, China

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Outline

Introduction

A toy example

- $1 + 2 + \cdots + 100$
- Compute the sum of a vector

Abstraction

- The whole job can be break into small parts and they can be done independently of each other.
- Map + Reduce

Useful cases

- Simulation
- Bootstrap, MCMC and cross validation, etc.
- Elementwisely update an vector in ADMM algorithm (Parallel in C++)

Basic paralle computation for simulation

- Start multiple R sessions
- Preparation: load necessary packages, etc.
- Run simulation scripts, possibly according to session ID.
- Collect and summary the results by hand.

Abstraction

- Create workers
- Prepare workers
- Run script in parallel and collect the results.

The `parallel` package

- It's derived from `snow` and `multicore` packages.
- Useful reference:
  - Parallel R. (This book is a bit old.)
  - `parallel`'s documentations.
  - `parallel`'s vignettes.

A simple template

```
library(parallel)
# use all the cores of this machine
cls <- makeCluster(detectCores())

# initializing workers
clusterEvalQ(cls, fun)
# pass VARLIST from master to all the workers
clusterExport(cls, VARLIST)


# split full index of all tasks to workers
idx_split <- clusterSplit(cls, idx_full)
# carry out the task parFUNCTION parallely
res <- parLapply(cls, idx_split, parFUNCTION)

# stop workers
stopCluster(cls)
```

A simple example

```
library(parallel)
a <- rnorm(12)
slow_function <- function(invec){
   ...     # a slow function
}

cls <- makeCluster(4)
ind_seq <- clusterSplit(cls, a)
clusterExport(cls, varlist = "slow_function")
res_par <- parSapply(cls, ind_seq, slow_function)
res <- sum(res_par)
```

Rabbit hole 1: PSOCK vs FORK

```
a <- rnorm(100)
```

PSOCK

```
cls <- makeCluster(4)      # default type is PSOCK
```

FORK

```
cls <- makeCluster(4, type = "FORK")    # NOT available on Windows
```

```
parSapply(cls, 1 : 10, function(id){
    return(a[id])
})
```

Rabbit hole 1: PSOCK vs FORK

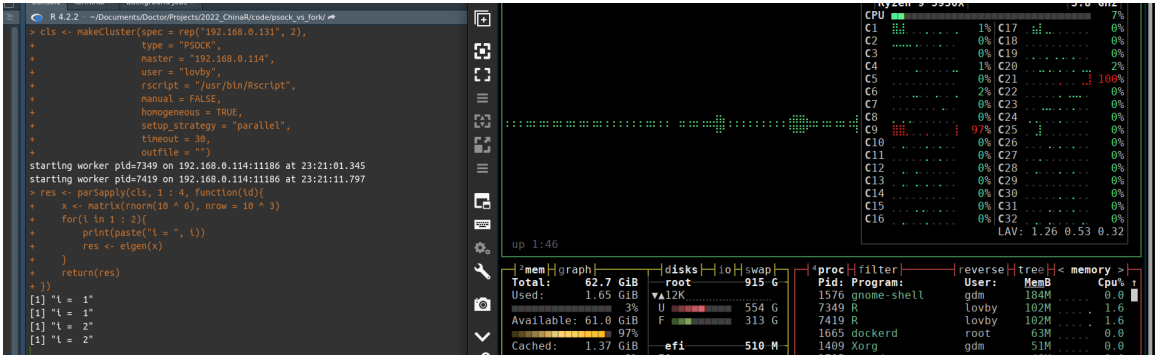

Figure 1: PSOCK connects to remote server

Rabbit hole 1: PSOCK vs FORK

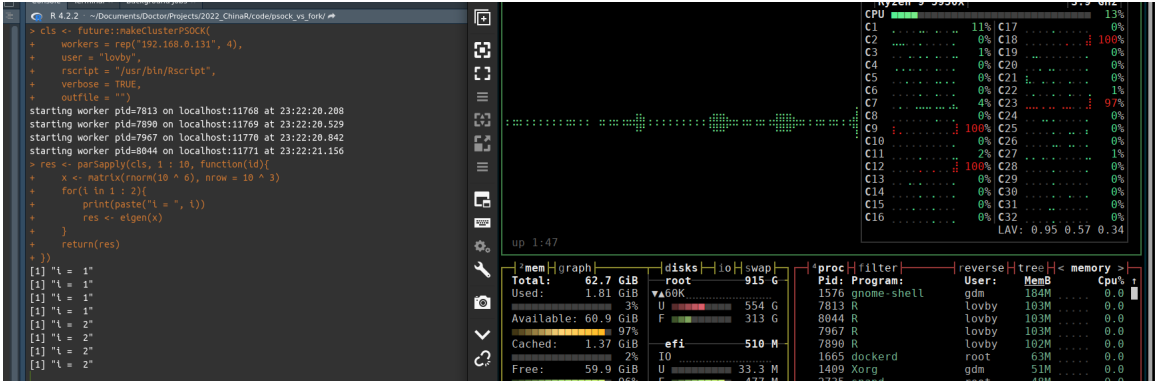

Figure 2: PSOCK (via future/parallely) connects to remote server

Rabbit hole 1: PSOCK vs FORK

Figure 3: Memory consumption of FORK, part 1

Rabbit hole 1: PSOCK vs FORK

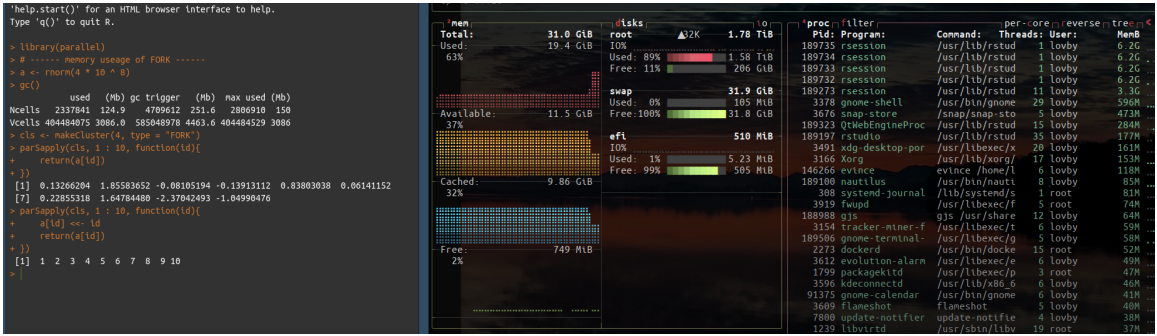

Figure 4: Memory consumption of FORK, part 2

Rabbit hole 1: PSOCK vs FORK

PSOCK

- Pros:
  - Use socket connection, a general approach.
  - All system, locally or remotely with suitable setup such as MPI
- Cons:
  - Might be hard to configure.
  - Manually transport the data.

FORK

- Pros: use FORK mechanism, no worry about variable transportation.
- Cons: Only for one machine, not available on Windows.

Rabbit hole 2: Parallel random number generation

```
> # --- PSOCK will have their own seed ---
> cls <- makeCluster(4)
> parSapply(cls, 1 : 4, function(id){
+     rnorm(10)
+ })
            [,1]       [,2]       [,3]       [,4]
 [1,] -0.1284523  0.90577746 -0.2007189  1.5838963
 [2,] -0.2812603 -0.12137209 -0.5616048  2.1205495
 [3,] -1.4523742 -0.82587203 -1.0321580 -0.7770089
 [4,]  0.2909059  0.60436821  0.1179803 -1.4674607
 [5,]  0.5116825  2.42765426 -1.3673113  1.5117072
 [6,] -1.7666148  0.50982495  0.5123056  0.3701816
 [7,]  0.5683548  0.55647039  1.1734904  0.7364532
 [8,]  0.6602347 -0.09715067 -1.3660750  1.1635798
 [9,]  0.1688014 -0.47356787 -1.5571017  0.4500263
[10,]  1.0467846  0.07022752  0.6334269 -0.5432841
```

(a) No control on PSOCK

```
> # --- fork will copy the seed setting of main session ---
> set.seed(10)
> cls <- makeCluster(4, type = "FORK")
> parSapply(cls, 1 : 4, function(id){
+     rnorm(10)
+ })
            [,1]        [,2]        [,3]        [,4]
 [1,]  0.01874617  0.01874617  0.01874617  0.01874617
 [2,] -0.18425254 -0.18425254 -0.18425254 -0.18425254
 [3,] -1.37133055 -1.37133055 -1.37133055 -1.37133055
 [4,] -0.59916772 -0.59916772 -0.59916772 -0.59916772
 [5,]  0.29454513  0.29454513  0.29454513  0.29454513
 [6,]  0.38979430  0.38979430  0.38979430  0.38979430
 [7,] -1.20807618 -1.20807618 -1.20807618 -1.20807618
 [8,] -0.36367602 -0.36367602 -0.36367602 -0.36367602
 [9,] -1.62667268 -1.62667268 -1.62667268 -1.62667268
```

(b) Same seed on FORK

Rabbit hole 2: Parallel random number generation

- Manually use `set.seed()` on every worker. not recommended
- Use 'L'Ecuyer-CMRG' multiple RNG stream.
  1. `RNGkind("L'Ecuyer-CMRG")` on your main session.
  2. `set.seed()` on your main session.
  3. `clusterSetupRNGstream()` to set your workers' seed.

Rabbit hole 3: Variable transportation

- Explicit functions and variables will always be transported.
- FORK will copy the main session at creation.
- Others should be taken care of by hand.
- Additional configuration of `clusterExport` when nested in a function call.

How many frameworks can one developer maintains?

There are so many different parallel backends:

- snow
- multicore
- parallel
- MPI
- Redis
- Hadoop
- Spark
- Slurm
- ...

How to support them? How to maintain code?

Foreach

`foreach` defines a simple but powerful framework for map/reduce parallel computation.

Package author/code writer

Decide which part of code can run in parallel.

End user

Decide how to run in parallel based on their available resources.

`foreach` is syntactically structured in the form of a for loop. But actually it works like -apply functions.

Foreach

```
library(foreach)
# library(doParallel)
# registerDoParallel()
a <- 10
foreach(i = 1 : 12, j = 12 : 1, .combine = rbind) %dopar%{
    Sys.sleep(0.5)
    # print will be dropped when run in parallel
    print(paste("i = ", i, ", j = ", j, sep = ""))
    # 'a' is passed automatically
    data.frame(i, j, a)
}
```

future

- `future` provides a simple and uniform way of evaluating R expressions asynchronously using various resources available to the user.
- Asynchronous computation. Not constrained by a for-loop or apply syntax.

future

```
library(future)
plan(cluster)

x <- future({
    x <- matrix(rnorm(10 ^ 6), nrow = 10 ^ 3)
    for(i in 1 : 5){
        print(paste("i = ", i))
        res <- eigen(x)
    }
    return(res)
}, seed = T)     # not block the main session

resolved(x)     # check whether the future is resolved
a <- rnorm(10)     # we can do other stuff at the main session
```

Futureverse

Available extensions for map-reduce:

- `future.apply`
- `doFuture`: backends for `foreach`, `BiocParallel` and `plyr`.
- `furrr`

Futureverse - future.apply

`future.apply` provides worry-free parallel alternatives to base-R "apply" functions.

```
library(future.apply)     # default plan is sequential
# plan(cluster)
x <- rnorm(16)
future_lapply(1 : 5, function(id){
    print(paste("id = ", id, sep = ""))     # normal print kept
    Sys.sleep(0.5)
    sum(x[1 : id])
})
```

Personal suggestions

- Nested parallel is NOT recommended. At least it should be done with careful configuration.
- `future.apply` vs `foreach`
  - Familiar with `foreach`: just use the `doFuture` backends.
  - New to parallel: `future.apply` is a good start point for your code.
  - `future` backend will relay the printed messages.
  - Performance in parallel are close, so-called.
  - Performance for sequential are slower than for-loop.

I want progress bars

- `RcppProgress` allows to display a progress bar in the R console for long running computations taking place in c++ code, supports OpenMP.
- `pbapply` is a lightweight package that adds progress bar to vectorized R functions ('*apply'). It supports several parallel backends.
- `progress` shows ASCII progress bars.
- `progressr` provides a minimal API for reporting progress updates in R.
  - Developer is responsible for providing progress updates.
  - End user decides if, when, and how progress should be presented.

progressr

```
library(progressr)
slow_sum <- function(x) {
    p <- progressr::progressor(along = x)
    sum <- 0
    for (kk in seq_along(x)) {
        Sys.sleep(0.5)
        sum <- sum + x[kk]
        p(message = sprintf("Added %g", x[kk]))
    }
    sum
}
# handlers("default")     # default handler is "txtprogressbar"
with_progress(y <- slow_sum(1:10))
handlers("progress")
with_progress(y <- slow_sum(1:10))
```

Profile parallel code (WIP)

Profiling 2 futures with 2 workers

```
plan(cluster, workers = 2)
fs <- lapply(1:2, function(x) future(slow(x))
vs <- value(fs)
```

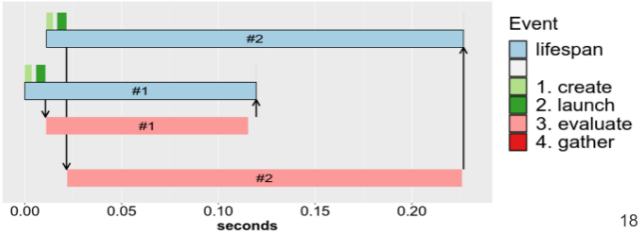

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Figure 6: Profile parallel code

Figure source at https://www.jottr.org/2022/06/23/future-user2022-slides/

Profile parallel code (WIP)

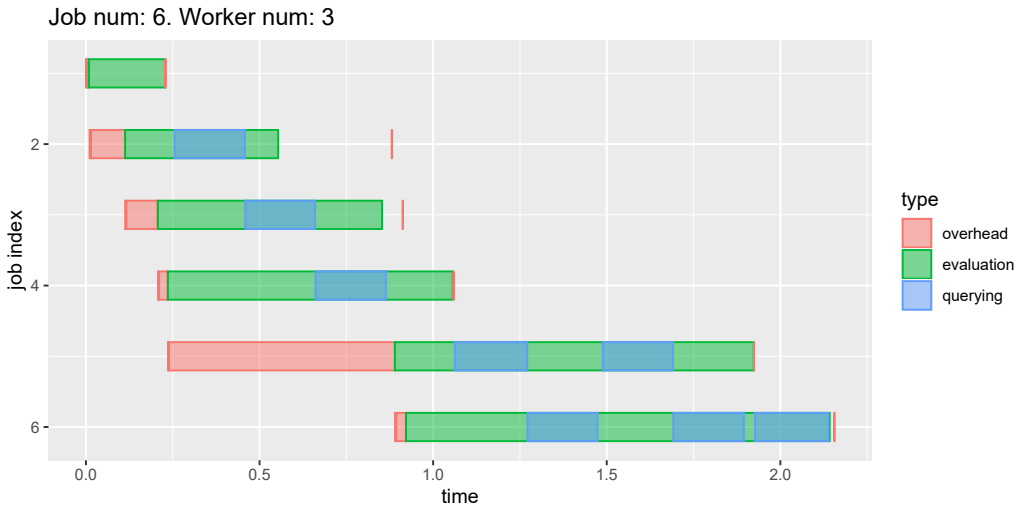
```
remotes::install_github(
    "git@github.com:HenrikBengtsson/future.git",
    ref = "9875992", force = TRUE)
```

```
> plan(cluster, workers = 2)
> slow_fcn <- function(x) {
+     Sys.sleep(x / 10)
+     sqrt(x)
+ }
>
> js <- capture_journals({
+     fs <- lapply(3:1, FUN = function(x) future(slow_fcn(x)))
+     value(fs)
+ })
> lapply(js, function(tndata){tndata[1 : 6, c("event", "type", "parent", "duration")]})
[[1]]
          event     type parent          duration
1        create overhead   <NA> 2.614021e-03 secs
6        launch overhead   <NA> 8.135939e-02 secs
2     getWorker overhead launch 1.218319e-04 secs
3   eraseWorker overhead launch 7.087874e-02 secs
4 attachPackages overhead launch 4.148483e-05 secs
5  exportGlobals overhead launch 8.690357e-04 secs

[[2]]
          event     type parent          duration
1        create overhead   <NA> 2.676725e-03 secs
6        launch overhead   <NA> 4.583597e-03 secs
2     getWorker overhead launch 1.337528e-04 secs
3   eraseWorker overhead launch 4.656315e-04 secs
4 attachPackages overhead launch 3.361702e-05 secs
5  exportGlobals overhead launch 6.408691e-04 secs
```

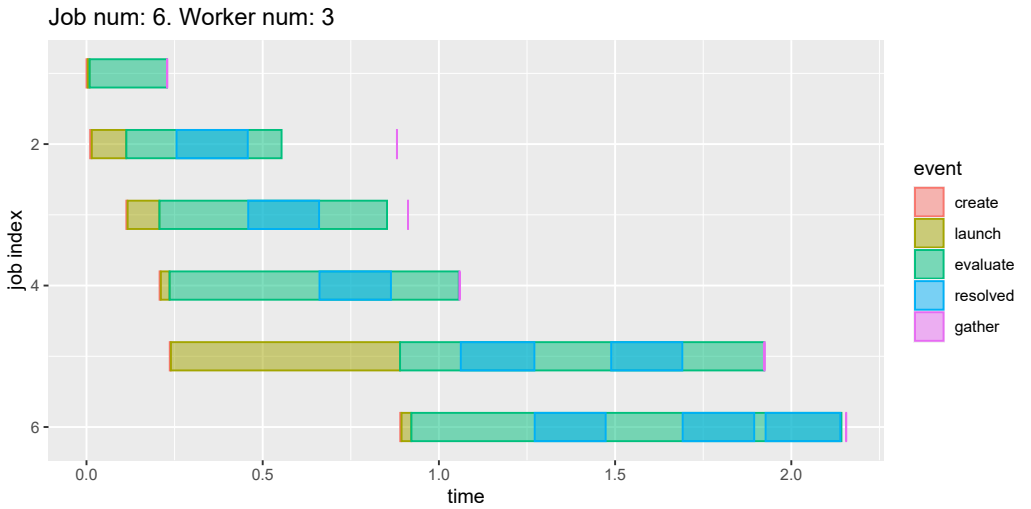
Profile parallel code (WIP)

```
library(future)
n_worker <- 3
n <- 6

plan(cluster, workers = n_worker)
slow <- function(x){
    Sys.sleep(x / 5)
    return(x)
}

tmp <- capture_journals({
    fs <- lapply(1 : n, function(x) future(slow(x)))
    vs <- value(fs)
})
```

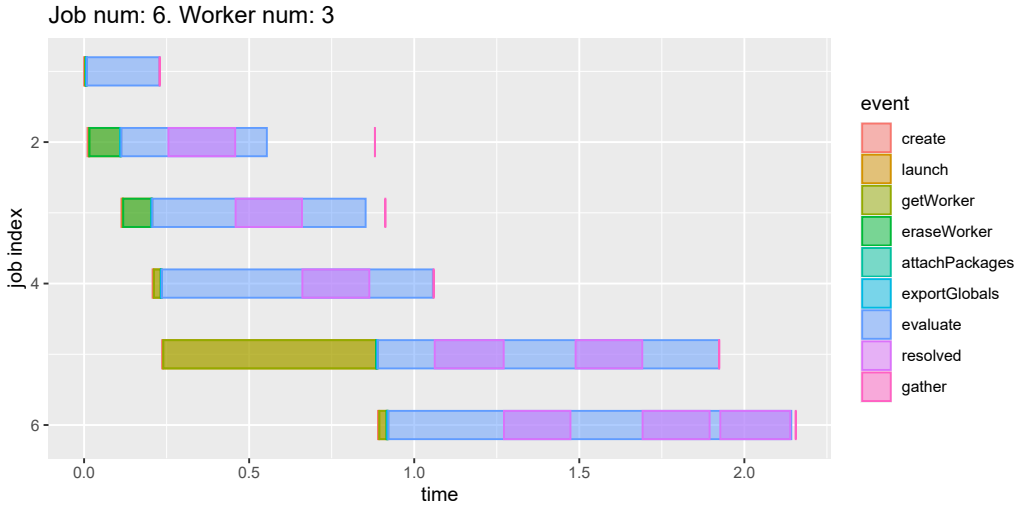
Profile parallel code (WIP)



Profile parallel code (WIP)



Profile parallel code (WIP)



Parallel is NOT all you need

How about we use $\frac{(1+n)\times n}{2}$?

Acknowledgement

Parallel computing with R using foreach, future, and other packages

BRYAN LEWIS

Future: Simple Async, Parallel & Distributed Processing in R - What's Next?

HENRIK BENGTSSON