

clustermq example

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Introduction

`clustermq` is an R package that uses the zeromq protocol for efficient inter-node/process communication. In contrast to `batchtools` that uses a disk-based registry, `clustermq` runs everything in-memory and hence has much better scalability.

Simple example

Using the `palmerpenguins` dataset we want to run some `glm`

```
compute <- function(n) {  
  
  library(palmerpenguins)  
  
  # Our dataset  
  x <- as.data.frame(penguins[c(4, 1)])  
  
  ind <- sample(344, 344, replace = TRUE)  
  result1 <-  
    glm(x[ind, 2] ~ x[ind, 1], family = binomial(logit))  
  coefficients(result1)  
}
```

Using this `compute()` function, we now simply can run

```
compute(1)
```

```
## (Intercept)    x[ind, 1]  
## 12.8465988   -0.7036583
```

If we now want to run the same `compute` function say a 100 times, we can use the `sapply` function

```
res<-sapply(1:100,compute)
```

Let's run this function a 10, 100 and 1000 times and measure the compute time

```
library(microbenchmark)  
microbenchmark(  
  sapply(1:10,compute),  
  sapply(1:100,compute),  
  sapply(1:1000,compute),  
  times=10)  
  
## Unit: milliseconds  
##          expr          min          lq          mean          median          uq  
##  sapply(1:10, compute)  18.15014  18.51515  19.47905  18.76681  18.94459  
##  sapply(1:100, compute) 193.11657 194.36330 208.46590 197.86827 203.32704
```

```
## supply(1:1000, compute) 1969.63796 1982.80374 2017.84963 2012.77071 2031.35082
##           max neval
##    26.5317    10
##   297.3029    10
##  2106.9649    10
```

Enter clustermq

Now let's do the same with clustermq.

```
library(clustermq)

## * Option 'clustermq.scheduler' not set, defaulting to 'SLURM'
## --- see: https://mschubert.github.io/clustermq/articles/userguide.html#configuration
system.time(res<-Q(compute, n=1:100, n_jobs=1))

## Submitting 1 worker jobs (ID: cmq9235) ...
## Running 100 calculations (0 objs/0 Mb common; 1 calls/chunk) ...
## [-----] 0% (1/1 wrk) eta: ?s[>-----]

##    user  system elapsed
##   0.374   0.034   3.240
```

Scaling up

```
microbenchmark(
  res<-Q(compute, n=1:1000, verbose=FALSE, n_jobs=1, chunk_size=10),
  res<-Q(compute, n=1:1000, verbose=FALSE, n_jobs=2, chunk_size=10),
  res<-Q(compute, n=1:1000, verbose=FALSE, n_jobs=4, chunk_size=10),
  res<-Q(compute, n=1:1000, verbose=FALSE, n_jobs=8, chunk_size=10),
  times=10
)

## Unit: seconds
##                                     expr
## res <- Q(compute, n = 1:1000, verbose = FALSE, n_jobs = 1, chunk_size = 10)
## res <- Q(compute, n = 1:1000, verbose = FALSE, n_jobs = 2, chunk_size = 10)
## res <- Q(compute, n = 1:1000, verbose = FALSE, n_jobs = 4, chunk_size = 10)
## res <- Q(compute, n = 1:1000, verbose = FALSE, n_jobs = 8, chunk_size = 10)
##      min      lq      mean  median      uq      max neval
## 5.229201 5.331659 6.037618 5.581053 5.990311 8.135010    10
## 4.531817 4.736806 5.152440 5.054040 5.117577 6.448664    10
## 3.236773 3.659275 4.325724 3.948953 4.352783 6.494752    10
## 3.435474 3.743023 4.159678 4.027089 4.194330 6.122911    10
```

Note the use of `chunk_size` above that is used to chunk individual tasks together.

foreach loops

Now let's run the same thing via foreach loops

```
computeforeach_cmq <- function(samples, tasks) {
  library(foreach)
  library(palmerpenguins)
```

```

# Register parallel backend to foreach
register_dopar_cmq(
  n_jobs = tasks,
  log_worker = FALSE,
  verbose=FALSE,
  chunk_size=10
)

# Our dataset
x <- as.data.frame(penguins[c(4, 1)])

# Number of samples to simulate
samples <- samples

# Main loop
foreach(i = 1:samples, .combine = rbind) %dopar% {
  ind <- sample(344, 344, replace = TRUE)
  result1 <-
    glm(x[ind, 2] ~ x[ind, 1], family = binomial(logit))
  coefficients(result1)
}
}

```

Now, let's test this `computeforeach_cmq` function for a couple of scenarios

```

library(clustermq)
library(microbenchmark)
microbenchmark(
  computeforeach_cmq(1000,1),
  computeforeach_cmq(1000,2),
  computeforeach_cmq(1000,4),
  computeforeach_cmq(1000,8),
  times=10
)

```

```

## Unit: seconds
##           expr      min       lq      mean   median      uq
## computeforeach_cmq(1000, 1) 5.112868 5.519198  6.172361 5.696144 6.856463
## computeforeach_cmq(1000, 2) 4.460139 4.494660 365.426522 5.193556 7.191374
## computeforeach_cmq(1000, 4) 3.489098 3.800440  4.712625 4.124666 6.212004
## computeforeach_cmq(1000, 8) 3.426540 3.969863  4.934567 4.455529 6.246246
##           max neval
##    8.239180     10
## 3604.555340     10
##    6.540094     10
##    6.782887     10

```

doFuture and future.batchtools

While there unfortunately is not yet a fully functional `future.clustermq` package, we have to make do with `future.batchtools` for the moment

```
library(doFuture)
```

```
## Loading required package: future
```

```
##
## Attaching package: 'future'
## The following object is masked from 'package:rmarkdown':
##
##      run
library(doRNG)

## Loading required package: rngtools
registerDoFuture()
library(future.batchtools)

## Loading required package: parallelly
Let's retry our computeforeach function again, but without the clustermq backend
computeforeach_future <- function(samples, tasks) {
  library(foreach)
  library(palmerpenguins)

  # Let's plan to have a maximum of tasks workers
  plan(batchtools_slurm, workers=tasks)

  # Our dataset
  x <- as.data.frame(penguins[c(4, 1)])

  # Number of samples to simulate
  samples <- samples

  # Main loop
  foreach(i = 1:samples, .combine = rbind, .options.future = list(chunk.size = 10)) %dorng% {
    ind <- sample(344, 344, replace = TRUE)
    result1 <-
      glm(x[ind, 2] ~ x[ind, 1], family = binomial(logit))
    coefficients(result1)
  }
}
```

Now, let's test this computeforeach_future function for a couple of scenarios

```
library(clustermq)
library(microbenchmark)
microbenchmark(
  computeforeach_future(1000,1),
  computeforeach_future(1000,2),
  computeforeach_future(1000,4),
  computeforeach_future(1000,8),
  times=10
)
```