Stat 8054 Lecture Notes: Parallel Computing in R

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1 License

2 R

- The version of R used to make this document is 4.0.2.
- The version of the `rmarkdown` package used to make this document is 2.3.
- The version of the `parallel` package used to make this document is 4.0.2. This is a "recommended" package that is installed by default in every installation of R, so the package version goes with the R version.

3 Introduction

The example that we will use throughout this document is simulating the sampling distribution of the MLE for Normal(θ, θ^2) data.

4 Set-Up

```
# sample size
n <- 10
# simulation sample size
nsim <- 1e4
# true unknown parameter value
# of course in the simulation it is known, but we pretend we don't
# know it and estimate it
theta <- 1

doit <- function(estimator, seed = 42) {
    set.seed(seed)
    result <- double(nsim)
    for (i in 1:nsim) {
        x <- rnorm(n, theta, abs(theta))
        result[i] <- estimator(x)
```

```
    }
    return(result)
}

mlogl <- function(theta, x) sum(- dnorm(x, theta, abs(theta), log = TRUE))

mle <- function(x) {
    theta.start <- sign(mean(x)) * sd(x)
    if (all(x == 0) || theta.start == 0)
        return(0)
    nout <- nlm(mlogl, theta.start, iterlim = 1000, x = x)
    if (nout$code > 3)
        return(NaN)
    return(nout$estimate)
}
```

- R function `doit` simulates `nsim` datasets, applies an estimator supplied as an argument to the function to each, and returns the vector of results.
- R function `mlogl` is minus the log likelihood of the model in question. We could easily change the code to do another model by changing only this function. (When the code mimics the math, the design is usually good.)
- R function `mle` calculates the estimator by calling R function `nlm` to minimize `mlogl`. The starting value `sign(mean(x)) * sd(x)` is a reasonable estimator because `mean(x)` is a consistent estimator of θ and `sd(x)` is a consistent estimator of $|\theta|$.

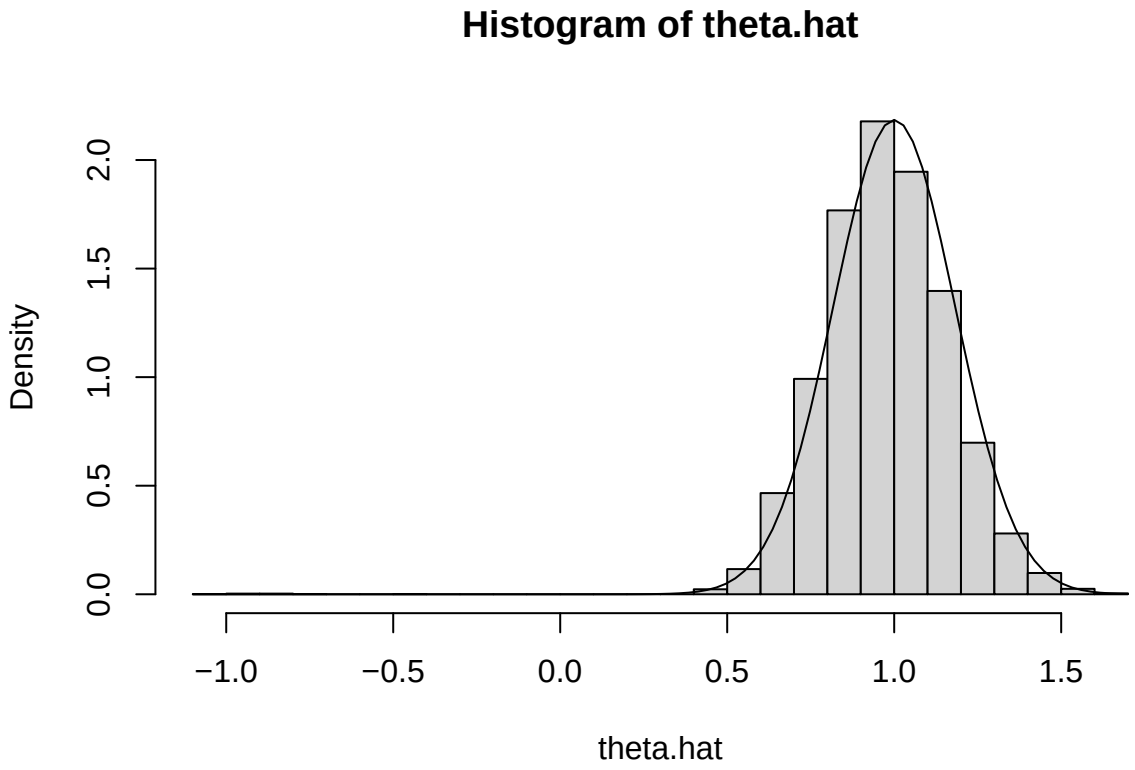
5 Doing the Simulation without Parallelization

5.1 Try It

```
theta.hat <- doit(mle)
```

5.2 Check It

```
hist(theta.hat, probability = TRUE, breaks = 30)
curve(dnorm(x, mean = theta, sd = theta / sqrt(3 * n)), add = TRUE)
```



The curve is the PDF of the asymptotic normal distribution of the MLE, which uses the formula

$$I_n(\theta) = \frac{3n}{\theta^2}$$

(the "usual" asymptotics of maximum likelihood).

Looks pretty good. The large negative estimates are probably not a mistake. The parameter is allowed to be negative, so sometimes the estimates come out negative even though the truth is positive. And not just a little negative because $|\theta|$ is also the standard deviation, so it cannot be small and the model fit the data.

```
sum(is.na(theta.hat))
```

```
## [1] 0
```

```
mean(is.na(theta.hat))
```

```
## [1] 0
```

```
sum(theta.hat < 0, na.rm = TRUE)
```

```
## [1] 9
```

```
mean(theta.hat < 0, na.rm = TRUE)
```

```
## [1] 9e-04
```

5.3 Time It

Now for something new. We will time it.

```
time1 <- system.time(theta.hat.mle <- doit(mle))
time1
```

```
##    user  system elapsed
##   0.842   0.004   0.848
```

The components of this vector are (these are taken from the R help page for R function `proc.time`, which R function `system.time` calls, and the UNIX man page for the UNIX system call `getrusage` system call, which `proc.time` calls)

- `user.self` the time the parent process (the R process executing the commands we see, like `doit`) spends in user mode
- `sys.self` the time the parent process spends in kernel model (doing system calls),
- `elapsed` the clock time,

We see that there is not a lot of difference between user mode time and elapsed time. We can take either to be the time.

5.4 Time It More Accurately

That's too short a time for accurate timing. So increase the number of iterations. Also we should probably average over several IID iterations to get a good average. Try again.

```
nsim <- 1e5
nrep <- 7
time1 <- NULL
for (irep in 1:nrep)
    time1 <- rbind(time1, system.time(theta.hat.mle <- doit(mle)))
time1
```

```
##      user.self sys.self elapsed user.child sys.child
## [1,]     7.315        0   7.314          0         0
## [2,]     7.081        0   7.081          0         0
## [3,]     7.772        0   7.773          0         0
## [4,]     7.479        0   7.479          0         0
## [5,]     7.446        0   7.446          0         0
## [6,]     7.570        0   7.569          0         0
## [7,]     7.613        0   7.614          0         0
```

Now we see two more components of `proc.time` objects

- `user.child` total user mode time for for all children of the calling process that have terminated and been waited for and grandchildren and further removed descendants, if all of the intervening descendants waited on their terminated children, which is a mouthful, here it is all the work done by the fork-and-exec'ed children, and
- `sys.child` like the preceding except kernel mode rather than user mode.

These components are in every `proc_time` object. The reason why we didn't see them before is something about what R function `print.proc_time` does. Now

```
class(time1)
```

```
## [1] "matrix" "array"
```

the printing is being done by R function `print.default` since there is no `print.matrix` and the class of what we are printing is no longer `proc_time`.

```
apply(time1, 2, mean)
```

```
##  user.self   sys.self    elapsed user.child  sys.child
##      7.468      0.000      7.468      0.000      0.000
```

```
apply(time1, 2, sd) / sqrt(nrep)
```

```
##  user.self   sys.self    elapsed user.child  sys.child
## 0.08418064 0.00000000 0.08432251 0.00000000 0.00000000
```

So we have about one and a half significant figures in our timing on this. Longer runs would have more accuracy.

6 Parallel Computing With Unix Fork and Exec

6.1 Introduction

This method is by far the simplest but

- it only works on one computer (using however many simultaneous processes the computer can do), and
- it does not work on Windows.

6.2 Toy Problem

First a toy problem that does nothing except show that we are actually using different processes.

```
library(parallel)
ncores <- detectCores()
mclapply(1:ncores, function(x) Sys.getpid(), mc.cores = ncores)
```

```
## [[1]]
## [1] 7171
##
## [[2]]
## [1] 7172
##
## [[3]]
## [1] 7173
##
## [[4]]
## [1] 7174
##
## [[5]]
## [1] 7175
##
## [[6]]
## [1] 7176
##
## [[7]]
## [1] 7177
##
## [[8]]
## [1] 7178
```

6.3 Warning

Quoted from the help page for R function `mclapply`

> It is *strongly discouraged* to use these functions in GUI or embedded environments, because it leads to several processes sharing the same GUI which will likely cause chaos (and possibly crashes). Child processes should never use on-screen graphics devices.

GUI includes RStudio. If you want speed, then you will have to learn how to use plain old R. The examples in the section on using clusters show that. Of course, this whole document shows that too. (No RStudio was used to make this document. In plain old R we said `library("rmarkdown")` and then `render("parallel.Rmd")`.)

6.4 Parallel Streams of Random Numbers

To get random numbers in parallel, we need to use a special random number generator (RNG) designed for parallelization.

```
RNGkind("L'Ecuyer-CMRG")
set.seed(42)
mclapply(1:ncores, function(x) rnorm(5), mc.cores = ncores)
```

```
## [[1]]
## [1]  1.11932846 -0.07617141 -0.35021912 -0.33491161 -1.73311280
##
## [[2]]
## [1] -0.2084809 -1.0341493 -0.2629060  0.3880115  0.8331067
##
## [[3]]
## [1]  0.001100034  1.763058291 -0.166377859 -0.311947389  0.694879494
##
## [[4]]
## [1]  0.2262605 -0.4827515  1.7637105 -0.1887217 -0.7998982
##
## [[5]]
## [1]  0.8584220 -0.3851236  1.0817530  0.2851169  0.1799325
##
## [[6]]
## [1] -1.1378621 -1.5197576 -0.9198612  1.0303683 -0.9458347
##
## [[7]]
## [1] -0.04649149  3.38053730 -0.35705061  0.17722940 -0.39716405
##
## [[8]]
## [1]  1.3502819 -1.0055894 -0.4591798 -0.0628527 -0.2706805
```

Just right! We have different random numbers in all our jobs. And it is reproducible.

But this may not work like you may think it does. If we do it again we get exactly the same results.

```
mclapply(1:ncores, function(x) rnorm(5), mc.cores = ncores)
```

```
## [[1]]
## [1]  1.11932846 -0.07617141 -0.35021912 -0.33491161 -1.73311280
##
## [[2]]
## [1] -0.2084809 -1.0341493 -0.2629060  0.3880115  0.8331067
##
## [[3]]
## [1]  0.001100034  1.763058291 -0.166377859 -0.311947389  0.694879494
##
```

```
## [[4]]
## [1]  0.2262605 -0.4827515  1.7637105 -0.1887217 -0.7998982
##
## [[5]]
## [1]  0.8584220 -0.3851236  1.0817530  0.2851169  0.1799325
##
## [[6]]
## [1] -1.1378621 -1.5197576 -0.9198612  1.0303683 -0.9458347
##
## [[7]]
## [1] -0.04649149  3.38053730 -0.35705061  0.17722940 -0.39716405
##
## [[8]]
## [1]  1.3502819 -1.0055894 -0.4591798 -0.0628527 -0.2706805
```

Running `mclapply` does not change `.Random.seed` in the parent process (the R process you are typing into). It only changes it in the child processes (that do the work). But there is no communication from child to parent *except* the list of results returned by `mclapply`.

This is a fundamental problem with `mclapply` and the fork-exec method of parallelization. And it has no real solution. You just have to be aware of it.

If you want to do exactly the same random thing with `mclapply` and get different random results, then you must change `.Random.seed` in the parent process, either with `set.seed` or by otherwise using random numbers *in the parent process*.

6.5 The Example

We need to rewrite our `doit` function

- to only do `1 / ncores` of the work in each child process,
- to not set the random number generator seed, and
- to take an argument in some list we provide.

```
doit <- function(nsim, estimator) {
    result <- double(nsim)
    for (i in 1:nsim) {
        x <- rnorm(n, theta, abs(theta))
        result[i] <- estimator(x)
    }
    return(result)
}
```

6.6 Try It

```
mout <- mclapply(rep(nsim / ncores, ncores), doit,
    estimator = mle, mc.cores = ncores)
lapply(mout, head)
```

```
## [[1]]
## [1] 0.9051972 0.9589889 0.9799828 1.1347548 0.9090886 0.9821320
##
## [[2]]
```

```
## [1] 0.8317815 1.3432331 0.7821308 1.2010078 0.9792244 1.1148521
##
## [[3]]
## [1] 0.8627829 0.9790400 1.1787975 0.7852431 1.2942963 1.0768396
##
## [[4]]
## [1] 1.0422013 0.9166641 0.8326720 1.1864809 0.9609456 1.3137716
##
## [[5]]
## [1] 0.8057316 0.9488173 1.0792078 0.9774531 0.8106612 0.8403027
##
## [[6]]
## [1] 1.0156983 1.0077599 0.9867766 1.1643493 0.9478923 1.1770221
##
## [[7]]
## [1] 1.2287013 1.0046353 0.9560784 1.0354414 0.9045423 0.9455714
##
## [[8]]
## [1] 0.7768910 1.0376265 0.8830854 0.8911714 1.0288567 1.1609360
```

6.7 Check It

Seems to have worked.

```
length(mout)
```

```
## [1] 8
```

```
sapply(mout, length)
```

```
## [1] 12500 12500 12500 12500 12500 12500 12500 12500
```

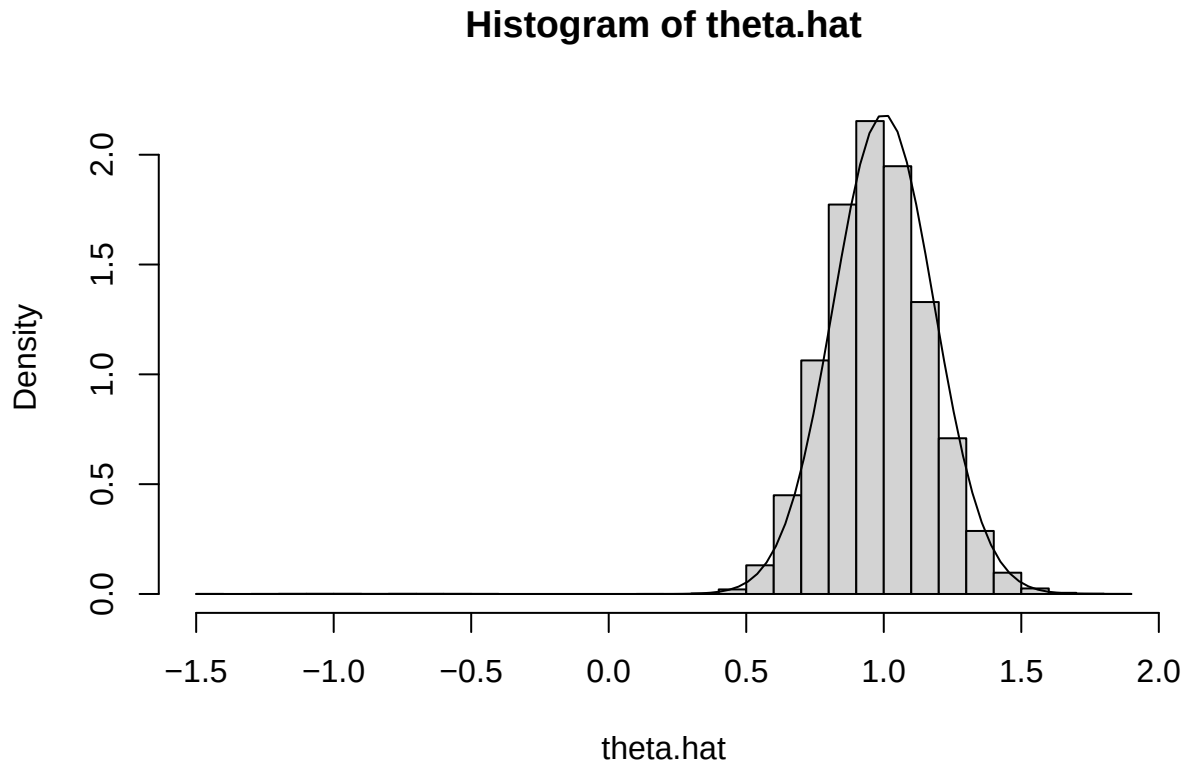
```
lapply(mout, head)
```

```
## [[1]]
## [1] 0.9051972 0.9589889 0.9799828 1.1347548 0.9090886 0.9821320
##
## [[2]]
## [1] 0.8317815 1.3432331 0.7821308 1.2010078 0.9792244 1.1148521
##
## [[3]]
## [1] 0.8627829 0.9790400 1.1787975 0.7852431 1.2942963 1.0768396
##
## [[4]]
## [1] 1.0422013 0.9166641 0.8326720 1.1864809 0.9609456 1.3137716
##
## [[5]]
## [1] 0.8057316 0.9488173 1.0792078 0.9774531 0.8106612 0.8403027
##
## [[6]]
## [1] 1.0156983 1.0077599 0.9867766 1.1643493 0.9478923 1.1770221
##
## [[7]]
## [1] 1.2287013 1.0046353 0.9560784 1.0354414 0.9045423 0.9455714
##
```

```
## [[8]]
## [1] 0.7768910 1.0376265 0.8830854 0.8911714 1.0288567 1.1609360
```

Plot it.

```
theta.hat <- unlist(mout)
hist(theta.hat, probability = TRUE, breaks = 30)
curve(dnorm(x, mean = theta, sd = theta / sqrt(3 * n)), add = TRUE)
```



6.8 Time It

```
time4 <- NULL
for (irep in 1:nrep)
    time4 <- rbind(time4, system.time(theta.hat.mle <-
        unlist(mclapply(rep(nsim / ncores, ncores), doit,
            estimator = mle, mc.cores = ncores))))
time4
```

```
##      user.self sys.self elapsed user.child sys.child
## [1,]     0.002    0.028   1.836     12.063     0.232
## [2,]     0.000    0.030   1.766     11.662     0.288
## [3,]     0.005    0.032   1.856     12.197     0.220
## [4,]     0.006    0.024   2.142     14.153     0.252
## [5,]     0.003    0.028   1.984     12.813     0.347
## [6,]     0.006    0.032   2.529     16.588     0.268
## [7,]     0.005    0.040   2.738     17.637     0.487
```

Now we see that, unlike when we had no parallelism, now `user.self` is almost no time. All the time is in `user.child`. The child processes are doing all the work. We also see that the total child time is far longer than the actual elapsed time (in the real world). So we are getting parallelism.

```
apply(time4, 2, mean)
```

```
##    user.self     sys.self      elapsed   user.child    sys.child
##  0.003857143  0.030571429  2.121571429 13.873285714  0.299142857
```

```
apply(time4, 2, sd) / sqrt(nrep)
```

```
##    user.self     sys.self      elapsed   user.child    sys.child
## 0.0008571429 0.0018880217 0.1417438765 0.8959501133 0.0350743622
```

We got the desired speedup. The elapsed time averages

```
apply(time4, 2, mean)["elapsed"]
```

```
##  elapsed
## 2.121571
```

with parallelization and

```
apply(time1, 2, mean)["elapsed"]
```

```
## elapsed
##   7.468
```

without parallelization. But we did not get an 8-fold speedup with 8 cores. There is a cost to starting and stopping the child processes. And some time needs to be taken from this number crunching to run the rest of the computer. However, we did get a 3.5-fold speedup. If we had more cores, we could do even better.

7 The Example With a Cluster

7.1 Introduction

This method is more complicated but

- it works on clusters like the ones at LATIS (College of Liberal Arts Technologies and Innovation Services) or at the Minnesota Supercomputing Institute.
- according to the documentation, it does work on Windows.

7.2 Toy Problem

First a toy problem that does nothing except show that we are actually using different processes.

```
library(parallel)
ncores <- detectCores()
cl <- makePSOCKcluster(ncores)
parLapply(cl, 1:ncores, function(x) Sys.getpid())
```

```
## [[1]]
## [1] 7211
##
## [[2]]
## [1] 7204
##
## [[3]]
## [1] 7208
```

```
##
## [[4]]
## [1] 7206
##
## [[5]]
## [1] 7210
##
## [[6]]
## [1] 7205
##
## [[7]]
## [1] 7209
##
## [[8]]
## [1] 7207
```

```
stopCluster(cl)
```

This is more complicated in that

- first you you set up a cluster, here with `makePSOCKcluster` but not everywhere — there are a variety of different commands to make clusters and the command would be different at LATIS or MSI — and
- at the end you tear down the cluster with `stopCluster`.

Of course, you do not need to tear down the cluster before you are done with it. You can execute multiple `parLapply` commands on the same cluster.

There are also a lot of other commands other than `parLapply` that can be used on the cluster. We will see some of them below.

7.3 Parallel Streams of Random Numbers

```
cl <- makePSOCKcluster(ncores)
clusterSetRNGStream(cl, 42)
parLapply(cl, 1:ncores, function(x) rnorm(5))
```

```
## [[1]]
## [1] -0.93907708 -0.04167943  0.82941349 -0.43935820 -0.31403543
##
## [[2]]
## [1]  1.11932846 -0.07617141 -0.35021912 -0.33491161 -1.73311280
##
## [[3]]
## [1] -0.2084809 -1.0341493 -0.2629060  0.3880115  0.8331067
##
## [[4]]
## [1]  0.001100034  1.763058291 -0.166377859 -0.311947389  0.694879494
##
## [[5]]
## [1]  0.2262605 -0.4827515  1.7637105 -0.1887217 -0.7998982
##
## [[6]]
## [1]  0.8584220 -0.3851236  1.0817530  0.2851169  0.1799325
##
## [[7]]
```

```
## [1] -1.1378621 -1.5197576 -0.9198612  1.0303683 -0.9458347
##
## [[8]]
## [1] -0.04649149  3.38053730 -0.35705061  0.17722940 -0.39716405
```

```
parLapply(cl, 1:ncores, function(x) rnorm(5))
```

```
## [[1]]
## [1] -2.1290236  2.5069224 -1.1273128  0.1660827  0.5767232
##
## [[2]]
## [1] 0.03628534 0.29647473 1.07128138 0.72844380 0.12458507
##
## [[3]]
## [1] -0.1652167 -0.3262253 -0.2657667  0.1878883  1.4916193
##
## [[4]]
## [1]  0.3541931 -0.6820627 -1.0762411 -0.9595483  0.0982342
##
## [[5]]
## [1]  0.5441483  1.0852866  1.6011037 -0.5018903 -0.2709106
##
## [[6]]
## [1] -0.57445721 -0.86440961 -0.77401840  0.54423137 -0.01006838
##
## [[7]]
## [1] -1.3057289  0.5911102  0.8416164  1.7477622 -0.7824792
##
## [[8]]
## [1]  0.9071634  0.2518615 -0.4905999  0.4900700  0.7970189
```

We see that clusters do not have the same problem with continuing random number streams that the fork-exec mechanism has.

- Using fork-exec there is a *parent* process and *child* processes (all running on the same computer) and the *child* processes end when their work is done (when `mclapply` finishes).
- Using clusters there is a *controller* process and *worker* processes (possibly running on many different computers) and the *worker* processes end when the cluster is torn down (with `stopCluster`).

So the worker processes continue and each remembers where it is in its random number stream (each has a different random number stream).

7.4 The Example on a Cluster

7.4.1 Set Up

Another complication of using clusters is that the worker processes are completely independent of the controller process. Any information they have must be explicitly passed to them.

This is very unlike the fork-exec model in which all of the child processes are copies of the parent process inheriting all of its memory (and thus knowing about any and all R objects it created).

So in order for our example to work we must explicitly distribute stuff to the cluster.

```
clusterExport(cl, c("doit", "mle", "mlogl", "n", "nsim", "theta"))
```

Now all of the workers have those R objects, as copied from the controller process right now. If we change them in the controller (pedantically if we change the R objects those *names* refer to) the workers won't know about it. Thus if we change these objects on the controller, we must re-export them to the workers.

7.4.2 Try It

So now we are set up to try our example.

```
pout <- parLapply(cl, rep(nsim / ncores, ncores), doit, estimator = mle)
```

7.4.3 Check It

Seems to have worked.

```
length(pout)
```

```
## [1] 8
```

```
sapply(pout, length)
```

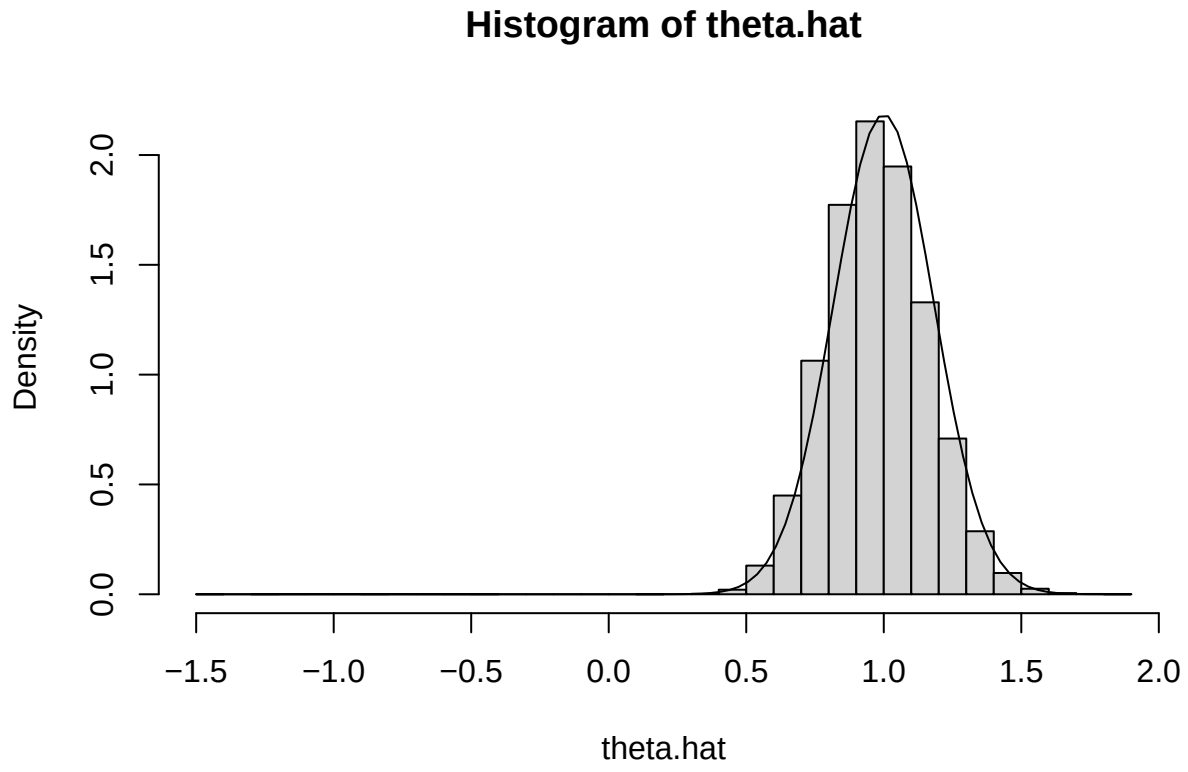
```
## [1] 12500 12500 12500 12500 12500 12500 12500 12500
```

```
lapply(pout, head)
```

```
## [[1]]
## [1] 1.0079313 0.7316543 0.4958322 0.7705943 0.7734226 0.6158992
##
## [[2]]
## [1] 0.9589889 0.9799828 1.1347548 0.9090886 0.9821320 1.0032531
##
## [[3]]
## [1] 1.3432331 0.7821308 1.2010078 0.9792244 1.1148521 0.9269000
##
## [[4]]
## [1] 0.9790400 1.1787975 0.7852431 1.2942963 1.0768396 0.7546295
##
## [[5]]
## [1] 0.9166641 0.8326720 1.1864809 0.9609456 1.3137716 0.9832663
##
## [[6]]
## [1] 0.9488173 1.0792078 0.9774531 0.8106612 0.8403027 1.1296857
##
## [[7]]
## [1] 1.0077599 0.9867766 1.1643493 0.9478923 1.1770221 1.2789464
##
## [[8]]
## [1] 1.0046353 0.9560784 1.0354414 0.9045423 0.9455714 1.0312553
```

Plot it.

```
theta.hat <- unlist(mout)
hist(theta.hat, probability = TRUE, breaks = 30)
curve(dnorm(x, mean = theta, sd = theta / sqrt(3 * n)), add = TRUE)
```



7.4.4 Time It

```
time5 <- NULL
for (irep in 1:nrep)
    time5 <- rbind(time5, system.time(theta.hat.mle <-
        unlist(parLapply(cl, rep(nsim / ncores, ncores),
            doit, estimator = mle))))
time5
```

```
##      user.self sys.self elapsed user.child sys.child
## [1,]     0.006    0.004   2.282          0         0
## [2,]     0.012    0.000   2.448          0         0
## [3,]     0.007    0.004   2.590          0         0
## [4,]     0.006    0.004   2.789          0         0
## [5,]     0.012    0.000   2.450          0         0
## [6,]     0.011    0.000   2.743          0         0
## [7,]     0.010    0.000   2.498          0         0
```

Now we are not seeing any child times because the workers are not children of the controller R process, they need not even be running on the same computer. If we wanted to know about times on the workers, we would have to run R function `system.time` on the workers and also include that information in the result somehow. So the only time of interest here is `elapsed`.

```
apply(time5, 2, mean)
```

```
##   user.self    sys.self     elapsed  user.child   sys.child
## 0.009142857 0.001714286 2.542857143 0.000000000 0.000000000
```

```
apply(time5, 2, sd) / sqrt(nrep)
```

```
##   user.self    sys.self     elapsed  user.child   sys.child
## 0.001033454 0.000808122 0.067355641 0.000000000 0.000000000
```

We got the desired speedup. The elapsed time averages

```
apply(time5, 2, mean)["elapsed"]
```

```
##  elapsed
## 2.542857
```

with parallelization and

```
apply(time1, 2, mean)["elapsed"]
```

```
## elapsed
##   7.468
```

without parallelization. But we did not get an 8-fold speedup with 8 cores. There is a cost to starting and stopping the child processes. And some time needs to be taken from this number crunching to run the rest of the computer. However, we did get a 2.9-fold speedup. If we had more cores, we could do even better.

We also see that this method isn't quite as fast as the other method. So why do we want it (other than that the other doesn't work on Windows)? Because it scales. You can get clusters with thousands of cores, but you can't get thousands of cores in one computer.

7.5 Tear Down

Don't forget to tear down the cluster when you are done.

```
stopCluster(cl)
```

8 LATIS

For more about the LATIS see https://cla.umn.edu/latis.

For more about the compute cluster `compute.cla.umn.edu` run by LATIS see https://cla.umn.edu/research-creative-work/research-development/research-computing-and-software.

For all the info on various queues and resource limits see https://neighborhood.cla.umn.edu/node/5371.

8.1 Fork-Exec

This is just like the fork-exec section above except for a few minor changes for running on LATIS.

8.1.1 Interactive Session

SSH into `compute.cla.umn.edu`. Then

```
qsub -I -l nodes=1:ppn=8
cd tmp/8054/parallel # or wherever
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/fork-exec.R
module load R/3.6.1
R CMD BATCH --vanilla fork-exec.R
cat fork-exec.Rout
exit
```

8.1.2 Batch Job

```
cd tmp/8054/parallel # or wherever
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/fork-exec.R
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/fork-exec.pbs
qsub fork-exec.pbs
```

If you want e-mail sent to you when the job starts and completes, then add the lines

```
### EMAIL NOTIFICATION OPTIONS ###
# Send email on a:abort, b:begin, e:end
#PBS -m abe
# Your email address
#PBS -M yourusername@umn.edu
```

to `fork-exec.pbs` where, of course, `yourusername` is replaced by your actual username.

You may also need to alter the line in the file `fork-exec.pbs` about `walltime`. This asks for 20 minutes. If the job doesn't finish in that amount of time, then it is killed. If you delete this line entirely, then the default two days.

The linux command

```
qstat
```

will tell you if your job is running.

The linux command

```
qdel jobnumber
```

where `jobnumber` is the actual job number shown by `qstat`, will kill the job.

You can log out of `compute.cla.umn.edu` after your job starts in batch mode. It will keep running.

8.2 MPI Cluster

MPI clusters are the way "big iron" does parallel processing. So if you ever want to move up to the clusters at the Minnesota Supercomputing Institute or even bigger clusters, you need to start here.

This is just like the cluster section above except for a few minor changes for running on LATIS.

8.2.1 Interactive Session

In order for an MPI cluster to work, we need to install R packages `Rmpi` and `snow` which LATIS does not install for us. So users have to install them themselves (like any other CRAN package they want to use). It also turns out that we have to load two modules rather than one: the module containing R and another module containing a newer version of openmpi than the default. This means we will also have to load these two modules whenever we want to use an MPI cluster.

```
qsub -I
module load R/3.6.1
module load openmpi/3.1.3
R --vanilla
options(repos = c(CRAN="https://cloud.r-project.org/"))
install.packages("Rmpi")
install.packages("snow")
q()
```

```
exit
```

R function `install.packages` will tell you that it cannot install the packages in the usual place and asks you if you want to install it in a "personal library". Say yes. Then it suggests a location for the "personal library". Say yes.

Now almost the same thing again (again we use only one node because we are only allowed one node for an interactive queue)

```
qsub -I -l nodes=1:ppn=8
cd tmp/8054/parallel # or wherever
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/cluster.R
module load R/3.6.1
module load openmpi/3.1.3
R CMD BATCH --vanilla cluster.R
cat cluster.Rout
exit
```

The `qsub` command says we want to use 8 cores on 1 node (computer). The interactive queue is not allowed to use more than one node.

8.2.2 Batch Job

Same as above *mutatis mutandis*

```
cd tmp/8054/parallel # or wherever
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/cluster.R
wget -N http://www.stat.umn.edu/geyer/8054/scripts/latis/cluster.pbs
qsub cluster.pbs
```

with the same comments about email and walltime.

8.3 Sockets Cluster on LATIS

You can make a sockets cluster on LATIS if you are only using one node. It works just like in the example in the main text.