Using R on HPC Clusters Part 2

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Get this presentation:

git clone https://github.com/RBigData/R4HPC.git

• Open

R4HPC_Part2.html

in your web browser (help ? toggle)

Slack workspace link for this workshop was emailed to you.

Many thanks to my colleagues and former colleagues who contributed to the software and ideas presented here. See the RBigData Organization on Github: https://github.com/RBigData. Also, many thanks to all R developers of packages used in this presentation.

Slides are made with the xaringan R package. It is an R Markdown extension based CAK On the JavaScript library remark.js.

Today's Package Installs

See R4HPC/code_4 R script and shell scripts for your machine



Running MPI on a Laptop

macOS in a Terminal window:

- brew install openmpi
- mpirun -np 4 Rscript your_spmd_code.R

Windows

- Web Page: https://docs.microsoft.com/en-us/message-passinginterface/microsoft-mpi
- Download: https://www.microsoft.com/en-us/download/details.aspx? id=100593
- pbdMPI has a Windows binary on CRAN



Revisithello_balance.Rincode_1

```
suppressMessages(library(pbdMPI))
   comm.print(sessionInfo())
   ## get node name
   host = system("hostname", intern = TRUE)
   mc.function = function(x) {
       Sys.sleep(1) # replace with your function for mclapply cores here
       Sys.getpid() # returns process id
   }
   ## Compute how many cores per R session are on this node
   local ranks query = "echo $OMPI COMM WORLD LOCAL SIZE"
   ranks_on_my_node = as.numeric(system(local_ranks_query, intern = TRUE))
   cores_on_my_node = parallel::detectCores()
   cores per R = floor(cores on my node/ranks on my node)
   cores_total = allreduce(cores_per_R) # adds up over ranks
   ## Run mclapply on allocated cores to demonstrate fork pids
   my_pids = parallel::mclapply(1:cores_per_R, mc.function, mc.cores = core
   my_pids = do.call(paste, my_pids) # combines results from mclapply
    ##
DAK RIDGE ame cores are shared with OpenBLAS (see flexiblas package)
                  or for other OpenMP enabled codes outside mclapply.
```

Working with a remote cluster using R



file:///Users/nk8/R4HPC/R4HPC_Part2.html#1



Running Distributed on a Cluster



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file:///Users/nk8/R4HPC/R4HPC_Part2.html#1

Section I: Environment and Workflow

Section II: Parallel Hardware and Software Overview

Section III: Shared Memory Tools

Section IV: Distributed Memory Tools









pbdR Project



pbdR											
R	Sca	ScaLAPACK		NetCDF4	ADIOS2	mpiP	fpmpi	ZeroMQ	cuRAND	cuBLAS	NVML
LAPACK	LAPACK P		CombBLAS	HDF5							
BLAS		BLACS									
		MPI						CUDA			

- Bridge HPC with high-productivity of R: Expressive for data and modern statistics
- Keep syntax identical to R, when possible
- Software reuse philosophy:
 - Don't reinvent the wheel when possible
 - Introduce HPC standards with R flavor
 - Use scalable HPC libraries with R convenience

CAK RIDGE National Laborato Simplify and use R intelligence where possible





Package pbdMPI

- Specializes in SPMD programming for HPC clusters
 - Manages printing from ranks
 - Provides chunking options
 - Provides communicator splits for multilevel parallelism
 - In situ capability to process data from other MPI codes without copy
- A derivation and rethinking of the Rmpi package aimed at HPC clusters
 - Simplified interface with fewer parameters (using R's S4 methods)
 - Faster for matrix and array data no serialization



Using R on HPC Clusters Part 2

Single Program Multiple Data (SPMD)



- One code and a parallel mindset
- A generalization of a serial code
- Many rank-aware operations are automated
- Collective operations are high level and easy to learn
- Explicit point-to-point communications are an advanced topic
- No manager, it is all cooperation





High-level Collective Communications

$$\mathbf{A} = \sum_{i=1}^{n} \mathbf{X}_{i}$$

pbdMPI:A = reduce(X)A = allreduce(X) $A = [X_1 | X_2 | \cdots | X_n]$ pbdMPI:A = gather(X)A = allgather(X)



Functions to Facilitate SPMD Programming



- **comm.chunk()** splits a number into chunks in various ways and various formats. Tailored for SPMD programming, returning correct (usually different) results to each rank.
- **comm.set.seed()** sets the seed of a parallel RNG. If diff = FALSE, then all ranks generate the same stream. Otherwise, ranks generate different streams.
- **comm.print()** and **comm.cat()** print by default from rank 0 only, with options to print from any or all ranks.





Hands on Session 5: Hello MPI Ranks



```
code_5/hello_world.R
```

```
suppressMessages(library(pbdMPI))
```

Rank distinguishes the parallel copies of the same code



Hands on Session 5: Random Forest with MPI



code_5/rf_mpi.R

```
suppressPackageStartupMessages(library(randomForest))
data(LetterRecognition, package = "mlbench")
library(pbdMPI, quiet = TRUE)
comm.set.seed(seed = 7654321, diff = FALSE)
n = nrow(LetterRecognition)
n test = floor(0.2 * n)
i_test = sample.int(n, n_test)
train = LetterRecognition[-i_test, ]
test = LetterRecognition[i_test, ][comm.chunk(n_test, form = "vector"),
comm.set.seed(seed = 1234, diff = TRUE)
my.rf = randomForest(lettr ~ ., train, ntree = comm.chunk(500), norm.vot
rf.all = allgather(my.rf)
rf.all = do.call(combine, rf.all)
pred = as.vector(predict(rf.all, test))
correct = allreduce(sum(pred == test$lettr))
comm.cat("Proportion Correct:", correct/(n_test), "\n")
```

AK REPOSITIZE()

Hands on Session 5: comm.chunk()

```
mpi_shorts/chunk.r
```

```
library( pbdMPI, quiet = TRUE )
my.rank = comm.rank( )
k = comm.chunk( 10 )
comm.cat( my.rank, ":", k, "\n", all.rank = TRUE, quiet = TRUE)
k = comm.chunk( 10 , form = "vector")
comm.cat( my.rank, ":", k, "\n", all.rank = TRUE, quiet = TRUE)
k = comm.chunk( 10 , form = "vector", type = "equal")
comm.cat( my.rank, ":", k, "\n", all.rank = TRUE, quiet = TRUE)
finalize( )
```



Hands on Session 5: other short MPI codes

bcast.r chunk.r comm_split.R cov.r gather-named.r gather.r gather-unequal.r hello-p.r hello.r map-reduce.r mcsim.r ols.r qr-cop.r rank.r reduce-mat.r timer.r

- These short codes only use pbdMPI and can run on a laptop in a terminal window if you installed OpenMPI
- On the clusters these can run on a login node with a small * number of ranks
- Wile in the mpi_shorts directory, run the following
 - o source ../code_4/modules_MACHINE.sh
 - mpirun -np 4 Rscript your_script.r

* Note that running long or large jobs on login nodes is strongly discouraged



Shared Memory - MPI or fork?

• fork via mclapply() + do.call() combine



• MPI replicated data + allreduce()



• MPI chunked data + allreduce()







Package pbdDMAT

- ScaLAPACK: Scalable LAPACK Distributed version of LAPACK (uses PBLAS/BLAS but not LAPACK)
 - 2d Block-Cyclic data layout mostly automated in pbdDMAT package
 - BLACS: Communication collectives for distributed matrix computation
 - PBLAS: BLAS distributed BLAS (uses shared memory BLAS within blocks)
- Most matrix operations in R code are identical to serial through overloading operators and ddmatrix class







Package pbdML

- A demonstration of pbdDMAT package capabilities
- Includes
 - Randomized SVD
 - Randomized principal components analysis
 - Robust Principal Component Analysis?" from https://arxiv.org/pdf/0912.3599.pdf



Hands on Session rsvd: Randomized sketching algorithms

Fast new alternatives to classical numerical linear algebra computations.

Guarantees are given with probability statements instead of classical error analysis.

Martinsson, P., & Tropp, J. (2020). Randomized numerical linear algebra: Foundations and algorithms. Acta Numerica, 29, 403-572. https://doi.org/10.48550/arXiv.2002.01387



Hands on Session rsvd: Randomized SVD via subspace of the second second

Given an $n \times p$ matrix X and k = r + 10, where r is the *effective rank* of X:

- 1. Construct a p imes k random matrix Ω
- 2. Form $Y = \overline{X}\Omega$
- 3. Decompose Y = QR

Q is an orthogonal basis for the columnspace of Y, which with high probability is the columnspace of X. To get the SVD of X:

- 1. Compute $C = Q^T X$
- 2. Decompose $C = \hat{U} \Sigma V^T$
- 3. Compute $U = Q\hat{U}$
- 4. Truncate factorization to r columns



mnist_rsvd.R

```
source("mnist_read_mpi.R") # reads blocks of rows
suppressMessages(library(pbdDMAT))
suppressMessages(library(pbdML))
init.grid()
## construct block-cyclic ddmatrix
bldim = c(allreduce(nrow(my_train), op = "max"), ncol(my_train))
gdim = c(allreduce(nrow(my_train), op = "sum"), ncol(my_train))
dmat_train = new("ddmatrix", Data = my_train, dim = gdim,
                 ldim = dim(my_train), bldim = bldim, ICTXT = 2)
cyclic_train = as.blockcyclic(dmat_train)
comm.print(comm.size())
t1 = as.numeric(Sys.time())
rsvd train = rsvd(cyclic train, k = 10, q = 3, retu = FALSE, retv = FALS
t2 = as.numeric(Sys.time())
t1 = allreduce(t1, op = "min")
t2 = allreduce(t2, op = "max")
comm.cat("Time:", t2 - t1, "seconds\n")
comm.cat("rsvd top 10 singular values:", rsvd_train$d, "\n")
finalize()
```







Package kazaam

- Distributed methods for tall matrices (and some for wide matrices) that exploit the short dimension for speed and long dimension for parallelism
- Tall matrices, shaq class, are chunked by blocks of rows adn wide matrices, tshaq class, by blocks of columns
- Much like pbdDMAT, most matrix operations in R code are identical to serial through overloading operators and shaq S4 class

Naming is a "tongue-in-cheek" play on 'Shaquille' 'ONeal' ('Shaq') and the film 'Kazaam'



Hands on Session kazaam

To be added

