Introduction to parallel computing with R - pbdMPI

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https://github.com/ResearchComputing/RMACC

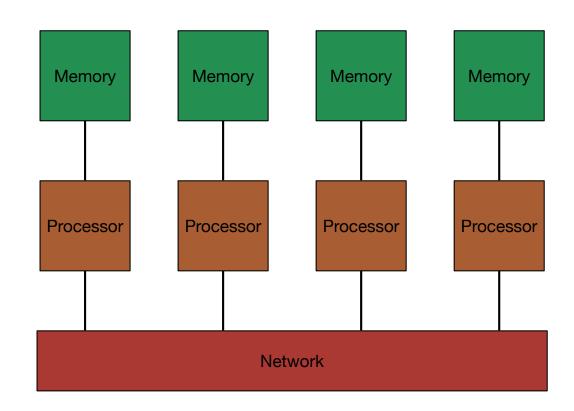
https://github.com/ResearchComputing/RMACC/blob/master/2017/Parallel_R/03-R-distributed.pdf

Outline

- Distributed parallel computing
- Quick overview over MPI (Message Passing Interface)
- Package pbdMPI
- Examples
 - Hello World
 - PI

Distributed Memory Computer

- Processors have different content in memory
- Data exchange by message passing



Execution

 You can run a MPI program with the following commands

\$ mpirun -n 24 Rscript yourRprogram.R

Run hello_print.R

• Example - Run the hello_print.R
\$ sinteractive --partition=shas --qos=debug \
 --time=30:00 --ntasks=10 --nodes=2 \
 --reservation=parallel-r
\$ module purge
\$ module load R
\$ module load openmpi
\$ cd \$HOME/RMACC/Parallel_R/examples/pbdMPI
\$ mpirun -n 10 Rscript hello_print.R

- Vary –n (needs to be lower than --ntasks)
- Is the output always in the same order?

Programming in MPI

MPI Communicator

- A collection of processors of an MPI program
- Used as a parameter for most MPI calls.
- Processors with in a communicator have a number
 - Rank: 0 to n-1
- comm
 - Contains all processors of your program run
- You can create new communicators that are subsets
 - All even processors
 - The first processor
 - All but the first processor

Programming in MPI

```
library(pbdMPI, quiet = TRUE)
init()

nprocs <- comm.size()
id <- comm.rank().
.
.
finalize()</pre>
```

Determine process id or *rank* (here = id) And number of processes (here = nprocs)

Package pdbMPI

Implements interface to MPI

```
> comm.print(variable, all.rank=TRUE)
> comm.size()
> comm.rank()
> comm.set.seed(diff=TRUE)
> pbdApply(X, margin, func, ...)
> pbdLapply(X, func, ...)
> pbdSapply(X, fun, ...)
> bcast
> allgather
> reduce
```

Broadcast

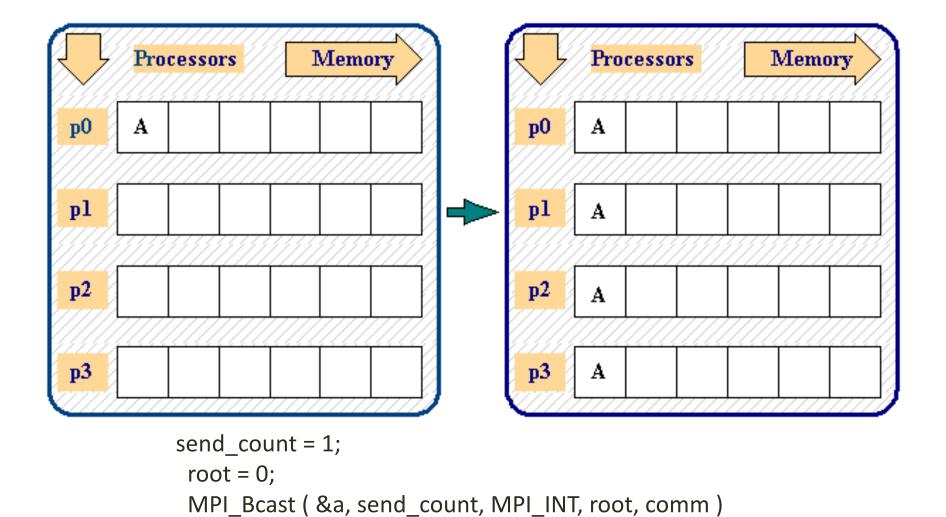
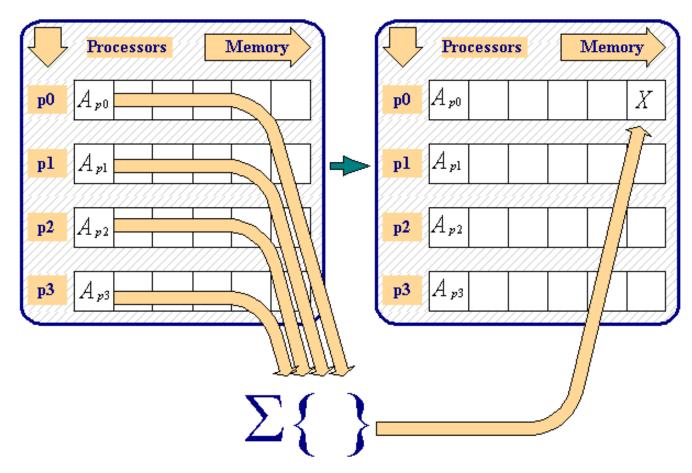


Figure from MPI-tutor: http://www.citutor.org/index.php

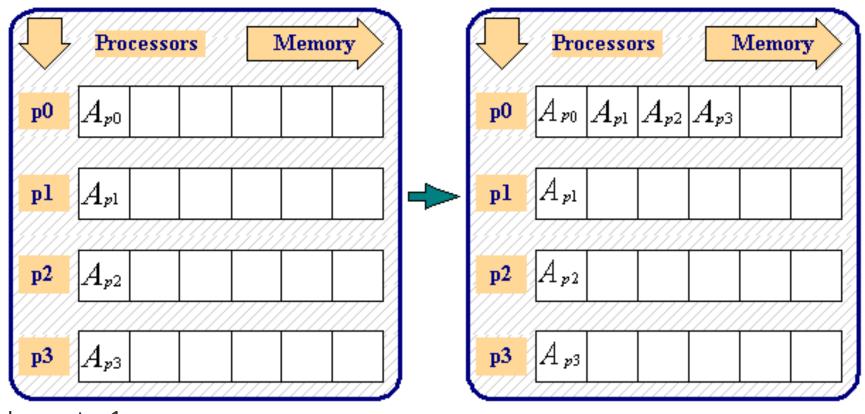
Reduction



```
count = 1;
rank = 0;
MPI_Reduce ( &a, &x, count, MPI_REAL, MPI_SUM, rank, MPI_COMM_WORLD );
```

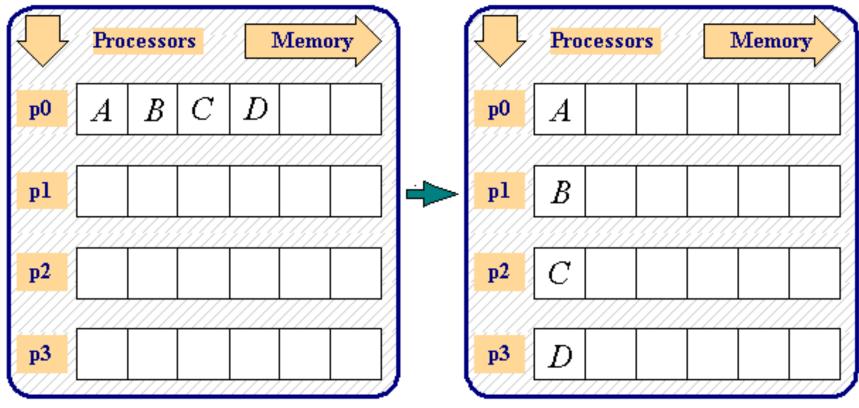
Figure from MPI-tutor: http://www.citutor.org/index.php

Gather



```
send_count = 1;
recv_count = 1;
recv_rank = 0;
MPI_Gather ( &a, send_count, MPI_REAL, &a, recv_count, MPI_REAL, recv_rank,
MPI_COMM_WORLD );
```

Scatter



```
recv_count = 1;
send_rank = 0;
MPI_Scatter ( &a, send_count, MPI_REAL,
       &a, recv_count, MPI_REAL,
       send_rank, MPI_COMM_WORLD );
```

Printing

- > comm.print("String", all.rank=TRUE|FALSE)
 - All processors have to participate
 - all.rank=TRUE prints on all ranks
- Globally print or cat a variable from specified processors
- By default message is shown on screen
- Warning: uses a barrier, so needs to be called by all processors
 - DEADLOCK danger
 - Barrier is a synchronization between all processes. All processes have to join the call and processes wait until all have called it

Deadlock

- Deadlock: process waiting for a condition that will never become true
- Easy to write send/receive code that deadlocks
 - Two processes: both receive before send
 - Send tag doesn't match receive tag
 - Process sends message to wrong destination process

Exercise – hello_deadLock.R

Run

```
$ mpirun -n 4 Rscript hello_deadLock.R
```

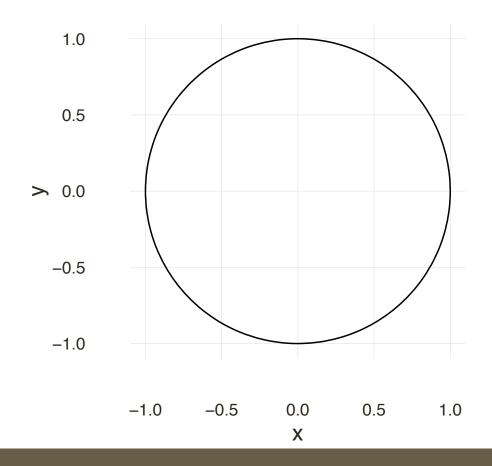
- What's happening?
- Try to fix the problem

pbdApply, pbdSapply

- \$ pbdSapply(n, approx.pi, pbd.mode="spmd")
 - pbd.mode
 - Single program multiple data spmd
 - Need to distribute the data
 - Scatter or execute code on all processes
 - Need to collect the data
 - Gather or reduce
 - Master Worker "mw"
 - Will distribute the first argument to the workers
 - Will get the result back
 - See later example

Calculate PI with Monte Carlo

• Goal: estimate the area of a circle with radius = 1 and area = π using Monte Carlo integration.



Exercise – pi_pbdSapply

- Is the program using the weak scaling or strong scaling approach?
- Run the program on your own node using
 - 4, 16 and 24 cores
- Modify the program so that it uses the other approach.
- result variable has no value after the reduce
 - How can we fix this?

Exercise – pi_mw_pbdSapply

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- Run the program on your own node using
 - 4, 16 and 24 cores
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- result variable has no value after the reduce
 - How can we fix this?

Questions?

- Email <u>rc-help@colorado.edu</u>
- Twitter: CUBoulderRC
- Slides:
 - https://github.com/ResearchComputing/RMACC/blob/mas ter/2017/Parallel_R/03-R-setup.pdf

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