Introducing R:
From Your Laptop to HPC and Big Data

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SC14

The pbdR Core Team

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pbdR
Programming with Big Data in R

Support

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About This Presentation

Downloads

This presentation is available at: http://r-pbd.org/tutorial

About This Presentation

Installation Instructions

Installation instructions for setting up a pbdR environment are available:

http://r-pbd.org/install.html

This includes instructions for installing R, MPI, and pbdR.

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Timings

Getting simple timings as a basic measure of performance is easy, and valuable.

- `system.time()` — timing blocks of code.
- `Rprof()` — timing execution of R functions.
- `Rprofmem()` — reporting memory allocation in R .
- `tracemem()` — detect when a copy of an R object is created.
- The **rbenchmark** package — Benchmark comparisons.

Performance Profiling Tools: system.time()

system.time() is a basic R utility for timing expressions

```r
x <- matrix(rnorm(20000*750), nrow=20000, ncol=750)

system.time(t(x) %*% x)
#     user  system elapsed
#    2.187   0.032   2.324

system.time(crossprod(x))
#     user  system elapsed
#    1.009   0.003   1.019

system.time(cov(x))
#     user  system elapsed
#    6.264   0.026   6.338
```

Performance Profiling Tools: Rprof()

Rprof() times the execution of all R functions:

```
Rprof(filename="Rprof.out", append=FALSE, interval=0.02,
  memory.profiling=FALSE, gc.profiling=FALSE,
  line.profiling=FALSE, numfiles=100L, bufsize=10000L)
```

```
x <- matrix(rnorm(10000*250), nrow=10000, ncol=250)

Rprof(interval=.99)
invisible(prcomp(x))
Rprof(NULL)

summaryRprof()
```

Performance Profiling Tools: Rprof()

```
$by.self
                self.time self.pct total.time total.pct
"La.svd"             0.68    69.39       0.72     73.47
"%*%"                0.12    12.24       0.12     12.24
"aperm.default"      0.04     4.08       0.04      4.08
"array"              0.04     4.08       0.04      4.08
"matrix"             0.04     4.08       0.04      4.08
"sweep"              0.02     2.04       0.10     10.20
### output truncated by presenter

$by.total
                 total.time total.pct self.time self.pct
"prcomp"               0.98    100.00      0.00     0.00
"prcomp.default"       0.98    100.00      0.00     0.00
"svd"                  0.76     77.55      0.00     0.00
"La.svd"               0.72     73.47      0.68    69.39
### output truncated by presenter

$sample.interval
[1] 0.02

$sampling.time
[1] 0.98
```

Performance Profiling Tools: Rprof()

```
$by.self
[1] self.time  self.pct   total.time total.pct
<0 rows> (or 0-length row.names)

$by.total
[1] total.time total.pct  self.time  self.pct
<0 rows> (or 0-length row.names)

$sample.interval
[1] 0.99

$sampling.time
[1] 0
```

Performance Profiling Tools: rbenchmark

rbenchmark is a simple package that easily benchmarks different functions:

```
x <- matrix(rnorm(10000*500), nrow=10000, ncol=500)

f <- function(x) t(x) %*% x
g <- function(x) crossprod(x)

library(rbenchmark)
benchmark(f(x), g(x))

#   test replications elapsed relative
# 1 f(x)          100  64.153    2.063
# 2 g(x)          100  31.098    1.000
```

1 Profiling and Benchmarking

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Other Profiling Tools

- perf
- PAPI
- MPI profiling: fpmpi, mpiP, TAU

Profiling MPI Codes with **pbdPROF**

1. Rebuild pbdR packages

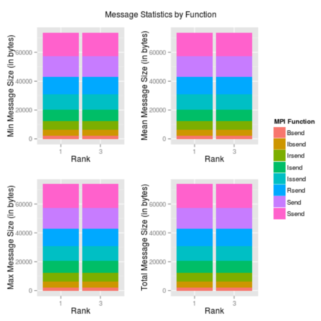
```
R CMD INSTALL pbdMPI_0.2-1.tar.gz \
    --configure-args= \
    "--enable-pbdPROF"
```

2. Run code

```
mpirun -np 64 Rscript my_script.R
```

3. Analyze results

```
library(pbdPROF)
prof <- read.prof( "output.mpiP")
plot(prof, plot.type="messages2")
```



Profiling with **pbdPAPI**

- Bindings for Performance Application Programming Interface (PAPI)
- Gathers detailed hardware counter data.
- High and low level interfaces

Function	Description of Measurement
`system.flips()`	Time, floating point instructions, and Mflips
`system.flops()`	Time, floating point operations, and Mflops
`system.cache()`	Cache misses, hits, accesses, and reads
`system.epc()`	Events per cycle
`system.idle()`	Idle cycles
`system.cpuormem()`	CPU or RAM bound*
`system.utilization()`	CPU utilization*

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Summary

- *Profile, profile, profile.*
- Use `system.time()` to get a general sense of a method.
- Use **rbenchmark**'s `benchmark()` to compare 2 methods.
- Use `Rprof()` for more detailed profiling.
- Other tools exist for more hardcore applications (**pbdPAPI** and **pbdPROF**).

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2 Wrapup

Summary

- Profile your code to understand your bottlenecks.
- pbdR makes distributed parallelism with R easier.
- Distributing data to multiple nodes
- For truly large data, I/O must be parallel as well.

The pbdR Project

- Our website: http://r-pbd.org/
- Email us at: RBigData@gmail.com
- Our google group: http://group.r-pbd.org/

Where to begin?

- The **pbdDEMO** package
  http://cran.r-project.org/web/packages/pbdDEMO/
- The **pbdDEMO** Vignette: http://goo.gl/HZkRt

Thanks for coming!

Questions?

pbdR

Programming with Big Data in R

http://r-pbd.org/

Come see our poster on Wednesday at 5:30!