Analyzing Analytics: Advanced Performance Analysis Tools for R

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Support

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- 2 Advanced Profilers
- 3 A Few Examples
- 4 Concluding Remarks



- 1 Why R?
- 2 Advanced Profilers
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"R? in *my* HPC?"

It's more likely than you think.

FREE PC CHECK!

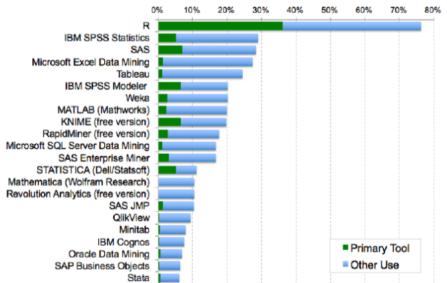


IEEE Spectrum's 2016 Ranking of Programming Languages

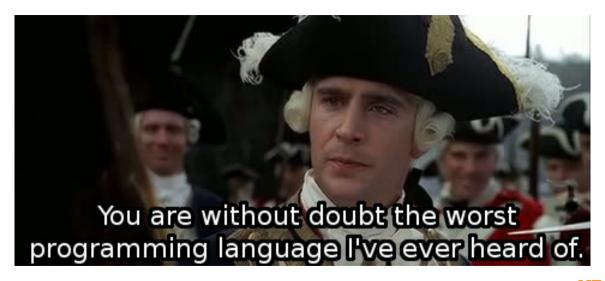
Language Rank Types		Types	Spectrum Ranking
1.	С	[] 🖵 🛢	100.0
2.	Java	\bigoplus \square \square	98.1
3.	Python	\bigoplus \Box	98.0
4.	C++	[] 🖵 🗰	95.9
5.	R	₽	87.9
6.	C#	\bigoplus \square \square	86.7
7.	PHP	\bigoplus	82.8
8.	JavaScript	$\bigoplus \square$	82.2
9.	Ruby	\bigoplus \Box	74.5
10.	Go	\bigoplus \Box	71.9



Rexer 2015 data scientist survey





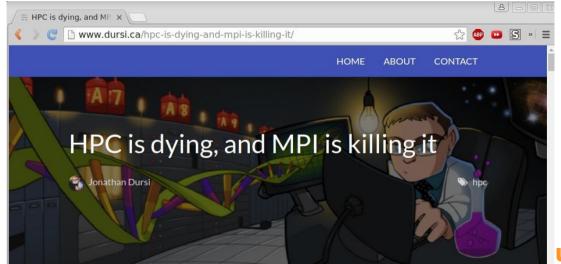




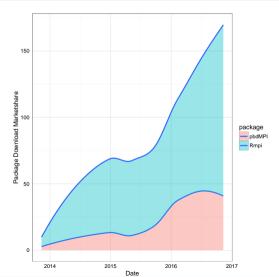




About Traditional HPC...



HPC may be dying, but we're behind the times





"OLCF Researchers Scale R to Tackle Big Science Data Sets"



- A problem that takes several hours on Apache Spark [was analyzed] in less than a minute using R on OLCF high-performance hardware.
- "... for situations where one needs interactive near-real-time analysis, the pbdR approach is much better."

```
https://www.hpcwire.com/2016/07/06/
olcf-researchers-scale-r-tackle-big-science-data-sets/
```



- 2 Advanced Profilers



Profiling in R Versus Traditional HPC

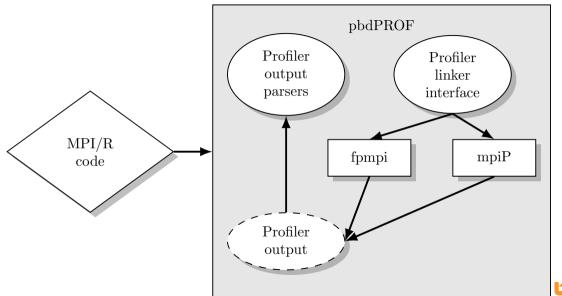
- Profiling in R (core): Stack sampler, some memory profilers.
- Every (other) profiling package in R: wall clock times.
- What's missing: MPI profilers, performance counters.



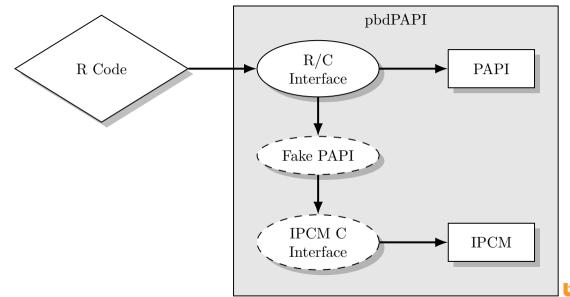
Three New R Packages

- pbdPROF MPI profiler support (fpmpi and mpiP).
- pbdPAPI PAPI bindings and utilities.
- hpcvis Plot methods for the above 2.







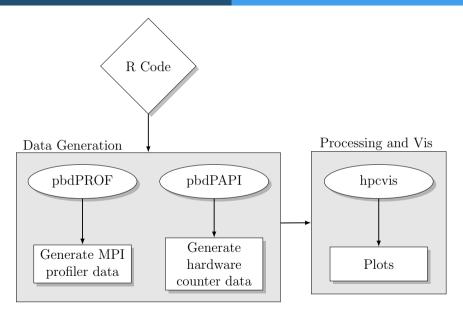




pbdPAPI High-Level Interface

Function	Measurement
system.cache()	Cache misses, hits, accesses
<pre>system.flops()</pre>	MFLOPS
<pre>system.idle()</pre>	ldle cycles
<pre>system.cpuormem()</pre>	Classify CPU/RAM bound
<pre>system.utilization()</pre>	CPU utilization







pbdPROF + hpcvis Syntax Example

```
library(pbdPROF)
library(hpcvis)

prof_file <- "R.4.26802.1.mpiP"

x <- read.prof(prof_file)

profplot(x, color=FALSE, stacked=FALSE, title=NULL, which=c(2,4))
profplot(x, plot.type="stats", color=FALSE, stacked=TRUE, title=NULL)</pre>
```

pbdPAPI + hpcvis Syntax Example

```
library(pbdPAPI)
library(hpcvis)

cb <- cachebench(foo(x), bar(x))
papiplot(cb, label.angle=15, levels=1:2)</pre>
```



Note

All plots for the remainder of this presentation were made with hpcvis.



- 1 Why R
- 2 Advanced Profilers
- 3 A Few Examples
 - Clustering
 - K-Means Clustering Algorithms
 - Distributed Clustering with pmclust
- 4 Concluding Remarks



Clustering Approaches

- K-means and GMM
- Two unsupervised learning approaches.
- Trying to discover latent groupings in the data.
- K-means
 - Cover data with k identical spheres.
- GMM
 - Can use different ellipsoids, pointing in different directions.



Now With Math

- Partition N data points in p dimensions into K clusters
- k-means model (stated as Gaussian mixture):

■
$$X_1, \dots, X_N \stackrel{iid}{\sim} \phi(\cdot|\boldsymbol{\mu}, \boldsymbol{\Sigma})$$

■ $\boldsymbol{\mu} = \{\mu_1, \dots, \mu_k\}$
■ $\boldsymbol{\Sigma} = \{\sigma I, \dots, \sigma I\}$
■ $\phi(\cdot|\boldsymbol{\mu}, \sigma I) = \sum_{k=1}^K \eta_k \phi_p(\cdot|\boldsymbol{\mu}_k, \sigma I)$
■ $2Kp + 1$ parameters

pmclust: Gaussian mixture model (GMM):

$$X_1, \dots, X_N \stackrel{iid}{\sim} \phi(\cdot|\boldsymbol{\mu}, \boldsymbol{\Sigma})$$

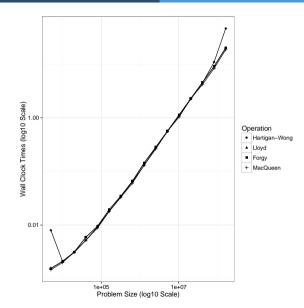
$$\boldsymbol{\mu} = \{\mu_1, \dots, \mu_k\}$$

$$\boldsymbol{\Sigma} = \{\Sigma_1, \dots, \Sigma_K\}$$

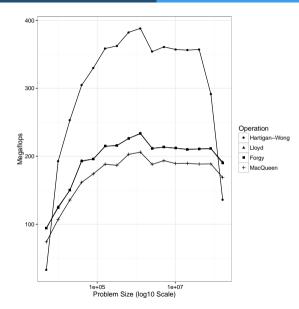
$$\boldsymbol{\phi}(\cdot|\boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{k=1}^K \eta_k \phi_p(\cdot|\mu_k, \Sigma_k)$$

$$\boldsymbol{\Sigma}(Kp + K \stackrel{p \times (p+1)}{2}) \text{ parameters}$$

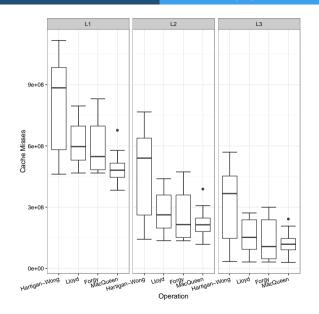




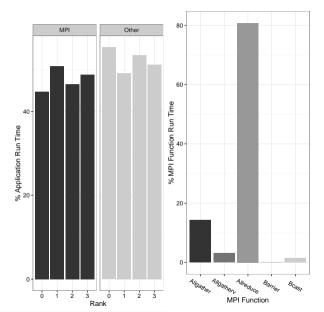




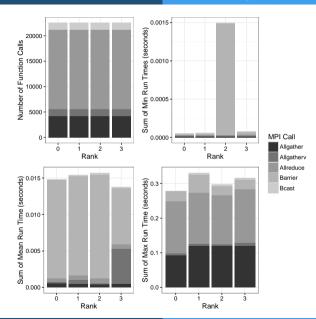














- 4 Concluding Remarks



Challenges

- pbdPAPI still difficult for R users to install.
- Mostly Linux-only.

Future Work

- Build a web interface?
- Integrate with tau?



\sim Thanks! \sim

Questions?

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