

# Programming with Big Data in R

Drew Schmidt and George Ostrouchov

<http://r-pbd.org/>

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A /ORNL PARTNERSHIP  
NATIONAL INSTITUTE FOR COMPUTATIONAL SCIENCES



# The pbdR Core Team

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## Support

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1 Introduction

2 pbdR

3 Benchmarks

4 Demos

## What is R?

- *lingua franca* for data analytics and statistical computing.
- Part programming language, part data analysis package.
- Dialect of S (Bell Labs).
- Syntax designed for data.



## What is R?

## Who uses R?

ORACLE®



MERCK

KICKSTARTER

Bank of America

The  
New York  
Times

Shell

mozilla  
FOUNDATION

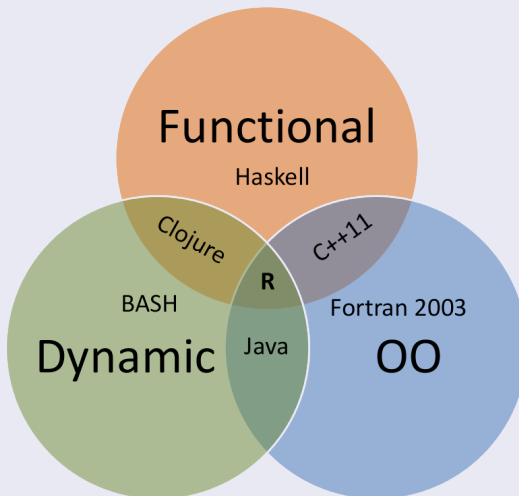
ORBITZ

LLOYD'S

Google eBay bing



## Language Paradigms



## Why R?

- 1 People love it.
- 2 Highly extensible (CRAN  $\approx$  5000 actively maintained packages).
- 3 Wealth of diverse analytical methods.
- 4 HPC community has growing need for data analytics.

## Problems with R

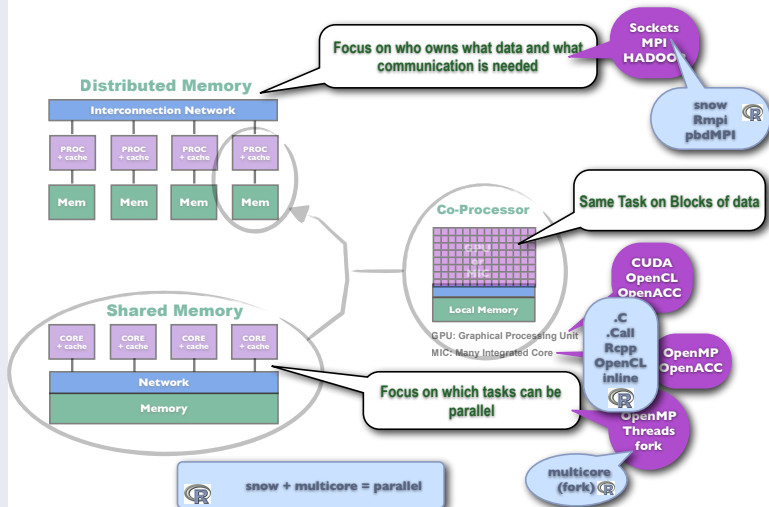
- 1 Slow.
- 2 If you don't know what you're doing, it's *really* slow.
- 3 Data science community has growing data size problem.
- 4 Chokes on big data.
- 5 Parallelism: “batteries not included”



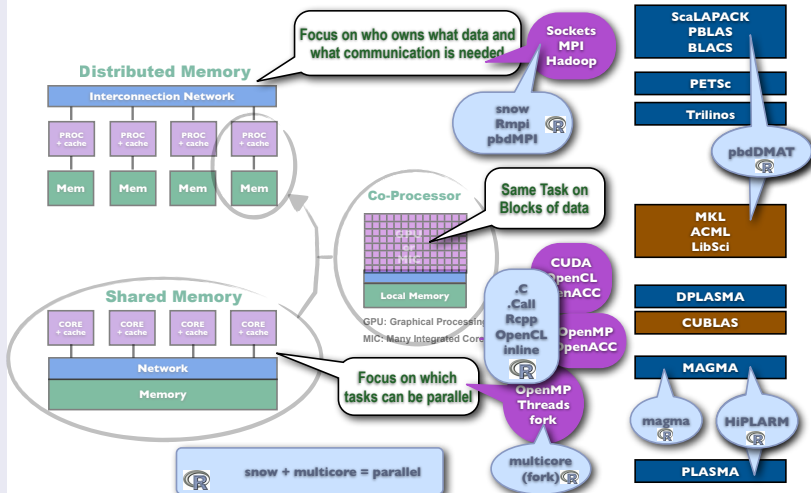
In spite of all this. . .



## R Interfaces to Native Tools



## R Interfaces to Scalable Math Libraries



# Contents

- 2 pbdR
  - The pbdR Project

## Programming with Big Data in R (pbdR)

*Productivity, Portability, Performance*

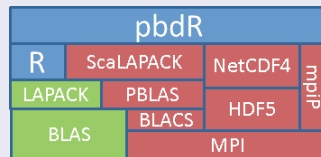
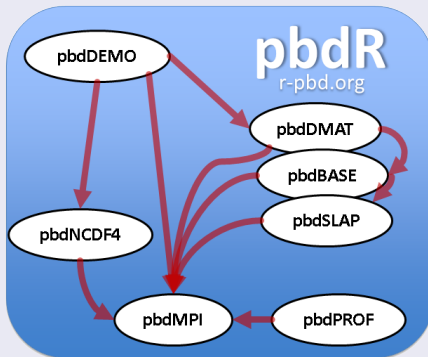


- *Free<sup>a</sup>* R packages.
- Bridging high-performance C with high-productivity of R
- Distributed data details implicitly managed.
- Methods have syntax *identical* to R.

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<sup>a</sup>MPL, BSD, and GPL licensed

## pbdR Packages



## pbdR Example Syntax

```
1 x <- x[-1, 2:5]
2 x <- log(abs(x) + 1)
3 xtx <- t(x) %*% x
4 ans <- svd(solve(xtx))
```

*The above runs on 1 core with R or 10,000 cores with pbdR*

## Profiling with pbdPROF

### 1. Rebuild **pbdR** packages

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

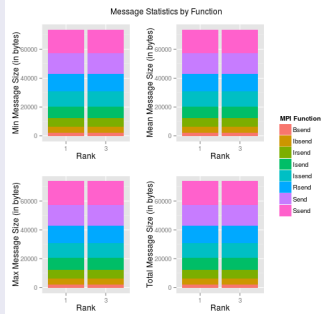
### 2. Run code

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

### 3. Analyze results

```
1 library(pbdPROF)
2 prof <- read.prof(
  "profiler_output.mpiP")
3 plot(prof)
```

### Publication-quality graphs





## pbdR on HPC Resources

### University of Tennessee

- Kraken (XSEDE)
- Nautilus
- Darter
- Newton

### Oak Ridge National Lab

- Titan
- Lens
- Chester
- Sith

### Other Resources

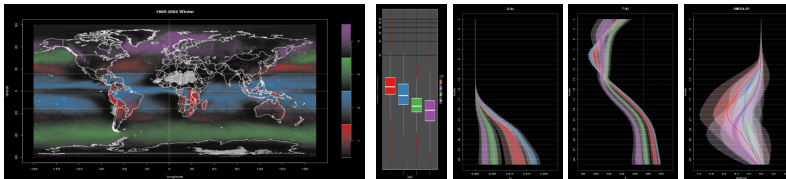
- Stampede, TACC (XSEDE)
- tara, UMBC
- Hopper, NERSC
- Edison, NERSC

If you are interested in installing pbdR: [RBigData@gmail.com](mailto:RBigData@gmail.com)

## Exploration of Climate Data with pbdR

- **2013 INCITE “Attributing Changes in the Risk of Extreme Weather and Climate” Michael Wehner, PI**
  - High resolution atmospheric model, CAM 5.1 (~25 km resolution)
  - Resolves processes responsible for extreme precipitation and storms
- **R and pbdR used for scalable analytics and graphics**
  - Advanced clustering capability (EM algorithm for Gaussian mixture models)

Behavior of extreme precipitation across atmospheric layers of moisture, temperature, and wind



W.-C. Chen, G. Ostrouchov, D. Pugmire, Prabhat, M. Wehner. A Parallel EM Algorithm for Model-Based Clustering Applied to the Exploration of Large Spatio-Temporal Data. *Technometrics* (online, in print: Fall 2013).

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1 Introduction

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## Non-Optimal Choices Throughout

- 1 Only libre software used (no MKL, ACML, etc.).
- 2 1 core = 1 MPI process.
- 3 No tuning for data distribution.

## Benchmark Data

- 1 Measure wallclock time for covariance and linear regression.
- 2 Random normal  $N(100, 10000)$ .
- 3 Local problem size of  $\approx 43.4\text{MiB}$ .
- 4 Three sets: 500, 1000, and 2000 columns.
- 5 Several runs at different core sizes within each set.

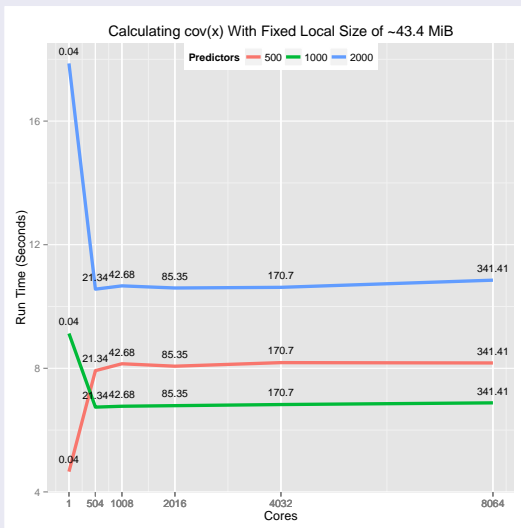


## Covariance Code

$$\text{cov}(x_{n \times p}) = \frac{1}{n-1} \sum_{i=1}^n (x_i - \mu_x)(x_i - \mu_x)^T$$

```
1 x <- ddmatrix("rnorm", nrow=n, ncol=p, mean=mean, sd=sd)
2
3 cov.x <- cov(x)
```

cov()



## Linear Model Code

Find  $\beta$  such that

$$\mathbf{y} = \mathbf{X}\beta + \epsilon$$

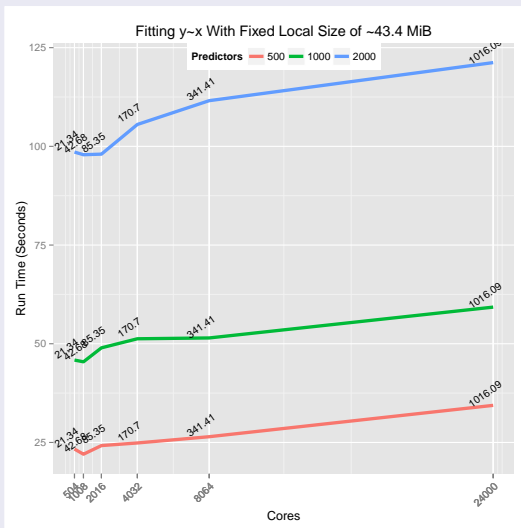
When  $\mathbf{X}$  is full rank,

$$\hat{\beta} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y}$$

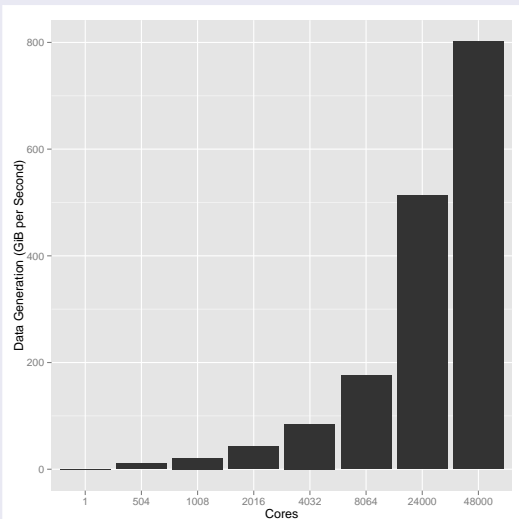
```
1 x <- ddmatrix("rnorm", nrow=n, ncol=p, mean=mean, sd=sd)
2 beta_true <- ddmatrix("runif", nrow=p, ncol=1)
3
4 y <- x %*% beta_true
5
6 beta_est <- lm.fit(x=x, y=y)$coefficients
```



## Linear Model Fitting

`lm.fit()`

## Data Generation



# Contents

## 4 Demos

- pbdMPI
- pbdDMAT
- RandSVD

## MPI Operations: The Gang's All Here

- **Communicator wrangling:** `init()`, `finalize()`
- **Rank query:** `comm.rank()`, `comm.size()`
- **Reduction:** `reduce(x, op='sum')`, `allreduce(x)`
- **Gather:** `gather(x)`, `allgather(x)`
- **Broadcast:** `bcast(x)`
- **Barrier:** `barrier()`
- **Send/Receive:** `send(x)`, `recv()`

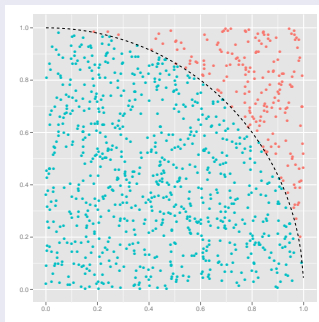
## MPI Operations for R Users

- **Printing:** `comm.print(x)`, `comm.cat(x)`
- **RNG Seeds:** `comm.set.seed(diff=T)`
- **Task Subsetting:** `get.jid(n)`
- **\*ply:**  
`pbdApply(X, MARGIN, FUN, ...)`  
`pbdLapply(X, FUN, ...)`  
`pbdSapply(X, FUN, ...)`

## Example 1: Monte Carlo Simulation

Sample  $N$  uniform observations  $(x_i, y_i)$  in the unit square  $[0, 1] \times [0, 1]$ . Then

$$\pi \approx 4 \left( \frac{\# \text{ Inside Circle}}{\# \text{ Total}} \right) = 4 \left( \frac{\# \text{ Blue}}{\# \text{ Blue} + \# \text{ Red}} \right)$$



## Distributed Matrices

Most problems in data science are matrix algebra problems, so:

Distributed matrices  $\implies$  Bigger data

## DMAT: 2-dimensional Block-Cyclic with 6 Processors

$$X = \begin{bmatrix} \begin{array}{cc|cc|cc|cc|c} X_{11} & X_{12} & X_{13} & X_{14} & X_{15} & X_{16} & X_{17} & X_{18} & X_{19} \\ X_{21} & X_{22} & X_{23} & X_{24} & X_{25} & X_{26} & X_{27} & X_{28} & X_{29} \\ \hline X_{31} & X_{32} & X_{33} & X_{34} & X_{35} & X_{36} & X_{37} & X_{38} & X_{39} \\ X_{41} & X_{42} & X_{43} & X_{44} & X_{45} & X_{46} & X_{47} & X_{48} & X_{49} \\ \hline X_{51} & X_{52} & X_{53} & X_{54} & X_{55} & X_{56} & X_{57} & X_{58} & X_{59} \\ X_{61} & X_{62} & X_{63} & X_{64} & X_{65} & X_{66} & X_{67} & X_{68} & X_{69} \\ \hline X_{71} & X_{72} & X_{73} & X_{74} & X_{75} & X_{76} & X_{77} & X_{78} & X_{79} \\ X_{81} & X_{82} & X_{83} & X_{84} & X_{85} & X_{86} & X_{87} & X_{88} & X_{89} \\ \hline X_{91} & X_{92} & X_{93} & X_{94} & X_{95} & X_{96} & X_{97} & X_{98} & X_{99} \end{array} \end{bmatrix}_{9 \times 9}$$

$$\text{Processor grid} = \begin{vmatrix} 0 & 1 & 2 \\ 3 & 4 & 5 \end{vmatrix} = \begin{vmatrix} (0,0) & (0,1) & (0,2) \\ (1,0) & (1,1) & (1,2) \end{vmatrix}$$



## Understanding DMAT: Local View

$\begin{bmatrix} X_{11} & X_{12} & X_{17} & X_{18} \\ X_{21} & X_{22} & X_{27} & X_{28} \\ X_{51} & X_{52} & X_{57} & X_{58} \\ X_{61} & X_{62} & X_{67} & X_{68} \\ X_{91} & X_{92} & X_{97} & X_{98} \end{bmatrix}$	5×4	$\begin{bmatrix} X_{13} & X_{14} & X_{19} \\ X_{23} & X_{24} & X_{29} \\ X_{53} & X_{54} & X_{59} \\ X_{63} & X_{64} & X_{69} \\ X_{93} & X_{94} & X_{99} \end{bmatrix}$	5×3	$\begin{bmatrix} X_{15} & X_{16} \\ X_{25} & X_{26} \\ X_{55} & X_{56} \\ X_{65} & X_{66} \\ X_{95} & X_{96} \end{bmatrix}$	5×2
$\begin{bmatrix} X_{31} & X_{32} & X_{37} & X_{38} \\ X_{41} & X_{42} & X_{47} & X_{48} \\ X_{71} & X_{72} & X_{77} & X_{78} \\ X_{81} & X_{82} & X_{87} & X_{88} \end{bmatrix}$	4×4	$\begin{bmatrix} X_{33} & X_{34} & X_{39} \\ X_{43} & X_{44} & X_{49} \\ X_{73} & X_{74} & X_{79} \\ X_{83} & X_{84} & X_{89} \end{bmatrix}$	4×3	$\begin{bmatrix} X_{35} & X_{36} \\ X_{45} & X_{46} \\ X_{75} & X_{76} \\ X_{85} & X_{86} \end{bmatrix}$	4×2

$$\text{Processor grid} = \begin{vmatrix} 0 & 1 & 2 \\ 3 & 4 & 5 \end{vmatrix} = \begin{vmatrix} (0,0) & (0,1) & (0,2) \\ (1,0) & (1,1) & (1,2) \end{vmatrix}$$

Randomized SVD<sup>1</sup>

## PROTOTYPE FOR RANDOMIZED SVD

Given an  $m \times n$  matrix  $A$ , a target number  $k$  of singular vectors, and an exponent  $q$  (say,  $q = 1$  or  $q = 2$ ), this procedure computes an approximate rank- $2k$  factorization  $U\Sigma V^*$ , where  $U$  and  $V$  are orthonormal, and  $\Sigma$  is nonnegative and diagonal.

## Stage A:

- 1 Generate an  $n \times 2k$  Gaussian test matrix  $\Omega$ .
- 2 Form  $Y = (AA^*)^q A\Omega$  by multiplying alternately with  $A$  and  $A^*$ .
- 3 Construct a matrix  $Q$  whose columns form an orthonormal basis for the range of  $Y$ .

## Stage B:

- 4 Form  $B = Q^*A$ .
- 5 Compute an SVD of the small matrix:  $B = \tilde{U}\Sigma V^*$ .
- 6 Set  $U = Q\tilde{U}$ .

**Note:** The computation of  $Y$  in step 2 is vulnerable to round-off errors. When high accuracy is required, we must incorporate an orthonormalization step between each application of  $A$  and  $A^*$ ; see Algorithm 4.4.

## ALGORITHM 4.4: RANDOMIZED SUBSPACE ITERATION

Given an  $m \times n$  matrix  $A$  and integers  $\ell$  and  $q$ , this algorithm computes an  $m \times \ell$  orthonormal matrix  $Q$  whose range approximates the range of  $A$ .

- 1 Draw an  $n \times \ell$  standard Gaussian matrix  $\Omega$ .
- 2 Form  $Y_0 = A\Omega$  and compute its QR factorization  $Y_0 = Q_0R_0$ .
- 3 **for**  $j = 1, 2, \dots, q$
- 4     Form  $\tilde{Y}_j = A^*Q_{j-1}$  and compute its QR factorization  $\tilde{Y}_j = \tilde{Q}_j\tilde{R}_j$ .
- 5     Form  $Y_j = A\tilde{Q}_j$  and compute its QR factorization  $Y_j = Q_jR_j$ .
- 6 **end**
- 7  $Q = Q_q$ .

## Serial R

```

1 randSVD <- function(A, k, q=3)
2 {
3   ## Stage A
4   Omega <- matrix(rnorm(n*2*k),
5                   nrow=n, ncol=2*k)
6   Y <- A %*% Omega
7   Q <- qr.Q(qr(Y))
8   At <- t(A)
9   for(i in 1:q)
10    {
11      Y <- At %*% Q
12      Q <- qr.Q(qr(Y))
13      Y <- A %*% Q
14      Q <- qr.Q(qr(Y))
15    }
16
17   ## Stage B
18   B <- t(Q) %*% A
19   U <- La.svd(B)$u
20   U <- Q %*% U
21   U[, 1:k]
22 }
```

<sup>1</sup>Halko N, Martinsson P-G and Tropp J A 2011 Finding structure with randomness: probabilistic algorithms for constructing approximate matrix decompositions *SIAM Rev.* **53** 217–88

## Randomized SVD

## Serial R

```

1 randSVD <- function(A, k, q=3)
2 {
3   ## Stage A
4   Omega <- matrix(rnorm(n*2*k),
5     nrow=n, ncol=2*k)
6   Y <- A %*% Omega
7   Q <- qr.Q(qr(Y))
8   At <- t(A)
9   for(i in 1:q)
10    {
11      Y <- At %*% Q
12      Q <- qr.Q(qr(Y))
13      Y <- A %*% Q
14      Q <- qr.Q(qr(Y))
15    }
16
17   ## Stage B
18   B <- t(Q) %*% A
19   U <- La.svd(B)$u
20   U <- Q %*% U
21   U[, 1:k]
22 }

```

## Parallel pbdR

```

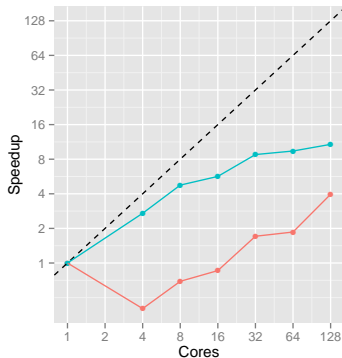
1 randSVD <- function(A, k, q=3)
2 {
3   ## Stage A
4   Omega <- ddmatrix("rnorm",
5     nrow=n, ncol=2*k)
6   Y <- A %*% Omega
7   Q <- qr.Q(qr(Y))
8   At <- t(A)
9   for(i in 1:q)
10    {
11      Y <- At %*% Q
12      Q <- qr.Q(qr(Y))
13      Y <- A %*% Q
14      Q <- qr.Q(qr(Y))
15    }
16
17   ## Stage B
18   B <- t(Q) %*% A
19   U <- La.svd(B)$u
20   U <- Q %*% U
21   U[, 1:k]
22 }

```

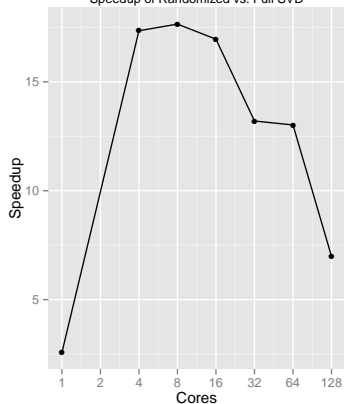
## Randomized SVD on $\approx 765$ MiB

30 Singular Vectors from a 100,000 by 1,000 Matrix

Algorithm — full randomized



30 Singular Vectors from a 100,000 by 1,000 Matrix  
Speedup of Randomized vs. Full SVD



Thanks for coming!

# Questions?



<http://r-pbd.org/>

Be sure to come to our R BoF: Wednesday 5:30-7:00 room 404