# pbdR: Harnessing HPC Research for Parallel Computing with R

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Oak Ridge National Laboratory and University of Tennessee

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## Support

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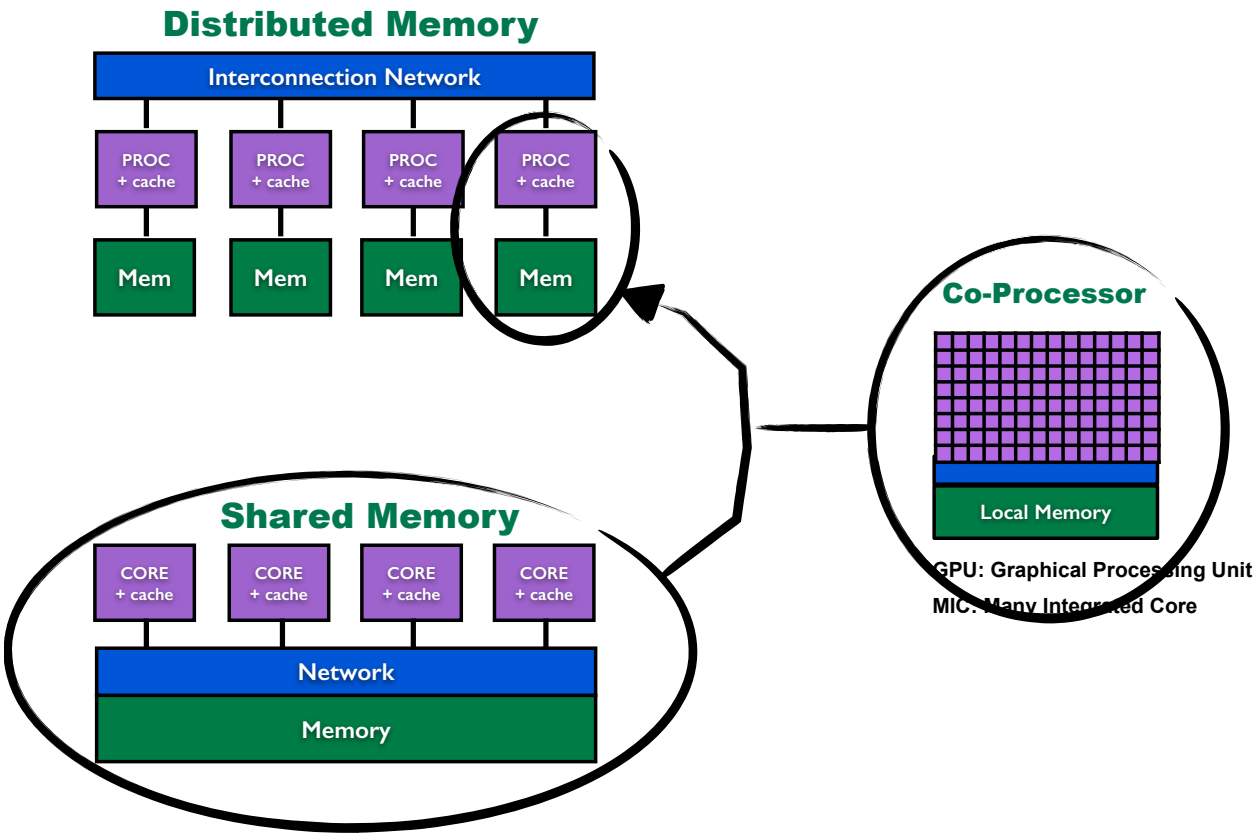
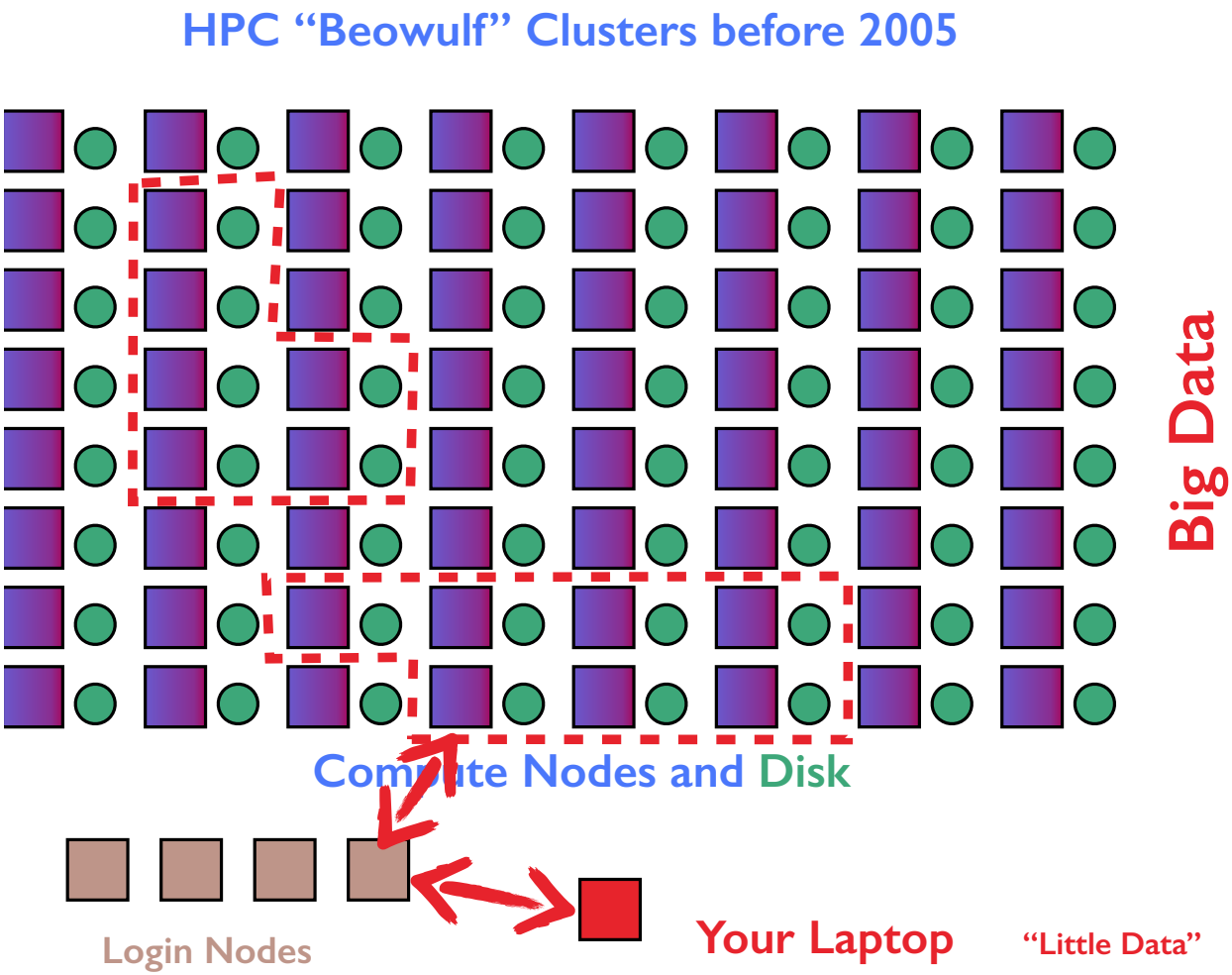
# Contents

# Cores and Co-Processors to Nodes



# Parallel Computing before Multicore



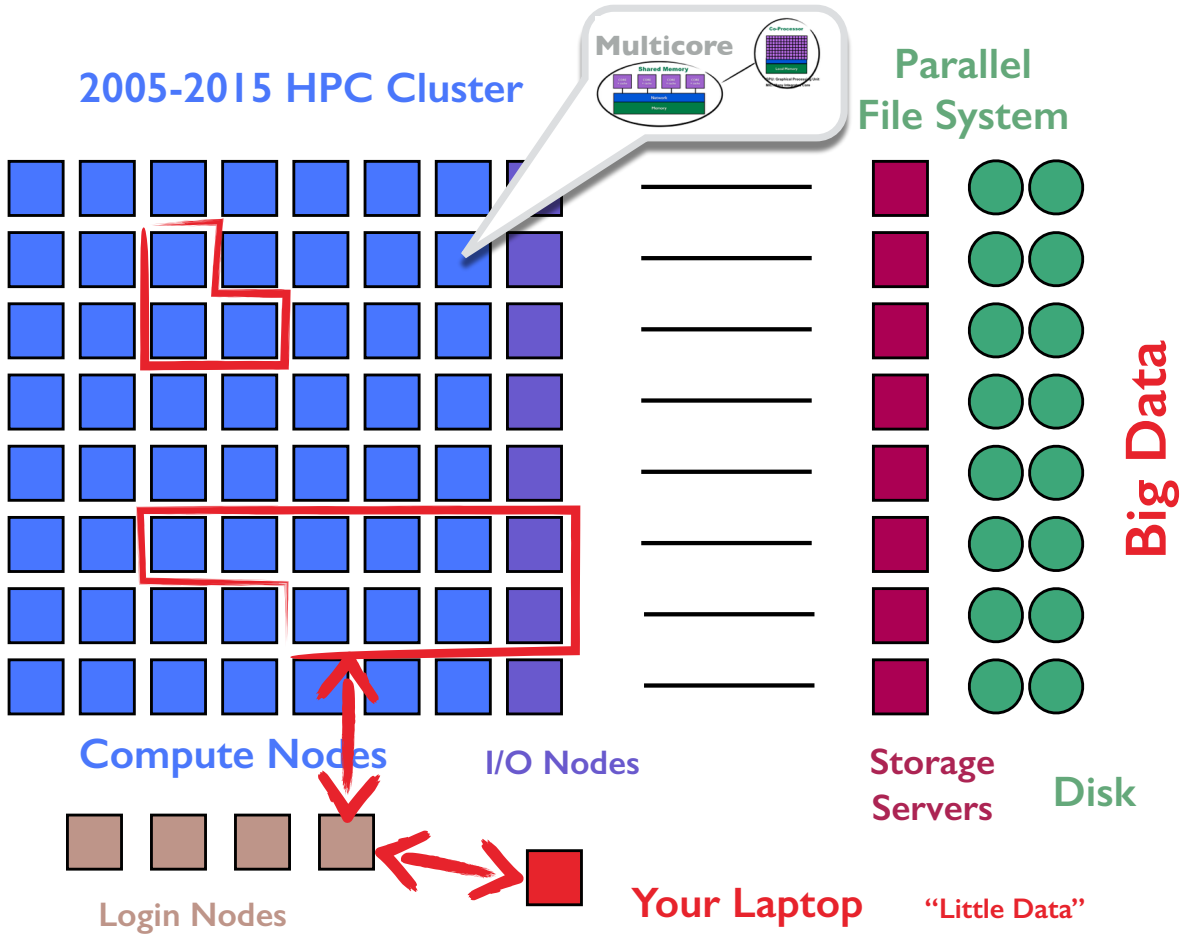

## Software Developments:

MPI is mature, MapReduce emerges

Parallel Libraries: PBLAS, ScaLAPACK, PETSc, etc.

Resource Manager: PBS mature, HADOOP emerges

# Multicore Emerges and Clusters become Diskless

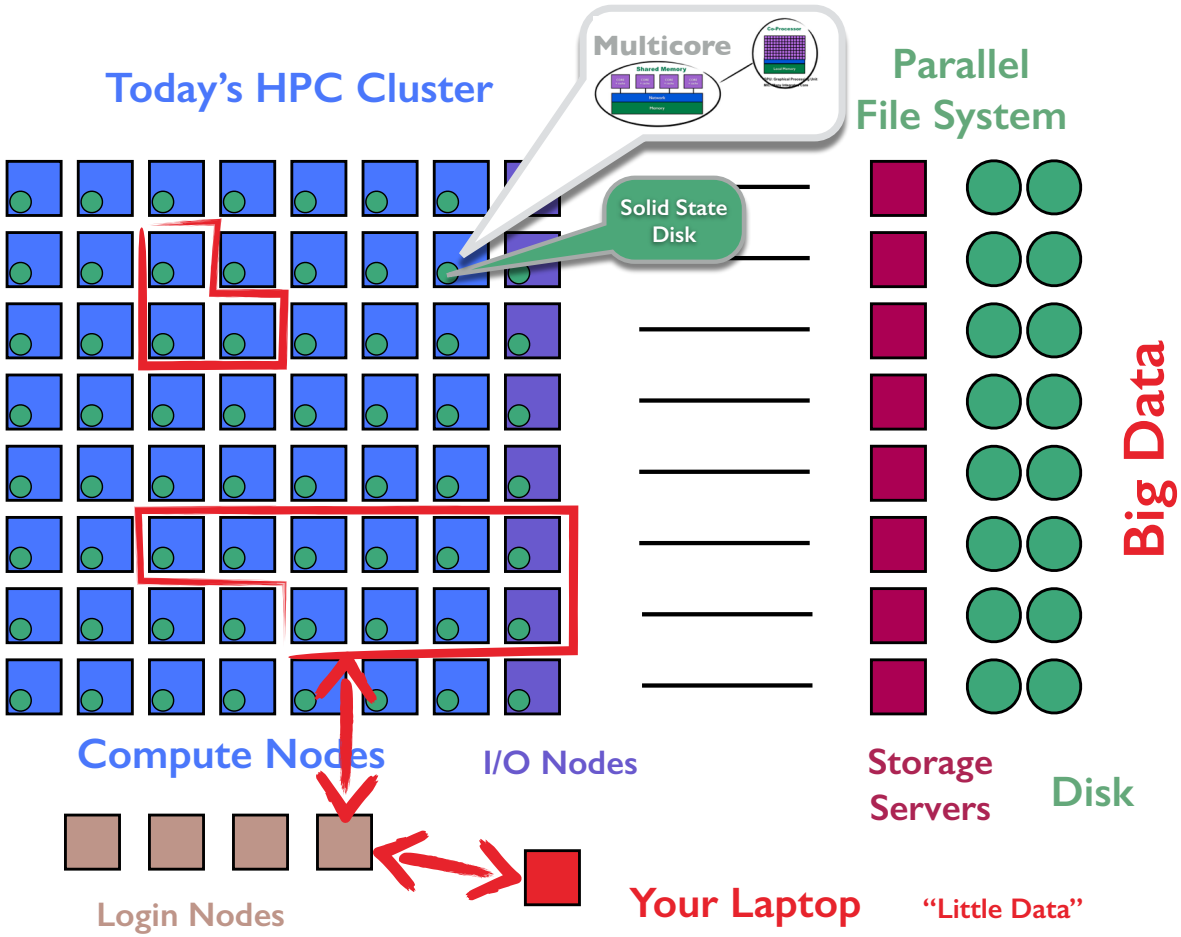



## Software Developments

OpenMP, CUDA, OpenCL, OpenACC

Libraries: PLASMA, MAGMA, CuBLAS

# Adding NVRAM to New HPC Systems

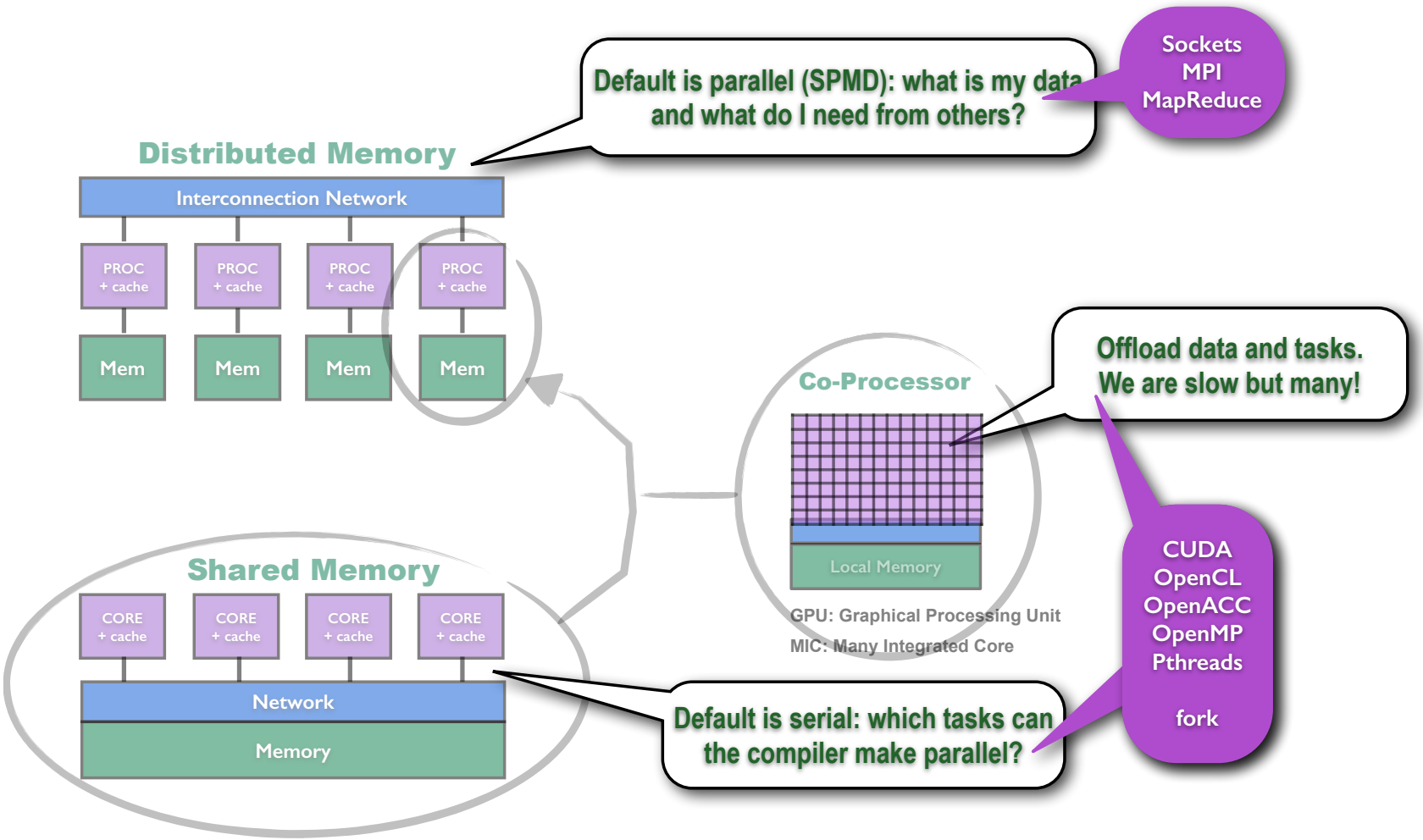



## Software Developments

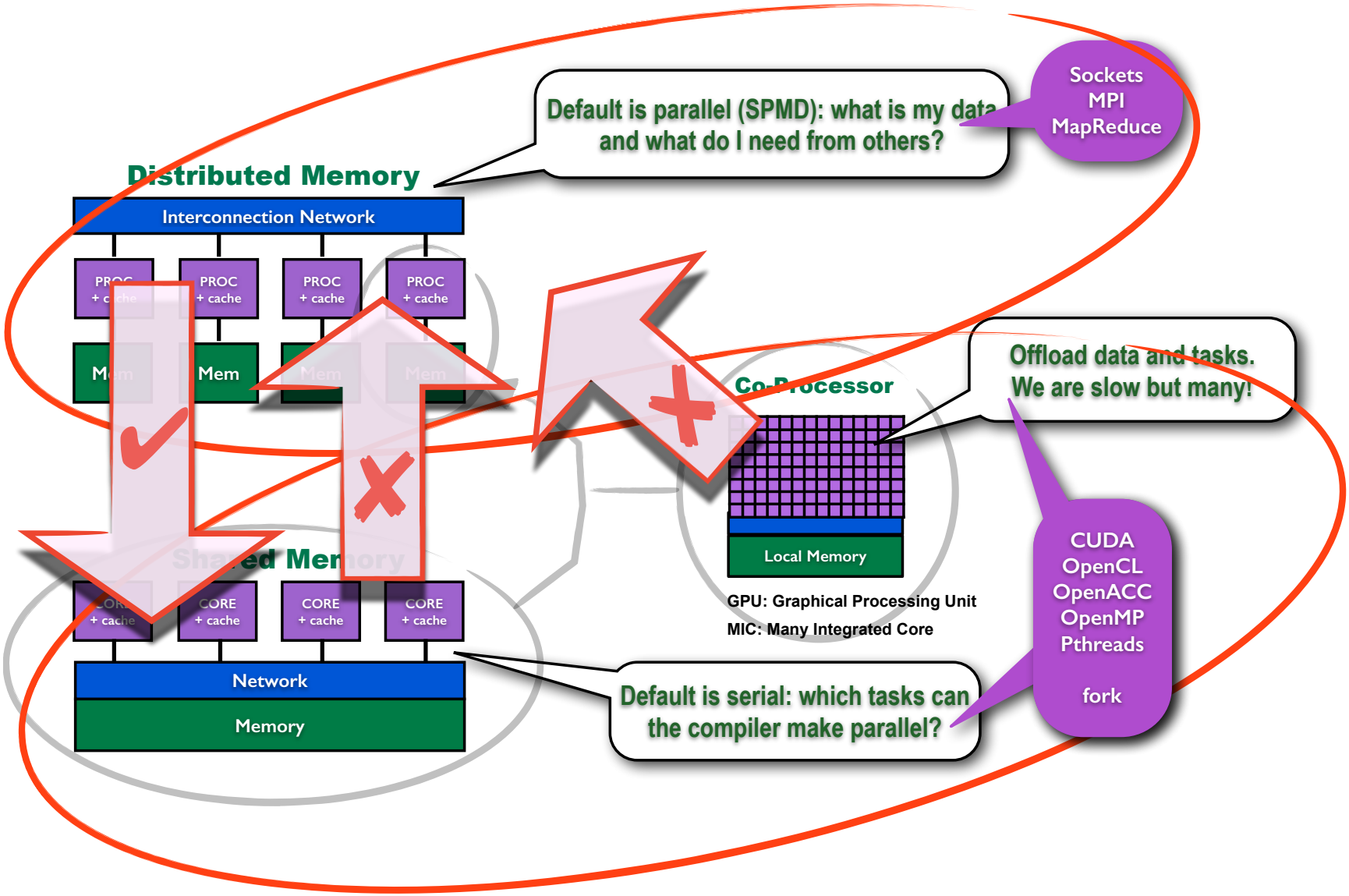
Libraries: DPLASMA, CombBLAS

HADOOP fades, Spark emerges

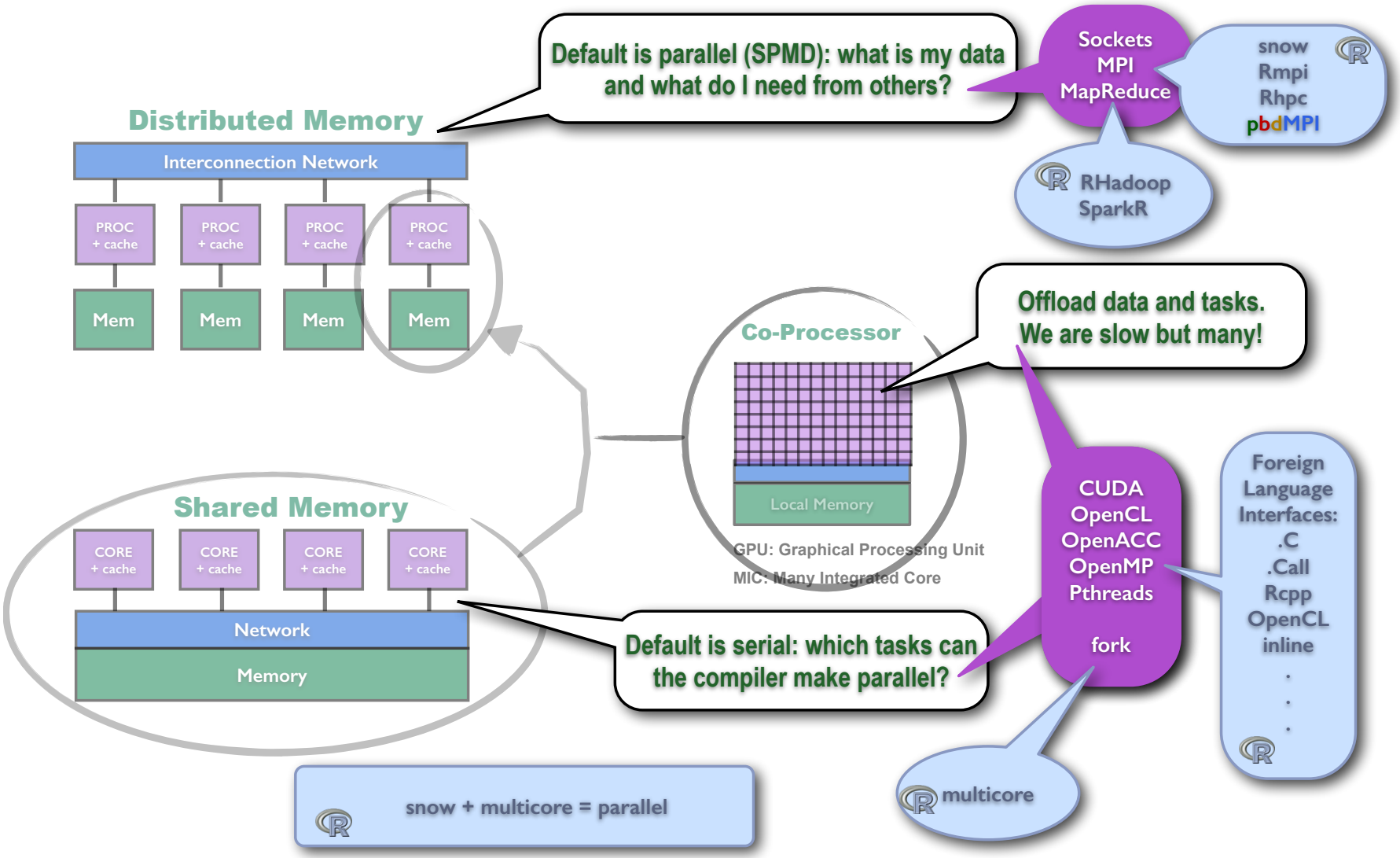
# "Native" Programming Models and Tools



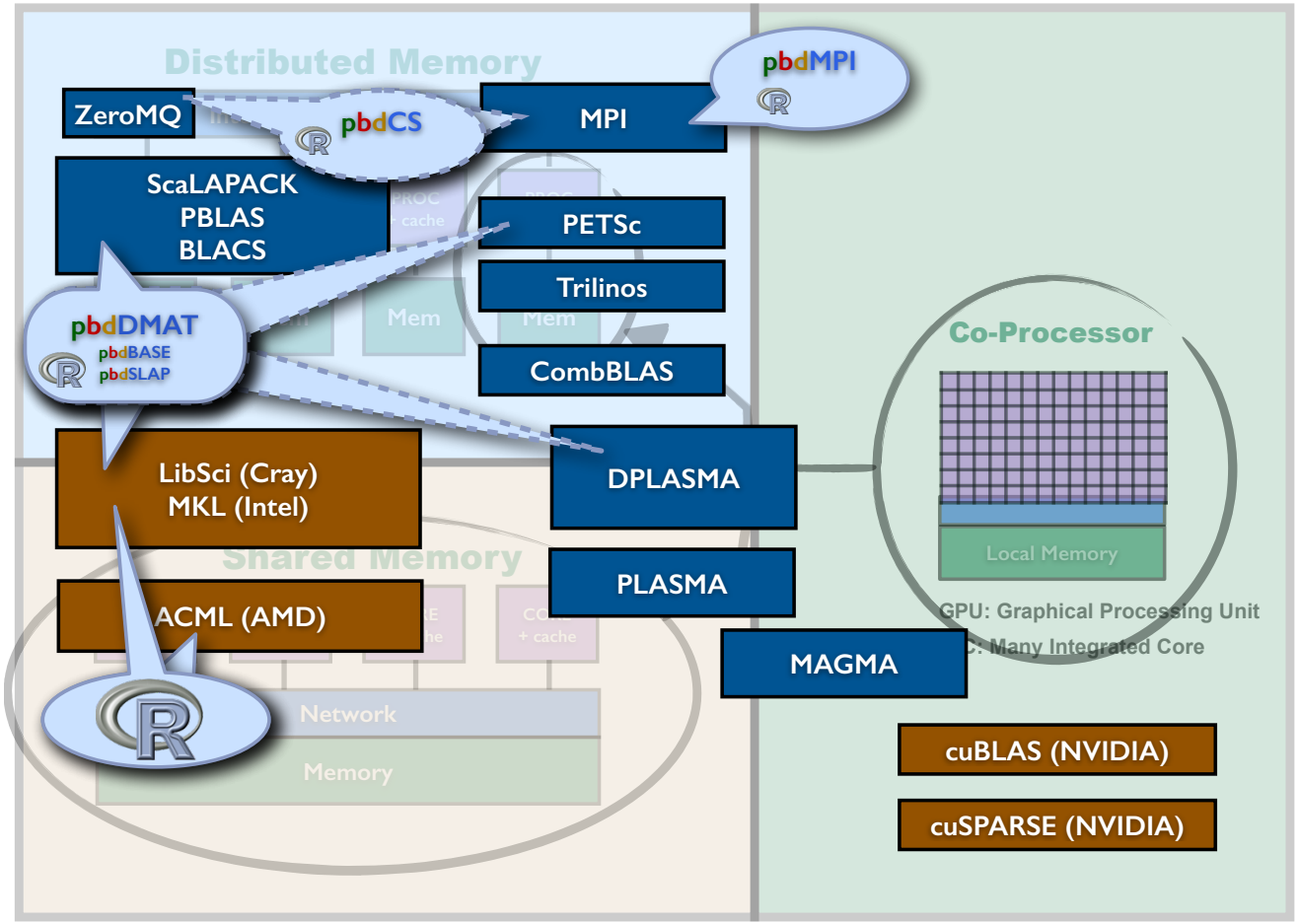
# Distributed Programming Works in Shared Memory

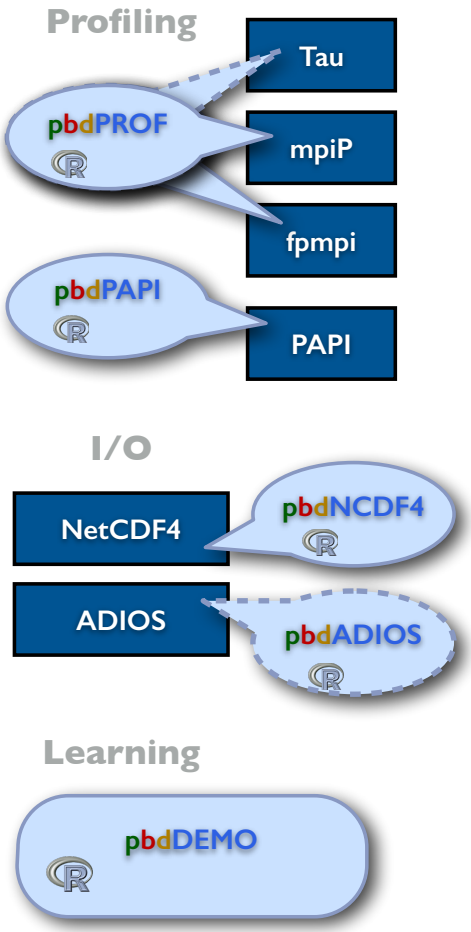


# R Interfaces to Low-Level Native Tools



# R and pbdR Interfaces to HPC Libraries



## Data analysis is interactive!

- Data reduction to knowledge
- Iterative process with same data
  - Exploration, model construction
  - Diagnostics of fit and quantification of uncertainty
  - Interpretation
- S (and R) interactive "answer" to batch data analysis
- Efficient use of expensive people

## Big platform computing is batch!

- Libraries built for batch computing
- Traditionally data generation by simulation science
- Efficient use of expensive platforms

## High-Level Language: Batch and Interactive Distinction Blurred.

- A function is a "batch" script
- R "An interactive environment to use batch scripts"

## Ideal solution: Interactive Client with a Batch Server

- Parallel visualization systems (VisIt and ParaView) are client-server (batch on server)
- Current pbdR packages address server side (batch)
- pbdCS 0.1-0 released on GitHub
  - Interactive SPMD
  - Based on ZeroMQ distributed messaging (pbdZMQ 0.1-1 on CRAN)
  - Bridge resource manager (pbdSCHED 0.1-0 on GitHub)
  - Site configuration file
  - Manage relationship of big data (server side) to little data (client side)

# Manager-Workers

- A serial program (Manager) divides up work and/or data
- Workers run in parallel without interaction
- Manager collects/combines results from workers
- Divide-Recombine fits this model

# MapReduce

- A concept born of a search engine
- Decouples certain coupled problems with an intermediate communication - shuffle
- User writes two serial codes: Map and Reduce

# MapReduce: a Parallel Search Engine Concept

## Search MANY documents — Serve MANY users

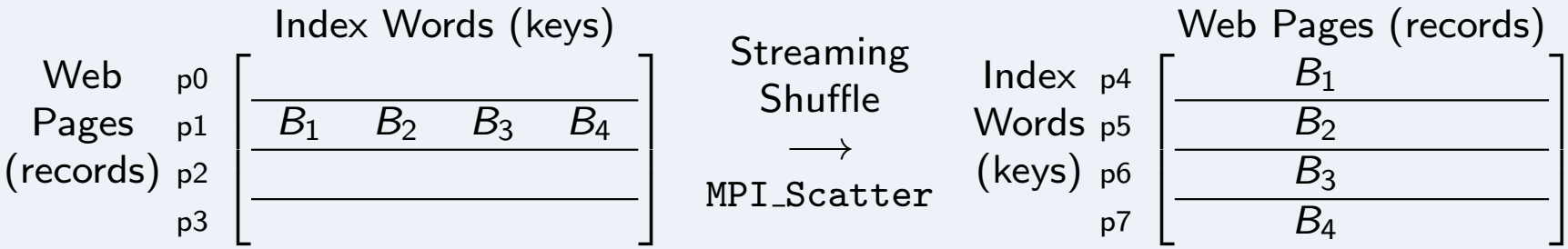
| Web Pages (records) | | Index Words (keys) | | | |
|---|---|---|---|---|---|
| | p0 | $A_1$ | $A_2$ | $A_3$ | $A_4$ |
| | p1 | $B_1$ | $B_2$ | $B_3$ | $B_4$ |
| | p2 | $C_1$ | $C_2$ | $C_3$ | $C_4$ |
| | p3 | $D_1$ | $D_2$ | $D_3$ | $D_4$ |

Shuffle $\longrightarrow$ `MPI_Alltoallv`

| Index Words (keys) | | Web Pages (records) | | | |
|---|---|---|---|---|---|
| | p0 | $A_1$ | $B_1$ | $C_1$ | $D_1$ |
| | p1 | $A_2$ | $B_2$ | $C_2$ | $D_2$ |
| | p2 | $A_3$ | $B_3$ | $C_3$ | $D_3$ |
| | p3 | $A_4$ | $B_4$ | $C_4$ | $D_4$ |

Matrix transpose in another language?

## Can use different sets of processors



# MPI and MapReduce

## Both Concepts are about Communitation

- One makes communication explicit, gives choices
- The other hides communication, gives one choice (shuffle)

# SPMD: Single Program Multiple Data

- The prevalent way of distributed programming
- Can handle tightly coupled parallel computations
- It is designed for batch computing
- There is usually no manager - rather, all cooperate
- Prime driver behind MPI specification

# Early SPMD Work in Statistics: Crossproduct (Row-Block)

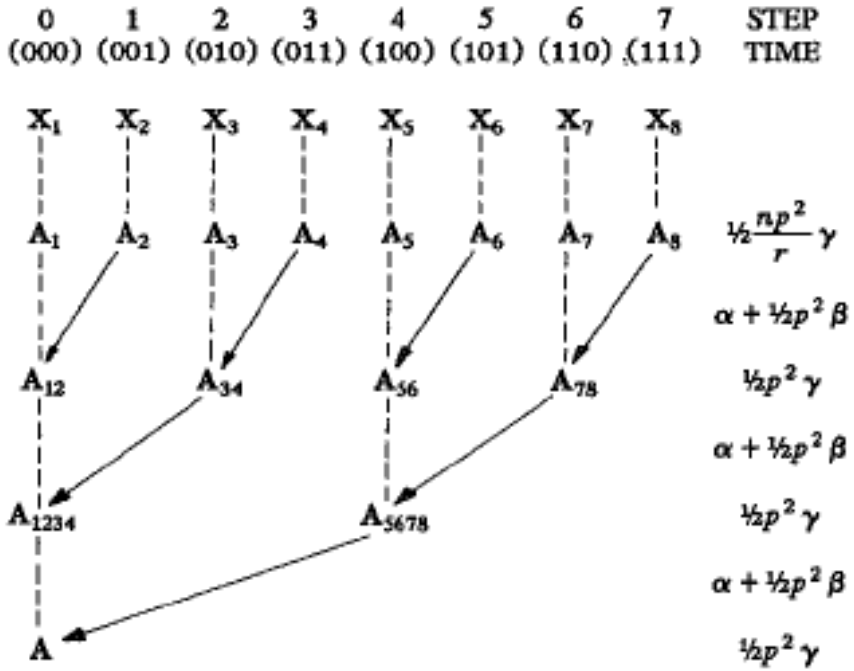



FIG. 4. *Computation of* $\mathbf{A} = \mathbf{X}'\mathbf{X}$ *on an 8-processor hypercube, with final result on processor 0.*

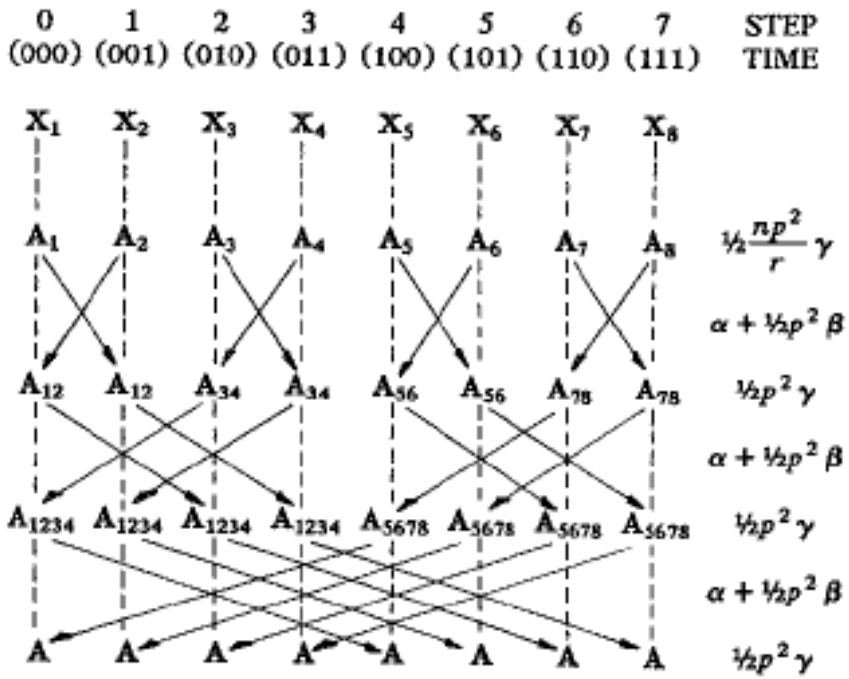



FIG. 6. *Computation of* $\mathbf{A} = \mathbf{X}'\mathbf{X}$ *on an 8-processor hypercube, with final result on all processors.*

## Hypercube: Individual send() and recv() over each dimension

Ostrouchov (1987). Parallel Computing on a Hypercube: An overview of the architecture and some applications. *Proceedings of the 19th Symposium on the Interface of Computer Science and Statistics*, p.27-32.

# Simplified with MPI (and further with pbdMPI)

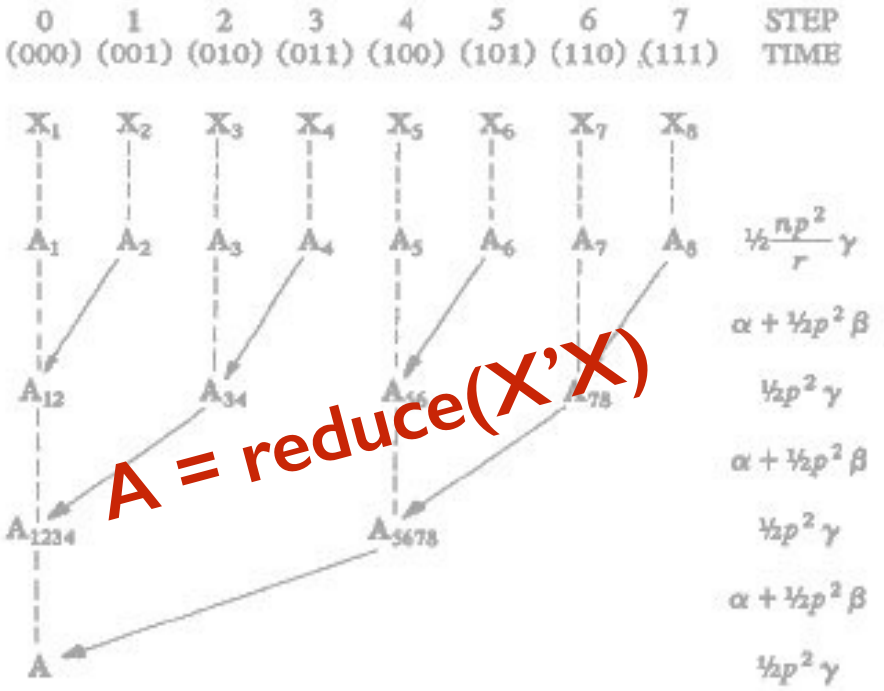



FIG. 4. *Computation of A = X'X on an 8-processor hypercube, with final result on processor 0.*

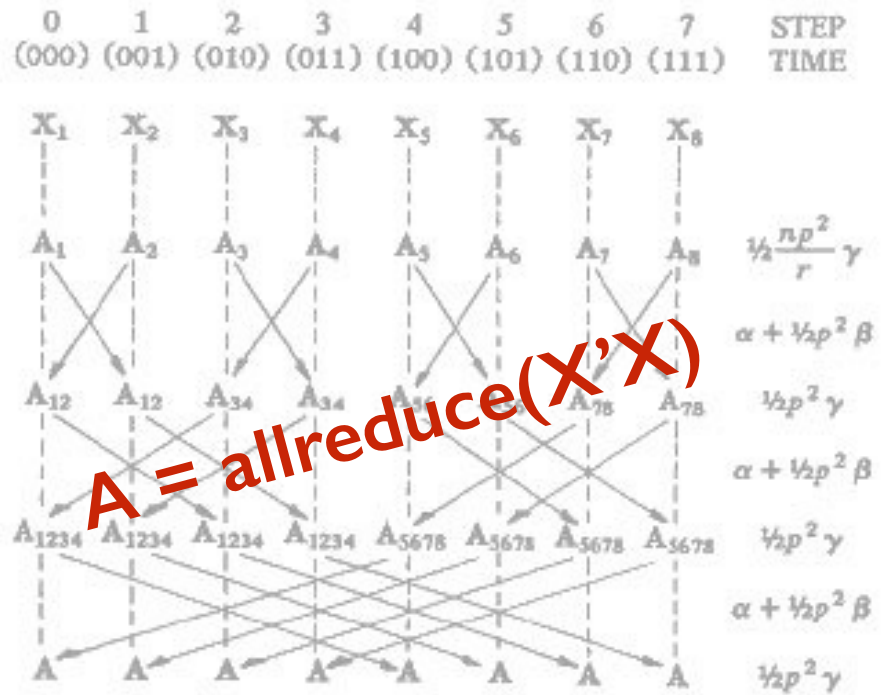



FIG. 6. *Computation of A = X'X on an 8-processor hypercube, with final result on all processors.*

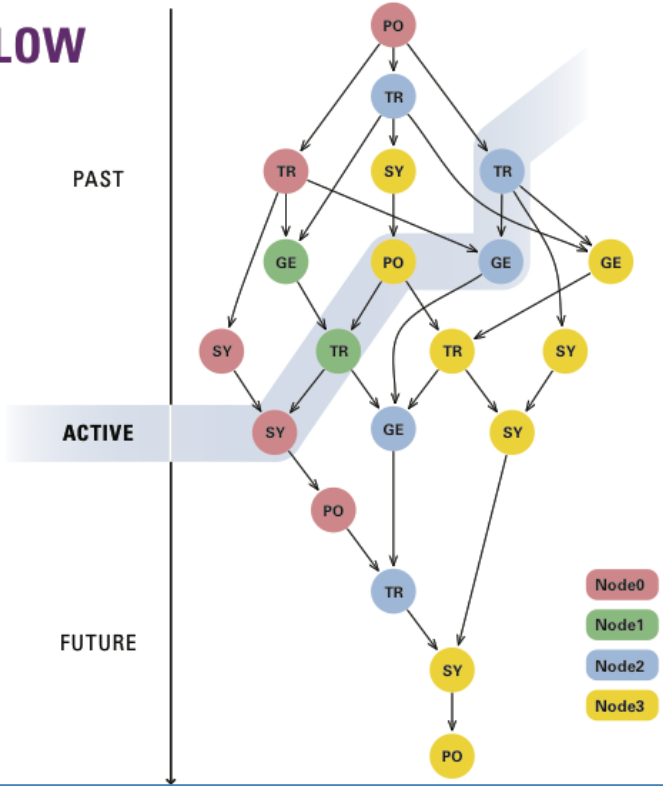
## Architecture-specific vendor optimizations

- Cray MPT
- SGI MPT

# Data-flow: Parallel Runtime Scheduling and Execution Controller (PaRSEC)

**EFFICIENT DATA FLOW REPRESENTATION**

| FEATURES |
| --- |
| Supports Distributed Heterogeneous Platforms |
| Sustained Performance |
| NUMA & Cache Aware Scheduling |
| State-of-the-art Algorithms |
| Capacity Level Scalability |
| Performance Portability |
| Implicit Communication |
| Communication Overlapping |



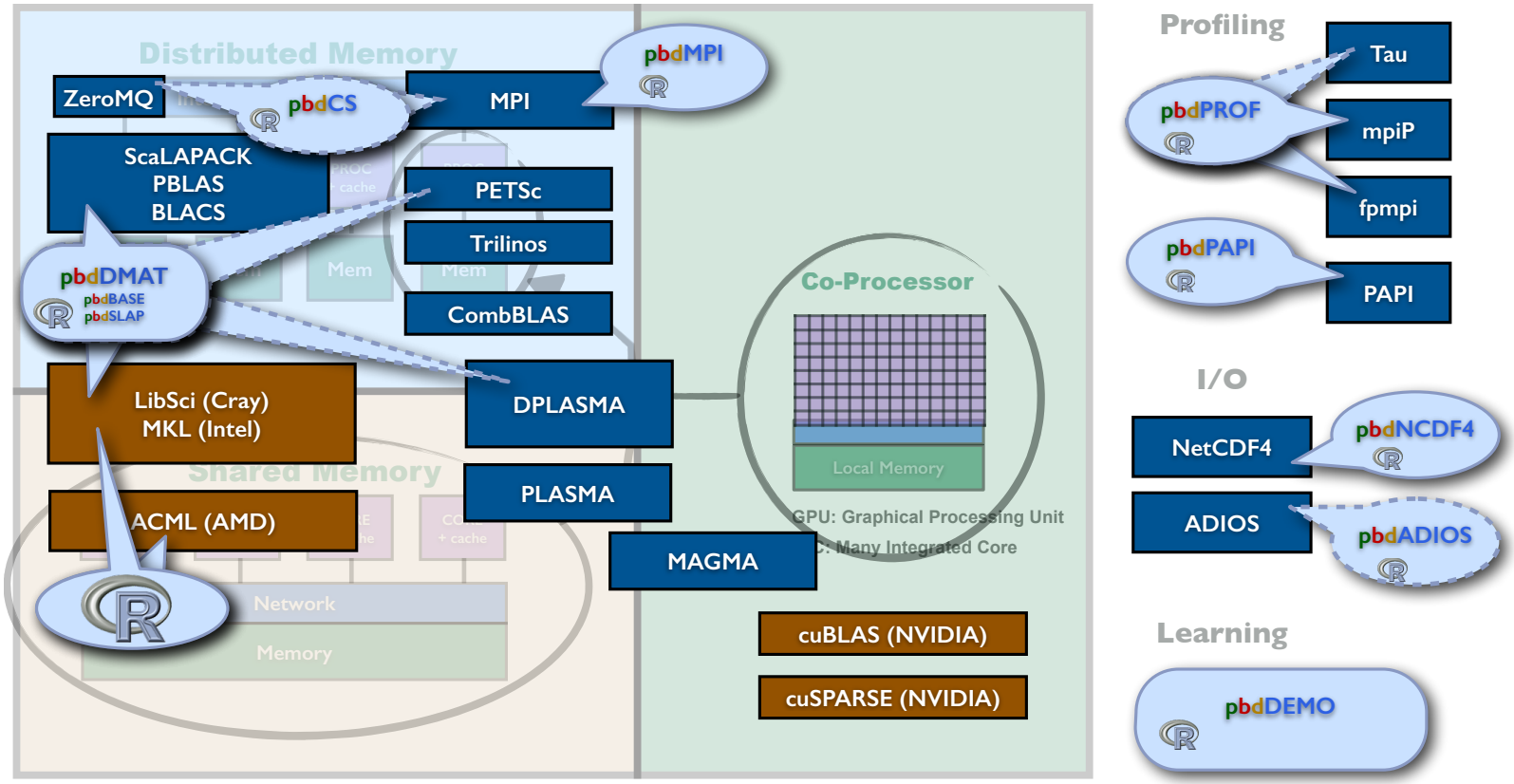

Graphic from icl.cs.utk.edu

Bosilca, G., Bouteiller, A., Danalis, A., Faverge, M., Herault, T., Dongarra, J. "PaRSEC: Exploiting Heterogeneity to Enhance Scalability," IEEE Computing in Science and Engineering, Vol. 15, No. 6, 36-45, November, 2013.

- Master data-flow controller runs distributed on all cores.
- Dynamic generation of current level in flow graph
- Effectively removes collective synchronizations

# Contents

# pbdR Interfaces to Libraries: Sustainable Path




## Why use HPC libraries?

- The libraries represent 30+ years of research by the HPC community
- *They're tested. They're fast. They're scalable.*
- Many science communities are invested in their API.
- HPC Simulation Science uses much of the same math as data analysis

2 pbdR

- The pbdR Project
- pbdMPI
- pbdDMAT
- RandSVD
- pbdMPI Example: Random Forest Prediction
- pbdMPI Example: Functional Data Analysis

## pbdMPI: Simplified, Extensible, and Fast Communication Operations

- S4 methods for collective communication: extensible to other R objects.
- Default methods (like `Robj` in **Rmpi**) check for data type: safe for general users.
- API is simplified: defaults in control objects.
- Array and matrix methods without serialization: faster than **Rmpi**.

| **pbdMPI** (S4) | **Rmpi** |
|---|---|
| `allgather` | `mpi.allgather`, `mpi.allgatherv`, `mpi.allgather.Robj` |
| `allreduce` | `mpi.allreduce` |
| `bcast` | `mpi.bcast`, `mpi.bcast.Robj` |
| `gather` | `mpi.gather`, `mpi.gatherv`, `mpi.gather.Robj` |
| `recv` | `mpi.recv`, `mpi.recv.Robj` |
| `reduce` | `mpi.reduce` |
| `scatter` | `mpi.scatter`, `mpi.scatterv`, `mpi.scatter.Robj` |
| `send` | `mpi.send`, `mpi.send.Robj` |

## Integer? Not always obvious in R.

```
> is.integer(1)
[1] FALSE
> is.integer(2)
[1] FALSE
> is.integer(1:2)
[1] TRUE
```

## pbdMPI lets R figure it out

Rmpi

```
# int
mpi.allreduce(x, type=1)
# double
mpi.allreduce(x, type=2)
```

pbdMPI

```
allreduce(x)
```

# Single Program (SPMD): Runs Asynchronous Parallel

## Rank Query Example

1_rank.r

```
1 library(pbdMPI, quiet = TRUE)
2 init()
3
4 my.rank <- comm.rank()
5 comm.print(my.rank, all.rank=TRUE)
6
7 finalize()
```

Execute this batch script via:

```
1 mpirun -np 2 Rscript 1_rank.r
```

Sample Output:

```
1 COMM.RANK = 0
2 [1] 0
3 COMM.RANK = 1
4 [1] 1
```

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# Mapping a Matrix to Processors

## Processor Grid Shapes

$$\begin{bmatrix} 0 & 1 & 2 & 3 & 4 & 5 \end{bmatrix} \qquad \begin{bmatrix} 0 & 1 & 2 \\ 3 & 4 & 5 \end{bmatrix} \qquad \begin{bmatrix} 0 & 1 \\ 2 & 3 \\ 4 & 5 \end{bmatrix} \qquad \begin{bmatrix} 0 \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{bmatrix}$$

(a) $1 \times 6$ (b) $2 \times 3$ (c) $3 \times 2$ (d) $6 \times 1$

Table: Processor Grid Shapes with 6 Processors

## 2×3 block-cyclic grid on 6 processors: Global view "ddmatrix" class

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

$$\text{Processor grid} = \left|\begin{array}{ccc} 0 & 1 & 2 \\ 3 & 4 & 5 \end{array}\right| = \left|\begin{array}{ccc} (0,0) & (0,1) & (0,2) \\ (1,0) & (1,1) & (1,2) \end{array}\right|$$

## 2×3 block-cyclic grid on 6 processors: Local view "ddmatrix" class

$$\left[\begin{array}{cc|cc} x_{11} & x_{12} & x_{17} & x_{18} \\ x_{21} & x_{22} & x_{27} & x_{28} \\ \hline x_{51} & x_{52} & x_{57} & x_{58} \\ x_{61} & x_{62} & x_{67} & x_{68} \\ \hline x_{91} & x_{92} & x_{97} & x_{98} \end{array}\right]_{5\times4} \quad \left[\begin{array}{cc|c} x_{13} & x_{14} & x_{19} \\ x_{23} & x_{24} & x_{29} \\ \hline x_{53} & x_{54} & x_{59} \\ x_{63} & x_{64} & x_{69} \\ \hline x_{93} & x_{94} & x_{99} \end{array}\right]_{5\times3} \quad \left[\begin{array}{cc} x_{15} & x_{16} \\ x_{25} & x_{26} \\ \hline x_{55} & x_{56} \\ x_{65} & x_{66} \\ \hline x_{95} & x_{96} \end{array}\right]_{5\times2}$$

$$\left[\begin{array}{cc|cc} x_{31} & x_{32} & x_{37} & x_{38} \\ x_{41} & x_{42} & x_{47} & x_{48} \\ \hline x_{71} & x_{72} & x_{77} & x_{78} \\ x_{81} & x_{82} & x_{87} & x_{88} \end{array}\right]_{4\times4} \quad \left[\begin{array}{cc|c} x_{33} & x_{34} & x_{39} \\ x_{43} & x_{44} & x_{49} \\ \hline x_{73} & x_{74} & x_{79} \\ x_{83} & x_{84} & x_{89} \end{array}\right]_{4\times3} \quad \left[\begin{array}{cc} x_{35} & x_{36} \\ x_{45} & x_{46} \\ \hline x_{75} & x_{76} \\ x_{85} & x_{86} \end{array}\right]_{4\times2}$$

$$\text{Processor grid} = \left|\begin{array}{ccc} 0 & 1 & 2 \\ 3 & 4 & 5 \end{array}\right| = \left|\begin{array}{ccc} (0,0) & (0,1) & (0,2) \\ (1,0) & (1,1) & (1,2) \end{array}\right|$$

## pbdR Example Syntax

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

*The above (and over 100 other functions) runs on 1 core with R or 10,000 cores with pbdR ddmatrix class*

```
1 > showClass("ddmatrix")
2 Class "ddmatrix" [package "pbdDMAT"]
3 Slots:
4 Name:      Data      dim     ldim    bldim    ICTXT
5 Class:   matrix numeric numeric numeric numeric
```

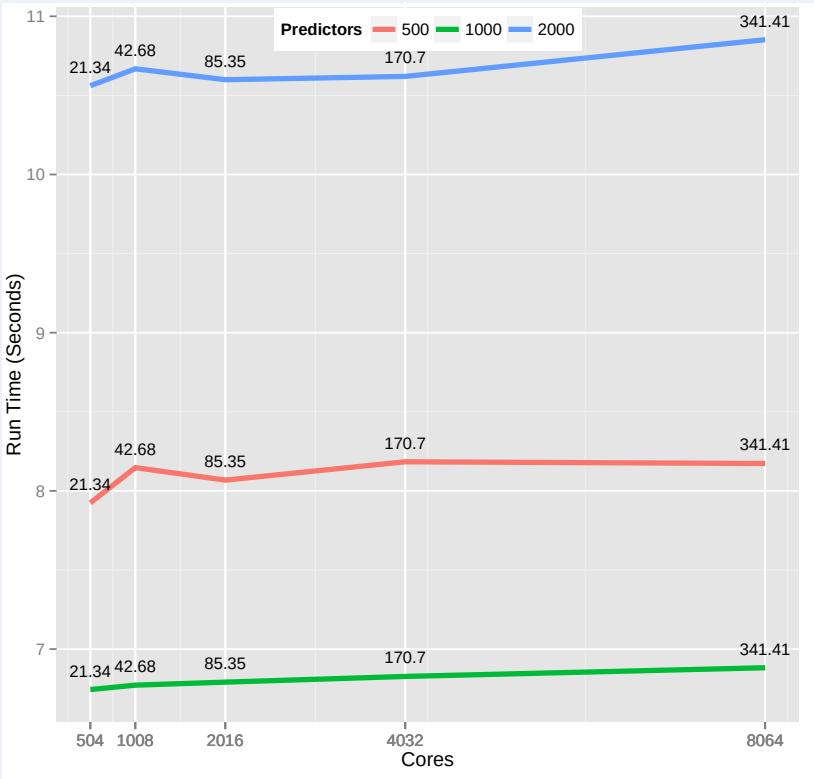
```
1 > x <- as.rowblock(x)
2 > x <- as.colblock(x)
3 > x <- redistribute(x, bldim=c(8, 8), ICTXT = 0)
```

## pbdDMAT Scalability Benchmarks

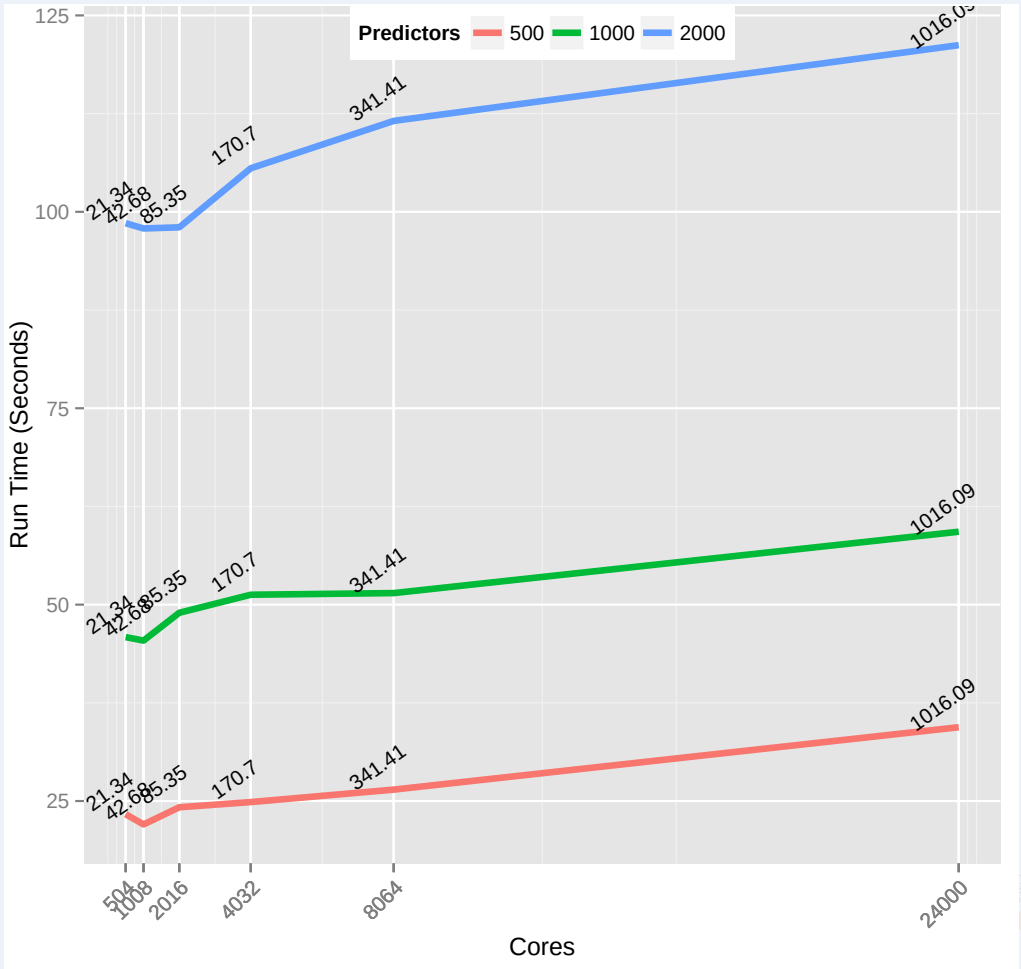
- Default choices throughout (no MKL, ACML, etc.)
- 1 core = 1 MPI process (Kraken: 6-core Opterons)
- Generate random matrix
  - Global Columns: 500, 1000, and 2000
  - Global Rows: fixed per core to make 43.4*MiB*
- Measure wall clock time
- "weak scaling" = global problem grows with core count

# pbdDMAT Scalability Benchmarks

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

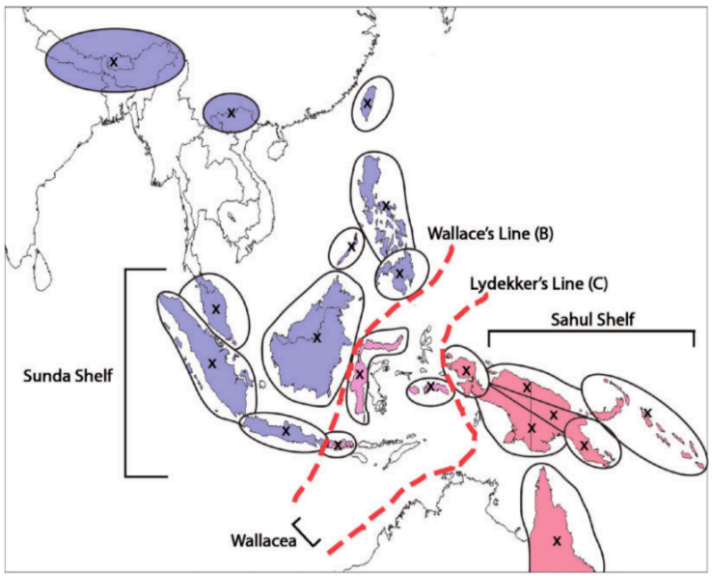


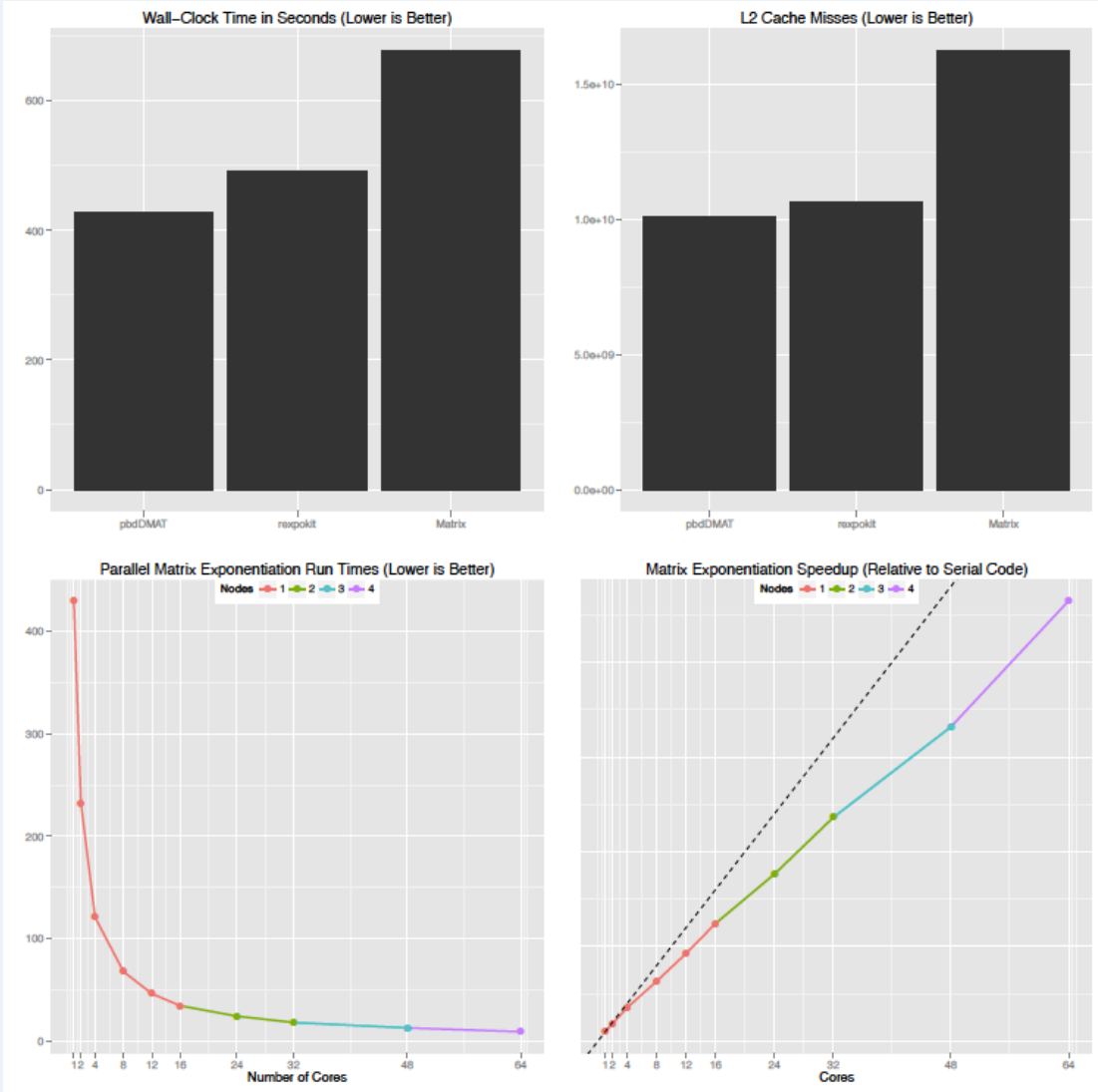

```
1 b <- ddmatrix("runif", nrow=p,
      ncol=1)
2 y <- x %*% b
3 b.hat <- lm.fit(x, y)$coefficients
```



# Matrix Exponentiation (pbdDMAT)

- Fitting biogeography models requires many matrix exponentiations
- Benchmark: Matrix exponential of $5000 \times 5000$ matrix.
- R 3.1.0, Matrix 1.1-2, rexpokit 0.25, pbdDMAT 0.3-0
- Libs: Cray LibSci, NETLIB ScaLAPACK, Compilers: gnu 4.8.2
- Configuration: 1 thread == 1 MPI rank == 1 physical core




Schmidt and Matzke (2014) Distributed matrix exponentiation, The R User Conference (UseR! 2014), Los Angeles, CA, August 2014

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## Randomized truncated SVD[1]

**Prototype for Randomized SVD**

*Given an $m \times n$ matrix $\boldsymbol{A}$, 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 $\boldsymbol{U\Sigma V}^*$, where $\boldsymbol{U}$ and $\boldsymbol{V}$ are orthonormal, and $\boldsymbol{\Sigma}$ is nonnegative and diagonal.*

**Stage A:**

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

**Stage B:**

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

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

**Algorithm 4.4: Randomized Subspace Iteration**

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

1 Draw an $n \times \ell$ standard Gaussian matrix $\boldsymbol{\Omega}$.
2 Form $\boldsymbol{Y}_0 = \boldsymbol{A\Omega}$ and compute its QR factorization $\boldsymbol{Y}_0 = \boldsymbol{Q}_0\boldsymbol{R}_0$.
3 **for** $j = 1, 2, \ldots, q$
4 Form $\widetilde{\boldsymbol{Y}}_j = \boldsymbol{A}^*\boldsymbol{Q}_{j-1}$ and compute its QR factorization $\widetilde{\boldsymbol{Y}}_j = \widetilde{\boldsymbol{Q}}_j\widetilde{\boldsymbol{R}}_j$.
5 Form $\boldsymbol{Y}_j = \boldsymbol{A}\widetilde{\boldsymbol{Q}}_j$ and compute its QR factorization $\boldsymbol{Y}_j = \boldsymbol{Q}_j\boldsymbol{R}_j$.
6 **end**
7 $\boldsymbol{Q} = \boldsymbol{Q}_q$.

### 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   }
```

[1] Halko, Martinsson, and Tropp. 2011. Finding structure with randomness: probabilistic algorithms for constructing approximate matrix decompositions *SIAM Review* **53** 217–288

## Randomized truncated SVD

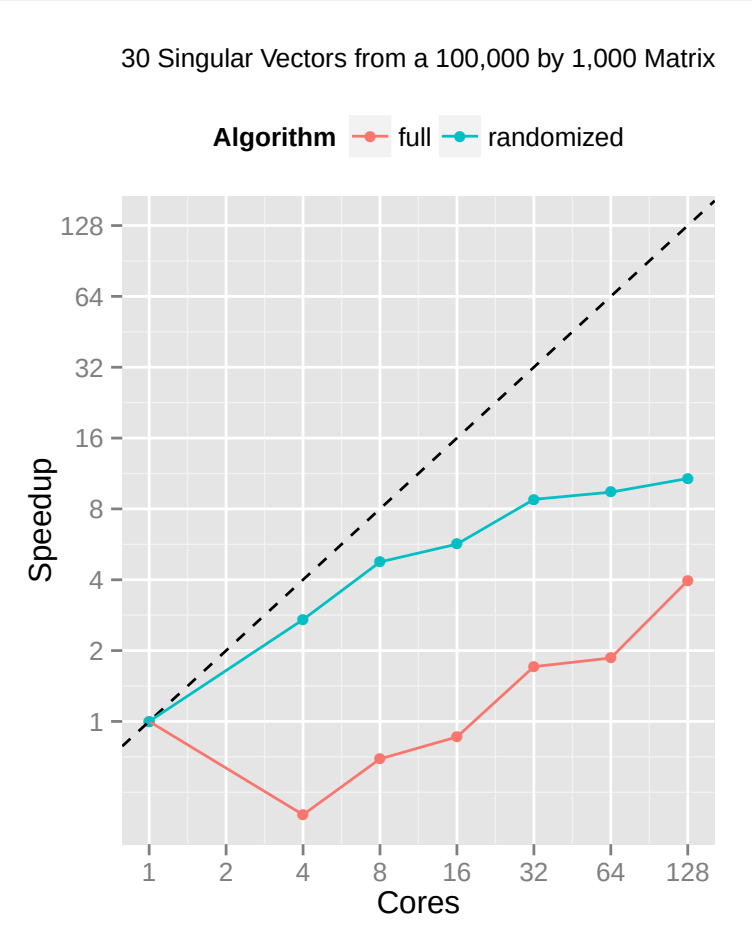
### Serial R

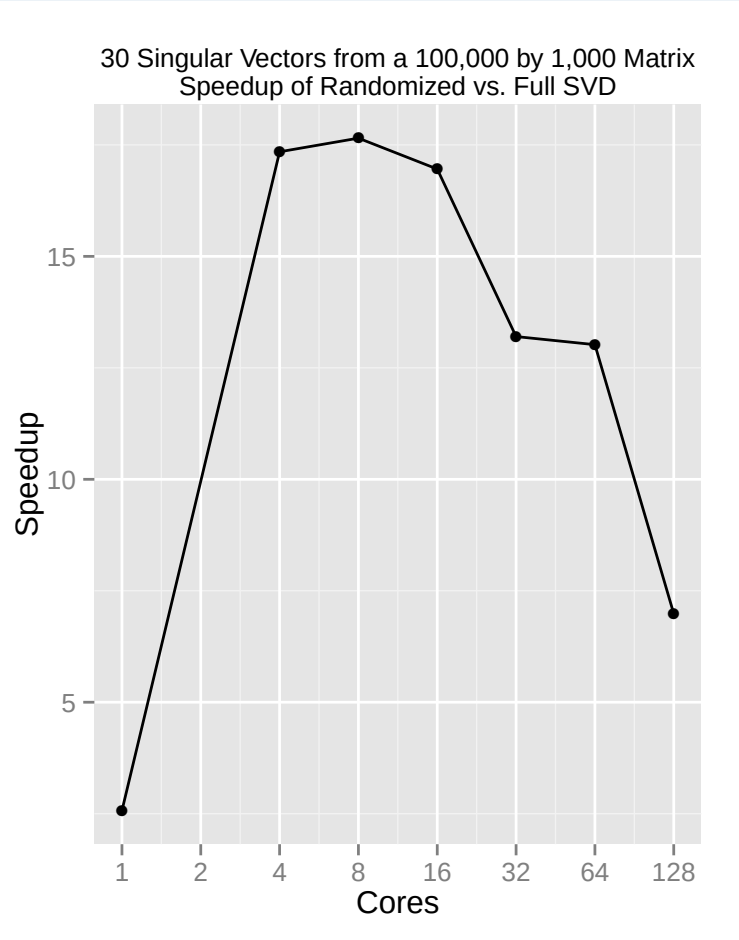
```
1  randSVD <- function(A, k, q=3)
2    {
3      ## Stage A
4      Omega <-  matrix(rnorm(n*2*k),
5          nrow=n, ncol=2*k)
6      Y <- A %*% Omega
7      Q <- qr.Q(qr(Y))
8      At <- t(A)
9      for(i in 1:q)
10       {
11         Y <- At %*% Q
12         Q <- qr.Q(qr(Y))
13         Y <- A %*% 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   }
```

# From journal to scalable code and scaling data in one day.



2 pbdR

- The pbdR Project
- pbdMPI
- pbdDMAT
- RandSVD
- pbdMPI Example: Random Forest Prediction
- pbdMPI Example: Functional Data Analysis

# Letter Recognition Data

## Example 1: Letter Recognition data from package **mlbench** (20,000 × 17)

```
[,1]  lettr  capital letter
[,2]  x.box  horizontal position of box
[,3]  y.box  vertical position of box
[,4]  width  width of box
[,5]  high  height of box
[,6]  onpix  total number of on pixels
[,7]  x.bar  mean x of on pixels in box
[,8]  y.bar  mean y of on pixels in box
[,9]  x2bar  mean x variance
[,10]  y2bar  mean y variance
[,11]  xybar  mean x y correlation
[,12]  x2ybr  mean of x^2 y
[,13]  xy2br  mean of x y^2
[,14]  x.ege  mean edge count left to right
[,15]  xegvy  correlation of x.ege with y
[,16]  y.ege  mean edge count bottom to top
[,17]  yegvx  correlation of y.ege with x
```

P. W. Frey and D. J. Slate (Machine Learning Vol 6/2 March 91): "Letter Recognition Using Holland-style Adaptive Classifiers".

## Example 1: Random Forest Algorithm

1. Build simple regression trees from random subsets of columns
2. Use model averaging for prediction
3. Package **randomForest** has a `combine()` function that enables the following parallel approach:
   1. Everyone gets the same training data
   2. Split regression tree building among processors (**randomForest**)
   3. Use `allgather` to bring built predictors to all
   4. Everyone `combine` predictors
   5. Split prediction work by blocks of rows
   6. Use `allreduce` to assess prediction
4. Steps (3) and (4) can be improved with a custom reduce/combine to take advantage of MPI vendor optimizations

# Example 1: Random Forest Code
# (Split learning by blocks of trees. Split prediction by blocks of rows.)

Serial Code 4_rf_s.r

```
1  library(randomForest)
2  library(mlbench)
3  data(LetterRecognition) # 26 Capital Letters Data 20,000 x 17
4  set.seed(seed=123)
5  n <- nrow(LetterRecognition)
6  n_test <- floor(0.2*n)
7  i_test <- sample.int(n, n_test) # Use 1/5 of the data to test
8  train <- LetterRecognition[-i_test, ]
9  test <- LetterRecognition[i_test, ]
10
11 ## train random forest
12 rf.all <- randomForest(lettr ~ ., train, ntree=500,
       norm.votes=FALSE)
13
14 ## predict test data
15 pred <- predict(rf.all, test)
16 correct <- sum(pred == test$lettr)
17 cat("Proportion Correct:", correct/(n_test), "\n")
```

# Example 1: Random Forest Code
# (Split learning by blocks of trees. Split prediction by blocks of rows.)

Parallel Code 4_rf_p.r

```
1  library(randomForest)
2  library(mlbench)
3  data(LetterRecognition)
4  comm.set.seed(seed=123, diff=FALSE) # same training data
5  n <- nrow(LetterRecognition)
6  n_test <- floor(0.2*n)
7  i_test <- sample.int(n, n_test) # Use 1/5 of the data to test
8  train <- LetterRecognition[-i_test, ]
9  test <- LetterRecognition[i_test, ][get.jid(n_test), ]
10
11 comm.set.seed(seed=1e6*runif(1), diff=TRUE)
12 my.rf <- randomForest(lettr ~ ., train, ntree=500%/%comm.size(),
       norm.votes=FALSE)
13 rf.all <- do.call(combine, allgather(my.rf))
14
15 pred <- predict(rf.all, test)
16 correct <- allreduce(sum(pred == test$lettr))
17 comm.cat("Proportion Correct:", correct/(n_test), "\n")
```

## Runs serial or on any number of cores

```
[beacon-login2 stats]$ time Rscript 4_rf_s.r
Proportion Correct: 0.96725
real 0m49.028s    user 0m48.626s    sys 0m0.335s
[beacon-login2 stats]$ time Rscript 4_rf_p.r
Proportion Correct: 0.96425
real 0m52.634s    user 0m51.914s    sys 0m0.598s
[beacon-login2 stats]$ time mpirun -np 2 Rscript 4_rf_p.r
Proportion Correct: 0.96425
real 0m28.349s    user 0m54.570s    sys 0m1.070s
[beacon-login2 stats]$ time mpirun -np 4 Rscript 4_rf_p.r
Proportion Correct: 0.963
real 0m16.380s    user 1m1.559s     sys 0m1.664s
[beacon-login2 stats]$ time mpirun -np 8 Rscript 4_rf_p.r
Proportion Correct: 0.963
real 0m11.010s    user 1m19.301s    sys 0m3.421s
[beacon-login2 stats]$ time mpirun -np 16 Rscript 4_rf_p.r
Proportion Correct: 0.9635
real 0m10.655s    user 2m32.508s    sys 0m6.624s
[beacon-login2 stats]$ time mpirun -np 32 Rscript 4_rf_p.r
Proportion Correct: 0.96325
real 0m21.692s    user 4m44.114s    sys 0m20.179s
```

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# fda.usc Package

## Profiling min.basis()

```
> summaryRprof()
$by.total
                      total.time  total.pct  self.time  self.pct
"min.basis"                12.32     100.00       0.00      0.00
"type.CV"                   6.54      53.08       0.02      0.16
"S.basis"                   5.76      46.75       0.00      0.00
"drop"                      4.20      34.09       0.00      0.00
"norm.fdata"                4.20      34.09       0.00      0.00
"metric"                    4.18      33.93       1.04      8.44
"%*%"                       3.98      32.31       3.98     32.31
"getbasispenalty"           2.72      22.08       0.02      0.16
"bsplinepen"                2.68      21.75       0.36      2.92
"int.simpson2"              2.54      20.62       1.96     15.91
"t"                         2.10      17.05       0.10      0.81
"ppBspline"                 1.60      12.99       0.82      6.66
. . .
```

# Example: min.basis() 110 lines — SPMD: Add 5, change 3

```
1  min.basis <- function(fdataobj, type.CV = GCV.S, . . ., ...)
2  {
3      . . . 13 lines
4      library(pbdMPI)
5      init()
6      my.k <- get.jid(lenlambda)
7      my.gcv <- array(Inf, dim = c(lenbasis, length(my.k)))
8      . . . 36 lines
9      for (i in 1:lenbasis) {
10         . . . 3 lines
11         for (k in my.k) {
12             S2 <- S.basis(tt, base, lambda[k])
13             my.gcv[i, k - my.k[1] + 1] <-
14                 type.CV(fdataobj, S = S2, W = W, trim =
                       par.CV$trim, draw = par.CV$draw, ...)
15         }
16     }
17     gcv <- do.call(cbind, allgather(my.gcv))
18     finalize()
19     . . . 48 lines
```

# Contents

3 pbdCS
- Client-Server Demo

# 0MQ

Some explanation goes here The demo goes here

# 4 Future Work

## Future Work

- Second year of a 3 year NSF grant to
  - Bring back interactivity via client/server (pbdCS 0.1-0)
  - Simplify parallel data input
  - Begin DPLASMA integration
  - Outreach to the statistics community
- DOE funding: In-situ or staging use with simulations
  - Machine learning from fusion simulation data
- Collaboration wishlist
  - RDD, HDFS, etc., file readers
  - Communicator integration with SparkR or Spark
  - Communicator integration with VisIt and ParaView
  - pbdCS integration with RStudio IDE
  - Instrumentation of various R packages with pbdR

## Where to learn more?

- http://r-pbd.org/
- **pbdDEMO** vignette
- Googlegroup:RBigDataProgramming