

A Quick Guide for the pbdDEMO Package

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Warning: This document is written to explain the main functions of **pbdDEMO** (Schmidt *et al.* 2012b), version 0.1-0. Every effort will be made to ensure future versions are consistent with these instructions, but features in later versions may not be explained in this document.

Information about the functionality of this package, and any changes in future versions can be found on website: “Programming with Big Data in R” at <http://r-pbd.org/>.

1. Introduction

This vignette is to explain some pbdR (Ostrouchov *et al.* 2012) examples which are higher level applications and may be commonly found in basic Statistics. The purposes is to show how to reuse the pre-exist functions, and quickly solve problems in an efficient way. The functions built for examples may not be exactly same idea of original R (R Core Team 2012) functions, but can be adjusted in similar wa. You are very welcome to use these as templates and rewrite your own functions or packages.

1.1. Installation

One can download **pbdDEMO** from CRAN at <http://cran.r-project.org>, and the intal-lation can be done with the following commands

Shell Command

```
tar zxvf pbdDEMO_0.1-0.tar.gz  
R CMD INSTALL pbdDEMO
```

Since **pbdDEMO** depends on other **pbdR** packages, please read the corresponding vignettes if installations did not succeed. We also provide several demos for the capability of **pbdR** packages which are explained correspondingly in the next few sections.

1.2. Notation

We presume that readers already have idea about SPMD programming. If not, please read **pbdMPI**’s vignette Chen *et al.* (2012b) first. If possible, readers are encouraged to run the demo of **pbdMPI** package and go through the code step by step.

Note that we tend to use suffix `.spmd` to indicate a distributed local object which is a portion of big object. As the usual R, Supposer \mathbf{X} is a very big matrix, then $\mathbf{X.spmd}$ ’s could be R objects distributed on all processors, and usually they have the same data type. \mathbf{X} could be a result of `cbind` or `rbind` on all $\mathbf{X.spmd}$ ’s. Examples can be found in the Section 3.

We also tend to assume common variables without suffix `.spmd` in SPMD programming. For instance, `y` could be an R object on all processors. Their dimension/attributes are allowed to be differed on some processors. In SPMD case, it may be a good idea to invent a `spmd` S4 class or methods for this purpose, but most S4 methods are sufficient and fast in most computation.

While in distributed computing, in contrast, it is a better idea to invent a `ddmatrix` class as in **pbdBASE** (Schmidt *et al.* 2012a) and **pbdDMAT** (Schmidt *et al.* 2012c), then let efficient libraries handle computing and avoid tedious coding. i.e. \mathbf{X} is a very big matrix, but `X.dmat` is in block-cyclic format where `X.dmat` can be utilized by most **pbdR** functions. Examples can be found in the Section ??.

2. Timing

Throughout ...

Part I

Ad Hoc Methods

3. Basic Statistics Examples

This section introduces four simple examples and explains a little about computing with distributed data. These implemented examples/functions are partly selected from the Cookbook of HPSC website (Chen and Ostrouchov 2011) at <http://thirteen-01.stat.iastate.edu/snoweye/hpsc/?item=cookbook>. Please see more details there.

As a matter of convention, throughout we will use the suffix `.spmd` to indicate the local piece of a “bigger” distributed object. In SPMD case, it may be a redundant idea to invent a `spmd` S4 class or methods for this purpose. The S3 class and methods are sufficient and fast in most SPMD case. In contrast, it is a better idea to invent a `ddmatrix` class as in **pbdBASE** (Schmidt *et al.* 2012a) and **pbdDMAT** (Schmidt *et al.* 2012c), then let efficient libraries handle computing and avoid tedious coding. A silly example can be found in the Section 3.5.

3.1. Monte Carlo Simulation

The demo command is

Shell Command

```
### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 4 Rscript -e "demo(monte_carlo, 'pbdDEMO', ask=F, echo=F)"
```

This is a simple Monte Carlo simulation example for numerically estimating π . Suppose we sample N uniform observations (x_i, y_i) inside (or perhaps on the border of) the unit square

$(0, 1) \times (0, 1)$, where $i = 1, 2, \dots, N$. Then

$$\pi \approx 4 \frac{L}{N} \quad (1)$$

where $0 \leq L \leq N$ is the number of observations sampled satisfying

$$x_i^2 + y_i^2 \leq 1$$

The intuitive explanation for this is strategy which is sometimes given belies a misunderstanding of infinite cardinalities, and infinite processes in general. We are not *approximating* an area, because to do so with points would be madness requiring a transfinite process.

In reality, we are evaluating the probability that someone throwing a 0-dimensional “dart” at the unit square will have that “dart” also land below the arc of the unit circle contained within the unit square. Formally, let U_1 and U_2 be random uniform variables, each from the closed unit interval $[0, 1]$. Define the random variable

$$X := \begin{cases} 1, & U_1^2 + U_2^2 \leq 1 \\ 0, & \text{otherwise} \end{cases}$$

Let $V_i = U_i^2$ for $i = 1, 2$. Then the expected value

$$\begin{aligned} E[X] &= P(V_1 + V_2 \leq 1) \\ &= \int_0^1 \int_0^{1-V_1} p(V_1, V_2) dV_2 dV_1 \\ &= \int_0^1 \int_0^{1-V_1} \left(\frac{1}{2\sqrt{V_1}} \right) \left(\frac{1}{2\sqrt{V_2}} \right) dV_2 dV_1 \\ &= \frac{1}{2} \int_0^1 \left(\frac{1-V_1}{V_1} \right)^{1/2} dV_1 \\ &= \frac{1}{2} \left[V_1 \left(\frac{1-V_1}{V_1} \right)^{1/2} - \frac{1}{2} \arctan \left(\frac{\left(\frac{1-V_1}{V_1} \right)^{1/2} (2V_1 - 1)}{2(V_1 - 1)} \right) \right]_{V_1 \rightarrow 0}^1 \\ &= \frac{1}{2} \cdot \frac{\pi}{2} \end{aligned}$$

and by sampling observations X_i for $i = 1, \dots, N$, by the Strong Law of Large Numbers

$$\bar{X}_N \xrightarrow{a.s.} \frac{\pi}{4} \quad \text{as } N \rightarrow \infty$$

In other words,

$$P \left(\lim_{N \rightarrow \infty} \bar{X}_N = \frac{\pi}{4} \right) = 1$$

Whence,

$$\frac{L}{N} \xrightarrow{a.s.} \frac{\pi}{4} \quad \text{as } N \rightarrow \infty$$

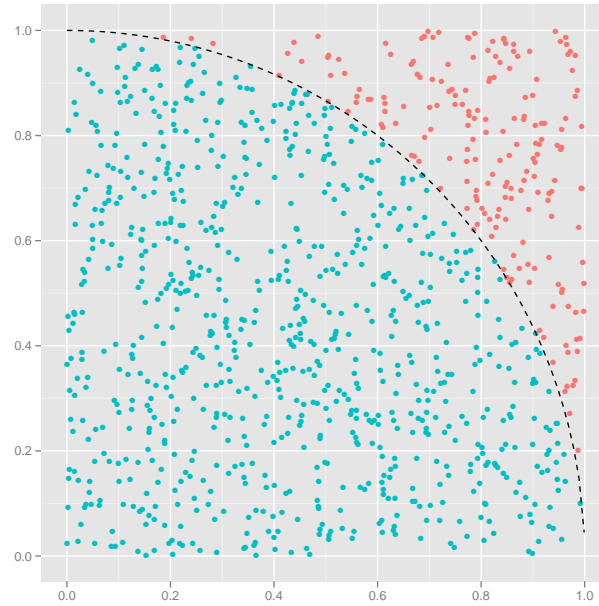


Figure 1: Approximating π by Monte Carlo methods

But because no one is going to read that, and if they do they'll just call me a grumpy old man, the misleading picture you desire can be found in Figure 1.

The key step of the demo code is in the next

R Code

```
N.spmd <- 1000
X.spmd <- matrix(runif(N.spmd * 2), ncol = 2)
r.spmd <- sum(rowSums(X.spmd^2) <= 1)
ret <- allreduce(c(N.spmd, r.spmd), op = "sum")
PI <- 4 * ret[2] / ret[1]
comm.print(PI)
```

In line 1, we specify sample size in `N.spmd` for each processor, and $N = D \times N.\text{spmd}$ if D processors are executed. In line 2, we generate samples in `X.spmd` for every processor. In line 3, we compute how many of radii are less than or equal to 1 for each processors. In line 4, we call `allreduce` to obtain total numbers across all processors. In line 5, we use the Equation (1). Since SPMD, `ret` is common on all processors, and so is `PI`.

3.2. Sample Mean and Sample Variance

The demo command is

Shell Command

```
### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
```

```
mpiexec -np 4 Rscript -e "demo(sample_stat,'pbdDEMO',ask=F,echo=F)"
```

Suppose $\mathbf{x} = \{x_1, x_2, \dots, x_N\}$ are observed samples, and N is potentially very large. We can distribute \mathbf{x} in 4 processors, and each processor roughly takes half of data. One simple way to compute sample mean \bar{x} and sample variance s_x is based on the formulas:

$$\begin{aligned}\bar{x} &= \frac{1}{N} \sum_{n=1}^N x_n \\ &= \sum_{n=1}^N \frac{x_n}{N}\end{aligned}\tag{2}$$

and

$$\begin{aligned}s_x &= \frac{1}{N-1} \sum_{n=1}^N (x_n - \bar{x})^2 \\ &= \frac{1}{N-1} \sum_{n=1}^N x_n^2 - \frac{2\bar{x}}{N-1} \sum_{n=1}^N x_n + \frac{1}{N-1} \sum_{n=1}^N \bar{x}^2 \\ &= \sum_{n=1}^N \left(\frac{x_n^2}{N-1} \right) - \frac{N\bar{x}^2}{N-1}\end{aligned}\tag{3}$$

where expressions (2) and (3) are one-pass algorithms in terms of C language which are potentially more stable and faster than the first expressions especially for large N . Here, only the first and second moments are implemented, while the extension of one-pass algorithms to higher order moments is also possible.

The demo command is

Shell Command

```
### At the shell prompt, run the demo with 2 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 2 Rscript -e "demo(sample_stat,'pbdDEMO',ask=F,echo=F)"
```

The demo `sample_stat` generates fake data on 2 processors, then utilize `mpi.stat` function as

The demo `sample_stat` generates fake data on 4 processors, then utilizes `mpi.stat` function as

R Code

```
mpi.stat <- function(x.spmd){
  ### For mean(x).
  N <- allreduce(length(x.spmd), op = "sum")
```

```

bar.x.spmd <- sum(x.spmd / N)
bar.x <- allreduce(bar.x.spmd, op = "sum")

### For var(x).
s.x.spmd <- sum(x.spmd^2 / (N - 1))
s.x <- allreduce(s.x.spmd, op = "sum") - bar.x^2 * (N / (N -
  1))

list(mean = bar.x, s = s.x)
} # End of mpi.stat().

```

where `allreduce` in **pbdMPI** (Chen *et al.* 2012a) can be utilized in this examples to aggregate local information across all processors.

3.3. Binning

The demo command is

Shell Command

```

### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 4 Rscript -e "demo(binning,'pbdDEMO',ask=F,echo=F)"

```

Binning is a classical statistics and can quickly summarize the data structure by setting some breaks between max and min of data. This is particularly a useful tool for constructing histograms and categorical data analysis.

The demo `binning` generates fake data on 4 processors, then utilize `mpi.bin` function as

R Code

```

mpi.bin <- function(x.spmd, breaks = pi / 3 * (-3:3)){
  bin.spmd <- table(cut(x.spmd, breaks = breaks))
  bin <- as.array(allreduce(bin.spmd, op = "sum"))
  dimnames(bin) <- dimnames(bin.spmd)
  class(bin) <- class(bin.spmd)
  bin
} # End of mpi.bin().

```

An easy implementation is to utilize `table` function to obtain local counts, then call `allreduce` to obtain global counts.

3.4. Quantile

The demo command is

Shell Command


```
### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 4 Rscript -e "demo(quantile,'pbdDEMO',ask=F,echo=F)"
```

Quantile is the other useful tool from fundamental statistics which provides data distribution for the desired value. This example can be extended to construct Q-Q plot, compute cumulative density function and nonparametric statistics, solve maximum likelihood estimators.

This is only an inefficient implementation to approximate a quantile and is not equivalent to the original `quantile` function in R. But in some sense, it should work well in large scale. The `demo quantile` generates fake data on 4 processors, then utilizes `mpi.quantile` function as

R Code

```
mpi.quantile <- function(x.spmd, prob = 0.5){
  if(sum(prob < 0 | prob > 1) > 0){
    stop("prob should be in (0, 1)")
  }

  N <- allreduce(length(x.spmd), op = "sum")
  x.max <- allreduce(max(x.spmd), op = "max")
  x.min <- allreduce(min(x.spmd), op = "min")

  f.quantile <- function(x, prob = 0.5){
    allreduce(sum(x.spmd <= x), op = "sum") / N - prob
  }

  uniroot(f.quantile, c(x.min, x.max), prob = prob[1])$root
} # End of mpi.quantile().
```

where a numerical function is solved by `uniroot` to find out the appropriate value such that cumulated probability is less than or equal to the specified quantile.

This simple example shows that the SPMD is greatly applicable on large scale data analysis and likelihood computing. Note that the `uniroot` call is working in parallel and on distributed data, i.e. other optimization functions such as `optim` and `nlm` can be utilized in the same way, since SPMD simply assumes every processors do the same work simultaneously.

3.5. Ordinary Least Squares

The demo command is

Shell Command

```
### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 4 Rscript -e "demo(ols,'pbdDEMO',ask=F,echo=F)"
```

Ordinary least squares (OLS) is perhaps *the* fundamental tool of the statistician. The goal is to find a solution β such that

$$\|X\beta - y\|_2^2 \quad (4)$$

which is minimized. In statistics, we tend to prefer to think of the problem as being of the form

$$y = X\beta + \epsilon$$

where y is $N \times 1$ observed vector, X is $N \times p$ designed matrix which is full rank and $N \gg p$, β is the interested parameters and unknown to be estimated, and ϵ is errors and to be minimized in norm.

Note that above, we do indeed mean (in fact, stress) *a* solution to the linear least squares problem. The full story is somewhat complicated. The short explanation is that for many applications a statistician will face, expression (4) will actually have a unique solution. But this is not always the case. Indeed, it may occur that there is an infinite family of solutions. So typically we go further and demand that a solution β be such that $\|\beta\|_2$ is at least as small as the corresponding norm of any other solution (although even this does not guarantee uniqueness).

A properly thorough treatment of the problems involved here go beyond the scope of this document, and require the reader have in-depth familiarity with linear algebra. For our purposes, the concise explanation above will suffice.

The classical Maximum Likelihood solution is given by:

$$\hat{\beta} = (X^t X)^{-1} X^t y \quad (5)$$

This example can be also generalized to weighted least square (WLS), and linear mixed effect models (LME).

The implementation is straight forward as

R Code

```
mpi.ols <- function(y.spmd, X.spmd){
  if(length(y.spmd) != nrow(X.spmd)){
    stop("length(y.spmd) != nrow(X.spmd)")
  }

  t.X.spmd <- t(X.spmd)
  A <- allreduce(t.X.spmd %*% X.spmd, op = "sum")
  B <- allreduce(t.X.spmd %*% y.spmd, op = "sum")

  solve(matrix(A, ncol = ncol(X.spmd))) %*% B
} # End of mpi.ols().
```

While this is a fine demonstration of the power of “getting your hands dirty”, this approach is only efficient for small N and small p . Worse, directly computing the product

$$X^t X$$

is often numerically non-stable. Instead, it is generally better (although much slower) to take an orthogonal factorization of the data matrix. Typically, the QR-decomposition is used to this end. Here $\mathbf{X} = \mathbf{Q}\mathbf{R}$, where \mathbf{Q} is orthogonal and \mathbf{R} is upper trapezoidal. This is beneficial, because orthogonal matrices are norm-preserving, and whence

$$\begin{aligned}\|\mathbf{X}\boldsymbol{\beta} - \mathbf{y}\|_2 &= \|\mathbf{Q}\mathbf{R}\boldsymbol{\beta} - \mathbf{y}\|_2 \\ &= \|\mathbf{Q}^T\mathbf{Q}\mathbf{R}\boldsymbol{\beta} - \mathbf{Q}^T\mathbf{y}\|_2 \\ &= \|\mathbf{R}\boldsymbol{\beta} - \mathbf{Q}^T\mathbf{y}\|_2\end{aligned}$$

The (arguably) much more well-known Singular Value Decomposition can also be used to develop yet another algebraically identical solution which is quite elegant. Here, if we take $\mathbf{X} = \mathbf{U}\boldsymbol{\Sigma}\mathbf{V}^T$, then it can be shown that “the” desired solution is given by

$$\boldsymbol{\beta} = \mathbf{V}\boldsymbol{\Sigma}^+\mathbf{U}^T\mathbf{y}$$

where $\boldsymbol{\Sigma}^+$ is the Moore-Penrose pseudoinverse of $\boldsymbol{\Sigma}$. However, this approach is handily the most computationally intensive.

The method utilizing QR to find a minimum norm solution has been implemented in **pbdDMAT** for objects of class **ddmatrix**. For larger problems, and especially those where numerical accuracy is important, it may be more convenient to simply convert `y.spm` and `X.spm` into block-cyclic format as in the Part II and to utilize **pbdBASE** and **pbdDMAT** for all matrix computation.

Part II

Distributed Matrix Methods

The **pbdBASE** and **pbdDMAT** packages offer a distributed matrix class, **ddmatrix**, as well as a collection of high-level methods for performing common matrix operations. For example, if you want to compute the mean of an R matrix `x`, you would call

```
mean(x)
```

That’s exactly the same command you would issue if `x` is no longer an ordinary R matrix, but a distributed matrix. These methods range from

Unfortunately, using these higher methods comes with a different cost: getting the data into the distributed matrix class. This can be especially frustrating because we assume that the any object of class **ddmatrix** is *block cyclically distributed*. This concept is discussed at length in the **pbdBASE** vignette [Schmidt et al. \(2012d\)](#), and we do not intend to discuss the concept of a block cyclic data distribution at length herein. However, we will demonstrate several examples of getting data into and out of the distributed block cyclic matrix format.

In short, once the hurdle of getting the data into the “right format” is out of the way, these methods offer very simple syntax (designed to mimic R as closely as possible) with the ability to scale computations on very large distributed machines.

4. Random Distributed Matrices

4.1. Fixed Global Dimension

4.2. Fixed Local Dimension

5. Reading Data

5.1. SPMD to DMAT

pbdDEMO also provides reader examples

Shell Command

```
### At the shell prompt, run the demo with 2 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 2 Rscript -e "demo(spm2dmat, 'pbdDEMO', ask=F, echo=F)"
```

Shell Command

```
### At the shell prompt, run the demo with 4 processors by
### (Use Rscript.exe for windows system)
mpiexec -np 4 Rscript -e "demo(dmat_random, 'pbdDEMO', ask=F, echo=F)"
```

5.2. CSV Files

It is simple enough to read in a csv file serially and then distribute the data out to the other processors.

However, this is inefficient, especially if the user has access to a parallel file system. In this case, several processes should be used to read parts of the file, and then distribute that data out to the larger process grid.

5.3. SQL Databases

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