

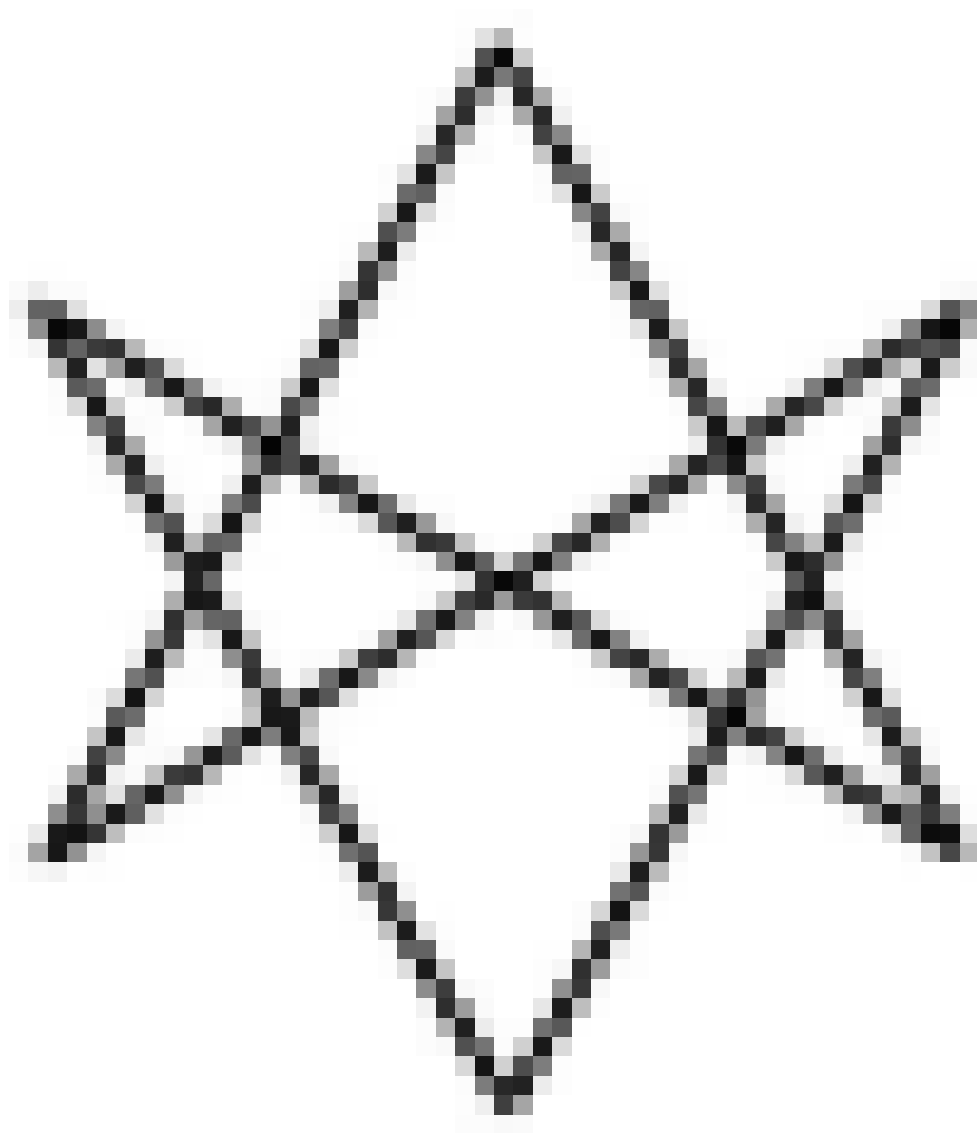
---

# GUIDE TO THE PBDML PACKAGE

---

AUGUST 11, 2020

DREW SCHMIDT  
WRATHEMATICS@GMAIL.COM



VERSION 0.1-1

## Acknowledgements and Disclaimer

Work for the **remoter** package is supported in part by the project \*Harnessing Scalable Libraries for Statistical Computing on Modern Architectures and Bringing Statistics to Large Scale Computing\* funded by the National Science Foundation Division of Mathematical Sciences under Grant No. 1418195.

Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation. The findings and conclusions in this article have not been formally disseminated by the U.S. Department of Health & Human Services nor by the U.S. Department of Energy, and should not be construed to represent any determination or policy of University, Agency, Administration and National Laboratory.

The **remoter** logo comes from the image “[Tradtelefon-illustration](#)”. Licensed under Public Domain via Commons.

This manual may be incorrect or out-of-date. The author(s) assume no responsibility for errors or omissions, or for damages resulting from the use of the information contained herein.

This publication was typeset using L<sup>A</sup>T<sub>E</sub>X.

# Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Installation . . . . .	1
<b>2</b>	<b>Dimension Reduction</b>	<b>1</b>
2.1	FLD . . . . .	1
2.2	Randomized SVD/PCA . . . . .	1
2.3	Decomp/Recomp . . . . .	3
<b>3</b>	<b>Legal</b>	<b>4</b>
<b>4</b>	<b>References</b>	<b>4</b>

# 1 Introduction

[3] [5] [1]

## 1.1 Installation

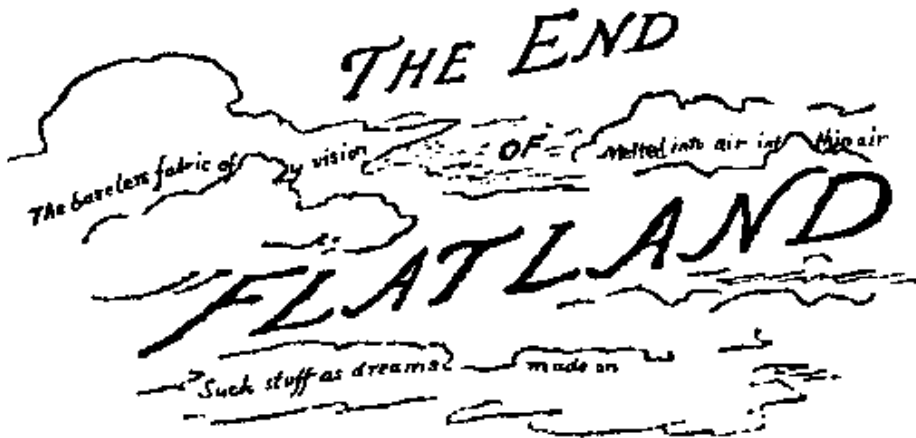
You can install the stable version from CRAN using the usual `install.packages()`:

```
install.packages("pbdML")
```

The development version is maintained on GitHub, and can easily be installed by any of the packages that offer installations from GitHub:

```
#### Pick your preference
devtools::install_github("RBigData/pbdML")
ghit::install_github("RBigData/pbdML")
remotes::install_github("RBigData/pbdML")
```

## 2 Dimension Reduction



“Be patient, for the world is broad and wide.” Image from *Flatland*

### 2.1 FLD

TODO

### 2.2 Randomized SVD/PCA

The singular value decomposition (SVD) is a matrix factorization, with numerous applications.

$$A = U\Sigma V^T$$

An application of the SVD well-known to statisticians is principal components analysis (PCA) [4].

A common technique is to compute the first 2 or 3 principal components in order to visualize high-dimensional data.

Estimation [2]

To show how this works, we generate a  $30000 \times 5000$  matrix with 3 different separate clusters:

```
gen <- function(m, n, mean, sd) matrix(rnorm(m*n, mean, sd), m, n)
```

```
m <- 10000
```

```
n <- 5000
```

```
sd <- 10
```

```
x1 <- gen(m, n, 0, sd)
```

```
x2 <- gen(m, n, 4, sd)
```

```
x3 <- gen(m, n, -2, sd)
```

```
x <- rbind(x1, x2, x3)
```

```
library(pbdML)
```

```
system.time({
```

```
  pc <- rpca(x, k=2)
```

```
})
```

```
## user system elapsed
```

```
## 8.908 4.028 11.674
```

Compare this to the full PCA computation:

```
system.time({
```

```
  pc.full <- prcomp(x)
```

```
})
```

```
## user system elapsed
```

```
## 644.632 159.220 240.094
```

The size comparisons are even more striking:

```
library(memuse)
```

```
memuse(x)
```

```
## 1.118 GiB
```

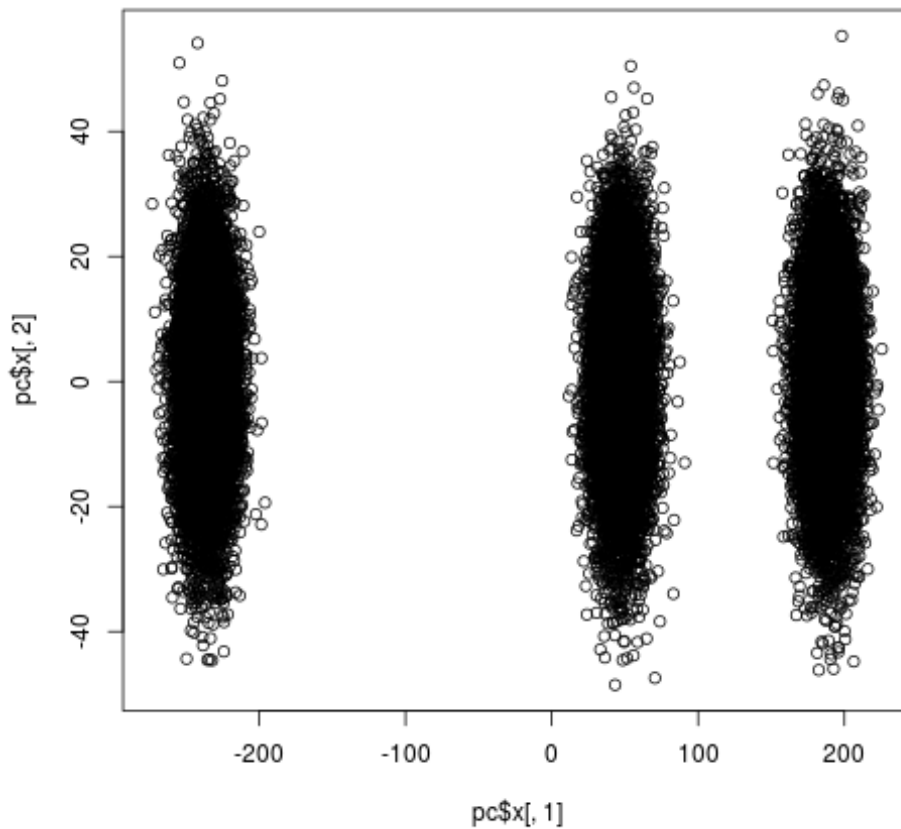
```
memuse(pc)
```

```
## 548.773 KiB
```

```
memuse(pc.full)
```

```
## 1.304 GiB
```

```
plot(pc$x[, 1], pc$x[, 2])
```



### 2.3 Decomp/Recomp

One day on Twitter, someone asked a very interesting question:



**Ahmed Moustafa**

@AhmedMoustafa

Help please on how to rebuild the matrix  
after excluding some principal components  
from a PCA analysis? #statistics #rstats  
#bioinformatics

6:10 AM - 22 Sep 2015

After some requests for clarification, the problem was stated as follows:



**Ahmed Moustafa**  
@AhmedMoustafa

@wrathematics I mean, is it possible to exclude the variance contributed by certain PCs from the original matrix?

7:36 AM - 22 Sep 2015

### 3 Legal

©2016–2017 Drew Schmidt.

Permission is granted to make and distribute verbatim copies of this vignette and its source provided the copyright notice and this permission notice are preserved on all copies.

Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation. The findings and conclusions in this article have not been formally disseminated by the U.S. Department of Health & Human Services nor by the U.S. Department of Energy, and should not be construed to represent any determination or policy of University, Agency, Administration and National Laboratory.

This manual may be incorrect or out-of-date. The authors assume no responsibility for errors or omissions, or for damages resulting from the use of the information contained herein.

### 4 References

#### References

- [1] Wei-Chen Chen, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu. pbdMPI: Programming with big data – interface to MPI, 2012. R Package, URL <http://cran.r-project.org/package=pbdMPI>.
- [2] Nathan Halko, Per-Gunnar Martinsson, and Joel A Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions. *SIAM review*, 53(2):217–288, 2011.
- [3] G. Ostrouchov, W.-C. Chen, D. Schmidt, and P. Patel. Programming with Big Data in R, 2012.
- [4] A.C. Rencher. *Methods of Multivariate Analysis*. Wiley series in probability and mathematical statistics. Probability and mathematical statistics. John Wiley & Sons, 2002.
- [5] Drew Schmidt, Wei-Chen Chen, George Ostrouchov, and Pragneshkumar Patel. pbdDMAT: Programming with big data – distributed matrix algebra computation, 2012. R Package.