

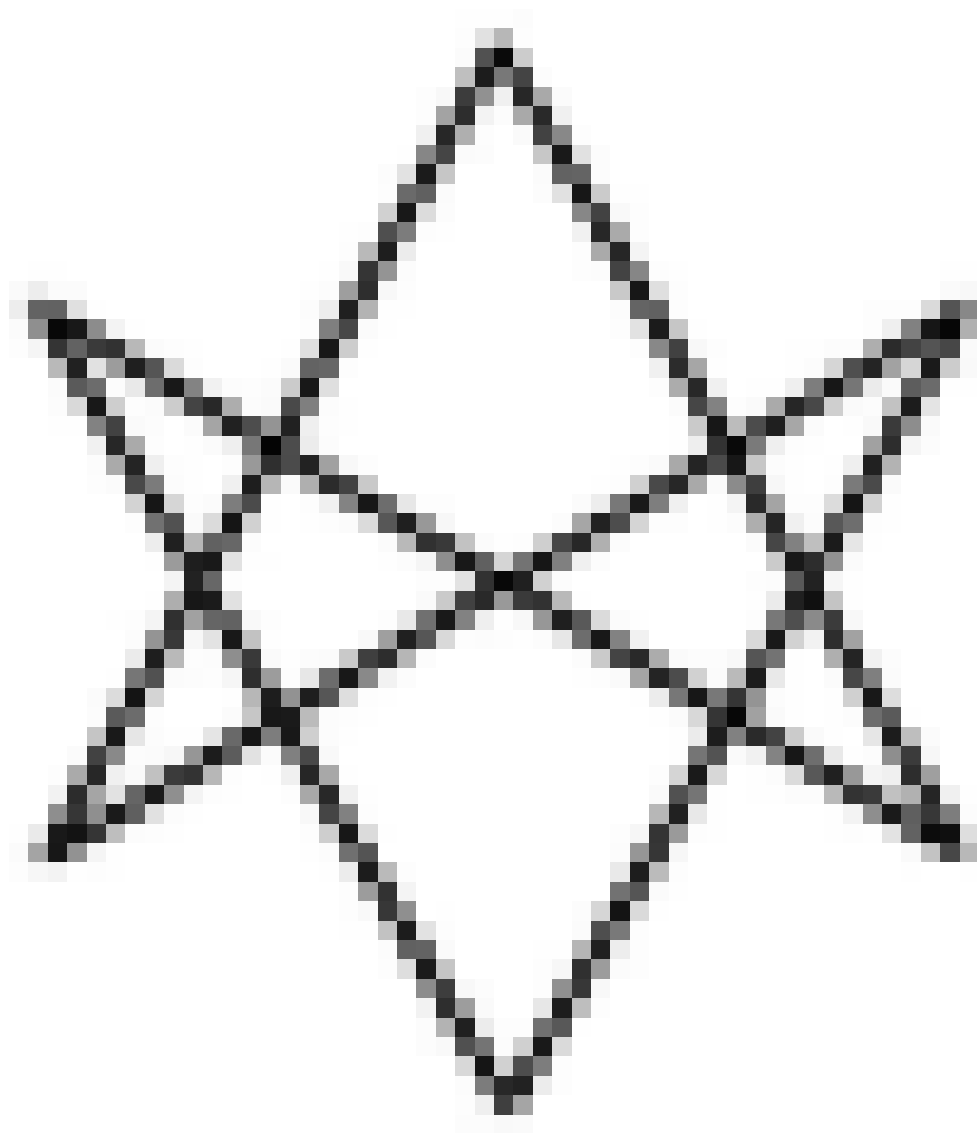
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# GUIDE TO THE PBDML PACKAGE

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VERSION 0.1-1

## Acknowledgements and Disclaimer

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# 1 Introduction

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## 1.1 Installation

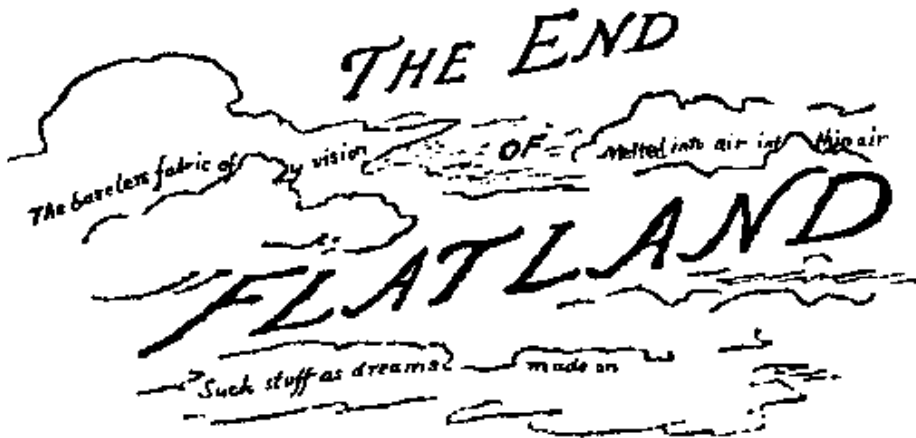
You can install the stable version from CRAN using the usual `install.packages()`:

```
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
```

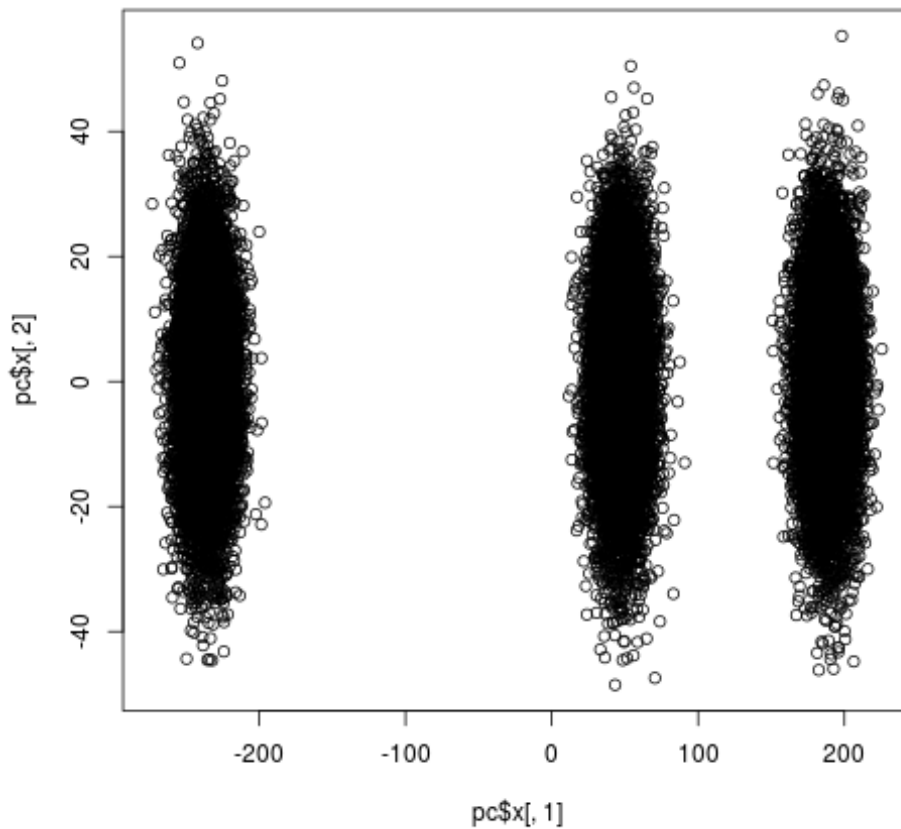
```
memuse(pc)
```

```
## 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

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### 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>.
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- [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.