

# The package {bigstatsr}: memory- and computation-efficient tools for big matrices stored on disk

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Slides: <https://privefl.github.io/RR18/bigstatsr.html>

# Introduction & Motivation

# About

I'm a PhD Student (2016-2019) in **Predictive Human Genetics** in Grenoble.

Disease  $\sim$  DNA mutations + ...



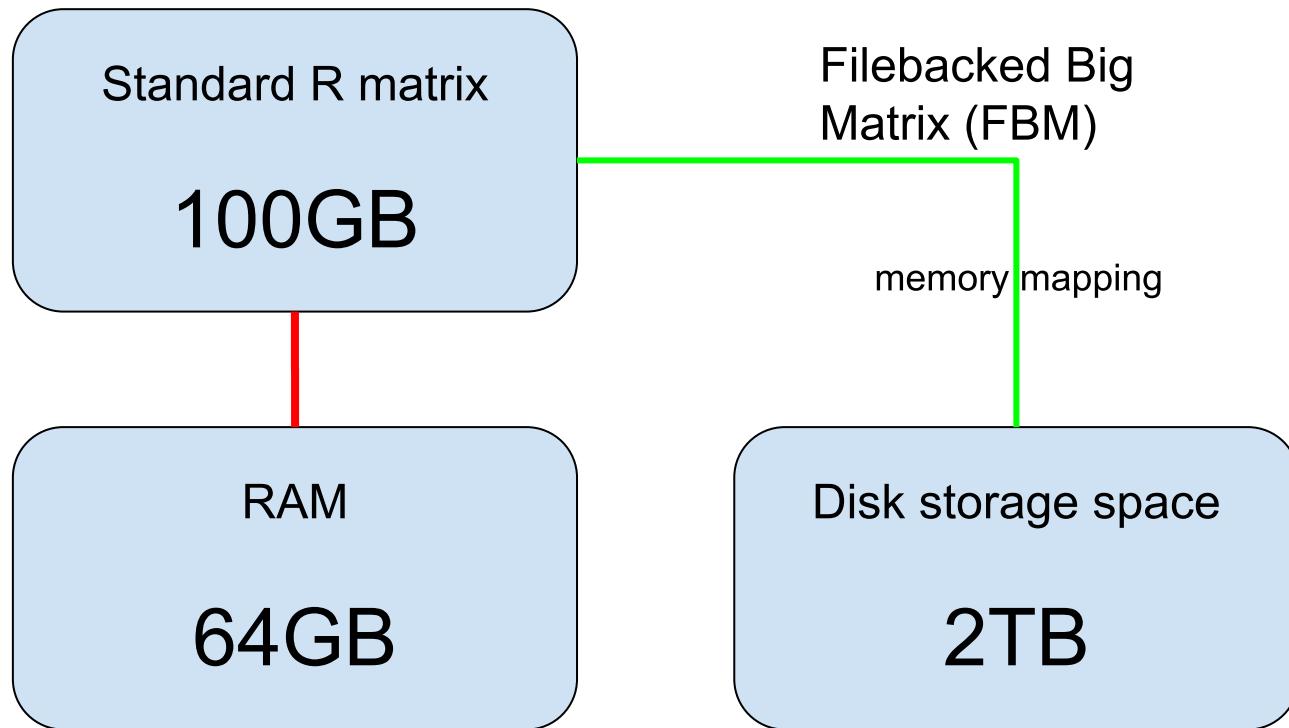
# Analyze very large genotype matrices

- previously: 15K x 280K, **celiac disease** (~30GB)
- currently: 500K x 500K, **UK Biobank** (~2TB)



But I still want to use ..

# The solution I found



Format FBM is very similar to format `filebacked.big.matrix` from package `{bigmemory}` (details in [this vignette](#)).

# Simple accessors

# Similar accessor as R matrices

```
X <- FBM(2, 5, init = 1:10, backingfile = "test")
```

```
X$backingfile
```

```
## [1] "/home/privef/Bureau/RR18/test.bk"
```

```
X[, 1] ## ok
```

```
## [1] 1 2
```

```
X[1, ] ## bad
```

```
## [1] 1 3 5 7 9
```

```
X[] ## super bad
```

```
## [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3    5    7    9
## [2,]    2    4    6    8   10
```

# Similar accessor as R matrices

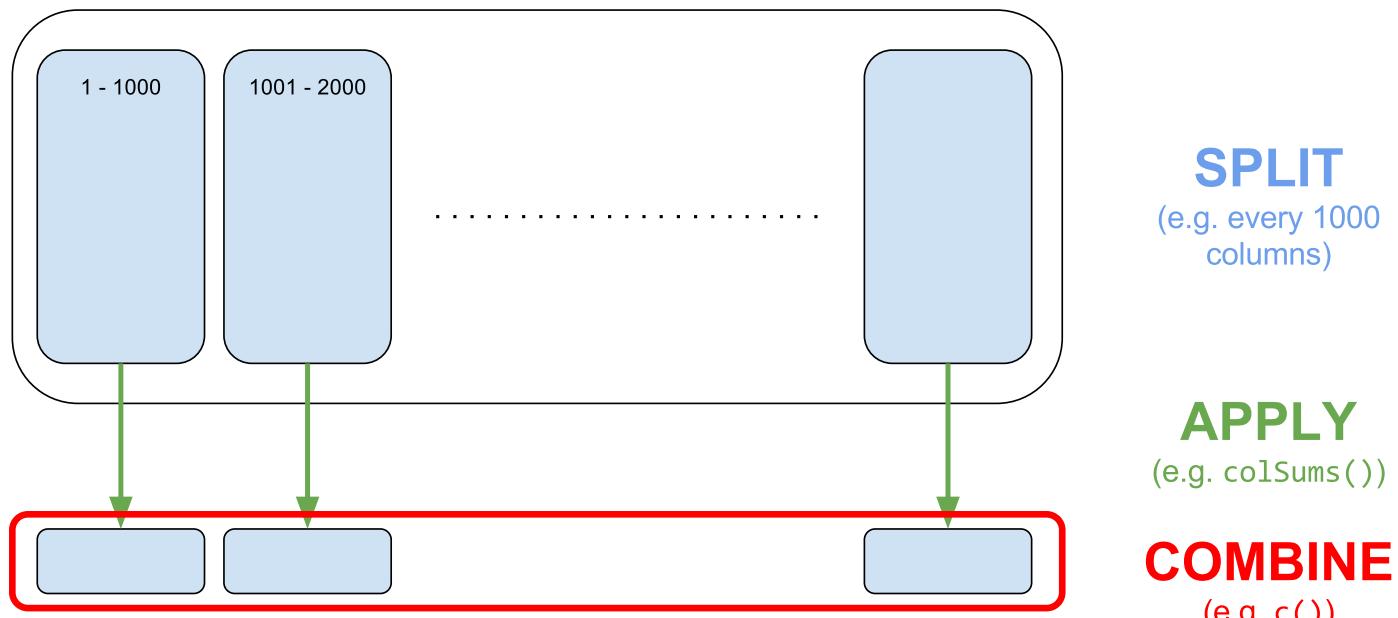
```
colSums(X[]) ## super bad
```

```
## [1] 3 7 11 15 19
```



# Split-(par)Apply-Combine Strategy

Apply standard R functions to big matrices (in parallel)



Implemented in `big_apply()`.

# Similar accessor as Rcpp matrices

```
// [[Rcpp::depends(BH, bigstatsr)]]
#include <bigstatsr/BMAcc.h>

// [[Rcpp::export]]
NumericVector big_columns(Environment BM) {

    XPtr<FBM> xpBM = BM["address"];
    BMAcc<double> macc(xpBM);

    size_t n = macc.nrow();
    size_t m = macc.ncol();

    NumericVector res(m);

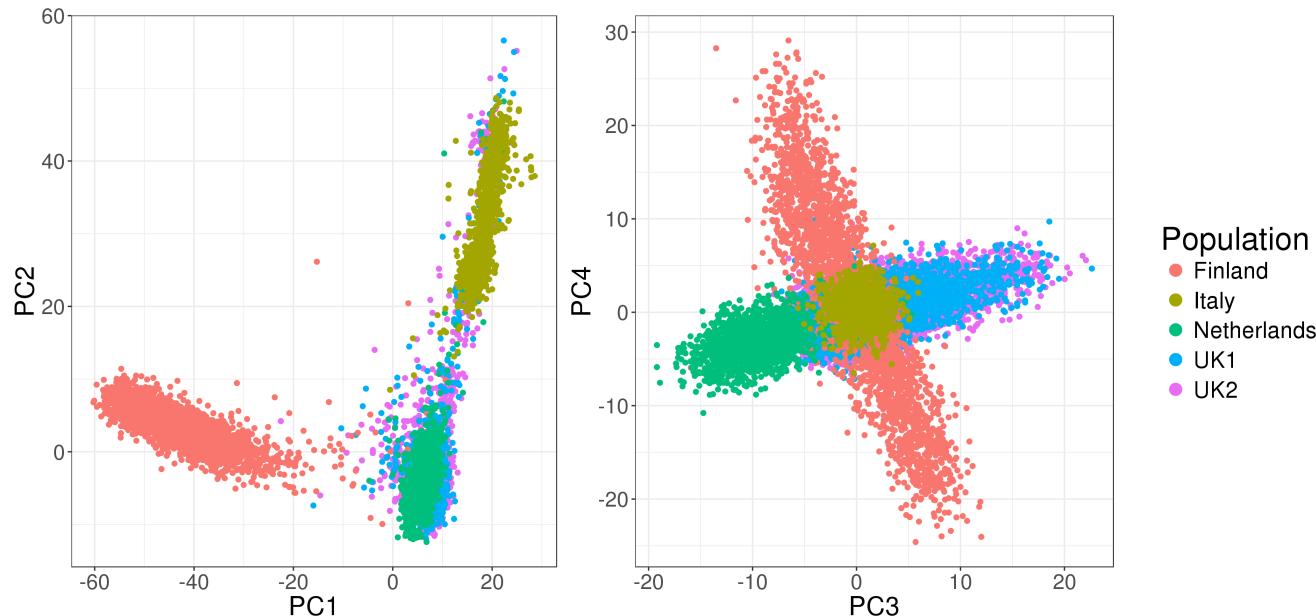
    for (size_t j = 0; j < m; j++)
        for (size_t i = 0; i < n; i++)
            res[j] += macc(i, j);

    return res;
}
```

Some examples  
from my work

# Partial Singular Value Decomposition

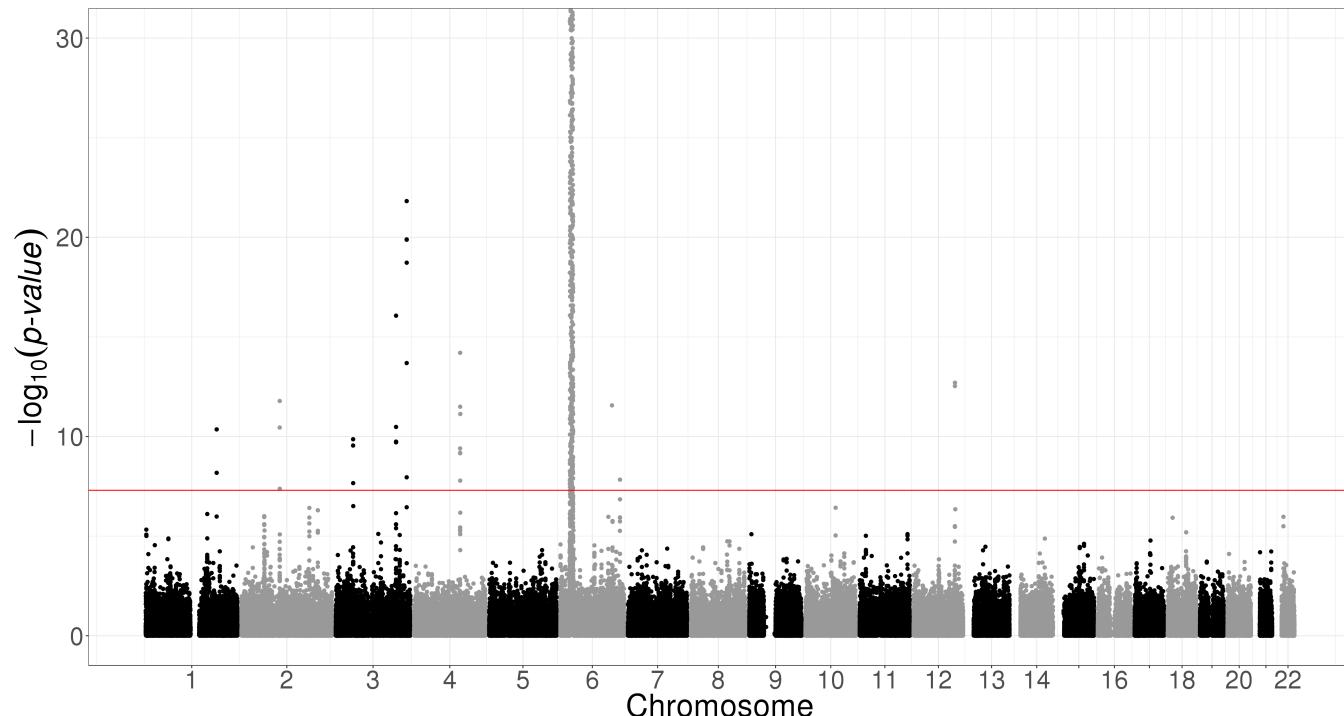
$15K \times 100K$  -- 10 first PCs -- 6 cores -- **1 min** (vs 2h in base R)



Implemented in `big_randomSVD()`, powered by R packages `{RSpectra}` and `{Rcpp}`.

# Multiple association testing

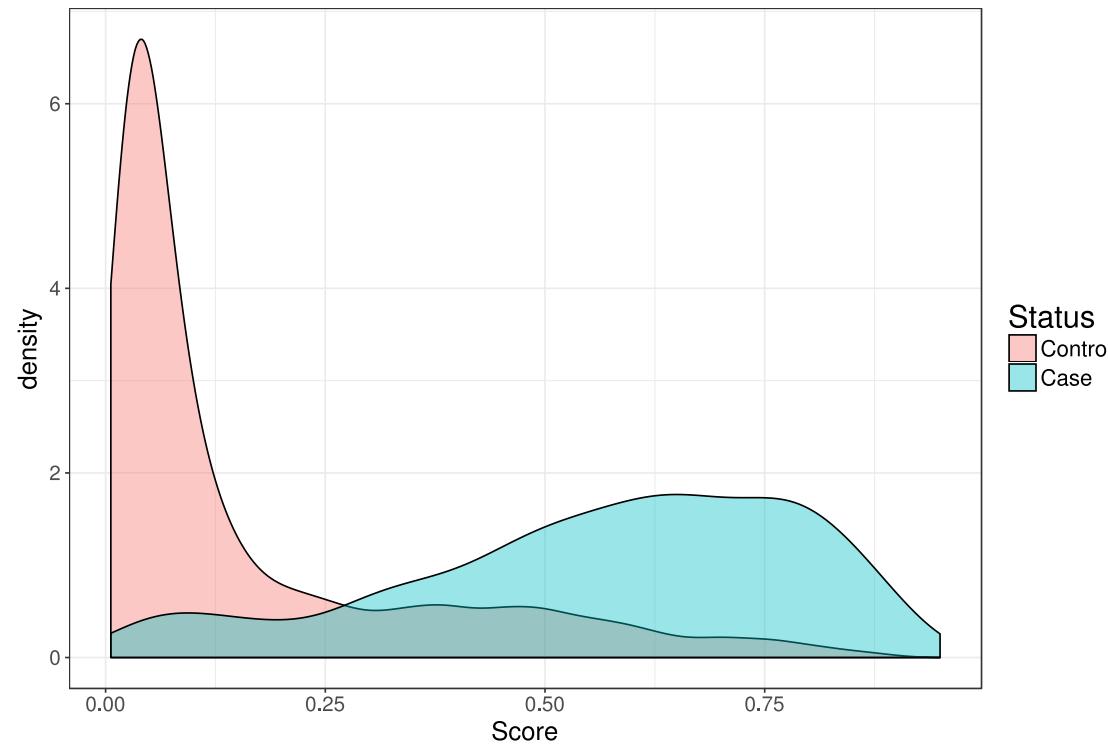
Which DNA mutations are associated with one disease?



# Sparse linear models

Predicting complex diseases via penalized logistic regression

$15K \times 280K$  -- 6 cores -- 2 min



# Conclusion

I'm able to run algorithms

on 100GB of data

in  on my computer

# Advantages of using FBM objects

- you can apply algorithms on **data larger than your RAM**,
- you can easily **parallelize** your algorithms because the data on disk is shared,
- you write **more efficient algorithms** (you do less copies and think more about what you're doing),
- you can use **different types of data**, for example, in my field, I'm storing my data with only 1 byte per element (rather than 8 bytes for a standard R matrix). See [the documentation of the FBM class](#) for details.

# R Packages

**Efficient analysis of large-scale genome-wide data  
with two R packages: bigstatsr and bigsnpr **

Florian Privé , Hugues Aschard, Andrey Ziyatdinov, Michael G B Blum 

*Bioinformatics*, bty185, <https://doi.org/10.1093/bioinformatics/bty185>

- {bigstatsr}: to be used by any field of research
- {bigsnpr}: algorithms specific to my field of research

# Contributors are welcomed!



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# Make sure to grab an hex sticker



# Thanks!

Presentation: <https://privefl.github.io/RR18/bigstatsr.html>

Package's website: <https://privefl.github.io/bigstatsr/>

DOI: [10.1093/bioinformatics/bty185](https://doi.org/10.1093/bioinformatics/bty185)



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