

# The R package **bigstatsr**: Memory- and Computation- Efficient Tools for Big Matrices

useR!2017 lightning talk

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# About

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

$\text{Disease} \sim \text{DNA mutations}$





# Very large genotype matrices

- currently: 15K x 300K, **celiac disease**
- soon: 500K x 800K, **UK Biobank**



# Problem I had

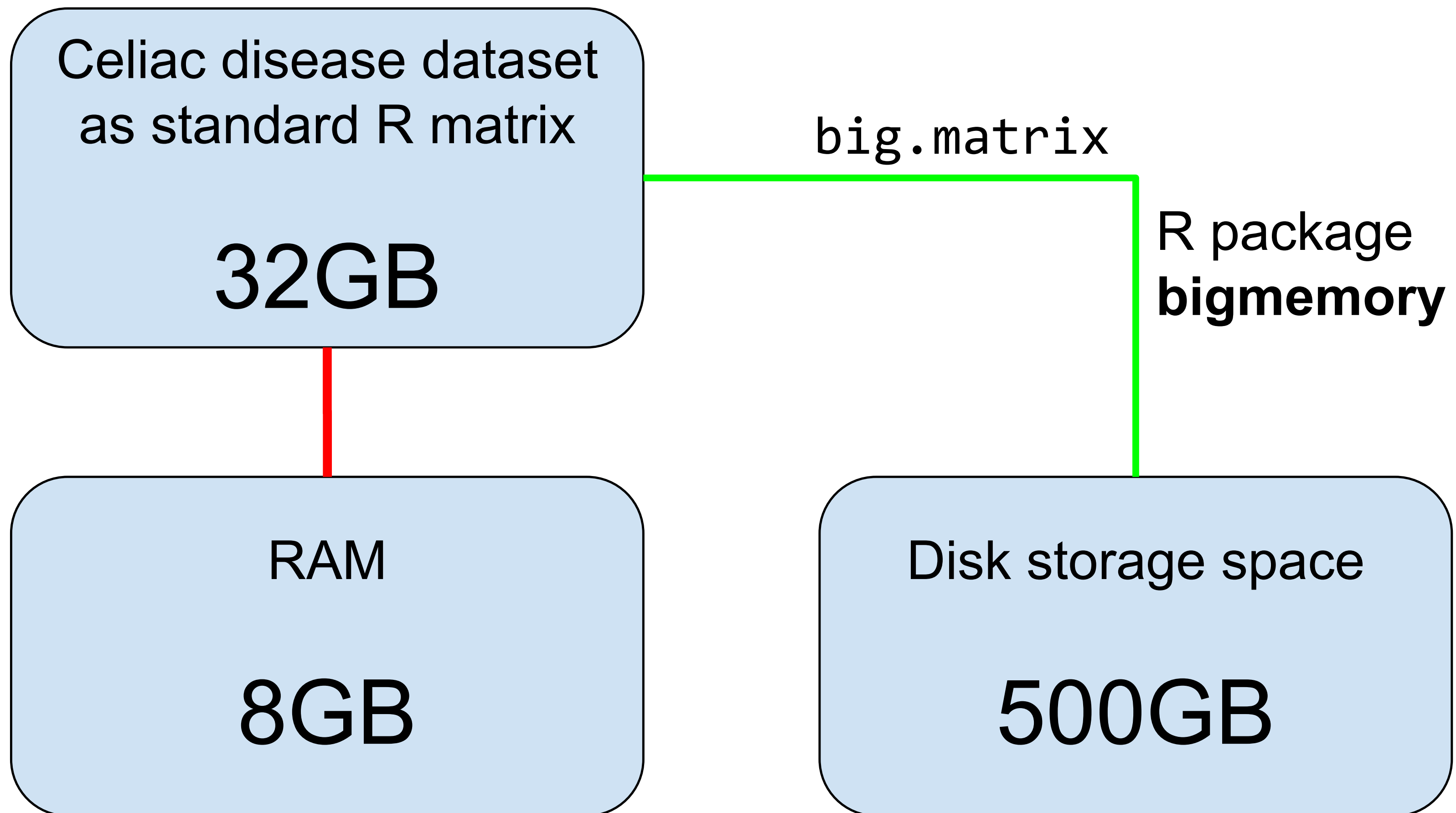
Celiac disease dataset  
as standard R matrix

**32GB**

RAM

**8GB**

# Solution I found



Michael J. Kane, John Emerson, Stephen Weston (2013).

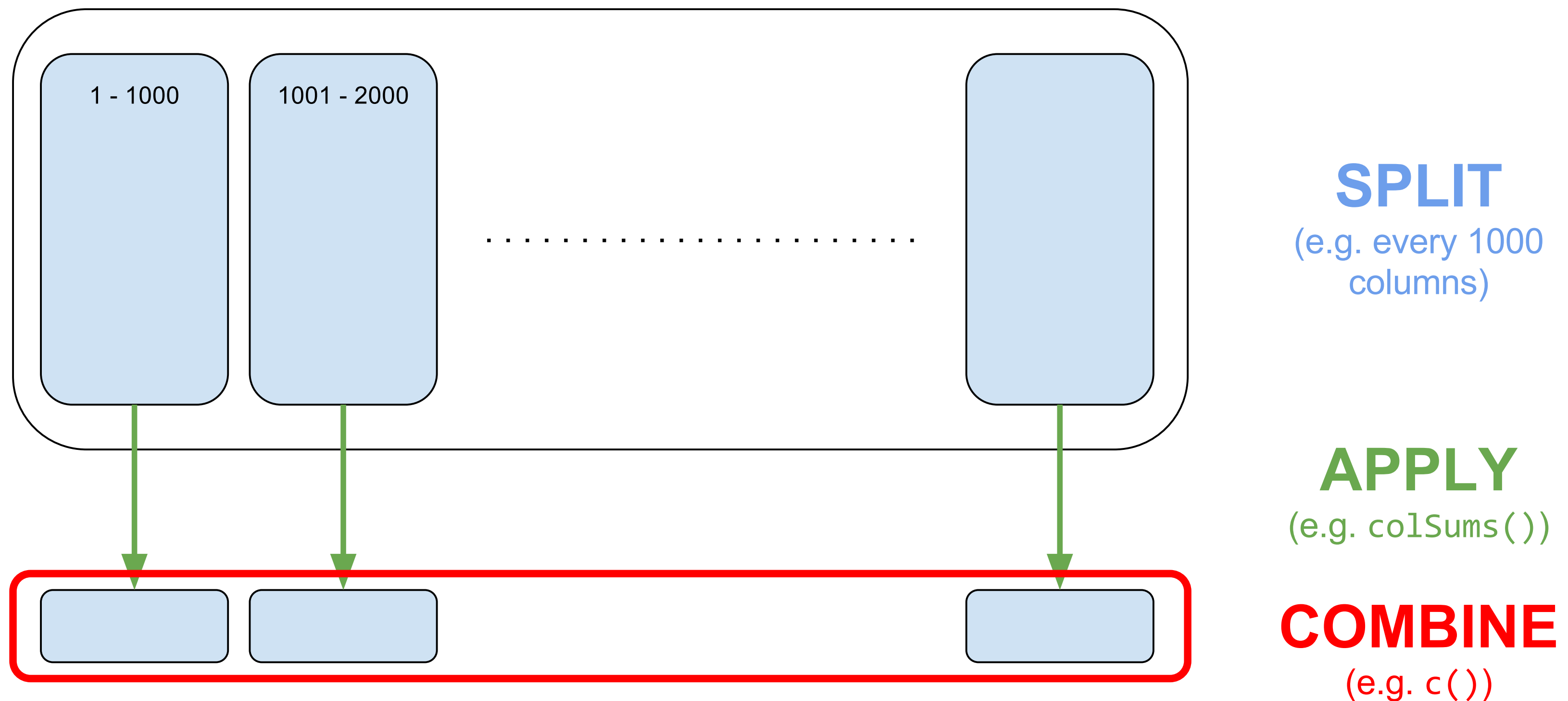
# Accesses almost as if the matrix were in memory

- in **R**: accesses with `[]`, as standard R matrices,
- in **Rcpp**: accesses single elements with `X(i, j)`, as standard Rcpp matrices.



# Split-(par)Apply-Combine Strategy

Apply standard R functions to big matrices (in parallel)



strategy coined by Hadley Wickham (2011)

# Matrix operations

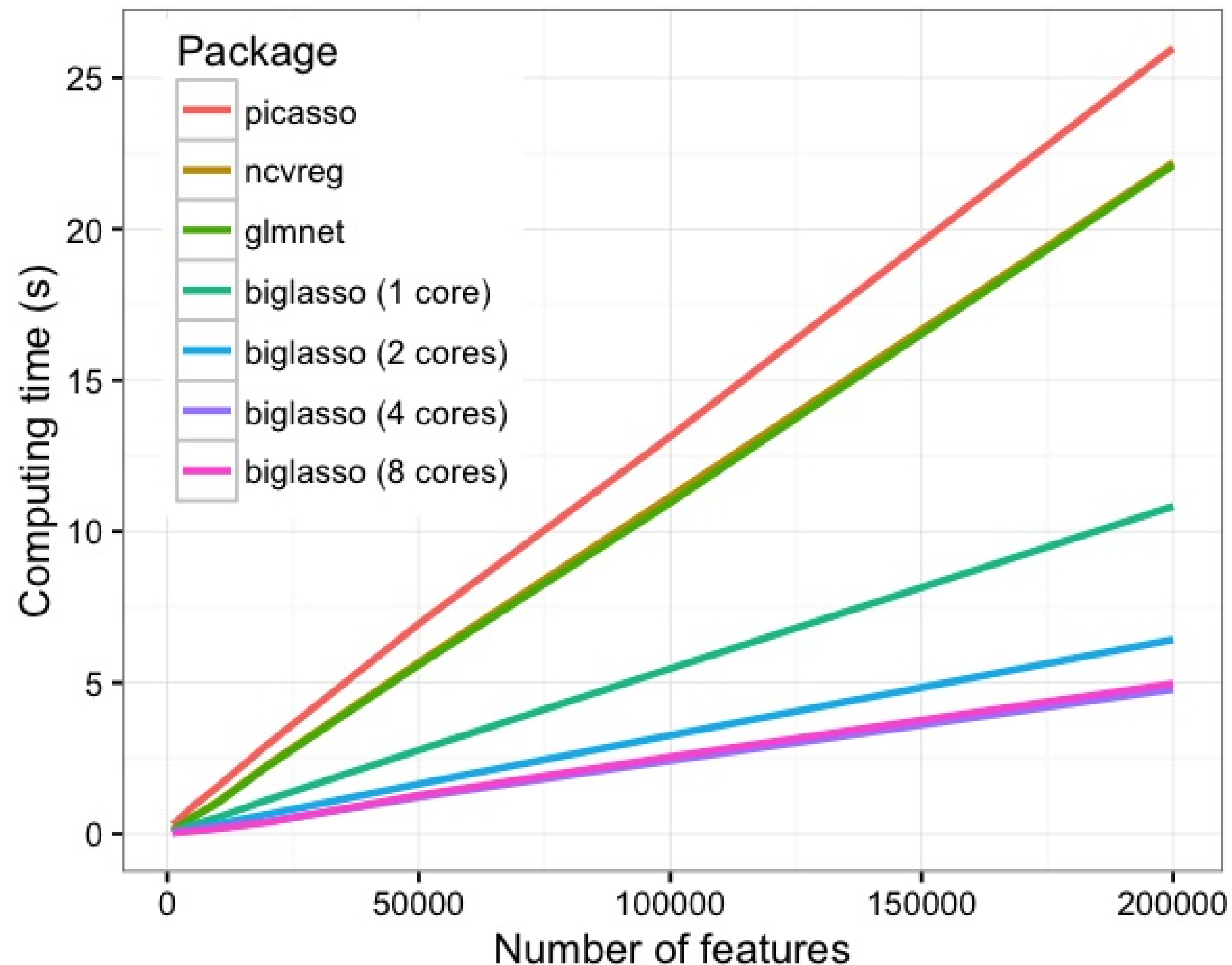
- (cross-)products with matrices/vectors
- special tricks for handling scaling ([vignette](#) and [blog post](#))

Example: computation of correlation of a 100,000 x 5000 matrix

- `cor`: 22 minutes
- `big_cor`: 1 minute

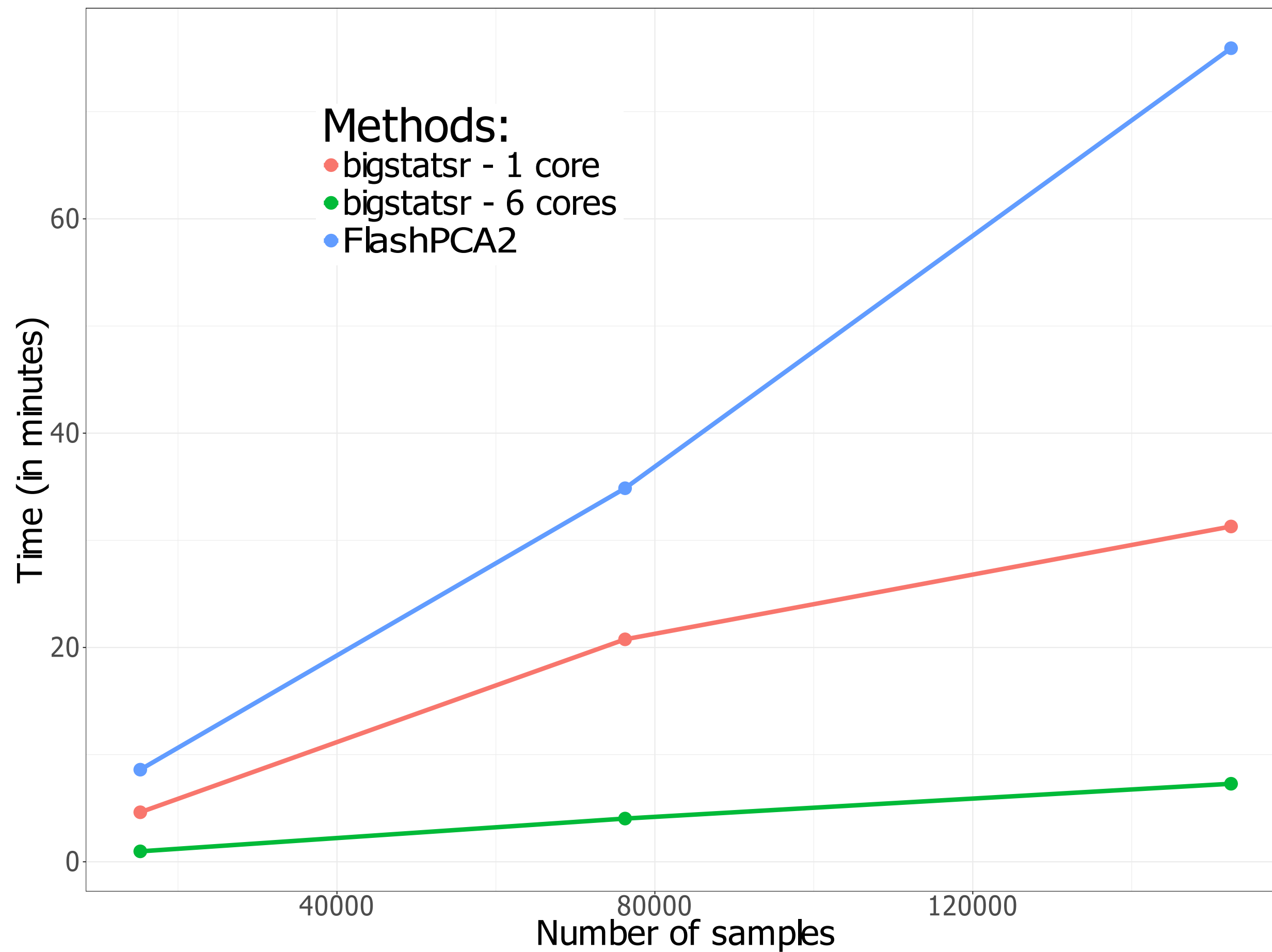


# Sparse linear models: **biglasso**



Zeng, Y., and Breheny, P. (2017).

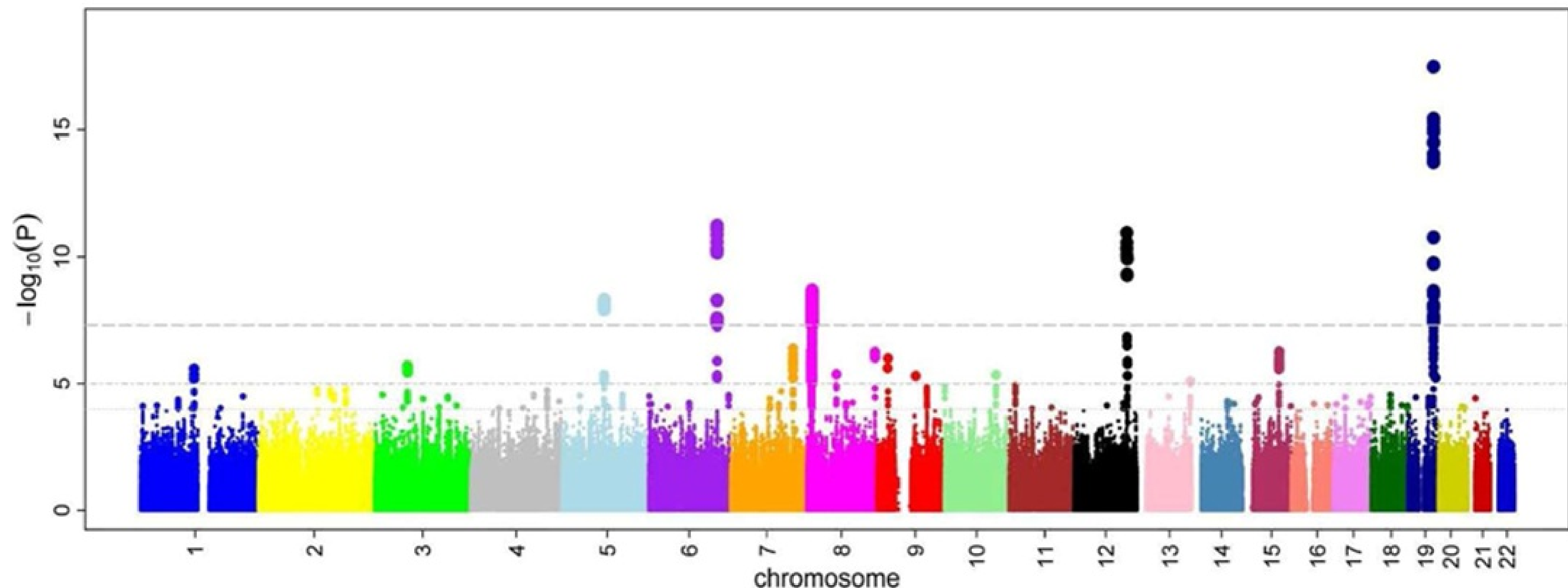
# Partial Singular Value Decomposition



based on R package **RSpectra**

# Test association of each variable with an outcome

In genetics, this is called a Genome-Wide Association Study (GWAS)





I'm now able  
to run algorithms  
on 100GB of data

# R Packages

bigmemory	`big.matrix` object
<b>bigstatsr</b>	Statistical functions for `big.matrix` objects <b>to be used by any field</b>
bigsnpr	Specific functions for SNP arrays

Paper in preparation: "Efficient management and analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr".



# Contributors are welcomed!





# Thanks!

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

Twitter and GitHub: [@privefl](#)

Presentation available online: <https://goo.gl/nNg0hw>

Slides created via the R package **xaringan**.