

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.

Disease \sim DNA mutations

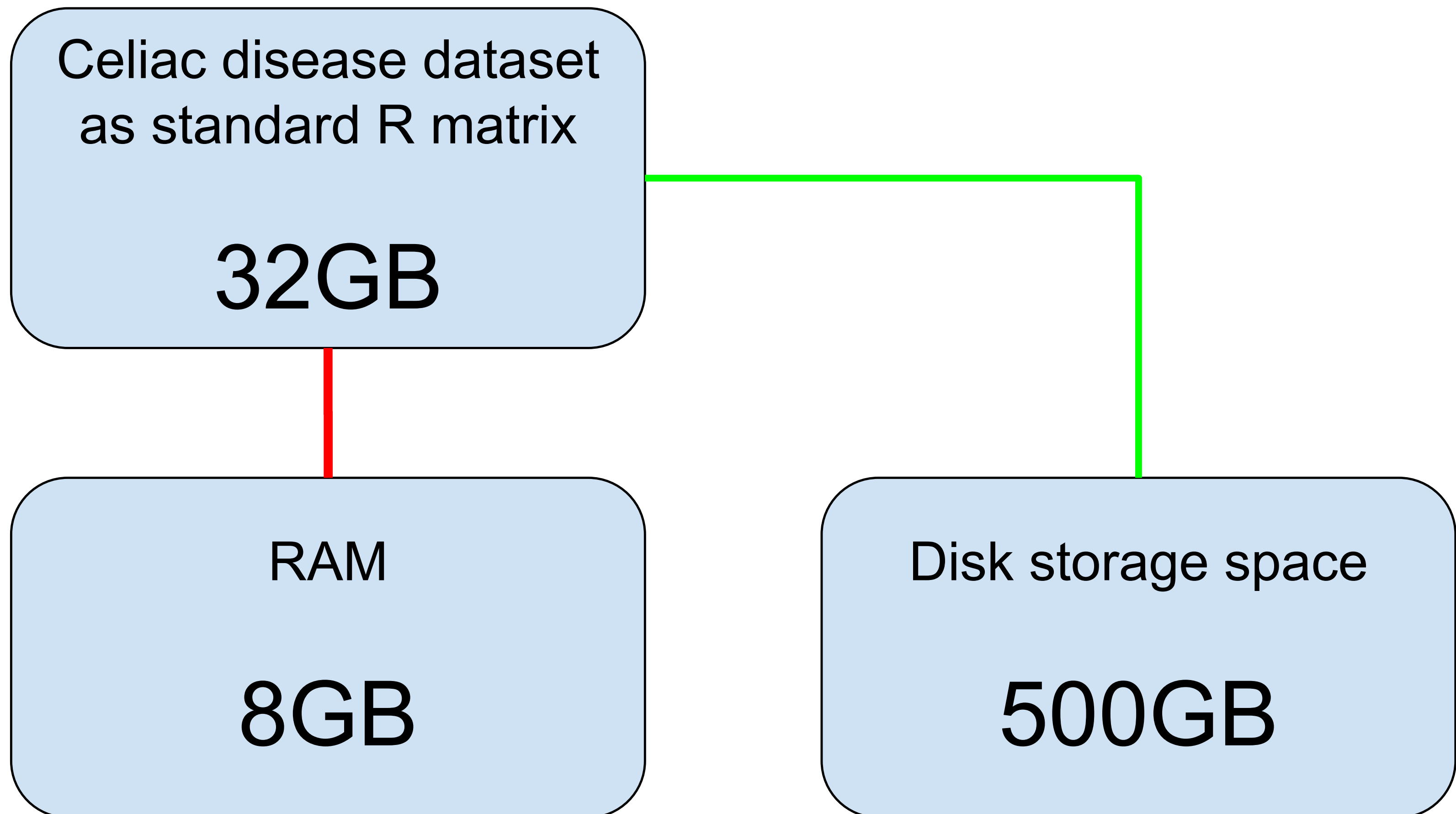


Very large genotype matrices

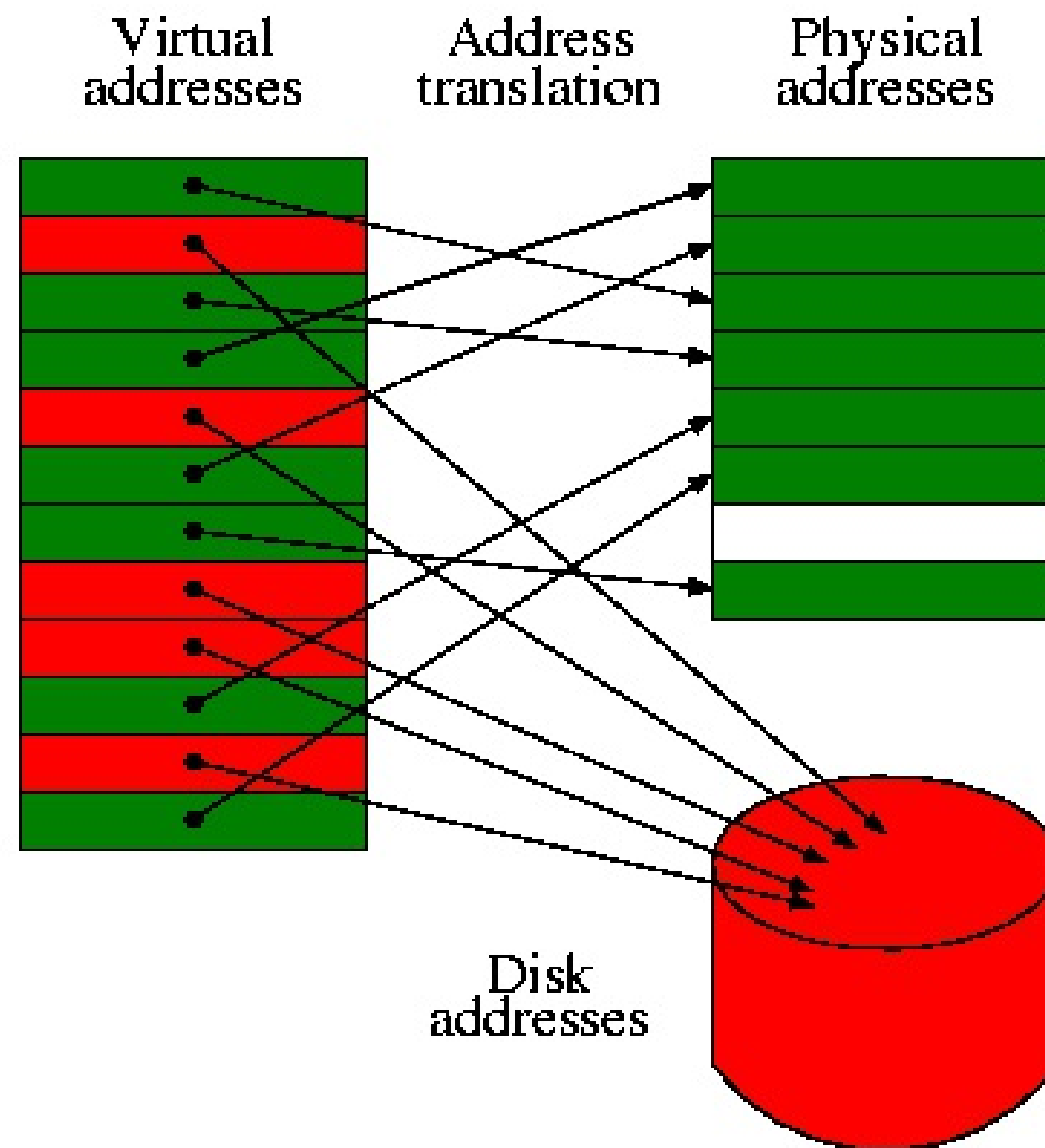
- currently: 15K x 300K, celiac disease
- soon: 500K x 800K, UK Biobank



Problem I had



Solution I found: R package bigmemory



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

Dependencies on bigmemory

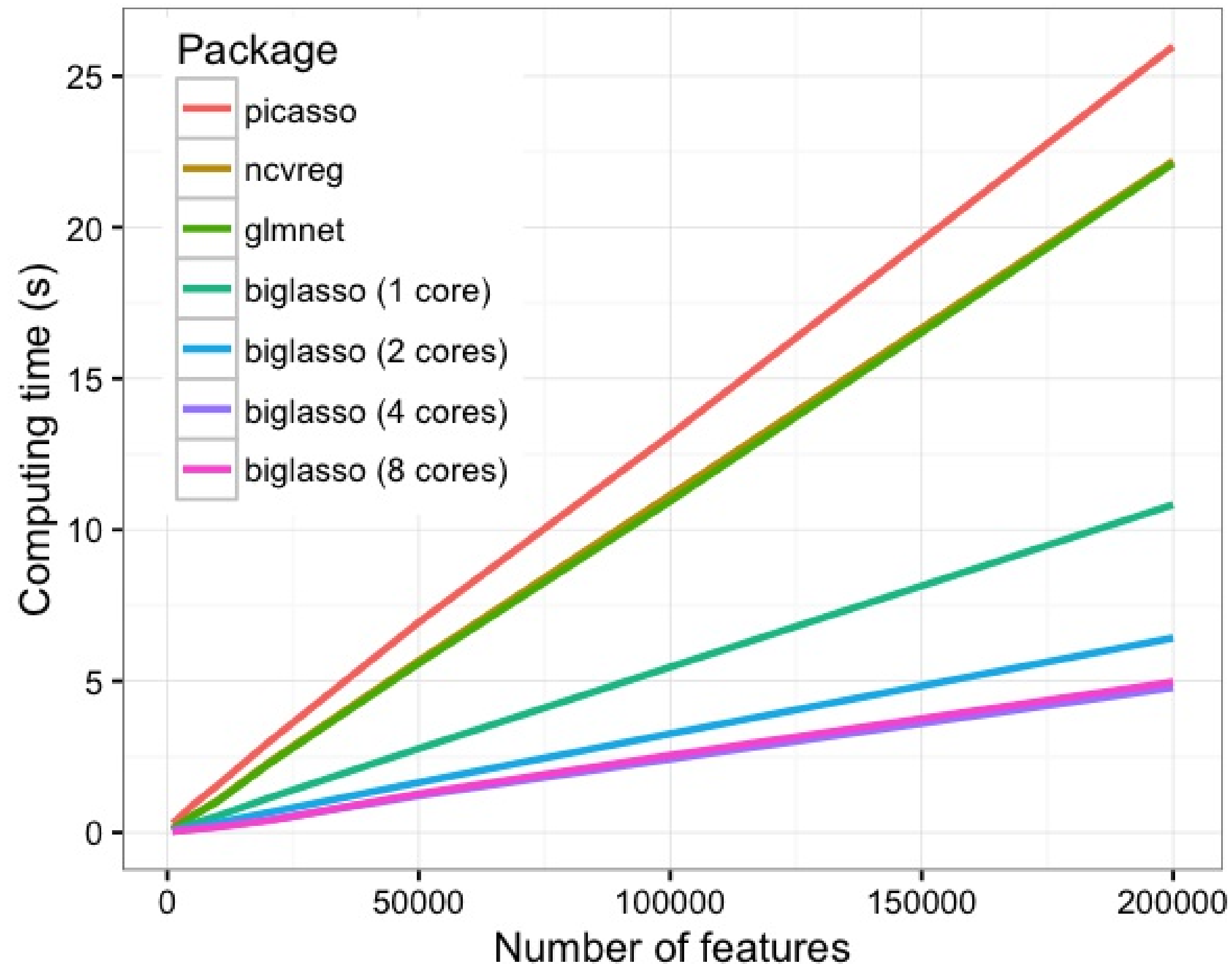
Reverse depends: [bigalgebra](#), [biganalytics](#), [bigFastlm](#), [bigKRLS](#),
[biglasso](#), [bigpca](#), [bigtabulate](#), [GHap](#), [oem](#)

Reverse imports: [BGData](#), [bigstep](#), [CollapsABEL](#), [cooccurNet](#),
[geneSLOPE](#), [kangar00](#), [mbest](#), [misclassGLM](#),
[multiplyr](#), [Rdsm](#), [s2dverification](#), [slimrec](#), [startR](#)

Reverse linking to: [bigalgebra](#), [biganalytics](#), [bigFastlm](#), [bigKRLS](#),
[biglasso](#), [bigtabulate](#), [oem](#), [sgd](#)

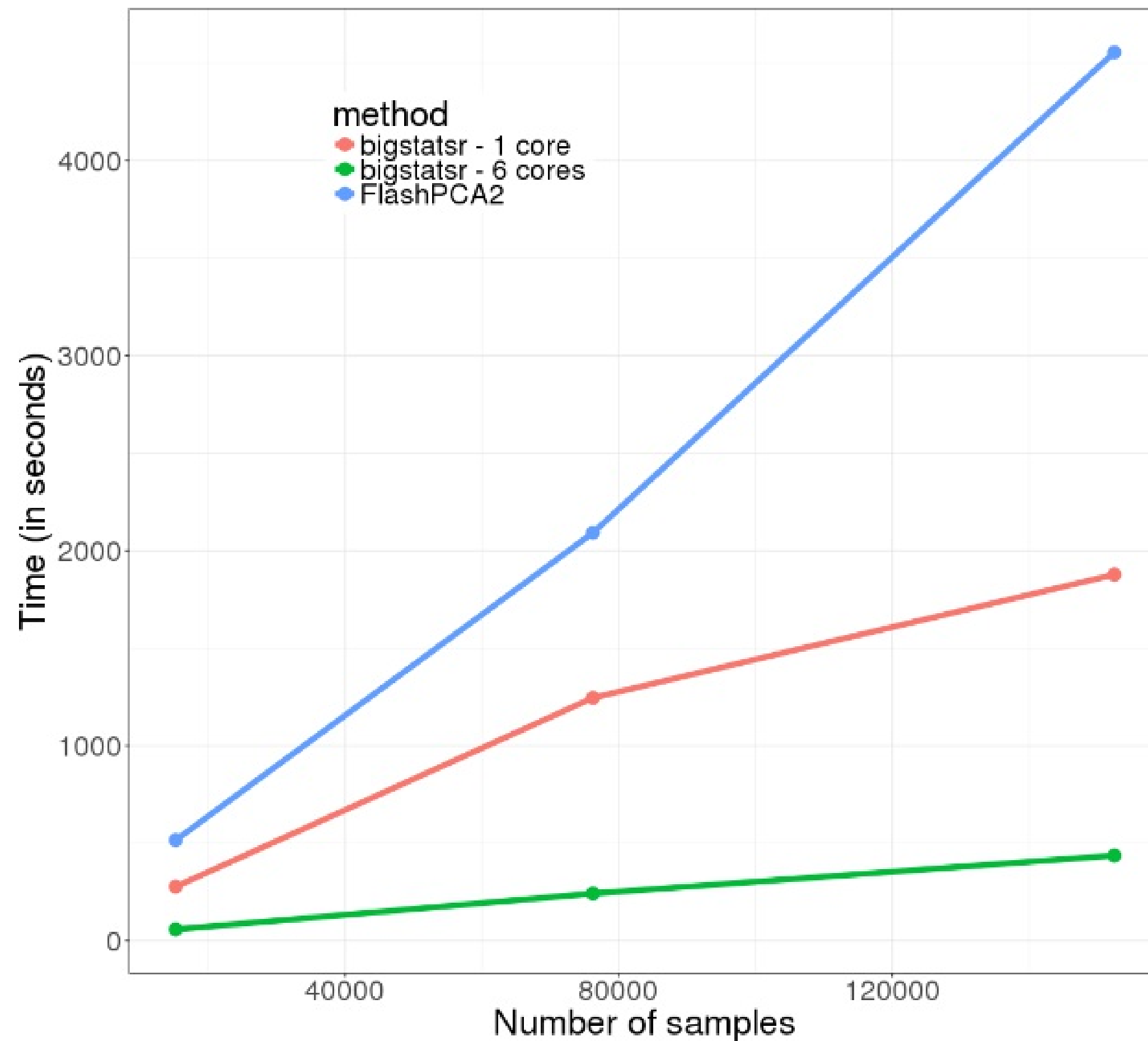
Reverse suggests: [bio3d](#), [filematrix](#), [matpow](#), [mlDNA](#), [nat.nblast](#),
[NetRep](#), [NMF](#), [PopGenome](#), [rsgcc](#), [sgd](#)

Sparse linear models: biglasso



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

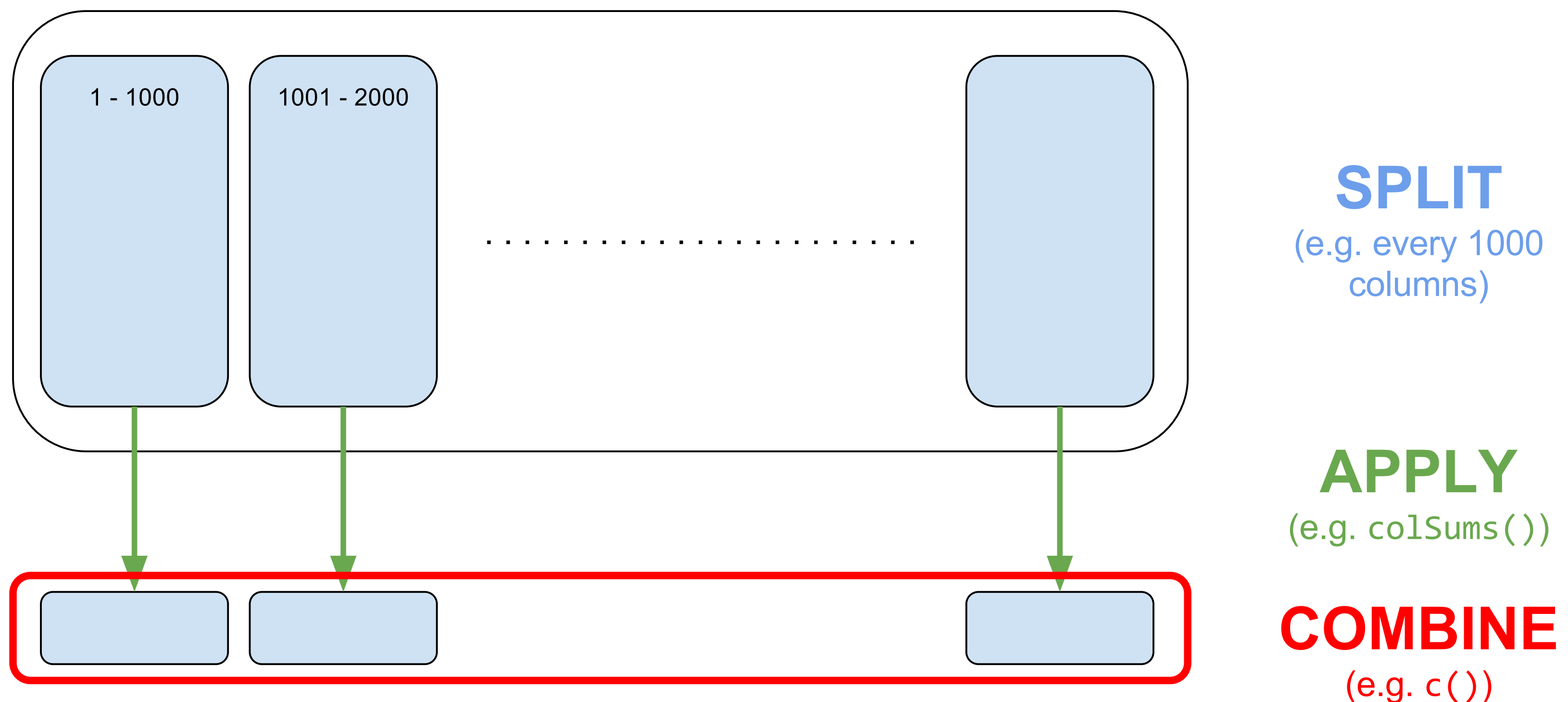
Partial Singular Value Decomposition



based on R package **RSpectra**

Split-(par)Apply-Combine Strategy

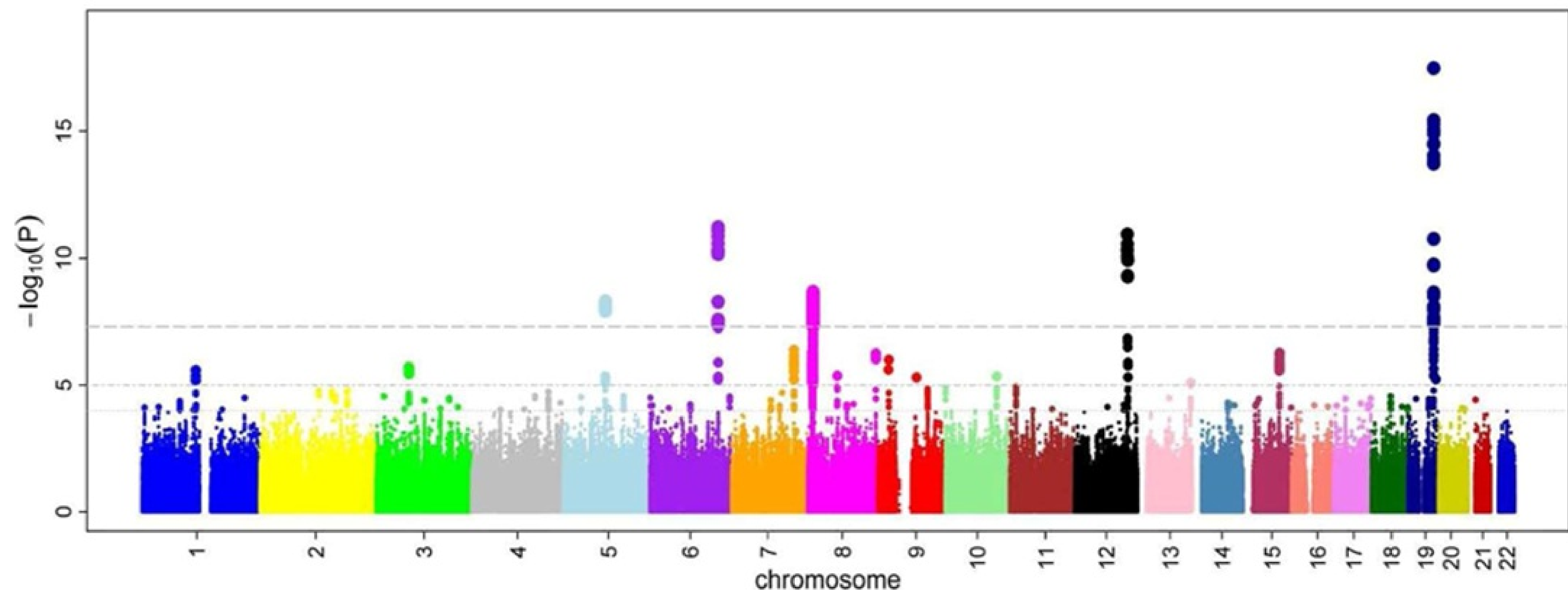
Apply standard R functions to big matrices (in parallel)



strategy coined by Hadley Wickham (2011)

Test association of each column with an outcome

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



Manhattan plot

R Packages

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

I'm now able
to run algorithms
on hundreds of
Gigabytes of data

Any contributor is 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**.