Journée des doctorants

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Outline

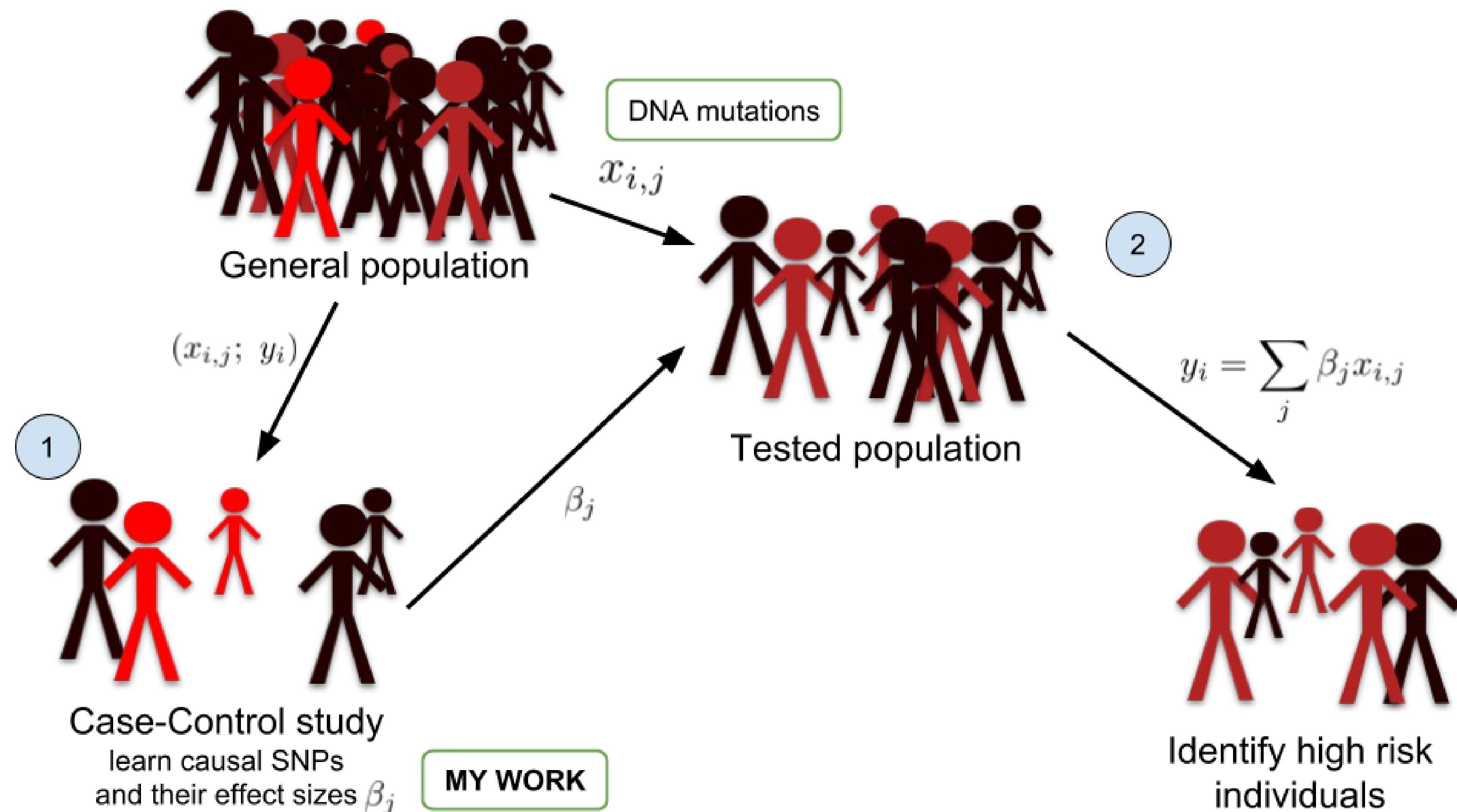1. Main objective of the thesis

2. R packages

3. Ongoing paper

4. Future work

Main objective

Compute Polygenic Risk Scores (PRS)

in order to identify high risk individuals

General population

DNA mutations

$x_{i,j}$

$(x_{i,j};\ y_i)$

1

Case-Control study
learn causal SNPs
and their effect sizes β_j

MY WORK

β_j

Tested population

2

$y_i = \sum_j \beta_j x_{i,j}$

Identify high risk
individuals

4 main difficulties

- Size of the data (dozens to hundreds of GB)

- Hundreds of thousands of correlated variables (variables with overlapping information)

- Generalization of models on different populations

- Integration of non-genetic data in the models

Big Data

Simpler solutions are easier to implement

What I want to be able to do

Data analysis on large-scale genotype matrices!

- Be fast to test many ideas quickly

    - code should be fast
    - I shouldn't have to make many conversions
    - it should be easily to combine multiple functions

- Not be restricted in my analysis

    - Basically use all I already know in R

- Work on my computer

    - I have 64 GB of RAM and 12 cores
    - Working on a server is not as easy as on my computer

Smooth and fast analysis!

Two R packages: bigstatsr and bigsnpr

## Statistical tools with big matrices stored on disk

- **bigstatsr** for many types of matrix, to be used by any field of research

- **bigsnpr** for functions that are specific to the analysis of genetic data

Submitted Manuscripts

STATUS	ID	TITLE	CREATED	SUBMITTED
Pending decision	BIOINF-2017-1798.R1	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr View Submission	31-Jan-2018	02-Feb-2018

Comparative performance

Computing partial SVD
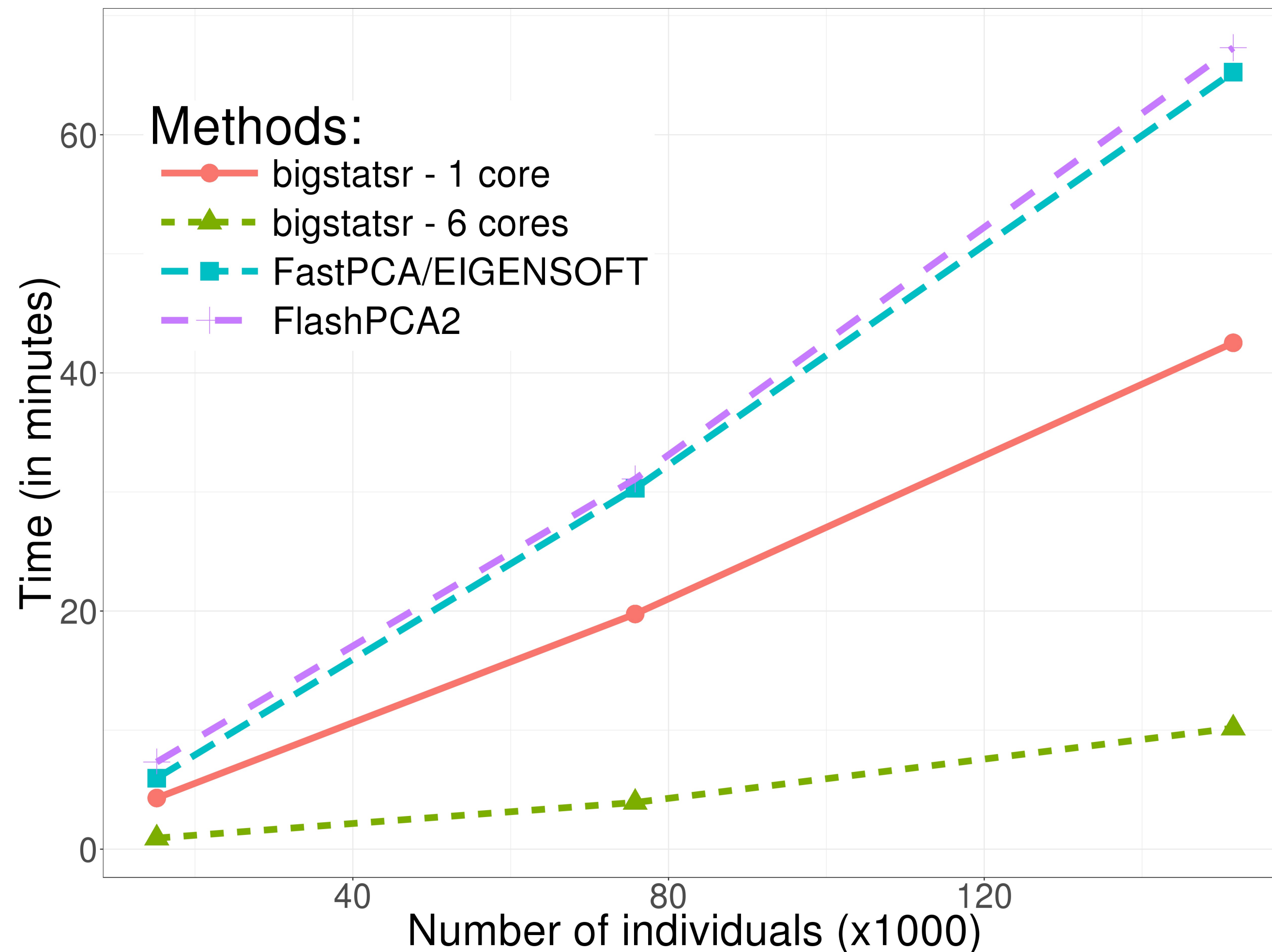
Ongoing paper

Comparison of methods for computing PRS

(will be submitted by the end of April)

Recall of what we want to achieve

Predict a phenotype: pitfalls of the widely-used model

- Weights learned independently

- Correlation is taken care of heuristically

- Regularization is taken care of heuristically

A better solution?

We can use **statistical learning methods**.

For example, we can use logistic regression on all variables at once by using a clever implementation.

Future work

UK Biobank

UK Biobank

It is an extremely large dataset with

- genetic data

- clinical data

- environmental data

Prospects

- [Paper 3, before the end of 2018] training in one population to improve training and prediction in another population

- [Paper 4, in 2019, while writing the thesis] assess how can we combine the information provided by genetic data with clinical and environmental data, possibly in a non-linear way

- find a job in Machine Learning in some company

Thanks!

Presentation available at

https://privefl.github.io/thesis-docs/JDD.html

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