

Sociogenomics

ACADEMIC YEAR 2021/2022.

Introduction

Nicola Barban



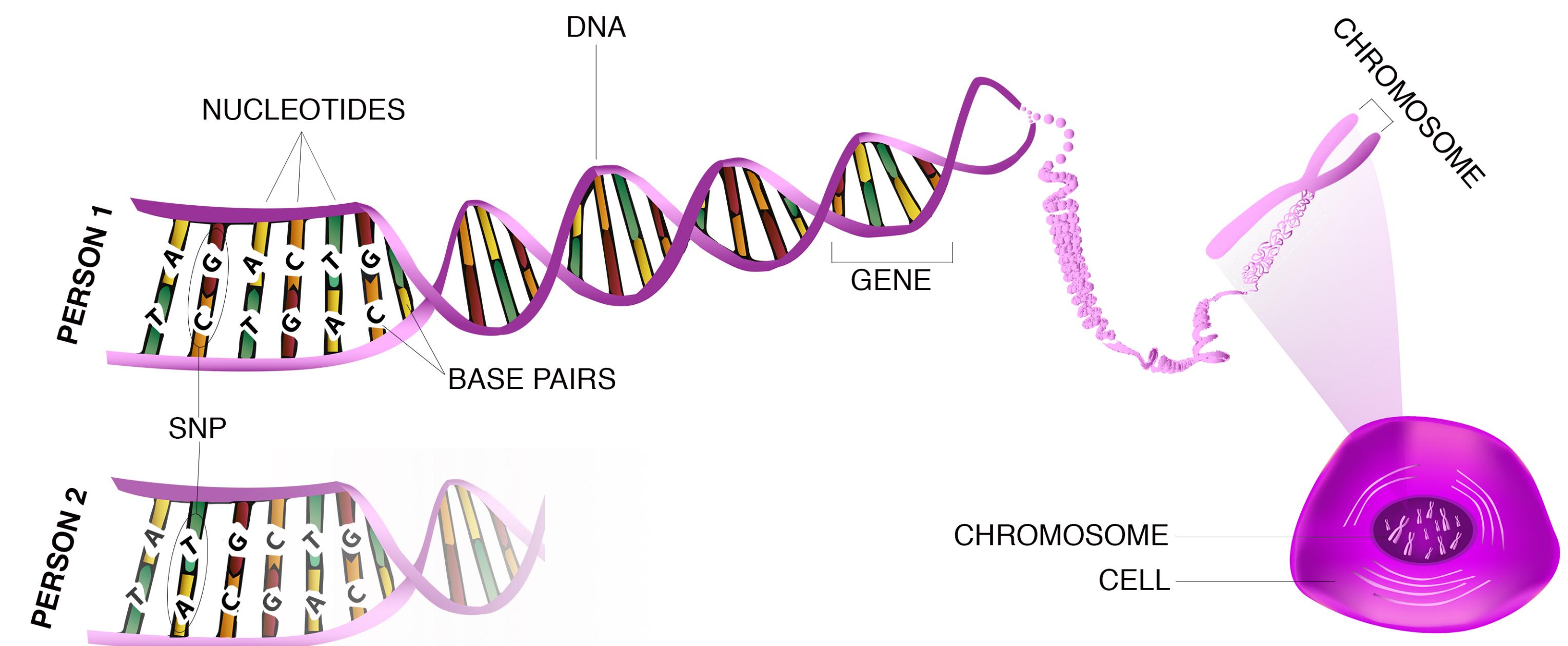
Outline

1. Why a course on “sociogenomics” ?
2. Learning objectives
3. Course Structure
4. Evaluation
5. Resources

1. Why a course on “sociogenomics” ?

The relevance of Human Genetics in the post-genomic era

Human Genetics is now relevant **beyond biology**, epidemiology and the medical sciences, with applications in psychology, psychiatric, statistics, demography, sociology and economics.



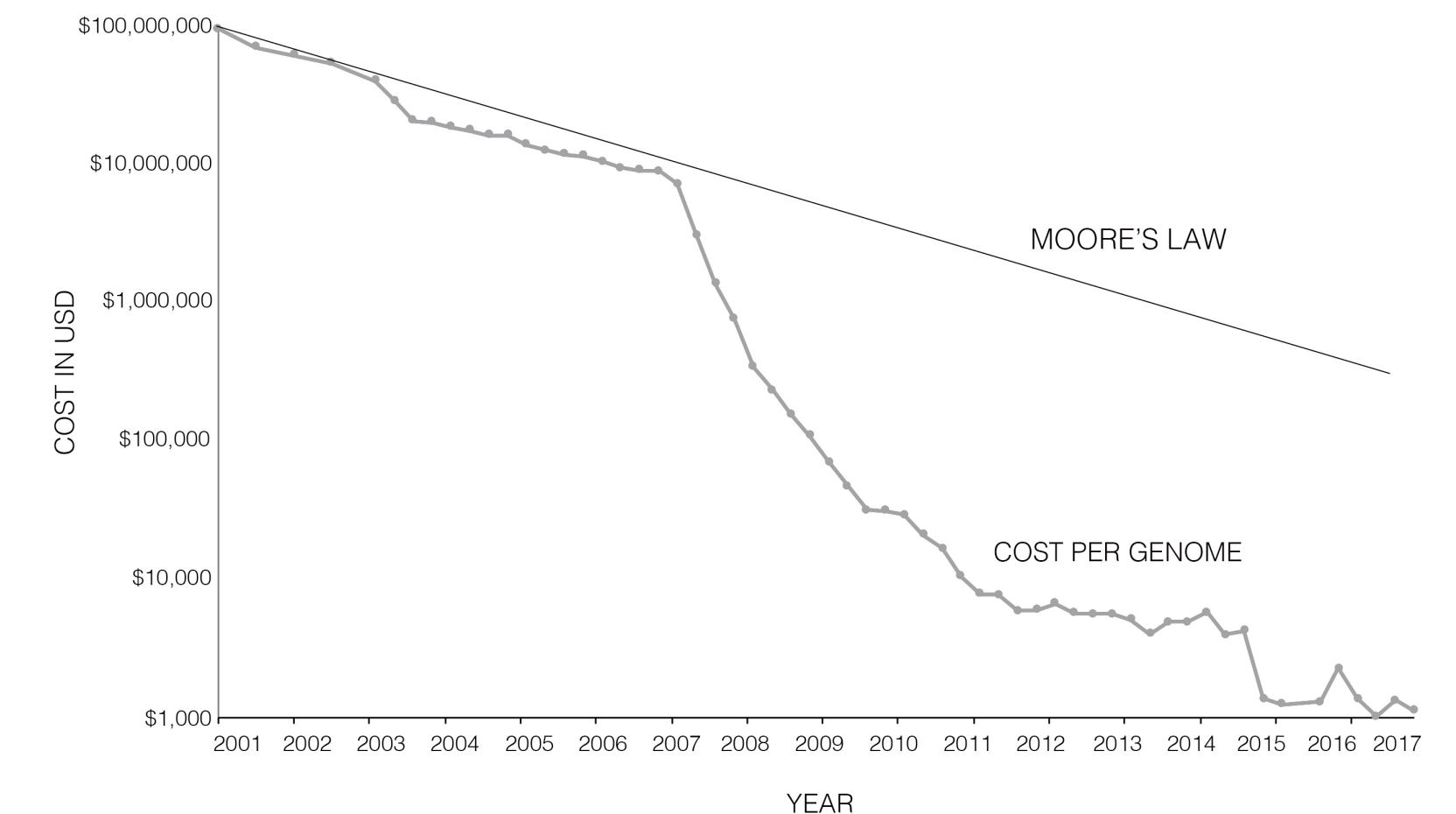


Give the most meaningful
gift this season

50% Off Health + Ancestry Kit

[Shop now](#)

Offer ends November 29.
Limit 3 kits.



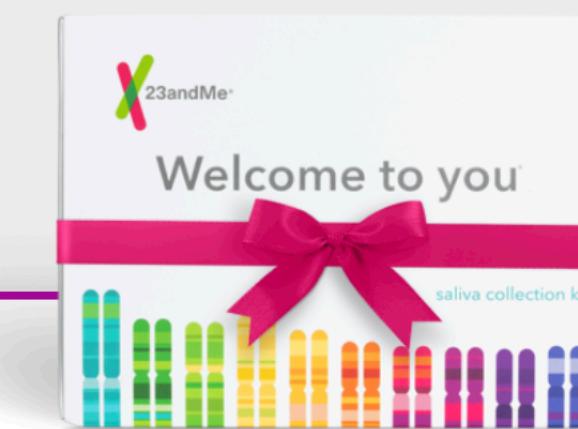
Ancestry + Traits Service

~~\$99~~ \$79



Health + Ancestry Service

~~\$199~~ \$99



23andMe+ Membership

~~\$199~~
\$99
+
~~\$29~~
\$9.99
kit
one year prepaid
membership

Ancestry Composition

Summary

Scientific Details

Frequently Asked Questions



Italy

Highly Likely Match

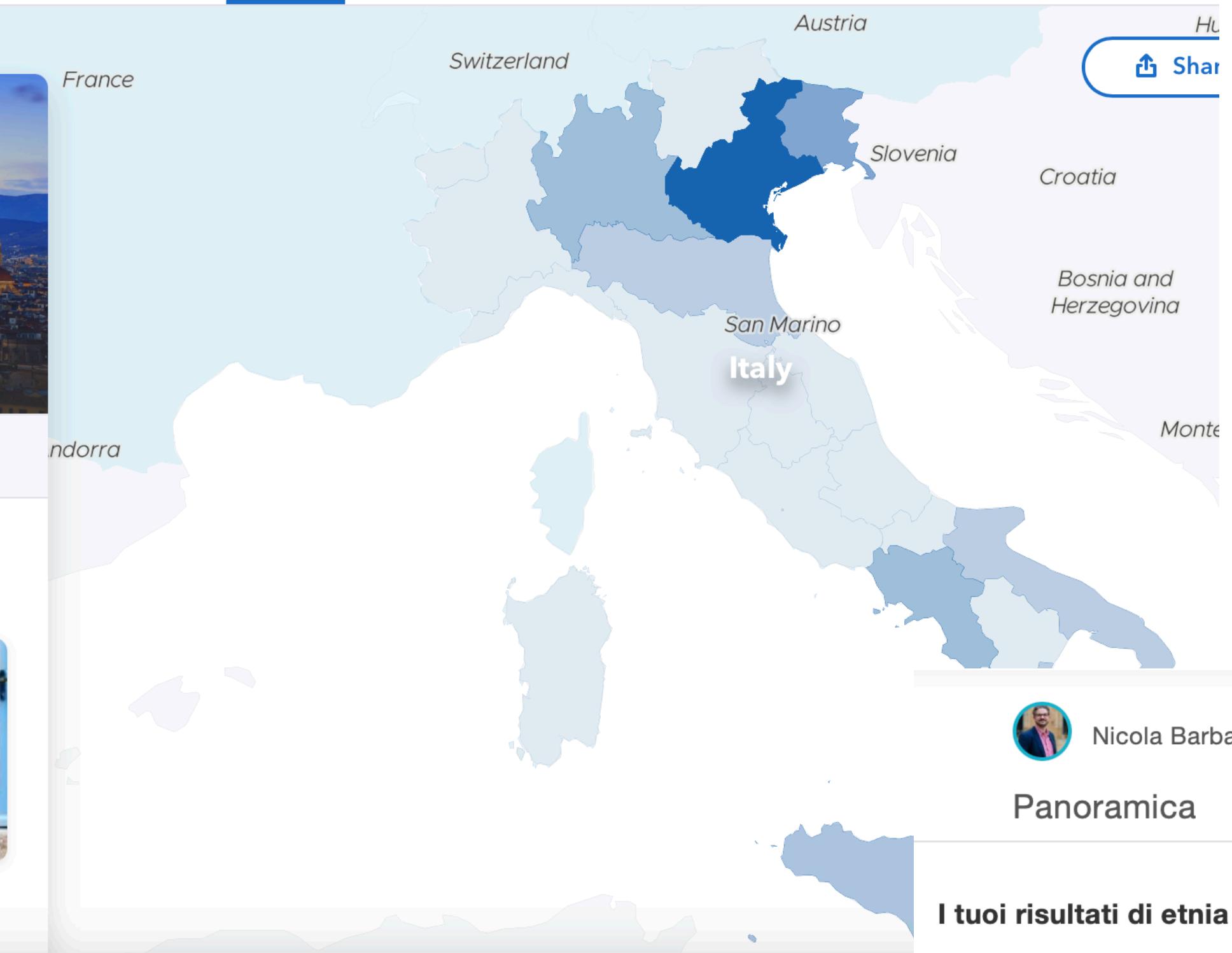
We did not detect enough evidence of recent ancestry from Malta.

LEARN MORE

Explore your
Italian heritage



23andme.com



Myheritage.com



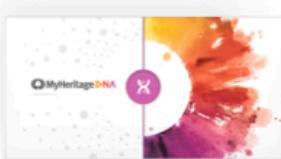
Nicola Barban, questo sei tu

Panoramica

Stima di Etnia

Corrispondenze DNA

Strumenti DNA



Esegui l'ana
Ottieni suggeri

I tuoi risultati di etnia

LIVELLO DI CONFIDENZA DEI GRUPPI GENETICI i

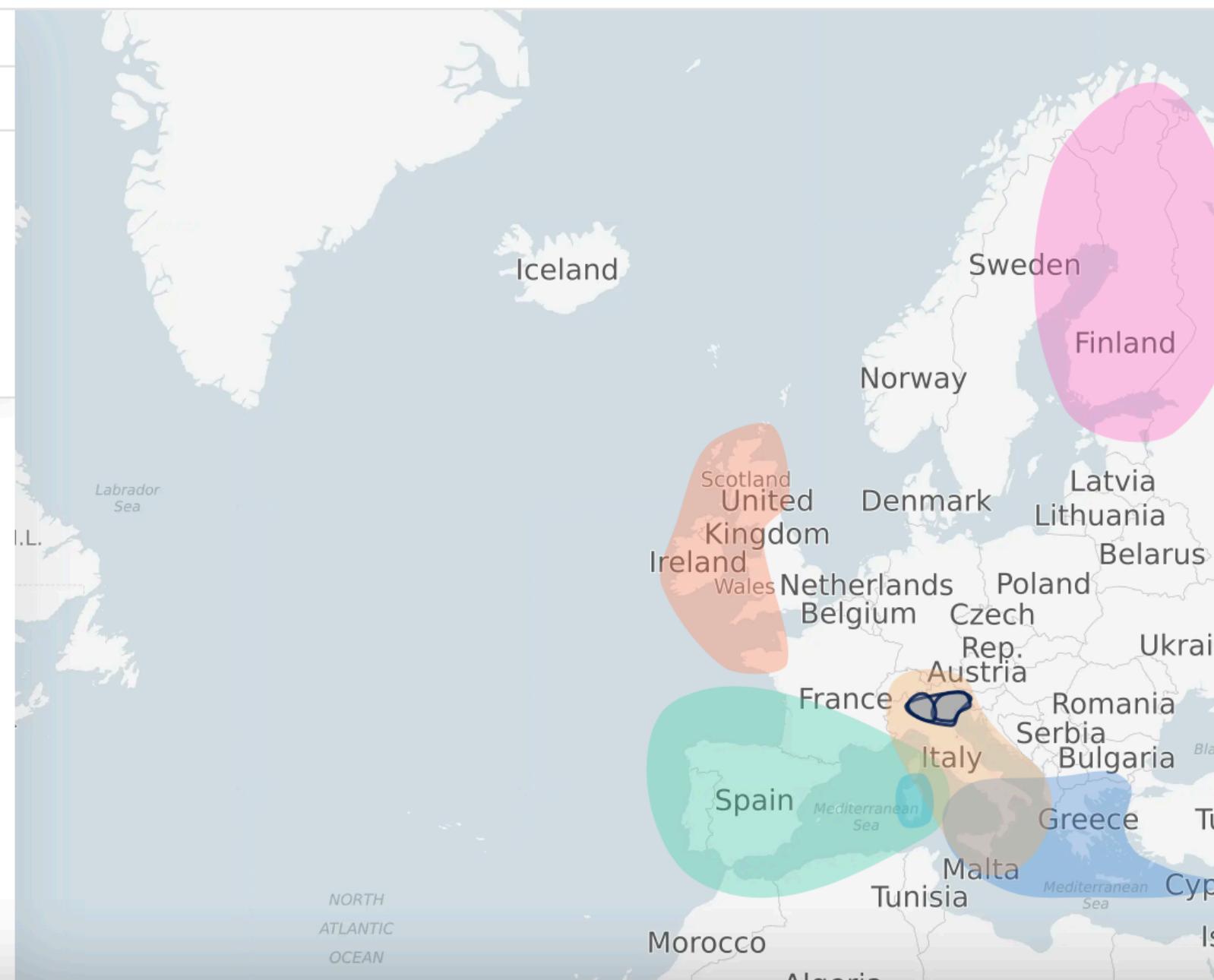
Elevato

Basso

Visualizzati 3/3

EUROPA

- | | |
|--|--------------|
| ● Italiano | 35,6% |
| ● Irlandese, scozzese e gallesse | 20,5% |
| ● Greco e italiano meridionale | 14,4% |
| ● Sardo | 13,7% |



NEWS | SCIENCE AND POLICY

We will find you: DNA search used to nab Golden State Killer can home in on about 60% of white Americans

Researchers call for limiting how ancestry databases can be used to protect privacy

11 OCT 2018 • BY JOCELYN KAISER



If you're white, live in the United States, and a distant relative has uploaded their DNA to a public ancestry database, there's a good chance an internet sleuth can identify you from a DNA sample you left somewhere. That's the conclusion of a new study, which finds that by combining an anonymous DNA sample with some basic information such as someone's rough age, researchers could narrow that person's identity to fewer than 20 people by starting with a DNA database of 1.3 million individuals.

Sociogenomics

In the social sciences there is a small, but rapidly growing, literature considering how genetic influences vary with **institutions**, **historical contexts**, **gender**, and other **environments**, sometimes placed under the umbrella terms **sociogenomics** or **social science genetics**

2.Learning Objectives (some examples)

1. Understand and work with molecular genetic data

Text PLINK files

*.ped

FID	ID	F	M	S	P	-GENETIC INFO-
CH18526	NA18526	0	0	2	1	G G G C C T T A A
CH18524	NA18524	0	0	1	1	G G G C C T T A A
CH18529	NA18529	0	0	2	1	C G G C C T T C A
CH18558	NA18558	0	0	1	1	G G G C C G T A A
CH18532	NA18532	0	0	2	1	G G G C C T T A A

*.map

Chr	SNP	SNP	Base-Pair
		Position	Coordinate
8	rs17121574	12.7991	12799052
8	rs754238	12.8481	12848056
8	rs11203962	12.8484	12848438
8	rs6999231	12.8623	12862253
8	rs17178729	12.867	12867001

Binary PLINK files

*.bed

Binary version
of the SNP info
of the *.ped
file which is
only readable by
your computer

*.fam

FID	ID	F	M	S	P
CH18526	NA18526	0	0	2	1
CH18524	NA18524	0	0	1	1
CH18529	NA18529	0	0	2	1
CH18558	NA18558	0	0	1	1
CH18532	NA18532	0	0	2	1

*.bim

Chr	SNP	SNP	Base-Pair	Allele1	Allele2
		Position	Coordinate		
8	rs17121574	12.7991	12799052	G	G
8	rs754238	12.8481	12848056	G	G
8	rs11203962	12.8484	12848438	C	G
8	rs6999231	12.8623	12862253	G	G
8	rs17178729	12.867	12867001	G	G

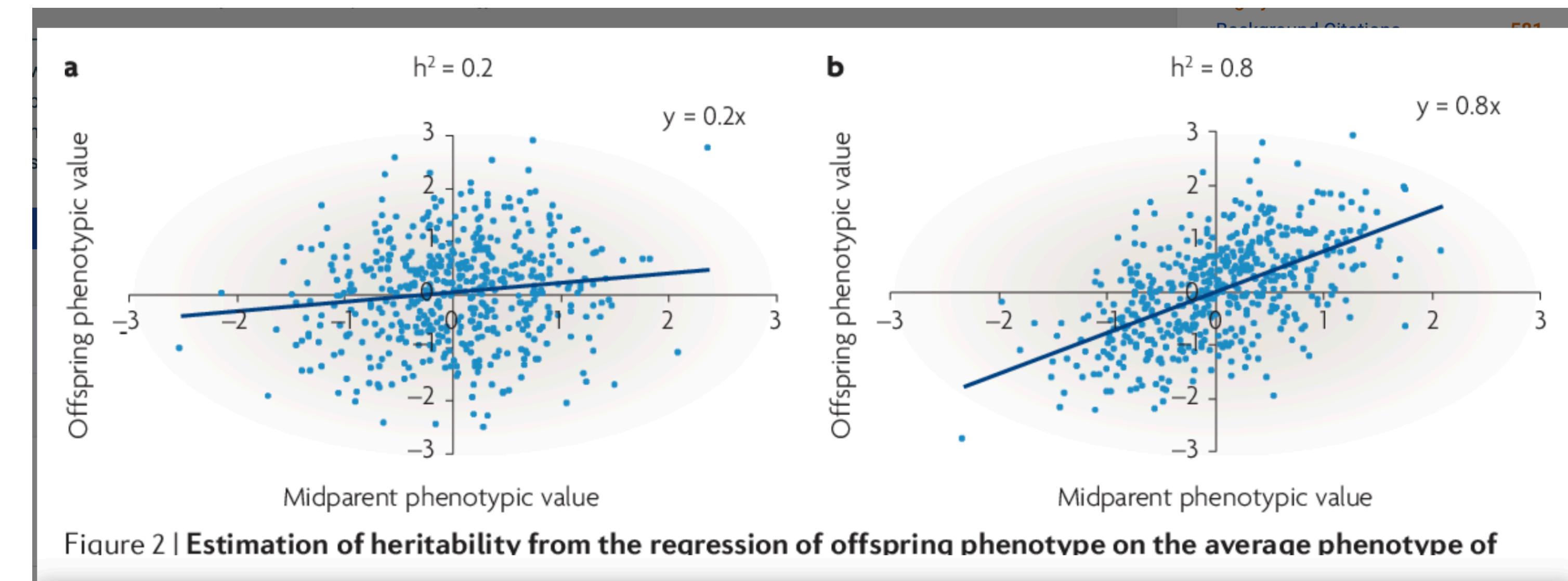
Covariates

FID	ID	Sex	Cohort	PC1	PC2	etc...
CH18526	NA18526	2	1	0.00542	-0.00876	
CH18524	NA18524	1	1	0.04517	-0.00761	
CH18529	NA18529	2	4	0.07776	-0.00231	
CH18558	NA18558	1	2	0.00125	0.00056	

2. Fundamentals of statistical genetics

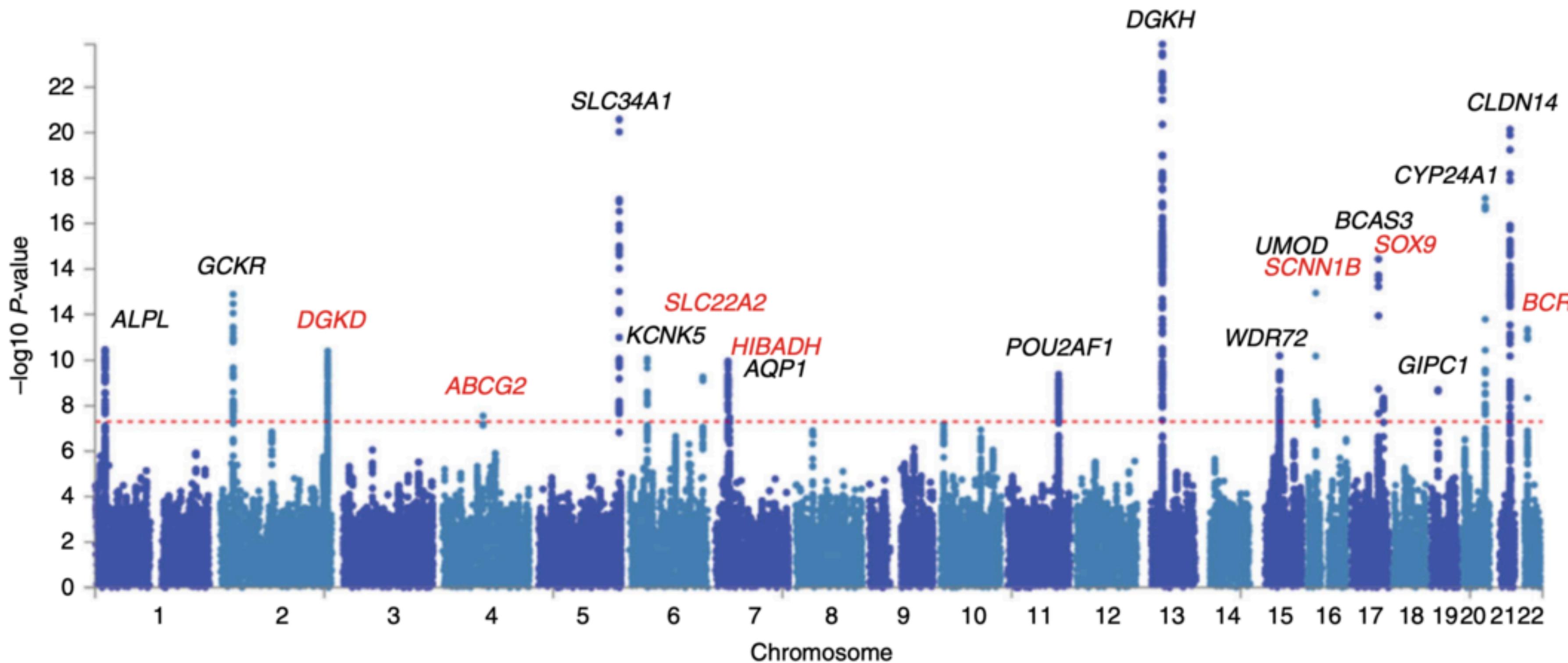
how much of the variation in a trait is due to variation in genetic factors?

Heritability (From twin studies to molecular genetics)



3. Genome Wide Association Studies

Associations between single-nucleotide polymorphisms (SNPs) and traits like major human diseases, traits, behaviours



4. Polygenic prediction

Genetic Weight

Your genes influence not just your weight, but also the impact of different healthy habits.

Overview

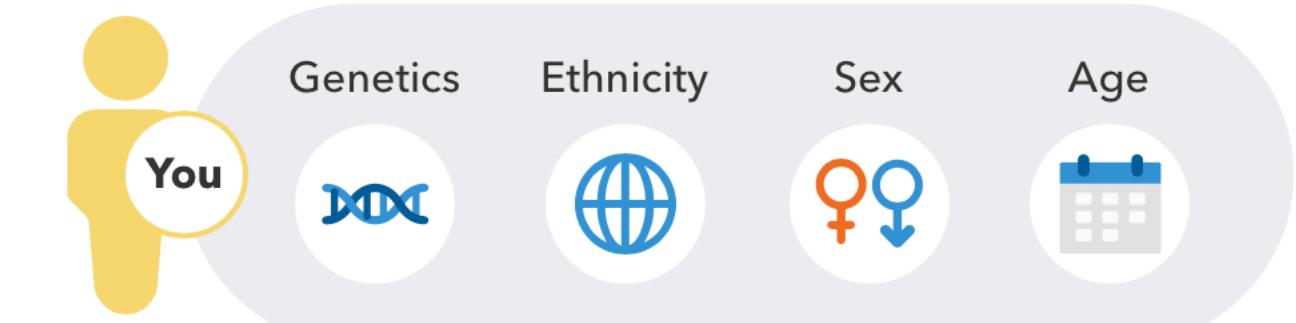
Scientific Details

How we determine your result

Can we use genetic information to “predict” a phenotype (trait)?

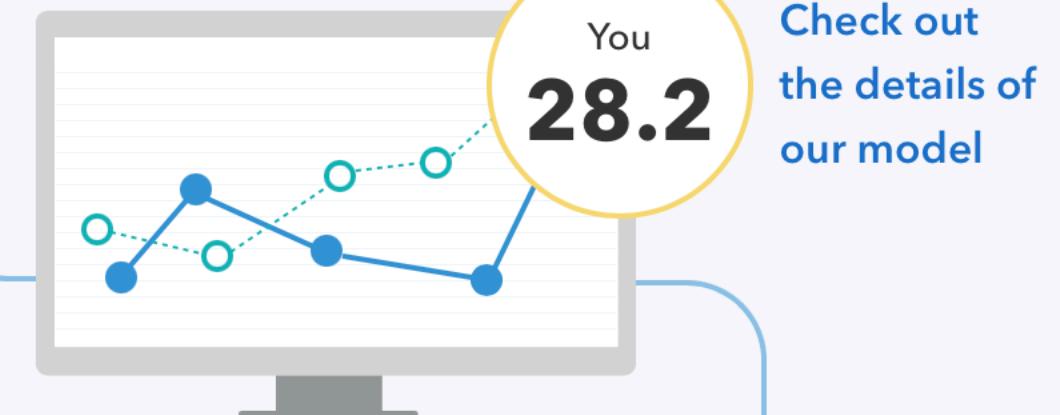
1. Collect some details from you.

You tell us your age, sex, height, weight, and ethnicity, so we can customize your result.



2. Calculate your score.

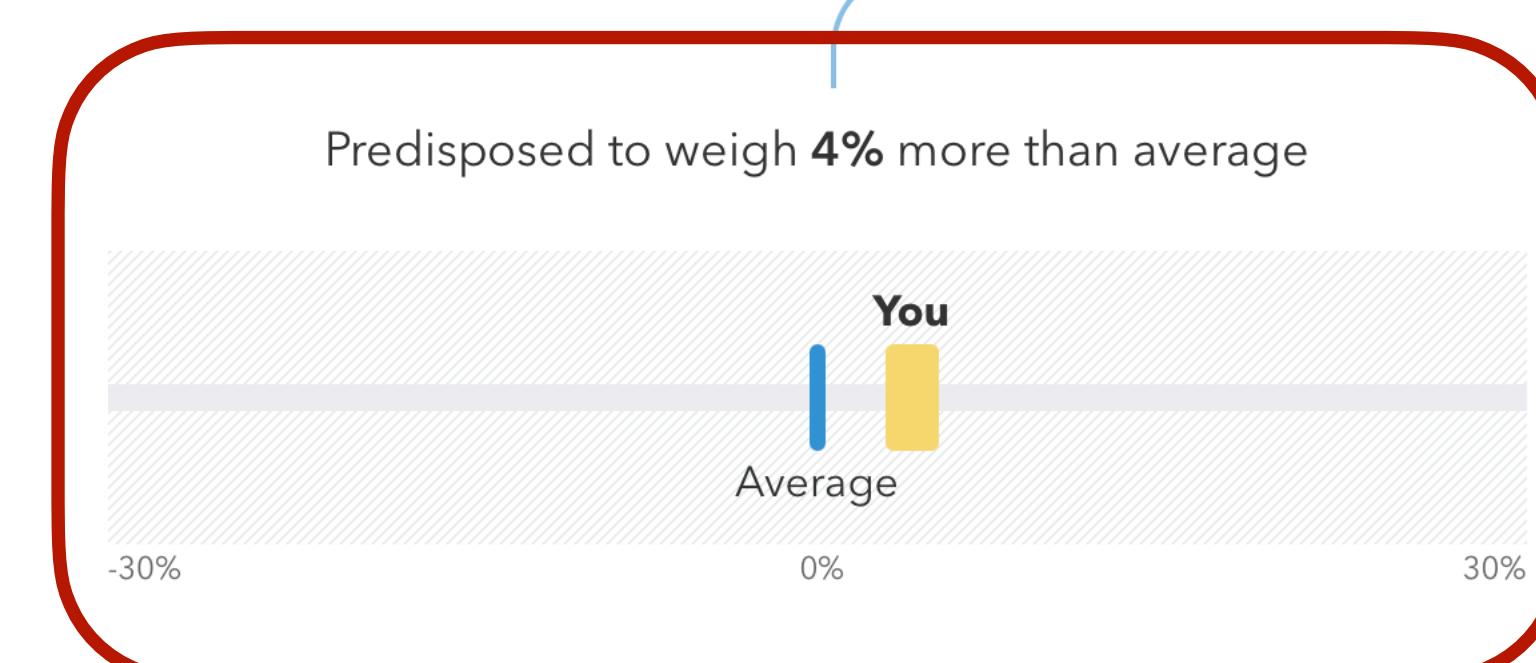
We use data from 23andMe research participants to create a genetic weight score based on your genotype at over 300 different genetic markers associated with weight. Based on your score, we then make a prediction about your BMI that also factors in your age, sex, and ethnicity.



3. Summarize your weight predisposition.

To determine whether you have a genetic tendency to weigh more or less than average, we compare your BMI prediction to other 23andMe participants of your age, sex, and ethnicity. Because average weights change with age, how your predisposition compares to average may also change slightly over time. [See our white paper about the science behind this report.](#)

Predisposed to weigh 4% more than average



30%

5. GxE interactions

...Educational policies may increase or decrease health differences, depending on whether they reinforce or counteract gene-related differences ...



Education can reduce health differences related to genetic risk of obesity

Silvia H. Barcellos^{a,1}, Leandro S. Carvalho^a, and Patrick Turley^{b,1}

^aCenter for Economic and Social Research, University of Southern California, Los Angeles, CA 90089; and ^bAnalytic and Translational Genetics Unit, Massachusetts General Hospital, Boston, MA 02114

Edited by Kenneth W. Wachter, University of California, Berkeley, CA, and approved September 4, 2018 (received for review February 16, 2018)

This work investigates whether genetic makeup moderates the effects of education on health. Low statistical power and endogenous measures of environment have been obstacles to the credible estimation of such gene-by-environment interactions. We overcome these obstacles by combining a natural experiment that generated variation in secondary education with polygenic scores for a quarter-million individuals. The additional schooling affected body size, lung function, and blood pressure in middle age. The improvements in body size and lung function were larger for individuals with high genetic predisposition to obesity. As a result, education reduced the gap in unhealthy body size between those in the top and bottom terciles of genetic risk of obesity from 20 to 6 percentage points.

education | health | gene-by-environment | obesity | genetics

Educational policies may increase or decrease health differ-

education on health (20, 21). We find that 14% of students completed an additional year of secondary education as a result of this reform. The combination of this experiment with the use of PGSS—instead of a candidate-gene approach—for a sample of a quarter-million individuals makes our analyses appropriately powered (22).

Before the release of the complete genetic data used in this study, we wrote a comprehensive preanalysis plan describing the construction of all variables to be used and the specification of all analyses to be run (ref. 22 and *SI Appendix*, section A). We strictly follow this plan below. Our plan was informed by previous work, which used nongenetic data to estimate how education affects the distribution of health in middle age (23). In that paper, we documented that the effects of education on health are concentrated at particular parts of the health distribution, which suggests that such effects vary across individuals (*SI Appendix*, section B).

6. Ethical Implications

- How to conduct responsible research?
- Who is going to benefit?
- Data privacy?
- Can genetic research lead to a more (un)equal society?
- Is there enough diversity in genetic research?
- What are the implication of genetic prediction?
- What are the risk of genetic editing?

3. Course Structure

Structure of the course

1. Lectures (interactions with students)
2. Invited lectures
 - Luca Pagani, molecular anthropologist, UniPD)
 - Pietro Biroli, economist, UniBO
3. Social Science Genomics Conference (18-20 May) - Optional
 - Melinda Mills (sociologist, Oxford)
 - Adam Rutherford, scientist author
 - Training on epigenetic by Meen Kumari, University of Essex
4. **Hands on laboratory (with your own laptop) HOW MANY OF YOU CAN BRING A LAPTOP DURING LECTURE?**

4. Evaluation

Course evaluation a.k.a exam

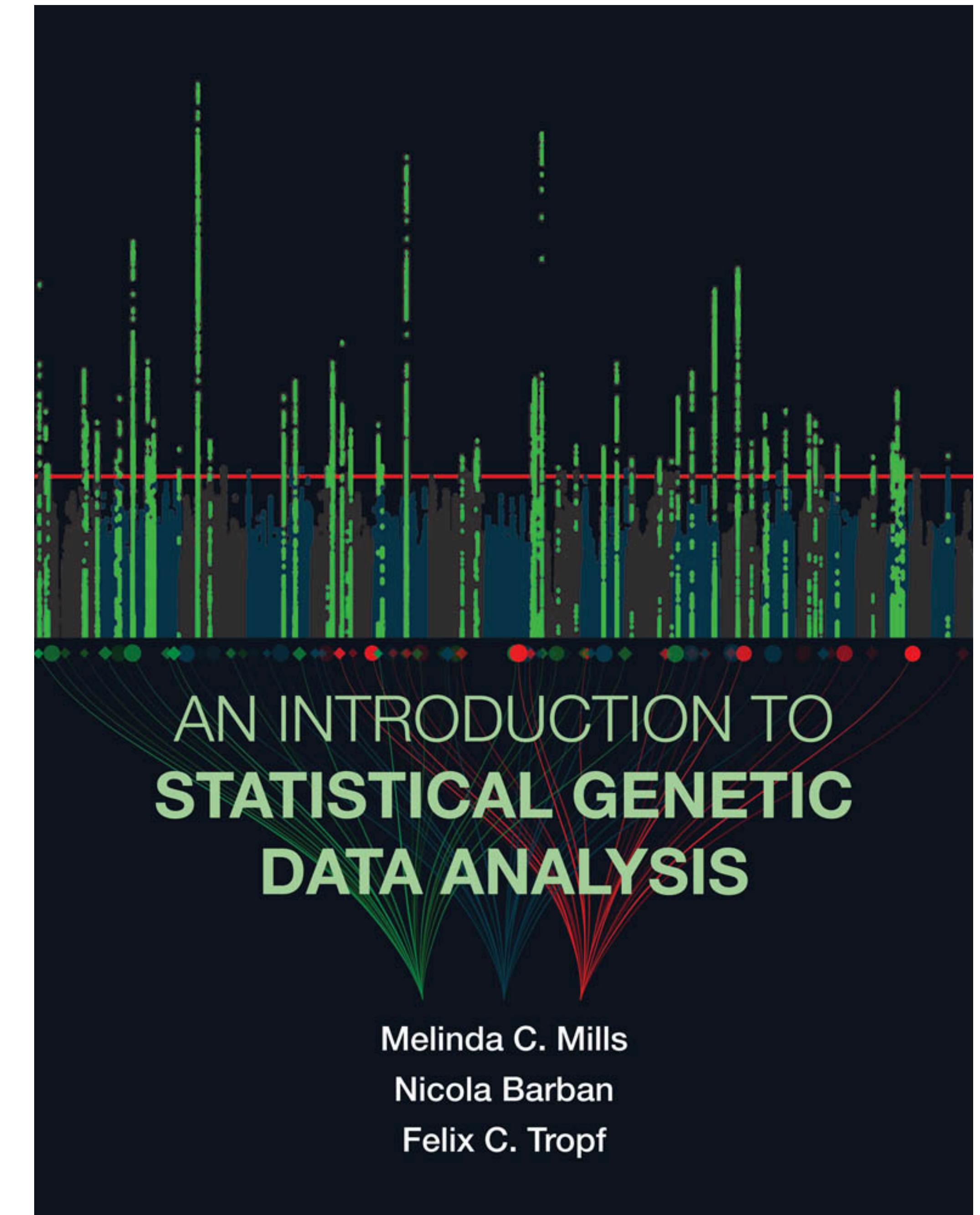
For students attending class regularly, the final evaluation will be composed by two parts:

1. Group or individual project/assignment (max 3 people). Instructions on the project will be distributed in class. **(60% of the final grade)**
2. Oral examination **(40% of the final grade)**

Students not attending class are invited to contact the instructor to discuss the examination.

4. Resources

Textbook



Additional Textbooks (Optional) + Assigned readings during class (not optional)

