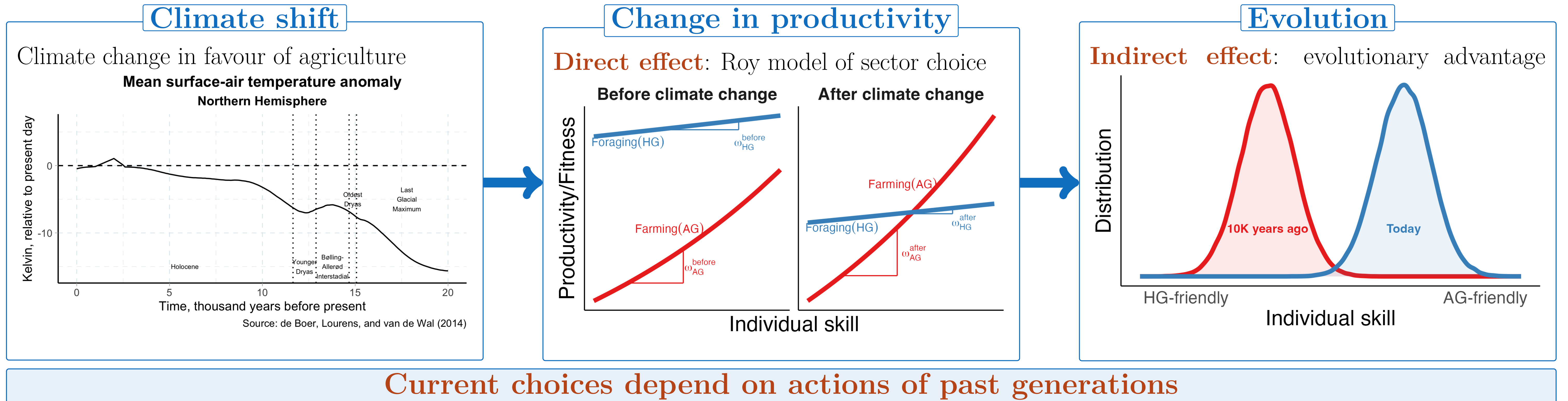


Selection and the Roy Model in the Neolithic Transition

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Technological shift and economic decisions



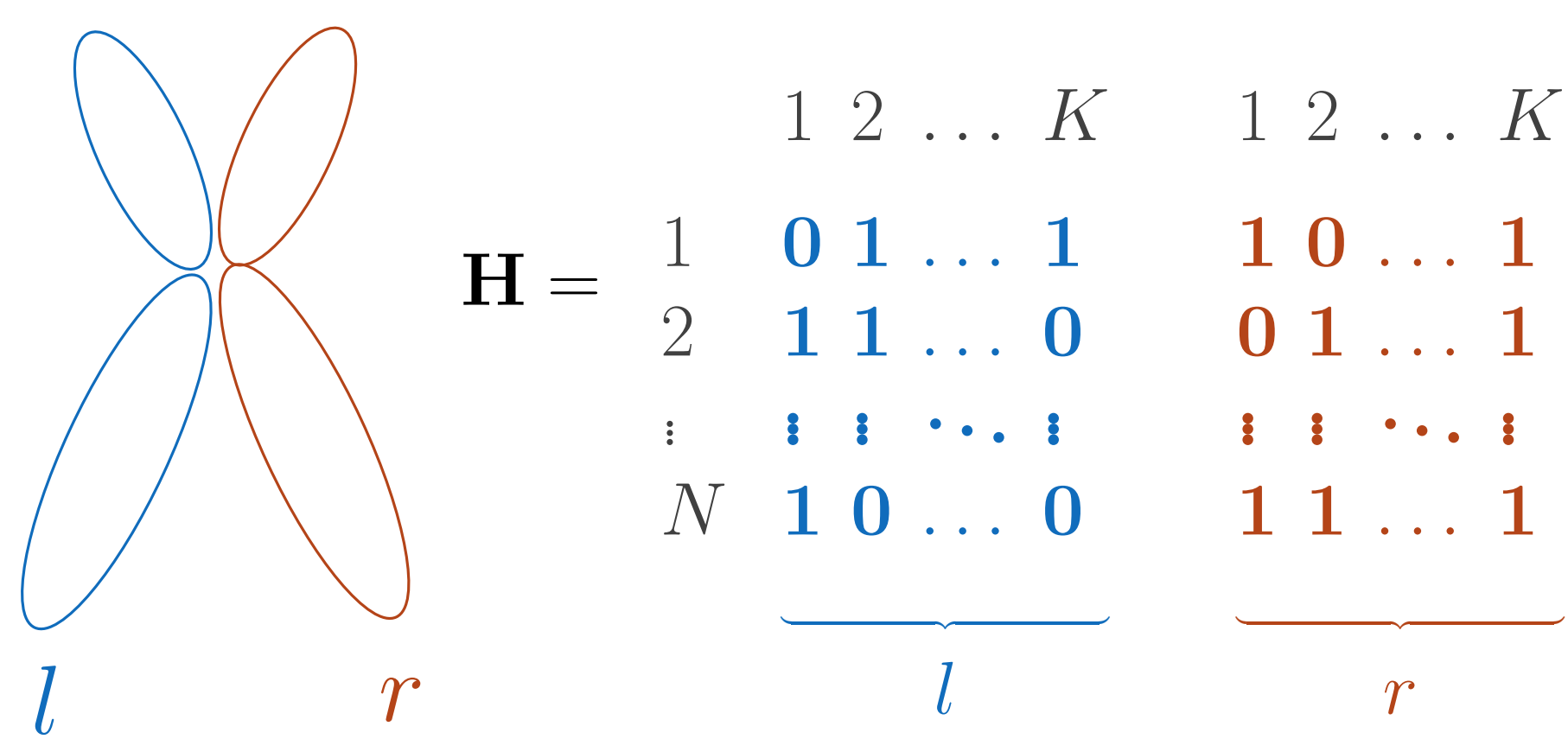
Modelling genetic evolution

Based on **Wright-Fisher** model with

- **population** size N
- K **genetic markers**
- coded $\{0, 1\}$ where 1 increases **skill**
- evolution over T **generations**

Unit of analysis - **haplotype pairs**

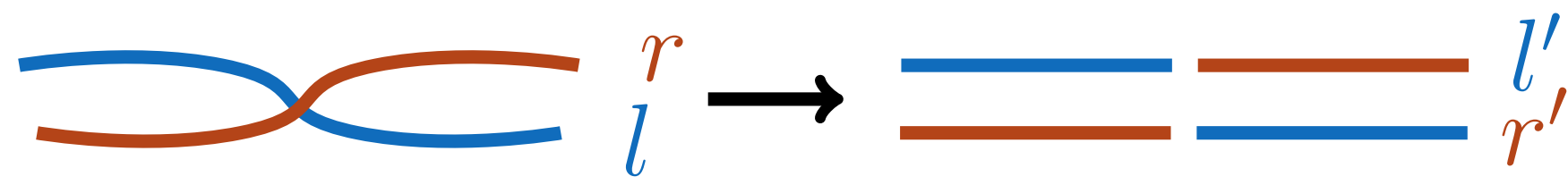
$$\mathbf{H} = (l, r) = (\{0, 1\}^K, \{0, 1\}^K)$$



Parents' haplotypes

Mutation: random switch $0 \leftrightarrow 1$

Recombination: random cross-over $l \leftrightarrow r$



Children's haplotypes

Random mating: parent haplotypes randomly matched to form a child haplotype.

Selection of the fittest: draw new generation from multinomial $\mathbf{mn}(N, F \otimes \mathbf{H})$

Fitness

Skill: linear **polygenic score** using GWAS β
 $z = \mathbf{H}(\beta\beta)'$

Occupation-specific fitness function
 $f(z, \tau) = R_\tau \exp(\omega_\tau z), \forall \tau \in \{HG, AG\}$

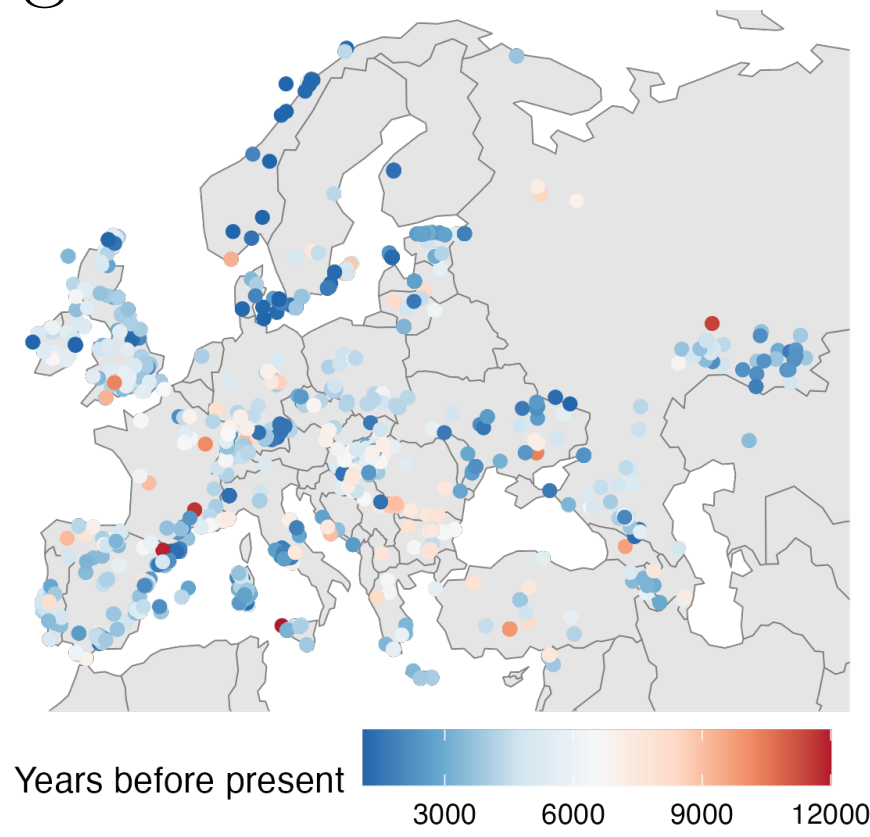
Fitness-maximising occupation choice
 $F = \max_\tau f(z, \tau)$

Parameters of interest: ω_τ
Average probability of skill-increasing alleles to pass into next generation.

Data and estimation

Data

Ancient DNA (David Reich Lab 2021) 2,328 ancient genomes



1000 Genomes

503 modern European genomes

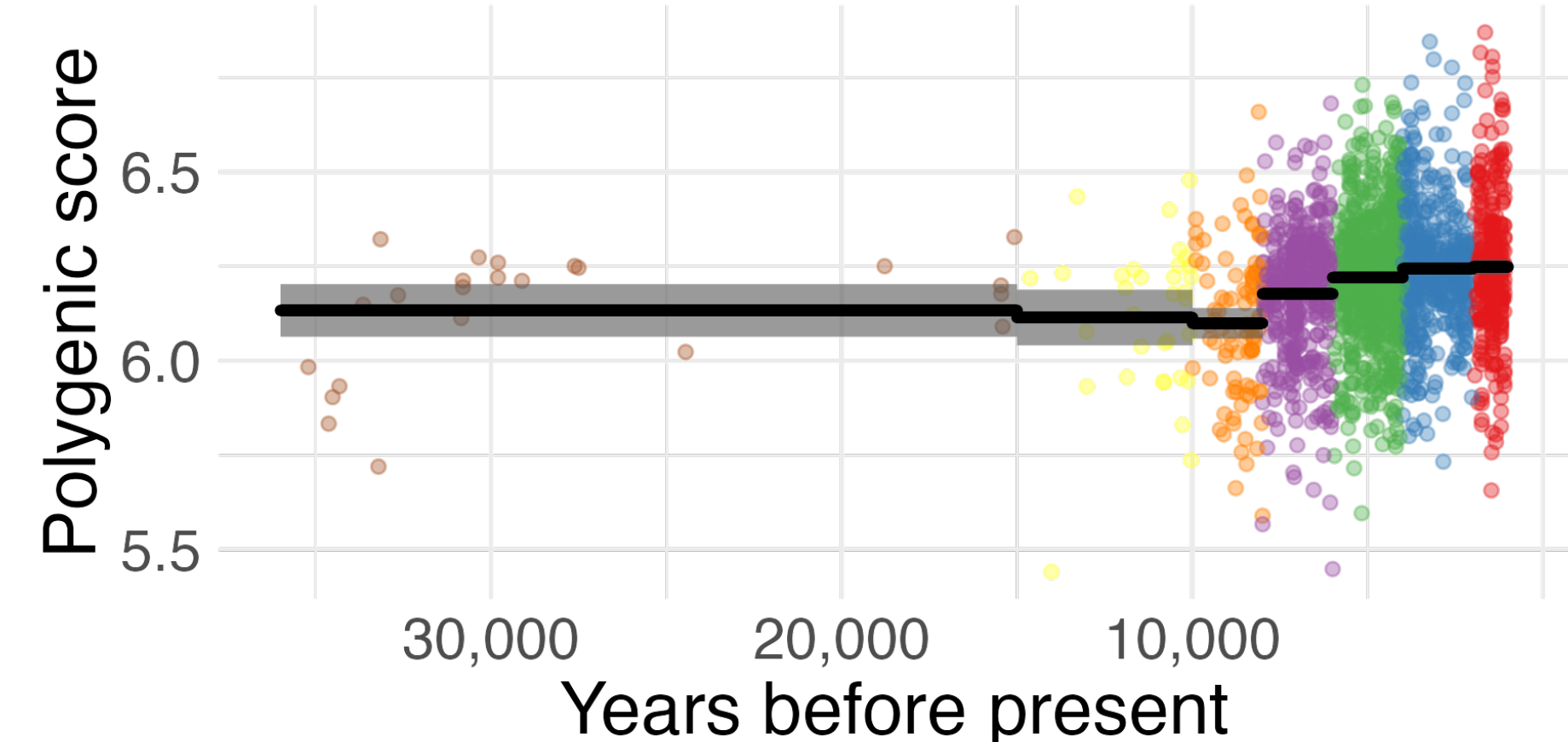
GWAS coefficients

Educational attainment (Lee et al. 2018)

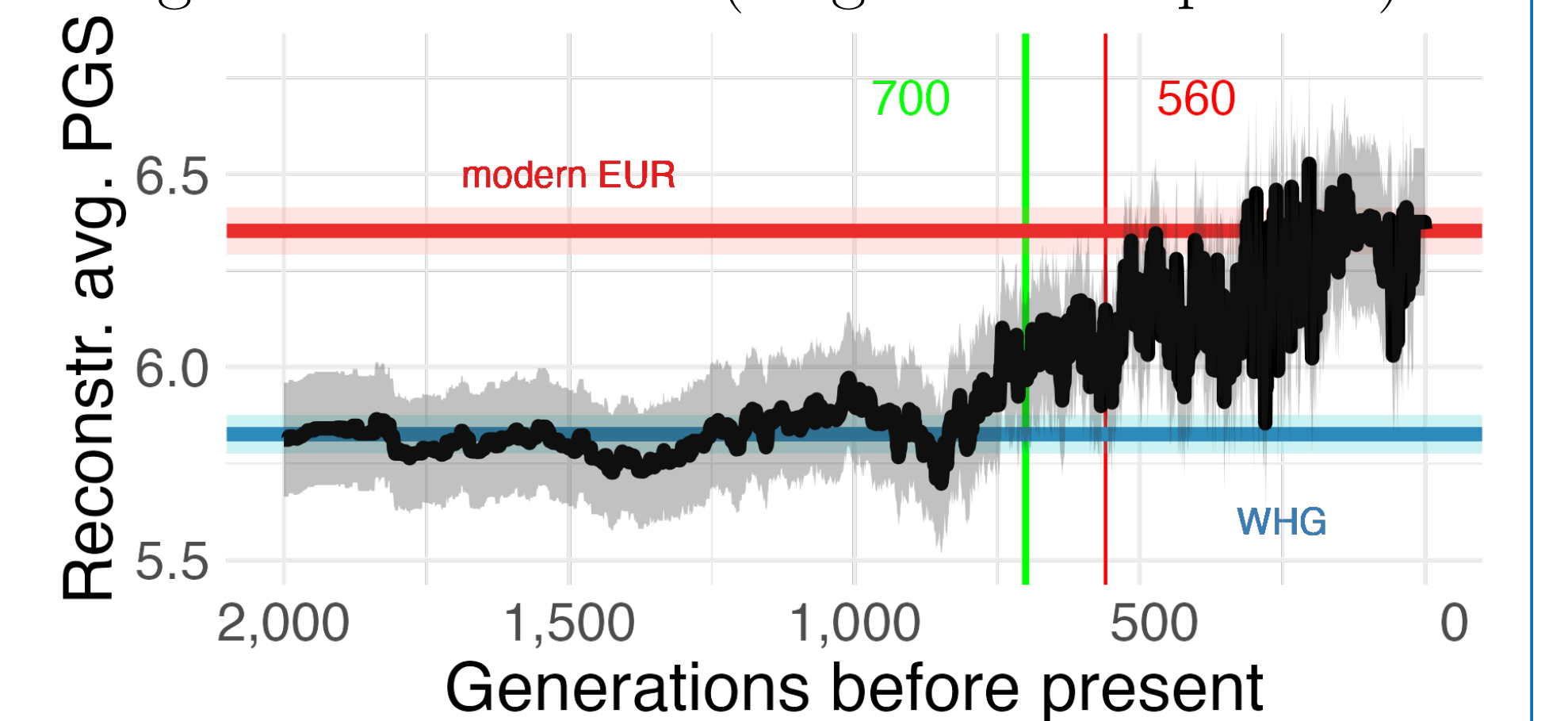
Polygenic scores

The data shows a jump in average PGS around 10K year (or 560 generations) ago

PGS of ancient DNA



Reconstructed PGS from modern DNA and Kingman's coalescent (Edge and Coop 2019)



Constant average PGS for thousands of generations before climate shift: $\omega_{HG} = 0$

References

- 1000 Genomes Project Consortium, A. Auton, L. D. Brooks, R. M. Durbin, E. P. Garrison, H. M. Kang, J. O. Korbel, et al. 2015. "A Global Reference for Human Genetic Variation." *Nature* 526, no. 7571 (2015): 68–74.
- David Reich Lab. 2021. "Allen Ancient DNA Resource (AADR): Downloadable Genotypes of Present-Day and Ancient DNA Data (v.44.3)." David Reich Lab, 2021.
- Edge, M. D., and G. Coop. 2019. "Reconstructing the History of Polygenic Scores Using Coalescent Trees." *Genetics* 211, no. 1 (2019): 235–262.
- Lee, J. J., R. Wedow, A. Okbay, E. Kong, O. Maghziyan, M. Zacher, T. A. Nguyen-Viet, et al. 2018. "Gene Discovery and Polygenic Prediction from a Genome-Wide Association Study of Educational Attainment in 1.1 Million Individuals." *Nature Genetics* 50, no. 8 (8): 1112–1121.

Estimation

Algorithm to estimate ω_{AG} :

1. Draw initial \mathbf{H} given ancient DNA
2. Simulate T generations multiple times
3. Get simulated lik. of modern DNA

