

Lecture 2

GWAS Unveiled: The Historical Journey and Fundamental Concepts

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What is Genome-wide Association Studies (GWAS)?

Statistical inference procedure based on **association testing** applied **genome-wide**.

Goal:

Identify genetic variants that are associated with traits/diseases.

Motivation:

Finding an address (before the invention of smartphones!): the **One O'Clock Gun** at Edinburgh Castle:

- Ask for directions to Edinburgh Castle. (**GWAS**)
- Once there, ask a staff member where to find the One O'Clock Gun.

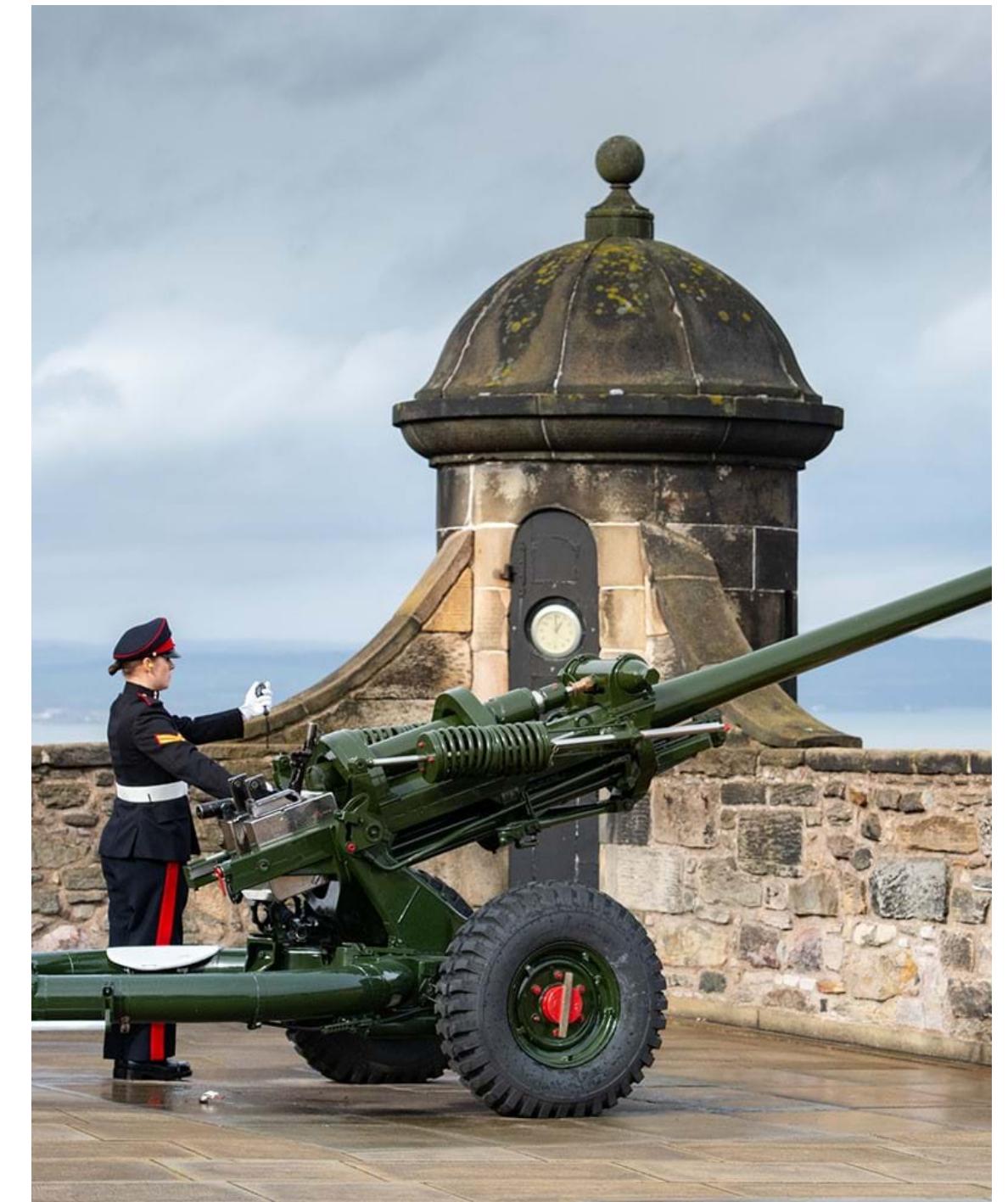


Figure is from: <https://www.edinburghcastle.scot/see-and-do/highlights/one-o'clock-gun>

Why GWAS?

- Identifies genetic variants associated with traits **without prior hypotheses**
- Highlights candidate genes and pathways
- Disease risk predictions



Historical Evolution of Quantitative Genetic Studies

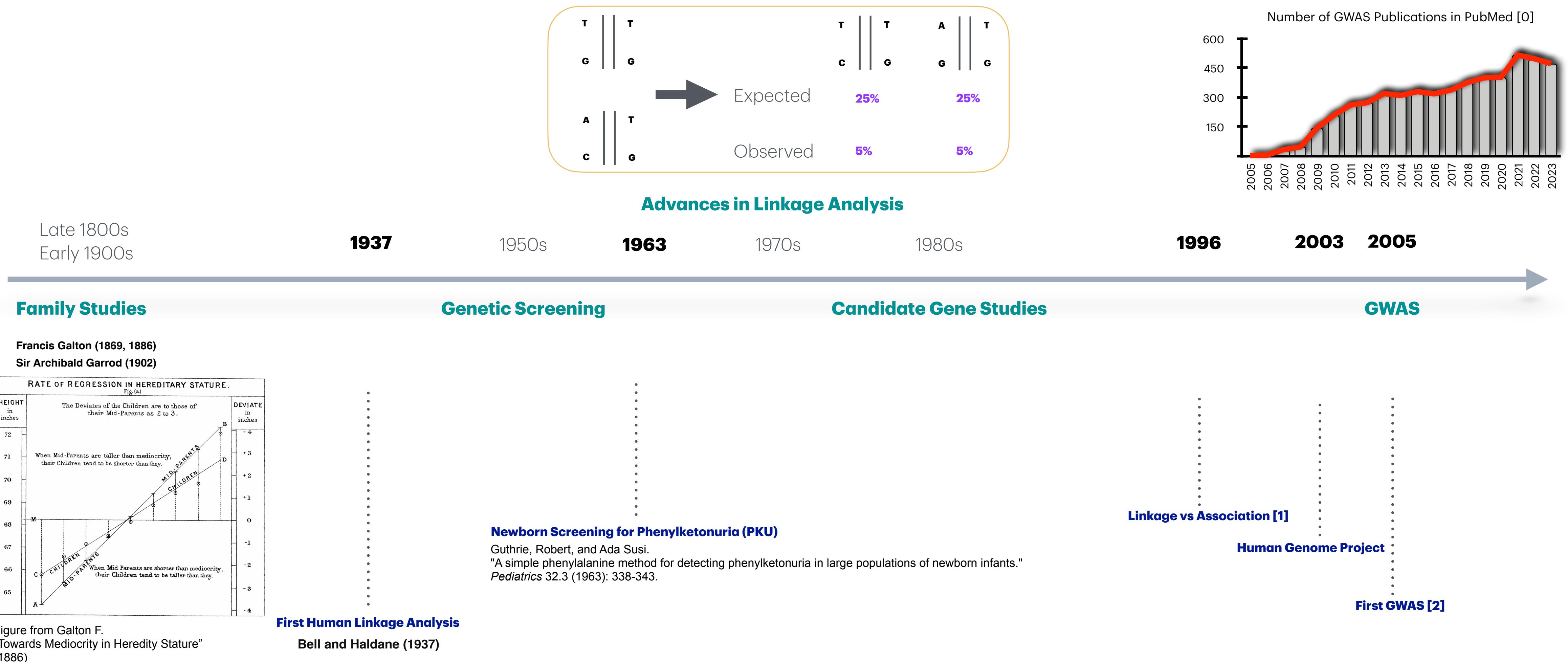


Figure from Galton F.
"Towards Mediocrity in Heredity Stature"
(1886)

First Human Linkage Analysis
Bell and Haldane (1937)

[0] [https://pubmed.ncbi.nlm.nih.gov/?term=%22genome-wide+association+study%22\[Title\]+AND+\(2005+\[Date+-+Publication\]+:+%222024+\[Date+-+Publication\]+\)](https://pubmed.ncbi.nlm.nih.gov/?term=%22genome-wide+association+study%22[Title]+AND+(2005+[Date+-+Publication]+:+%222024+[Date+-+Publication]+))
 [1] Risch, Neil, and Kathleen Merikangas. "The future of genetic studies of complex human diseases." *Science* 273.5281 (1996): 1516-1517.
 [2] Klein, Robert J., et al. "Complement factor H polymorphism in age-related macular degeneration." *Science* 308.5720 (2005): 385-389.

The GWAS Catalog

Published Genome-Wide Associations as of July 2019
 $p \leq 5 \times 10^{-8}$ for 17 trait categories



"The Catalog **was founded** by the **NHGRI** in **2008**, in response to the rapid increase in the number of published genome-wide association studies (GWAS)." [3]

"As of **2024-11-20**, the GWAS Catalog contains **7083** publications, **692444** top associations and **96947** full summary statistics." [4]



NHGRI-EBI GWAS Catalog
www.ebi.ac.uk/gwas

http://ftp.ebi.ac.uk/pub/databases/gwas/timeseries/current/GWAS_Catalog_annotated_diagram.pdf

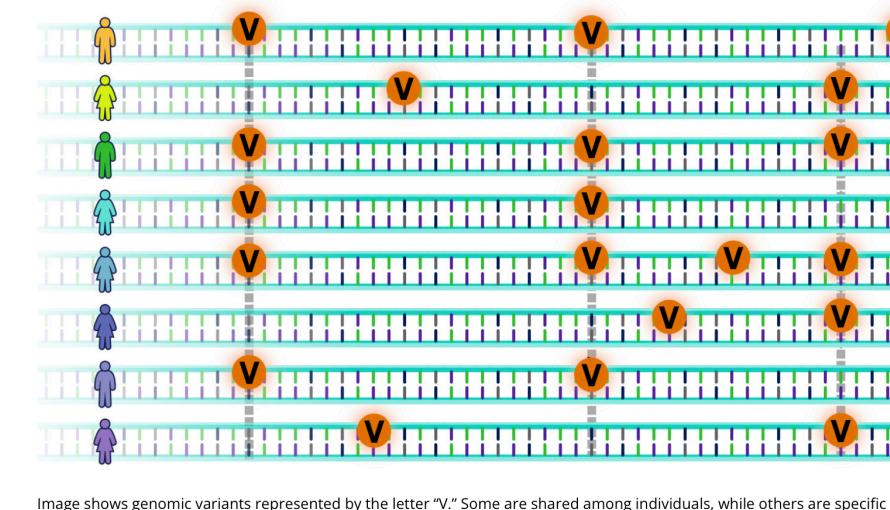
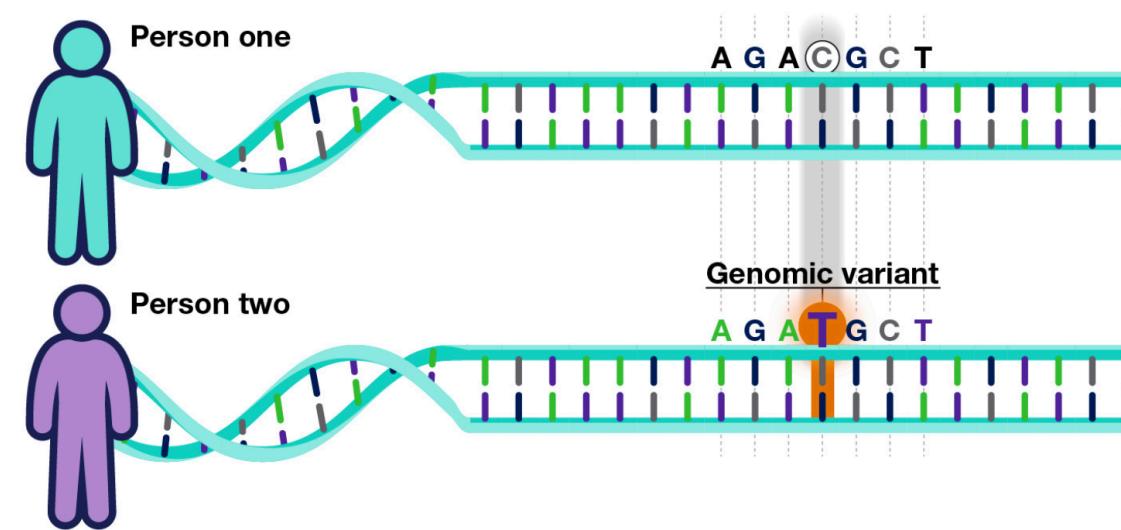
[3] <https://www.ebi.ac.uk/gwas/docs/about>
[4] <https://www.ebi.ac.uk/gwas/home>

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Fundamental Concepts in GWAS

Genomic variant (g)



Figures are from: <https://www.genome.gov/Health/Genomics-and-Medicine/Polygenic-risk-scores>

Manhattan plot

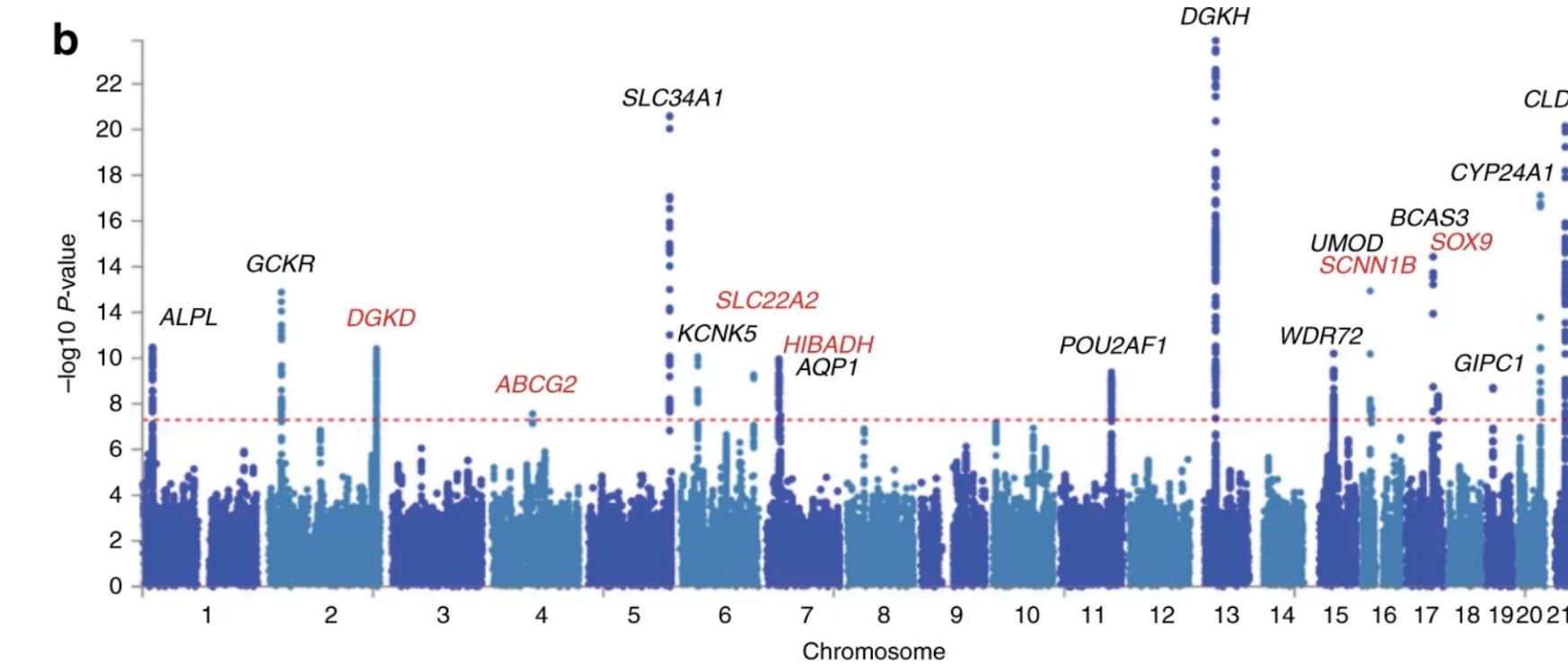
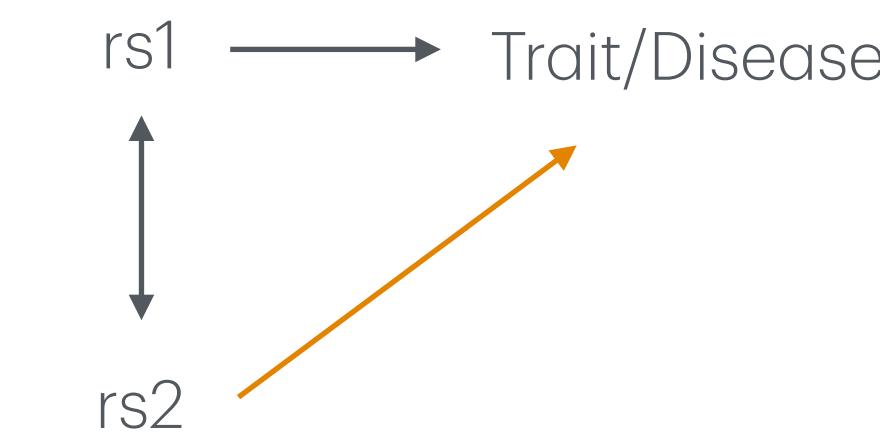


Figure is from:

Howles, S.A., Wiberg, A., Goldsworthy, M. et al. Genetic variants of calcium and vitamin D metabolism in kidney stone disease. *Nat Commun* **10**, 5175 (2019).



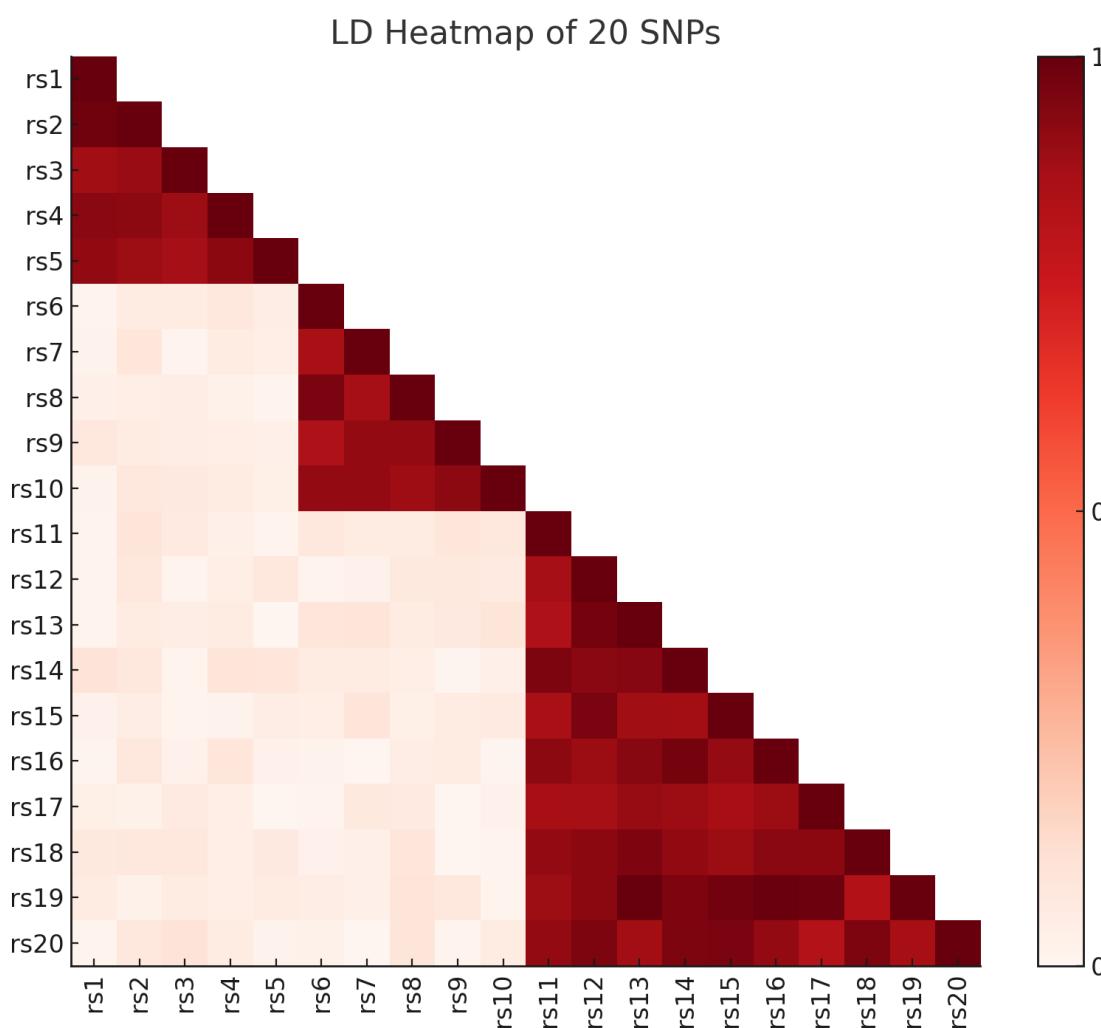
Effect size Measures the impact of a genetic variant on a particular trait or phenotype of interest.



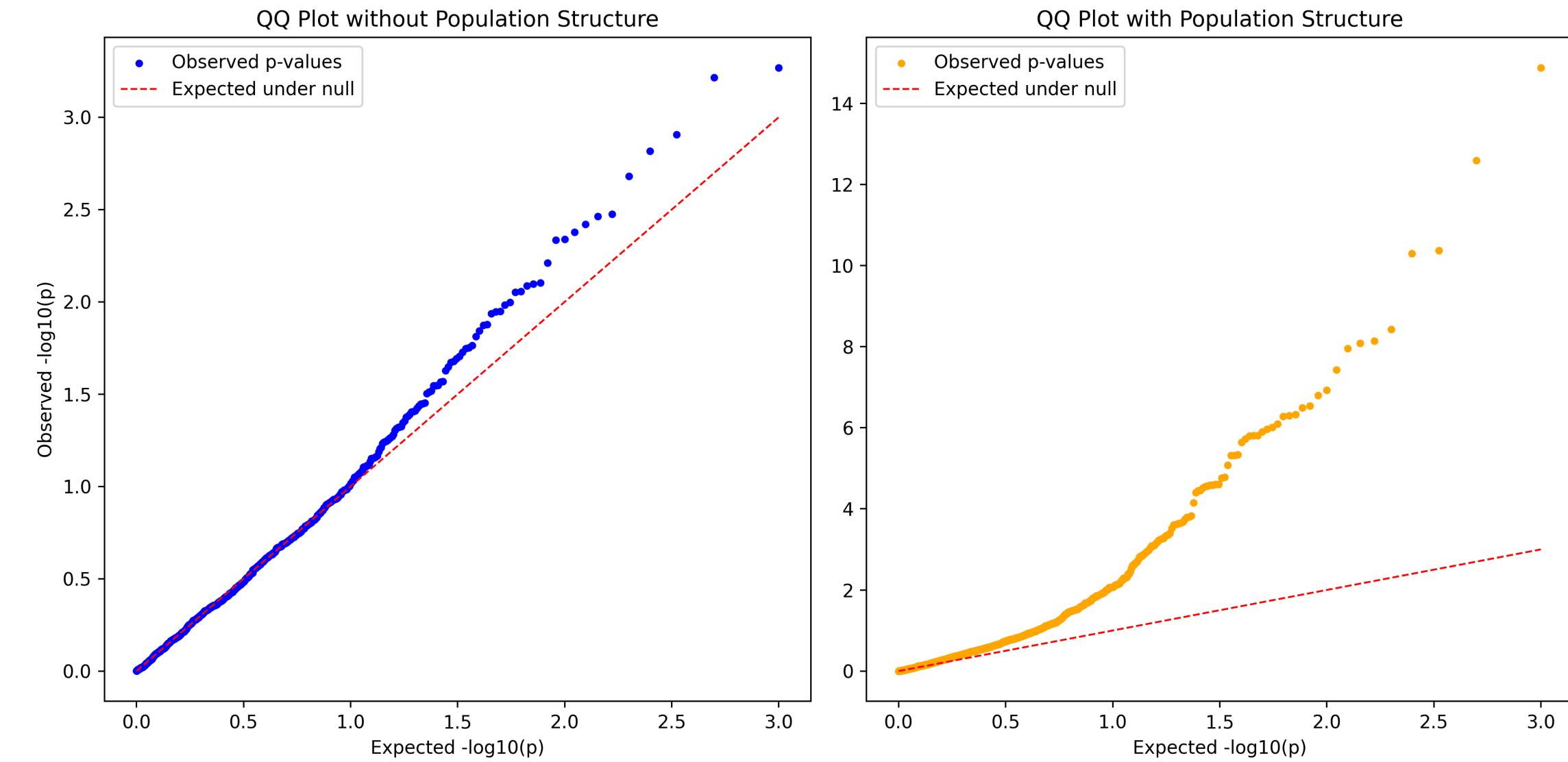
Fundamental Concepts in GWAS

Linkage Disequilibrium (LD)

non-random association of alleles (at different loci).



QQ plot



Population structure

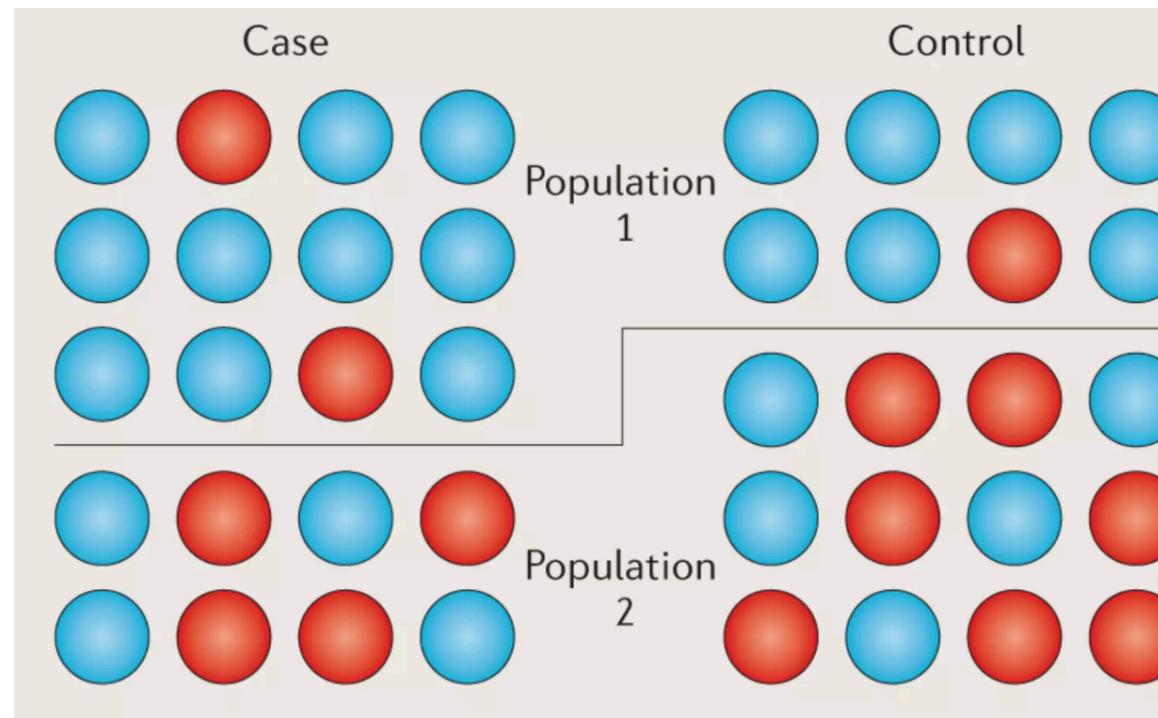


Figure is from: Balding, D. A tutorial on statistical methods for population association studies. *Nat Rev Genet* **7**, 781–791 (2006).

Genomic Inflation Factor (λ)

$$\lambda = \frac{\text{Median(Observed Test Statistics)}}{\text{Median(Expected Test Statistics under the null)}}$$

$\lambda > 1$ might indicate the presence of population structure

Fundamental Concepts in GWAS

Identity by State (IBS)

Identical genetic segments between individuals.

Identity by Descent (IBD)

Identical genetic segments between individuals due to inheritance.

Coefficient of relationship (r)

A measure of biological relationship between individuals. Examples:

$$r(\text{self}, \text{self}) = 1, r(\text{self}, \text{son}) = 0.5, r(\text{self}, \text{daughter}) = 0.5, r(\text{self}, \text{father}) = 0.5, r(\text{self}, \text{mother}) = 0.5$$

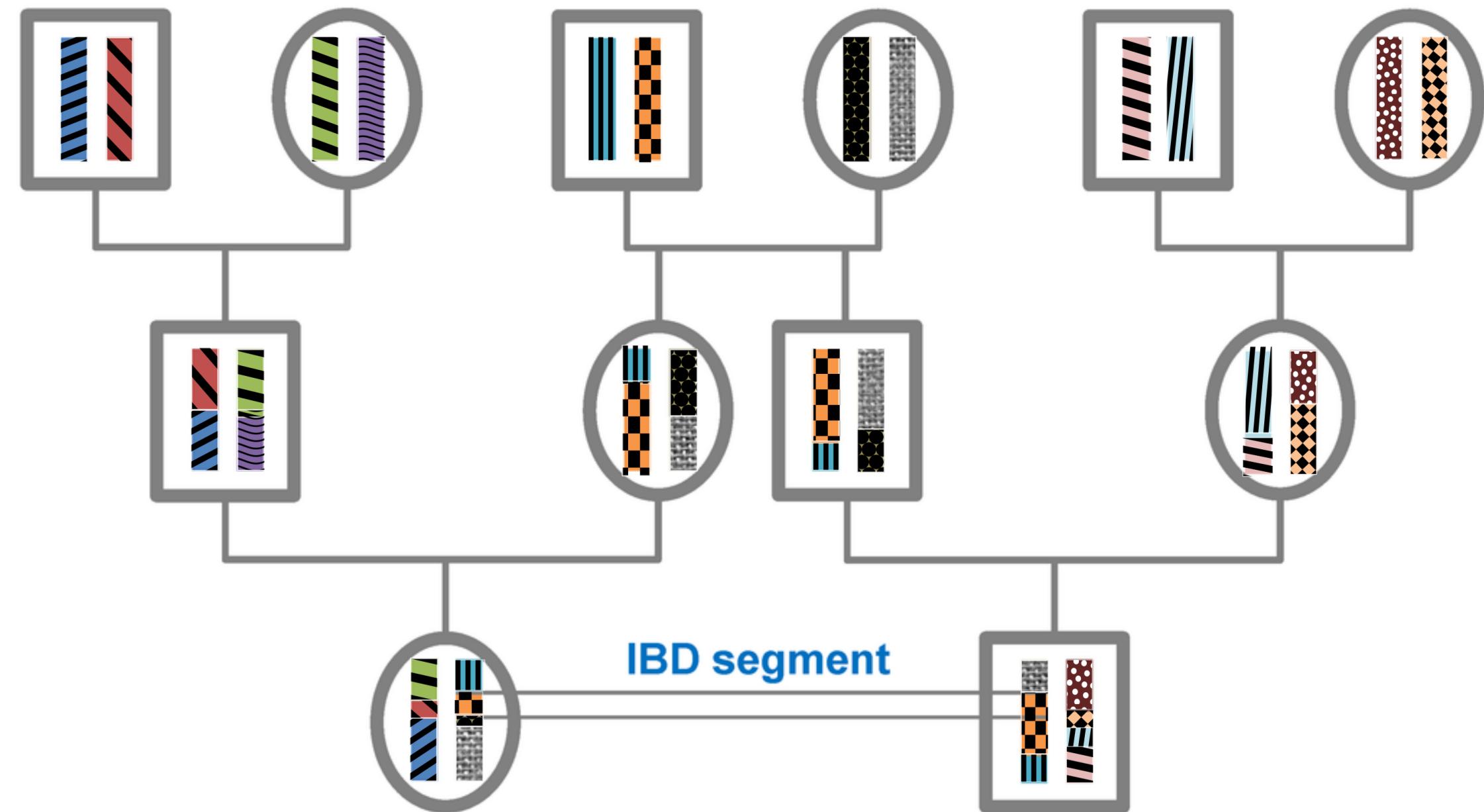


Figure is from: https://en.wikipedia.org/wiki/Identity_by_descent

Fundamental Concepts in GWAS

Minor Allele Frequency (MAF)

The frequency of the less common allele in a given population.

Hardy-Weinberg Equilibrium (HWE)

HWE describes a stable state where allele and genotype frequencies remain constant over time in a given population, provided random mating occurs and there is no influence of evolutionary forces such as selection, mutation, migration, or genetic drift..

Genetic Relationship Matrix

A matrix $\pi = [\pi_{i,j}]$ that estimates the genetic relatedness between individuals based on their genotypes.

$$\pi_{i,j} = \frac{1}{M} \sum_{k=1}^M \frac{(g_{ki} - 2f_i)(g_{kj} - 2f_j)}{2f_i(1-f_i)}.$$



What's Next

1. Association Analysis by Linear Regression
2. Why Linear Regression does not work?
3. Association Analysis by Linear Mixed Models
4. Advantages and (further) Challenges

