

Measuring relatedness in human populations from DNA

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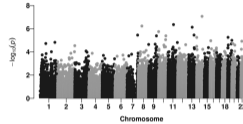
Why study relatedness?



Human genetics is fascinating!



Heritability of complex traits

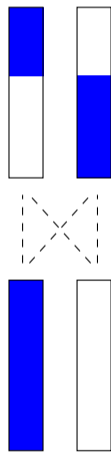
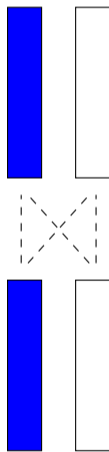
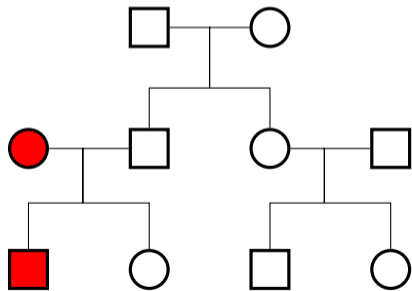


Search for disease-causing genetic variants

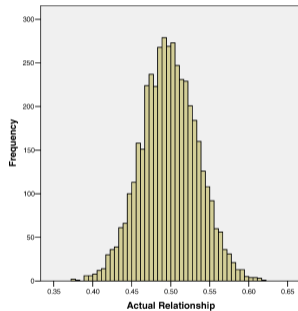
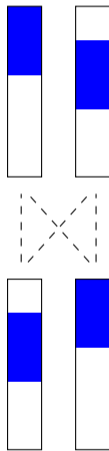
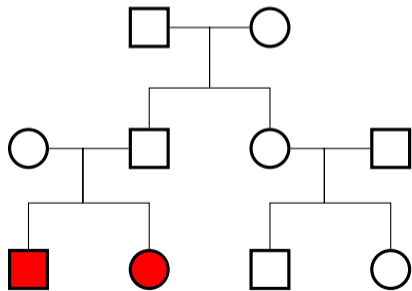


Animal and plant breeding

The kinship coefficient for parent-child: $\frac{1}{4}$

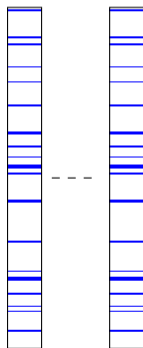
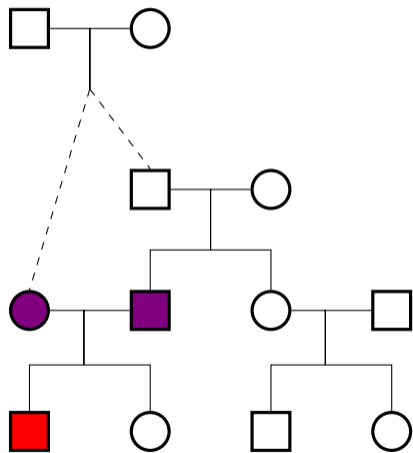


The kinship coefficient for siblings: $\frac{1}{4}$ on average



Visscher *et al.* (2006)

The inbreeding coefficient in populations



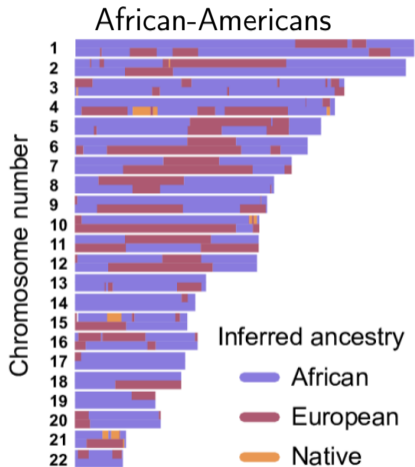
Measurements relative to a reference pop.:

Inbreeding = 0 in the local population

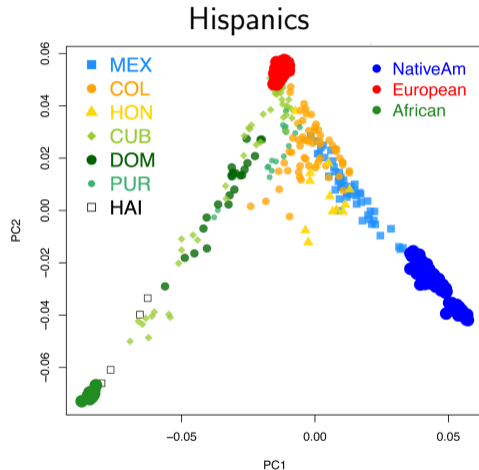
Inbreeding ≥ 0 relative to a distant ancestral population

Better measured using covariance

Recently admixed populations



Baharian *et al.* (2016)



Moreno-Estrada *et al.* (2013)

Kinship model for genotypes

symbol	meaning
T	ref ancestral population
i	locus index
j, k	individual indexes
p_i^T	ref allele frequency
x_{ij}	genotype (num ref alleles)
φ_{jk}^T	kinship of j, k
f_j^T	inbreeding of j

Statistical model:

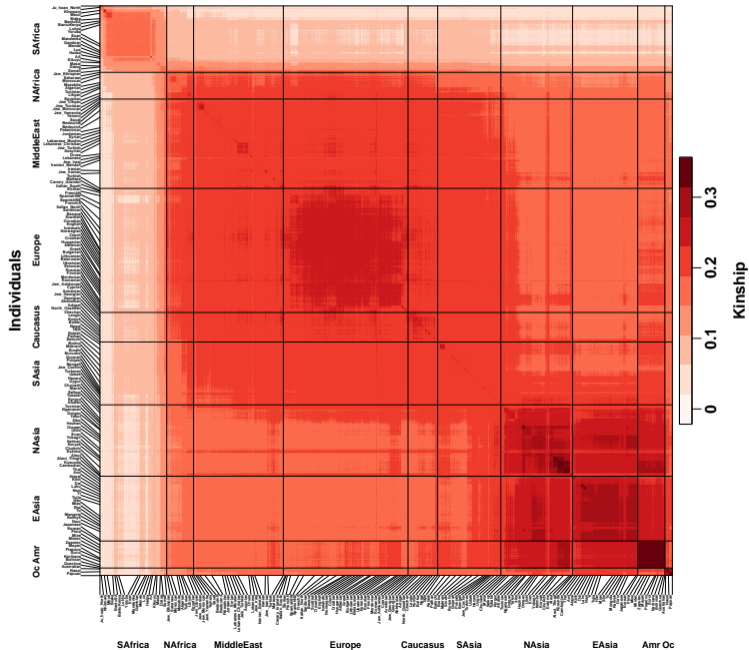
$$E[x_{ij} | T] = 2p_i^T,$$

$$\text{Var}(x_{ij} | T) = 2p_i^T (1 - p_i^T) (1 + f_j^T),$$

$$\text{Cov}(x_{ij}, x_{ik} | T) = 4p_i^T (1 - p_i^T) \varphi_{jk}^T.$$

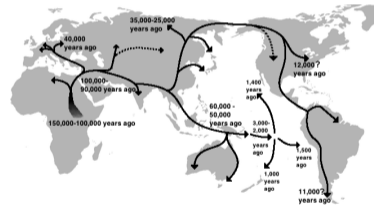
(Wright 1921, 1951; Malécot 1948; Jacquard 1970).

We developed a new kinship estimation framework that works for arbitrary population structures!

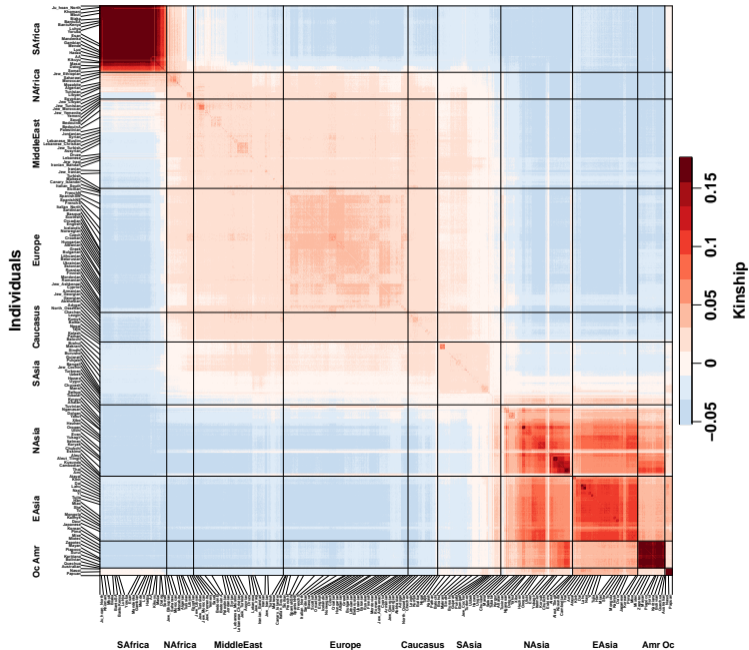


New kinship estimates

Genotypes from "Human Origins" (Lazaridis et al. 2014, 2016)

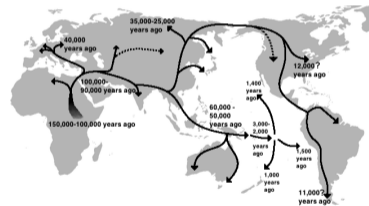


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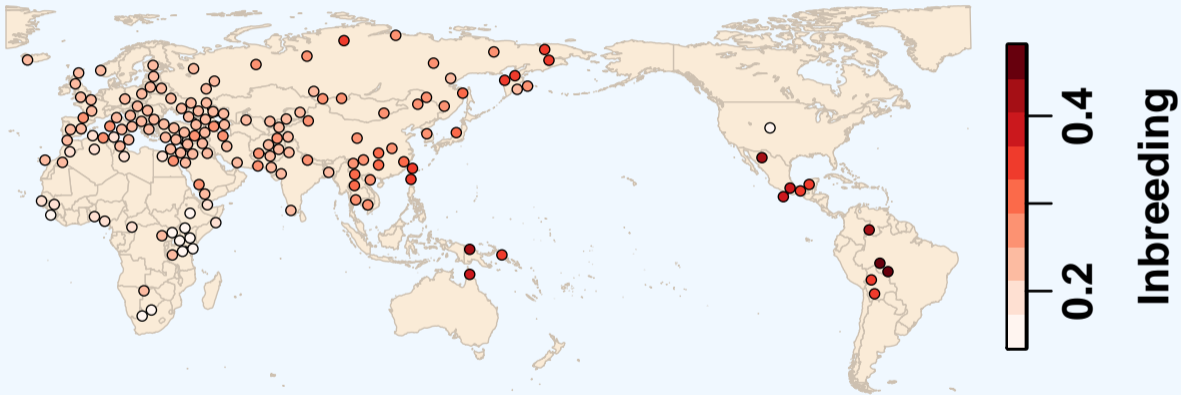
Standard kinship estimates

Genotypes from "Human Origins" (Lazaridis et al. 2014, 2016)



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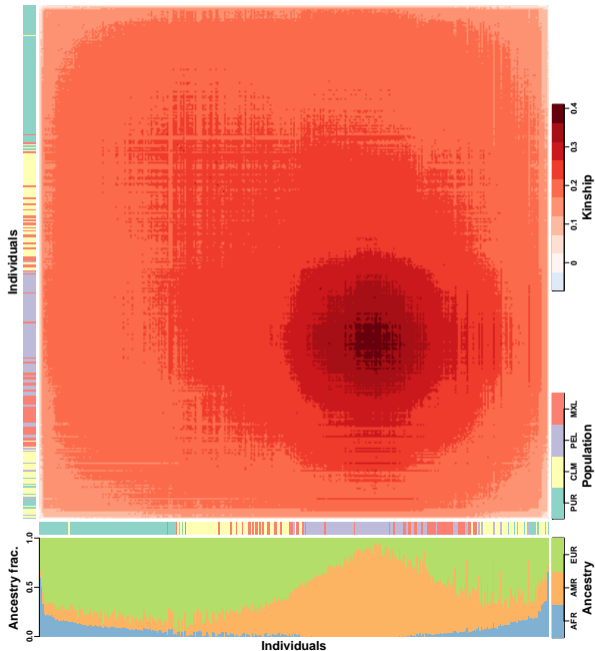
Population-level inbreeding



Kinship driven by admixture in Hispanics

New kinship estimates

Genotypes from the 1000 Genomes Project (2012)



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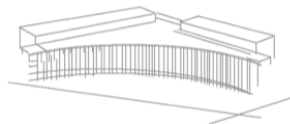
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