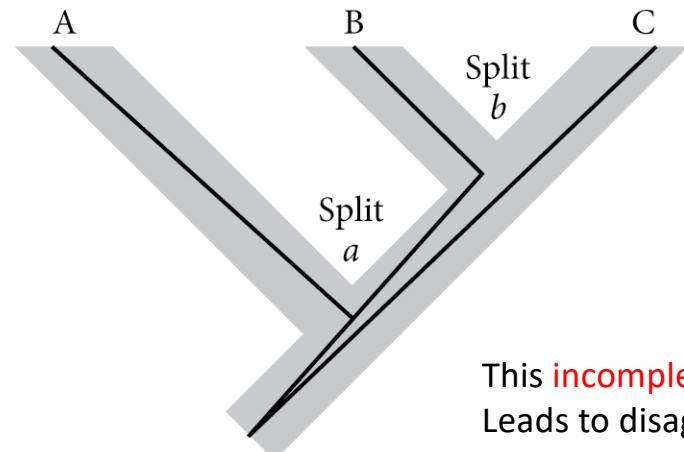
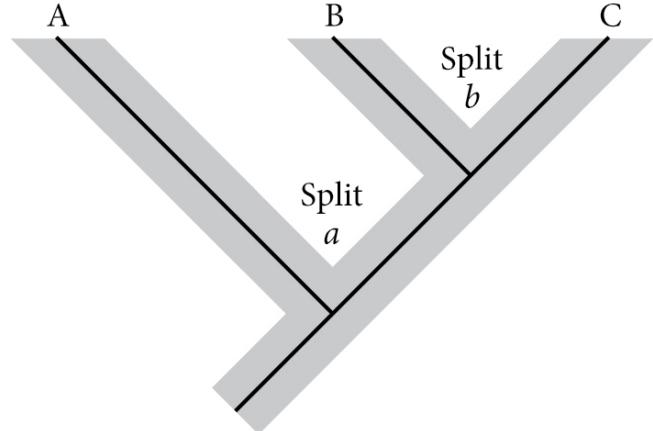


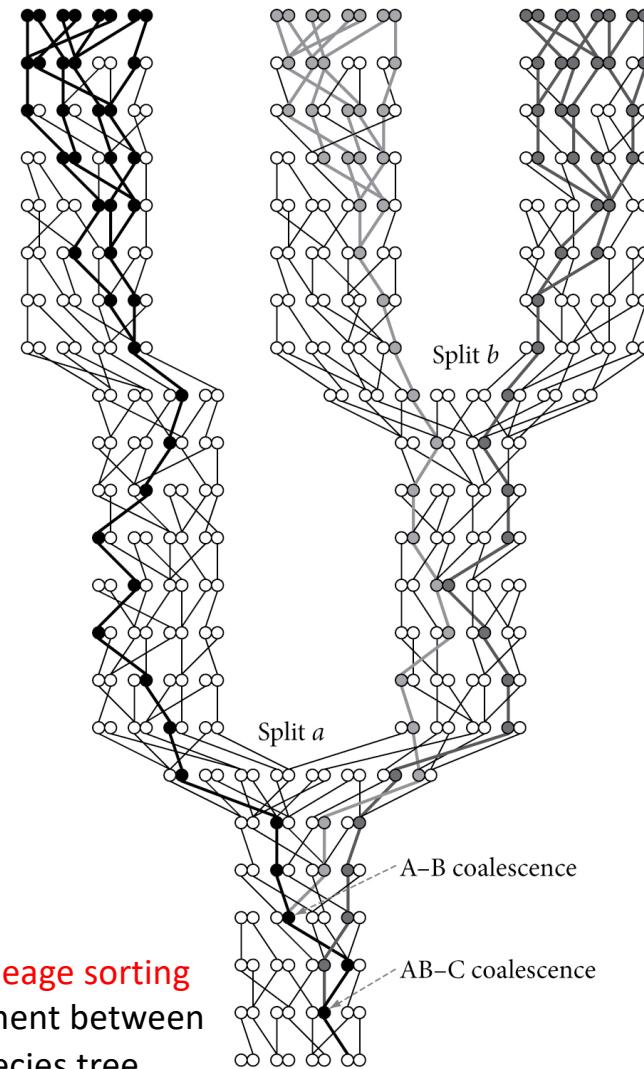
Project
overview



© Jon Fjeldså



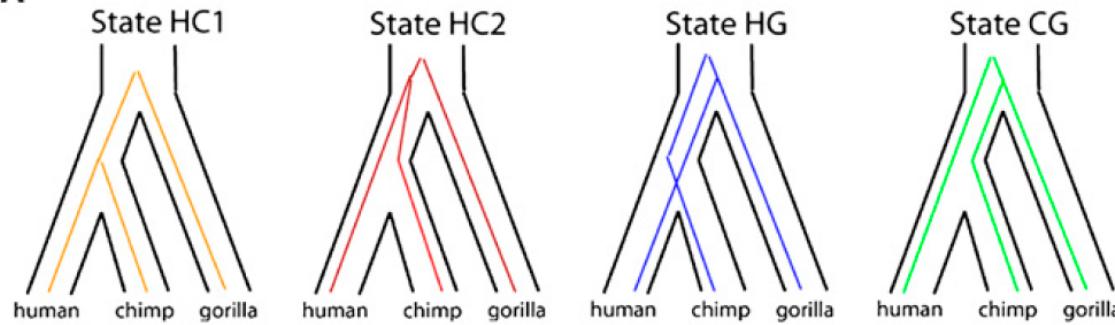
This **incomplete lineage sorting**
Leads to disagreement between
Gene trees and species tree.



Baum & Smith book

Human-Chimp-Gorilla incomplete lineage sorting

A



Species tree:

Uninformative

Agrees

Two speciation events

$n = 3$



5 patterns

Disagrees

1	0	0	1	0
0	1	0	1	0
0	0	1	1	0

1 pattern

0

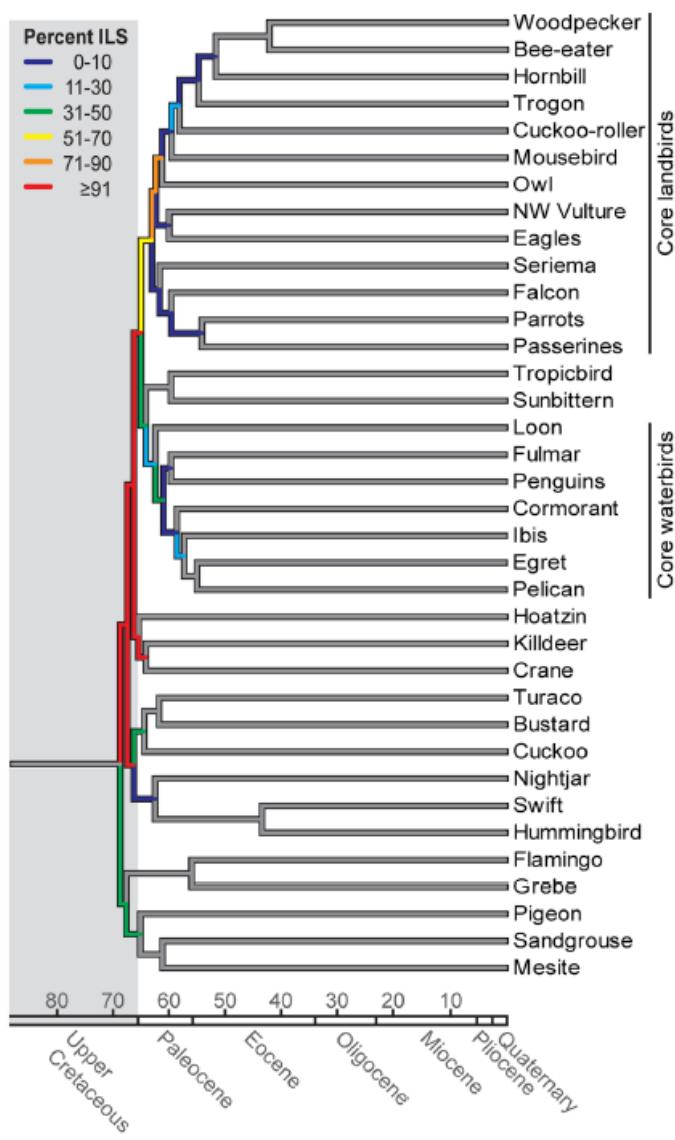
2 patterns

0

1

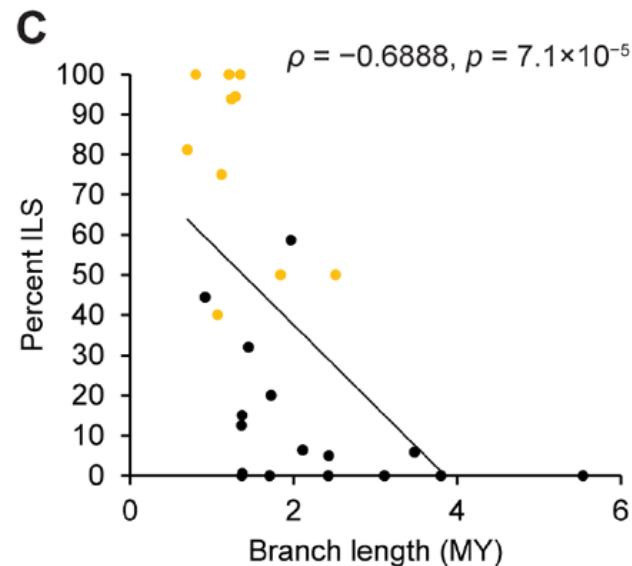
1

1

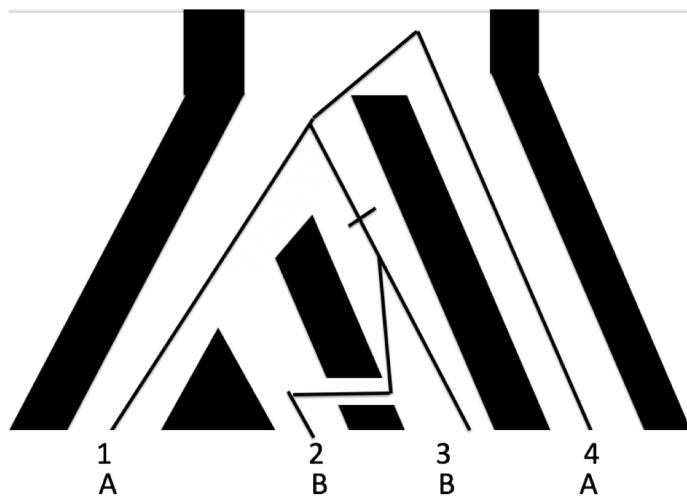
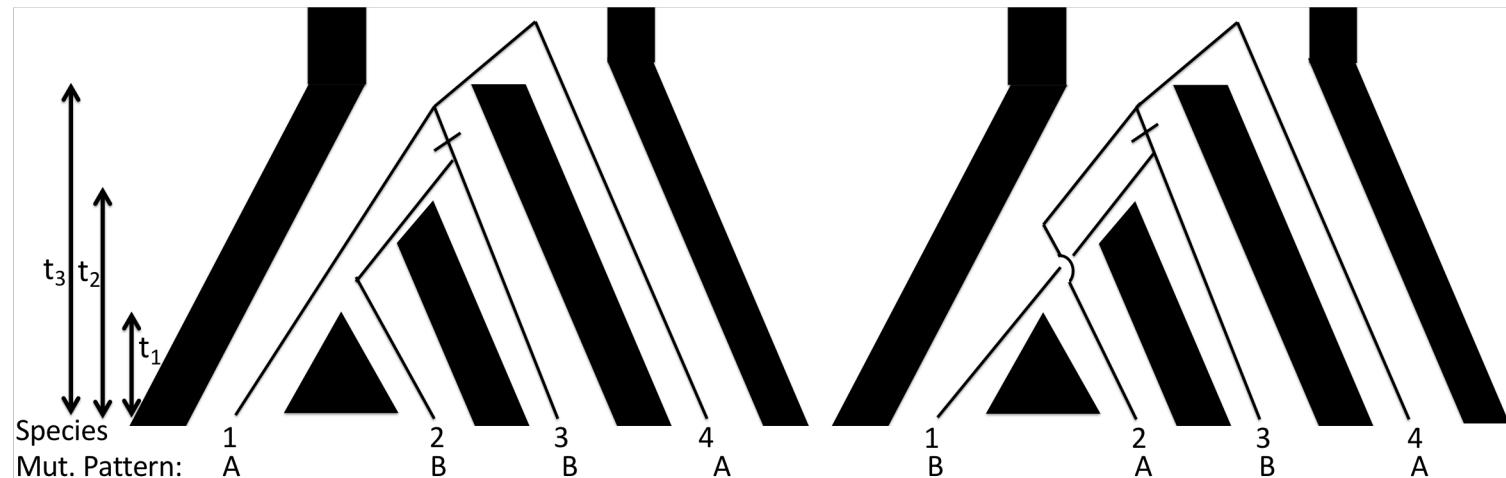


The Dynamics of Incomplete Lineage Sorting across the Ancient Adaptive Radiation of Neoavian Birds

Alexander Suh*, Linnéa Smeds, Hans Ellegren

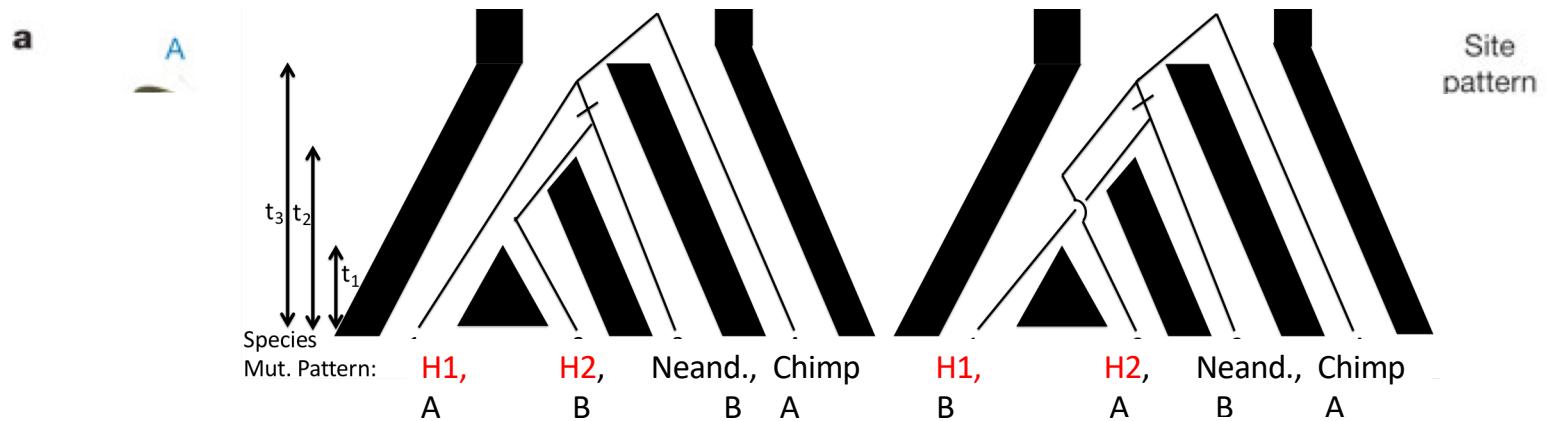


Gene tree-species tree conflict can result from introgression or incomplete lineage sorting



Distinguishing incomplete lineage sorting from
introgression (ABBA-BABA statistic)
Under incomplete lineage sorting & no introgression
Number of ABBA loci = Number of BABA loci
 $D = (\#(BABA) - \#(ABBA))/C, C = \#(ABBA) + \#(BABA)$

Green et al 2010, Nature



Under incomplete lineage sorting & no introgression

Number of ABBA loci = Number of BABA loci

$$D = (\#(BABA) - \#(ABBA))/C; C = \#(ABBA) + \#(BABA)$$

Genetic history of an archaic hominin group from Denisova Cave in Siberia

David Reich^{1,*}, Richard E. Green^{3,4,*}, Martin Kircher^{1*}, Johannes Krause^{3,5*}, Nick Patterson^{2*}, Eric Y. Durand⁶, Bence Viola^{3,7*}, Adrian W. Briggs^{3,5}, Udo Stenzel³, Philip L. F. Johnson³, Tomislav Maricic³, Jeffrey M. Good⁸, Tomas Marques-Bonet^{10,11}, Can Alkan¹⁰, Qiaomei Fu^{3,12}, Swapna Mallik^{1,2}, Heng Li¹³, Matthias Meyer⁹, Evan E. Eichler¹⁰, Mark Stoneking³, Michael Richards^{7,13}, Sahra Talamo⁹, Michael V. Shunkov¹⁴, Anatoli P. Derevianko¹⁴, Jean-Jacques Hublin¹, Janet Kelso³, Montgomery Slatkin⁶ & Svante Pääbo³

Table 1 | Sharing of derived alleles between present-day and archaic hominins

Sample H ₁	Sample H ₂	Source of data for H ₁ and H ₂	D(H ₁ , H ₂ , Neanderthal, chimpanzee)					D(H ₁ , H ₂ , Denisova, chimpanzee)				
			n _{BABA}	n _{ABBA}	D (%)	s.e. (%)	Z-score	n _{BABA}	n _{ABBA}	D (%)	s.e. (%)	Z-score
African/African*												
San	Yoruba	Ref. 8	23,690	23,855	-0.3	0.6	-0.6	39,042	39,019	0.0	0.5	0.1
Eurasian/African*												
French	San	Ref. 8	25,242	22,982	4.7	0.6	7.6†	39,838	38,495	1.7	0.5	3.4†
French	Yoruba	Ref. 8	21,794	19,890	4.6	0.7	6.9†	34,262	33,078	1.8	0.5	3.6†
Han	San	Ref. 8	25,081	22,470	5.5	0.6	8.5†	38,815	37,439	1.8	0.5	3.4†
Han	Yoruba	Ref. 8	21,741	19,412	5.7	0.7	7.9†	33,182	32,184	1.5	0.5	2.8
Eurasian/Melanesian*												
French	Papuan1	Ref. 8	15,523	15,548	-0.1	0.8	-0.1	23,509	25,470	-4.0	0.7	-5.7†
Han	Papuan1	Ref. 8	15,059	14,677	1.3	0.9	1.5	22,262	24,198	-4.2	0.7	-5.8†
Melanesian/African*												
Papuan1	San	Ref. 8	21,985	20,366	3.8	0.7	5.1†	35,923	32,841	4.5	0.6	7.2†
Papuan1	Yoruba	Ref. 8	19,107	17,646	4.0	0.8	4.9†	30,995	28,186	4.7	0.6	7.4†



Do your genes make you a criminal?

In the US a murderer is claiming his crime was the tragic consequence of being born a killer. Steve Connor reports on new arguments over whether some people are destined to be bad

STEVE CONNOR | Sunday 12 February 1995



Overweight? Maybe You Really Can Blame Your Genes



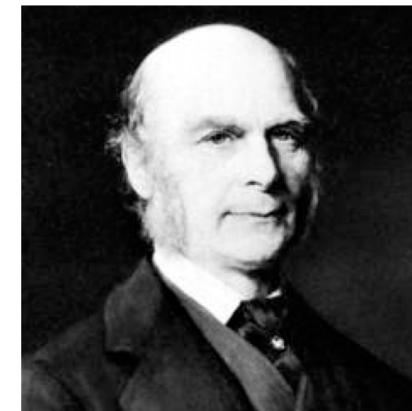
Phenotypic Resemblance between relatives

- Covariance
- Correlation
- Slope of linear regression

Francis Galton

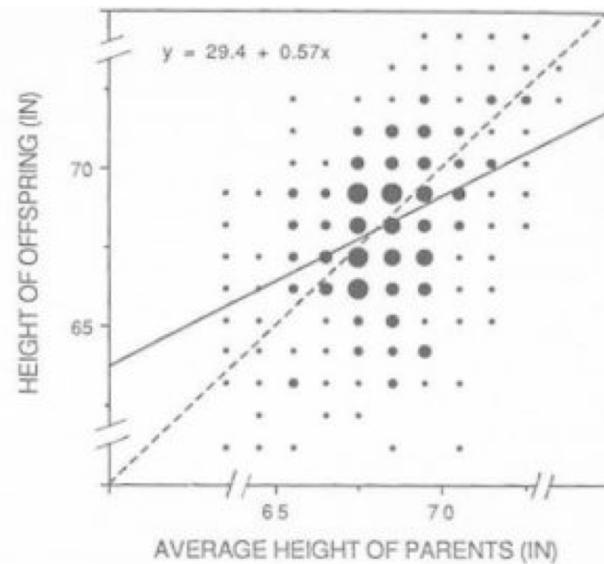
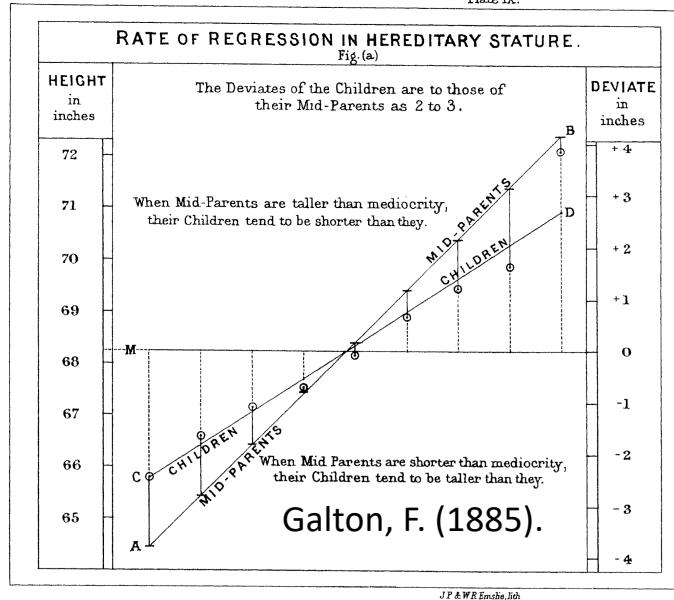
Phenotypic variation within a population is usually continuous, often has a normal distribution.

Inheritance is the blending together of parental phenotypes.



Regression towards mediocrity (the mean)

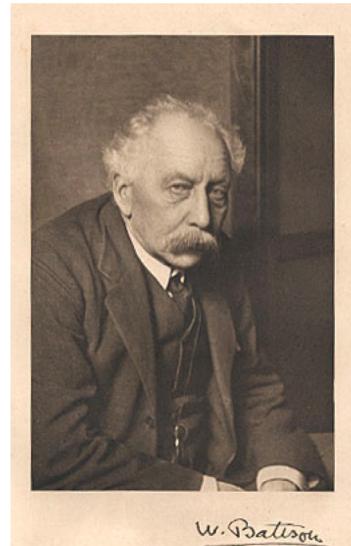
Plate IX.



Resemblance between relatives

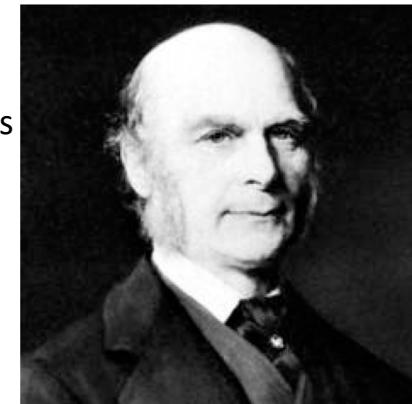


Gregor Mendel
And the Mendelians
e.g. Bateson



Galton

And the Biometrists
e.g. Pearson and
Weldon



R.A. Fisher (1918)

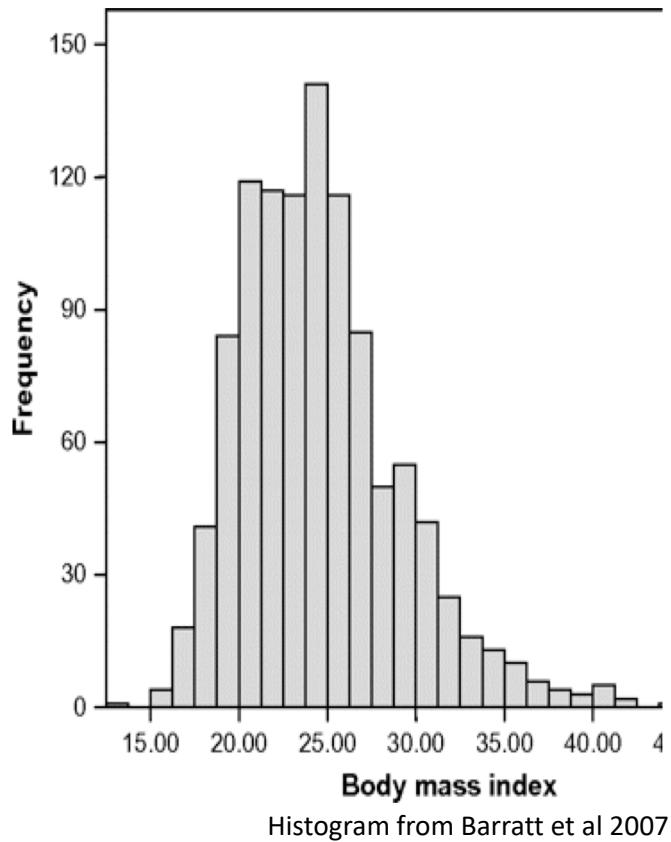
"The correlations between relatives on the supposition of Mendelian inheritance"

- Reconciled these two views by showing that the mendelian inheritance of many alleles, each of small effect, gave rise to:
 - Resemblance between relatives.
 - regression towards the mean.

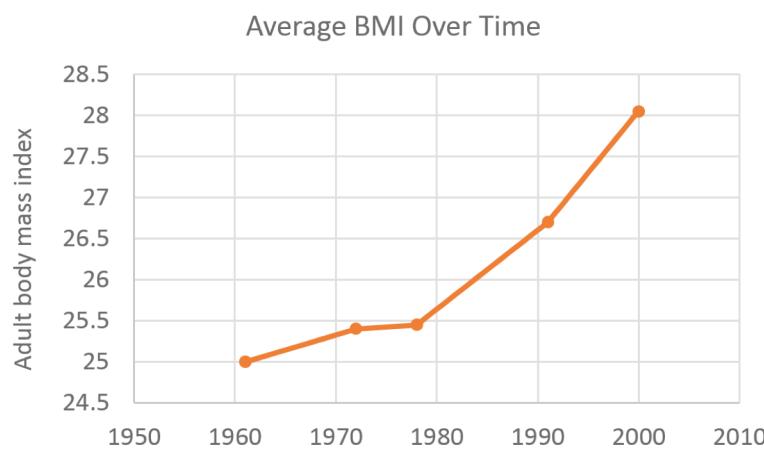


The apparent 'blending' of traits is due to inheritance $\frac{1}{2}$ alleles from Mum and $\frac{1}{2}$ from Dad.

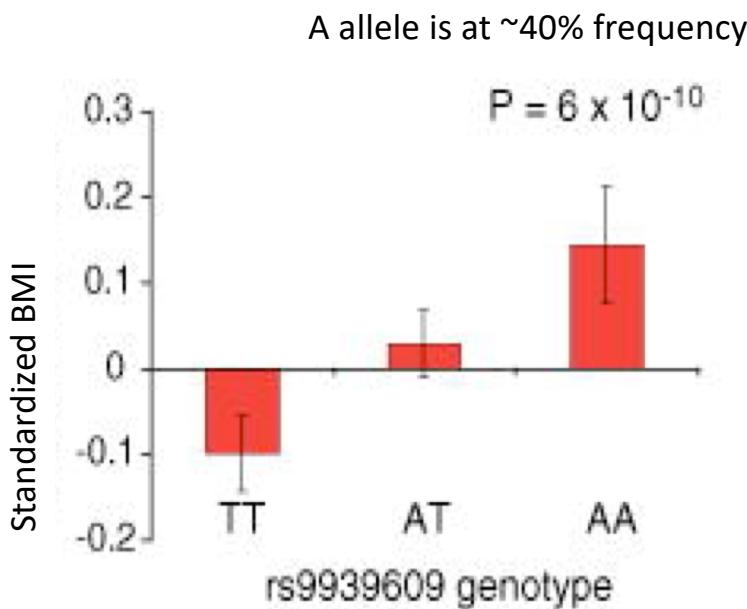
To what extent is my weight genetic?



My height ~6 foot
My weight ~160 pounds
My BMI 21.7



Phenotypes are always due to the interaction of genes and environments.



A Common Variant in the *FTO* Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity

Timothy M. Frayling,^{1,2*} Nicholas J. Timpson,^{3,4*} Michael N. Weedon,^{1,2*} Eleftheria Zeggini,^{3,5*}

My BMI is 22.4

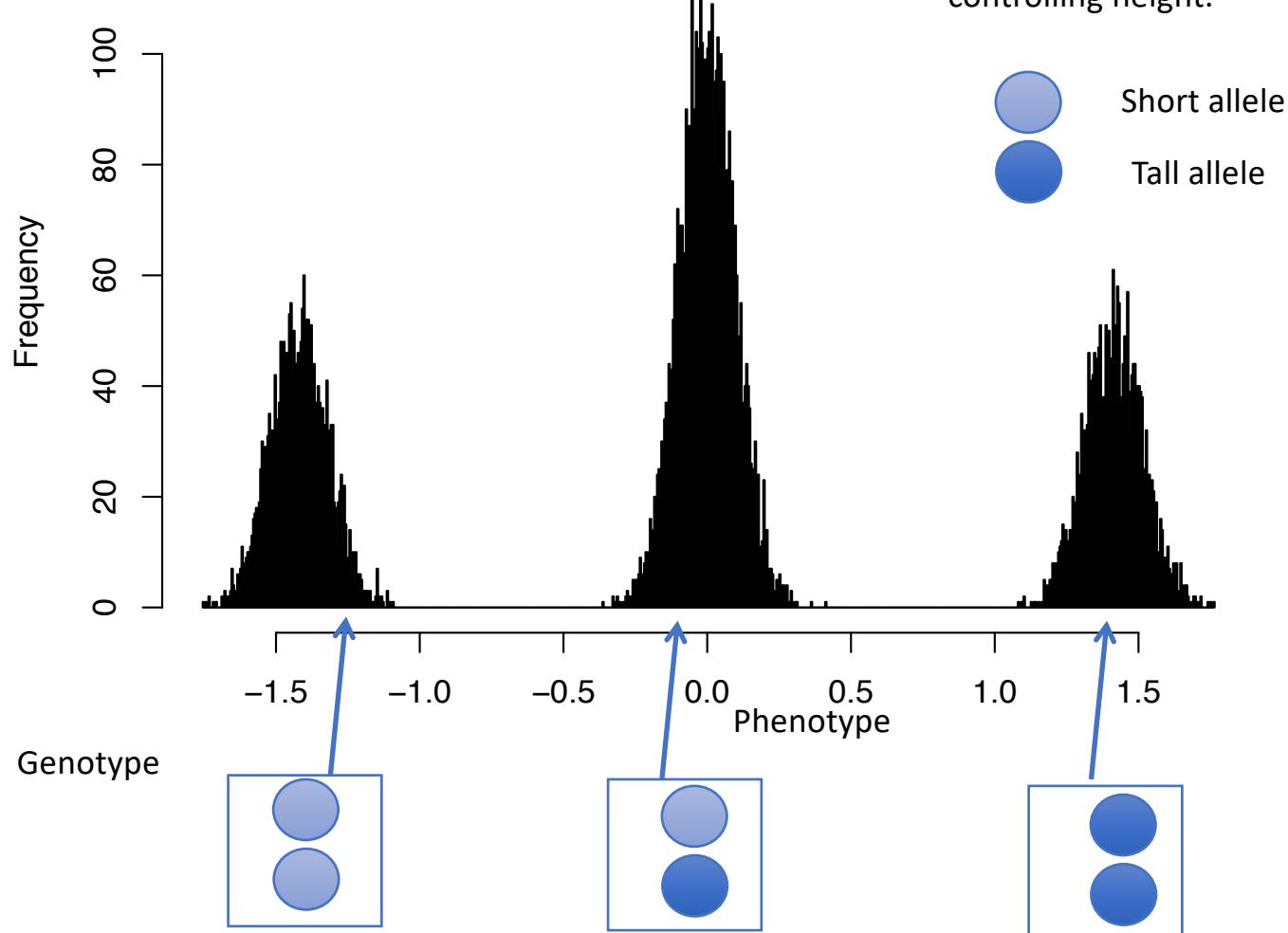
Top 6 Alleles associated with BMI:

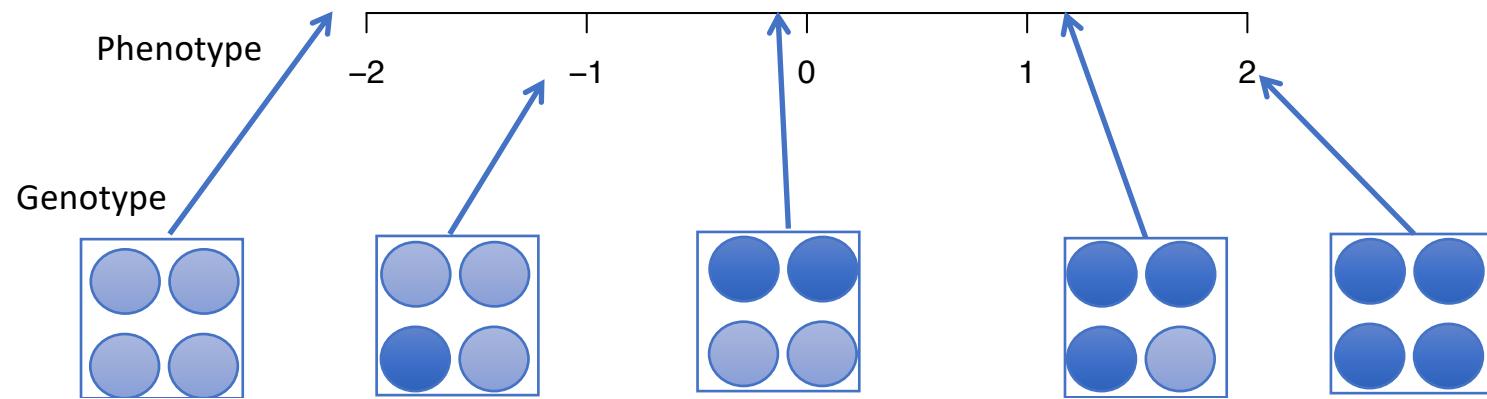
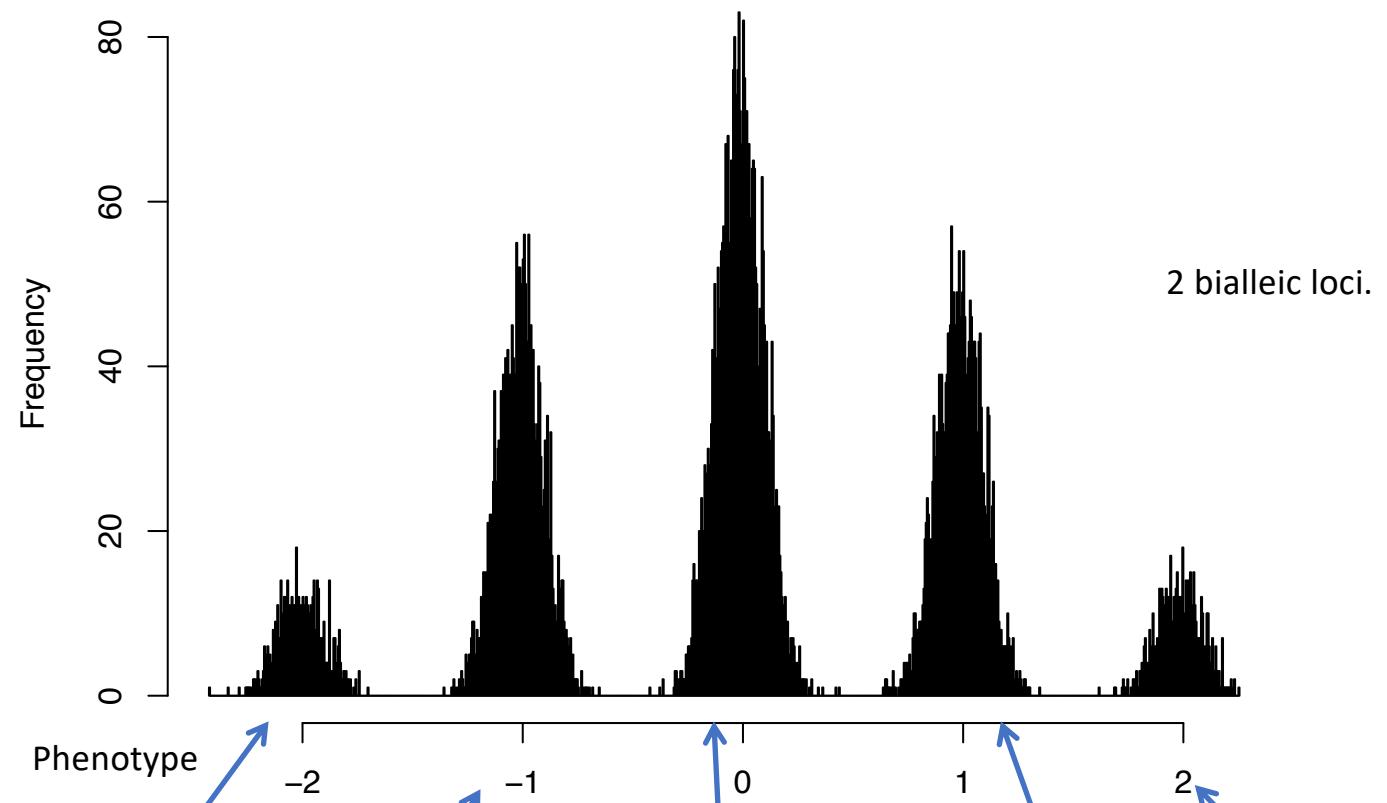
SNP name	My Genotype	Avg. Effect on BMI*
rs3751812	GT	0.33 for each T
rs10871777	AA	0.2 for each G
rs13130484	CC	0.19 for each T
rs4788102	GG	0.15 for each A
rs10838738	AA	0.07 for each G
rs3101336	CT	0.1 for each C

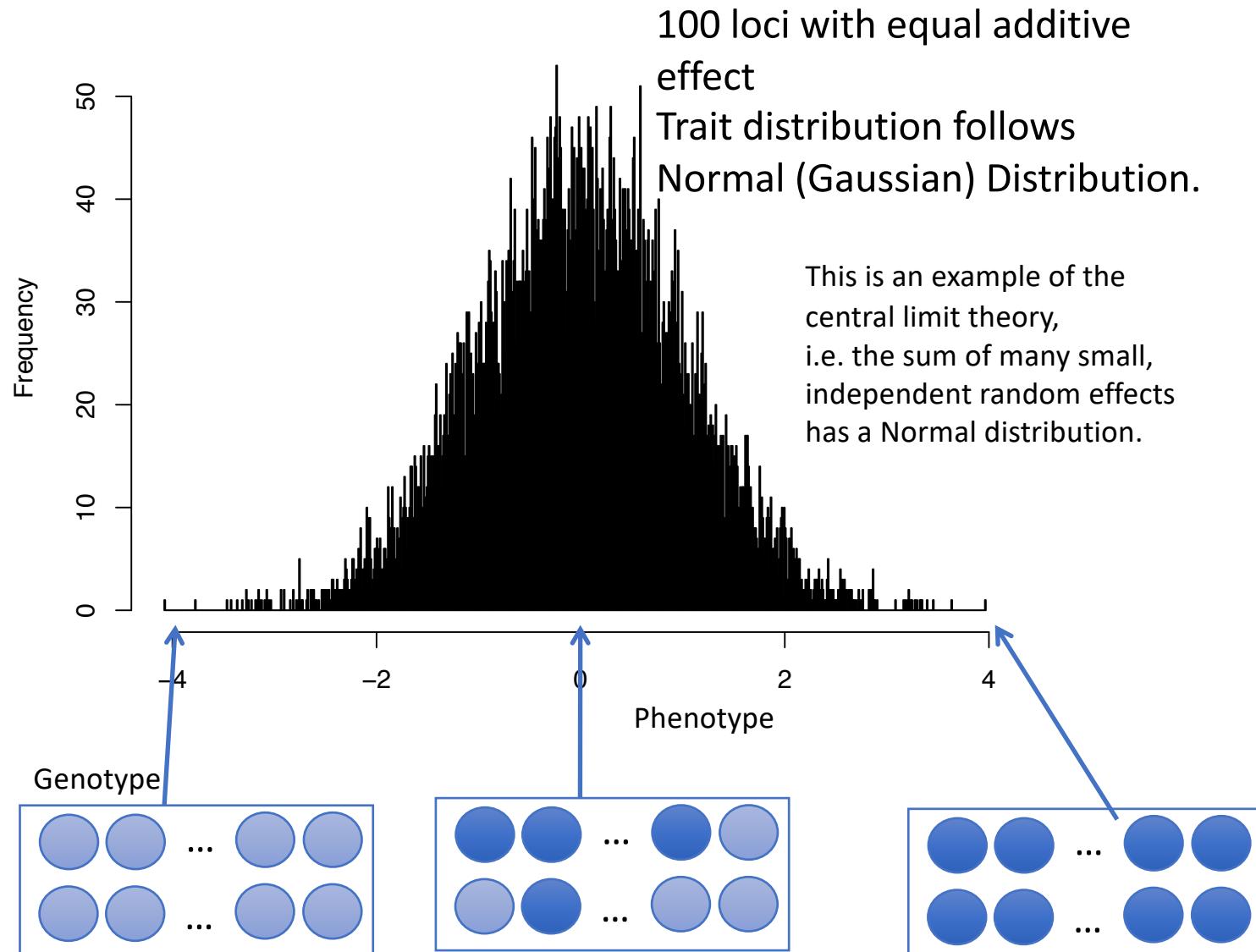
There are many hundreds more genetic variants contributing to BMI.

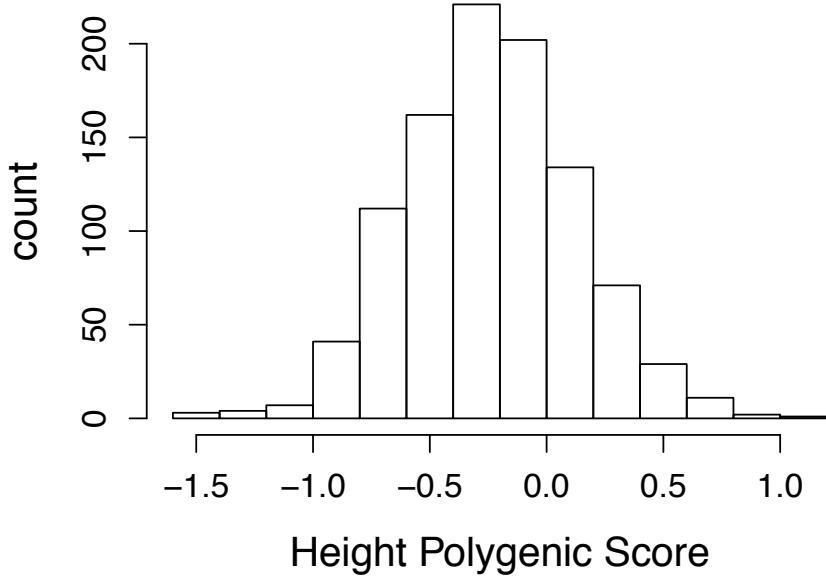
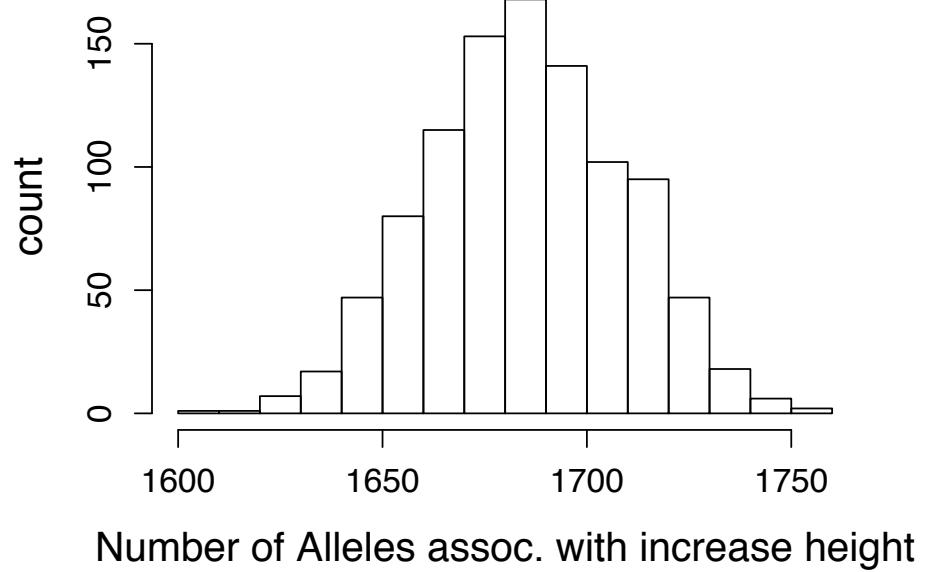
*Calculated by 23&Me.

Two alleles at a single locus controlling height.









Resemblance between relatives in Quantitative traits

- Individual 1's phenotype = X_1
- Individual 2's phenotype = X_2
- Want to know the $\text{cov}(X_1, X_2)$
- = $\text{Cov}((X_{1M} + X_{1P} + X_{1E}), (X_{2M} + X_{2P} + X_{2E}))$