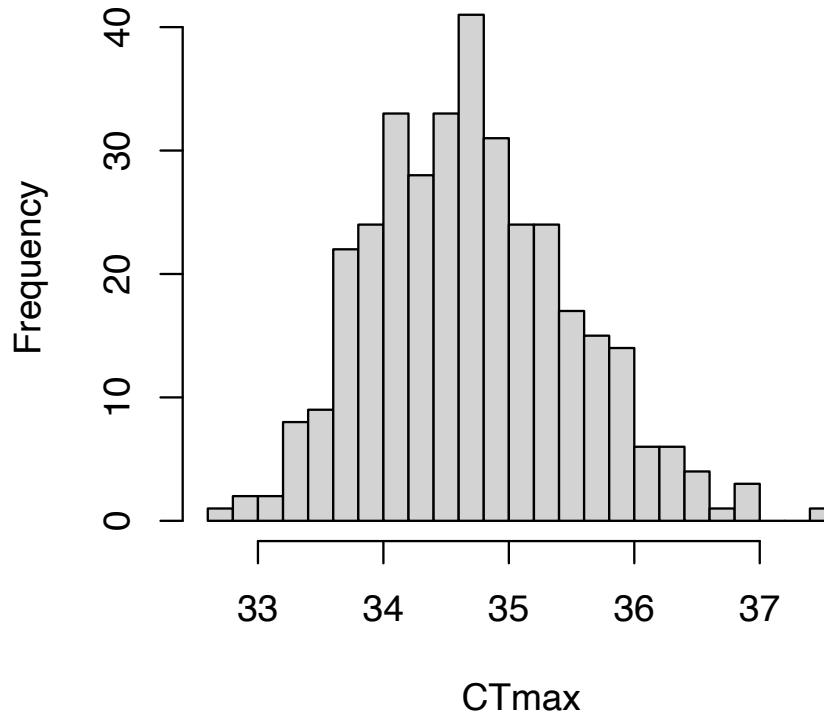


Quantitative genetics

What is a phenotype?

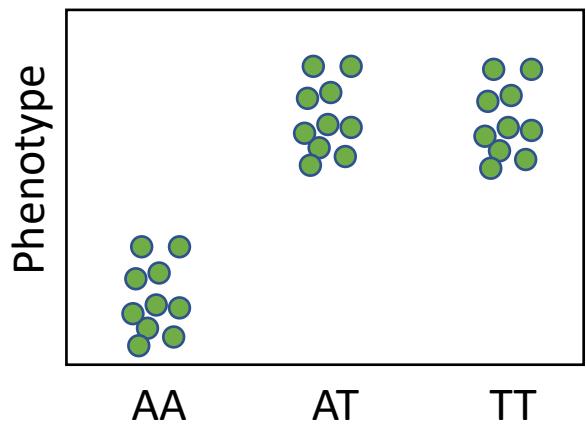
- any measurable aspect of an organism
- Discrete versus quantitative traits

- How does phenotypic variation among individuals in a population arises as a result of genetic variation in the population

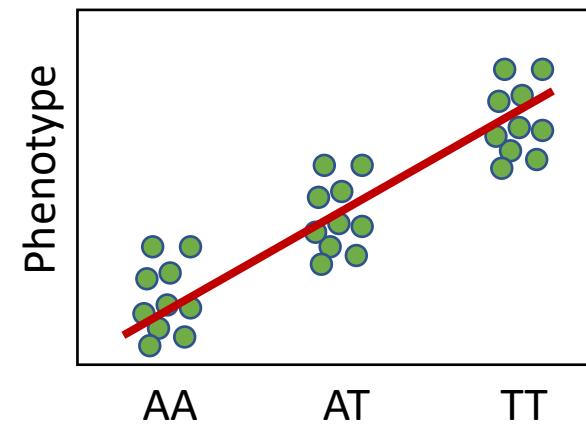


- How do we square continuous traits with mendelian genetics?

Dominant/recessive

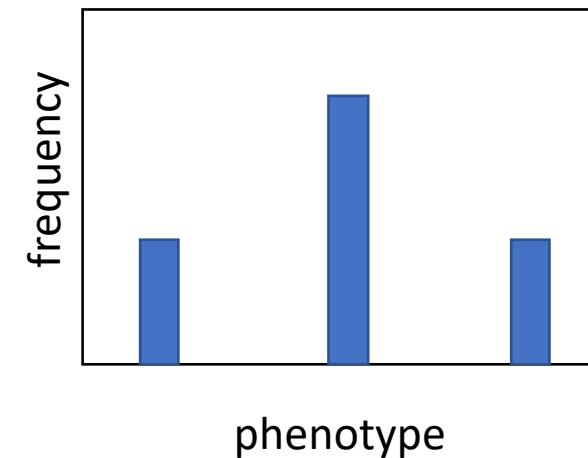
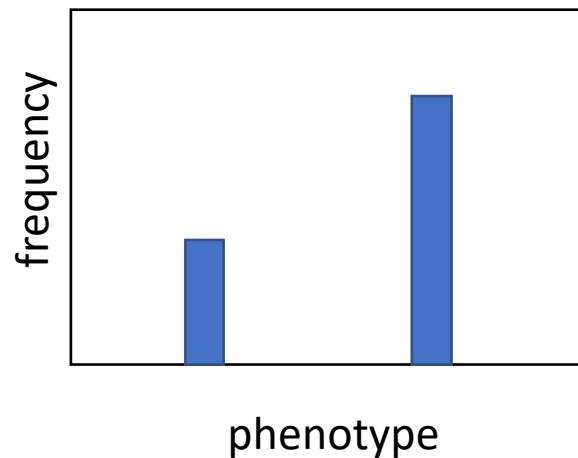


additive



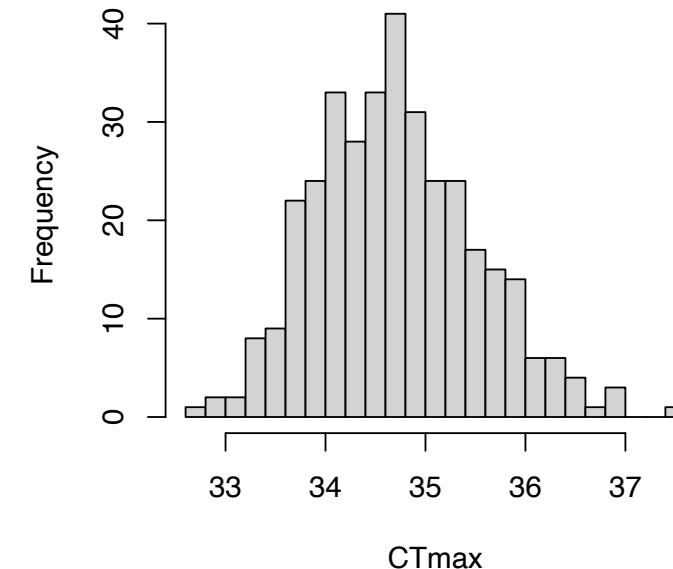
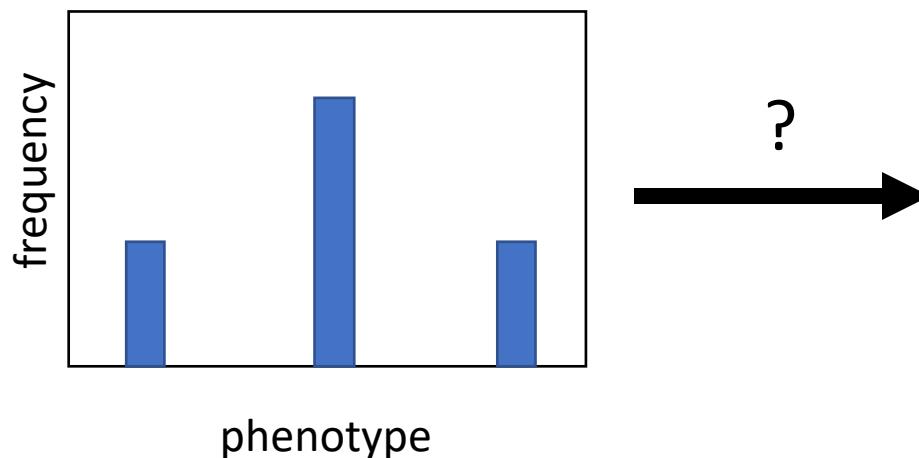
$$X \sim \mu + a_i G_i$$

μ = mean phenotype
 a_i = slope (effect size)
 G_i = genotype (0, 1, 2)



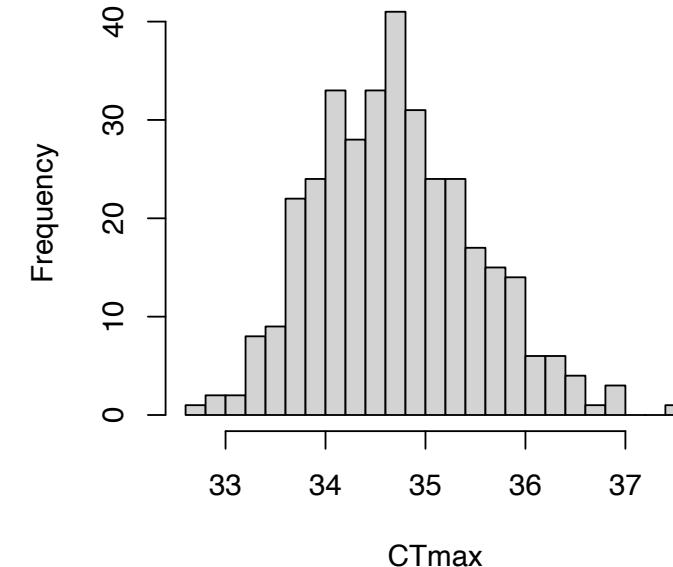
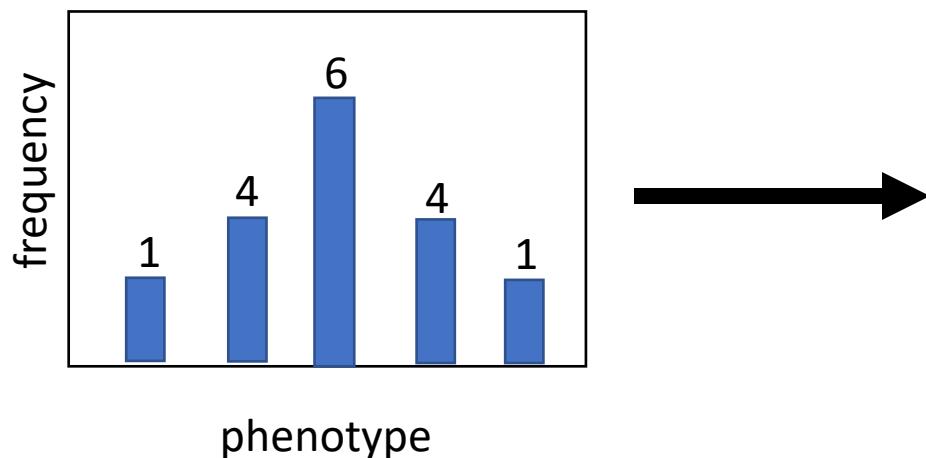
Additive single locus

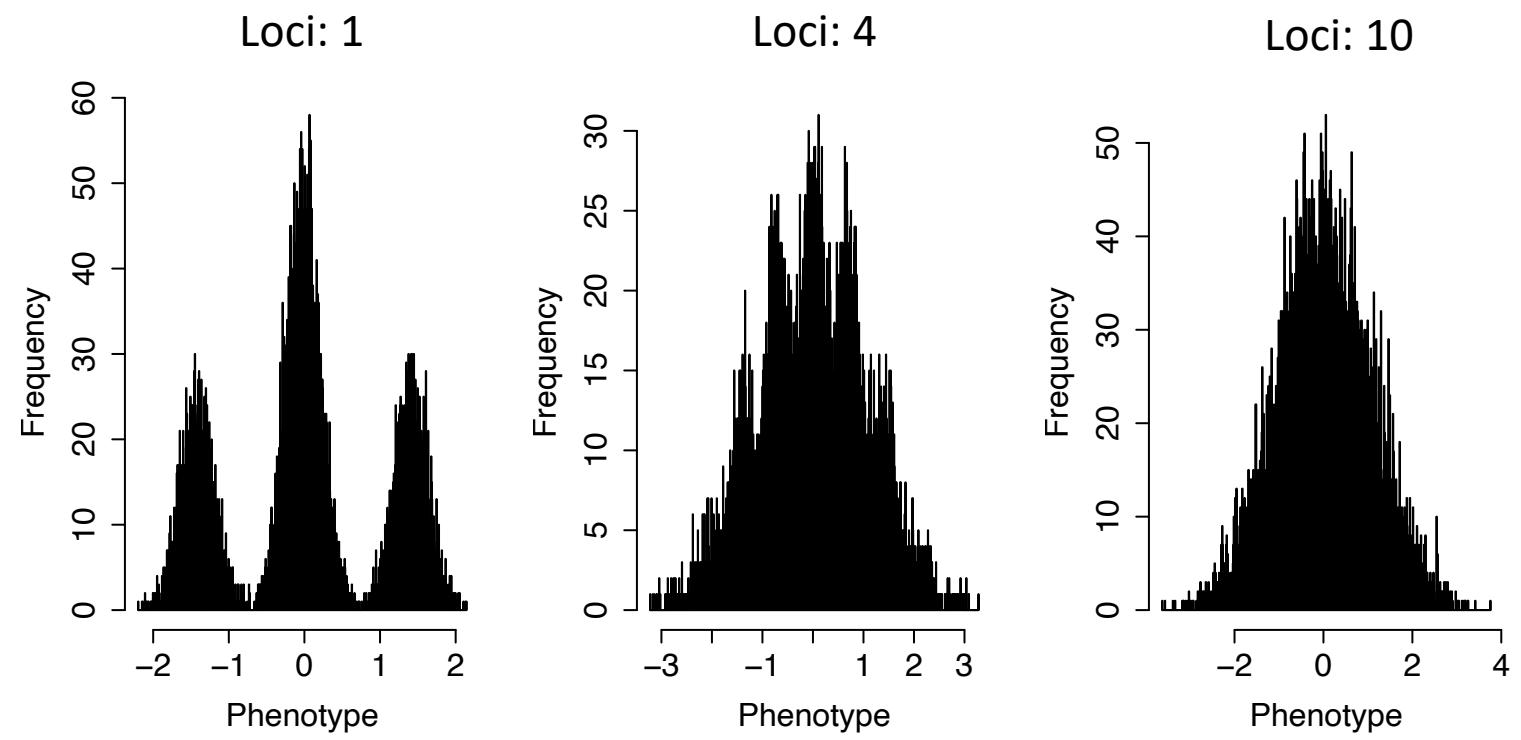
Genotype	Number of alleles	Frequency	Phenotype
AA	2	$\frac{1}{4}$	$\mu + 2a$
Aa	1	$\frac{1}{2}$	$\mu + a$
aa	0	$\frac{1}{4}$	μ



Additive two loci

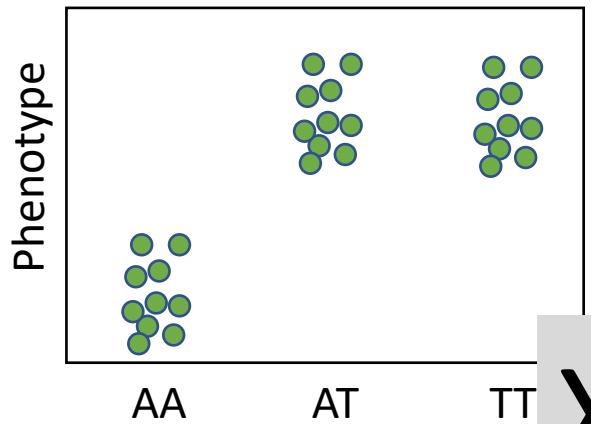
Genotype	Number of alleles	Frequency	Phenotype
AABB	4	1/16	$\mu + 4a$
AABb, AaBB	3	4/16	$\mu + 3a$
AaBb + aaBB	2	6/16	$\mu + 2a$
Aabb + aaBb	1	4/16	$\mu + a$
aabb	0	1/16	μ



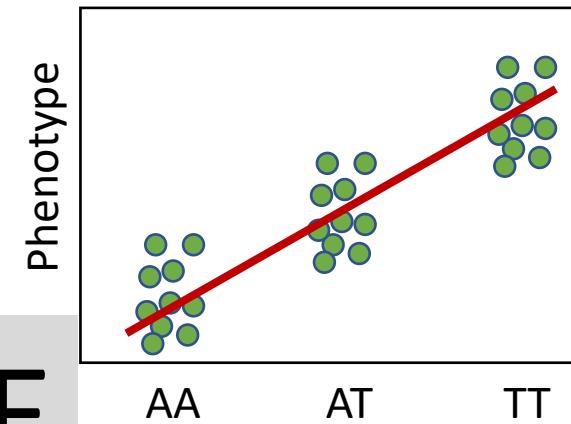


Why do we have noise in the phenotypes?

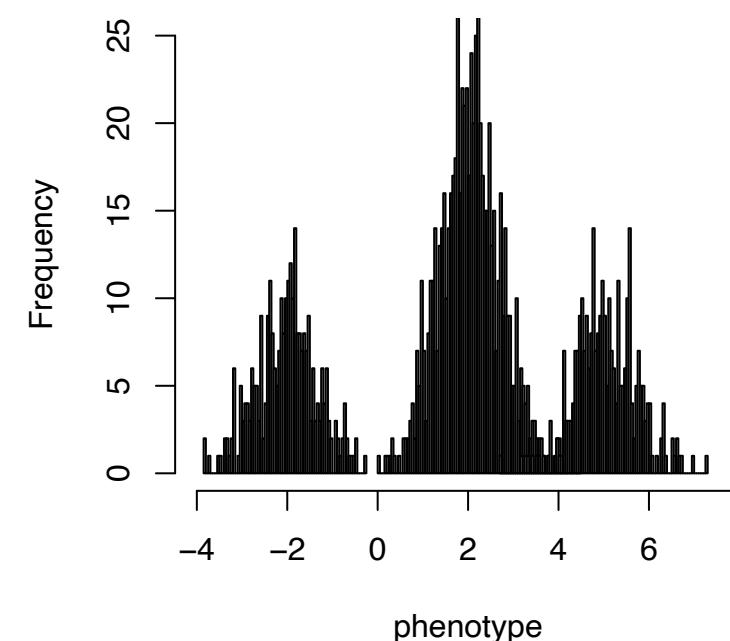
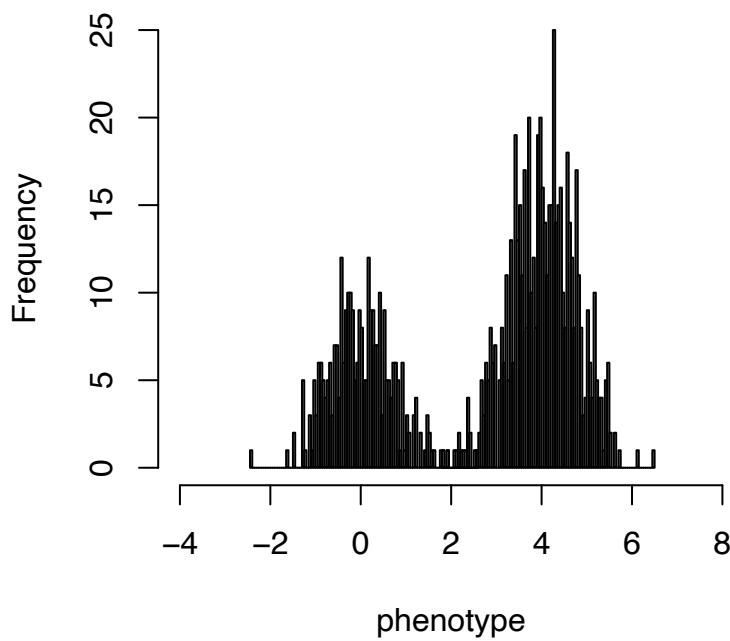
Dominant/recessive



additive

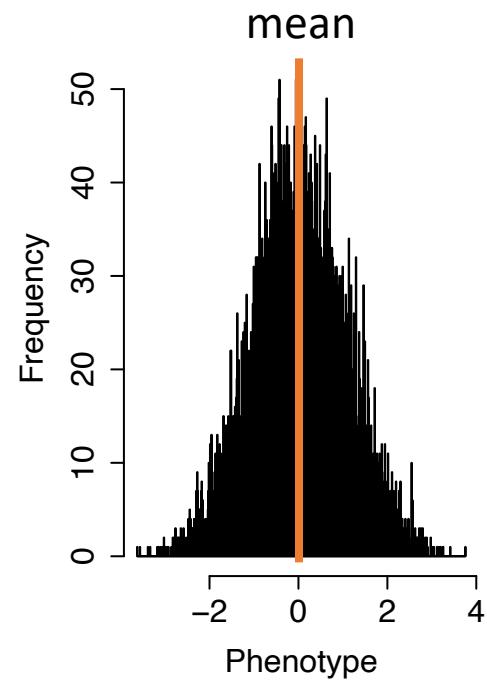


$$X = G + E$$



- Quantitative traits → traits you can measure, continuous
- Quantitative traits causes by many loci (polygenic), environment
- The goal of quantitative genetics is to understand the variance of traits

- The goal of quantitative genetics is to understand the variance of traits



Phenotypic variance = Genetic variance + Environmental variance

$$V_P = V_G + V_E$$

$$V_P = V_G + V_E$$

Heritability

- The proportion of total phenotypic variance due to genetic effects

Broad-sense heritability

$$H^2 = \frac{V_G}{V_G + V_E}$$

Q1: In humans, what is the heritability of having a head?

Q2: Imagine you estimate heritability of temperature tolerance of copepods on the west shore.

Next year you repeat your experiment on the east shore and find your estimation has decreased.

What explains this?

$$V_P = V_G + V_E$$

Heritability

- The proportion of total phenotypic variance due to genetic effects

Broad-sense heritability

$$H^2 = \frac{V_G}{V_G + V_E}$$

$$V_G = V_A + V_I$$

Narrow-sense heritability

$$h^2 = \frac{V_A}{V_G + V_E}$$

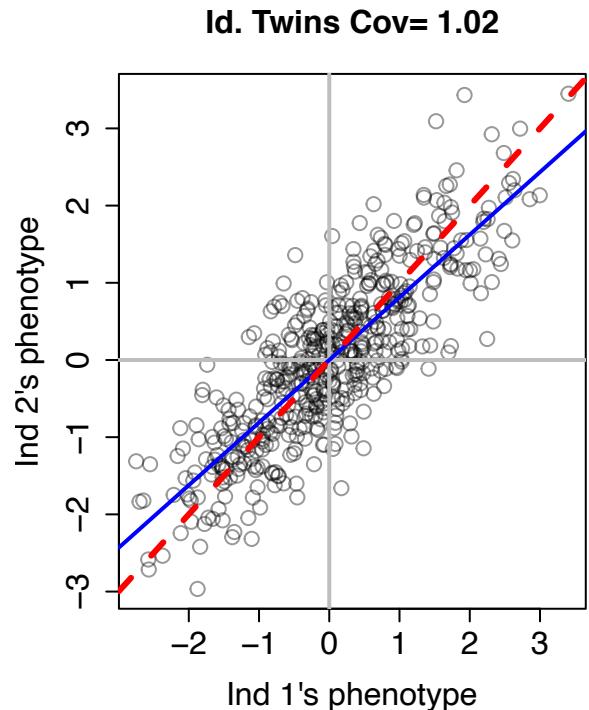
proportion of variance explained by
the additive effect of loci

This is what is passed on to offspring

How to estimate h^2

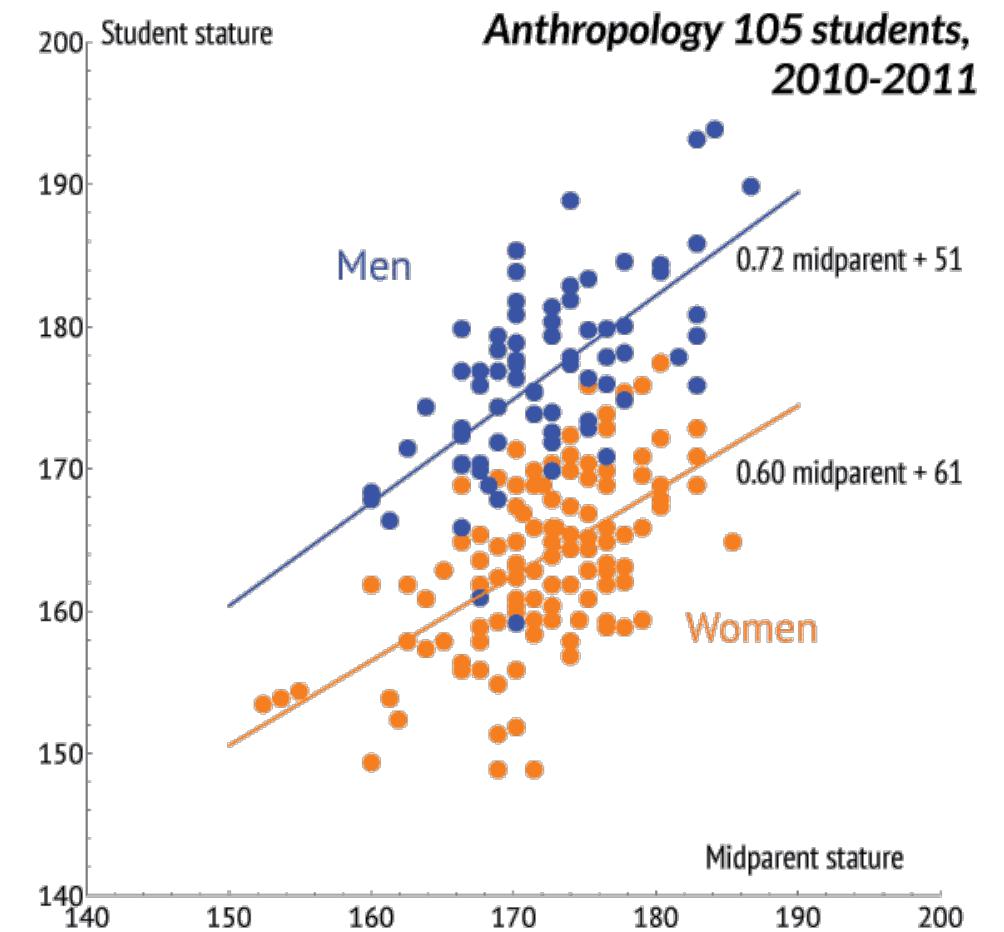
- Covariance between relatives
 - Covariance is degree that x and y deviate from their mean in the same way.

If $V_A = 1$



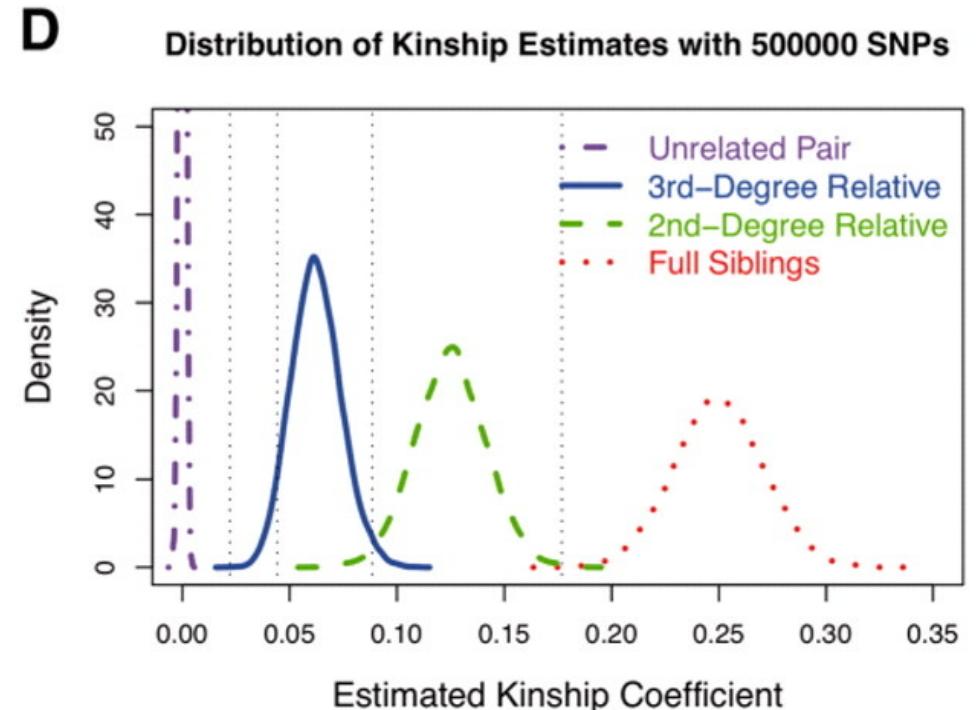
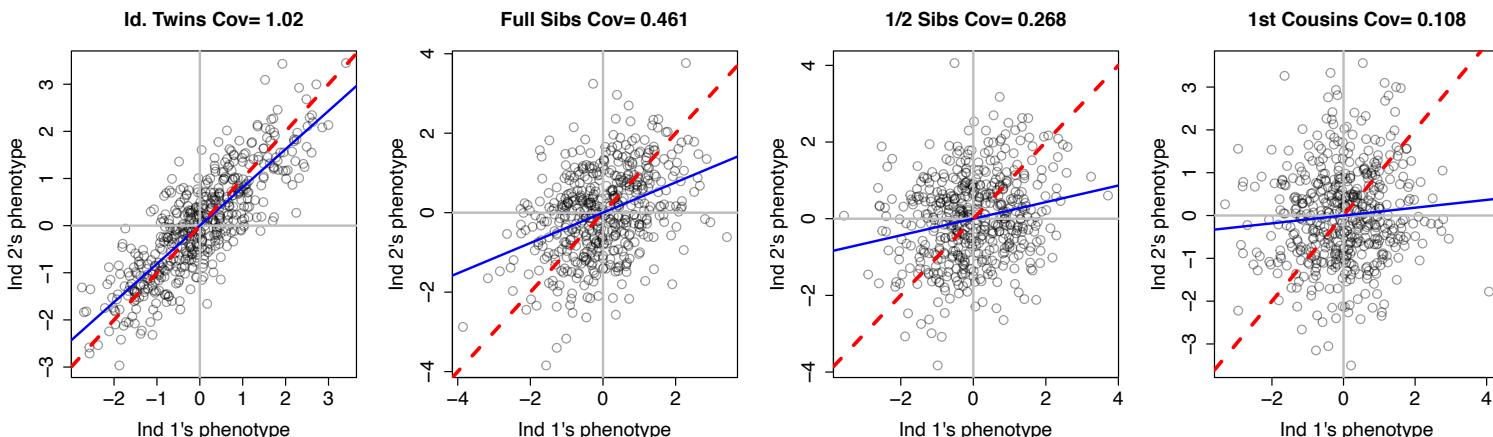
Parent-offspring covariance

- $\text{Cov}(\text{parent}, \text{offspring}) = \frac{V_A}{2}$
 - Why divide by 2?
- Regression of mid-parent phenotype with offspring
- We don't need to know anything about the genes
- Can use same principles for other related individuals



Estimating heritability from genomic data

- Can't generate families for all systems.
 - Time consuming, logically impossible
- Can estimate relatedness of individuals from genomic data
- Then we can apply the same principles as before



Manichaikul et al., 2010

2nd-degree relatives:

- half-sibs, aunts/unles and niece/nephew and grandparent-grandchild pairs)

3rd-degree relatives:

- first cousins

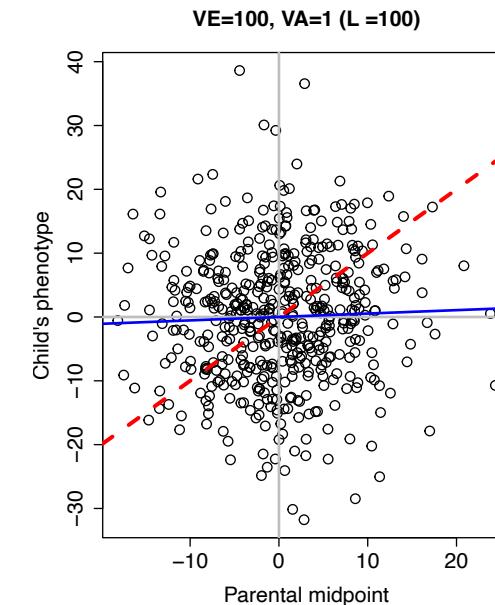
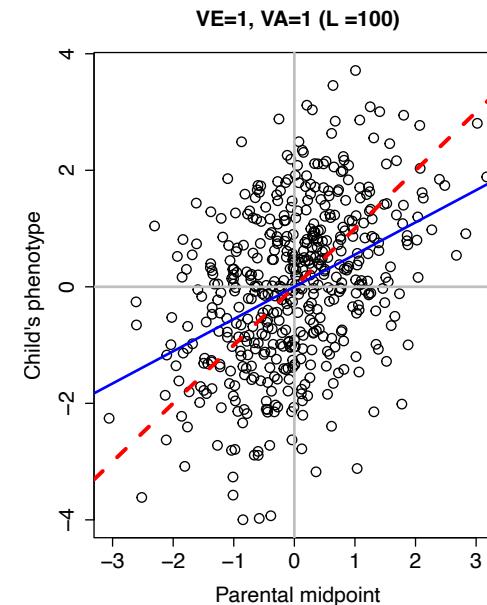
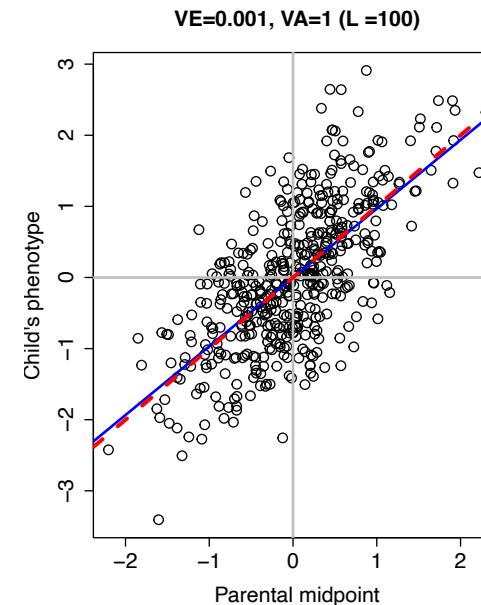
Typical h^2 values

Table 10.1 Approximate values of the heritability of various characters in animal species. The estimates are rounded to the nearest 5 per cent; their errors range from about 2 per cent to about 10 per cent.

	$h^2(\%)$	R
<i>Man</i>		
Stature	65	
Serum immunoglobulin (IgG) level	45	
<i>Cattle</i>		
Body weight (adult)	65	
Butterfat, %	40	
Milk-yield	35	
<i>Pigs</i>		
Back-fat thickness	70	
Efficiency of food conversion	50	
Weight gain per day	40	
Litter size	5	
<i>Poultry</i>		
Body weight (at 32 wks)	55	
Egg weight (at 32 wks)	50	
Egg production (to 72 wks)	10	
<i>Mice</i>		
Tail length (at 6 wks)	40	
Body weight (at 6 wks)	35	
Litter size (1st litters)	20	
<i>Drosophila melanogaster</i>		
Abdominal bristle number	50	
Body size	40	
Ovary size	30	
Egg production	20	

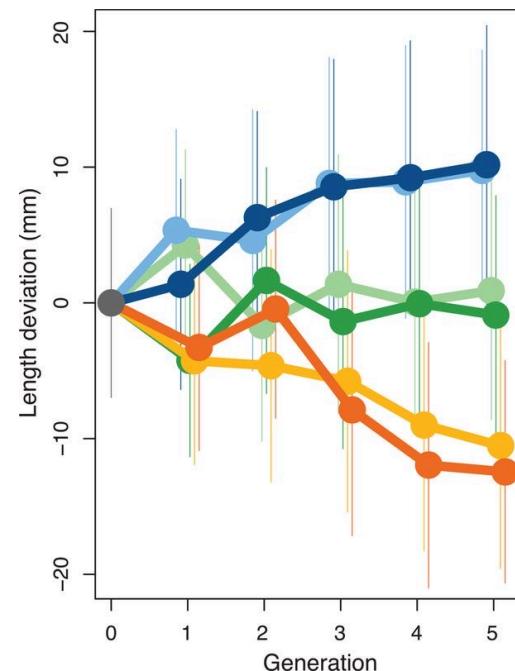
Important to remember

- Heritability estimates are not transferrable between populations or environments or time
- Given constant V_A , how could heritability change?



Why do we care about heritability?

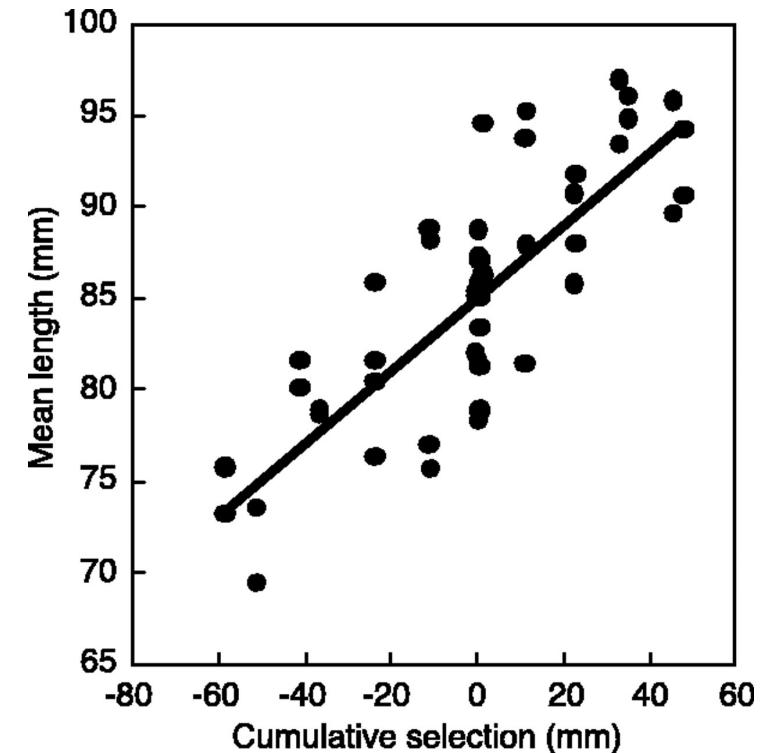
- If we know heritability, can predict responses to selection
- Breeder's equation:
 - $R = h^2 S$



Therkildsen et al., 2019

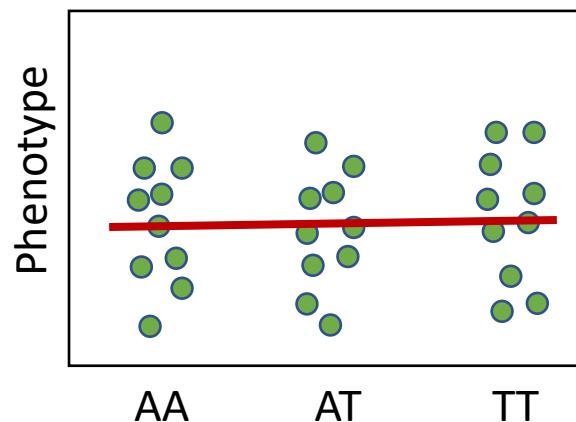
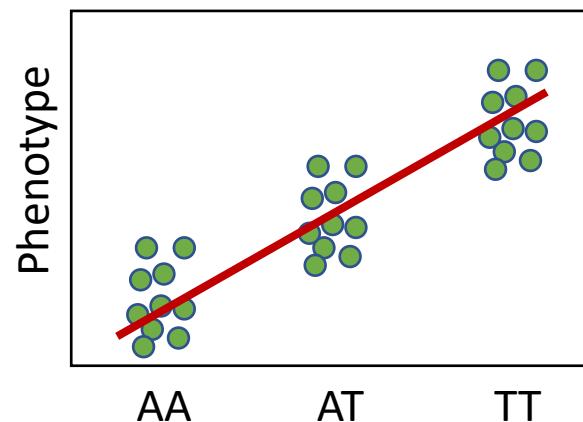
Sustaining Fisheries Yields Over Evolutionary Time Scales

David O. Conover* and Stephan B. Munch



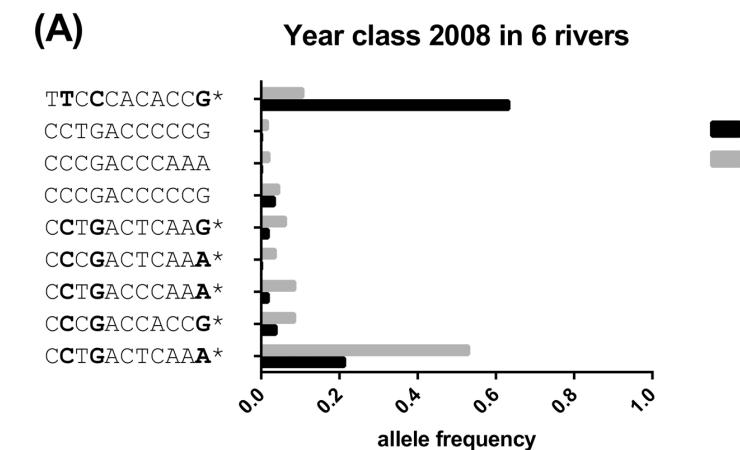
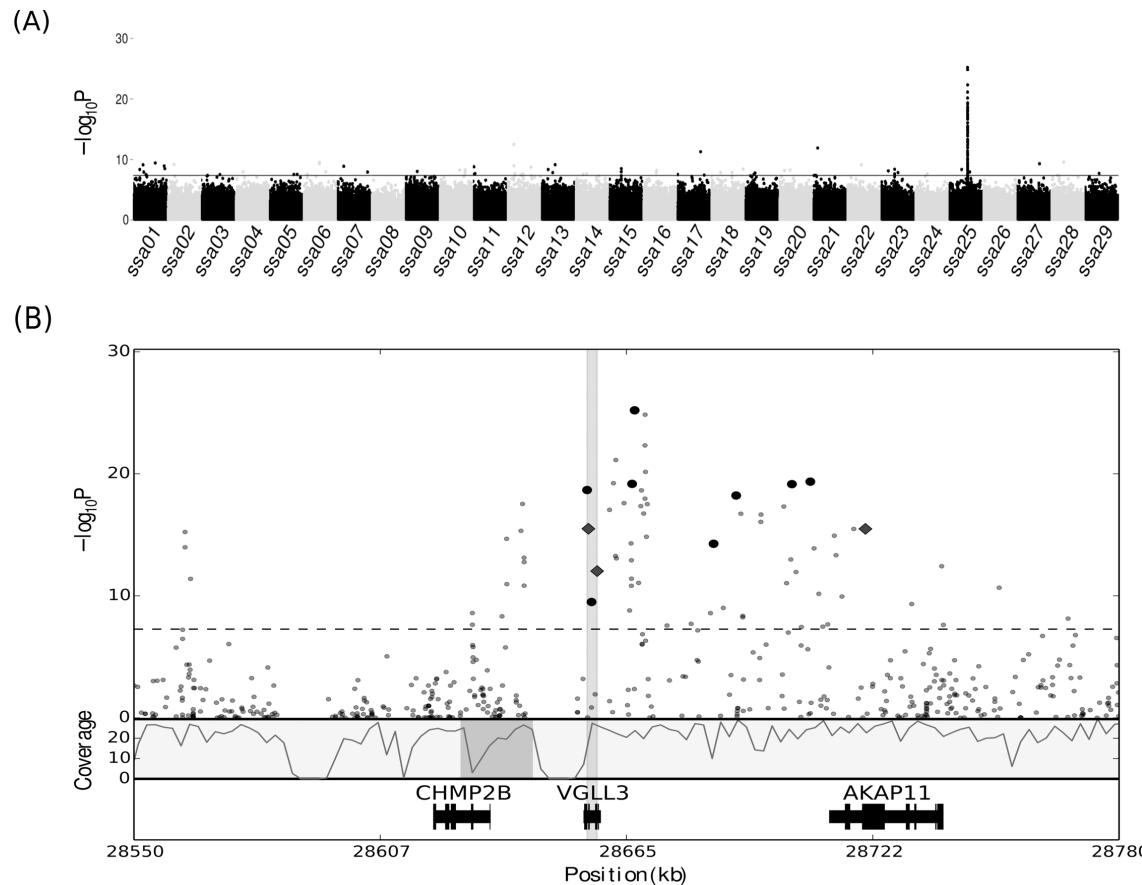
Genome-wide association studies

- Identify genotype-phenotype associations
- In contrast to QTL mapping, relies on natural levels of linkage



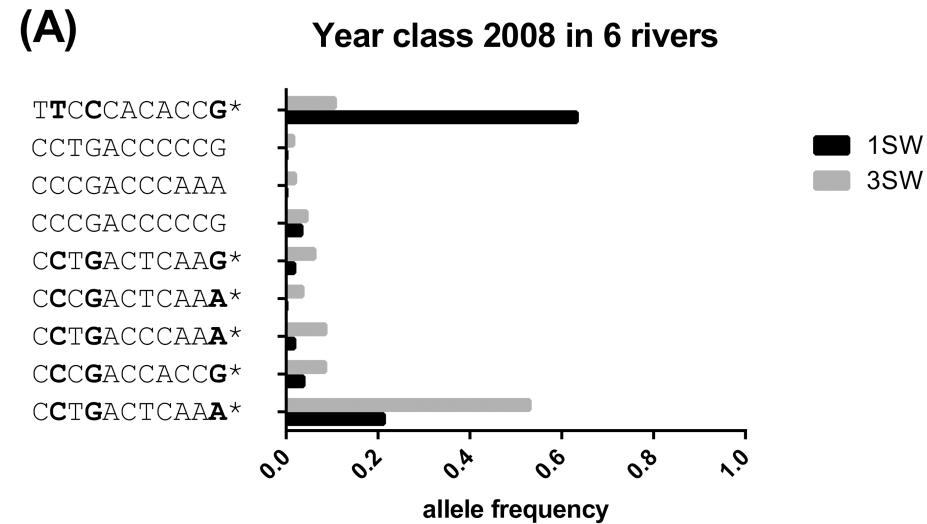
The *vgl3* Locus Controls Age at Maturity in Wild and Domesticated Atlantic Salmon (*Salmo salar* L.) Males

Fernando Ayllon, Erik Kjærner-Semb, Tomasz Furmanek, Vidar Wennevik, Monica F. Solberg, Geir Dahle, Geir Lasse Taranger,
Kevin A. Glover, Markus Sällman Almén, Carl J Rubin, Rolf B. Edvardsen, Anna Wargelius 



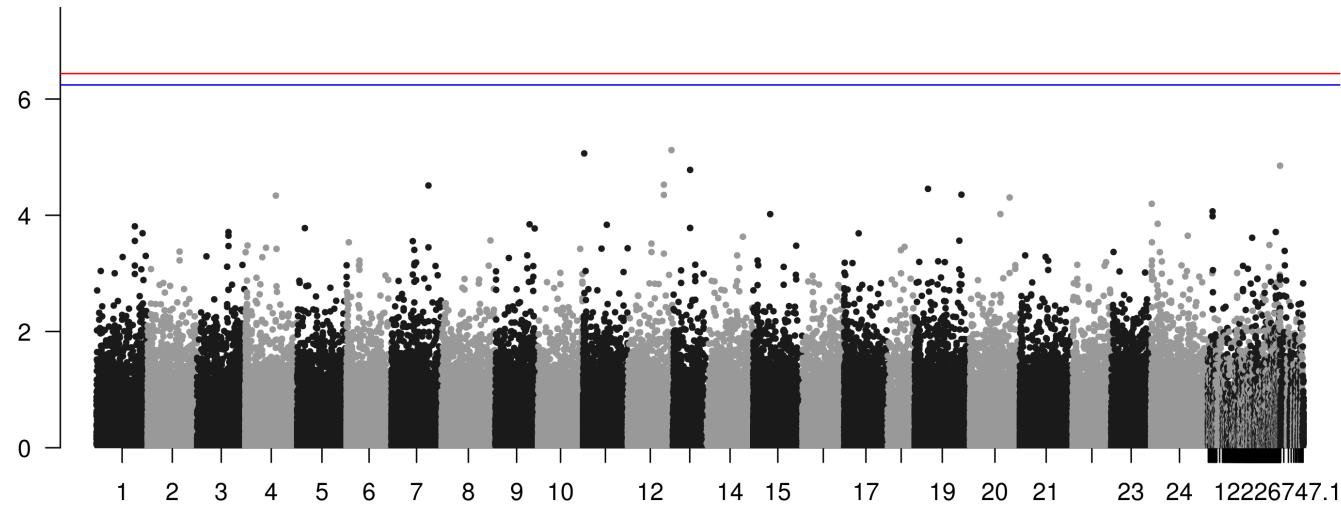
Why do we care about heritability?

- We can manage populations
- Overlapping in distributions and genetics, but are distinct



A more typical result....

Why a lack of significance?

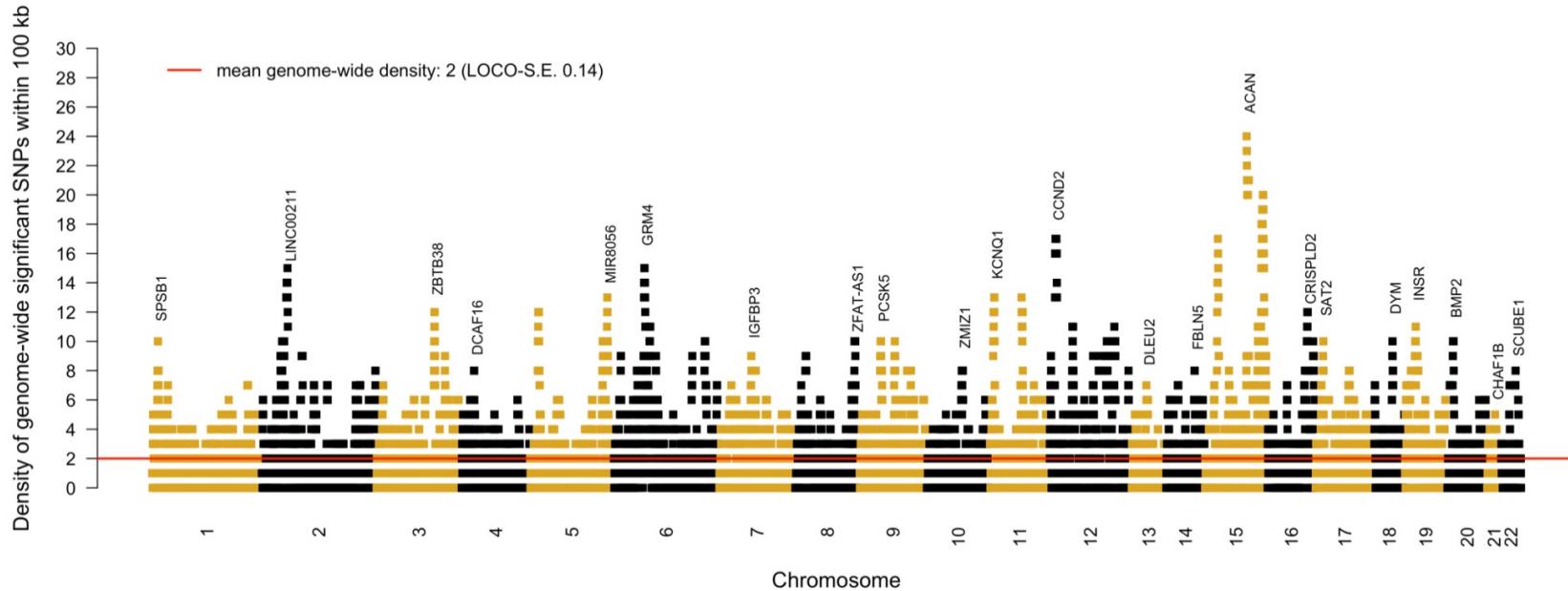


Many (most?) phenotypes are quantitative and polygenic

Huge sample sizes needed

12,111 SNPs account for 40% of phenotypic variance in human height

5.4 Million Individuals

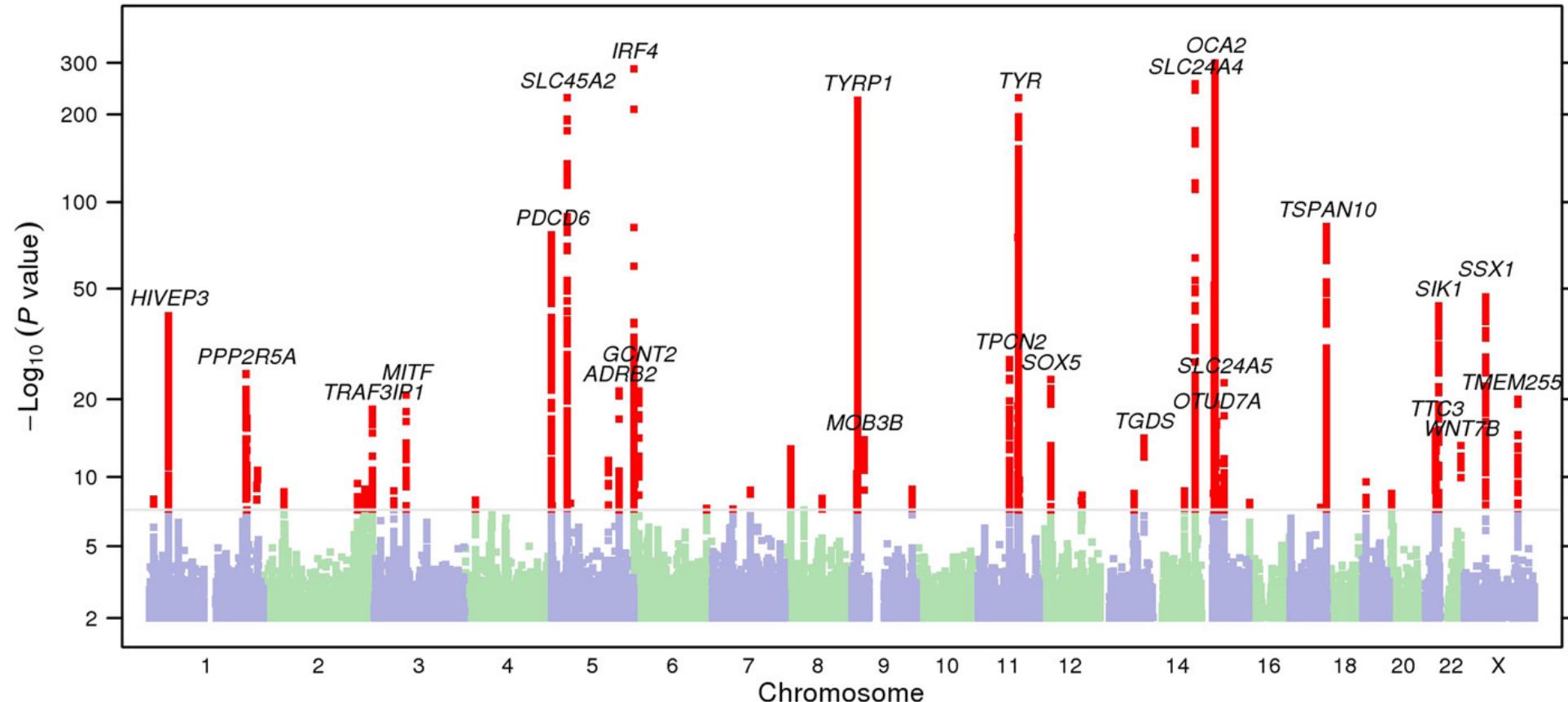


But isn't heritability of height ~0.7?

- Missing heritability problem

"A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries"

“simple” traits probably not so simple

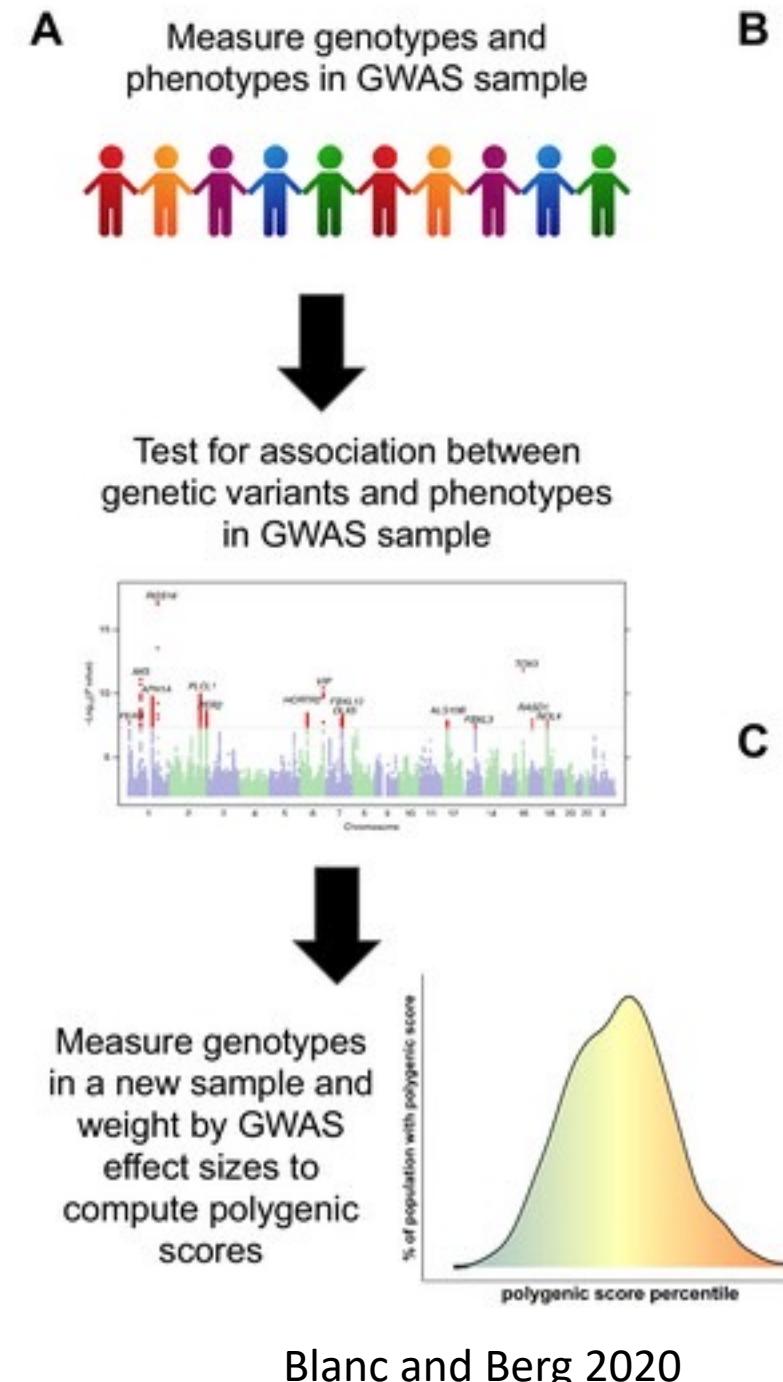
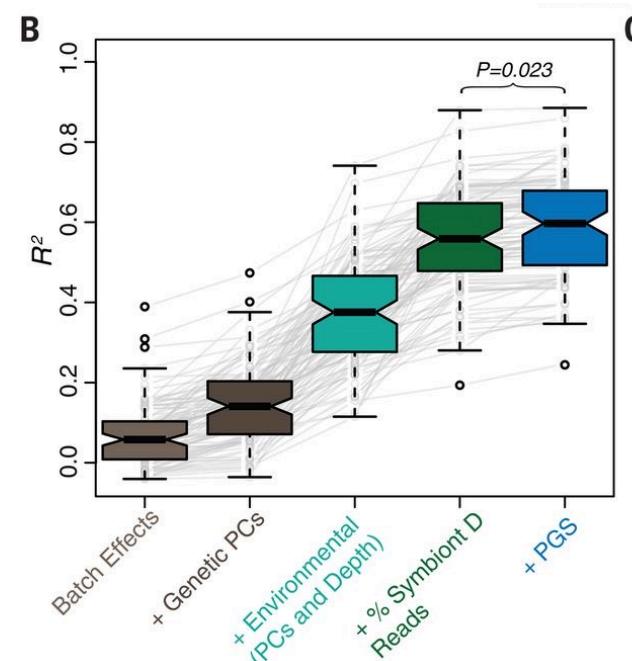


124 loci are associated with human eye color.
Explain 53% of the variation

Polygenic scores

- Value that represents an estimated contribution of a genome to a phenotype
- sum of the estimated effect sizes of the genetic variants in the genome
 - Considering all loci, not just significant.

Polygenic score to predict risk of coral bleaching



Paper for discussion

Low potential for evolutionary rescue from climate change in a tropical fish

Rachael Morgan^{a,1} , Mette H. Finnøen^a , Henrik Jensen^b , Christophe Pélabon^b , and Fredrik Jutfelt^a 

Quantitative genetics and racism

Eugenics and racism long a part of quantitative genetics.

Debates of genetic basis of IQ, behavior, etc.

"red hair effects"

Race is a social construct:

- Lewontin showed that: 85.4% of the total genetic variation observed occurred within each group.
- vast majority of genetic differences are found within populations rather than between them.
- two random individuals from any one group (which could be a continent or even a local population) are almost as different as any two random individuals from the entire world

Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals

[James J. Lee](#), [Robbee Wedow](#), ... [David Cesarini](#)

+ Show authors

Polygenic scores explain 11% of the variation