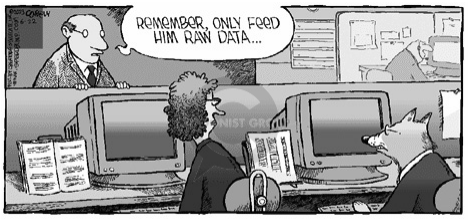
Psych 3102
Introduction to Behavior Genetics

Lecture 10
Quantitative genetic theory
Model-fitting



Basic underlying tenet behind all methods:

Methods allow us to
1.

2.

3.

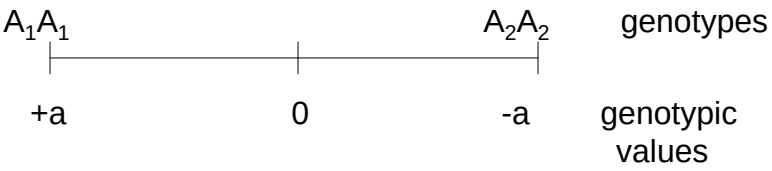
methods are not as direct and powerful as animal studies

All models are still based on segregation at a single locus

SINGLE-GENE MODEL

Consider a single locus with 2 alleles A_1 and A_2

assign genotypic values to show effects of each allele on phenotype:



where heterozygote falls on this scale depends on nature of allelic interaction at the locus

heterozygous genotype is given value d

d =

d =

d =

ADDITIVE GENETIC VARIATION - the additive effects of alleles

- phenotypic effect of the alleles is the mathematical sum of all alleles present for the trait since all alleles have an effect
- additive alleles produce predictable phenotypic scores in offspring -

- this gives us a prediction about the offspring that can be tested

at a single locus, we have evidence of

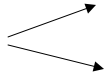
NON-ADDITIVE GENETIC VARIATION - the result of dominant alleles

- dominant alleles produce dominance deviation

=

- dominance produces unpredictable results for the scores of offspring
- offspring score depends on combination of alleles inherited and is NOT just an average of parental scores

Variance components so far:

Variance due to genes 

POLYGENIC MODEL

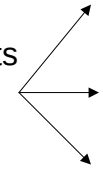
extending the single-gene model to accommodate traits influenced by many genes

additive and dominance effects are just summed over loci

But

new source of variation :

epistasis

Genetic components of variance (G) 

G = A + D + I

PHENOTYPIC VALUES

considered to be the sum of all genetic and environmental effects

individual phenotypic scores are combined and phenotypic values are measured as deviations from the population mean

for analysis, deviations from the mean are converted into variances

Phenotype value =

Variance components are now:

$V_{(P)}$ =

observed variation in population	variation due to environment	variation due to genes	variation due to interaction between genes & environment	correlation between genetic and environmental effects

Inbred strains: $V_{(G)}$ =

so, $V_{(P)}$=

Humans : only less direct estimates possible from resemblance between relatives

in the case of MZ twins, $V_{(G)}$= 0 and $V_{(P)}$= $V_{(E)}$

Genotype x Environment interaction

- genotype and environment are not independent
- gene effects are modified by environment (and vice versa)
- gene effects can be changed by certain environments
- effects can be quite large

liability to become a smoker (Heath et al, 2002)

both genes and environments have main effects

but there is extra liability, more than additive effects, due to interaction

25% of total variance is from interaction between genetic risk alleles and environment that encourages smoking

Genotype x Environment correlation

- genotype and environment are not independent
- neither main effect is altered
- because of choice, certain genotypes are more common in certain specific environments than others

people with talent to play certain sports as a result of their genotype (muscle type, size, height, aerobic capacity etc)

are found more frequently in an environment where their sport is played

– genotypes present in members of competitive basketball teams are NOT a random selection