



Heritability

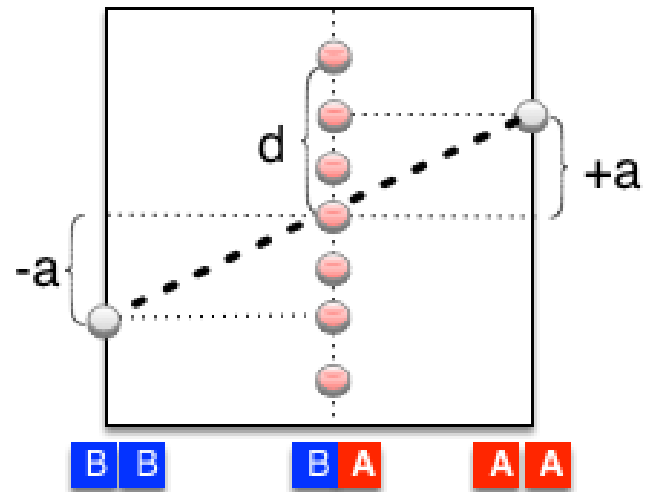
Jinliang Yang
Oct. 29th, 2018

Announcements

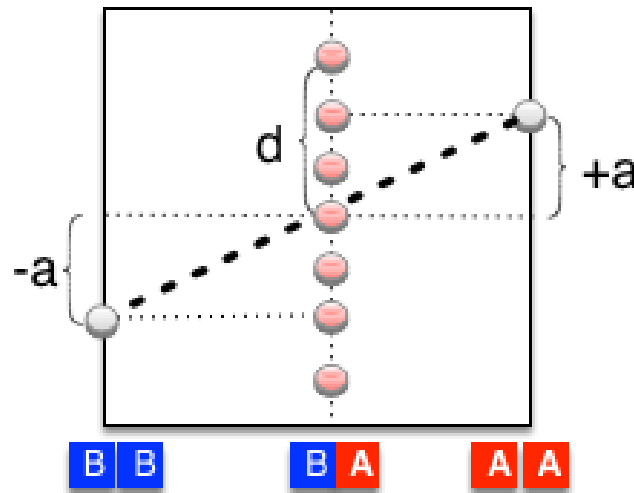
HW due **Oct. 31st (W) 8:00am**

Previous Exam posted on Canvas

Mode of inheritance



Mode of inheritance



- $d > a, \frac{d}{a} > 1$: Overdominance
- $d = a, \frac{d}{a} = 1$: Complete dominance
- $0 < d < a, 0 < \frac{d}{a} < 1$: Incomplete (partial) dominance
- $d = 0, \frac{d}{a} = 0$: Pure additive
- $-a < d < 0, -1 < \frac{d}{a} < 0$: Incomplete (partial) recessive
- $d = -a, \frac{d}{a} = -1$: Complete recessive
- $d < -a, \frac{d}{a} < -1$: Underdominance

Genetic covariances for general relatives

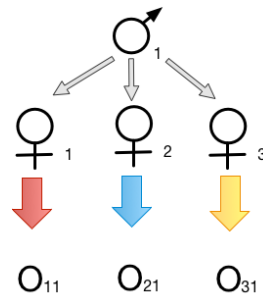
$$Cov_G = 2f_{XY}\sigma_A^2 + \Delta_{XY}\sigma_D^2$$

$$Cov_G = r\sigma_A^2 + u\sigma_D^2$$

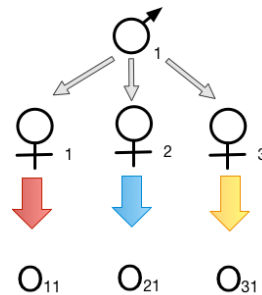
Note that u is normally zero unless they IBD through **both of their respective parents**. for example, full sibs and double first cousins.

Relationship		Coancestry	r (of σ_A^2)	u (of σ_D^2)
First degree	Parent:offspring	1/4	1/2	0
Second degree	Half sibs	1/8	1/4	0
	Full sibs	1/4	1/2	1/4
	Grantparent:offspring	1/8	1/4	0
Third degree	great-grantparent:offspring	1/16	1/8	0

A simple half-sib design



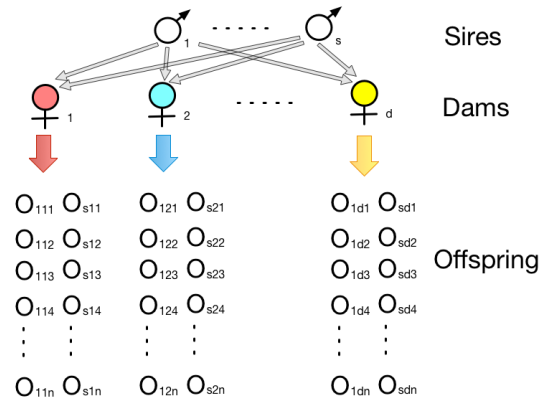
A simple half-sib design



From the lab, we can extract $\text{Cov}(\text{HS}) = \text{Var}(\text{Dam})$.

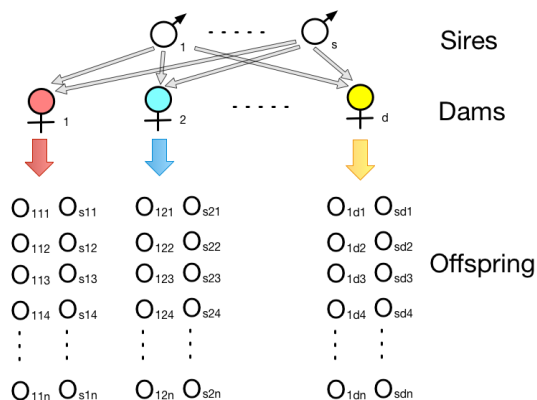
Sib Analysis

If we have a balanced design of s sires each mated to d dams, and each dam has n progenies.



Sib Analysis

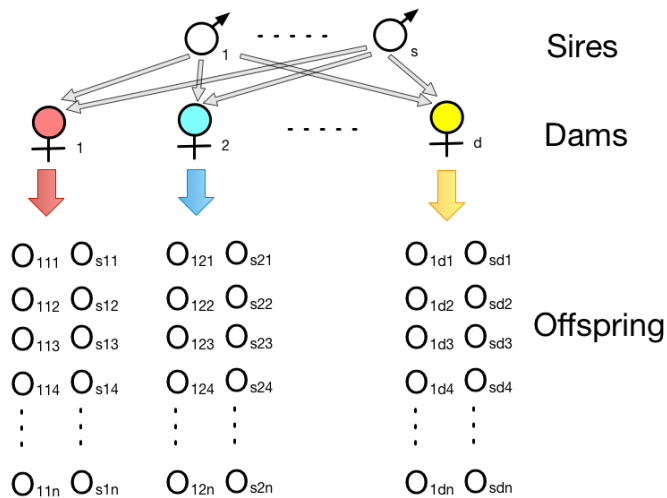
If we have a balanced design of s sires each mated to d dams, and each dam has n progenies.



Then we have the following ANOVA table.

Source	df	MS	Expectation of MS
Sires	$s-1$	MS_s	?
Dams (Within Sires)	$s(d-1)$	MS_d	?
Within Dams	$sd(n-1)$	MS_w	?

Expectation of MS



MS within (residual error)

Source	df	MS	Expectation of MS
Sires	$s-1$	MS_s	?
Dams (Within Sires)	$s(d-1)$	MS_d	?
Within Dams	$sd(n-1)$	MS_w	$= \sigma_w^2$

MS Between Dams (within Sires)

The variance among dams is calculated by taking the **average value for each full-sib family (the offspring of each dam)** and averaging these means, after correcting for differences among sire means.

Source	df	MS	Expectation of MS
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So the between-dam component is estimated as:

$$MS_d = \sigma_W^2 + n\sigma_D^2 = MS_w + n\sigma_D^2$$

$$\sigma_D^2 = \frac{1}{n}(MS_d - MS_w)$$

MS Between Sires

Similarly, the variance among sires is found by taking **the mean of all offspring of each sire** and calculating the variance of these sire means.

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Sires	s-1	MS_s	$= \sigma_W^2 + n\sigma_D^2 + dn\sigma_S^2$
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$$\sigma_s^2 = \frac{1}{dn}(MS_s - MS_d)$$

Interpretation of variance components

Phenotypic variance

Phenotypic variance is the sum (σ_T^2) of the three observational components:

$$\begin{aligned}V_P &= \sigma_T^2 \\ &= \sigma_s^2 + \sigma_d^2 + \sigma_w^2\end{aligned}$$

Between-sire component σ_s^2

This is the **variance between the means of half-sib families** and it therefore estimates the phenotypic **covariance of half sibs**.

$$\sigma_s^2 = Cov(HS) = \frac{1}{4}\sigma_A^2$$

- A key concept in the **analysis of variance (ANOVA)** is that the variance between groups is equal to the covariance within groups.

Interpretation of variance components

Within-progeny component σ_w^2

- A key concept in the **analysis of variance (ANOVA)** is that the variance between groups is equal to the covariance within groups.
- It follows that **a within-group component = total variance - covariance of members of the groups.**

Within-dams are full-sibs, therefore,

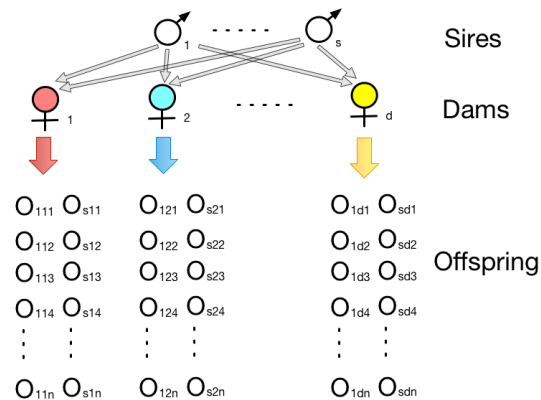
$$\begin{aligned}\sigma_w^2 &= V_p - Cov(FS) \\ &= \sigma_A^2 + \sigma_D^2 + \sigma_E^2 - \left(\frac{1}{2}\sigma_A^2 + \frac{1}{4}\sigma_D^2\right) \\ &= \frac{1}{2}\sigma_A^2 + \frac{3}{4}\sigma_D^2 + \sigma_E^2\end{aligned}$$

Interpretation of variance components

Between-dam component σ_d^2

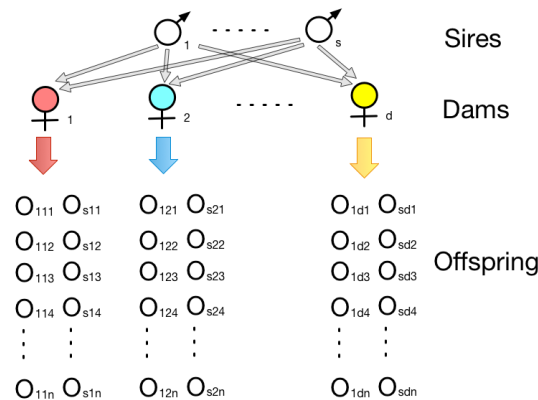
$$\begin{aligned}\sigma_d^2 &= \sigma_P^2 - \sigma_s^2 - \sigma_d^2 \\ &= \sigma_A^2 + \sigma_D^2 + \sigma_E^2 - \frac{1}{4}\sigma_A^2 - \left(\frac{1}{2}\sigma_A^2 + \frac{3}{4}\sigma_D^2 + \sigma_E^2\right) \\ &= \frac{1}{4}\sigma_A^2 + \frac{1}{4}\sigma_D^2\end{aligned}$$

Summary



Observational		Covariance and causal components estimated
Sires	$\sigma_s^2 = Cov(HS)$	$= \frac{1}{4}\sigma_A^2$
Dams	$\sigma_d^2 = Cov(FS) - Cov(HS)$	$= \frac{1}{4}\sigma_A^2 + \frac{1}{4}\sigma_D^2$
Progeny	$\sigma_w^2 = V_P - Cov(FS)$	$= \frac{1}{2}\sigma_A^2 + \frac{3}{4}\sigma_D^2$
Total	$\sigma_T^2 = V_P = \sigma_s^2 + \sigma_d^2 + \sigma_w^2$	$= \sigma_A^2 + \sigma_D^2 + \sigma_E^2$
Sires + Dams	$\sigma_s^2 + \sigma_d^2 = Cov(FS)$	$= \frac{1}{2}\sigma_A^2 + \frac{1}{4}\sigma_D^2$

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Sires + Dams	$\sigma_s^2 + \sigma_d^2 = Cov(FS)$	$= \frac{1}{2}\sigma_A^2 + \frac{1}{4}\sigma_D^2$

Special environmental conditions are shared for given offspring of particular sires. σ_E^2 can therefore, be partitioned into σ_{Ec}^2 and σ_{Ew}^2 .

A sib experiment

- A balanced experimental data collected from 100 sires each mated to 2 dams.
- Have body length records of 3 male and 3 female offspring from each dam.
- Get h^2 for body length?

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ANOVA table for body length:

Source	Value	Mean Sq
Between Sires	7.83	MS_s
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Within progenies	1.27	MS_w

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Get heritability:

$$\sigma_W^2 = MS_w = 1.27$$

$$\sigma_D^2 = (MS_d - \sigma_W^2)/n = (4.51 - 1.27)/6 = 0.54$$

$$\sigma_S^2 = (MS_s - \sigma_d^2)/(dn) = (7.83 - 4.51)/(2 \times 6) = 0.277$$

$$\sigma_P^2 = \sigma_D^2 + \sigma_S^2 + \sigma_W^2 = 1.27 + 0.54 + 0.277 = 2.087$$

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$$\sigma_P^2 = \sigma_D^2 + \sigma_S^2 + \sigma_W^2 = 1.27 + 0.54 + 0.277 = 2.087$$

$$\sigma_S^2 = \sigma_A^2/4$$

$$\sigma_A^2 = 0.277 \times 4 = 1.108$$

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2} = 1.108/2.087 = 0.53$$

Why estimate heritability?

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- Comparison between traits
- Predict response to selection
- Power of gene mapping studies
- Efficiency of prediction of genetic risk of disease

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Estimation

- h^2 influenced by allele frequencies, and therefore differ from one population to another
- Depends on environments and number of measurements,
- Varies from traits to traits

Narrow sense heritability

- Parents transmit only one allele to offspring
- Most relative share only one or zero alleles that are IBD, therefore, only share the average effect of one allele.

Therefore, the **narrow sense heritability** (h^2) is the most important component.

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Breeding

Heritability in the narrow sense (h^2):

- is a fundamental statistics we use in predicting response to selection
- and is very informative for designing breeding schemes
- enters to almost every formula connected with breeding methods.

Regression

From Math foundation:

$$b_{XY} = \frac{\text{Cov}(X, Y)}{\text{Var}(Y)}$$

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Breeding value and phenotypic value

$$\begin{aligned} b_{AP} &= \frac{Cov(A, P)}{\sigma_P^2} \\ &= \frac{Cov(A, A + D + I + E)}{\sigma_P^2} \\ &= \frac{Cov(A, A)}{\sigma_P^2} = \frac{\sigma_A^2}{\sigma_P^2} = h^2 \end{aligned}$$

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Therefore, $h^2 = b_{AP}$ is the regression coefficient of breeding value on phenotypic value

Correlation

From Math foundation:

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The correlation between A and P

$$\begin{aligned} r_{AP} &= \frac{Cov(A, P)}{\sqrt{\sigma_A^2 \sigma_P^2}} \\ &= \frac{Cov(A, A + D + I + E)}{\sqrt{\sigma_A^2 \sigma_P^2}} \\ &= \frac{\sigma_A^2}{\sqrt{\sigma_A^2 \sigma_P^2}} = \frac{\sigma_A}{\sigma_P} = h \end{aligned}$$

In animal breeding

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In plant breeding

We might be using the average of a family in a plot, i.e. ear to row, and thus we will need to consider heritability of a family average.