

## Animal Models

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### Introduction

In animal model, observations per animal and all factors affecting the observations are described including an animal additive genetic effect

Additive genetic effects are random &  
 Expected value of zero &  
 Covariance matrix (additive genetic relationship matrix) is **A**

Assumptions: trait is influenced by infinite number of loci each and small, and population with random mating

## Example Situation

Sheep are scanned at maturity by ultrasound(US) to determine the amount of fat surrounding the muscle

A model :  $US_{Fat} = YearMonth + FMG + b(Age\ at\ US) + Animal + Residual$

Year-month of birth is fixed,  
 FMG, flock-year-management group effect (random),  
 Age at ultrasound is a covariate,  
 Animal additive genetic effects ,  
 Residual effects

## Example Situation

Fat thickness is in millimeters.

The purpose of the analysis is to estimate the variances, and estimate breeding values of animals

Animals have only one US Fat measurement  
 And they have not been pre-selected on the basis of any other trait

The sex is assumed to not have any effect on the measurements

## Estimation of Variances

Two methods of estimating variances are used

One is called Restricted Maximum Likelihood (or REML)

REML has several different ways of being calculated. One is called Derivative Free REML (DFREML), and another is called Average Information REML (AIREML)

## Estimation of Variances

To employ REML, needs to assume observations follow a normal distribution

Both DFREML and AIREML try to maximize the log of the likelihood function, but in different ways

The details of the methodology are too complex for this course

## Practical example

❑ To illustrate the method of estimating variances, it is nearly impossible using small examples. Thus, a good example is difficult to present

❑ The estimation of variances requires data on at least a few thousand animals (2000 or more), more animals => sharper will be the peak at the maximum of the likelihood function

❑ Success also depends on the number of unknown parameters in the model

## Changes in Variances

❑ Variance parameters tend to not change very much over time

❑ Variances do not need to be re-estimated very often

❑ Usually parameters need to be re-estimated every time the model is changed (adding or deleting factors to the model)

### Breed or Country Differences

- Variance parameters may be specific to a breed
  - Ex. Holsteins have larger variances for milk production because Holsteins produce more milk than the other breeds
  - Ex. Charolais beef cattle grow more rapidly than Hereford or Angus
  
- Variances may also be specific to a breed within a particular country

### Genetic Evaluation and Rankings of Animals

- If heritability is estimated to be 0.30, then genetic evaluations that are calculated using either 0.20 or 0.40 would not greatly re-rank animals
  - using 0.20 , EBVs have a smaller range in values
  - using 0.40 , EBVs have a bigger range
  
- Using the correct variance is important for measuring genetic trends, but not for ranking animals for selection

### Repeated Records

- Animals are observed more than once for a trait, as get older between observations
  
- An important questions:
  - observation at one age is a different trait from observation at a later age? Is the genetic correlation between the observations less than 1?
  
- Assuming that the genetic correlation is not greatly less than 1, then there are repeated records on an animal
  
- There are permanent environmental factors that are not genetic, but affect observations of one animal

### Repeatability

- Repeatability( $r$ ), is a number between 0 and 1, the degree of permanent environmental effects
- Let  $\sigma^2_p$  be the variance of permanent environmental effects,  $\sigma^2_a$  is the additive genetic variance,  $\sigma^2_e$  is the residual variance

$$\sigma^2_y = \sigma^2_a + \sigma^2_p + \sigma^2_e$$

$$r = (\sigma^2_a + \sigma^2_p) / \sigma^2_y$$

$$h^2 = \sigma^2_a / \sigma^2_y$$

- ❖  $\sigma^2_p$  is often smaller than  $\sigma^2_a$

- In animal model where animals have only one record and no progeny, reliabilities of EBVs can go no higher than the heritability of the trait
- more progeny & repeated records per animal, reliability go as high as 100%
- Reliabilities account for
  - 1) number of records on the animal
  - 2) number of progeny the animal has
  - 3) number and type of relatives in the data
  - 4) number of animals in each breed
  - 5) total number of observations in the data set
  - 6) number of factors in the model
  - 7) variance parameters relative to the residual variance

## Inbreeding & Additive Genetic Relationship

### Inbreeding and Relationship

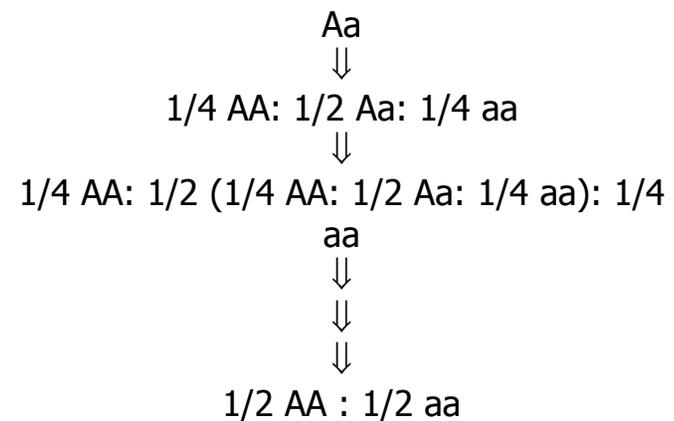
#### Inbreeding

mating of related individuals

mating of individuals more closely related than the average of the breed

animal is inbred if, and only if, its parents are related

### Genetic results from inbreeding



### Genetic result of inbreeding

increased homozygosity

if there is dominance:

aa may be inferior

inbreeding will cause decrease  
in performance

### Phenotypic result of inbreeding

inbreeding depression

decline in performance from mating  
related individuals

result of inbreeding when there is  
non-additive gene action  
(dominance)

### Phenotypic result of inbreeding

inbreeding depression

more pronounced for lowly  
heritable traits

<u>class of trait</u>	<u>inbreeding depression</u>
Reproduction	high
growth	moderate
carcass	low

### Measurement of inbreeding

inbreeding coefficient (F)

degree of homozygosity

% increase in homozygosity above  
the average of the breed

if  $F = .25$  the animal is 25% more  
homozygous than  
the average of the  
breed

## Inbreeding coefficient (F)

minimum value = 0  
maximum value = 1

for livestock  
rare for  $F > .6$

lab animals  
F can approach .9

plants with self-fertilization  
F can approach 1.0

## Avoidance of inbreeding

need to keep inbreeding at low level

$F > .1$  time to think about it  
 $F > .2$  time to worry about it

producers should not actively pursue  
inbreeding

## Avoidance of inbreeding

avoid mating close relatives  
nothing closer than cousins

keep ratio of males / females high

keep replacements from several families

avoid bottlenecks (period of reduced  
census number)

## Calculation of Inbreeding coefficient (F)

$$F_X = \sum \left[ \left( \frac{1}{2} \right)^{n+1} (1 + F_A) \right]$$

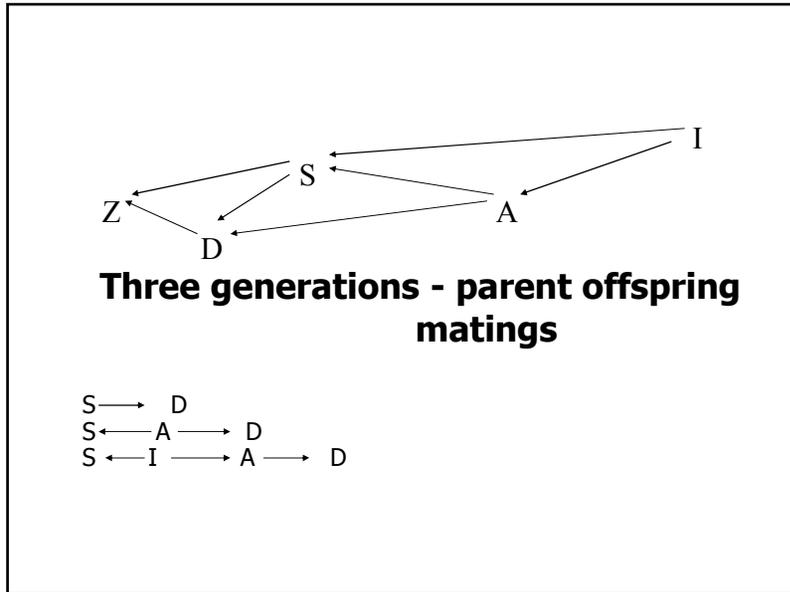
$F_X$  = inbreeding coefficient of individual X

$\Sigma$  = summation sign

n = number of segregations (arrows) between  
the sire and dam in each separate path

$F_A$  = inbreeding coefficient of the common  
ancestor in each path

common ancestor - appears in both sire and  
dam portions of the pedigree



\* Inbreeding of S  
 path  $\textcircled{I} \rightarrow A$

value =  $\frac{1}{2}^{1+1} (1+0) = .25$

$F_S = .25^*$	1	$\frac{1}{2}^{1+1} (1+.25)$	= .3125
$F_A = 0$	2	$\frac{1}{2}^{2+1} (1+0)$	= .125
$F_I = 0$	3	$\frac{1}{2}^{3+1} (1+0)$	= .0625
		$\Sigma =$	.500

F = .50

**Additive genetic relationship matrix**

**A**

	1	2	3	4	5	6	7	
1	(-,-)	1	0	0	0	$\frac{1}{2}$	$\frac{1}{2}$	0
2	(-,-)	0	1	0	0	$\frac{1}{2}$	$\frac{1}{2}$	0
3	(-,-)	0	0	1	0	0	0	$\frac{1}{2}$
4	(-,-)	0	0	0	1	0	0	$\frac{1}{2}$
5	(1,2)	$\frac{1}{2}$	$\frac{1}{2}$	0	0	1	$\frac{1}{2}$	0
6	(1,2)	$\frac{1}{2}$	$\frac{1}{2}$	0	0	$\frac{1}{2}$	1	0
7	(3,4)	0	0	$\frac{1}{2}$	$\frac{1}{2}$	0	0	1