Variance and Inbreeding

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Assumption

- Variance of breeding value u_i: $var(u_i) = (A)_{ii}\sigma_u^2$
- Diagnoal elements of numerator relationship matrix A

$$(A)_{ii} = (1 + F_i)$$

where

F_i	inbreeding coefficient of animal i
σ_u^2	genetic additive variance

- The higher F_i, the higher the similarity, the higher the variance

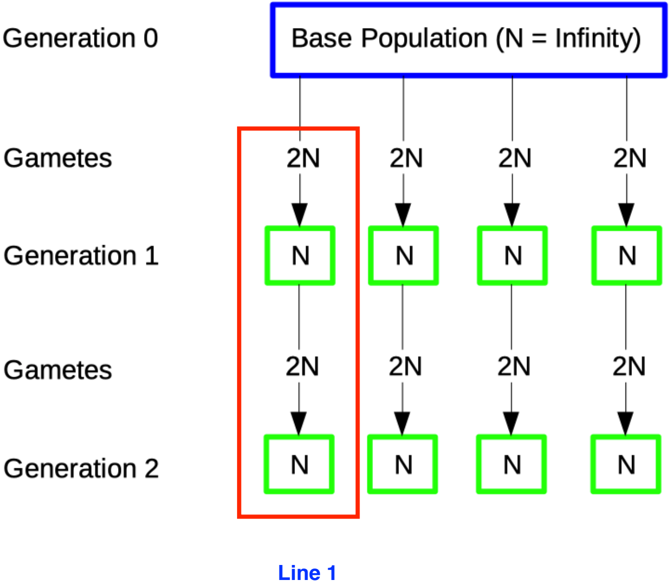
→ Contradiction?

Variance and Inbreeding

- Relationship between variance and inbreeding
- How does inbreeding affect the genetic variance?
- How do we get inbreeding in a population?

→ Population separates into different lines

Population with Inbreeding



Assumptions

- N individuals
- self-fertilizing, shedding constant rate of eggs and sperm
- at a given locus: alleles in base population are non-identical by descent
- N individuals produce $2N$ gametes (eggs and sperm) at constant rate
- probability that a pair of gametes taken at random carry identical alleles: $1/2N$
- probability corresponds to the **inbreeding coefficient** (F)

Inbreeding Coefficient

- In generation 1:

$$F_1 = \frac{1}{2N}$$

- second generation
  - either de-novo match of alleles or
  - the same alleles from generation 1

$$F_2 = \boxed{\frac{1}{2N}} + (1 - \frac{1}{2N}) * F_1$$

- new variable $\Delta F = \frac{1}{2N}$, then

$$F_2 = \Delta F + (1 - \Delta F) * F_1$$

continue with F3, F4, …

Inbreeding Coefficient II

- Generation t: $F_t = \Delta F + (1 - \Delta F) * F_{t-1}$
- Solving for ΔF

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

- Panmicitic Index $P = 1 - F$

$$\frac{P_t}{P_{t-1}} = 1 - \Delta F$$

$$P_t = (1 - \Delta F)^t * P_0 \text{ with } P_0 = 1$$

$$F_t = 1 - (1 - \Delta F)^t$$

Inbreeding coefficient Ft in generation t as a function of the Increase of F and the generation number t

Variance of Gene Frequency

- Allele frequencies (p and q) no longer constant in lines → variation
- Variance of change of q (same for p)

$$\sigma^2_{\Delta q} = \frac{p_0 q_0}{2N} = p_0 q_0 \Delta F$$

- Variance of q (same for p)

$$\sigma^2_q = p_0 q_0 F$$

Genotype Frequencies

- Average genotype frequency of homozygotes across all lines: $\overline{q^2}$
- Definition of variance

$$\sigma_q^2 = \overline{q^2} - \bar{q}^2$$

where $\bar{q}$ is the mean allele frequency across all lines and hence is the same as q_0 in the base population

- Therefore

$$\overline{q^2} = q_0^2 + \sigma_q^2 = q_0^2 + p_0 q_0 F$$

Genotype Frequencies II

Table 1: Genotype Frequencies for a bi-allelic locus, expressed in terms of inbreeding coefficient F

Genotype	Original Frequencies	Changes due to inbreeding
A_1A_1	p_0^2	$+p_0q_0F$
A_1A_2	$2p_0q_0$	$-2p_0q_0F$
A_2A_2	q_0^2	$+p_0q_0F$

Base Population

Later generations with lines

Changes of Mean Value

Table 2: Derivation of Inbreeding Depression

Genotype	Frequency	Value	Product
A_1A_1	$\bar{p}^2 + \bar{p}\bar{q}F$	a	$(\bar{p}^2 + \bar{p}\bar{q}F)a$
A_1A_2	$2\bar{p}\bar{q} - 2\bar{p}\bar{q}F$	d	$(2\bar{p}\bar{q} - 2\bar{p}\bar{q}F)d$
A_2A_2	$\bar{q}^2 + \bar{p}\bar{q}F$	$-a$	$-(\bar{q}^2 + \bar{p}\bar{q}F)a$

Sum of Product-Column corresponds to MF

Inbreeding Depression

$$\begin{aligned} M_F &= (\bar{p}^2 + \bar{p}\bar{q}F)a + (2\bar{p}\bar{q} - 2\bar{p}\bar{q}F)d - (\bar{q}^2 + \bar{p}\bar{q}F)a \\ &= a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q} - 2d\bar{p}\bar{q}F \\ &= a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q}(1 - F) \\ &= M_0 - 2d\bar{p}\bar{q}F \end{aligned}$$

Inbreeding depression

M0 is the population mean in the base population

Changes of Variance

- Only additive locus
- Within line: as before

$$\begin{aligned} V_{\bar{G}} &= 2(\bar{pq})a^2 \\ &= 2p_0q_0(1-F) \\ &= V_G(1-F) \end{aligned}$$

- New variance component: between line

$$var(M) = \sigma_M^2 = 4a^2\sigma_q^2 = 4a^2p_0q_0F = 2FV_G$$

Summary

Table 3: Partitioning of the variance in a population with inbreeding coefficient F

New source of variation between lines

Source	Variance
Between lines	$2FV_G$
Within lines	$(1 - F)V_G$
Total	$(1 + F)V_G$

Why is the variance of the true breeding value dependent on F var(u_i) = (1 + F_i) * var(g) ?

Increased inbreeding (F) leads to a shift in the genotype frequencies, such that the frequency of heterozygous genotypes descreases, but the frequencies of homozygous genotypes increases, this leads to a higher frequency of genotypes which show larger difference between their genotypic values and therefore the variation is increased