

Variance and Inbreeding

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Assumption

- ▶ Diagonal elements of numerator relationship matrix A

$$(A)_{ii} = (1 + F_i)\sigma_u^2$$

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

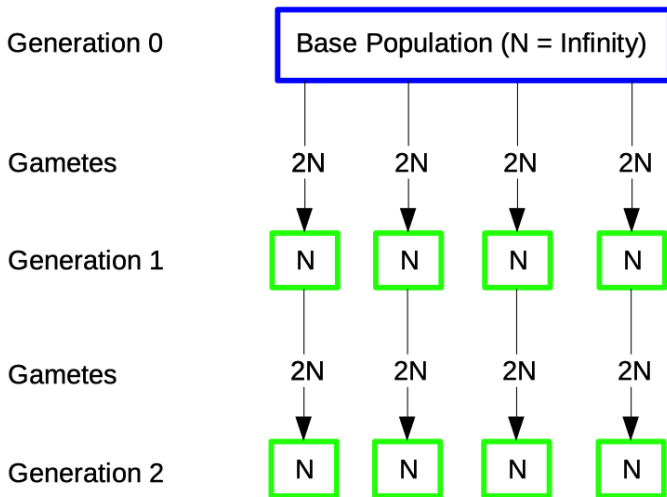
→ Contradiction?

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

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

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

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

Inbreeding Coefficient II

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

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

- ▶ Panmictic Index $P = 1 - F$

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

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

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

Variance of Gene Frequency

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

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

- ▶ Variance of q (same for p)

$$\sigma_q^2 = p_0 q_0 F$$

Genotype Frequencies

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

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

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

- ▶ Therefore

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

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	$+p_0q_0F$

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	$\bar{q}^2 + \bar{p}\bar{q}F$	$-a$	$-(\bar{q}^2 + \bar{p}\bar{q}F)a$

Inbreeding Depression

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

Changes of Variance

- ▶ Only additive locus
- ▶ Within line: as before

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

- ▶ New variance component: between line

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

Summary

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

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