Day 1
Basics: Response to Selection

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Learning objectives

Lecture

- Refresh The Response to Selection Theory
- Components of the Breeder's Equation
- Briefly look at Multi-Trait Selection

Practical

- Simulate Response to Selection of a Single Trait in AlphaSimR
- Simulate Response to Selection of Multiple Traits in AlphaSimR

Selective breeding

- **Selection:** Superior individuals with desirable traits are chosen to be the parents of the next generation.

- **Mating:** The selected individuals are then crossed and their offspring inherit the desired traits from their parents.

- **Repeat:** The process repeated over multiple generations to increase the performance of desired traits.

Response to selection to measure or predict the change in performance of traits from one generation to the next.
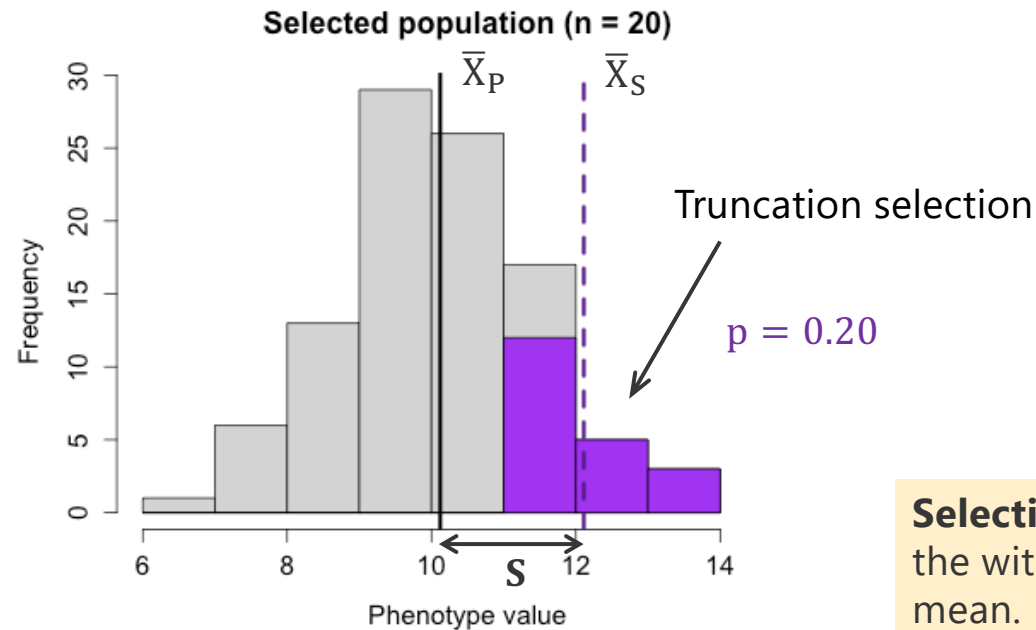
Response to selection

Initial population (n = 100)
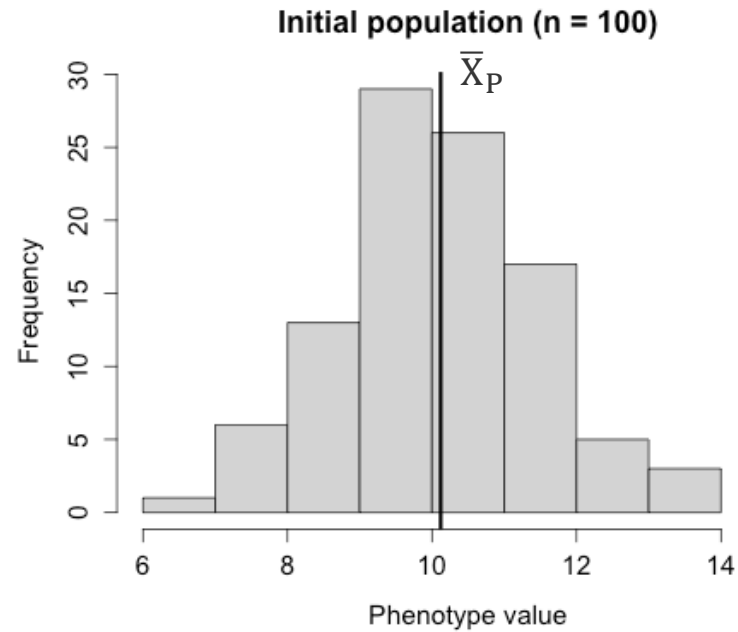
$\overline{X}_P = 10.12$ mean of the population

Response to selection: selection

Selected population (n = 20)

Truncation selection

$p = 0.20$

> **Selection differential** measures the within-generation change in mean.

$\overline{X}_P = 10.12$ mean of the population
$\overline{X}_S = 12.11$ mean of the selected individuals
$S = \overline{X}_S - \overline{X}_P = 1.99$ selection differential

Response to selection: mating

Offspring population (n = 100)
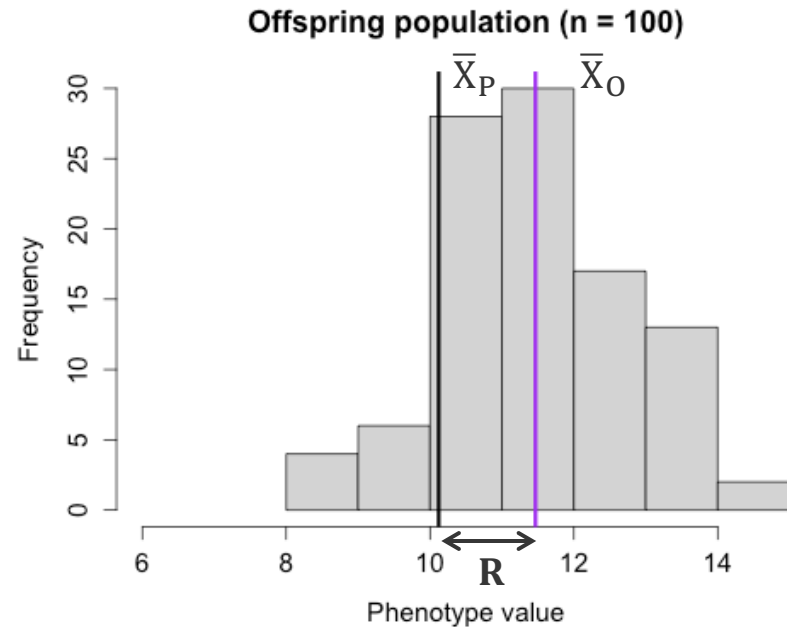
Response to selection measures the between-generation change in mean.

$\overline{X}_P = 10.12$ mean of the population
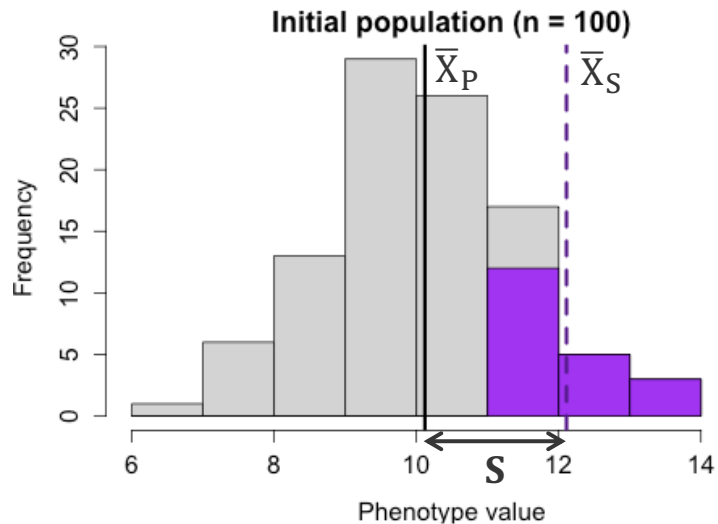$\overline{X}_S = 12.11$ mean of the selected individuals
$S = \overline{X}_S - \overline{X}_P = 1.99$ selection differential
$\overline{X}_O = 11.46$ mean of the offspring population
$R = \overline{X}_O - \overline{X}_P = 1.34$ response to selection

Response to selection

$\overline{X}_P = 10.12$ mean of the population
$\overline{X}_S = 12.11$ mean of the selected individuals
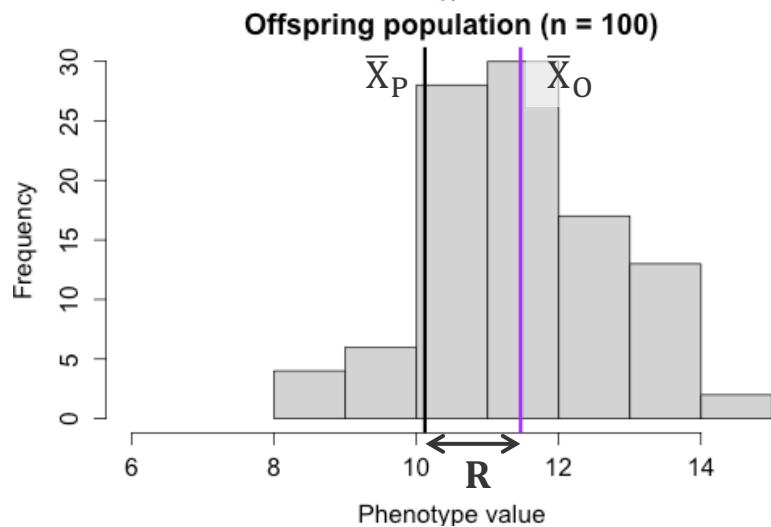$S = \overline{X}_S - \overline{X}_P = 1.99$ selection differential
$\overline{X}_O = 11.46$ mean of the offspring population
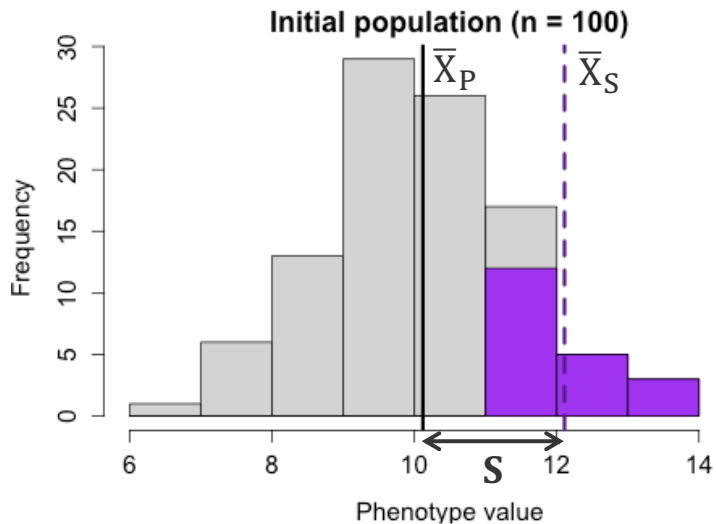$R = \overline{X}_O - \overline{X}_P = 1.34$ response to selection

Typically, $\overline{X}_S > \overline{X}_O > \overline{X}_P$

$\overline{X}_O > \overline{X}_P$
- Some selected parents have favourable genotypes and pass favourable alleles to their offspring

Response to selection

$$\overline{X}_P = 10.12 \qquad \text{mean of the population}$$
$$\overline{X}_S = 12.11 \qquad \text{mean of the selected individuals}$$
$$S = \overline{X}_S - \overline{X}_P = 1.99 \quad \text{selection differential}$$
$$\overline{X}_O = 11.46 \qquad \text{mean of the offspring population}$$
$$R = \overline{X}_O - \overline{X}_P = 1.34 \quad \text{response to selection}$$

Typically, $\overline{X}_S > \overline{X}_O > \overline{X}_P$

$\overline{X}_O < \overline{X}_S$

- Some selected parents do not have favourable genotypes and their good phenotypes result from a favourable environment.
- Alleles, not genotypes, are transmitted and good genotypes are disrupted by Mendelian sampling and recombination.

Response to selection

$\overline{X}_P = 10.12$ mean of the population
$\overline{X}_S = 12.11$ mean of the selected individuals
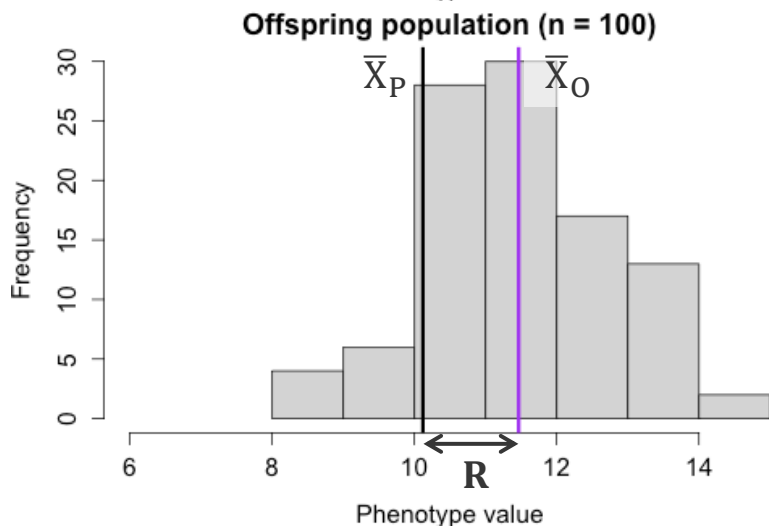$S = \overline{X}_S - \overline{X}_P = 1.99$ selection differential
$\overline{X}_O = 11.46$ mean of the offspring population
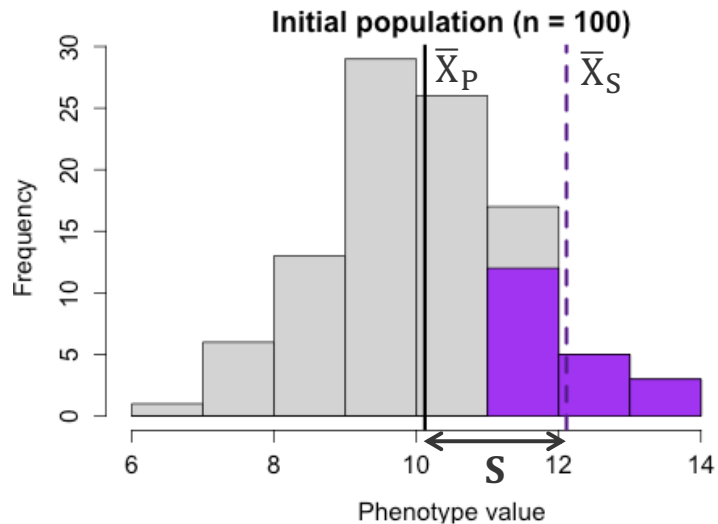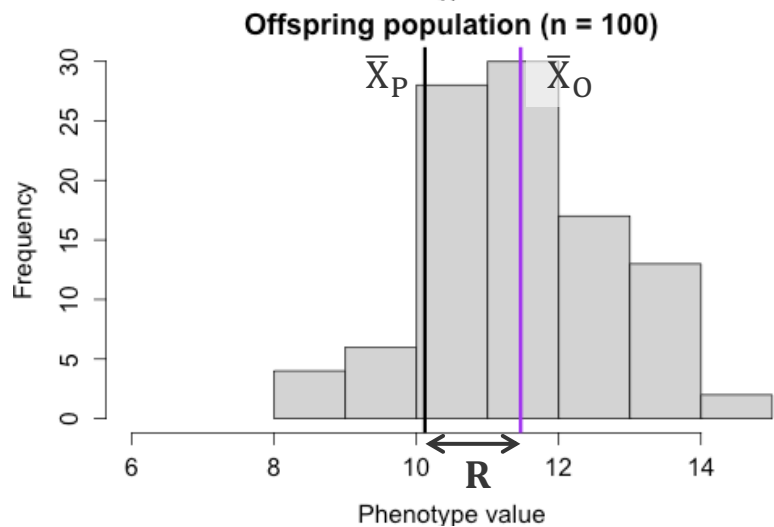$R = \overline{X}_O - \overline{X}_P = 1.34$ response to selection

$\overline{X}_O = 10.12 + 1.34 = 11.46$

Response to selection

$\overline{X}_P = 10.12$ mean of the population

$\overline{X}_S = 12.11$ mean of the selected individuals

$S = \overline{X}_S - \overline{X}_P = 1.99$ selection differential

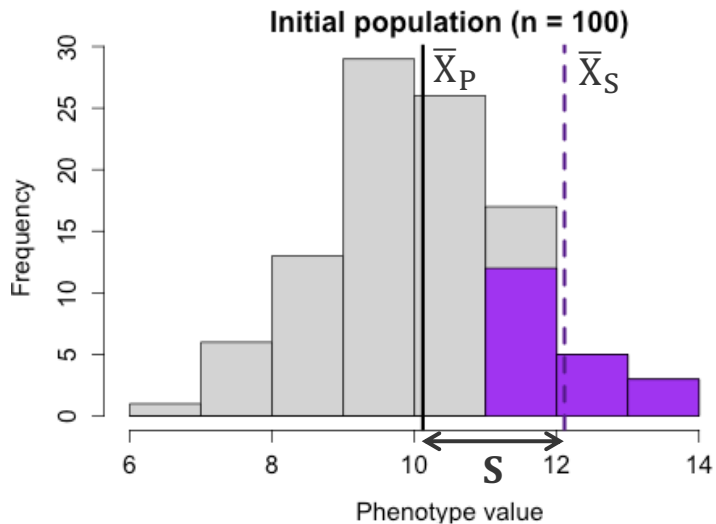$\overline{X}_O = 11.46$ mean of the offspring population

$R = \overline{X}_O - \overline{X}_P = 1.34$ response to selection

$$\overline{X}_O = 10.12 + 1.34 = 11.46$$

$$\overline{X}_O = \overline{X}_P + R = \overline{X}_P + h^2 S$$
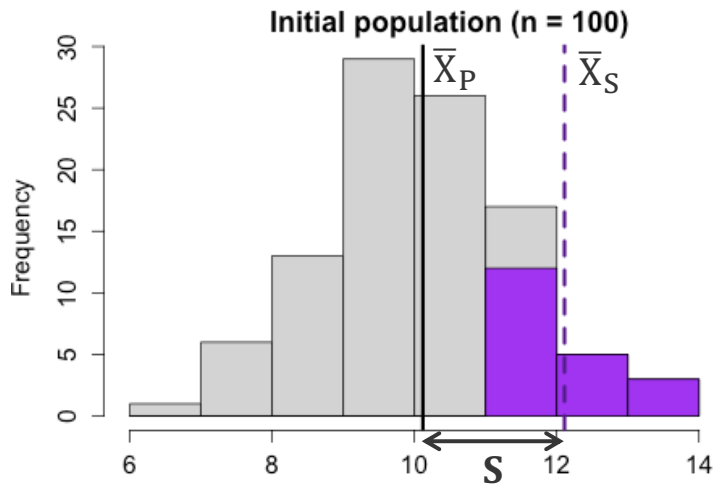
$$\mathbf{R = h^2 S}$$

h^2 is the proportion of S that gets transmitted to the next generation.
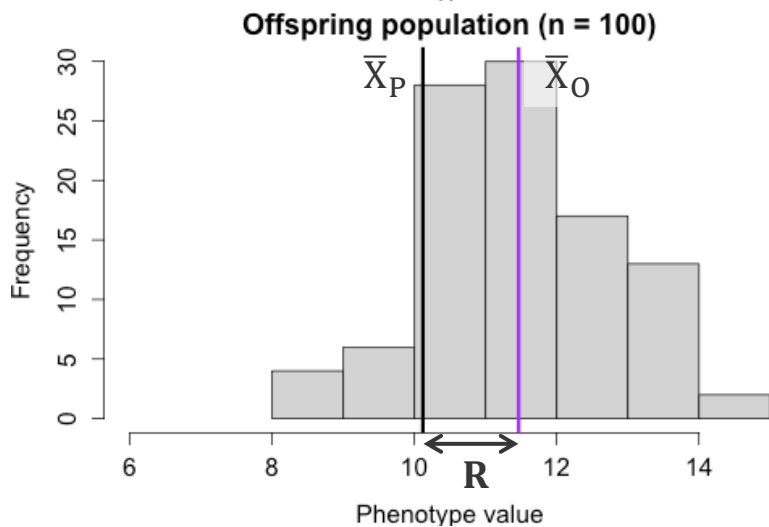
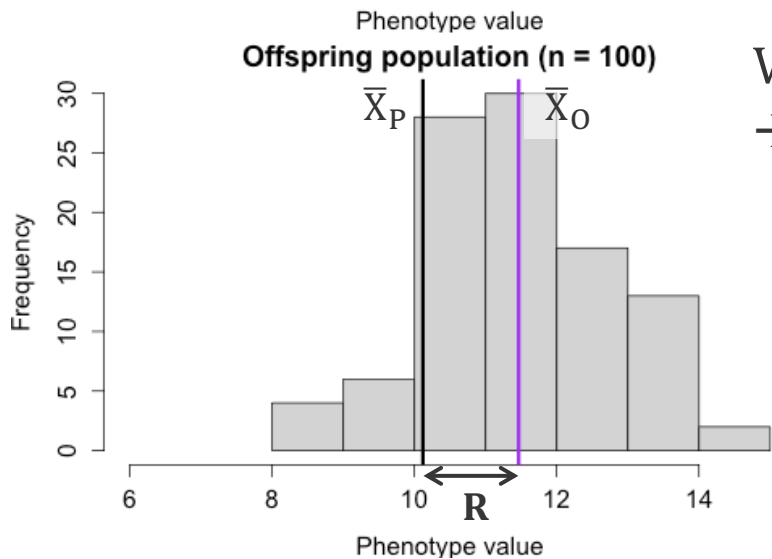S is a measure of selection, R the actual response. One can get lots of selection but no response.

Effect of selection on variance

Initial population (n = 100)

Offspring population (n = 100)

$V_{P_P} = 1.96$ variance of the parental population

$V_{P_S} = 0.50$ variance of the selected population
→ Variance of selected individuals is reduced by factor k
$$V_{P_S} = (1 - k)V_{P_P}, \text{ where } k = i(i - x) \text{ (Bulmer, 1971)}$$

$V_{P_O} = 1.60$ variance of the new population
→ Variance partially recovered in a new population by Mendelian sampling and recombination among offspring
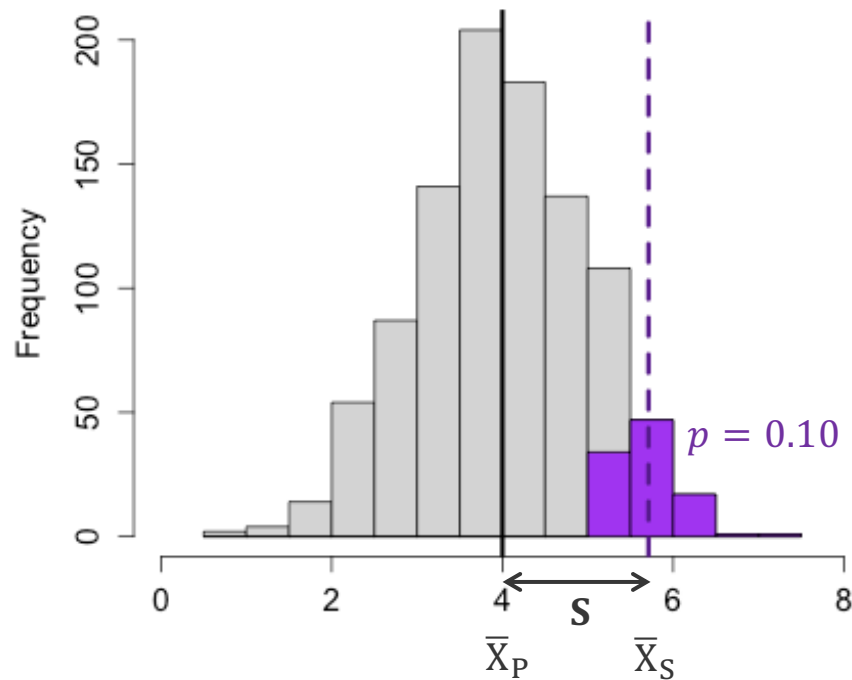$$V_{P_O} = (1 - 1/2h^4k)V_{P_P}$$

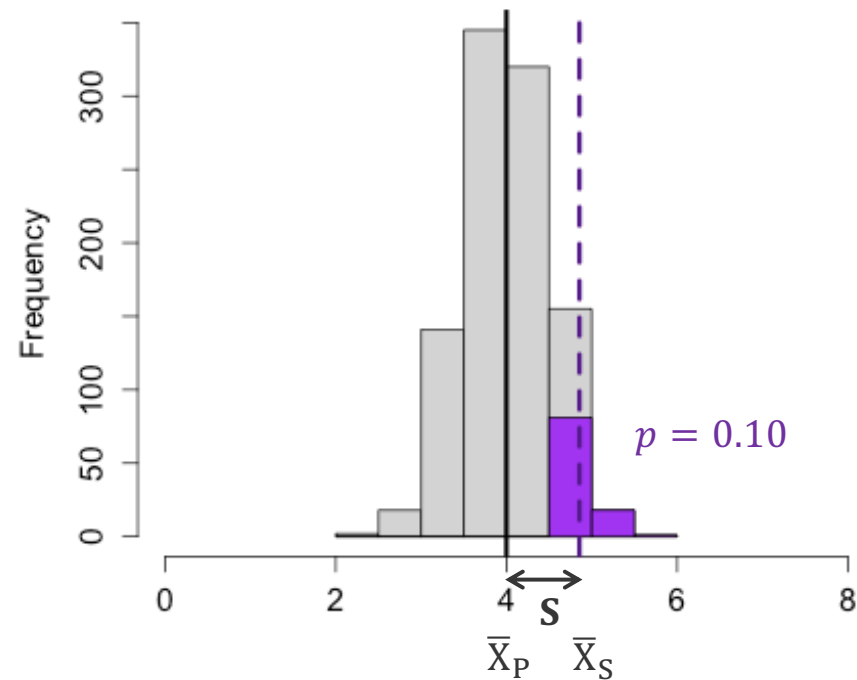# Selection differential

Selection differential is a function of

- the trait variability, and
- the proportion of individuals selected.

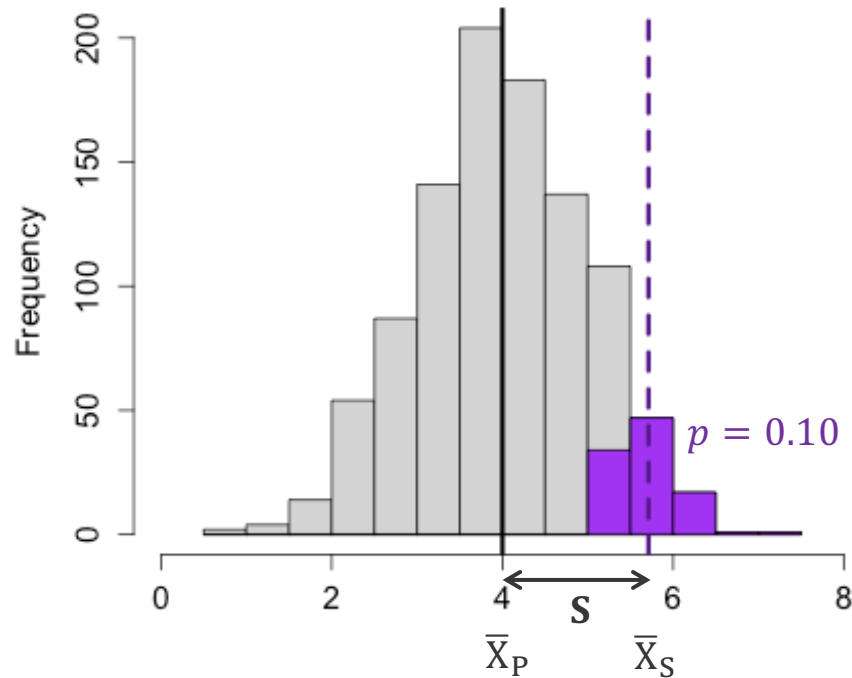# Selection differential: variability of the trait

$$i = (\overline{X}_S - \overline{X}_P)/\sigma_P = S/\sigma_P$$

Selection intensity (or standardised selection differential), expressed in standard deviation units of phenotype, provides a generalized measure for comparison between populations/traits.
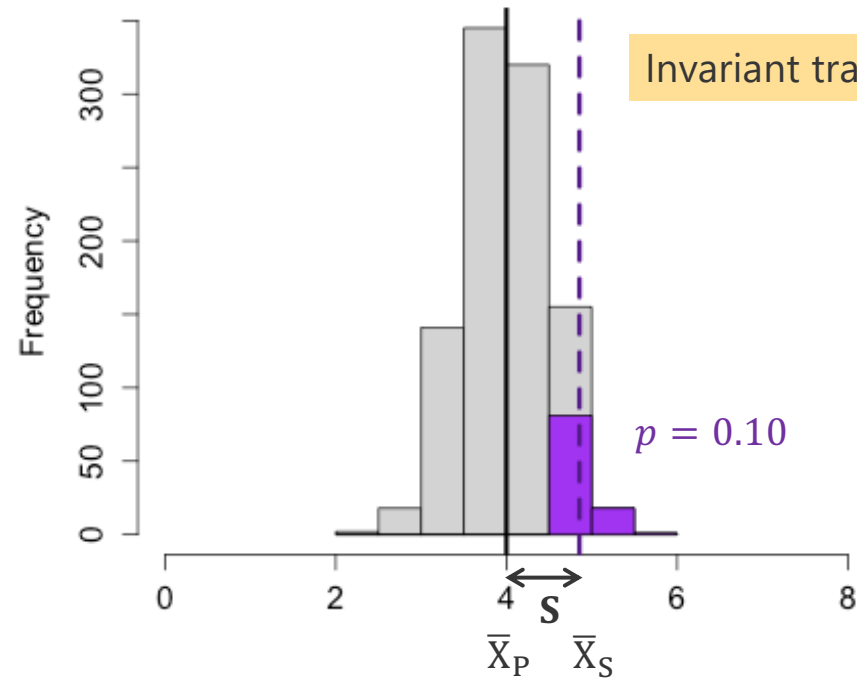
Selection differential: variability of the trait

varP = 1; p = 0.10

$p = 0.10$

$\overline{X}_P$ $\overline{X}_S$

$S = 1.71\sigma_P$

varP = 0.25; p = 0.10

Invariant trait → low S

$p = 0.10$

$\overline{X}_P$ $\overline{X}_S$

$S = 0.86\sigma_P$

$$i = (\overline{X}_S - \overline{X}_P)/\sigma_P = S/\sigma_P \rightarrow \mathbf{S = i\sigma_P}$$

Selection intensity = how many standard deviations the mean of selected individuals is away from the population mean.

Selection differential: proportion of selected
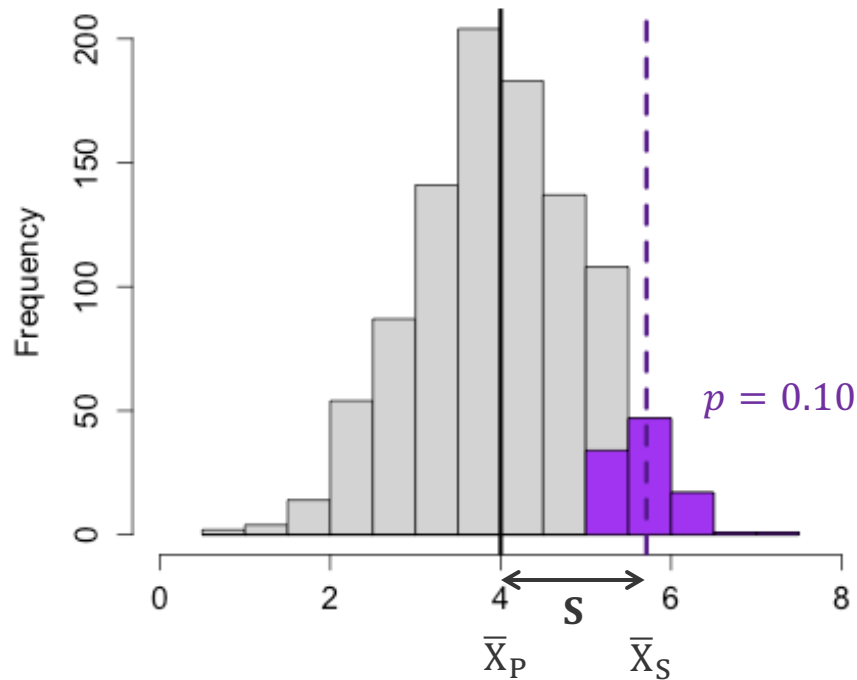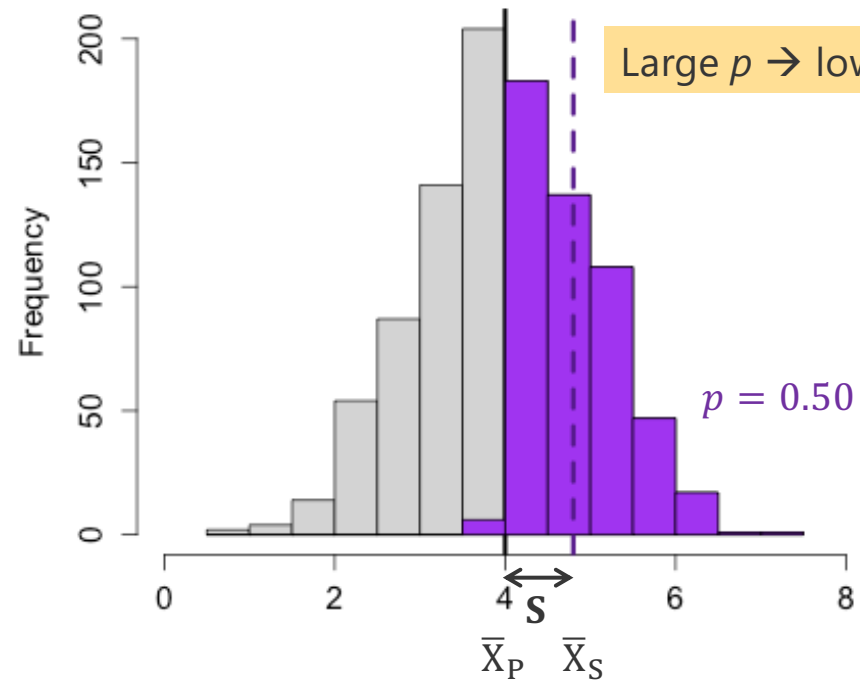
$$i = (\bar{X}_S - \bar{X}_P)/\sigma_P = S/\sigma_P \rightarrow S = i\sigma_P = (z/p)\sigma_P$$

The proportion of selected individuals can be translated into **expected selected intensity** (assuming the trait is normally distributed).

Selection differential: proportion of selected

$$i = z/p$$

$\sigma = 1$

Height of truncation point

$p\%$

z

$0 \quad\quad x \quad i$
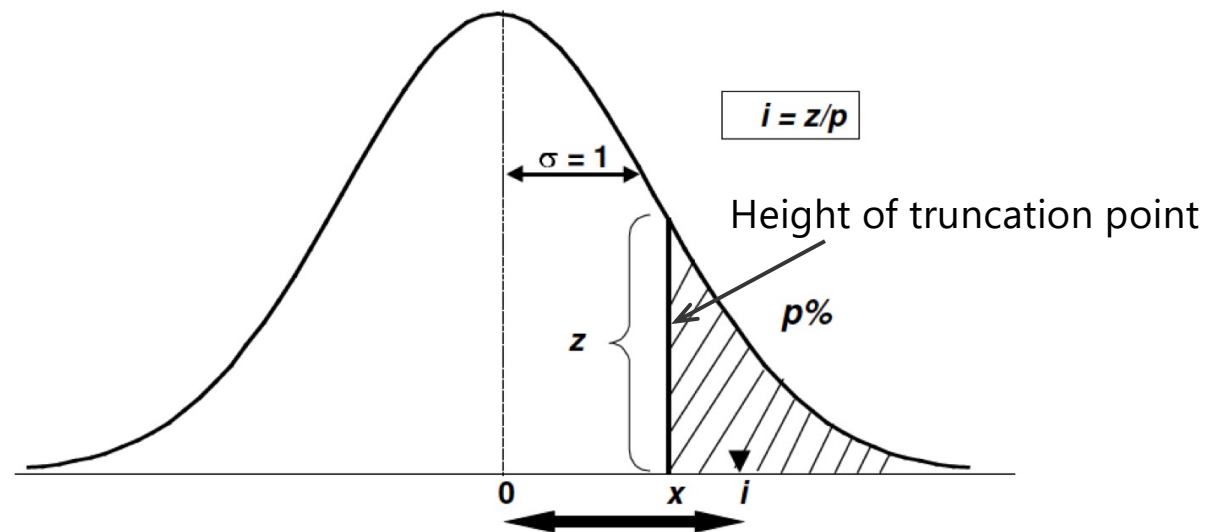
In R command: $i = \text{dnorm}(\text{qnorm}(1 - p))/p$

$$\mathbf{i} = (\overline{X}_S - \overline{X}_P)/\sigma_P = S/\sigma_P \ \rightarrow\ S = i\sigma_P = (z/p)\sigma_P$$

Expected selection intensity = allows a breeder to choose an expected value
of i before selection to calculate an expected gain

The Breeder's Equation

$$R = h^2 S = h^2 i\, \sigma_P = h^2 \left(^z/_p\right)\sigma_P$$

The Breeder's Equation

$$R = h^2S = h^2i\,\sigma_P = h^2\left(^z/_p\right)\sigma_P$$

$$\downarrow$$

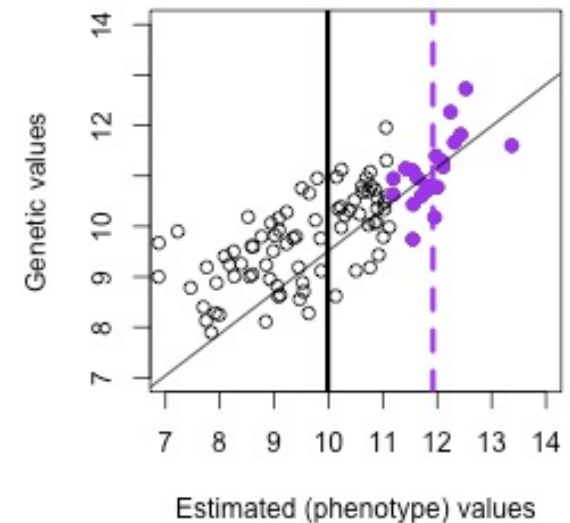$$R = b_{AP}i\sigma_P$$

$$\downarrow$$

$$R = \frac{r\sigma_A}{\cancel{\sigma_P}}\,i\cancel{\sigma_P}$$

$$\downarrow$$

$$R = ri\sigma_A$$

$$h^2 = b_{AP} = \frac{r\sigma_A}{\sigma_P}$$

$$a = \bar{x} + b_{AP}x + e, \text{ where } b_{AP} = h^2$$

The Breeder's Equation – *key drivers of selection*

$$\Delta G = \frac{ir\sigma_A}{L}$$ (Lush, 1937)

i	selection intensity
r	accuracy of selection
σ_A	genetic variance
L	generation interval
ΔG	expected gain per unit of time

Selection intensity (i)

higher intensity → more gain, more inbreeding, more genetic variance loss
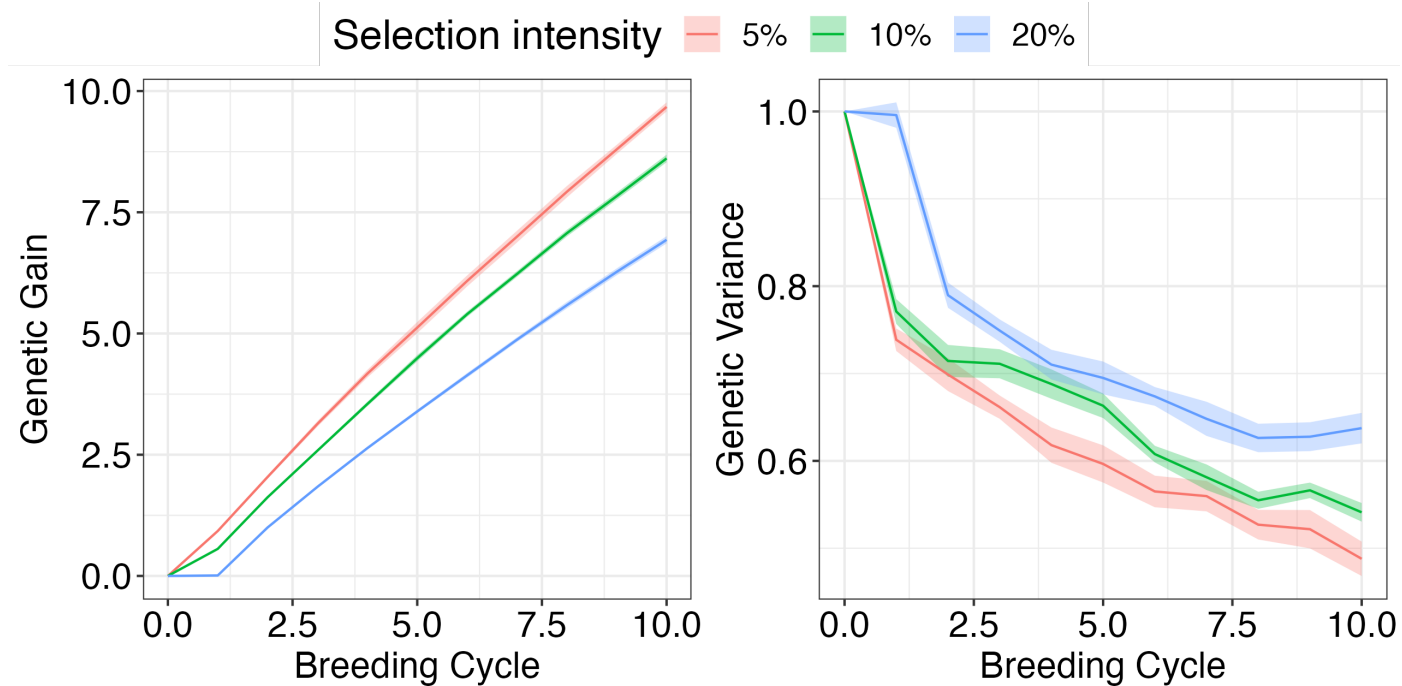
Increase i: genotype more individuals without phenotypes

Accuracy of selection (r)

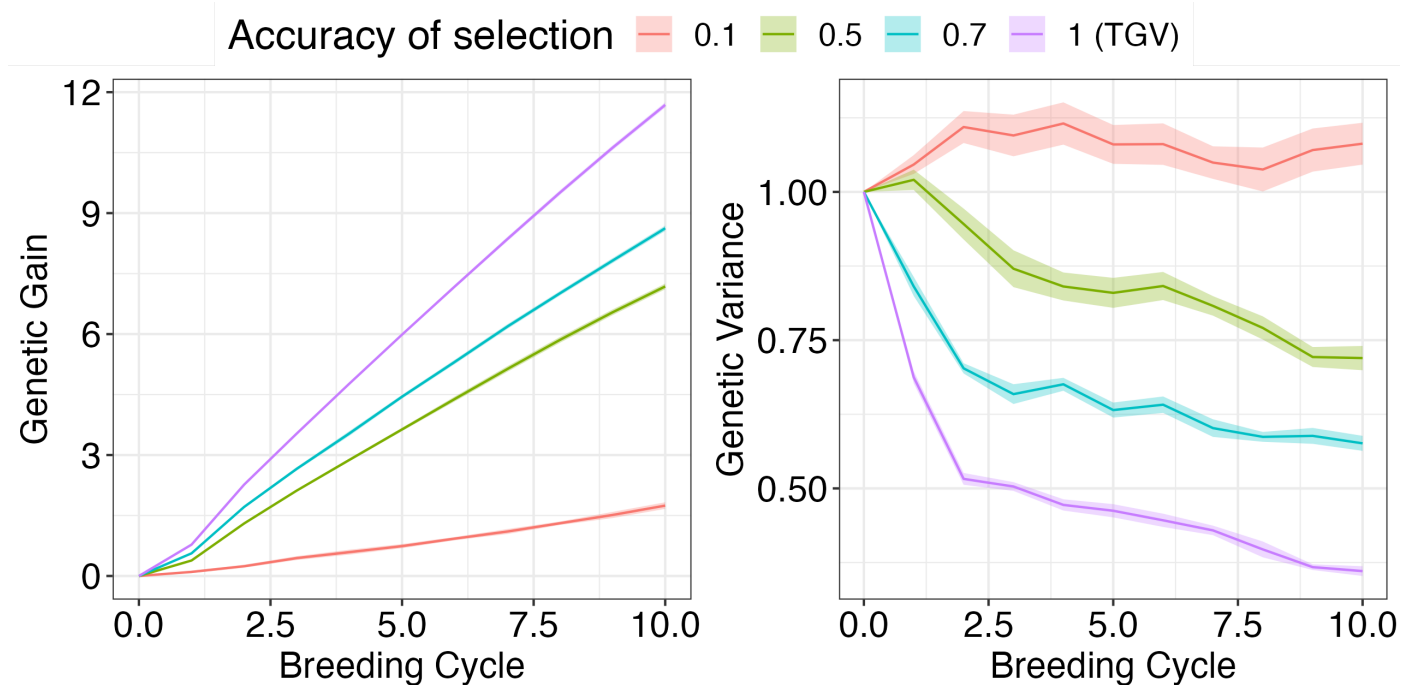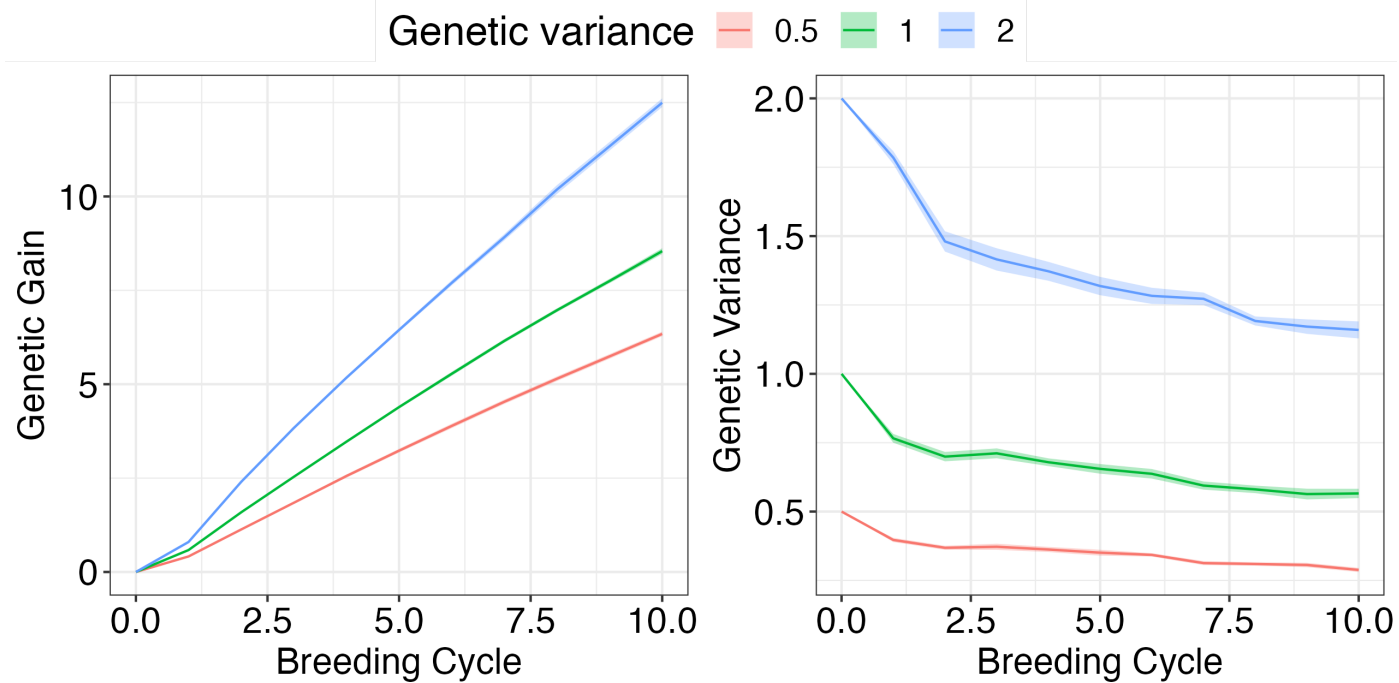higher accuracy → more gain, more inbreeding, more genetic variance loss

Increase r: more information, indirect selection, good phenotypes, good experimental design, kinship information

Genetic variance (σ_A)

higher genetic variance → more gain

Genetic variance — 0.5 — 1 — 2

Maintain σ_A: minimising inbreeding, introduction of new genetic material

Generation interval (L)

increased generation interval → increase in response, more inbreeding, more genetic variance loss
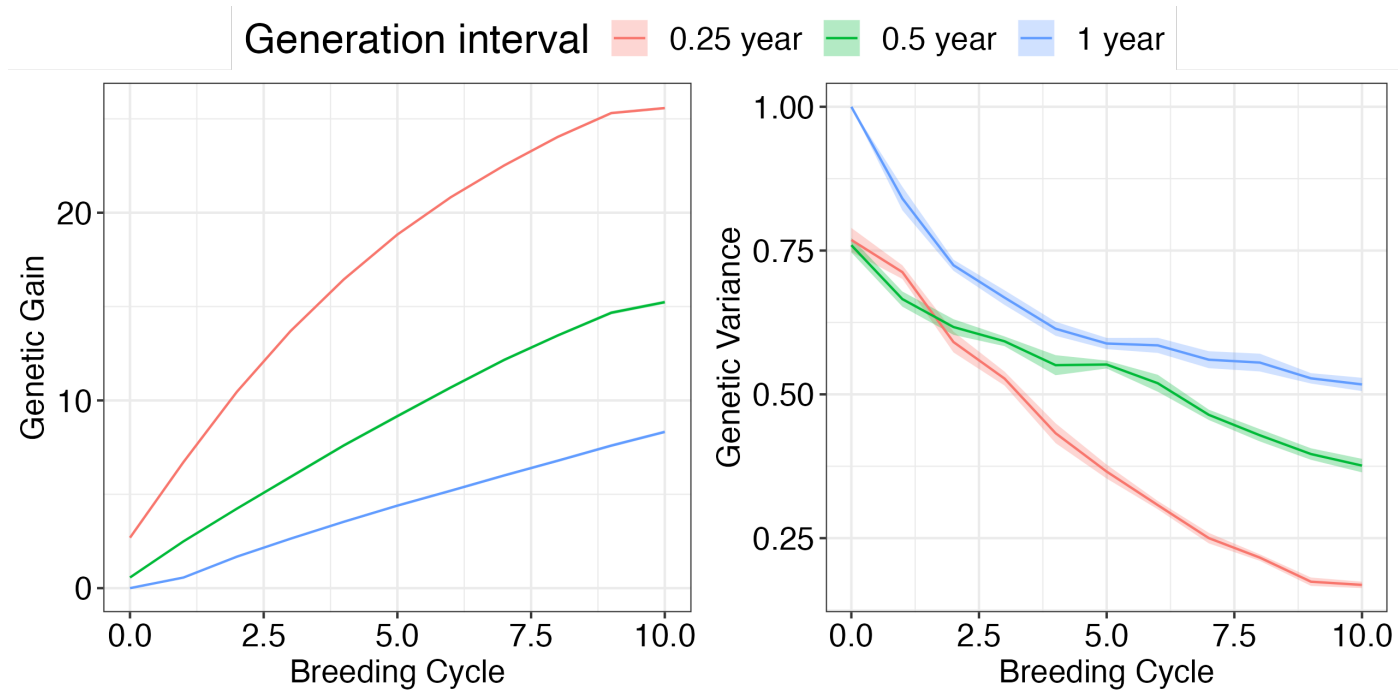
Increase L: early genotype selection (with/without phenotypes), make crosses ahead of results, out of season nurseries

Multiple Trait Selection: Correlated Response

$$CR_2 = ih_1 r_A \sigma_{A2}$$

CR_2 correlated response for Trait 2 when selection imposed on Trait 1

i selection intensity on Trait 2

h_1 accuracy of selection for Trait 1

r_A genetic correlation between Trait 1 and 2

σ_{A2} genetic variance of Trait 2

Selection for one trait will cause a **correlated response to selection** in a second trait if a *genetic correlation* exists between the two traits.

Multiple Trait Selection: Index Selection

$$I = b_1 X_1 + b_2 X_2 + ... + b_n X_n, \text{ where } \mathbf{b} = \mathbf{P}^{-1}\mathbf{Ga} \text{ (Hazel, 1943)}$$

X_i phenotypic value for trait i

$\mathbf{b}$ $n \times 1$ vector of weights for the n traits

$\mathbf{G}$ $n \times n$ genetic covariance matrix between the n traits

$\mathbf{P}^{-1}$ $n \times n$ inverse phenotype covariance matrix between the n traits

$\mathbf{a}$ $n \times 1$ vector of economic weights for the n traits

Index selection involves selecting for several traits simultaneously on the basis of a *single index value.*

Selection index is usually a linear function of different traits, each trait being given a certain weight according to its Importance.

Multi-Trait Version of The Breeder's Equation

$$\Delta\mathbf{G} = \mathbf{G}\mathbf{P}^{-1}\mathbf{S}$$

$\mathbf{G}$	$n \times n$ genetic covariance matrix between n traits
$\mathbf{P}^{-1}$	$n \times n$ inverse phenotype covariance matrix between n traits
$\mathbf{S}$	$n \times 1$ selection differential vector for n traits
$\Delta\mathbf{G}$	expected within-generation gain for n traits

AlphaSimR demonstration

5 minute tutorial + 20 minute exercise

Simulate Response to Selection of a Single Trait in AlphaSimR

5 minute tutorial + 20 minute exercise

Simulate Response to Selection of Multiple Traits in AlphaSimR

Remaining time or homework

Independent Exercise