Computation of selection differential and intensity of selection

Selection is differential reproduction and survival of genotype which may be natural, artificial or both. It is a process that involves forces that determine which animals in a given generation will breed and produce the next generation. Selection may be natural selection i.e causal forces are from natural origin or artificial selection which is under human control. In either case, the genetic effect is the same. The process of change in gene frequencies normally moves at a faster rate with artificial selection than with normal selection. Selection for a quantitative trait brings about changes in mean performance of the progeny generation over the parental generation. This change in performance of progeny due to artificial selection is referred to as response to selection or genetic gain.

Selection Differential

Changes in the trend in a population or an individual herd with time are due to both genetic and environmental factors. Any genetic improvement can be gained by computing the selection differential and multiplying them by appropriate heritability value. Selection differential can be accurately determined and it is found to be large enough to express any genetic change. The selection differential is the difference between the performance of those individuals which are selected to be parents and the average of all individuals in the population. Due to varying percentage of offspring required by different species to maintain the population, their selection differential can vary according to their reproductive rate. There are also differences in the selection differential attained for males and females. It is obvious that if the selection differential is increased, a more progress can be achieved.

Selection differential is the only factor that a man can consider to improve his herd. Unless the selected animals are better than the average of the population, no improvement can be made in the subsequent generation.

It is computed as the difference between the mean of the selected parents (P_S) and mean of the population prior to selection (P_O) and is symbolized as (S). It is a measure of the phenotypic superiority of the selected parents over the population from which the parents were selected. It carries the unit of the measurement of the trait.

\[ S = P_S - P_O \]
When selection is applied in both the sexes, the selection differential is calculated separately by each sex and the mean of the two selection differential is obtained as:

\[
\text{Average } S = \frac{S \text{ (male)} + S \text{ (female)}}{2}
\]

Selection differential can be expressed in standard deviation units \((\sigma_p)\) by assuming the trait to be normally distributed. The standardized selection differential is referred to as selection intensity \((i)\). Selection intensity does not carry any unit of measurement. Selection intensity can be calculated as:

\[
\text{Selection intensity } (i) = \frac{S}{\sigma_p}
\]

If the phenotypic values are normally distributed and the proportion of the population saved for breeding is known. The value of the selection intensity can be known directly from the following table:

<table>
<thead>
<tr>
<th>Per cent selected</th>
<th>P</th>
<th>i</th>
<th>Per cent selected</th>
<th>P</th>
<th>i</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.01</td>
<td>2.67</td>
<td>15</td>
<td>0.15</td>
<td>1.55</td>
</tr>
<tr>
<td>2</td>
<td>0.02</td>
<td>2.42</td>
<td>20</td>
<td>0.20</td>
<td>1.40</td>
</tr>
<tr>
<td>3</td>
<td>0.03</td>
<td>2.27</td>
<td>25</td>
<td>0.25</td>
<td>1.27</td>
</tr>
<tr>
<td>4</td>
<td>0.04</td>
<td>2.15</td>
<td>30</td>
<td>0.30</td>
<td>1.16</td>
</tr>
<tr>
<td>5</td>
<td>0.05</td>
<td>2.06</td>
<td>40</td>
<td>0.40</td>
<td>0.97</td>
</tr>
<tr>
<td>6</td>
<td>0.06</td>
<td>1.99</td>
<td>50</td>
<td>0.50</td>
<td>0.80</td>
</tr>
<tr>
<td>7</td>
<td>0.07</td>
<td>1.92</td>
<td>60</td>
<td>0.60</td>
<td>0.64</td>
</tr>
<tr>
<td>8</td>
<td>0.08</td>
<td>1.86</td>
<td>70</td>
<td>0.70</td>
<td>0.50</td>
</tr>
<tr>
<td>9</td>
<td>0.09</td>
<td>1.80</td>
<td>80</td>
<td>0.80</td>
<td>0.35</td>
</tr>
<tr>
<td>10</td>
<td>0.10</td>
<td>1.76</td>
<td>90</td>
<td>0.90</td>
<td>0.20</td>
</tr>
</tbody>
</table>
The average 8 week body weight of a broiler flock was 1200 grams. Male and female selected as breeders averaged 1600 and 1400 grams respectively. Calculate:

A) The selection differential for a) male  b) female  c) average for both the sexes

B) If selection had not been practiced in males, what would be the selection differential for males and average selection differential for males and average selection differential for both the sexes?

\[
\begin{align*}
\text{A) } & \quad \overline{P} = 1200 \text{ grams} \\
& \quad P_{Sm} = 1600 \text{ grams} \\
& \quad P_{SF} = 1400 \text{ grams} \\
\text{a) } & \quad S_m = 1600 - 1200 \\
& \quad = 400 \text{ grams} \\
\text{b) } & \quad S_f = 1400 - 1200 \\
& \quad = 200 \text{ grams} \\
\text{c) } & \quad S_{av} = \frac{400 + 200}{2} \\
& \quad = 300 \text{ grams} \\
\text{B) In case no selection have been practiced in case of males then} \\
& \quad S_m = 0 \\
& \quad S_f = 200 \\
& \quad S_{av} = \frac{200 + 0}{2} = 100 \text{ grams}
\end{align*}
\]
Exercise 2

In a normally distributed population with mean of 1200 grams and standard deviation of 100 grams, the selected parents were superior over the population average by 200 grams. Calculate

a) Selection intensity

b) Interpret its value in terms of percentage of the parents retained for breeding
Exercise 3

Following are the yearling weight of 20 bulls on a performance test. The mean is 100 kg.

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>102</td>
<td>102</td>
<td>98</td>
<td>101</td>
<td>117</td>
</tr>
<tr>
<td>109</td>
<td>104</td>
<td>103</td>
<td>112</td>
<td>111</td>
</tr>
<tr>
<td>103</td>
<td>110</td>
<td>97</td>
<td>113</td>
<td>96</td>
</tr>
<tr>
<td>115</td>
<td>101</td>
<td>102</td>
<td>106</td>
<td>105</td>
</tr>
</tbody>
</table>

a) Assume that the top bull is used in an A.I. stud, what is the selection differential?
b) What is the selection differential of the three best bulls?
c) What is the selection differential of the five best bulls?
d) If standard deviation is 0.64 what will be the intensity of selection in all cases?
Exercise 4

Find out the observed selection differential, standardized and effective (Weighted) selection differential from the data given below with mean = 1900 units and $\sigma_p = 16$ units.

<table>
<thead>
<tr>
<th>Sire No.</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trait</td>
<td>2000</td>
<td>1970</td>
<td>1920</td>
<td>1880</td>
<td>1850</td>
<td>1900</td>
<td>11520</td>
</tr>
<tr>
<td>No. of progeny</td>
<td>10</td>
<td>15</td>
<td>12</td>
<td>14</td>
<td>11</td>
<td>8</td>
<td>70</td>
</tr>
</tbody>
</table>
Estimation of Generation interval

Generation interval:

Generation interval is defined as the average age of parents when all their offspring are born. It is the average of the length of time between the births of certain animals and the birth of all their progeny. For example, if a cow has 10 calves in her life time when she was 2, 3, 5, 6, 8, 9, 10, 11, 12 and 14 years of age, the generation interval just far her family is 8 years. In reality the generation interval for all cattle is about 6 or 7 years, one year poultry and for pigs 2 – 3 years. Generation interval affects genetic progress because longer generation interval slows down the overall progress. Greater progress can be obtained in those species that has shorter generation interval. Poultry and swine have shorter generation interval than cattle or other livestock species. Because they produce more progeny. That is why so much greater progress has apparently occurred in poultry and swine during last 30 – 40 years.

The generation interval is computed as the time interval between the two successive generations (i.e. parents and offspring generation) with respect to same stage of life cycle. If the male and female parents vary in the age when their offspring are born, then the generation interval should be computed separately for the two sexes.

\[
\text{Average G.I} = \frac{\text{G.I (male)} + \text{G.I (female)}}{2}
\]

Example

Given below are the months of birth of sires and dams of pigs born in January, 1995

Calculate:

a. Generation interval for the sires and dams.

b. Average generation interval for the two sexes.

<table>
<thead>
<tr>
<th>Pig No.</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>Sire</td>
<td>July,93</td>
<td>Nov.,93</td>
<td>May,93</td>
<td>Nov.,93</td>
</tr>
<tr>
<td>Dam</td>
<td>Oct.,93</td>
<td>Feb.,93</td>
<td>Jan.,94</td>
<td>Dec.,92</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Generation interval of sire

<table>
<thead>
<tr>
<th>Sire</th>
<th>Date of Birth</th>
<th>Generation Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>July 93 to January 95</td>
<td>18 months</td>
</tr>
<tr>
<td>2</td>
<td>Nov., 93 to January 95</td>
<td>14 months</td>
</tr>
<tr>
<td>3</td>
<td>May, 93 to January 95</td>
<td>20 months</td>
</tr>
<tr>
<td>4</td>
<td>Nov., 93 to January 95</td>
<td>14 months</td>
</tr>
<tr>
<td>5</td>
<td>Jan., 94 to January 95</td>
<td>12 months</td>
</tr>
</tbody>
</table>

### Generation interval of Dams

<table>
<thead>
<tr>
<th>Dam</th>
<th>Date of Birth</th>
<th>Generation Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Oct., 93 to January 95</td>
<td>15 months</td>
</tr>
<tr>
<td>2</td>
<td>Feb., 93 to January 95</td>
<td>23 months</td>
</tr>
<tr>
<td>3</td>
<td>Jan, 93 to January 95</td>
<td>12 months</td>
</tr>
<tr>
<td>4</td>
<td>Dec., 93 to January 95</td>
<td>25 months</td>
</tr>
<tr>
<td>5</td>
<td>Oct., 94 to January 95</td>
<td>15 months</td>
</tr>
</tbody>
</table>

### Average generation interval

<table>
<thead>
<tr>
<th>Sire/Dam</th>
<th>GI_s + GI_f</th>
<th>Average GI of both Sexes</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>18 + 15/2</td>
<td>33/2</td>
</tr>
<tr>
<td>2</td>
<td>14 + 23/2</td>
<td>37/2</td>
</tr>
<tr>
<td>3</td>
<td>20 + 12/2</td>
<td>32/2</td>
</tr>
<tr>
<td>4</td>
<td>14 + 25/2</td>
<td>39/2</td>
</tr>
<tr>
<td>5</td>
<td>12 + 15/2</td>
<td>27/2</td>
</tr>
</tbody>
</table>
Exercise 1. The data given below are the date of birth of the parents of calves born in January 2007. Calculate the generation interval for sires and dams for each calf separately and average generation interval for the two sexes.

<table>
<thead>
<tr>
<th>Animal no</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Exercise 2

The age at first kidding of 500 goats is given here. Find out the G.I. for age at first kidding.

<table>
<thead>
<tr>
<th>Age at first kidding (Years)</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of Goats</td>
<td>140</td>
<td>170</td>
<td>100</td>
<td>90</td>
</tr>
</tbody>
</table>
Exercise 3

Find out the generation interval of cow born in July, 90. The cow has produced first calf in Sept., 93 after that it has produced 5 calves during her life time with calving interval as 14 months.
Expected genetic gain

Response to selection can be defined as the difference of mean phenotypic value between the offspring of the selected parents and the whole of the selected parents before selection. It is also called as expected genetic gain and shall be symbolized by (R or ΔG). Selection response depends upon heritability of the character (h²) and Selection differential (SD)

\[ R = h^2 \times SD \]

The expected genetic gain per generation or response per generation can be estimated by

Response / generation = h² x SD

Response / year = (h² x SD) / Generation Interval

If selection differential is expressed in terms of intensity of selection (i) and phenotypic standard deviation then SD = i x σₚ and selection response become

\[ R = h^2 \times SD \]

\[ R = h^2 \times i \times \sigma_p \]

We know that h = σₐ / σₚ

Or, σₐ = h x σₚ

Then above equation of selection response can also be written as follows

\[ R = h \times i \times \sigma_A \]

If two sexes have variable selection differential and generation interval then response per year can be calculated as follows

\[ \Delta G / Year = \left[ \frac{1}{2} h^2 \times S_m + h^2 \times S_f \right] \frac{S_F}{G.I_m \times G.I_f} \]

Where,

\[ h^2 = \text{Heritability of the trait.} \]
Sm = Selection differential for males
Sf = Selection differential for females
G. Im = Generation interval for males
G. If = Generation interval for females.

The formula for expected genetic gain can also be written in terms of selection intensity (i) as:

\[ \frac{\Delta G}{\text{Year}} = r_{AP} \times i \times \sigma_A \frac{h}{G.I} \]

Where, \( r_{AP} \) = accuracy of selection and is computed as the correlation between the breeding value and the criterion of selection (performance of individual or pedigree or family or progeny) and equals square root of heritability ‘h’ for individual selection. Its value varies for different basis of selection

Considering, different selection intensities and different generation intervals for the two sexes. \( \Delta G \) can be computed as:

\[
\frac{\Delta G}{\text{Year}} = \left( \frac{1}{2} \frac{h \times \sigma_A \times i_m}{G.I_m} + \frac{h \times \sigma_A \times i_f}{G.I_f} \right)
\]

Where,

h = Square root of heritability of the trait.
i_m = Selection intensity for males
i_f = Selection intensity for female.
Example:

In a flock of Japanese quails, 4 weeks body weights averaged 135 gm. The selected quails had average body weight of 150 gms. The $h^2$ of body weight is 0.3. One generation of quails can be obtained in 4 months. Calculate

a) Selection differential
b) Expected genetic gain per generation and per year
c) Expected mean 4 week body weight in the next generation and after one year
d) How many year required to double the 4 week body weight of the quail flock

Average 4 week body weight of the flock (Po) = 135 gms
Average 4 week body weight of the selected birds (Ps) = 150 gms

$h^2 = 0.3$

Generation Interval (G.I) = 4 months

a) Selection differential,

$$S = [Ps - Po] = 150 - 135 = 15 \text{ grams}$$

b) Expected genetic gain per generation,

$$\Delta G = h^2 \times S = 0.3 \times 15 = 4.5 \text{ gram}$$

One generation = 4 months

Generations per year = $12 / 4$

$$4.5 \times 12$$

Expected genetic gain per year = $\frac{4.5 \times 12}{4} = 13.5 \text{ grams}$

c) Expected average 4 week body weight after one year = $135 + 13.5 = 148.5 \text{ grams}$

d) No. of years required to double the 4 week body weight of the quail flock = 10

Correlated Response to selection:

When selection is practiced for a given trait, a change in the mean performance of the progeny generation with respect to this trait is quite naturally expected. The genetic gain in the trait under selection is then referred to as “direct response” or “direct genetic gain”. When selection for a given trait results in a change in the other trait of the progeny, the change is referred to as “correlated response”. The correlated response is due to genetic association of the trait under selection with other trait which has been not subjected to selection. It can be computed as:

$$\Delta G / X = h_x \times i_x \times \sigma_{A(Y)} \times r_{G(XY)}$$
Since \( \sigma_{P(Y)} = h_Y \times \sigma_{P(Y)} \), Therefore the formula can be rewritten as:

\[
\Delta G/ X = h_X \times h_Y \times i_x \times r_{G(XY)} \times \sigma_{P(Y)} \times r_{G(XY)}
\]

Where,

\( \Delta G/ X \) = Expected correlated response in trait ‘Y’ when selection is for trait ‘X’.

\( h_x \) = Square root of heritability of the trait being selected (X)

\( h_Y \) = Square root of heritability of the trait Y

\( i_x \) = Selection intensity for trait X

\( \sigma_{A(Y)} \) = Additive genetic standard deviation for trait Y

\( \sigma_{P(Y)} \) = Phenotypic standard deviation for trait Y

\( r_{G(XY)} \) = genetic correlation between X & Y

**Example:**

Given below is the information for lactation milk yield (X) and age at first calving (Y) in a dairy cattle herd:

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean</th>
<th>( \sigma_P )</th>
<th>( h^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lactation milk yield</td>
<td>2000 liters</td>
<td>200 liters</td>
<td>0.25</td>
</tr>
<tr>
<td>Age at first calving</td>
<td>36 months</td>
<td>9 months</td>
<td>0.16</td>
</tr>
</tbody>
</table>

The genetic correlation between milk yield and age at first calving is – 0.30. If the best 40% of the parents (both sexes) are retained for breeding, calculate:

a) The excepted direct response to selection in milk yield.
b) The correlated response in age at first calving .
c) The expected average Lactation milk yield in the next generation.
d) The expected average age at first calving of the next generation.
e) Comment on the correlated response in age at first calving.
   a) \( R = i \sigma_Y h^2 \)
   b) \( i = 0.97 \) (40%) from table
\[ R = 0.97 \times 200 \times 0.25 = 48.5 \text{ liters} \]

b) \[ R_Y = i \times h \times \sigma_{AY} \]

\[ h^2 = 0.25, \ h = 0.5 \]

\[ \sigma_{A(Y)} = h_Y \times \sigma_p \times r_{A(XY)} \]

\[ = 0.4 \times 9 = 3.6 \]

\[ R_Y = 0.97 \times 0.5 \times 3.6 \times (-0.3) = -0.5231 \text{ months} \]

Negative sign means age at first calving decreases by 0.5238 months.

c) \[ P_{s(X)} = R + P_o \]

\[ = 48.5 + 2000 = 2048.5 \text{ liters} \]

d) \[ P_{(Y)} = R_Y + P_o = -0.5238 + 36 = 35.48 \]

e) With increase in milk yield we expect decline in age at 1\textsuperscript{st} calving.
Exercise 1

Calculate the expected genetic gain per generation and per annum using the values given below. Find out the number of years required to double the milk yield.

Selection intensity \( (i) = 0.9 \)

Standard deviation \( (\sigma_p) = 100 \) grams

Heritability \( (h^2) \) = 0.4

Herd average = 1500 kgs.

Generation interval = 6 years
Exercise 2

The average milk yield of dairy farm is 1005 kg per lactation of 305 days. A cow and bull is selected for breeding purpose has average milk yield 1500 kg and 2000 kg respectively. The milk yield is 30% heritable. Calculate expected genetic gain in the offspring produced by the selected parents.
Exercise 3

An average egg production of a flock is 100 eggs per year. Sire birds were selected and they have an average of 150 eggs. If the heritability value of egg production is 0.3. Determine:

a) Genetic gain per generation and per year
b) Average egg production after five years
c) How many years will be required to increase the average egg production to its present value?
Exercise 4.

The average annual greasy fleece weight of a flock of sheep was 2.0 kg and after culling the low producers, the average increased to 2.5 kg. The EPA of 10 rams used in the flock was 3.0 kg after culling the low producers, the average increased to 4.0 kg. Assume the $h^2$ of fleece production as 0.4 and generation interval from dam to daughter as 4 years and that of sire to daughter as 3 years. Estimate the expected genetic gain per generation and per year.
MOST PROBABLE PRODUCING ABILITY

Life time averages which show the ability of certain individuals to repeat a high level of performance over a long period of time are very important in animal breeding. The record should be accurate and should be corrected for certain environmental factors before the individuals in the herd are compared.

Lush has suggested a formula for adjusting the records of cows with different number of records to the same basis and has called this as the Most Probable Producing Ability (MPPA) of an individual.

\[
\text{MPPA} = \text{Herd Average} + \frac{n \cdot r}{1 + (n - 1) \cdot r} \times \text{Individuals own average} - \text{Herd average}
\]

- \( n \) = Number of records for each individual
- \( r \) = Repeatability estimate for one record

Life time averages are important in selection for traits in which the repeatability is low. A consistently high performance over a period of many years is a good indication that the animal possesses desirable genes for several traits. Both male and female replacements from such dams should be selected.

**Exercise 1**

Calculate Most Probable Producing Ability for weaning weight of calves if the herd average is 50 kg. and the repeatability is 0.4. Cow No. 1 has weaned three calves with average weaning weight as 60 Kg. and cow No. 2 has weaned 5 calves with average weaning weight as 70 Kg.
Exercise 2

The average milk production in a lactation of Tharparkar herd is 1800 kg. The milk production of 4 cows in different lactation is given as under:

<table>
<thead>
<tr>
<th>Cow No.</th>
<th>Lactation 1</th>
<th>Lactation 2</th>
<th>Lactation 3</th>
<th>Lactation 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1820</td>
<td>1860</td>
<td>---</td>
<td>---</td>
</tr>
<tr>
<td>2</td>
<td>1810</td>
<td>1836</td>
<td>1860</td>
<td>1840</td>
</tr>
<tr>
<td>3</td>
<td>1830</td>
<td>1850</td>
<td>1870</td>
<td>--</td>
</tr>
<tr>
<td>4</td>
<td>1840</td>
<td>---</td>
<td>---</td>
<td>---</td>
</tr>
</tbody>
</table>

Taking the repeatability of milk yield as 0.40, estimate the MPPA of all the cows and rank them.
Calculation of inbreeding coefficient and coefficient of relationship

The major genetic consequence of inbreeding is to increase the homozygosity at the expense of total heterozygosity existing in base population. The percent increase in homozygosity or decrease in heterozygosity in an inbred individual in relation to other non-inbred individuals of the base population is called inbreeding coefficient (F) was proposed by Sewall Wright (1921).

The inbreeding coefficient (F) is also defined as the probability that the two alleles at a locus in an individual are identical by descent. Two genes are said to be identical by descent if they arise from the direct replication of the same gene from a common ancestor in an earlier generation. The value of coefficient inbreeding (F) ranges from 0 to 1 or 0 to 100%. As the value of F increases, the relative proportion of heterozygosity declines in a proportionate amount equal to (1-F).

**Formula used:**

As inbreeding coefficient depends on the relationship of its ancestor or parents, the inbreeding coefficient of an individuals (Fx) will be:

\[ F_x = \frac{1}{2} (\text{covariance of parents}) = \frac{1}{2} \sum \left[ \left(\frac{1}{2}\right)^n (1+F_A) \right] = \sum \left[ \left(\frac{1}{2}\right)^{n+1} (1+F_A) \right] \]……………………..(1)

Where,

- \( F_x \) = Inbreeding coefficient of individual X
- \( \sum \) = summation sign
- \( i = 1 \) to \( k \) number of common ancestor
- \( n \) = number of arrows connecting the sire and dam through the common ancestor
- \( F_A \) = Inbreeding the coefficient of common ancestor of parent of X

The above formula can also be represented in following ways:

(1) \[ F_x = \sum \left[ \left(\frac{1}{2}\right)^n (1+F_A) \right] \]………………..(2)

Where,

- \( N\) = Number of individual in any path of relationship counting the parents of X, the common ancestor and all individuals in the path connecting parents to common ancestor.

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

If the common ancestor is not inbred, then

\[ F_x = \sum \left(\frac{1}{2}\right)^{n+1} \]……………………..(3)
Where,

\[ n = \text{Number of generation/arrows connecting between common ancestor and one parent (Sire) of } X \]
\[ n' = \text{Number of generations / arrows connecting between the common ancestor and other parent (dam) of } X \]
\[ F_X = \text{Inbreeding coefficient of individual } X \]
\[ l = \text{Constant for halving of relationship between parents of } X \]

**Example:** Calculate the inbreeding coefficient from the following pedigree of a half sib mating

```
D  B  D
  |   |
 X E  D
  |
 C F
```

**Solution:**

1. Prepare the arrow diagram in the following way:

```
B  D
  |
X  E  D
  |
C F
```

2. Locate the common ancestor from which two or more than two arrows are emerging i.e. D here.

3. As the common ancestors are not inbred, the following formula will be used

\[ F_X = \sum \left( \frac{1}{2} \right)^{\text{Path}} \]

4. **Calculate the \( F_X \) in the following way:**

<table>
<thead>
<tr>
<th>CA</th>
<th>Path</th>
<th>n</th>
<th>n'</th>
<th>Contribution of each path/ C.A.</th>
</tr>
</thead>
<tbody>
<tr>
<td>D</td>
<td>X ← B ← D ← C ← X</td>
<td>1</td>
<td>1</td>
<td>((1/2)^{1+1+1} = (1/2)^3 = 1/8 = 0.125)</td>
</tr>
</tbody>
</table>

**Total**

\[ F_X = .125 \]

5. **Conclusion:** The inbreeding coefficient of X (\( F_X \)) in the above pedigree is 0.125 or 12.5%
Exercise 1. Calculate the Inbreeding coefficient from the following pedigree of a full sib mating

```
S
X
D
```

```
F
C
C
F
```
Exercise 2. Find the inbreeding coefficient of Z (Fz) from the following pedigree.
Exercise 3. Calculate the inbreeding coefficient (Fx) from the following pedigree of sire and daughter mating:
Exercise 4. Estimate the inbreeding coefficient ($F_x$) from the following pedigree
Exercise 5. Calculate the inbreeding coefficient of individual X from the following pedigree
Exercise 6. Find out the inbreeding coefficient of individual X in the following arrow diagram of pedigree:
**Measurement of Relationship (Coefficient of Relationship)**

The coefficient for expressing the degree of relationship between two individuals was developed by Wright. It measures the probable proportion of genes that are the same in two individuals due to their common ancestry, over and above that in the base population.

Parent-offspring relationships are the simplest. They are fundamental to all other degrees of relationships as these represent combinations of several parent-offspring relationships. Since half the genes of any animal come from his sire and half from his dam, any offspring is 50 per cent related to each parent. Since each parent in turn received half his genes from his sire and half from his dam and half is transmitted to each offspring, on the average 25 per cent of the genes of any animal originally came from each grandparent. Thus, on the average, an animal is 25 per cent related to each of his grandparents. Again it should be kept in mind that the relationship between two individuals is the extra similarity in the genes they possess due to their common ancestry. Many of their genes will already be alike because of the high frequency of these genes in the population (breed).

The key to measuring relationship is the number of generations between the two animals being studied and their common ancestor or ancestors. The first step in computing a relationship coefficient consists of counting the number of generations intervening between some common ancestor and the two descendants in question.

To calculate coefficient of the relationship between X and Y, X and Y have two common ancestors, S and D. When there are two or more common ancestors, the contributions of each are added to arrive at the complete coefficient of relationship.
Relationship of X and Y

<table>
<thead>
<tr>
<th>Common ancestor</th>
<th>n</th>
<th>Contributions</th>
</tr>
</thead>
<tbody>
<tr>
<td>S</td>
<td>2</td>
<td>((\frac{1}{2})^2 = \frac{1}{4} = 0.25)</td>
</tr>
<tr>
<td>D</td>
<td>2</td>
<td>((\frac{1}{2})^2 = \frac{1}{4} = 0.25)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sum = 0.50</td>
</tr>
</tbody>
</table>

Thus X and Y have 0.5 of their genes in common and are related 50 per cent. You can readily calculate the relationship of half brothers as 25 per cent. In the above example you may wonder why A, B, C, and E were not considered as common ancestors of X and Y. The answer is that they make their contributions only through S or D, not through both. For example, the only way A is an ancestor of both X and Y is through S, and by including S as a common ancestor, we automatically take care of A’s contributions. If A had been an ancestor of both S and D, we would have included him as a common ancestor, since he could have contributed the same genes to X and Y through both S and D.

Methods to compute coefficient of relationship

There are two methods for computing coefficient of relationship

1. **Genetic variance-covariance method:**

\[
R_{xy} = \frac{\text{Genetic covariance (X,Y)}}{\sqrt{\text{(genetic variance X)}} \sqrt{\text{(genetic variance Y)}}}
\]

Where, Genetic covariance (X,Y) = \(\sum \left[ \frac{1}{2} \right]^{n+\bar{n}+1} (1 + F_A) \)

Genetic variance (X) = 1 + Fx

Genetic variance (Y) = 1 + FY

2. **Wright’s Method of path coefficient:** The coefficient of relationship is computed as

a. **Direct relatives**

b. **Collateral relatives**

a. **Direct relationship:** Any two individuals are said to be directly related if one is a direct ancestor and other is descendant i.e. they belong to the different generations. eg: sire-son, dam –son, sire-daughter, dam-daughter. It arises when out of two related individuals one is a direct ancestor and other is descendent.

\[
R_{AX} = \left[ \sum \left(\frac{1}{2}\right)^{n+\bar{n}} \right] \left[ \sqrt{1+F_A}/\sqrt{1+Fx} \right]
\]

Where,

\(R_{AX}\) = coefficient of relationship between ancestor (A) and descendent (X)

\(N = (n+\bar{n})\) = numbers generation connecting the ancestor and descendent

\(\frac{1}{2}\) = stands for halving the sampling process of inheritance in each generation
F_A = Inbreeding Coefficient of ancestor (A)
F_X = Inbreeding Coefficient of descendent (X)

However, if the ancestor and the descendent both are non-inbred then formula
\[
R_{AX} = \sum (1/2)^{n+n'}
\]

**Collateral relationship:** Any two individuals are said to collaterally related if neither is an ancestor nor a descendent of the other i.e. usually belongs to different generations.

1) Full sibs
2) Half sibs
3) Half first cousins
4) Single first cousins
5) Double first cousins

\[
R_{XY} = \left[ \sum \left( \frac{1}{2} \right)^{n+n'} \frac{1+FA}{\sqrt{1+F_X}} \frac{1+FY}{\sqrt{1+F_Y}} \right]
\]

Where,
- \( R_{XY} \) = coefficient of relationship between the individual (X) and (Y)
- \( n+n' \) = numbers generation connecting the individual (X) and (Y) through their common ancestor
- \( \frac{1}{2} \) = stands for halving the sampling process of inheritance in each generation
- \( F_A \) = Inbreeding Coefficient of ancestor (A)
- \( F_X \) = Inbreeding Coefficient of descendent (X)
- \( F_Y \) = Inbreeding Coefficient of descendent (Y)

When neither of the individual are inbred then formula
\[
R_{AX} = \sum (1/2)^{n+n'}
\]

Find the coefficient relationship between full sibs (X and Y) from the following pedigree

```
X
  A
  B
```

```
Y
  A
  B
```
Solution:
1. Prepare the arrow diagram in the following ways:

\[ \text{X} \leftrightarrow \text{A} \]
\[ \text{Y} \leftrightarrow \text{B} \]

1. Locate the common ancestor of X and Y having the emergence of two or more than two arrow are i.e. A and B

2. Formula Used:
   As the individual X and Y are the collateral relatives and neither of the common ancestor nor any of the individual is inbred, the following formula will be used
   \[ F_X = \sum \frac{1}{2}^{n+n'} \]

3. Calculate the \(R_{XY}\) in the following way:

<table>
<thead>
<tr>
<th>Common ancestor</th>
<th>Path</th>
<th>n</th>
<th>n'</th>
<th>(F_A)</th>
<th>(F_X)</th>
<th>(F_Y)</th>
<th>Contribution of each path/ C.A.</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>X\leftrightarrow A \rightarrow Y</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>((1/2)^{1+1} = 1/4 = 0.25)</td>
</tr>
<tr>
<td>B</td>
<td>X\leftrightarrow B \rightarrow Y</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>((1/2)^{1+1} = 1/4 = 0.25)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>(F_X = 0.50)</td>
</tr>
</tbody>
</table>

4. Conclusion:
   The relationship coefficient of \(R_{XY}\) in the above pedigree is 0.50 or 50%.
Exercise 1. Calculate coefficient of relationship between half sibs (X and Y) from the following pedigree.
Exercise 2. Find the coefficient of relationship between X and Y from the following pedigree:
Exercise 3. Calculate the relationship coefficient between S and D from the following pedigree.
Exercise 4. Estimate the relationship coefficient between son (X) and sire (S) in the following pedigree.
ESTIMATION OF HETEROSIS

Heterosis can be defined as the increased performance of offspring over the parents resulting from crossing of different breeds/strains/lines etc. It is the result of non-additive gene action. The term “heterosis” was coined by G.H. Shull (1914). Heterosis can be positive (hybrid vigour) or negative depending upon the trait. The amount of heterosis usually depends upon the extent of the heterozygosity attained by the hybrids, which in turn is based on the diversity of sire and dam lines crossed. It also depends on the degree of dominance, over dominance and epistasis. It may be of three types:

1. **Individual Heterosis:** Improvement in performance in an individual (over the mean of its parents) that is not attributed to maternal, paternal or sex-linked effects.

2. **Maternal Heterosis:** Heterosis in population attributed to using crossbred dams instead of purebred dams.

3. **Paternal Heterosis:** Refers to heterosis in using crossbred sires instead of purebred sires on the performance of the progeny.

Maximum hybrid vigour is observed in F₁ (Σdy²) and the animals are likely to be phenotypically uniform in the expression of different traits. But the heterosis diminishes in F₂ (1/2 Σdy²) by inter-se mating. Hybrid vigour has been used extensively in the productions of broilers, layers, commercial swine and production of mules.

**Measures of Heterosis – two ways.**

1. Amount by which F₁s (i.e. offspring’s) exceed the best parent.

   \[
   \text{Heterosis (\%) = } \frac{\text{(Mean of offspring’s – Mean of best parent)}}{\text{Mean of best parent}} \times 100
   \]

2. Amount by which F₁s exceed the average of two parents (mid – parent value).

   \[
   \text{Heterosis (\%) = } \frac{\text{(Mean of offspring’s – Mean of two parents)}}{\text{Mean of best parent}} \times 100
   \]
The second measure is most commonly used in animal breeding. In the F₂ generation, the heterosis is reduced to one-half of its value in the F₁.

Effect of proportion of genes from one breed on maximum heterosis possible from crossbreeding. The maximum heterosis possible in crossbreeding programme depends on relative contribution of genes from different breed. Maximum possible heterosis in particular cross is calculated with the help of following formula

Proportion of maximum possible heterosis = 2 (100- percent of genes from predominant breed)

According to this formula maximum heterosis possible in two breed cross is when there is 50:50 contribution from both the breed.

Exercise 1. Estimate the maximum possible heterosis in two breed rotational crossbreeding programme up to ten generation of crossing and conclude the results
Exercise 2

The average body weight at first calving of pure Holstein-Friesian and pure Sahiwal cows was 525 kg and 375 kg, respectively. The average body weight of Holstein-Friesian X Sahiwal cows was 485 kg. Calculate % heterosis and predict the average body weight at first calving in F₂ which is produced by interse mating of F₁ crossbreds.
Exercise 3

The average age at first calving of HF and Sahiwal and their crosses was 28.7, 47.8 and 43.2 months.

a) Calculate the % heterosis
b) Predict the average age at first calving in F₂ produced by inter-se-mating of F₁ crossbreds.
Exercise 4

In a strain crossing programme, the performance of two strains of broilers for 6-week body weight was recorded to be 1500 and 1300 g and the heterosis was computed to be 7.14%. Compute the average performance of F1 offspring.
Computation of Sire Indices

When an individual is mated to a number of individuals taken at random from the population, then its breeding value is twice the mean deviation of the progeny from the population mean. This deviation is doubled because only half of the genes are transmitted to the progeny from the sire and the other half coming at random from the population.

The objective of sire evaluation is to estimate the additive genetic value (breeding value) of a sire on the basis of performance of all of its progeny from different dams randomly mated to the sire. Depending on the information available various methods are present by which these information can be combined into index known as sire index to give the estimate of the sire’s genetic potential.

Various Sire Indices are as follows:

1. Simple Daughter Average Index ($I_1$): Given by Edwards (1932). It simply uses the average production of bull’s daughters as being indicative of his transmitting ability of milk production.

$$I_1 = D$$

Where, $D$ = daughter’s average

2. Equi-parent or Intermediate Index ($I_2$): Hansson (1913) proposed this index and it is also known as Yapp’s index or Mount Hope Index. This index makes adjustment for the variation in production level of dam.

$$I_2 = 2D – M$$

Where, $D$ = daughter’s average, $M$ = Average of the mates of the sire or Dam’s average

This index is based on the assumption that the dams and daughters are raised under similar conditions so that the daughter dam difference reflects the sire effects.

2. Corrected Daughter Average Index ($I_3$): Given by Krishan (1956), this index is superior to $I_1$ and $I_2$ as it corrects for the production level of dams allotted to the sire over herd average. The daughters average is corrected for the differences in the production level of their dams by the correction factor $b (\overline{M} - \overline{H})$.

$$I_3 = \overline{D} – b (\overline{M} - \overline{H}) = \overline{D} – 0.5h^2 (\overline{M} - \overline{H})$$

Searle (1964) compared records of daughters with those of their herd mates in the same year and referred to as contemporary e comparison.
Where, \( b = 0.5h^2 \) or the intrasire regression of daughters on dam, 
\( \bar{H} = \) Herd average, \( n = \) Number of daughters

3. **Contemporary Daughter Average Index (I₄):** The herdmate or contemporary comparisons reduce the environmental variation due to herd, year and season. The records of the daughters of a sire are compared with the daughters of all other sires in the same herd calved in the same month. This was proposed by Sunderasan (1965)

\[
I₄ = \bar{H} + \frac{0.5h^2}{1 + (n + 1) t} \frac{1}{(D - CD)}
\]

Where, \( CD = \) Average of contemporary daughters of the sire
\( t = \) intraclass correlation

4. **Corrected Contemporary Daughter Average Index (I₅):** This index is an extension of the contemporary daughter’s average index. This index besides adjusting the number of the progeny and period to period variation also adjust for the differences in production levels of dams allotted to different sires. Proposed by Sunderasan (1965), it is known as Dairy Search Index.

\[
I₅ = \bar{H} + \frac{1}{n + 12} \frac{1}{(D - CD)} - b(M - CM)
\]

Where, \( CM = \) Average of contemporary mates

5. **Least squares constants:** The sire constants are obtained by least squares technique which adjusts the data for all the environmental effects including the non orthogonality in data. These sire constant are used in getting the sire index as

\[
I = \frac{2nh^2}{4 + (n - 1) h^2} \frac{1}{(S_i)}
\]

Where, \( S_i \) is the sire constant for \( i^{th} \) sire
Exercise 1. Sires A and B produced 4 and 5 daughters, compute the sire indexes for milk yield on the basis of following information:

<table>
<thead>
<tr>
<th>Sire</th>
<th>Daughter’s Production (kg)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
</tr>
<tr>
<td>A</td>
<td>1800</td>
</tr>
<tr>
<td>B</td>
<td>2000</td>
</tr>
</tbody>
</table>

Exercise 2. The average milk production of Sahiwal herd comprising 150 progenies of 6 sires is 2000 kg with h2 of milk yield as 0.30. the average milk production and no. of progenies per sire is given below

<table>
<thead>
<tr>
<th>Sire No.</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>30</td>
<td>20</td>
<td>25</td>
<td>15</td>
<td>10</td>
<td>50</td>
</tr>
<tr>
<td>X</td>
<td>1600</td>
<td>2250</td>
<td>1840</td>
<td>2200</td>
<td>2300</td>
<td>2100</td>
</tr>
</tbody>
</table>

Rank each sire based on their breeding value
Exercise 3. From the following data on milk yield construct the sire indices by Simple daughter average index, equiparent index, corrected daughter average index (both methods) and Dairy Search Index.

<table>
<thead>
<tr>
<th>Sire no.</th>
<th>Daughters’ records</th>
<th>Dam’s average</th>
<th>Contemporary Daughters</th>
<th>Contemporary Dams</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>1252, 1858, 2343, 1880, 1532, 1743, 1274, 1806</td>
<td>1600</td>
<td>1930</td>
<td>1550</td>
</tr>
<tr>
<td>2.</td>
<td>1780, 1510, 1781, 1561, 1744</td>
<td>1340</td>
<td>1710</td>
<td>1310</td>
</tr>
<tr>
<td>3.</td>
<td>2455, 1498</td>
<td>1680</td>
<td>2200</td>
<td>1590</td>
</tr>
<tr>
<td>4.</td>
<td>1581, 2051, 2100, 1583, 2155, 2178</td>
<td>1500</td>
<td>2000</td>
<td>1490</td>
</tr>
<tr>
<td>5.</td>
<td>1258, 1616, 1424</td>
<td>1315</td>
<td>1510</td>
<td>1300</td>
</tr>
</tbody>
</table>

h² of milk yield = 0.28, population mean (H) = 1660
Computation of Selection Index

In total score method or selection index method, two or more trait of an individual are combined to obtain a single index value by assigning weights to each trait. This value is known as total score & symbolized by ‘I’

The animals that have highest score or selection index value are selected for producing future progeny of desired traits. The weights (b) assigned for different traits depend upon economic values of the traits, heritability of the characters and genetic & phenotypic correlation among the traits. Therefore, for developing selection index, the following population parameters must be known:

1. Heritability of each trait
2. Phenotypic and genetic variance of each trait
3. Genetic and phenotypic correlation between each pair of traits
4. Relative economic values for different traits.

The selection index value for the individual can be written in the following form:

\[ I = b_1X_1 + b_2X_2 + b_3X_3 + \ldots \ldots b_nX_n \]

Where,

\( b_1, b_2, \ldots b_n \) are the weights given to each trait (these weights are common for individuals of a population)

\( X_1, X_2, \ldots X_n \) are the performance records for various traits of the same individual

Selection Index (Total Score) is the best method for simultaneous selection for multi traits. There is simple and easy approach for construction of selection index by setting up the normal simultaneous equation. For example, when only two traits are involved the equation will be

\[ b_1\sigma^2_p_1 + b_2\sigma^2_p_1p_2 = a_1\sigma^2_G_1 + a_2\sigma^2G_1G_2 \]

\[ b_1\sigma p_1p_2 + b_2\sigma^2 p_2 = a_1\sigma G_1G_2 + a_2\sigma^2 G_2 \]

Where,

\( \sigma^2_p_1 = \) Phenotypic variance of \( X_1 \) trait; \( \sigma^2_p_2 = \) Phenotypic variance of \( X_2 \) trait

\( \sigma^2G_1 = \) Genetic variance of \( X_1 \) trait; \( \sigma^2G_2 = \) Genetic variance of \( X_2 \) trait
\( \sigma_{p1 \ p2} = \) Phenotypic covariance between X1 and X2 traits
\( \sigma_{G1 \ G2} = \) Genetic covariance between X1 and X2 traits
\( a1 = \) Relative Economic value for X1 trait
\( a2 = \) Relative Economic value for X2 trait
\( b1 = \) Weights given for X1 trait
\( b2 = \) Weights given for X2 trait

**Steps for Construction of Selection Index for Two Traits**

1. Set the normal simultaneous equation 1 & 2 by putting the values
   \[
   b_1 \sigma^2_{p1} + b_2 \sigma_{p1 \ p2} = a_1 \sigma^2_{G1} + a_2 \sigma_{G1 \ G2} \tag{1}
   \]
   \[
   b_1 \sigma_{p1 \ p2} + b_2 \sigma^2_{p2} = a_1 \sigma_{G1 \ G2} + a_2 \sigma^2_{G2} \tag{2}
   \]
2. Solve the right hand side of both the equations by multiplying the economic values with the additive genetic variance and genetic covariance
3. The equation one is divided by phenotypic covariance \( \sigma_{p1 \ p2} \) to obtain equation (3)
4. The equation two (2) is divided by phenotypic variance of X2 trait \( \sigma^2_{p2} \) to obtain equation (4)
5. Subtract the equation (4) from (3) to obtain equation (5)
6. By solving equation (5), get the value of \( b1 \)
7. Substitute the value of \( b1 \) in equation (5) and get value of \( b2 \)
8. Construct the selection index as follows:
   \[
   I = b_1 X_1 + b_2 X_2
   \]
Exercise 1. Given the following information construct a selection index to maximize genetic gain in aggregate genetic rate.

\[ h^2_x = 0.5, \quad h^2_y = 0.1, \quad a_x = 1, \quad a_y = 4, \quad r_{g \,(xy)} = 0.4, \quad r_{p \,(xy)} = 0.4 \]
Exercise 2. Based on first lactation milk yield (kg) and age at first calving using the following statistics, construct the selection index.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Economic value (a)</th>
<th>Genetic variance (V&lt;sub&gt;A&lt;/sub&gt;)</th>
<th>Phenotypic variance (V&lt;sub&gt;p&lt;/sub&gt;)</th>
<th>Covariance A</th>
<th>Covariance P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk Yield</td>
<td>1.00</td>
<td>84687.21</td>
<td>125423.41</td>
<td>-42.26</td>
<td>111.989</td>
</tr>
<tr>
<td>(X&lt;sub&gt;1&lt;/sub&gt;)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AFC (X&lt;sub&gt;2&lt;/sub&gt;)</td>
<td>- 5.84</td>
<td>13.678</td>
<td>17.498</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Exercise 3. The breeder has developed the following selection index for egg number ($X_1$) and egg weight ($X_2$) for twenty hens and ranks them according to their index.

$$I = 0.46X_1 + 0.35X_2$$

<table>
<thead>
<tr>
<th>Hen No.</th>
<th>Egg Nos.</th>
<th>Egg weight (gms)</th>
<th>Total score</th>
<th>Rank</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>89</td>
<td>56</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>93</td>
<td>56</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>87</td>
<td>59</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>85</td>
<td>57</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>87</td>
<td>58</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>92</td>
<td>57</td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>91</td>
<td>55</td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>93</td>
<td>54</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>88</td>
<td>57</td>
<td></td>
<td></td>
</tr>
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