1. Introduction
Way back in 1865, Mendel was able to recognize the statistical nature of genetical variables. Based on this premise, Fisher, Swell Wright and Haldane developed the generalization theories applicable to more complex genetical phenomena. Generally, the qualitative characters are analyzed at population level and quantitative characters are analyzed from a point of view of plant or animal improvement. Here, only quantitative characters are considered and analyses like, path analysis, diallel analysis and line × tester analysis are discussed.

2. Path Analysis
The theory of path coefficients is established as a general statistical method for cause and effect analysis in a system of correlated variables. If the cause and effect relationship is well defined, it is possible to represent the whole system of variables in the form of a diagram, known as path diagram. Let the yield 'Y' in barely (effect) be linearly related to various casual factors like number of ears per plant ($X_1$), number of grains per ear ($X_2$) and 100 grain weight ($X_3$) etc. It is also assumed that these factors show the following type of association with one another (Fig.1).

From the figure it is obvious that yield is the result of $X_1$, $X_2$ and $X_3$ and some other undefined factors designated by R. Further, $X_1$, $X_2$ and $X_3$ in turn are also correlated. In the figure a, b, c and h are the path-coefficients due to respective variables.
Definitions
Path coefficient is defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, i.e., if Y is the effect and X₁ is the cause, the path-coefficient for the path from cause X₁ to the effect Y, denoted by (X₁ → Y), is \( \sigma_{X_1} / \sigma_Y \).

Path coefficient for the path from any cause to the effect is defined as the standardized partial regression coefficient of the effect on that cause.

The advantage of the path diagram is that a set of simultaneous equations can be written directly from the diagram and a solution of these equations provides information on the direct and indirect contribution of these causal factors to the effect. The theoretical basis of these equations may be explained as below:

Let \( r(X_1, Y) \) be the correlation between \( X_1 \) and \( Y \) as shown in the Fig. 1.

Assuming that
\[
Y = X_1 + X_2 + X_3 + R
\]
it can be shown that
\[
r(X_1, Y) = \frac{\sigma_{X_1}}{\sigma_Y} + \frac{\sigma_{X_2}}{\sigma_Y} + \frac{\sigma_{X_3}}{\sigma_Y}
\]
where, as per definition,
\[
\frac{\sigma_{X_1}}{\sigma_Y} = 'a' \text{ the path coefficient from } X_1 \text{ to } Y.
\]
\[
\frac{\sigma_{X_2}}{\sigma_Y} = 'b' \text{ the path coefficient from } X_2 \text{ to } Y.
\]
\[
\frac{\sigma_{X_3}}{\sigma_Y} = 'c' \text{ the path coefficient from } X_3 \text{ to } Y.
\]
Thus, \( r(X_1, Y) = a + r(X_1, X_2)b + r(X_1, X_3)c \).

Similarly, one can work out the equations for \( r(X_2, Y), r(X_3, Y) \) and \( r(R, Y) \) and finally can get a set of simultaneous equations as given below:
\[
r(X_1, Y) = a + r(X_1, X_2)b + r(X_1, X_3)c
\]
\[
r(X_2, Y) = a + r(X_2, X_1)b + r(X_2, X_3)c
\]
\[
r(X_3, Y) = r(X_3, X_1)a + r(X_3, X_2)b + c
\]
r = (R, Y) = h

Considering only the first three factors, i.e., $X_1$, $X_2$ and $X_3$, the simultaneous equations given above can be presented in matrix notations as:

$$
\begin{bmatrix}
    r_{X1Y} \\
    r_{X2Y} \\
    r_{X3Y}
\end{bmatrix} =
\begin{bmatrix}
    r_{X1X1} & r_{X1X2} & r_{X1X3} \\
    r_{X2X1} & r_{X2X2} & r_{X2X3} \\
    r_{X3X1} & r_{X3X2} & r_{X3X3}
\end{bmatrix} \begin{bmatrix}
    a \\
    b \\
    c
\end{bmatrix}
$$

Say, $A = B \cdot C \Rightarrow C = B^{-1}A$, provided $B$ is non-singular matrix.

After having calculated the values of path coefficients, i.e., $C$, it is possible to obtain the path value for residual $R$ in the following way:

From the model given in the diagram (Fig. 1) it is obvious that:

$$Y = X_1 + X_2 + X_3 + R$$

and hence,

$$\sigma_Y^2 = \sigma_{X1}^2 + \sigma_{X2}^2 + \sigma_{X3}^2 + \sigma^2 R + 2\sigma_{X1X2} + 2\sigma_{X2X3} + 2\sigma_{X1X3}$$

where, $\sigma_{X1X2} = r(X_1, X_2)\sigma_{X1}\sigma_{X2}$.

The contribution of residual is thus,

$$h^2 = 1 - a^2 - b^2 - c^2 - 2r(X_1X_2)ab - 2r(X_1X_3)ac - 2r(X_2X_3)bc.$$

Example

In a replicated trial ($r = 4$), eight varieties of barely were tested and the observations were recorded on number of ears per plant (Table 1), ear length (Table 2), 100-grain weight (Table 3) and grain yield per plant (Table 4) (Singh and Chaudhary, 1995) as listed below:

<table>
<thead>
<tr>
<th>Parents</th>
<th>R-I</th>
<th>R-II</th>
<th>R-III</th>
<th>R-IV</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50.2</td>
<td>41.4</td>
<td>36.2</td>
<td>39.8</td>
<td>167.6</td>
</tr>
<tr>
<td>2</td>
<td>41.8</td>
<td>47.2</td>
<td>39.6</td>
<td>46.6</td>
<td>175.2</td>
</tr>
<tr>
<td>3</td>
<td>39.2</td>
<td>37.6</td>
<td>38.8</td>
<td>33.6</td>
<td>149.2</td>
</tr>
<tr>
<td>4</td>
<td>37.8</td>
<td>49.6</td>
<td>35.4</td>
<td>41.8</td>
<td>164.6</td>
</tr>
<tr>
<td>5</td>
<td>35.6</td>
<td>31.4</td>
<td>33.2</td>
<td>29.8</td>
<td>130.0</td>
</tr>
<tr>
<td>6</td>
<td>53.4</td>
<td>50.2</td>
<td>49.6</td>
<td>57.8</td>
<td>211.0</td>
</tr>
<tr>
<td>7</td>
<td>43.8</td>
<td>46.8</td>
<td>41.4</td>
<td>43.6</td>
<td>175.6</td>
</tr>
<tr>
<td>8</td>
<td>50.6</td>
<td>47.8</td>
<td>41.8</td>
<td>46.8</td>
<td>187.0</td>
</tr>
<tr>
<td>Total</td>
<td>352.4</td>
<td>352.0</td>
<td>316.0</td>
<td>339.8</td>
<td>1360.2</td>
</tr>
</tbody>
</table>
Table 2. Data on ears per length

<table>
<thead>
<tr>
<th>Parents</th>
<th>R-I</th>
<th>R-II</th>
<th>R-III</th>
<th>R-IV</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>20.5</td>
<td>20.6</td>
<td>20.5</td>
<td>19.6</td>
<td>81.2</td>
</tr>
<tr>
<td>2.</td>
<td>19.5</td>
<td>20.1</td>
<td>19.3</td>
<td>20.1</td>
<td>79.0</td>
</tr>
<tr>
<td>3.</td>
<td>19.0</td>
<td>18.5</td>
<td>18.1</td>
<td>19.3</td>
<td>74.9</td>
</tr>
<tr>
<td>4.</td>
<td>20.0</td>
<td>20.3</td>
<td>20.6</td>
<td>20.3</td>
<td>81.2</td>
</tr>
<tr>
<td>5.</td>
<td>20.0</td>
<td>20.8</td>
<td>20.3</td>
<td>19.9</td>
<td>81.0</td>
</tr>
<tr>
<td>6.</td>
<td>19.2</td>
<td>19.5</td>
<td>20.3</td>
<td>19.9</td>
<td>78.9</td>
</tr>
<tr>
<td>7.</td>
<td>19.5</td>
<td>20.4</td>
<td>20.7</td>
<td>20.3</td>
<td>80.9</td>
</tr>
<tr>
<td>8.</td>
<td>19.7</td>
<td>19.8</td>
<td>20.1</td>
<td>20.5</td>
<td>80.1</td>
</tr>
<tr>
<td>Total</td>
<td>157.4</td>
<td>160.0</td>
<td>159.9</td>
<td>159.9</td>
<td>637.2</td>
</tr>
</tbody>
</table>

Table 3. Data on 100-Grain Weight (g)

<table>
<thead>
<tr>
<th>Parents</th>
<th>R-I</th>
<th>R-II</th>
<th>R-III</th>
<th>R-IV</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>3.9</td>
<td>4.0</td>
<td>3.8</td>
<td>3.9</td>
<td>15.6</td>
</tr>
<tr>
<td>2.</td>
<td>3.7</td>
<td>3.6</td>
<td>3.6</td>
<td>3.7</td>
<td>14.6</td>
</tr>
<tr>
<td>3.</td>
<td>4.5</td>
<td>4.6</td>
<td>4.6</td>
<td>4.7</td>
<td>18.4</td>
</tr>
<tr>
<td>4.</td>
<td>4.3</td>
<td>4.4</td>
<td>4.2</td>
<td>4.3</td>
<td>17.2</td>
</tr>
<tr>
<td>5.</td>
<td>4.1</td>
<td>4.0</td>
<td>4.2</td>
<td>4.1</td>
<td>16.4</td>
</tr>
<tr>
<td>6.</td>
<td>4.2</td>
<td>4.5</td>
<td>4.3</td>
<td>4.5</td>
<td>17.5</td>
</tr>
<tr>
<td>7.</td>
<td>4.3</td>
<td>4.3</td>
<td>4.2</td>
<td>4.3</td>
<td>17.1</td>
</tr>
<tr>
<td>8.</td>
<td>4.2</td>
<td>4.0</td>
<td>4.3</td>
<td>4.1</td>
<td>16.6</td>
</tr>
<tr>
<td>Total</td>
<td>33.2</td>
<td>33.4</td>
<td>33.2</td>
<td>33.6</td>
<td>133.4</td>
</tr>
</tbody>
</table>

Table 4. Data on Grain Yield (g)

<table>
<thead>
<tr>
<th>Parents</th>
<th>R-I</th>
<th>R-II</th>
<th>R-III</th>
<th>R-IV</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>104.9</td>
<td>84.3</td>
<td>77.0</td>
<td>76.5</td>
<td>342.7</td>
</tr>
<tr>
<td>2.</td>
<td>88.0</td>
<td>106.5</td>
<td>89.8</td>
<td>108.7</td>
<td>393.0</td>
</tr>
<tr>
<td>3.</td>
<td>80.0</td>
<td>71.3</td>
<td>77.5</td>
<td>69.5</td>
<td>298.3</td>
</tr>
<tr>
<td>4.</td>
<td>80.8</td>
<td>106.5</td>
<td>83.3</td>
<td>95.9</td>
<td>366.5</td>
</tr>
<tr>
<td>5.</td>
<td>60.0</td>
<td>52.5</td>
<td>53.0</td>
<td>51.0</td>
<td>216.5</td>
</tr>
<tr>
<td>6.</td>
<td>96.4</td>
<td>98.8</td>
<td>99.1</td>
<td>107.2</td>
<td>401.5</td>
</tr>
<tr>
<td>7.</td>
<td>91.4</td>
<td>99.7</td>
<td>83.3</td>
<td>89.5</td>
<td>363.9</td>
</tr>
<tr>
<td>8.</td>
<td>91.8</td>
<td>84.8</td>
<td>70.0</td>
<td>81.5</td>
<td>328.1</td>
</tr>
<tr>
<td>Total</td>
<td>693.3</td>
<td>704.4</td>
<td>633.0</td>
<td>679.8</td>
<td>2710.5</td>
</tr>
</tbody>
</table>

Here, SPAR1 package will be used to solve the problem for finding direct and indirect paths. Further, inferences can be drawn from the results obtained.

3. Diallel Analysis

Few Definitions

**Diallel cross**: A diallel cross is a set of all possible matings between several genotypes which may be individuals, clones, homozygous lines etc.
**General Combining ability:** The General Combining ability (g.c.a.) of an inbred line is defined as the average performance of the hybrids which this line produces with other lines chosen from a random mating population. In general terms, such an effect is genic and therefore its variance, taking into account epistatic interactions of digenic type and denoted by $\sigma_{gca}^2$ is given by:

$$\sigma_{gca}^2 = \frac{1}{2} \sigma_A^2 + \frac{1}{4} \sigma_{AA}^2$$

**Specific combining ability:** It refers to a pair of inbred lines involved in a cross. The specific combining ability (s.c.a) of a cross is defined as the deviation of the performance of the cross from the expectation on the basis of the average g.c.a effects of the two lines involved. Its existence indicates non-additive genetic effects and therefore its variance, denoted by $\sigma_{sca}^2$, is given by:

$$\sigma_{sca}^2 = \sigma_D^2 + \frac{1}{2} \sigma_{AA}^2 + \sigma_{AD}^2 + \sigma_{DD}^2$$

It may also be noted that the total genotypic variance is related to these two variances in the following manner:

$$\sigma_G^2 = \sigma_A^2 + \sigma_D^2 + \sigma_{AA}^2 + \sigma_{AD}^2 + \sigma_{DD}^2$$

$$= 2\sigma_{gca}^2 + \sigma_{sca}^2$$

Here, emphasis will be given only on diallel analysis by Griffing method (1956). For $p$ inbred lines, the total number of all possible crosses are $p^2$. However, there are situations (determined mainly by the requirements of the breeding programme) where lesser number of crosses may be made. The diallel system may be classified into four types. These are:-

1. A set of $p^2$ crosses including selfings and reciprocal crosses.
2. A set of $\frac{p(p+1)}{2}$ crosses including selfings and only one set of $F^1$ crosses.
3. A set of $p(p-1)$ crosses using $F^1$ crosses and their reciprocals but excluding selfings and
4. A set of $\frac{p(p-1)}{2}$ crosses using only one set of $F^1$ crosses and excluding selfings.

Griffing has used the term “method” for what has been called "types" above. It is presumed that the experiment has been conducted in a randomized complete block design using $t (=1,2, ..., p^2)$ crosses in $b$ blocks having $c$ observation in each of the $tb$ plots. The model for the analysis is:

$$Y_{ijkl} = \mu + t_{ij} + b_k + (tb)_{jk} + e_{ijkl} ; i, j = 1, 2, ..., p; j = 1, 2, ..., b; k = 1, 2, ..., c;$$

where $Y_{ijkl}$ is the value of the $i$th observation from $ij$th cross in the $k$th block, $\mu$ the population mean, $t_{ij}$ the effect of the $ij$th cross, $b_k$ the effect of the $k$th block, $(tb)_{jk}$ the
interaction resulting from the \( ij \)th cross with the \( k \)th block and \( e_{ijkl} \) the deviation of \( Y_{ijkl} \) from its expectation. The analysis of diallel crosses can be considered under two assumptions, that is, when different effects in the model are considered as either fixed or random.

**Model-I (Fixed effects)**

Here, the effects \( t_{ij} \), \( b_k \) and \((tb)_{ijk}\) are assumed as fixed while the deviation \( e_{ijkl} \) is assumed as random and normally distributed. In this model, the primary interest is the study of the performance of the parents through their hybrids and to identify promising crosses. Since the material is to be treated as a population the inferences drawn are applicable strictly to the specific material studied.

**Model-II (Random effects)**

All the effects \( t_{ij} \), \( b_k \), \((tb)_{ijk}\) and \( e_{ijkl} \) are assumed to be random and distributed normally. Here the stress is upon the variability in the population and not much upon the performance of individual parental line or a cross. Essential features of the analysis of variance along with the expectations of mean squares for "varieties", "blocks × varieties" and "plants within plots" are given for the two models in Table 5.

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>MS</th>
<th>Expectation of MS Model-I</th>
<th>Expectation of MS Model-II</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blocks (B)</td>
<td>b - 1</td>
<td>MB</td>
<td>( v + tck_b )</td>
<td>( v + cv_{tb} + ctv_b )</td>
</tr>
<tr>
<td>Varieties (T)</td>
<td>t - 1</td>
<td>MT</td>
<td>( v + bck_t )</td>
<td>( v + cv_{tb} + cbv_t )</td>
</tr>
<tr>
<td>B × T</td>
<td>( (b-1)(t-1) )</td>
<td>MBT</td>
<td>( v + ck_{tb} )</td>
<td>( v + cv_{tb} )</td>
</tr>
<tr>
<td>Plant within plot</td>
<td>bt(c - 1)</td>
<td>ME</td>
<td>( v )</td>
<td>( v )</td>
</tr>
</tbody>
</table>

where

\[
\begin{align*}
  k_b &= \frac{\sum b_i^2}{b - 1}; \\
  k_t &= \frac{\sum t_i^2}{t - 1}; \\
  k_{tb} &= \frac{\sum \sum (tb)_{ij}^2}{(t - 1)(b - 1)}
\end{align*}
\]

and \( \nu_x \) is the population variance of \( x \). The appropriate F-tests for varieties from Table 5 are:

- **Model-I** \( F[t - 1, bt(c - 1)] = \frac{MT}{ME} \)
- **Model-II** \( F[t - 1, (b - 1)(t - 1)] = \frac{MT}{MBT} \)

where the degrees of freedom for the numerator and the denominator are given in the parenthesis along F. It must be mentioned that in the detailed analysis the term \( t_{ij} \) can be split as:
\[ t_{ij} = g_i + g_j + s_{ij} + r_{ij} \] (F1 and reciprocal crosses)
\[ t_{ij} = g_i + g_j + s_{ij} \] (F1 but no reciprocal crosses)

where \( g_i \) is the gca effect of the \( i \)th parent, \( s_{ij} \) the gca effect resulting from the crossing of \( i \)th with the \( i \)th parent and \( r_{ij} \) the reciprocal effect involving the reciprocal crosses between these two parents. The subsequent analysis of the data for combining ability is done by the varietal means taken over the \( b \) blocks. The error mean squares for the two models (1 and 2) are calculated as \( ME^1 = [ME/bc] \) and \( ME^2 = [MBE/bc] \). In either case \( E(ME) = v \). Since the analysis is done on varietal mean basis, the two models in terms of means are different in form. For fixed effects the constraints are:

\[
\sum_k b_k = 0; \sum_k (tb)_{ijk} = 0
\]

The above constraints do not apply to the random effects model. Using \( Y_{ij} \) as the new symbol for the \( ij \)th varietal mean the two models (1 and 2) are now given by

\[ Y_{ij} = \mu + t_{ij} + \frac{\sum_k \sum l e_{ijkl}}{bc} \]

and

\[ Y_{ij} = \mu + t_{ij} + \frac{\sum_k b_k}{b} + \frac{\sum_k (tb)_{ijk}}{b} + \frac{\sum_k \sum l e_{ijkl}}{bc} \]

**Notation for summation**
The notation used can be better understood from the pattern of cells involved in the two-way tables for the 4 methods as given in Table 6. The mean values are denoted by \( Y_{ij} \). The illustration is for a \( 3 \times 3 \) diallel.

<table>
<thead>
<tr>
<th>Method - 1</th>
<th>Method - 2</th>
<th>Method - 3</th>
<th>Method - 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>( Y_{11} ) ( Y_{12} ) ( Y_{13} )</td>
<td>( Y_{11} ) ( Y_{12} ) ( Y_{13} )</td>
<td>( \cdot ) ( Y_{12} ) ( Y_{13} )</td>
<td>( \cdot ) ( Y_{12} ) ( Y_{13} )</td>
</tr>
<tr>
<td>( Y_{21} ) ( Y_{22} ) ( Y_{23} )</td>
<td>( \cdot ) ( Y_{22} ) ( Y_{23} )</td>
<td>( Y_{21} ) ( \cdot ) ( Y_{23} )</td>
<td>( \cdot ) ( \cdot ) ( Y_{23} )</td>
</tr>
<tr>
<td>( Y_{31} ) ( Y_{32} ) ( Y_{33} )</td>
<td>( \cdot ) ( \cdot ) ( Y_{33} )</td>
<td>( Y_{31} ) ( Y_{32} ) ( \cdot )</td>
<td>( \cdot ) ( \cdot ) ( \cdot )</td>
</tr>
</tbody>
</table>

**Method - 1**
\[ Y_i = \sum_j Y_{ij}; Y_j = \sum_i Y_{ij}; Y_{..} = \sum_i \sum_j Y_{ij} \]

**Method - 2**
\[ Y_{i.} = \sum_j Y_{ij}; Y_{.j} = Y_{ji}; Y_{..} = \sum_i \sum_j Y_{ij} \]
Method - 3
\[ Y_{i} = \sum_{i} Y_{ij}; \quad Y_{j} = \sum_{j} Y_{ij}; \quad Y_{..} = \sum_{i} \sum_{j} Y_{ij} \]

Method – 4
\[ Y_{i} = \sum_{i<j} Y_{ij}; \quad Y_{..} = \sum_{i<j} \sum_{j} Y_{ij} \]

**Statistical Analysis**
In what follows only the method – 4 of Griffing's approach is being presented (analysis by other methods will be explained through SPAR1). Variances of variance components, treatment of mixed models and the extension of the technique to two and more variables are not included.

Method - 4:
Let us consider the models I and II for fixed and random effects as
\[ Y_{ij} = \mu + g_i + g_j + s_{ij} + \left( \frac{1}{bc} \right) \sum_{k=1}^{b} \sum_{l=1}^{c} e_{ijkl} \]
and
\[ Y_{ij} = \mu + g_i + g_j + s_{ij} + \left( \frac{1}{b} \right) \sum_{k=1}^{b} b_k + \left( \frac{1}{c} \right) \sum_{l=1}^{c} (tb)_{ijk} + \left( \frac{1}{bc} \right) \sum_{k=1}^{b} \sum_{l=1}^{c} e_{ijkl} \]
\((i, j = 1, 2, ..., p; k = 1, 2, ..., b; l = 1, 2, ..., c) \text{ and } s_{ij} = s_{ji}.\)

Restrictions imposed upon the parameters of model-I are:
\[ \sum_{i} g_i = 0; \quad \sum_{i} \sum_{j} s_{ij} = 0 \]

Sum of squares:
\[ SSG = \frac{1}{p-2} \sum_{i} Y_{i..}^2 - \frac{4}{p(p-2)} Y_{..}^2 \]
\[ SSS = \sum_{i<j} \sum_{j} Y_{ij}^2 - \left( \frac{1}{p-2} \right) \sum_{i} \sum_{j} Y_{ij}^2 + \frac{2}{(p-1)(p-2)} Y_{..}^2 \]

The analysis of variance and the expectation of mean squares are given in Table 7.

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>Expectation of Mean Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>gca</td>
<td>p-1</td>
<td>SSG</td>
<td>MG</td>
<td>( v + (p-2)\left( \frac{1}{p-1} \right) \sum_{i} g_i^2 )</td>
</tr>
<tr>
<td>sca</td>
<td>p(p-3)/2</td>
<td>SSS</td>
<td>MS</td>
<td>( v + \left[ \frac{2}{p(p-3)} \right] \sum_{i&lt;j} s_{ij}^2 )</td>
</tr>
<tr>
<td>Error</td>
<td>2/m</td>
<td>SSE</td>
<td>ME</td>
<td>( v )</td>
</tr>
</tbody>
</table>

\( v + v_S + (p-2)v_g \)  
\( v + v_S \)
The estimates of various effects in the model are:

\[ \hat{\mu} = \frac{2Y}{p(p-1)} \]
\[ \hat{g}_i = \frac{pY_i - 2Y}{p(p-1)} \]
\[ S_{ij} = Y_{ij} - \frac{Y_i + Y_j}{p-2} + \frac{2Y}{(p-1)(p-2)} \]

The estimates of variance components are obtained by equating the observed variance to their expectations given in Table 7 and they are:

\[ \hat{\nu}_g = \frac{1}{p-2}(MG - MS) \]
\[ \hat{\nu}_s = MS - ME \]

F-tests of significance associated with Model-I: Let df(x) be the degrees of freedom for the factor x where x stands for the symbols g or s. The primary interest in Model I is the overall heterogeneity of the estimates within each class. It will be seen from the analysis of variance Table 7 that the appropriate tests are:

\[ F(df(x), vb(c-1)) = \frac{Mx}{ME} \]

F-tests of significance associated with Model-II:

The primary interest in this model is the estimation of variability parameters \( \nu_g \) or \( \nu_s \). Hence suitable procedures have to be adopted to test the significance of \( \nu_x \). A study of the variance component in Table 7 reveals that variance components can be tested by calculating 'F' as a ratio of the concerned observed mean square and another suitable observed mean square. For testing \( \hat{\nu}_g = 0 \) and \( \hat{\nu}_s = 0 \) the following statistics are used:

\[ F[p-1, df(S)] = \frac{MG}{MS} \]
\[ F[df(r),(v-1)(b-1)] = \frac{MR}{ME^2} \]

**Exercise**

In an experiment on Barley, six inbred lines were crossed in possible combinations excluding self and reciprocals, the total entry being \( p(p-1)/2 \) (i.e. 15 in case of \( p=6 \) parents). The crosses were sown in randomized complete block design with two replicates. The observations on the average number of kernels per head are given below:

<table>
<thead>
<tr>
<th>Cross</th>
<th>Block 1</th>
<th>Block 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1×2</td>
<td>47.60</td>
<td>48.70</td>
</tr>
<tr>
<td>1×3</td>
<td>40.53</td>
<td>38.15</td>
</tr>
<tr>
<td>1×4</td>
<td>31.30</td>
<td>30.75</td>
</tr>
</tbody>
</table>
Some Statistical Techniques in Plant Breeding Experiments

Using SPAR1 package the above diallel cross will be analyzed for estimating general and specific combining abilities and their variances and estimates of variances. Based on the results obtained inferences will be drawn.

4. Line × Tester Analysis

When a breeding programme envisages the study of the performance of a large number of inbred lines termed "lines" with a view to choosing promising combiners they are crossed with a set of few inbred lines termed "testers" of proven merit. If the number of lines and testers are $l$ and $t$ respectively, the number of crosses or hybrids or full-sib progenies is $lt$. Let the $lt$ crosses along with or without lines and testers be tried in a randomized complete block design with $r$ replications. The linear model involving effects pertaining to combining ability is:

$$y_{ijk} = \mu + l_i + t_j + (lt)_{ij} + r_k + e_{ijk}$$

where $y_{ijk}$ is the value of the cross obtained from $i^{th}$ line and $j^{th}$ tester in the $k^{th}$ replication, $\mu$ a general parameter common to all the plots, $l_i$ the gca effect of the $i^{th}$ line, $t_j$ the gca effect of the $j^{th}$ tester, $(lt)_{ij}$ the gca (interaction) effect of the $ij^{th}$ cross, $r_k$ the effect of the $k^{th}$ replication and $e_{ijk}$ the deviation of $y_{ijk}$ from its expectation. It is assumed that the effects $l$, $t$, $lt$, $r$ and $e$ are random and $\mu$ is fixed. Least square technique leads to the following analysis of variance (Essential features of the analysis of variance are given in Table 8.).

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>Expectation of MS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications (R)</td>
<td>r - 1</td>
<td>SSR</td>
<td>MR</td>
<td>$v + ltv_r$</td>
</tr>
<tr>
<td>Lines (L)</td>
<td>l - 1</td>
<td>SSL</td>
<td>ML</td>
<td>$v + rv_{lt} + rv_{t}$</td>
</tr>
<tr>
<td>Testers (T)</td>
<td>t - 1</td>
<td>SST</td>
<td>MT</td>
<td>$v + rv_{lt} + rv_{t}$</td>
</tr>
<tr>
<td>L × T</td>
<td>(l-1) (t-1)</td>
<td>SSLT</td>
<td>MLT</td>
<td>$v + rv_{lt}$</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (lt-1)</td>
<td>SSE</td>
<td>ME</td>
<td>$v$</td>
</tr>
</tbody>
</table>

where $v$ is the population error variance and $v_l, v_t$ etc. are the population variances corresponding to lines and testers etc. The various sum of squares are calculated as:
Some Statistical Techniques in Plant Breeding Experiments

\[ \text{CF} = \frac{Y^2}{r \times t} \]

\[ \text{TSS} = \sum_{k} \sum_{j} \sum_{i} y_{ijk}^2 \quad \text{CF} \]

\[ \text{SSR} = \sum_{k} \frac{Y^2}{\text{lt}} \quad \text{CF} \]

\[ \text{SSL} = \frac{1}{t} \sum_{i} \quad \text{CF} \]

\[ \text{SSLT} = \frac{\sum_{i} \sum_{j} \sum_{r} Y_{ijr}^2}{r} \quad \text{CF} - \text{SSL} - \text{SST} \]

\[ \text{SSE} = \text{TSS} - \frac{\sum_{j} \sum_{i} Y_{ijr}^2}{r} + \text{CF} \]

where (.) in the suffix of \( Y \) follows the conventional notation used for the summation over the appropriate variable.

The estimates of parameters are given by

\[ \hat{\mu} = \frac{Y_{\ldots}}{ltr} \]

\[ \hat{\beta}_i = \frac{Y_{i\ldots}}{ltr} \]

\[ \hat{\beta}_{ij} = \frac{Y_{ij\ldots}}{ltr} \]

\[ \hat{(\beta)_{ij}} = \frac{Y_{ijr}}{r} - \frac{Y_{i\ldots}}{ltr} \]

The variances of estimates of parameters can be computed as

\[ \text{var} (\hat{\mu}) = \frac{1}{rlt} \hat{\nu} \]

\[ \text{var} (\hat{\beta}_i) = \frac{(t - 1)\hat{\nu}}{rlt} \]

\[ \text{var} (\hat{\beta}_{ij}) = \frac{2}{rt} \hat{\nu} \]

\[ \text{var} ((\hat{\beta})_{ij} - \hat{\beta}_{kj}) = \frac{2(t - 1)}{rt} \hat{\nu} \]

\[ \text{var} ((\hat{\beta})_{ij} - \hat{\beta}_{km}) = \frac{2(t - 1)}{r} \hat{\nu} \]

where \( \hat{\nu} \) is the estimate of \( \nu \) and equal of ME. The estimates of variance components can also be computed as by equating the expectations of means squares to the observed values and it is easily seen that:

\[ \hat{\nu}_l = \frac{ML - MT}{rt} \]

\[ \hat{\nu}_t = \frac{MT - MLT}{rl} \]

\[ \hat{\nu}_{lt} = \frac{MLT - ME}{r} \]

The plant breeders are always interested to know the estimates of variance components of \( \text{gca} \) and \( \text{sca} \) effects. The variance \( \nu_l \) and \( \nu_t \) are associated with \( \text{gca} \) while \( \nu_{lt} \) is associated with \( \text{sca} \) effects. It may be pointed out that the term \( \text{gca} \) variance is generally used to tell about \( \nu_l, \nu_t, \nu_l + \nu_t, \frac{ML + MT - 2MLT}{r(l + t)} \) etc. The term \( \text{sca} \) variance however, can be used for \( \nu_{lt} \) without ambiguity.
Tests of significance of estimates of variance components
The different variance components \( \hat{v}_1, \hat{v}_t, \) and \( \hat{v}_{lt} \) can be tested by calculating F- as a ratio of two observed variances. For testing the null hypotheses

1. \( \hat{v}_1 = \hat{v}_{gca} = 0, \)
   calculate F \( (d_1, d_2) = \frac{ML}{MLT} \) where \( d_1 = 1-1; d_2 = (1-1)(t-1) \)

2. \( \hat{v}_t = \hat{v}_{gca} = 0 \)
   calculate F \( (d_1, d_2) = \frac{MT}{MLT} \) where \( d_1 = t-1; d_2 = (1-1)(t-1) \)

3. \( \hat{v}_{lt} = \hat{v}_{sca} = 0 \)
   calculate F \( (d_1, d_2) = \frac{MLT}{ME} \) where \( d_1 = (1-1)(t01); d_2 = (r-1)(lt-1) \)
   and when

4. \( \hat{v}_{gca} = ML + MT - 2MLT \)
   and \( \hat{v}_{gca} = 0 \)
   calculate F \( (d_1, d_2) = M^* \) where \( M^* = \frac{ML + MT}{2} \)
   \( d_1 = \frac{(ML + MT)^2(1-1)(t-1)}{(t-1)(ML)^2 + (1-1)(MT)^2}; d_2 = (1-1)(t-1) \)

5. \( \hat{v}_{gca} = \hat{v}_1 + \hat{v}_t = \frac{1}{r(t+1)}(1-1)(t01) \)
   and \( \hat{v}_{gca} = 0 \)
   calculate F \( (d_1, d_2) = M^* \) where \( M^* = \frac{(1)(ML) + t(MT)}{1+t} \)
   \( d_1 = \frac{(1)(ML) + t(MT)2(1-1)(t-1)}{(t-1)(ML)^2 + (1-1)(t-1)}; d_2 = (1-1)(t-1) \)

In all the above expressions \( d_i \) and \( d_c \) denote the degrees of freedom corresponding to the numerator and denominator of the right hand side of expression for F.

Exercise
Suppose there are 3 testes and 5 lines and 5 x 3 =15 crosses. These crosses along with 8 parents, i.e., 5 lines and 3 testers, total entry being 23, were tested in a R.B.D. with 4 replications and the data on grain yield were obtained (Table 9).

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>R1</th>
<th>R2</th>
<th>R3</th>
<th>R4</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1×6</td>
<td>74.40</td>
<td>70.86</td>
<td>60.94</td>
<td>68.00</td>
<td>274.20</td>
</tr>
<tr>
<td>1×7</td>
<td>91.82</td>
<td>99.18</td>
<td>118.88</td>
<td>120.68</td>
<td>430.56</td>
</tr>
<tr>
<td>1×8</td>
<td>48.08</td>
<td>62.10</td>
<td>58.54</td>
<td>41.84</td>
<td>210.56</td>
</tr>
</tbody>
</table>
### ANOVA for Line × tester Analysis including parents

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>3</td>
<td>83.000</td>
<td>23.667</td>
<td>0.304</td>
</tr>
<tr>
<td>Treatments</td>
<td>22</td>
<td>32552.940</td>
<td>1479.679</td>
<td>16.249</td>
</tr>
<tr>
<td>Parents</td>
<td>7</td>
<td>6299.620</td>
<td>899.945</td>
<td>9.882</td>
</tr>
<tr>
<td>Parents vs. crosses</td>
<td>1</td>
<td>53.666</td>
<td>53.666</td>
<td>0.589</td>
</tr>
<tr>
<td>Crosses</td>
<td>14</td>
<td>26199.654</td>
<td>1871.404</td>
<td>20.550</td>
</tr>
<tr>
<td>Lines</td>
<td>4</td>
<td>10318.361</td>
<td>M&lt;sub&gt;l&lt;/sub&gt;=2579.590</td>
<td>1.457</td>
</tr>
<tr>
<td>Testers</td>
<td>5</td>
<td>1718.925</td>
<td>M&lt;sub&gt;t&lt;/sub&gt;=859.463</td>
<td>0.485</td>
</tr>
<tr>
<td>Lines × Testers</td>
<td>8</td>
<td>14162.368</td>
<td>M&lt;sub&gt;1×t&lt;/sub&gt;=1770.296</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>66</td>
<td>6010.295</td>
<td>M&lt;sub&gt;e&lt;/sub&gt;=91.650</td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>91</strong></td>
<td><strong>38646.235</strong></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

It is to be noted here that M.S. due to lines (M<sub>l</sub>) and testers (M<sub>t</sub>) are to be tested against the M.S. due to lines × testers (M<sub>1×t</sub>). The latter is, in turn tested against M.S. due to error (M<sub>e</sub>). The gca and sca effects, variance components and estimates of variance components are further obtained from SPAR1 package.