

Automatic report for a Randomized Complete Block Design (RCBD)

International Potato Center

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1. Model specification and data description

There are data from 27 genotypes evaluated using a randomized complete block design with 3 blocks. The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where

- y_{ij} is the observed response with genotype i and block j .
- μ is the mean response over all genotypes and blocks.
- τ_i is the effect for genotype i .
- β_j is the effect for block j .
- ϵ_{ij} is the error term.

In this model we assume that the errors are independent and have a normal distribution with common variance, that is, $\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$.

2. Analysis for trait Vine vigor 1 estimating 1-9

2.1. ANOVA

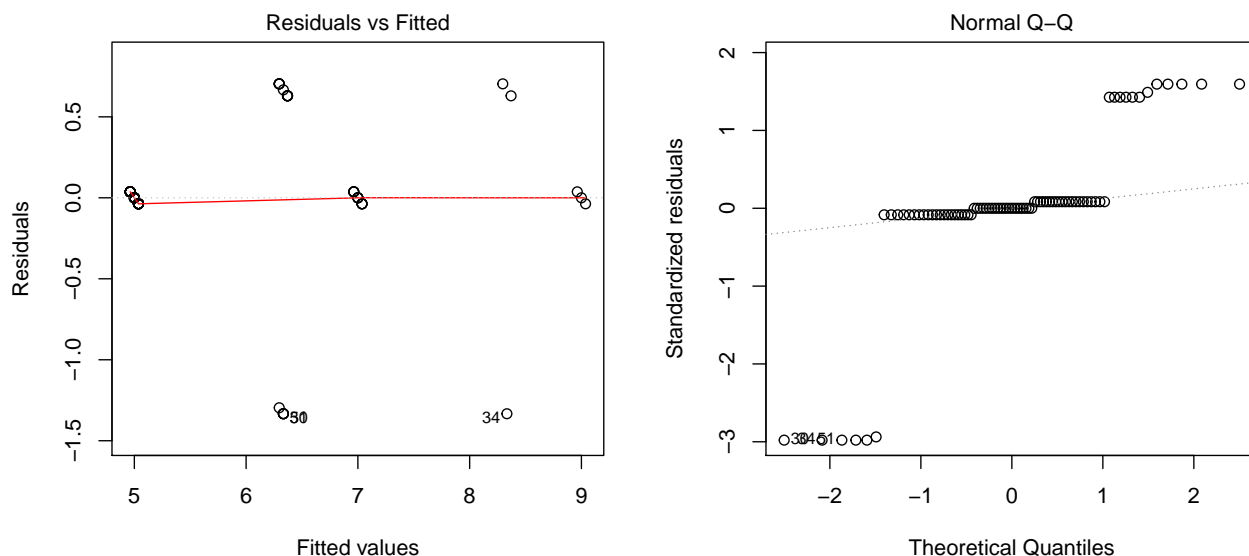
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

```
## Analysis of Variance Table
##
## Response: "Vine vigor 1 estimating 1-9"
##           Df Sum Sq Mean Sq F value    Pr(>F)
## germplasmName 26 102.222   3.9316 14.6809 6.966e-16 ***
## REP           2   2.074   1.0370   3.8723 0.02706 *
## Residuals     52  13.926   0.2678
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 9.427%. The p-value for genotypes is 6.966e-16 which is significant at the 5% level.

2.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

2.3. Genotype means

Below are the sorted means for each genotype with letters indicating if there are significant differences using the multiple comparisons method of Tukey at the 5% level.

##		trt	means	M
## 1	MGSG	1051-1	9.000000	a
## 2	MGSG	1006-9	8.333333	ab
## 3	Chingova		7.000000	bc
## 4	MGSG	1007-9	7.000000	bc
## 5	MGSG	1015-17	7.000000	bc
## 6	MGSG	1065-4	7.000000	bc
## 7	MGSG	1004-27	6.333333	cd
## 8	MGSG	1006-7	6.333333	cd
## 9	MGSG	1008-8	6.333333	cd
## 10	MGSG	1010-10	6.333333	cd
## 11	MGSG	1032-3	6.333333	cd
## 12	Jonathan		5.000000	d
## 13	MGSG	1001-36	5.000000	d
## 14	MGSG	1001-7	5.000000	d
## 15	MGSG	1002-49	5.000000	d
## 16	MGSG	1003-27	5.000000	d
## 17	MGSG	1004-2	5.000000	d
## 18	MGSG	1005-17	5.000000	d
## 19	MGSG	1007-13	5.000000	d
## 20	MGSG	1009-3	5.000000	d
## 21	MGSG	1010-4	5.000000	d
## 22	MGSG	1011-5	5.000000	d
## 23	MGSG	1012-9	5.000000	d
## 24	MGSG	1015-2	5.000000	d
## 25	MGSG	1061-3	5.000000	d
## 26	MGSG	1068-1	5.000000	d

```
## 27 Resisto      5.000000 d
```

2.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

```
##              Variance  Std.Dev.
## germplasmName 1.22127255 1.1051120
## REP          0.02849003 0.1687899
## Residual      0.26780627 0.5175000
```

3. Analysis for trait Virus symptoms 1 estimating 1-9

3.1. ANOVA

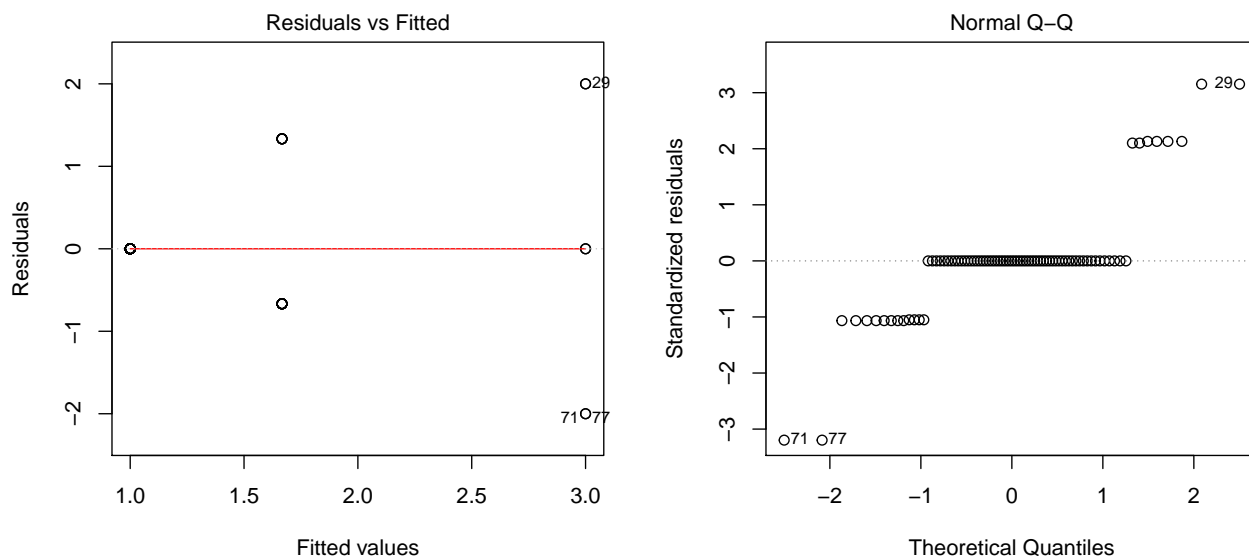
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

```
## Analysis of Variance Table
##
## Response: "Virus symptoms 1 estimating 1-9"
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## germplasmName 26 24.8889  0.95726   1.6000 0.07453 .
## REP           2  0.8889  0.44444   0.7429 0.48073
## Residuals     52 31.1111  0.59829
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 59.94%. The p-value for genotypes is 0.07453 which is not significant at the 5% level.

3.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

3.3. Genotype means

The means of your genotypes are:

```
##      Chingova      Jonathan MSGS 1001-36 MSGS 1001-7 MSGS 1002-49
##      1.666667      1.000000      1.000000      1.666667      1.000000
## MSGS 1003-27 MSGS 1004-2 MSGS 1004-27 MSGS 1005-17 MSGS 1006-7
##      3.000000      1.000000      1.666667      1.000000      1.666667
## MSGS 1006-9 MSGS 1007-13 MSGS 1007-9 MSGS 1008-8 MSGS 1009-3
##      1.000000      3.000000      1.000000      1.000000      1.666667
## MSGS 1010-10 MSGS 1010-4 MSGS 1011-5 MSGS 1012-9 MSGS 1015-17
##      1.000000      1.000000      1.000000      1.000000      1.000000
## MSGS 1015-2 MSGS 1032-3 MSGS 1051-1 MSGS 1061-3 MSGS 1065-4
##      1.000000      1.666667      1.000000      1.000000      1.000000
## MSGS 1068-1      Resisto
##      1.000000      1.000000
```

3.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

```
##      Variance Std.Dev.
## germplasmName 0.1215575 0.3486509
## REP          0.0000000 0.0000000
## Residual      0.5925926 0.7698004
```

4. Analysis for trait Virus symptoms 2 estimating 1-9

4.1. ANOVA

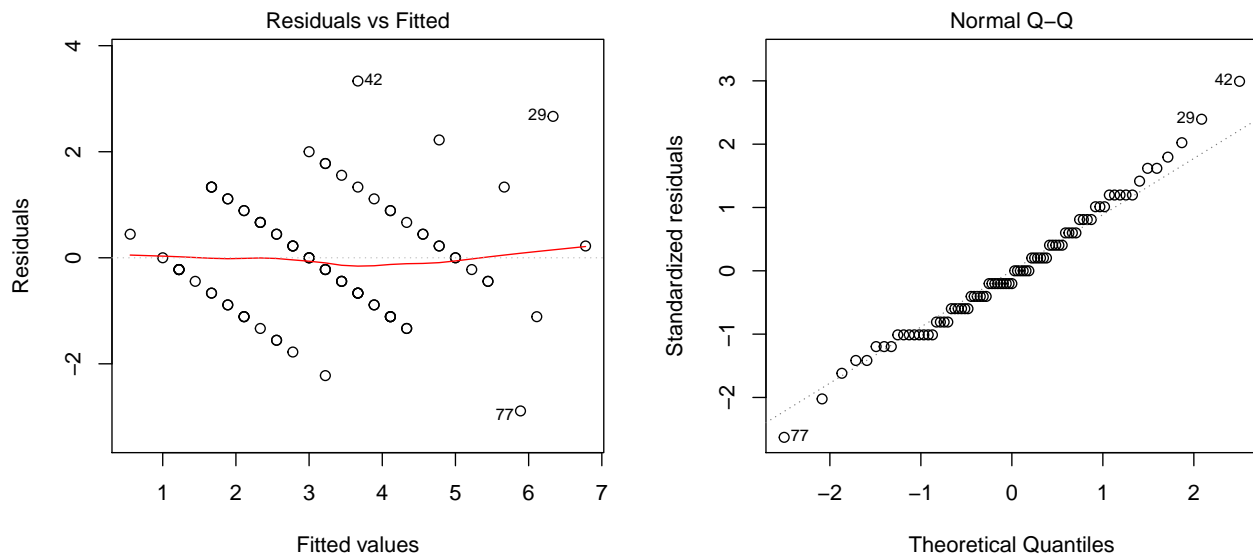
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

```
## Analysis of Variance Table
##
## Response: "Virus symptoms 2 estimating 1-9"
##           Df Sum Sq Mean Sq F value    Pr(>F)
## germplasmName 26 141.728   5.4511   3.0211 0.0003426 ***
## REP           2   15.506   7.7531   4.2968 0.0187489 *
## Residuals     52   93.827   1.8044
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 42.02%. The p-value for genotypes is 0.0003426 which is significant at the 5% level.

4.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

4.3. Genotype means

Below are the sorted means for each genotype with letters indicating if there are significant differences using the multiple comparisons method of Tukey at the 5% level.

```
##           trt      means  M
## 1  MSGS 1003-27 6.333333  a
```

```
## 2  MSGS 1007-13 5.666667  ab
## 3  MSGS 1004-27 5.000000  abc
## 4  MSGS 1006-7  5.000000  abc
## 5  MSGS 1002-49 4.333333  abc
## 6  MSGS 1006-9  4.333333  abc
## 7  MSGS 1032-3  4.333333  abc
## 8  MSGS 1001-7  3.666667  abc
## 9  MSGS 1007-9  3.666667  abc
## 10 MSGS 1009-3  3.666667  abc
## 11 MSGS 1010-4  3.666667  abc
## 12 MSGS 1015-17 3.666667  abc
## 13 MSGS 1051-1  3.666667  abc
## 14 Chingova      3.000000  abc
## 15 MSGS 1001-36 3.000000  abc
## 16 MSGS 1061-3  3.000000  abc
## 17 MSGS 1065-4  3.000000  abc
## 18 MSGS 1004-2  2.333333  abc
## 19 MSGS 1005-17 2.333333  abc
## 20 MSGS 1010-10 2.333333  abc
## 21 MSGS 1068-1  2.333333  abc
## 22 Jonathan      1.666667  bc
## 23 MSGS 1008-8  1.666667  bc
## 24 MSGS 1011-5  1.666667  bc
## 25 MSGS 1012-9  1.666667  bc
## 26 Resisto       1.666667  bc
## 27 MSGS 1015-2  1.000000   c
```

4.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

```
##              Variance Std.Dev.
## germplasmName 1.2155746 1.1025310
## REP           0.2203229 0.4693856
## Residual      1.8043685 1.3432678
```

5. Analysis for trait Weight of commercial storage roots measuring kg per plot

5.1. ANOVA

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

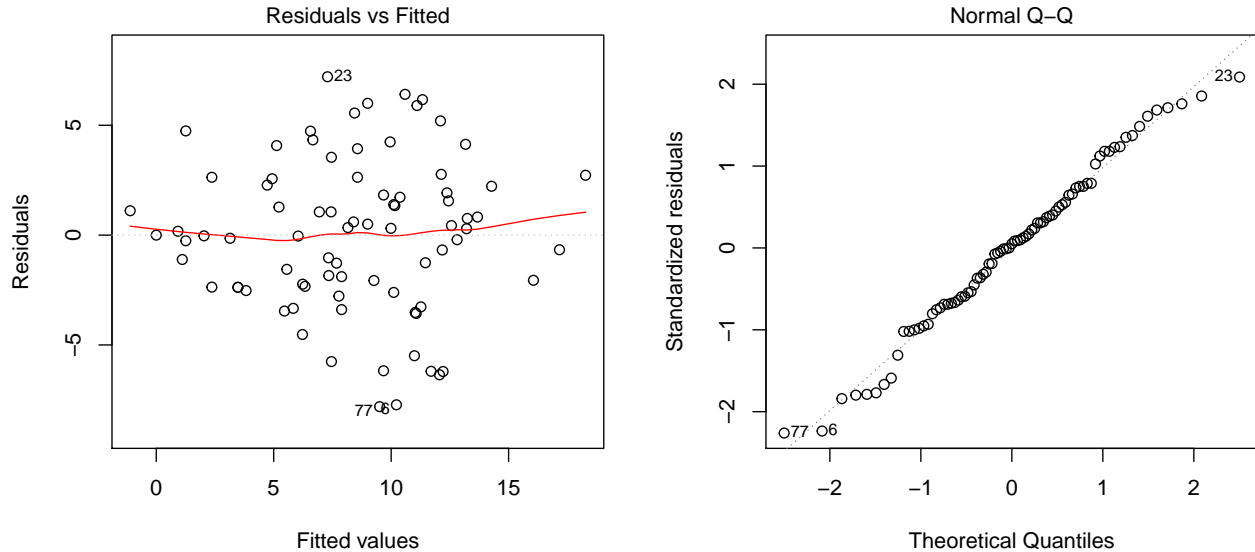
```
## Analysis of Variance Table
##
## Response: "Weight of commercial storage roots measuring kg per plot"
##      Df Sum Sq Mean Sq F value    Pr(>F)
## germplasmName 26 1221.52   46.981    2.6002 0.001676 **
## REP           2  102.38    51.190    2.8332 0.067937 .
## Residuals     52  939.55    18.068
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 51.01%. The p-value for genotypes is 0.001676 which is significant at the 5% level.

5.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

5.3. Genotype means

Below are the sorted means for each genotype with letters indicating if there are significant differences using the multiple comparisons method of Tukey at the 5% level.

##		trt	means	M
## 1	MGSG	1015-2	17.166667	a
## 2	MGSG	1001-7	13.166667	ab
## 3	MGSG	1010-10	12.566667	ab
## 4	MGSG	1065-4	12.133333	ab
## 5	MGSG	1009-3	12.100000	ab
## 6	MGSG	1006-7	11.700000	ab
## 7	MGSG	1051-1	11.333333	ab
## 8	MGSG	1061-3	11.266667	ab
## 9	MGSG	1005-17	11.100000	ab
## 10	MGSG	1010-4	11.066667	ab
## 11	MGSG	1002-49	9.266667	ab
## 12	MGSG	1001-36	9.000000	ab
## 13	MGSG	1004-27	9.000000	ab
## 14	Chingova		8.566667	ab
## 15	MGSG	1007-13	8.566667	ab


```
## 16 MSGS 1003-27 8.400000 ab
## 17 MSGS 1006-9 7.333333 ab
## 18 MSGS 1011-5 6.666667 ab
## 19 MSGS 1004-2 6.566667 ab
## 20 MSGS 1012-9 6.333333 ab
## 21 MSGS 1015-17 6.233333 ab
## 22 Resisto 5.833333 ab
## 23 MSGS 1008-8 4.933333 ab
## 24 Jonathan 2.366667 b
## 25 MSGS 1068-1 2.366667 b
## 26 MSGS 1007-9 2.033333 b
## 27 MSGS 1032-3 0.000000 b
```

5.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

```
##          Variance Std.Dev.
## germplasmName 9.637726 3.104469
## REP          1.226747 1.107586
## Residual     18.068314 4.250684
```

6. Analysis for trait Weight of non-commercial storage roots measuring kg per plot

6.1. ANOVA

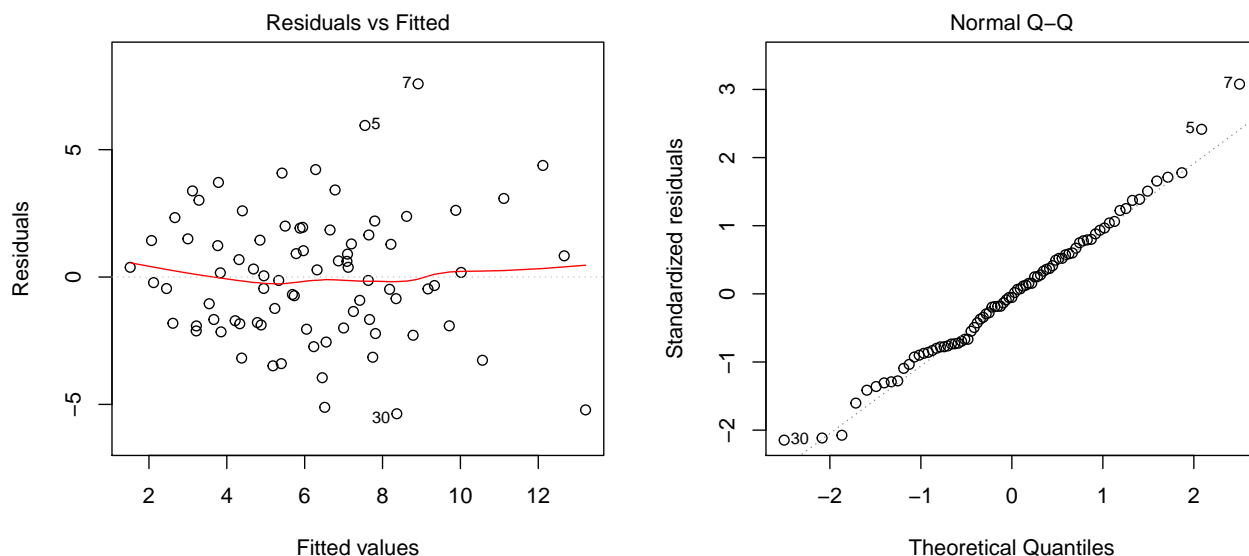
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

```
## Analysis of Variance Table
##
## Response: "Weight of non-commercial storage roots measuring kg per plot"
##          Df Sum Sq Mean Sq F value Pr(>F)
## germplasmName 26 484.13 18.6203  1.9595 0.01958 *
## REP          2  18.79  9.3970  0.9889 0.37887
## Residuals    52 494.13  9.5025
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 49.05%. The p-value for genotypes is 0.01958 which is significant at the 5% level.

6.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals—for instance a funnel shape—suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

6.3. Genotype means

Below are the sorted means for each genotype with letters indicating if there are significant differences using the multiple comparisons method of Tukey at the 5% level.

##		trt	means	M
## 1	MGSG	1009-3	12.666667	a
## 2	MGSG	1004-2	10.566667	ab
## 3	MGSG	1061-3	9.333333	ab
## 4	MGSG	1001-36	9.166667	ab
## 5	MGSG	1004-27	8.366667	ab
## 6	MGSG	1005-17	7.800000	ab
## 7	MGSG	1006-7	7.666667	ab
## 8	MGSG	1015-17	7.633333	ab
## 9	MGSG	1051-1	7.200000	ab
## 10	MGSG	1010-4	7.100000	ab
## 11	MGSG	1001-7	7.000000	ab
## 12	MGSG	1010-10	6.866667	ab
## 13	MGSG	1002-49	6.233333	ab
## 14	MGSG	1011-5	5.966667	ab
## 15	Chingova		5.733333	ab
## 16	Jonathan		5.500000	ab
## 17	MGSG	1065-4	5.400000	ab
## 18	MGSG	1012-9	5.333333	ab
## 19	MGSG	1006-9	5.233333	ab
## 20	MGSG	1008-8	4.400000	ab
## 21	Resisto		4.333333	ab
## 22	MGSG	1007-9	3.833333	ab
## 23	MGSG	1015-2	3.766667	ab
## 24	MGSG	1003-27	3.666667	ab
## 25	MGSG	1007-13	3.000000	ab
## 26	MGSG	1032-3	2.666667	b

```
## 27 MSGG 1068-1 2.066667 b
```

6.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

```
##          Variance Std.Dev.
## germplasmName 3.040567 1.743722
## REP          0.000000 0.000000
## Residual     9.498642 3.081987
```

7. Analysis for trait Weight of vines measuring kg per plot

7.1. ANOVA

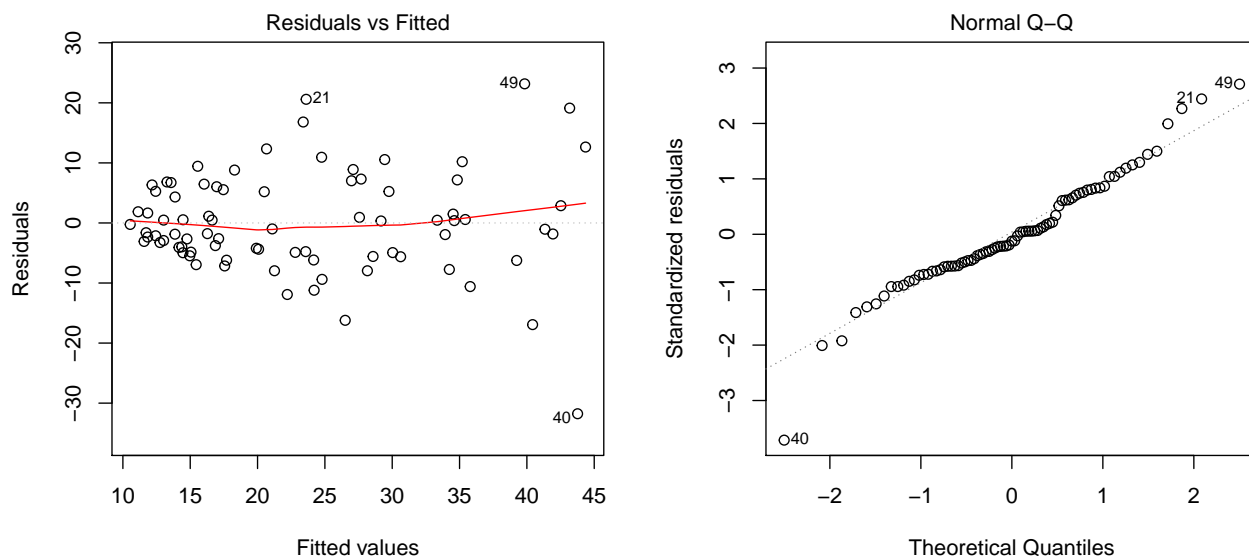
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

```
## Analysis of Variance Table
##
## Response: "Weight of vines measuring kg per plot"
##          Df Sum Sq Mean Sq F value    Pr(>F)
## germplasmName 26 7649.4  294.208   2.6341 0.001473 **
## REP           2   22.9   11.429   0.1023 0.902916
## Residuals     52 5808.1  111.694
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The coefficient of variation for this experiment is 44.96%. The p-value for genotypes is 0.001473 which is significant at the 5% level.

7.2. Assumptions

Don't forget the assumptions of the model. It is supposed that the errors are independent with a normal distribution and with the same variance for all the genotypes. The following plots must help you evaluate this:



Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

7.3. Genotype means

Below are the sorted means for each genotype with letters indicating if there are significant differences using the multiple comparisons method of Tukey at the 5% level.

##		trt	means	M
## 1	MGSG	1015-2	43.76667	a
## 2	MGSG	1051-1	41.93333	a
## 3	MGSG	1032-3	39.83333	a
## 4	MGSG	1005-17	35.20000	a
## 5	MGSG	1007-9	34.83333	a
## 6	MGSG	1015-17	33.93333	a
## 7	Chingova		30.03333	a
## 8	MGSG	1065-4	29.16667	a
## 9	MGSG	1003-27	27.56667	a
## 10	MGSG	1006-9	27.10000	a
## 11	MGSG	1006-7	24.20000	a
## 12	MGSG	1008-8	24.16667	a
## 13	MGSG	1068-1	22.80000	a
## 14	MGSG	1004-2	20.66667	a
## 15	MGSG	1010-10	20.50000	a
## 16	MGSG	1061-3	17.70000	a
## 17	MGSG	1009-3	16.96667	a
## 18	Resisto		16.86667	a
## 19	MGSG	1012-9	16.03333	a
## 20	MGSG	1004-27	14.96667	a
## 21	MGSG	1010-4	14.46667	a
## 22	MGSG	1002-49	14.16667	a
## 23	Jonathan		13.86667	a
## 24	MGSG	1001-7	12.43333	a
## 25	MGSG	1011-5	12.43333	a
## 26	MGSG	1001-36	12.16667	a

```
## 27 MSGG 1007-13 11.13333 a
```

7.4. Variance components

Below are the variance components for this model, under the assumption that genotypes and blocks are random. Here the model is fitted using REML and missing values are not estimated.

##	Variance	Std.Dev.
## germplasmName	62.07585	7.878823
## REP	0.00000	0.000000
## Residual	107.98074	10.391378