ANOVA for a RCBD trial:
PTLB199909_OXAPMP_B3C1OXA00-03

rsimon using HIDAP

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Contents

Author affiliations:

Citation: Bonierbale, Merideth; Gastelo Manuel (1999). *PTLB199909_OXAPMP_B3C1OXA00-03*. Dataset version: 1. Dataset fingerprint (UNF): ASDFHSJKDF525423. Url: http://dataverse.cipotato.org/123456.

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# This is an automatedly created report.

# See more details in section on materials.
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Alternate formats:

Abstract

This trial has the identifier PTLB199909_OXAPMP_B3C1OXA00-03. It was conducted under the supervision of Bonierbale, Merideth; Gastelo Manuel as a Preliminary Trial as part of a Yield Breeding Program in , PERU in 1999. A total of 26 clones (including reference clones) were evaluated for NTP, PGH, Plant_Vigor, Flower, LB1, LB2, LB3, LB4, LB5, LB6, LB7, AUDPC, rAUDPC, SAUDPC, NMTP, NoMTWP, TTWP, TTYNA, MTWP, MTYNA, ATMW, AVDM, SG, FFR, TEXFR, Chip_Color traits.

Materials and Methods

Location characterization

Installation

Geographic and climate characterization

Weather during planting season

Soil

Field management

Observations on special events

Materials

Trait descriptions (from ontology)

Model specification and data description

There is data from 26 treatments, evaluated using a randomize complete block design with 4 blocks. The statistical model is

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

where

- y_{ij} is the observed response with treatment i and block j.
- μ is the mean response over all treatments and blocks.
- τ_i is the effect for treatment 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, $\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$.

The following traits are analyzed: **SG, FFR, TEXFR, Chip_Color, LB3**

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Computational tools

This report was created using i386-w64-mingw32, i386, mingw32, i386, mingw32, , 3, 2.2, 2015, 08, 14, 69053, R, R version 3.2.2 (2015-08-14), Fire Safety on a i386-w64-mingw32/i386 (32-bit) running Windows 7 x64 (build 7601) Service Pack 1 in . The following base packages were loaded: **stats, graphics, grDevices, utils, datasets, methods, base** and the following additional packages: **hidap, knitr, qtl, qtlcharts, fbsites, rmarkdown, leaflet, shinyBS, shinyFiles, rhandsontable, shinydashboard, shiny**.

Results

Raw data

Trait summaries

Trait analyses

Analysis for trait SG

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

Table 1: Table continues below

|	Df	Sum Sq	Mean Sq	F value
INSTN	25	0.0062656	0.000250624	17.4424
REP	3	3.41691e-05	1.13897e-05	0.792675
Residuals	75	0.00107765	1.43687e-05	NA

	Pr(>F)
INSTN	4.98796e-22
REP	0.501768
Residuals	NA

The p-value for treatments is 0.00000000000000000000498796 which is significant at the 5% level.

The means of your treatments are:

INSTN	SG
CIP377744.1	1.07
CIP384866.5	1.06
CIP391004.18	1.07
CIP391011.17	1.08
CIP391046.14	1.05
CIP391047.34	1.06
CIP391065.69	1.07
CIP391580.30	1.07
CIP392617.54	1.08
CIP392634.49	1.07
CIP392637.10	1.07
CIP392639.31	1.05

INSTN	SG
CIP392639.34	1.06
CIP392640.18	1.07
CIP392657.171	1.07
CIP392657.8	1.06
CIP393077.54	1.07
CIP393079.24	1.07
CIP393227.66	1.07
CIP393248.55	1.07
CIP393339.242	1.06
CIP393371.58	1.08
CIP393385.39	1.06
CIP393385.47	1.07
CIP393453.198	1.06
CIP720064	1.05
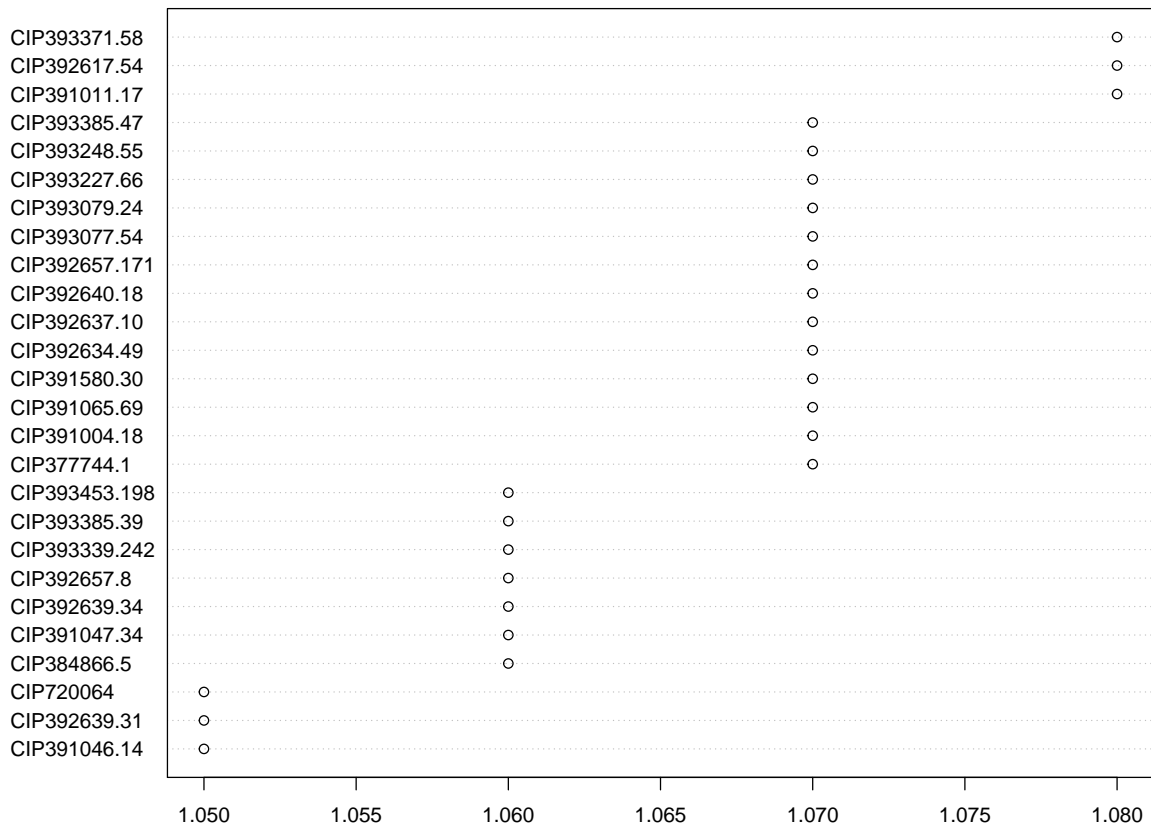
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
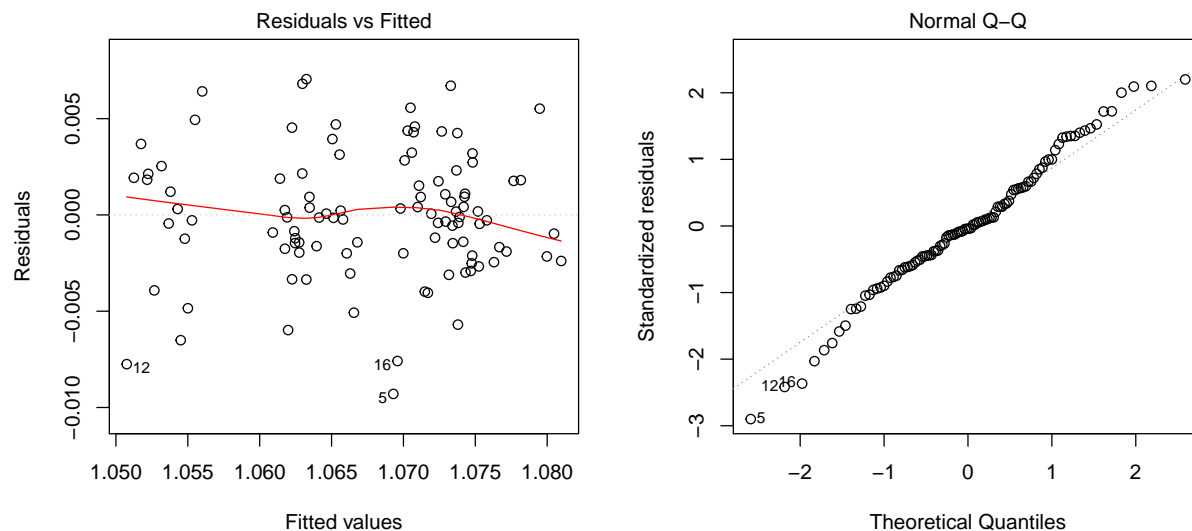
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait FFR

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

Table 4: Table continues below

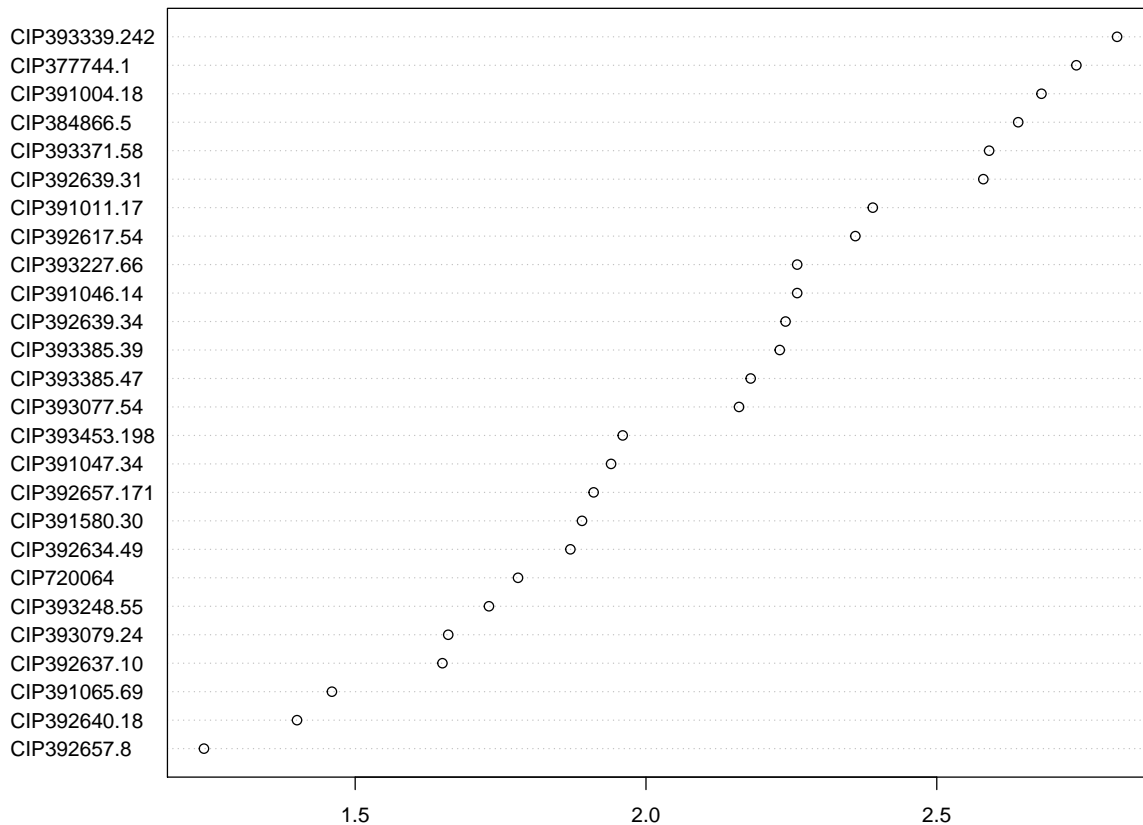|	Df	Sum Sq	Mean Sq	F value
INSTN	25	18.8385	0.753542	2.98694
REP	3	0.0820313	0.0273438	0.108387
Residuals	75	18.9209	0.252279	NA

	Pr(>F)
INSTN	0.000138696
REP	0.954949
Residuals	NA

The p-value for treatments is 0.000138696 which is significant at the 5% level.

The means of your treatments are:

INSTN	FFR
CIP377744.1	2.74
CIP384866.5	2.64
CIP391004.18	2.68
CIP391011.17	2.39
CIP391046.14	2.26
CIP391047.34	1.94

5

INSTN	FFR
CIP391065.69	1.46
CIP391580.30	1.89
CIP392617.54	2.36
CIP392634.49	1.87
CIP392637.10	1.65
CIP392639.31	2.58
CIP392639.34	2.24
CIP392640.18	1.4
CIP392657.171	1.91
CIP392657.8	1.24
CIP393077.54	2.16
CIP393079.24	1.66
CIP393227.66	2.26
CIP393248.55	1.73
CIP393339.242	2.81
CIP393371.58	2.59
CIP393385.39	2.23
CIP393385.47	2.18
CIP393453.198	1.96
CIP720064	1.78

CIP393339.242
CIP377744.1
CIP391004.18
CIP384866.5
CIP393371.58
CIP392639.31
CIP391011.17
CIP392617.54
CIP393227.66
CIP391046.14
CIP392639.34
CIP393385.39
CIP393385.47
CIP393077.54
CIP393453.198
CIP391047.34
CIP392657.171
CIP391580.30
CIP392634.49
CIP720064
CIP393248.55
CIP393079.24
CIP392637.10
CIP391065.69
CIP392640.18
CIP392657.8

Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

Residuals vs Fitted
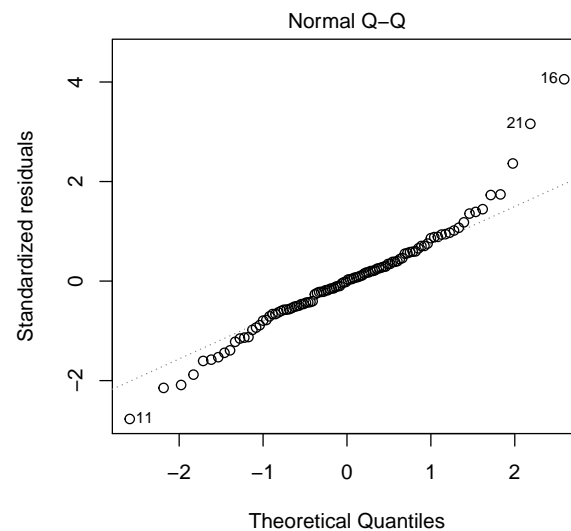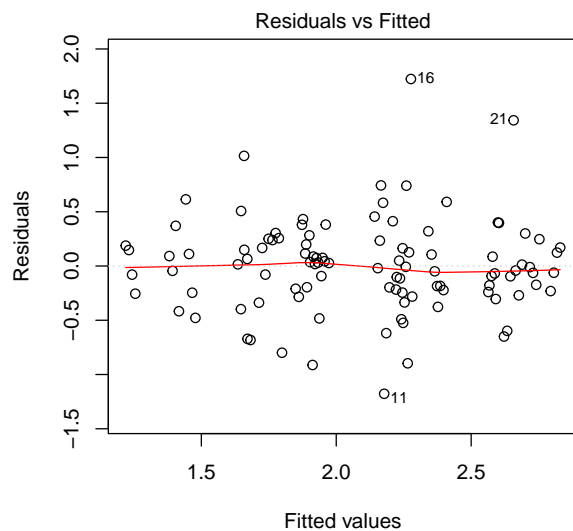
Normal Q–Q

Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait TEXFR

You have fitted a linear model for a RCBD. The ANOVA table for your model is:
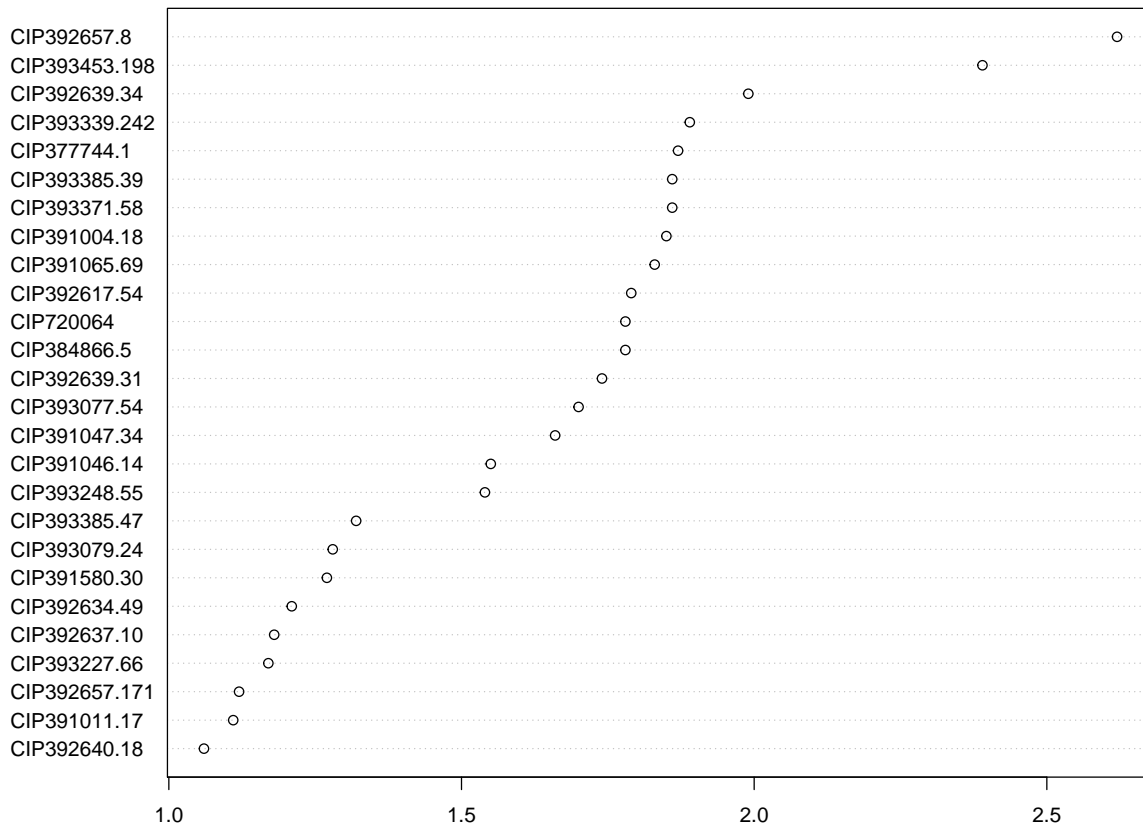
Table 7: Table continues below

	Df	Sum Sq	Mean Sq	F value
INSTN	25	15.5839	0.623358	10.2469
REP	3	0.0939364	0.0313121	0.514715
Residuals	75	4.56254	0.0608339	NA

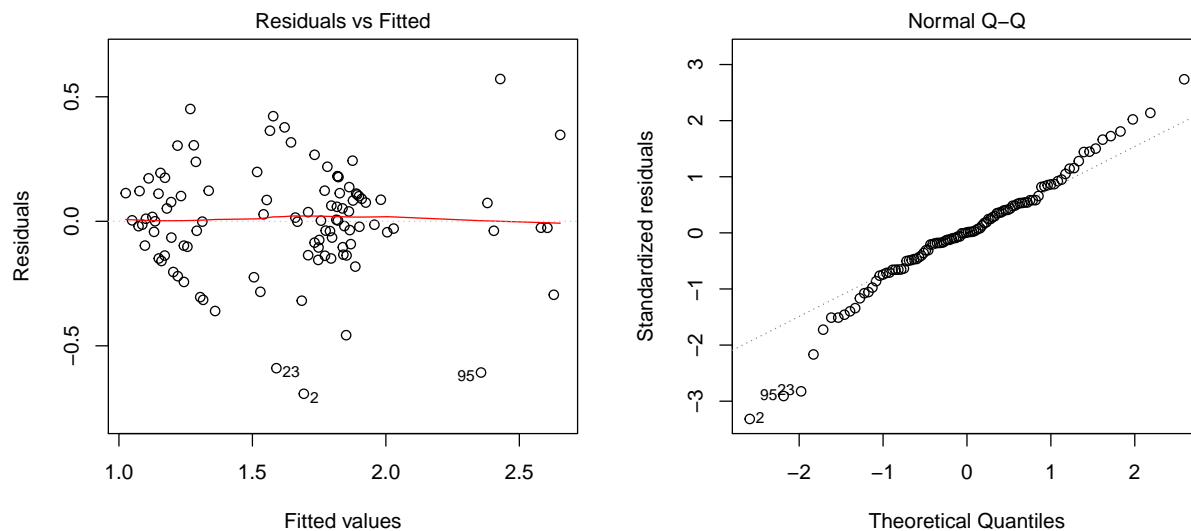|	Pr(>F)
INSTN	1.95109e-15
REP	0.673395
Residuals	NA

The p-value for treatments is 0.00000000000000195109 which is significant at the 5% level.

The means of your treatments are:

INSTN	TEXFR
CIP377744.1	1.87
CIP384866.5	1.78
CIP391004.18	1.85
CIP391011.17	1.11
CIP391046.14	1.55
CIP391047.34	1.66
CIP391065.69	1.83
CIP391580.30	1.27
CIP392617.54	1.79
CIP392634.49	1.21
CIP392637.10	1.18
CIP392639.31	1.74
CIP392639.34	1.99
CIP392640.18	1.06
CIP392657.171	1.12
CIP392657.8	2.62
CIP393077.54	1.7
CIP393079.24	1.28
CIP393227.66	1.17
CIP393248.55	1.54
CIP393339.242	1.89
CIP393371.58	1.86
CIP393385.39	1.86
CIP393385.47	1.32
CIP393453.198	2.39
CIP720064	1.78

CIP392657.8
CIP393453.198
CIP392639.34
CIP393339.242
CIP377744.1
CIP393385.39
CIP393371.58
CIP391004.18
CIP391065.69
CIP392617.54
CIP720064
CIP384866.5
CIP392639.31
CIP393077.54
CIP391047.34
CIP391046.14
CIP393248.55
CIP393385.47
CIP393079.24
CIP391580.30
CIP392634.49
CIP392637.10
CIP393227.66
CIP392657.171
CIP391011.17
CIP392640.18

1.0   1.5   2.0   2.5

Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

Residuals vs Fitted

Residuals

0.5   0.0   −0.5

1.0   1.5   2.0   2.5

Fitted values

23
2
95

Normal Q–Q

Standardized residuals

3   2   1   0   −1   −2   −3

−2   −1   0   1   2

Theoretical Quantiles

95 23
2

Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait Chip_Color

You have fitted a linear model for a RCBD. The ANOVA table for your model is:
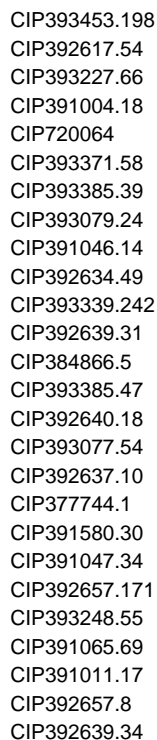
Table 10: Table continues below

	Df	Sum Sq	Mean Sq	F value
INSTN	25	13.6983	0.547932	3.50708
REP	3	0.0498749	0.016625	0.106409
Residuals	75	11.7177	0.156236	NA

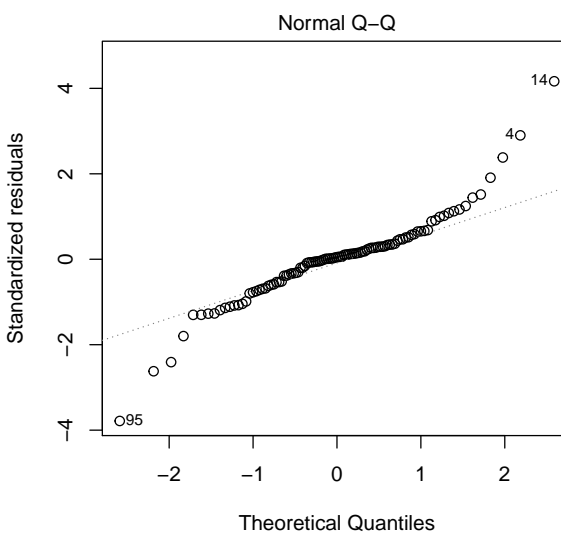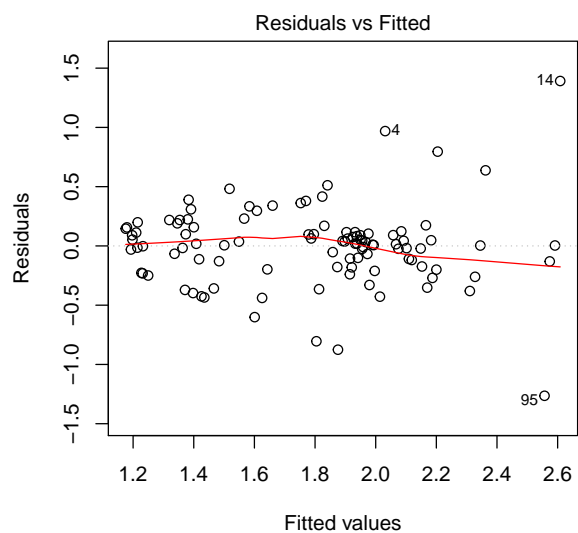|	Pr(>F)
INSTN	1.40209e-05
REP	0.956097
Residuals	NA

The p-value for treatments is 0.0000140209 which is significant at the 5% level.

The means of your treatments are:

INSTN	Chip_Color
CIP377744.1	1.57
CIP384866.5	1.9
CIP391004.18	2.17
CIP391011.17	1.22
CIP391046.14	1.96
CIP391047.34	1.41
CIP391065.69	1.35
CIP391580.30	1.49
CIP392617.54	2.34
CIP392634.49	1.94
CIP392637.10	1.63
CIP392639.31	1.92
CIP392639.34	1.2
CIP392640.18	1.8
CIP392657.171	1.4
CIP392657.8	1.21
CIP393077.54	1.78
CIP393079.24	1.97
CIP393227.66	2.18
CIP393248.55	1.37
CIP393339.242	1.93
CIP393371.58	2.08
CIP393385.39	2.01
CIP393385.47	1.85
CIP393453.198	2.58
CIP720064	2.09

CIP393453.198
CIP392617.54
CIP393227.66
CIP391004.18
CIP720064
CIP393371.58
CIP393385.39
CIP393079.24
CIP391046.14
CIP392634.49
CIP393339.242
CIP392639.31
CIP384866.5
CIP393385.47
CIP392640.18
CIP393077.54
CIP392637.10
CIP377744.1
CIP391580.30
CIP391047.34
CIP392657.171
CIP393248.55
CIP391065.69
CIP391011.17
CIP392657.8
CIP392639.34

1.2 1.4 1.6 1.8 2.0 2.2 2.4 2.6

Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

Residuals vs Fitted

Residuals

14

4

95

1.2 1.4 1.6 1.8 2.0 2.2 2.4 2.6

Fitted values

Normal Q–Q

Standardized residuals

14

4

95

−2 −1 0 1 2

Theoretical Quantiles

Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait LB3

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

|	Df	Sum Sq	Mean Sq	F value	Pr(>F)
INSTN	25	15339.7	613.587	13.7459	5.74463e-19
REP	3	458.413	152.804	3.42321	0.0214143
Residuals	75	3347.84	44.6378	NA	NA

The p-value for treatments is 0.0000000000000000574463 which is significant at the 5% level.

The means of your treatments are:

INSTN	LB3
CIP377744.1	12.5
CIP384866.5	30
CIP391004.18	5
CIP391011.17	10
CIP391046.14	47.5
CIP391047.34	17.5
CIP391065.69	16.2
CIP391580.30	15
CIP392617.54	3.75
CIP392634.49	6.25
CIP392637.10	6.25
CIP392639.31	31.2
CIP392639.34	31.2
CIP392640.18	5
CIP392657.171	10
CIP392657.8	36.2
CIP393077.54	5
CIP393079.24	7.5
CIP393227.66	8.75
CIP393248.55	12.5
CIP393339.242	5
CIP393371.58	3.75
CIP393385.39	20
CIP393385.47	6.25
CIP393453.198	13.8
CIP720064	37.5
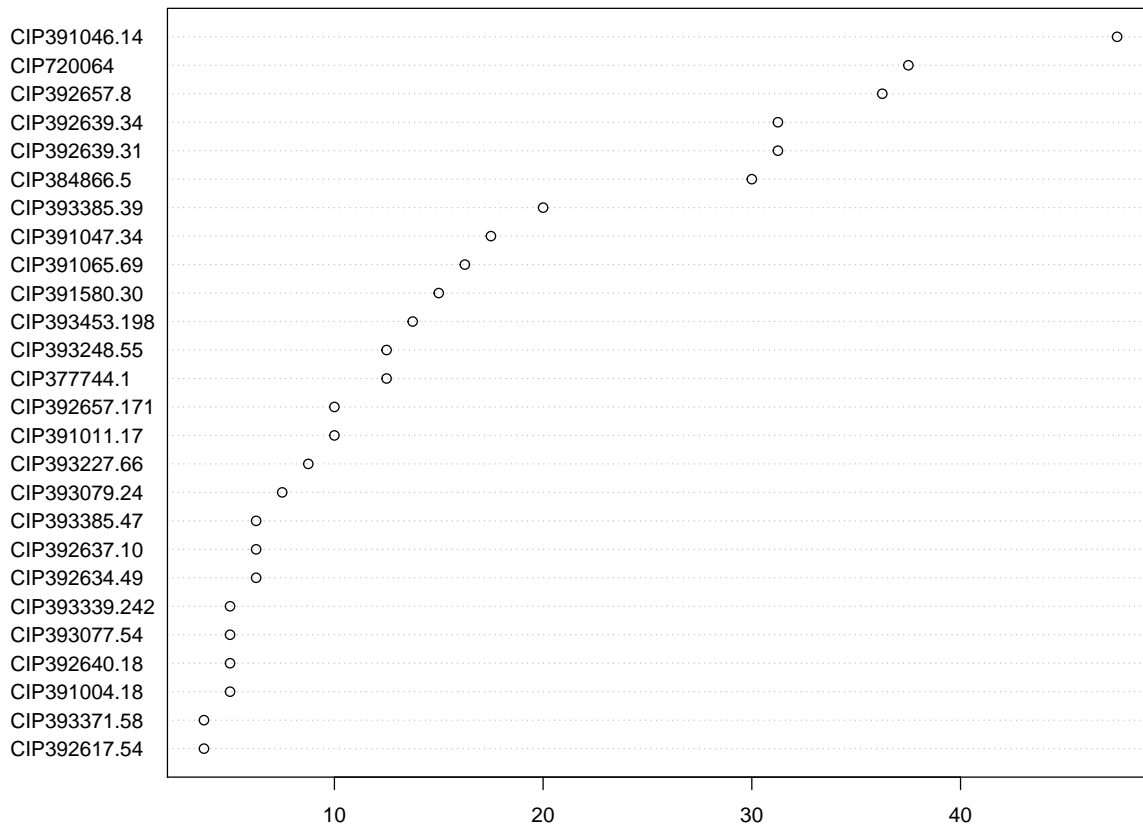
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
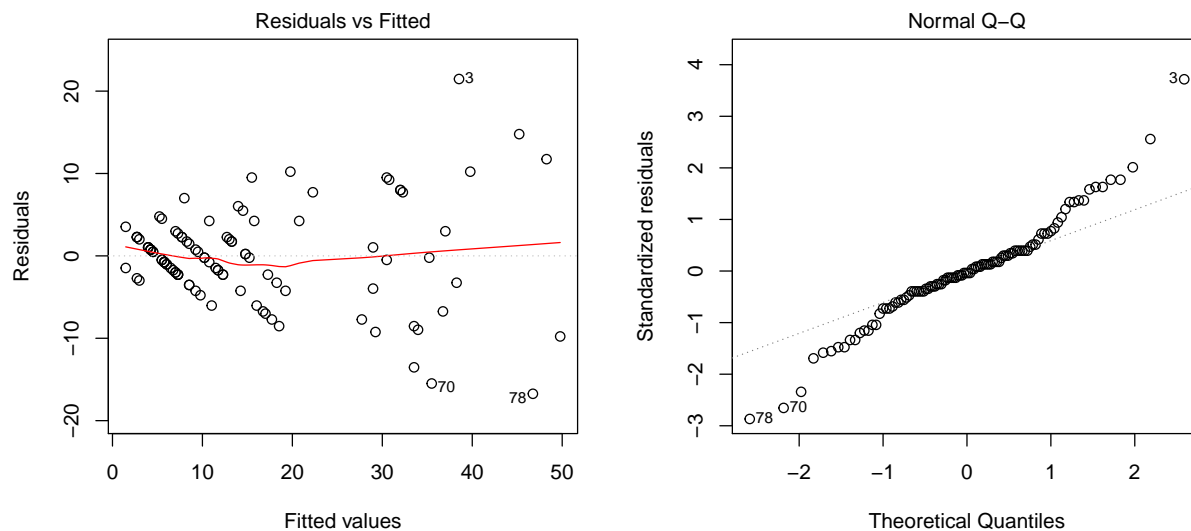
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Trait correlations

Variety candidate selection

Summary

References

Data sources

Literature