ANOVA for a RCBD trial: PTLB199909_OXAPMP_B3C1OXA00-03

rsimon using HIDAP

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Contents

Author affiliations:

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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: **PGH, TTWP, SAUDPC**

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: **knitr, qtl, qtlcharts, rmarkdown, leaflet, shinyBS, shinyFiles, shinyTree, rhandsontable, shinydashboard, shiny**.

Results

Raw data

Trait summaries

Trait analyses

Analysis for trait PGH

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	0.757384	0.0302954	2.77571
REP	3	0.00481025	0.00160342	0.146908
Residuals	75	0.818584	0.0109145	NA

|	Pr(>F)
INSTN	0.000357177
REP	0.931363
Residuals	NA

The p-value for treatments is 0.000357177 which is significant at the 5% level.

The means of your treatments are:

INSTN	PGH
CIP377744.1	2
CIP384866.5	2
CIP391004.18	1.6
CIP391011.17	2
CIP391046.14	2
CIP391047.34	2
CIP391065.69	2
CIP391580.30	2
CIP392617.54	1.89
CIP392634.49	1.96
CIP392637.10	1.99
CIP392639.31	2

INSTN	PGH
CIP392639.34	2
CIP392640.18	1.99
CIP392657.171	2
CIP392657.8	2
CIP393077.54	1.86
CIP393079.24	1.86
CIP393227.66	1.98
CIP393248.55	2
CIP393339.242	2
CIP393371.58	1.87
CIP393385.39	2
CIP393385.47	1.94
CIP393453.198	2
CIP720064	2
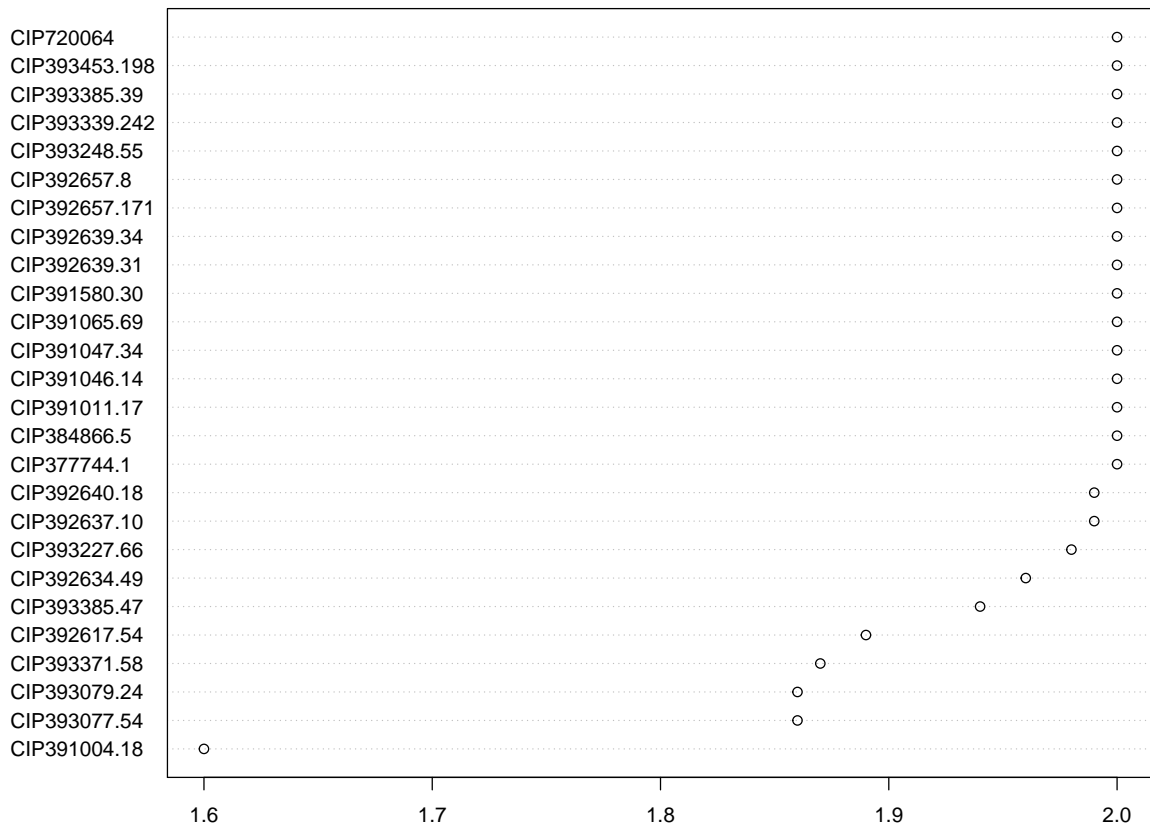
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
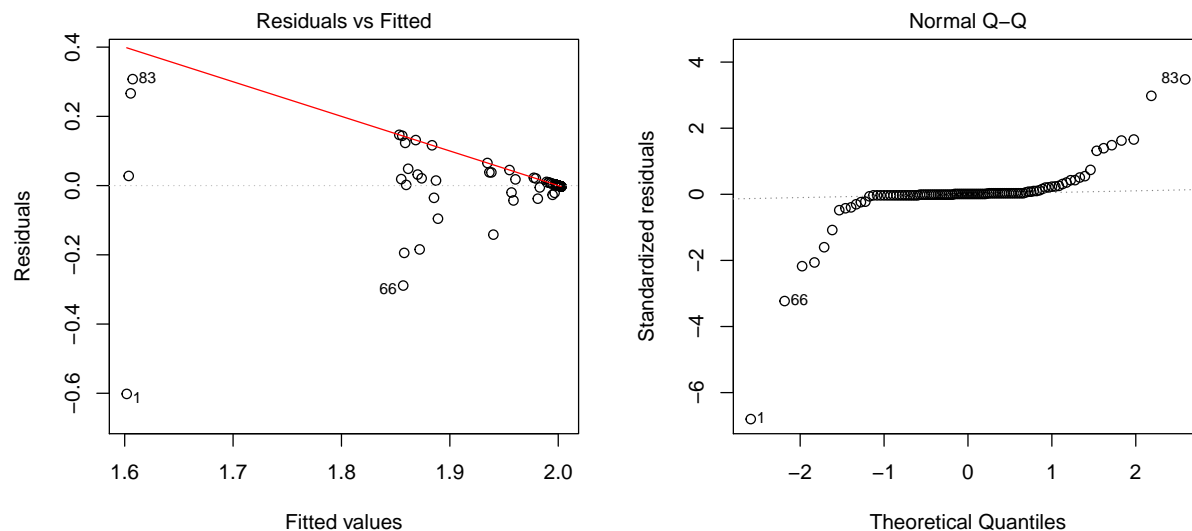
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait TTWP

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	911.808	36.4723	17.7319	3.02346e-22
REP	3	1.22178	0.407261	0.198	0.897444
Residuals	75	154.266	2.05688	NA	NA

The p-value for treatments is 0.000000000000000000000302346 which is significant at the 5% level.

The means of your treatments are:

INSTN	TTWP
CIP377744.1	2.64
CIP384866.5	1.55
CIP391004.18	9.59
CIP391011.17	7.11
CIP391046.14	2.05
CIP391047.34	4.83
CIP391065.69	3.98
CIP391580.30	6.85
CIP392617.54	12
CIP392634.49	8.55
CIP392637.10	6.75
CIP392639.31	2.24
CIP392639.34	4.17
CIP392640.18	6.62
CIP392657.171	5.57

5

INSTN	TTWP
CIP392657.8	5.07
CIP393077.54	7.79
CIP393079.24	7.47
CIP393227.66	7.95
CIP393248.55	7.3
CIP393339.242	2.51
CIP393371.58	11.8
CIP393385.39	3.41
CIP393385.47	8.55
CIP393453.198	3.45
CIP720064	1.15
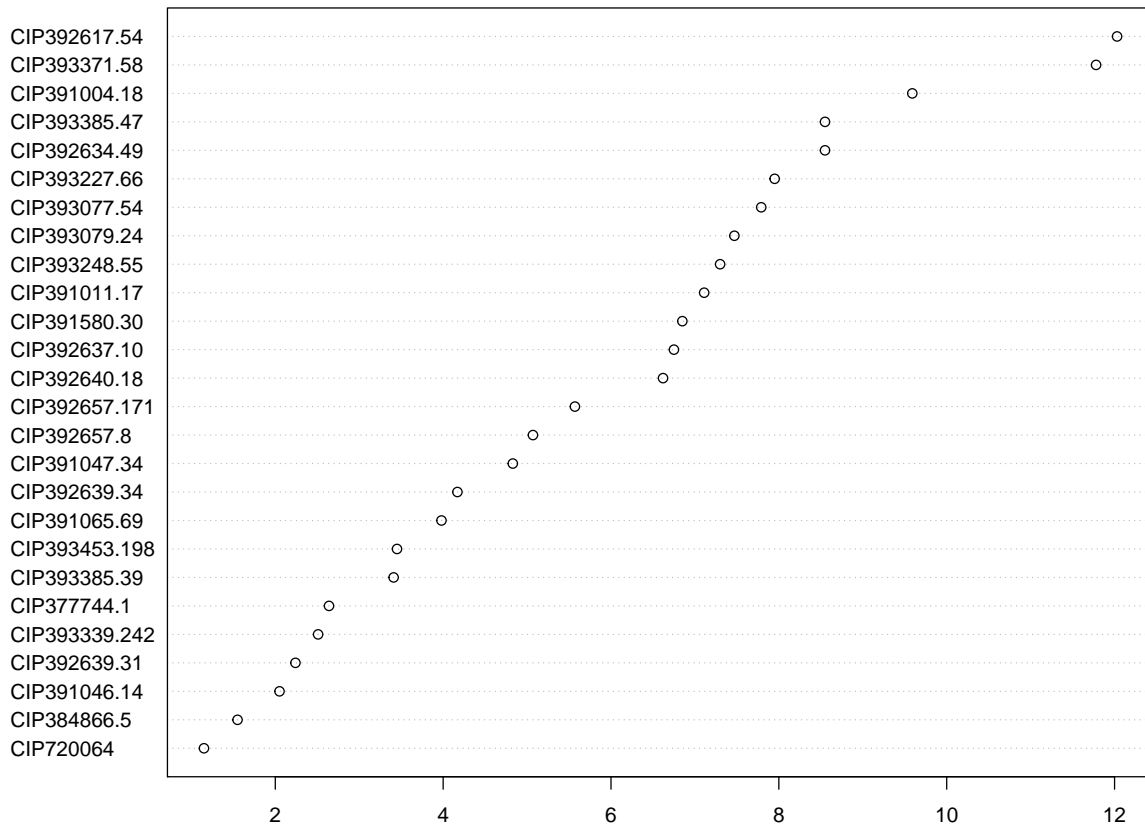
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
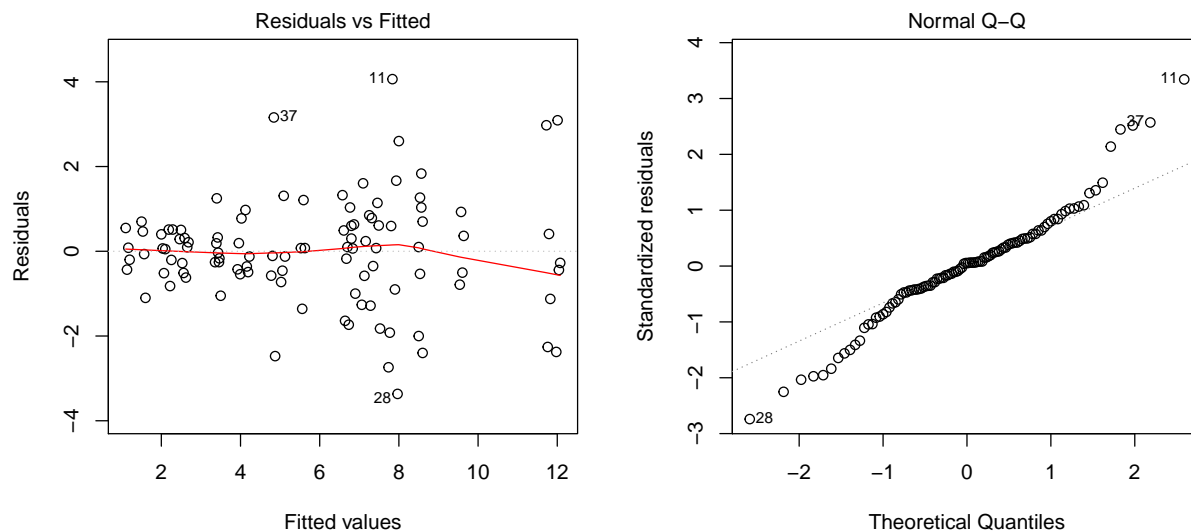
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis for trait SAUDPC

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	474.856	18.9942	72.8625	8.23293e-43
REP	3	1.80106	0.600353	2.30297	0.0838393
Residuals	75	19.5514	0.260686	NA	NA

The p-value for treatments is 0.000000000000000000000000000000000000000823293 which is significant at the 5% level.

The means of your treatments are:

INSTN	SAUDPC
CIP377744.1	2.15
CIP384866.5	6.08
CIP391004.18	0.675
CIP391011.17	2.67
CIP391046.14	7.42
CIP391047.34	4.25
CIP391065.69	4.67
CIP391580.30	3.33
CIP392617.54	0.525
CIP392634.49	1.3
CIP392637.10	1.77
CIP392639.31	6.45
CIP392639.34	4.35
CIP392640.18	1.6

7

INSTN	SAUDPC
CIP392657.171	1.98
CIP392657.8	7.17
CIP393077.54	0.875
CIP393079.24	0.975
CIP393227.66	1.2
CIP393248.55	3.77
CIP393339.242	1.12
CIP393371.58	0.7
CIP393385.39	2.88
CIP393385.47	1.2
CIP393453.198	3.9
CIP720064	6
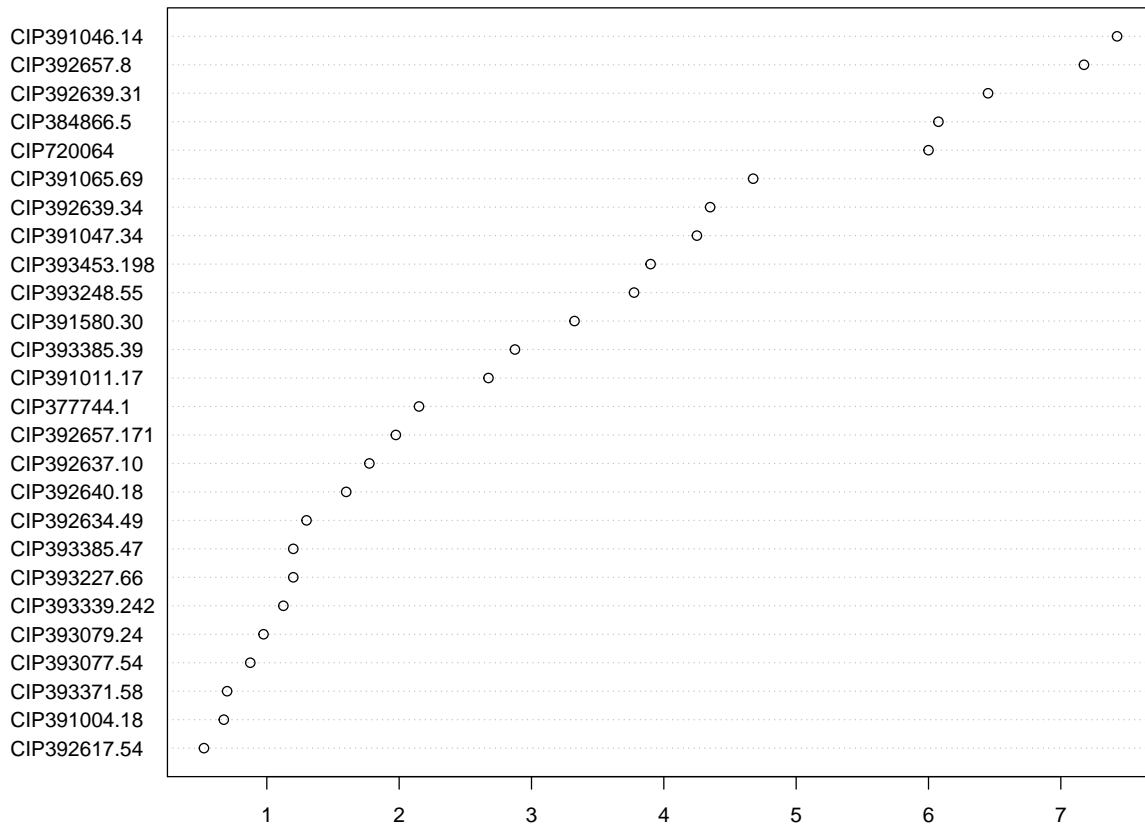
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
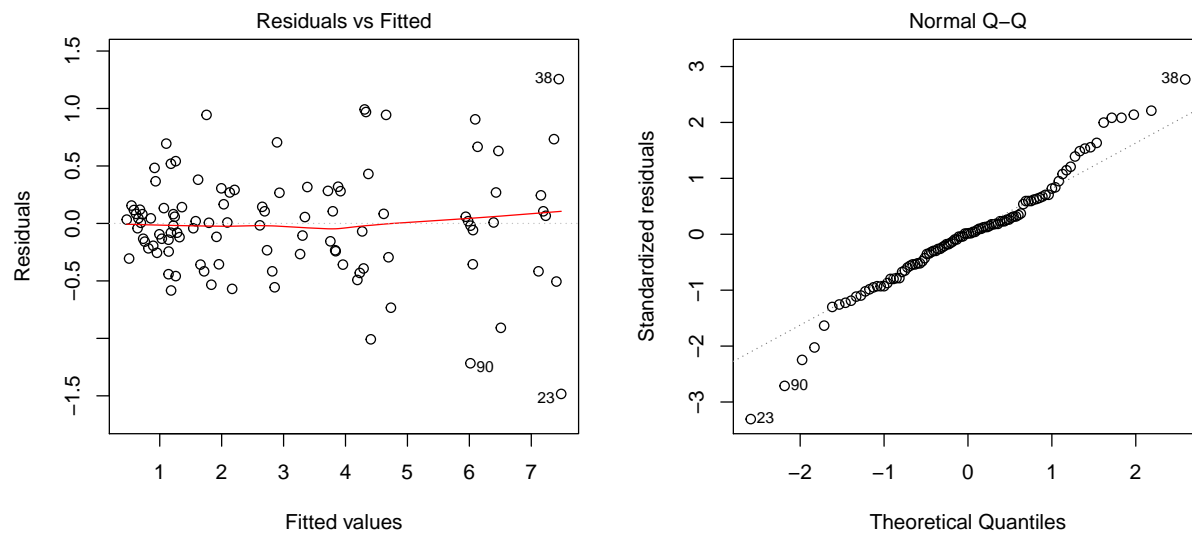
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Trait correlations

Variety candidate selection

Summary

References

Data sources

Literature