ANOVA for a RCBD trial: PTLB199909\_OXAPMP\_B3C1OXA00-03

rsimon using HIDAP

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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>.

# This is an automatedly created report.  
  
# See more details in section on materials.

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

where

* is the observed response with treatment and block .
* is the mean response over all treatments and blocks.
* is the effect for treatment .
* is the effect for block .
* is the error term.

In this model we assume that the errors are independent and have a normal distribution with common variance, that is, .

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 continues below

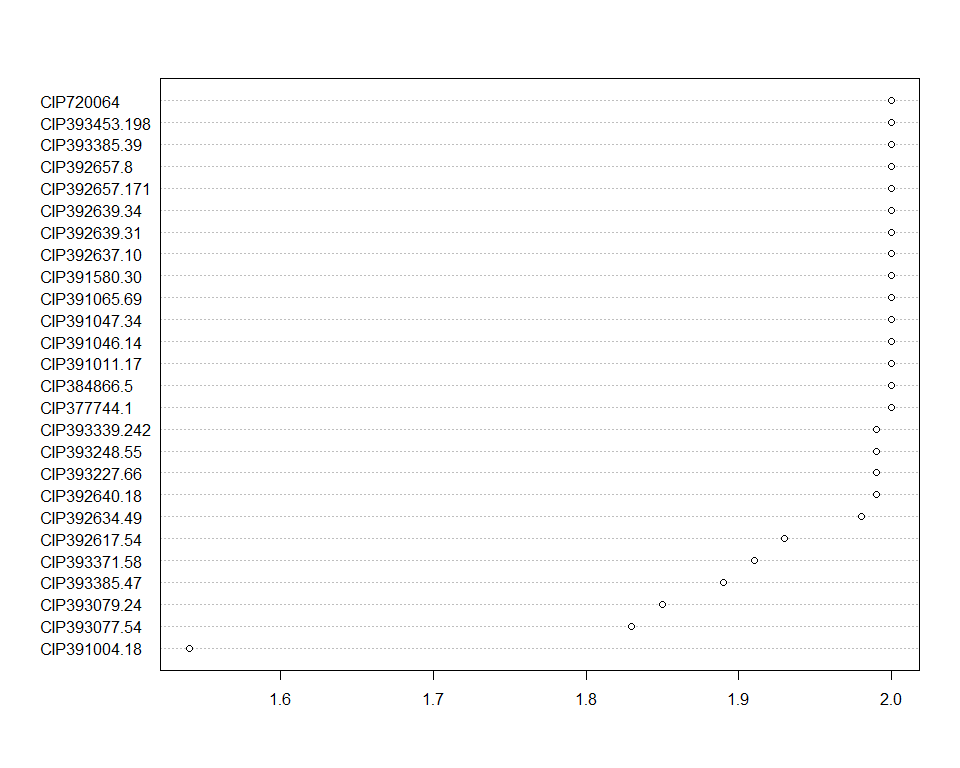
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value |
| **INSTN** | 25 | 0.95268 | 0.0381072 | 3.11004 |
| **REP** | 3 | 0.00129773 | 0.000432576 | 0.0353038 |
| **Residuals** | 75 | 0.918971 | 0.0122529 | NA |

|  |  |
| --- | --- |
|  | Pr(>F) |
| **INSTN** | 8.01855e-05 |
| **REP** | 0.991041 |
| **Residuals** | NA |

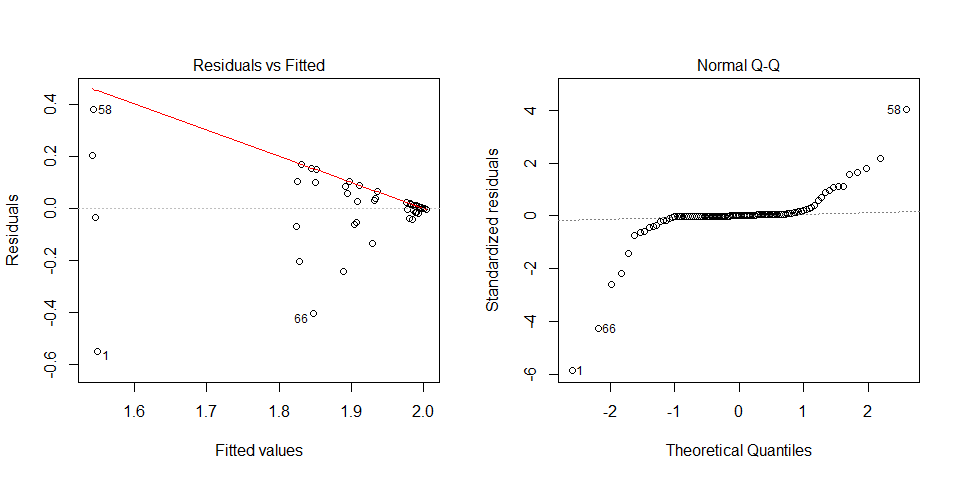
The p-value for treatments is 0.0000801855 which is significant at the 5% level.

The means of your treatments are:

|  |  |
| --- | --- |
| INSTN | PGH |
| CIP377744.1 | 2 |
| CIP384866.5 | 2 |
| CIP391004.18 | 1.54 |
| CIP391011.17 | 2 |
| CIP391046.14 | 2 |
| CIP391047.34 | 2 |
| CIP391065.69 | 2 |
| CIP391580.30 | 2 |
| CIP392617.54 | 1.93 |
| CIP392634.49 | 1.98 |
| CIP392637.10 | 2 |
| CIP392639.31 | 2 |
| CIP392639.34 | 2 |
| CIP392640.18 | 1.99 |
| CIP392657.171 | 2 |
| CIP392657.8 | 2 |
| CIP393077.54 | 1.83 |
| CIP393079.24 | 1.85 |
| CIP393227.66 | 1.99 |
| CIP393248.55 | 1.99 |
| CIP393339.242 | 1.99 |
| CIP393371.58 | 1.91 |
| CIP393385.39 | 2 |
| CIP393385.47 | 1.89 |
| 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

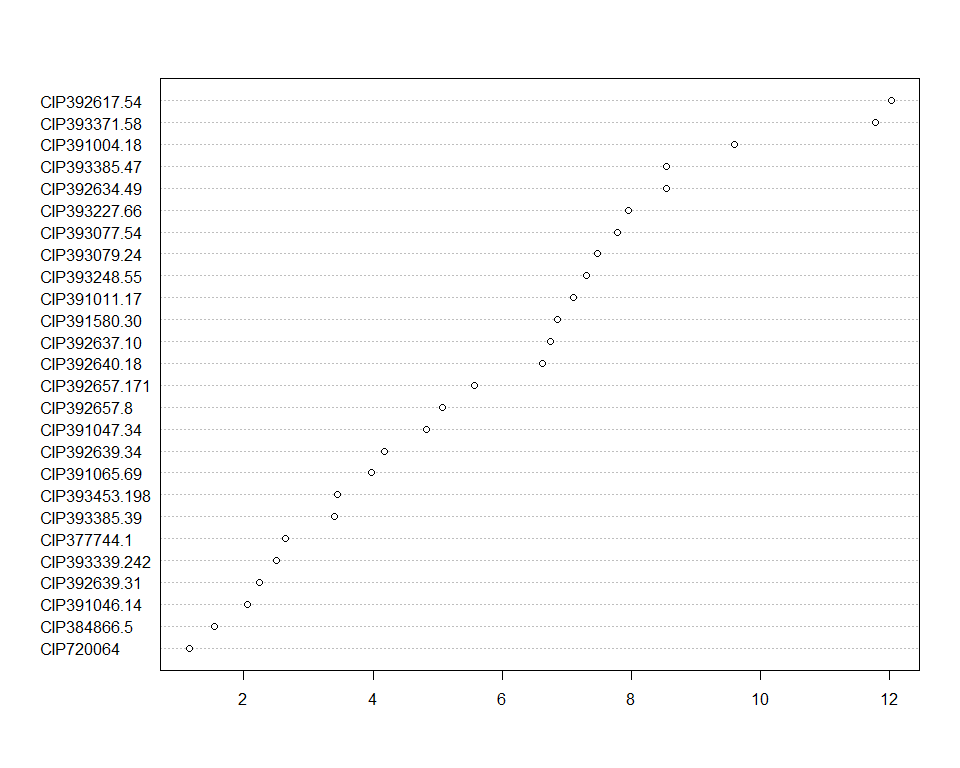
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | 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 |

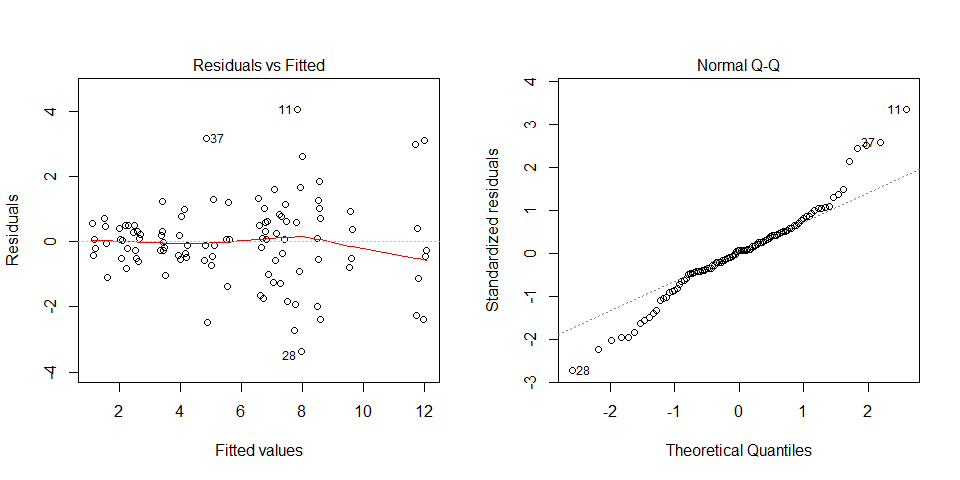
The p-value for treatments is 0.000000000000000000000302346 which is significant at the 5% level.

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 |
| 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

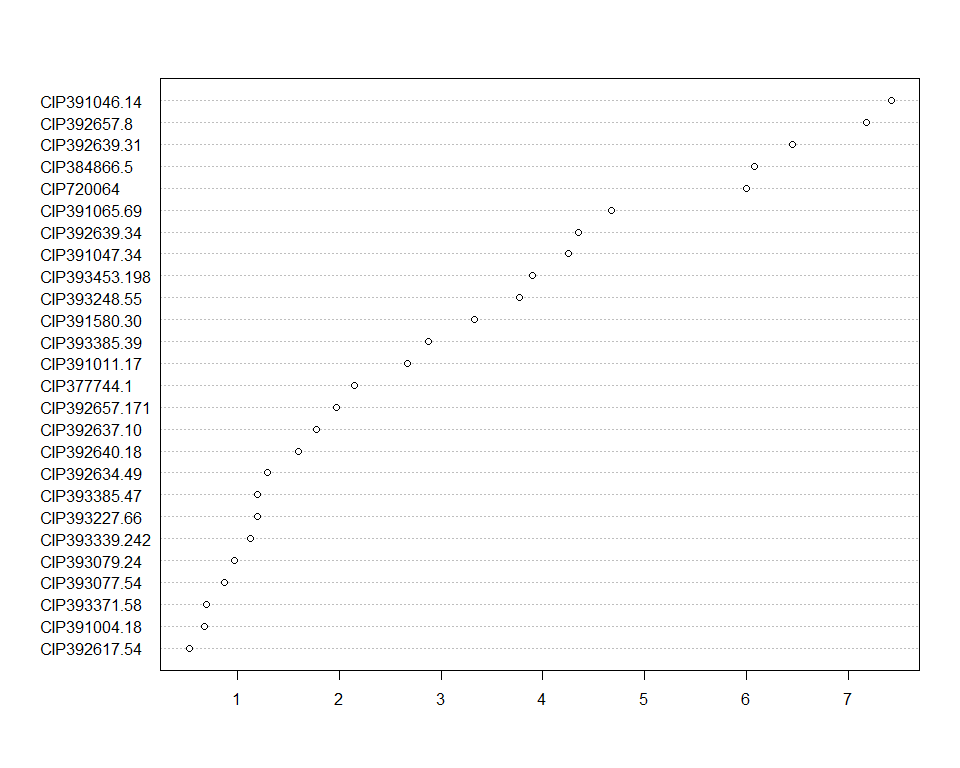
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | 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 |

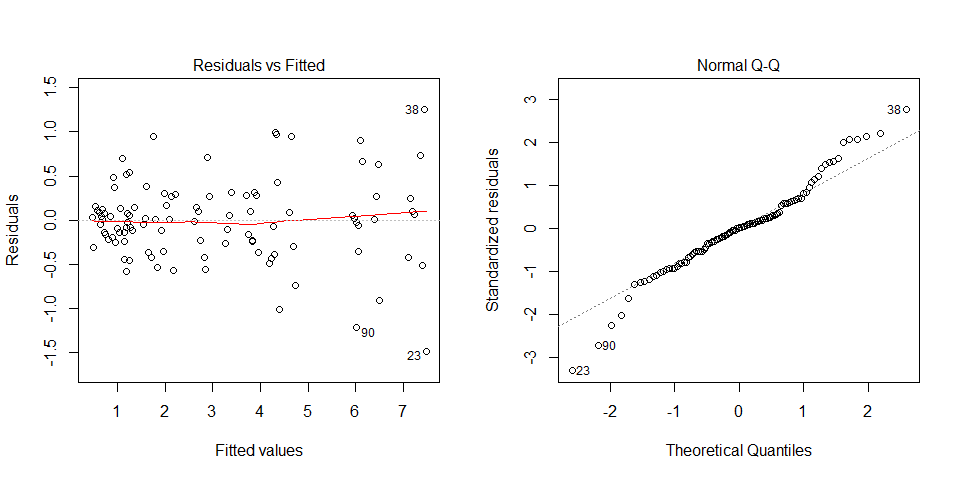
The p-value for treatments is 0.000000000000000000000000000000000000000000823293 which is significant at the 5% level.

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 |
| 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