Automatic report for a Completely Randomized Design (CRD)

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# 1. Model specification and data description

There are data from 4 treatments evaluated using a completely randomized design. The statistical model is

where

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

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

# 2. Analysis for trait Wheat\_Total biomass (including all roots and spikes)\_Fresh weight\_g

## 2.1. ANOVA

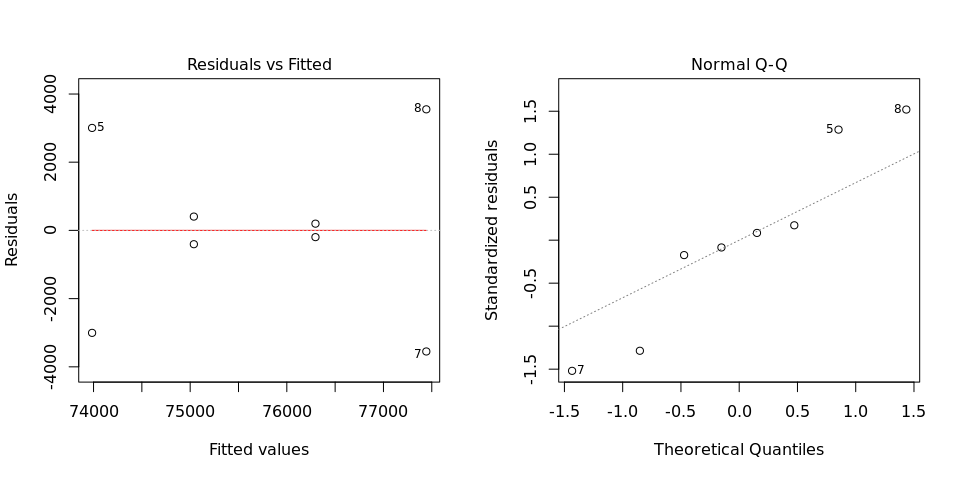
You have fitted a linear model for a CRD. The ANOVA table for your model is:

## Analysis of Variance Table  
##   
## Response: "Wheat\_Total biomass (including all roots and spikes)\_Fresh weight\_g"  
## Df Sum Sq Mean Sq F value Pr(>F)  
## TREATMENT 3 13549463 4516488 0.4136 0.7529  
## Residuals 4 43678213 10919553

The coefficient of variation for this experiment is 4.366%. The p-value for treatments is 0.7529 which is not 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 treatments. The following residuals plots must help you evaluate this:



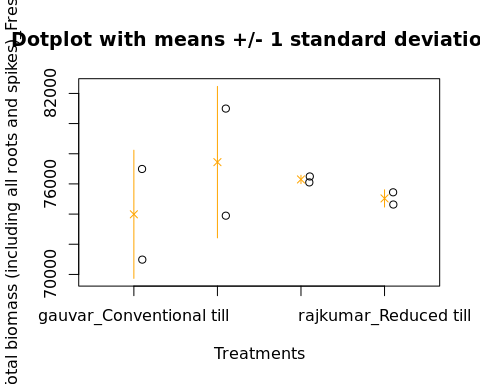
Any trend in the residuals in the left plot would violate the assumption of independence while a trend in the variability of the residuals –for instance a funnel shape– suggests heterogeneity of variances. Departures from the theoretical normal line on the right plot are symptoms of lack of normality.

## 2.3. Treatment means

The means of your treatments are:

## gauvar\_Conventional till gauvar\_Reduced till   
## 73985.0 77443.5   
## rajkumar\_Conventional till rajkumar\_Reduced till   
## 76296.5 75038.0

It is always good to have some visualization of the data. Because the number of treatments in your experiment is not so big, we can plot the data for each treatment:



## 2.4. Variance components

Below are the variance components for this model, under the assumption that treatments are random. Here the model is fitted using REML.

## boundary (singular) fit: see ?isSingular

## Variance Std.Dev.  
## TREATMENT 0 0.000  
## Residual 8175382 2859.263