

Single trial analysis for

1 General information

Analysis done on	18-03-26 14:33:20
Pipeline version	0.0.0.9000
Mixed model engine	lme4

2 Description of the fitted model

Trait	yield
Experimental design features	block (R)
Spatial model	FALSE
Genotype	fixed

3 Summary of the results

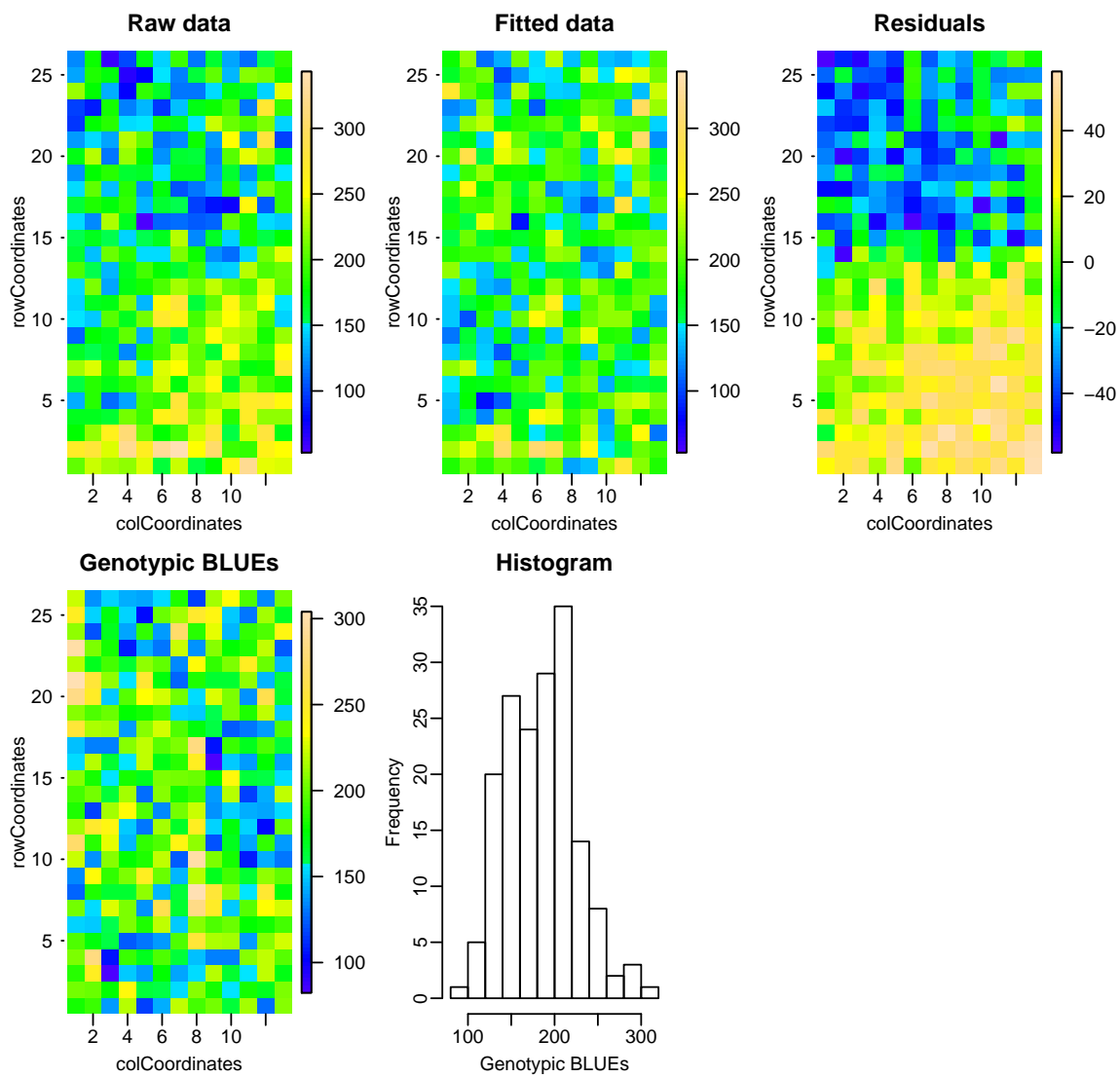
Table 1: Size of the data set and eight number descriptives

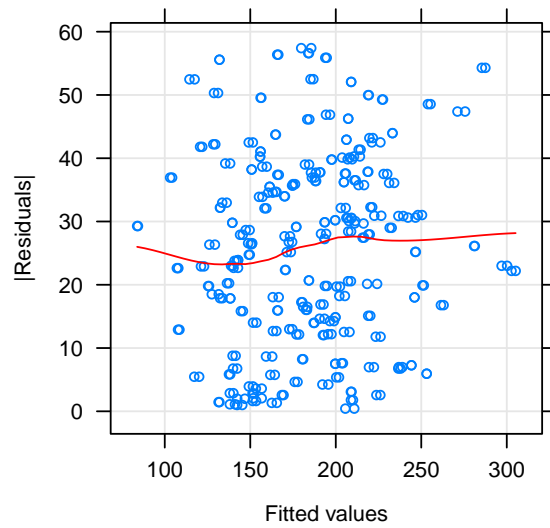
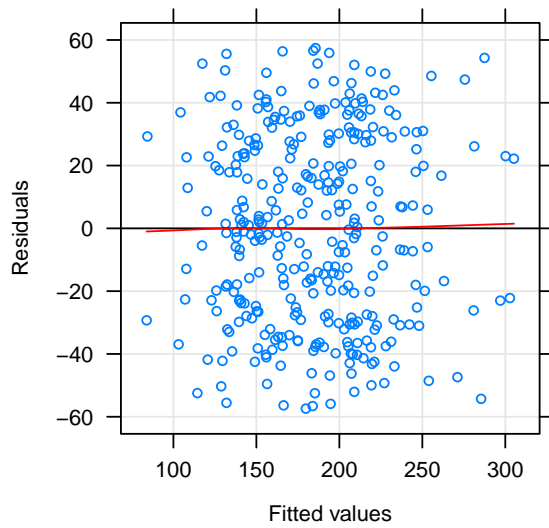
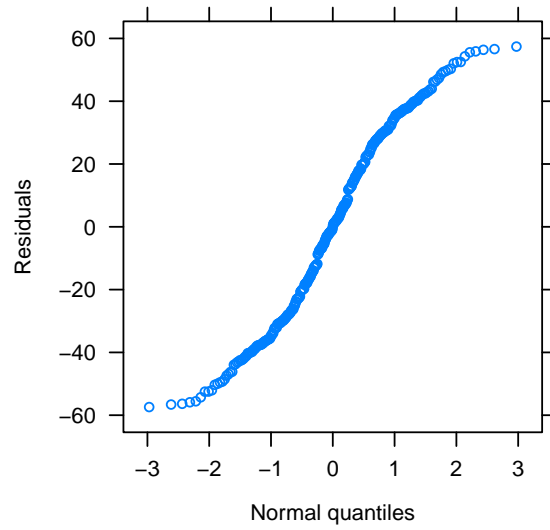
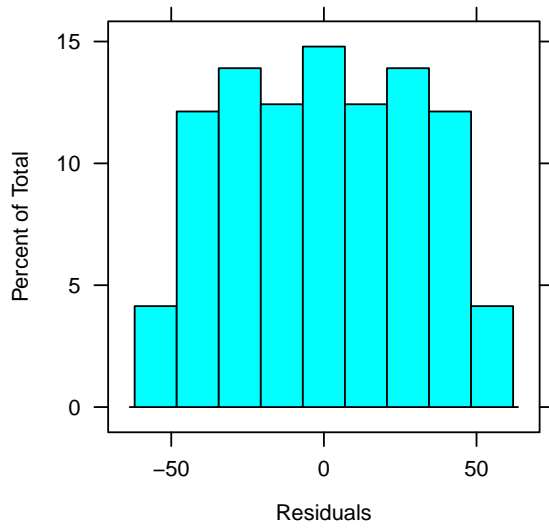
Number of observations	338.00
Number of missing values	0.00
Mean	184.16
Median	179.81
Min	54.58
Max	341.77
Lower quartile	148.56
Upper quartile	220.50
Variance	2569.23

Table 2: Variance components

	Variance
Block	20.01
Residual	1805.46

4 Diagnostic plots





5 List of best 10% genotypes with highest BLUEs

genotype	yield	SE
SB023	302.84	30.19
SB025	297.84	30.19
SB022	285.13	30.19
SB032	280.96	30.19
SB011	272.45	30.19
SB156	262.77	30.19
SB055	253.21	30.19
SB020	253.08	30.19
SB144	251.55	30.19
SB045	250.07	30.19
SB054	246.51	30.19
SB031	245.69	30.34
SB027	244.27	30.19
SB128	243.91	30.34
SB194	239.22	30.19
SB077	238.66	30.19
SB093	236.58	30.19

