

# Model report

2018-01-02 09:08:17

## 1 Description of the fitted model

Trait	yield
Experimental design features	replicate (F) + row(replicate) (R) + col(replicate) (R)
Spatial model	2 dimensional P-splines
Genotype	fixed

## 2 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

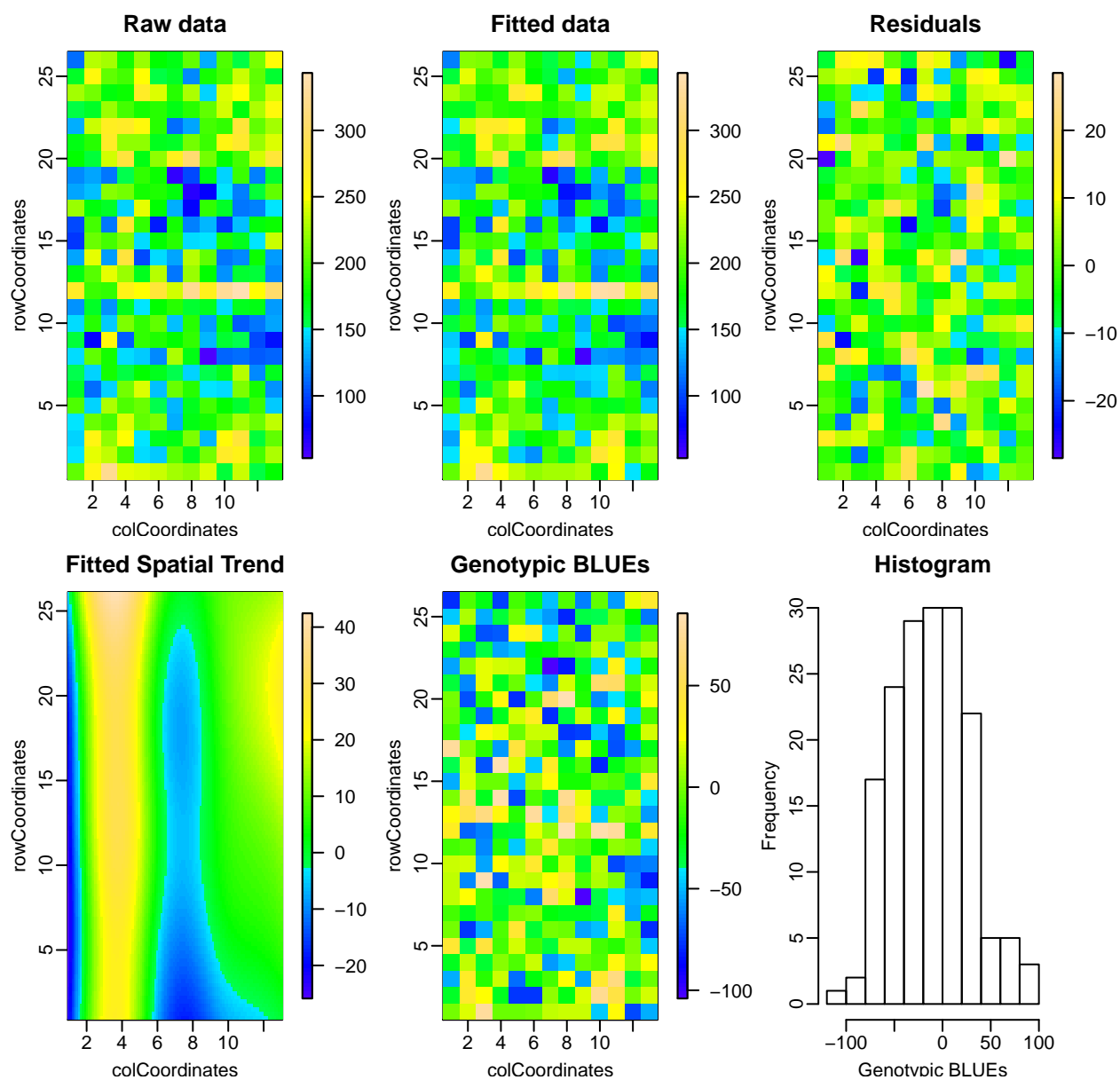
Table 2: Effective dimensions

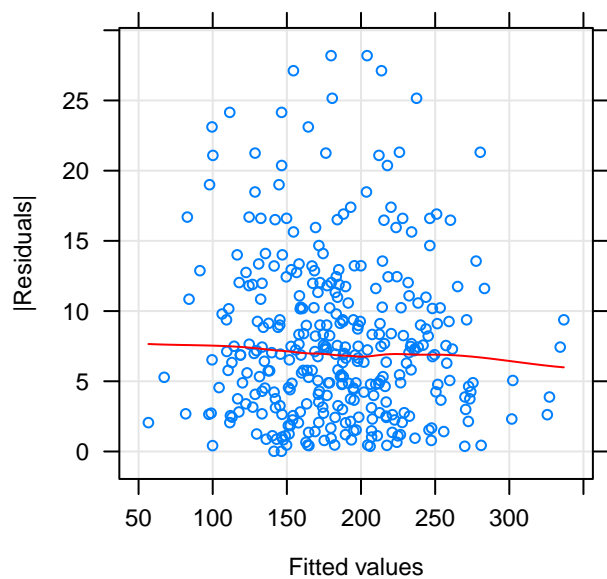
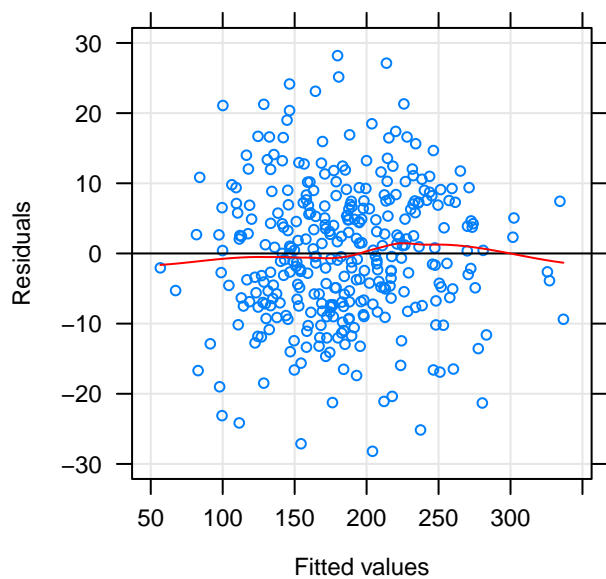
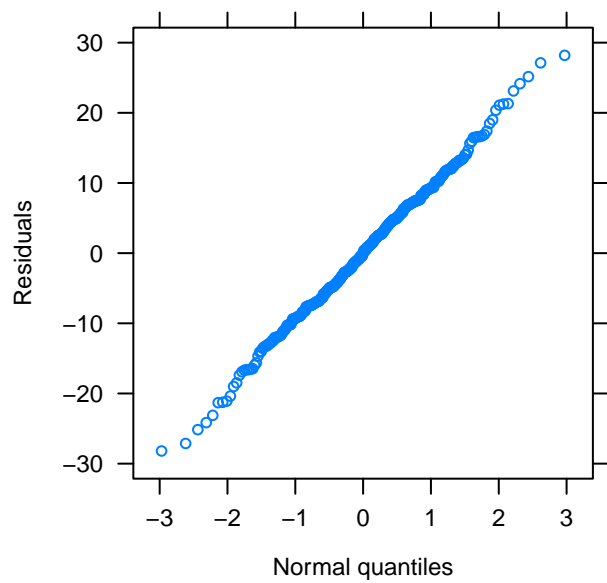
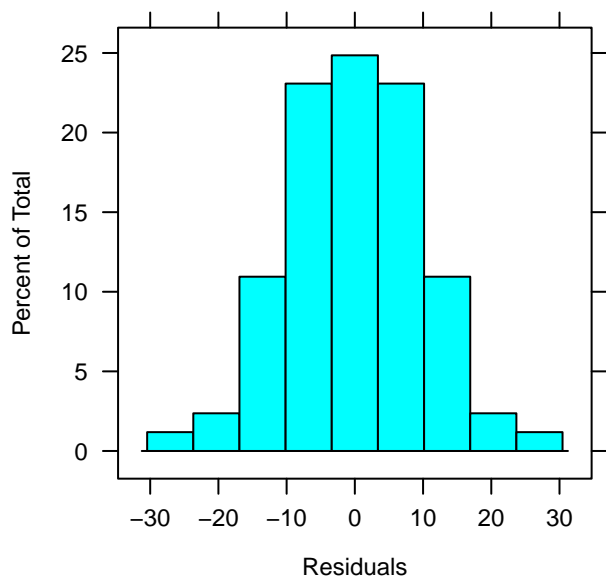
	Effective	Model	Nominal	Ratio	Type
Genotype	168.0	168	168	1.00	F
Intercept	1.0	1	1	1.00	F
Replicate	1.0	1	1	1.00	F
Row(replicate)	18.3	52	51	0.36	R
Col(replicate)	1.1	26	25	0.04	R
Linear trend along cols	1.0	1	1	1.00	S
Linear trend along rows	1.0	1	1	1.00	S
Linear trend along rows and cols	1.0	1	1	1.00	S
Smooth trend along cols	4.2	8	8	0.52	S
Smooth trend along rows	0.0	14	14	0.00	S
Linear trend in rows changing smoothly along cols	0.0	8	8	0.00	S
Linear trend in cols changing smoothly along rows	1.3	14	14	0.09	S
Smooth-by-smooth interaction trend over rows and cols	2.3	28	28	0.08	S
Total	200.2	323	321	0.62	
Residual	137.8				
Number of observations	338				

Table 3: Variance components

	Variance
Row(replicate)	233.60
Col(replicate)	4.99
Smooth trend along cols	22290.00
Smooth trend along rows	0.00
Linear trend in rows changing smoothly along cols	1.00
Linear trend in cols changing smoothly along rows	28.82
Smooth-by-smooth interaction trend over rows and cols	465.30
Residual	234.50

### 3 Diagnostic plots





## 4 List of best 10% genotypes

genotype	BLUEs	SE
SB025	297.93	13.75
SB032	297.77	14.51
SB023	296.40	13.61
SB022	291.29	14.43
SB011	290.38	13.95
SB144	287.02	14.18
SB156	281.01	14.80
SB031	273.75	14.56
SB055	272.72	14.23
SB054	270.55	14.87
SB143	260.58	14.96
SB194	258.68	14.00
SB183	255.15	14.91
SB020	253.16	13.15
SB155	253.15	13.77
SB140	253.07	14.69
SB128	252.18	15.89

