

## Solution to Exercise 11.2 (Version 1, 3/5/15)

from **Statistical Methods in Biology: Design & Analysis of Experiments and Regression (2014)** S.J. Welham, S.A. Gezan, S.J. Clark & A. Mead. Chapman & Hall/CRC Press, Boca Raton, Florida. ISBN: 978-1-4398-0878-8

© S J Welham, S A Gezan, S J Clark & A Mead, 2015.

**Exercise 11.2** (Data: courtesy P. Lutman, Rothamsted Research)

Weeds within a crop can greatly decrease yield and there is interest in the impact of different weed species, both alone and in combination. A RCBD with two blocks of 30 plots was set up to investigate the effect of different densities of barley and chickweed on the yield of a linseed crop. There were 29 treatments in total: a factorial combination of five densities of barley with five densities of chickweed (25 treatments), with duplicates of the control (no weeds), plus two higher densities of each of the individual species (four treatments). File DENSITY.DAT holds the unit numbers (*ID*), structural factors (Block, Plot), the applied seed rate of barley and chickweed (variates *B*, *C*) and the resulting grain yield (variate *Grain*).

Create factor versions of the weed density variates. Write down an explanatory model in terms of these factors, identify the structural component of the model for this trial, and fit the model using both components (the intra-block analysis). Is there any evidence of an interaction between the weed species? Identify the predictive model and write down its form. Produce predictions with SE for each combination of weed seed densities present in the trial. (We re-visit these data in Exercise 17.9.)

### Data 11.2 (DENSITY.DAT)

Linseed grain yields (Grain) from a two-block RCBD set up to investigate the effect of different densities of barley (B) and chickweed (C):

ID	Block	Plot	B	C	Grain	ID	Block	Plot	B	C	Grain
1	1	1	50	400	0.503	31	2	1	50	200	0.601
2	1	2	100	100	0.634	32	2	2	0	0	1.140
3	1	3	300	800	0.215	33	2	3	300	0	0.176
4	1	4	25	800	0.364	34	2	4	100	800	0.302
5	1	5	0	0	1.217	35	2	5	0	1200	0.466
6	1	6	400	0	0.152	36	2	6	50	800	0.362
7	1	7	25	0	0.929	37	2	7	0	100	1.090
8	1	8	0	800	0.501	38	2	8	0	200	1.042
9	1	9	50	100	0.675	39	2	9	25	800	0.336
10	1	10	100	0	0.525	40	2	10	300	200	0.136
11	1	11	300	0	0.232	41	2	11	200	0	0.170
12	1	12	300	100	0.193	42	2	12	300	400	0.053
13	1	13	0	0	1.290	43	2	13	100	400	0.348
14	1	14	100	800	0.194	44	2	14	50	400	0.467
15	1	15	50	200	0.849	45	2	15	400	0	0.136
16	1	16	0	600	0.408	46	2	16	300	100	0.214
17	1	17	100	400	0.360	47	2	17	0	600	0.394
18	1	18	25	400	0.367	48	2	18	100	100	0.435

19	1	19	50	800	0.484	49	2	19	25	200	0.748
20	1	20	100	200	0.372	50	2	20	0	400	0.967
21	1	21	0	400	0.700	51	2	21	0	0	1.253
22	1	22	25	100	0.694	52	2	22	25	0	0.965
23	1	23	300	400	0.192	53	2	23	0	800	0.310
24	1	24	50	0	0.579	54	2	24	25	400	0.657
25	1	25	0	100	1.115	55	2	25	25	100	0.919
26	1	26	300	200	0.098	56	2	26	100	0	0.455
27	1	27	0	200	1.100	57	2	27	50	100	0.556
28	1	28	0	1200	0.293	58	2	28	50	0	0.737
29	1	29	200	0	0.096	59	2	29	300	800	0.100
30	1	30	25	200	0.599	60	2	30	100	200	0.501

### Solution 11.2

We will name the factor versions of the  $B$  and  $C$  variates as **Brate** and **Crate**, respectively. These factors are crossed rather than nested, but we do not have a factorial set due to the additional higher densities (600 and 1200 for chickweed, 200 and 400 for barley). We can verify this with a table of counts of the factor combinations present (Table S11.2.1). It is straightforward to verify that this crossed structure is not orthogonal. The explanatory component of the model can be written as

Explanatory component: [1] + Brate\*Crate

**Table S11.2.1.** Number of replicates present for each combination of barley and chickweed seed rates.

		Seed rate (density) of chickweed						
		0	100	200	400	600	800	1200
Seed rate (density) of barley	0	4	2	2	2	2	2	2
	25	2	2	2	2	0	2	0
	50	2	2	2	2	0	2	0
	100	2	2	2	2	0	2	0
	200	2	0	0	0	0	0	0
	300	2	2	2	2	0	2	0
	400	2	0	0	0	0	0	0

The experiment was laid out as a RCBD with two blocks, so the structural component is nested. The full model for grain yield therefore takes the form

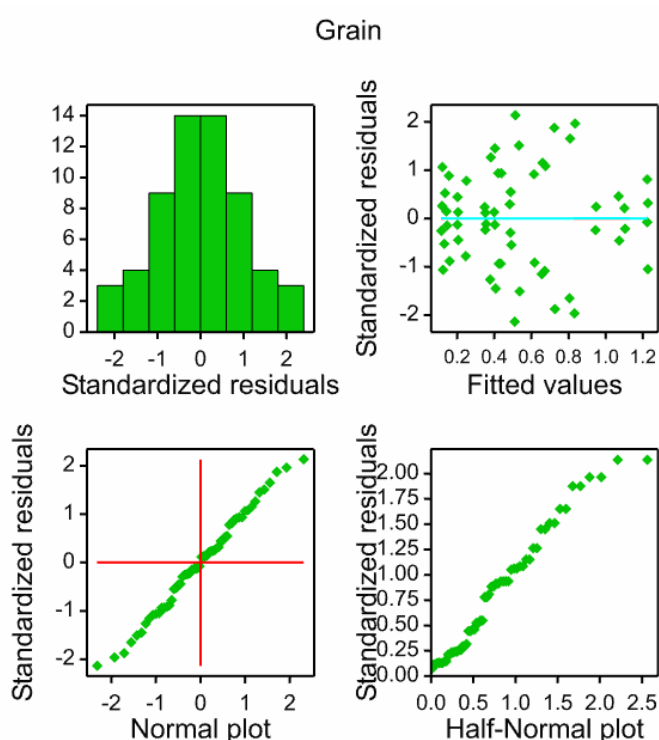
Response variable: *Grain*  
 Structural component: Block / Plot  
 Explanatory component: [1] + Brate\*Crate

Because we have a RCBD, we can fit this non-orthogonal structure using an intra-block analysis without losing any information on the explanatory component (since no treatment comparisons are

made between blocks). The model specification for the intra-block analysis is:

Response variable: *Grain*  
 Explanatory component: [1] + Block + Brate\*Crate

We know that the structure is non-orthogonal, so should fit the explanatory model in both orders (Brate before Crate and vice versa). We first fit in the order given and check the residual plots, shown in Figures S11.2.1 and S11.2.2. There is some pattern in the plots of both the residuals and absolute residuals plotted against fitted values, as there appear to be larger discrepancies between replicates with predicted values in the middle of the yield range than at the extremes. There is no obvious biological reason for this, but neither is there enough evidence to assert a pattern of variance heterogeneity here, and so we accept the analysis.

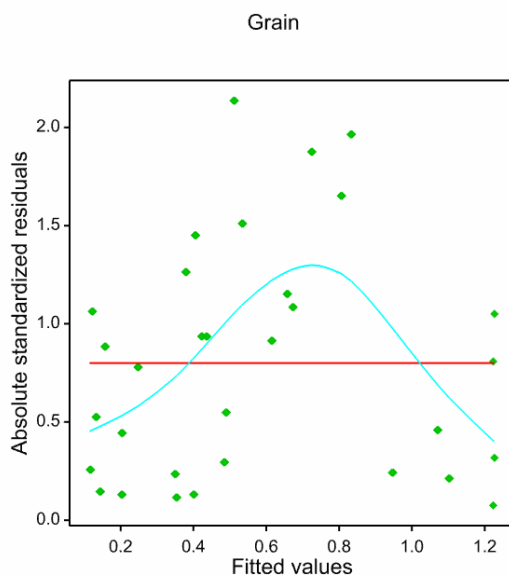


**Figure S11.2.1.** Residual plots for Grain variate from initial model (default set of composite plots from GenStat).

Table S11.2.2 shows sequential ANOVA tables for the main effect of Brate fitted before the main effect of Crate, and vice versa. Notice that the df for the interaction term is smaller than we would predict from the number of levels of each factor because of the large number of missing combinations. The variance ratios indicate the presence of an interaction between the two weeds (Brate.Crate,  $F_{16,30} = 3.767$ ,  $P < 0.001$ ). Note also that the variance ratios for the main effects are very much larger than that for the interaction.

Predictions should be made from the full model, averaging over blocks. The terms in the predictive model are [1] + Block + Brate\*Crate, with averages taken over factor Block. The resulting predictions are in Table S11.2.3 and Figure S11.2.3. The predictions show that yield decreases with the density of both chickweed and barley seed rates. Once the yield is depressed by the presence of one weed type, the presence of the second has less impact, hence the requirement for the interaction

term in the model. The decrease of yield is not linear in terms of the seed densities, but we might still model the pattern in terms of a polynomial response and this is the subject of Exercise 17.9.



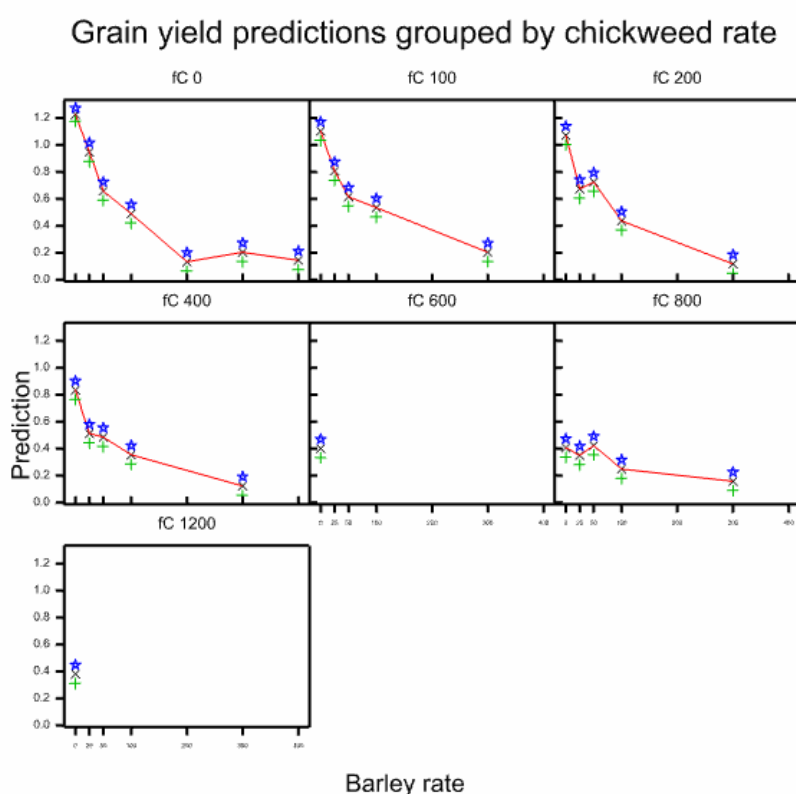
**Figure S11.2.2.** Plot of absolute residuals vs fitted values for grain variate from initial model.

**Table S.11.2.2** Sequential ANOVA tables for a crossed model for the grain yield. Br denotes factor Brate and Cr denotes factor Crate. SS = sum of squares, MS = mean square, VR = variance ratio.

Sequence 1					Sequence 2				
Source	df	SS	MS	VR	Source	df	SS	MS	VR
+ Block	1	0.0002	0.0002	0.020	+ Block	1	0.0002	0.0002	0.020
+ Brate	6	3.7462	0.6244	67.115	+ Crate	6	0.9399	0.1566	16.839
+ Crate	6	2.1486	0.3581	38.494	+ Brate	6	4.9549	0.8258	88.770
+ Br.Cr	16	0.5607	0.0350	3.767	+ Cr.Br	16	0.5607	0.0350	3.767
Residual	30	0.2791	0.0093		Residual	30	0.2791	0.0093	
Total	59	6.7348			Total	59	6.7348		

**Table S.11.2.3.** Predicted mean grain yield for each combination of barley and chickweed seed rates tested in the experiment, with SE shown in parenthesis.

		Seed rate (density) of chickweed						
		0	100	200	400	600	800	1200
Seed rate (density) of barley	0	1.225 (0.0482)	1.102 (0.0682)	1.071 (0.0682)	0.833 (0.0682)	0.401 (0.0682)	0.405 (0.0682)	0.379 (0.0682)
	25	0.947 (0.0682)	0.806 (0.0682)	0.673 (0.0682)	0.512 (0.0682)	-	0.350 (0.0682)	-
	50	0.658 (0.0682)	0.615 (0.0682)	0.725 (0.0682)	0.485 (0.0682)	-	0.423 (0.0682)	-
	100	0.490 (0.0682)	0.534 (0.0682)	0.436 (0.0682)	0.354 (0.0682)	-	0.248 (0.0682)	-
	200	0.133 (0.0682)	-	-	-	-	-	-
	300	0.204 (0.0682)	0.204 (0.0682)	0.117 (0.0682)	0.122 (0.0682)	-	0.157 (0.0682)	-
	400	0.144 (0.0682)	-	-	-	-	-	-



**Figure S.11.2.3.** Predicted mean grain yield (red line with black cross) for each combination of barley and chickweed seed rates tested in the experiment, with limits of  $\pm$ SE (prediction+SE = blue star, prediction-SE = green cross).