

## Residual Analysis for two-way ANOVA

The twoway model with  $K$  replicates, including interaction, is  $Y_{ijk} = \mu_{ij} + \epsilon_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \epsilon_{ijk}$  with  $i = 1, \dots, I$ ,  $j = 1, \dots, J$ ,  $k = 1, \dots, K$ .

In carrying out the  $F$  tests for interaction, and for the main effects of factors A and B, we have assumed that  $\epsilon_{ijk}$  are as sample from  $N(0, \sigma^2)$ .

Among other things, this means that:

- the distribution of the errors (and in particular, the variance  $\sigma^2$ ) does not differ depending on the level of factor A, the level of factor B, or the mean of the response ( $\mu_{ij} = \mu + \alpha_i + \beta_j + \gamma_{ij}$ )
- the errors are a sample from a normal distribution

If these assumptions hold, then the p-values for the tests of interaction and main effects are valid. If the assumptions do not hold, then the p-values may substantially over- or under-estimate the evidence against the null hypotheses.

**Residuals** are usually defined as the difference “data-prediction”.

In the twoway anova model with interaction, the predicted value of  $Y_{ijk}$  is  $\hat{\mu}_{ij}$ , and so the residuals are

$$r_{ijk} = Y_{ijk} - \hat{\mu}_{ij} = Y_{ijk} - \bar{Y}_{ij}.$$

(Another way of writing the residual for the twoway model with interaction is  $r_{ijk} = Y_{ijk} - \hat{\mu} - \hat{\alpha}_i - \hat{\beta}_j - \hat{\gamma}_{ij}$ .)

If the sample size is moderately large, the residuals should be approximately equal to the errors  $\epsilon_{ijk}$ , and so we use the residuals (which are known to us) in place of the errors  $\epsilon_{ijk}$  (which are unknown) to assess the plausibility of the model assumptions.

The following plots are often useful in this regard:

1. A QQ plot of the residuals is used to assess the assumption of normality of errors
2. To assess the assumption that the distribution of the errors (in particular the variance of the distribution) does not depend on the levels of either factor A or factor B, the residuals should be plotted against:
  - (a) the levels of factor A
  - (b) the levels of factor B
  - (c) the fitted values  $\bar{Y}_{ij}$ .

Example: A two factor experiment was carried out in which the survival times (in units of 10 hours) were measured for groups of four animals (replicates) randomly allocated to three poisons and four treatments.

The data were as follows:

Poison	Treatment	Data			
I	A	0.31	0.45	0.46	0.43
II	A	0.36	0.29	0.40	0.23
III	A	0.22	0.21	0.18	0.23
I	B	0.82	1.10	0.88	0.72
II	B	0.92	0.61	0.49	1.24
III	B	0.30	0.37	0.38	0.29
I	C	0.43	0.45	0.63	0.76
II	C	0.44	0.35	0.31	0.40
III	C	0.23	0.25	0.24	0.22
I	D	0.45	0.71	0.66	0.62
II	D	0.56	1.02	0.71	0.38
III	D	0.30	0.36	0.31	0.33

The data were entered into minitab, and a twoway anova was carried out, as follows:

```
MTB > print c1
```

```
0.31    0.45    0.46    0.43
0.36    0.29    0.40    0.23
0.22    0.21    0.18    0.23
0.82    1.10    0.88    0.72
0.92    0.61    0.49    1.24
0.30    0.37    0.38    0.29
0.43    0.45    0.63    0.76
0.44    0.35    0.31    0.40
0.23    0.25    0.24    0.22
0.45    0.71    0.66    0.62
0.56    1.02    0.71    0.38
0.30    0.36    0.31    0.33
```

```
MTB > set c2
DATA> 4(1 1 1 1 2 2 2 2 3 3 3 3)
```

```
DATA> set c3
DATA> 12(1) 12(2) 12(3) 12(4)
```

```
MTB > twoway c1 c2 c3;
SUBC> residuals c4;
SUBC> fits c5.
```

Two-way ANOVA: C1 versus C2, C3

Source	DF	SS	MS	F	P
C2	2	1.03301	0.516506	23.22	0.000
C3	3	0.92121	0.307069	13.81	0.000
Interaction	6	0.25014	0.041690	1.87	0.112
Error	36	0.80073	0.022242		
Total	47	3.00508			

S = 0.1491    R-Sq = 73.35%    R-Sq(adj) = 65.21%

```
MTB > nscores c4 c6
```

The normal scores and residual plots are as follows:

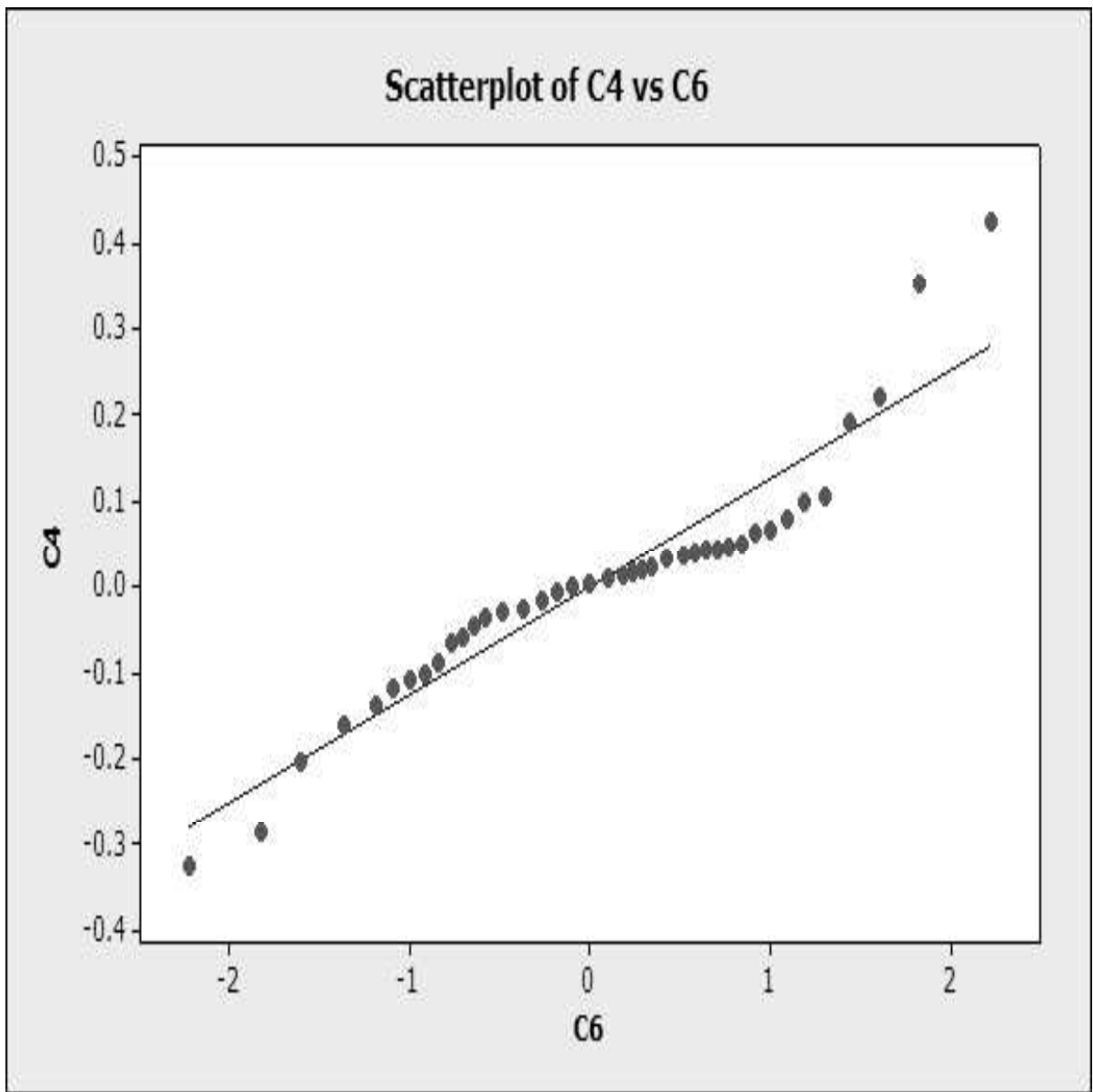


Figure 1: Normal scores plot of residuals

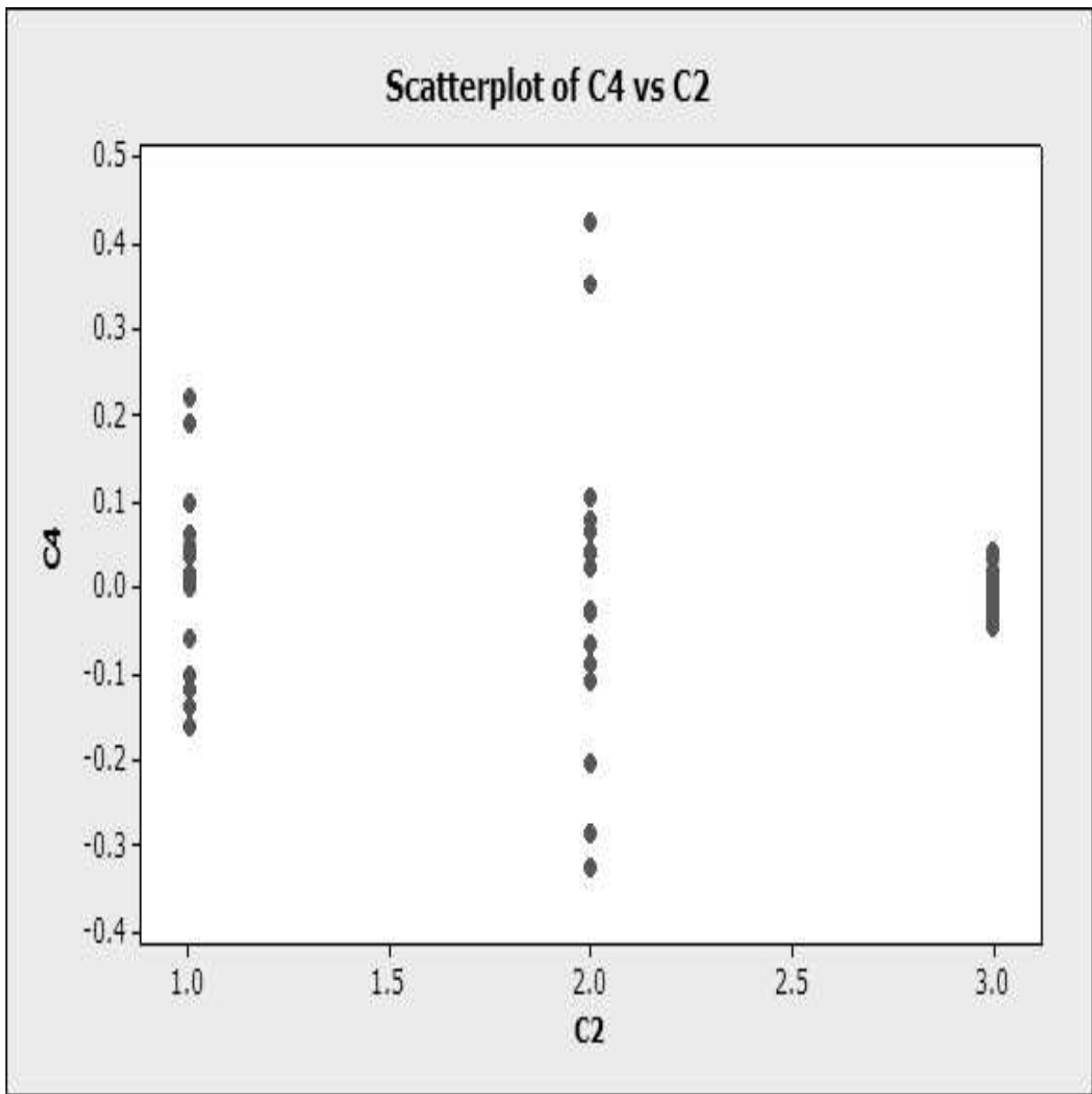


Figure 2: Plot of residuals vs type of poison

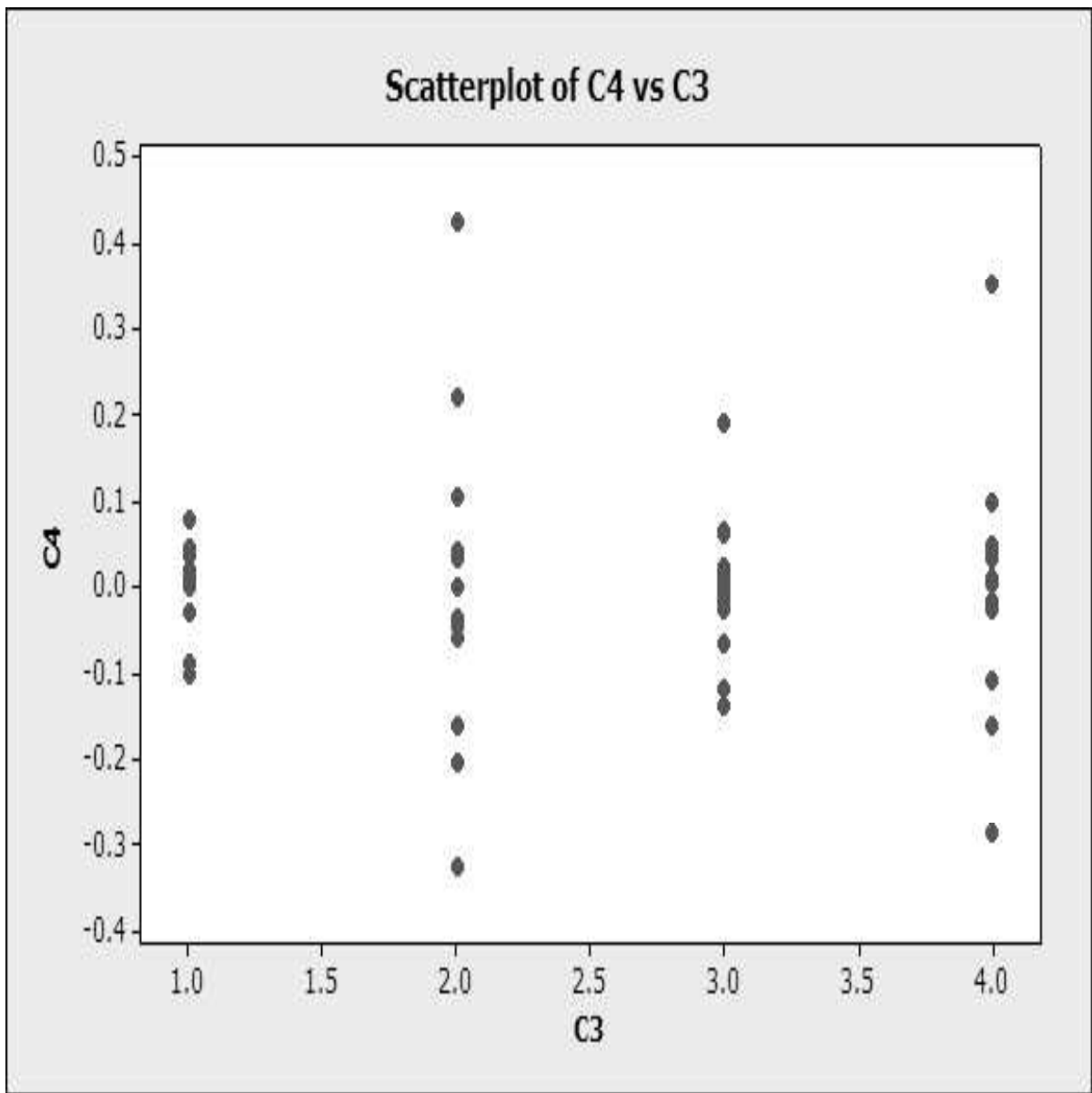


Figure 3: Plot of residuals vs treatment

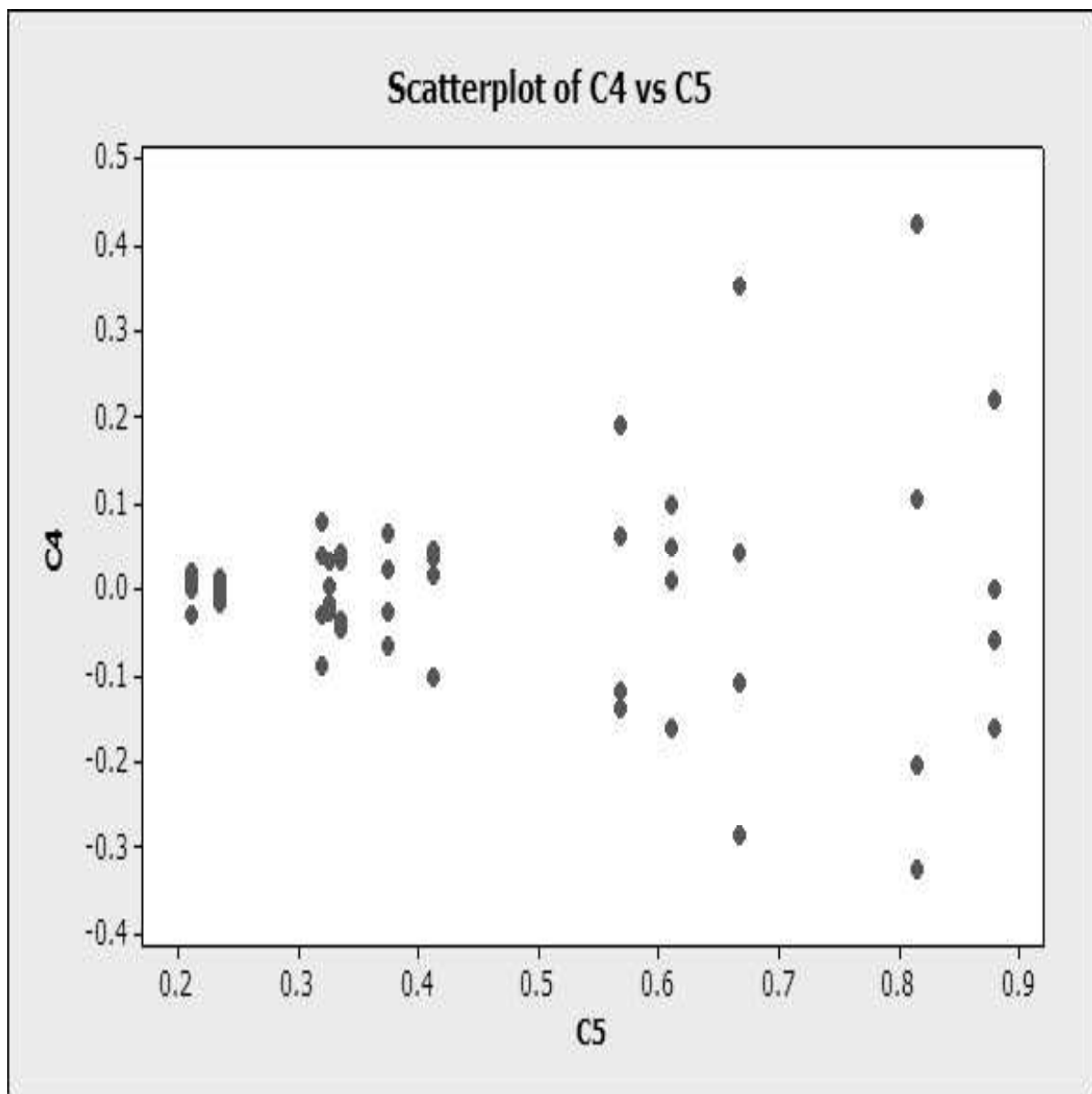


Figure 4: Plot of residuals vs fitted values

If the QQ plot shows evidence of non-normality, or if the distribution of the residuals appears to depend on the levels of one or both factors, then the inferences (eg p-values) concerning the model parameters may be invalid.

In this case, the QQ plot provides some suggestion of non-normality. The plots of residual vs factor level suggest that the variance of the residuals is not constant across



levels of either factor. A definite pattern can be seen in the plot of residuals vs predicted values, in which variance of the residual is increasing as the fitted value increases. This suggests that the variance of  $Y$  is increasing with the mean of  $Y$ . Consequently, our conclusions regarding the significance of effects and interactions may be in error due to incorrect assumptions.

In such cases, one approach which is often taken is to try to find a **transformation of the dependent variable** to a form for which the model assumptions are better satisfied. Transformations which are sometimes tried are to replace  $Y$  by  $\sqrt{Y}$ ,  $\log(Y)$ , or  $1/Y$ .

There are some results from probability and statistical theory which provide techniques to search for so-called **variance stabilizing transformations**. These ideas are studied in some higher level statistics courses. After careful examination of the pattern of residuals, we are led to consider the reciprocal transformation,  $Z_{ijk} = 1/Y_{ijk}$ . (In this case, where  $Y$  are measurements of time, then  $Z = 1/Y$  are described as **rates**, and have units of 1/time.)

A twoway model was fit for  $Z_{ijk}$ , leading to the following output:

```
MTB > let c7=1/c1
MTB > twoway c7 c2 c3;
SUBC> residuals c8;
SUBC> fits c9.
```

Two-way ANOVA: C7 versus C2, C3

Source	DF	SS	MS	F	P
C2	2	34.8771	17.4386	72.63	0.000
C3	3	20.4143	6.8048	28.34	0.000
Interaction	6	1.5708	0.2618	1.09	0.387
Error	36	8.6431	0.2401		
Total	47	65.5053			

S = 0.4900    R-Sq = 86.81%    R-Sq(adj) = 82.77%

```
MTB > nscores c8 c10
```

The normal scores and residual plots for the transformed data are as follows:

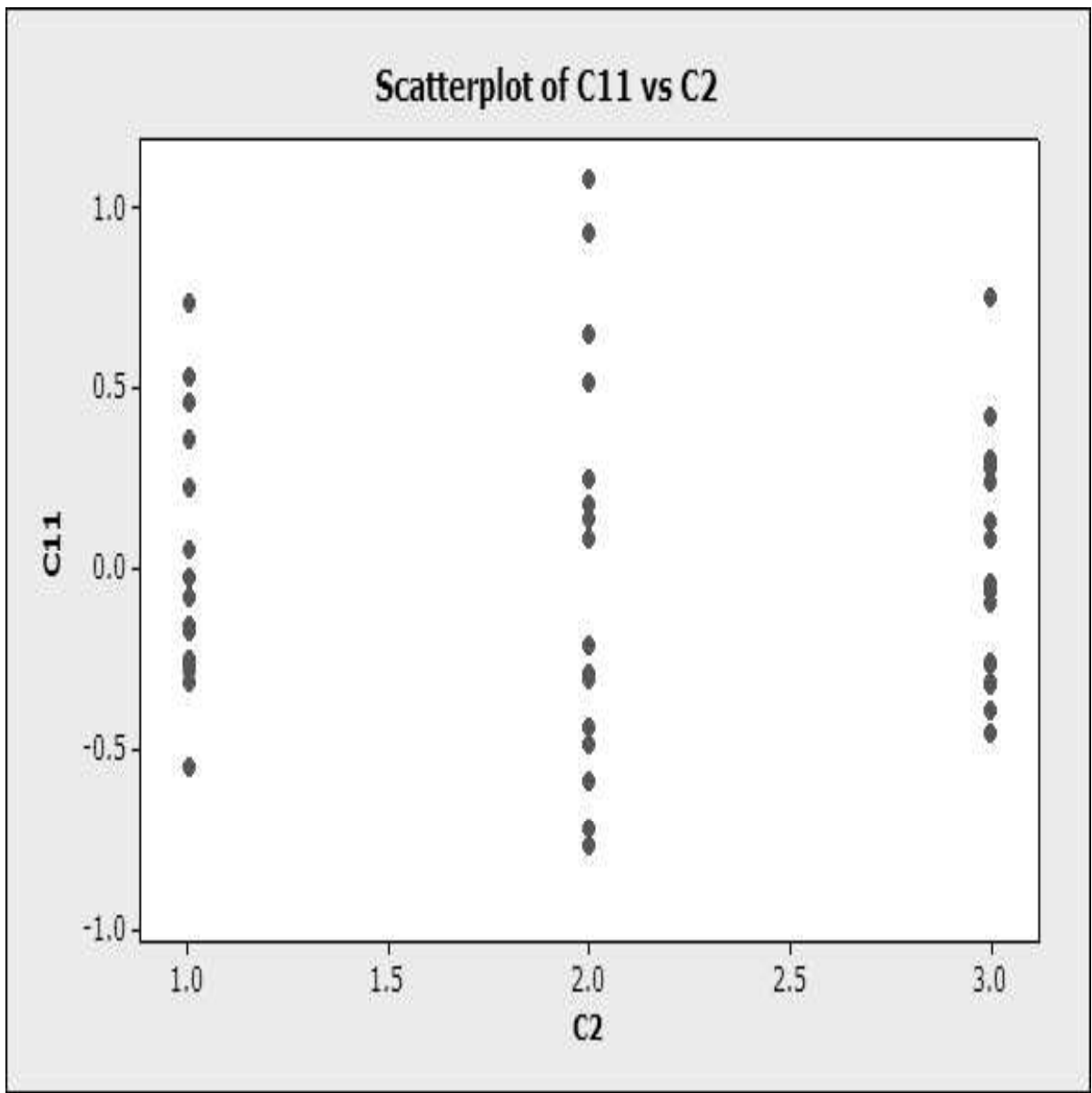


Figure 5: Plot of residuals vs poison - transformed data

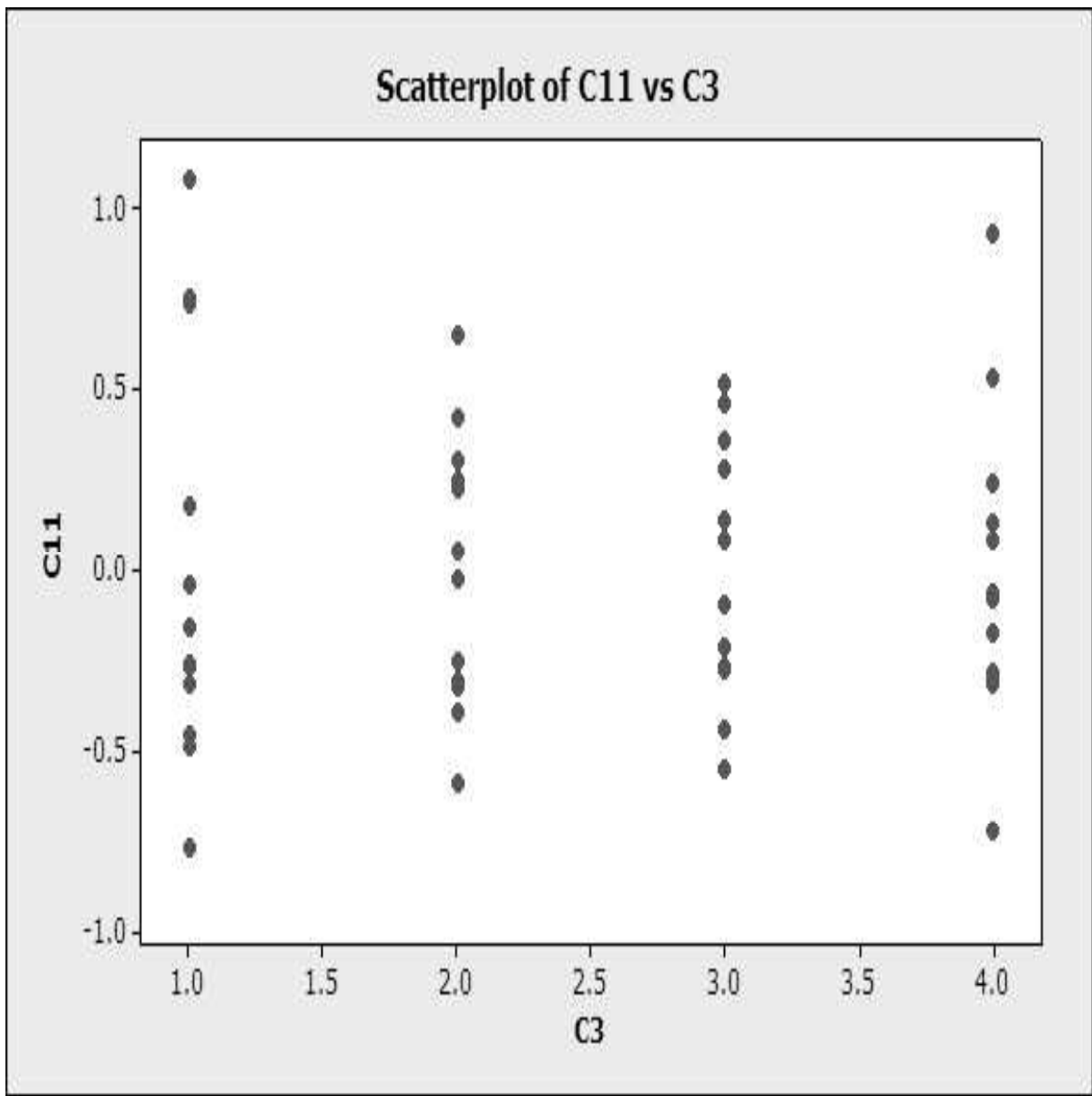


Figure 6: Plot of residuals vs treatment - transformed data

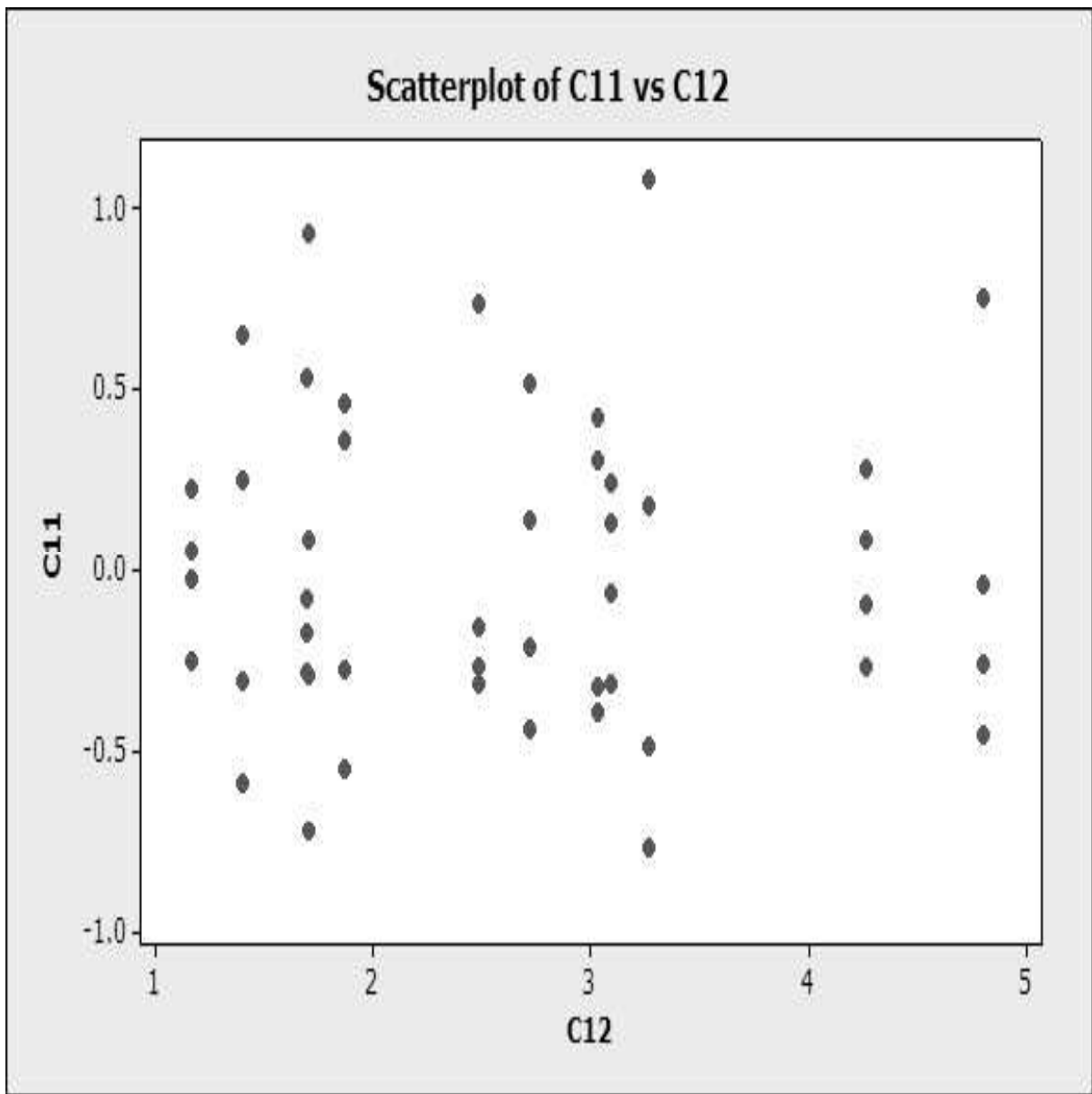


Figure 7: Plot of residuals vs fitted values - transformed data

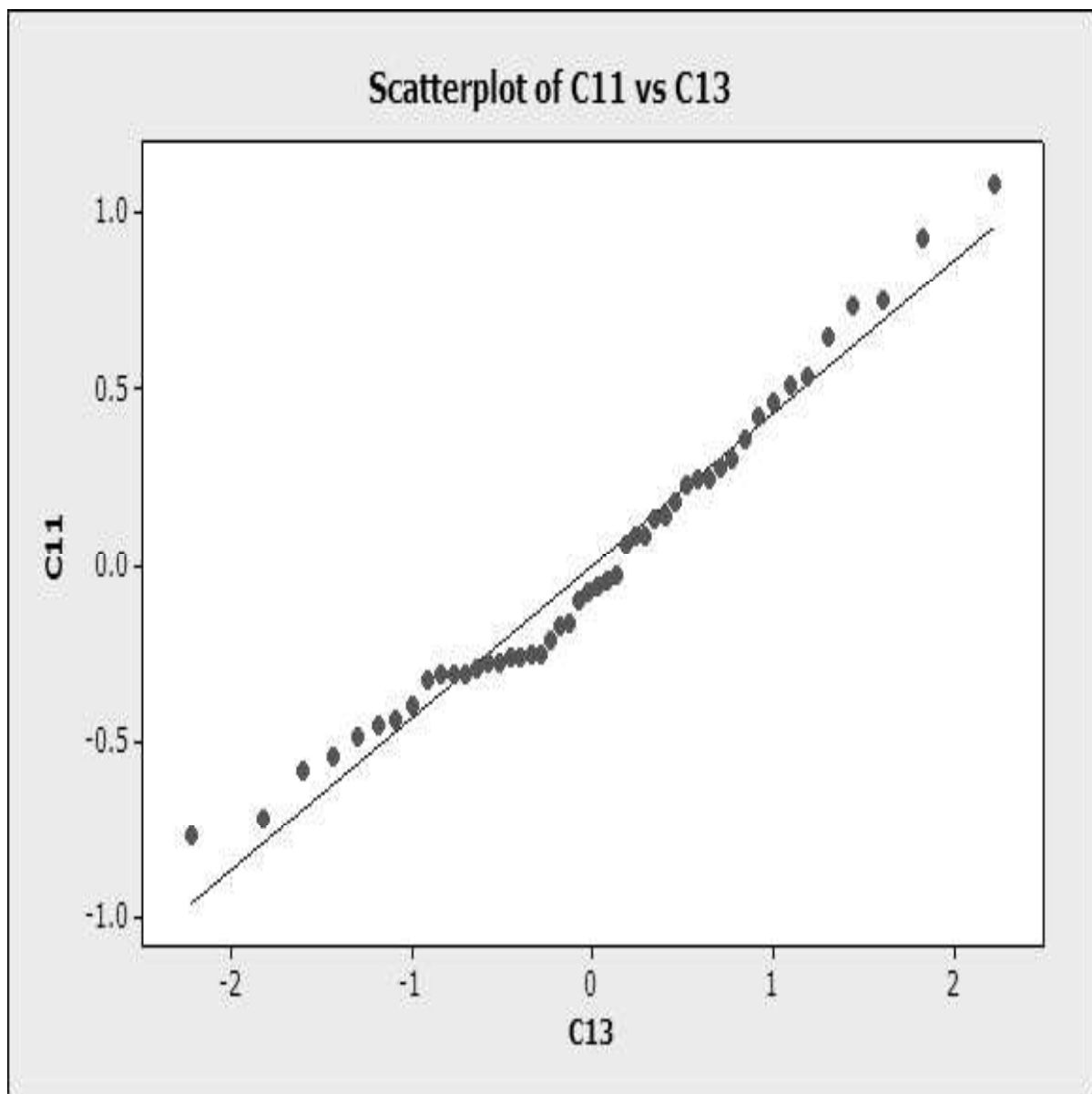


Figure 8: Normal scores plot of residuals - transformed data

These residual plots suggest few departures from the model assumptions, and so we can be confident about the validity of our conclusions for the transformed data.

Reference: Box and Cox (1964) An analysis of transformation. *J.Roy.Stat.Soc.B*, **26**, 211.

The data were part of a larger investigation to combat the effects of toxic agents.