

Chapter 2

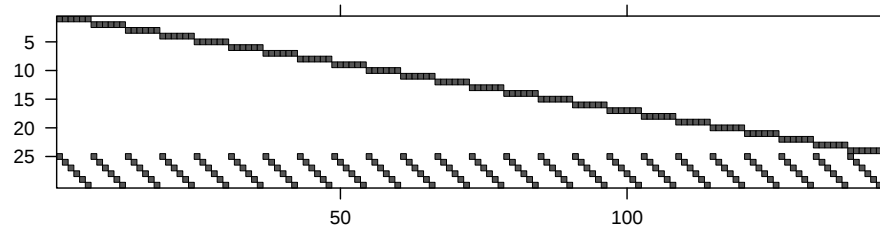


Fig. 2.3 Image of the transpose of the random-effects model matrix, Z , for model fm2. The non-zero elements, which are all unity, are shown as darkened squares. The zero elements are blank.

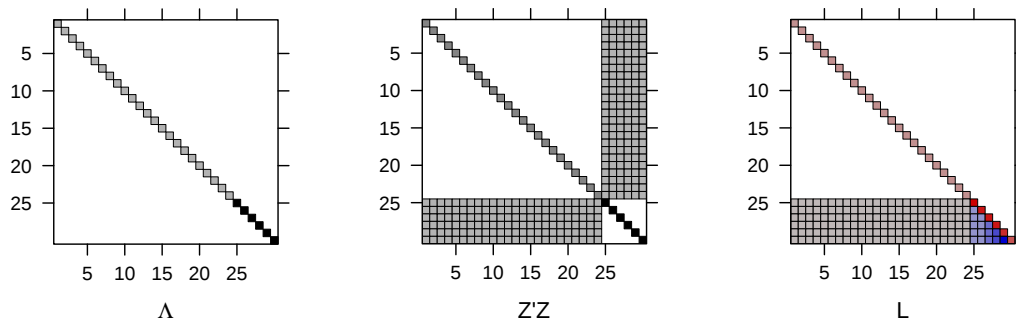


Fig. 2.4 Images of the relative covariance factor, Λ , the cross-product of the random-effects model matrix, $Z'Z$, and the matrix L .

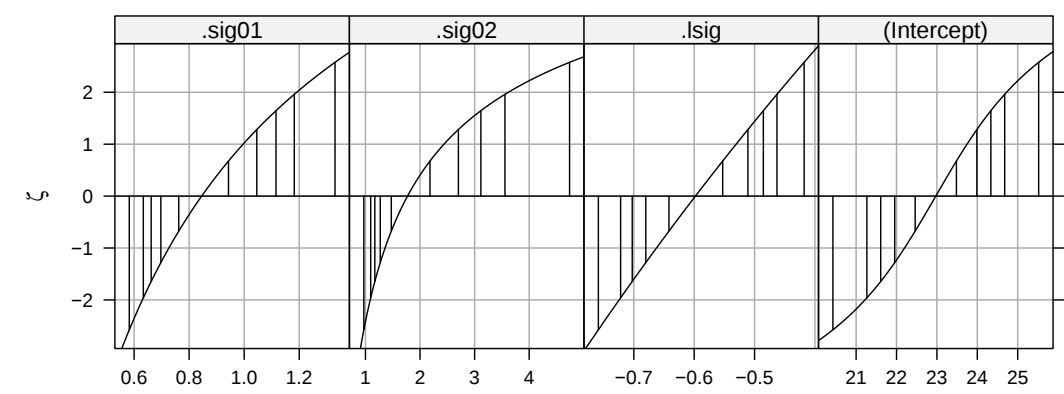


Fig. 2.5 Profile zeta plot of the parameters in model fm2.

of σ

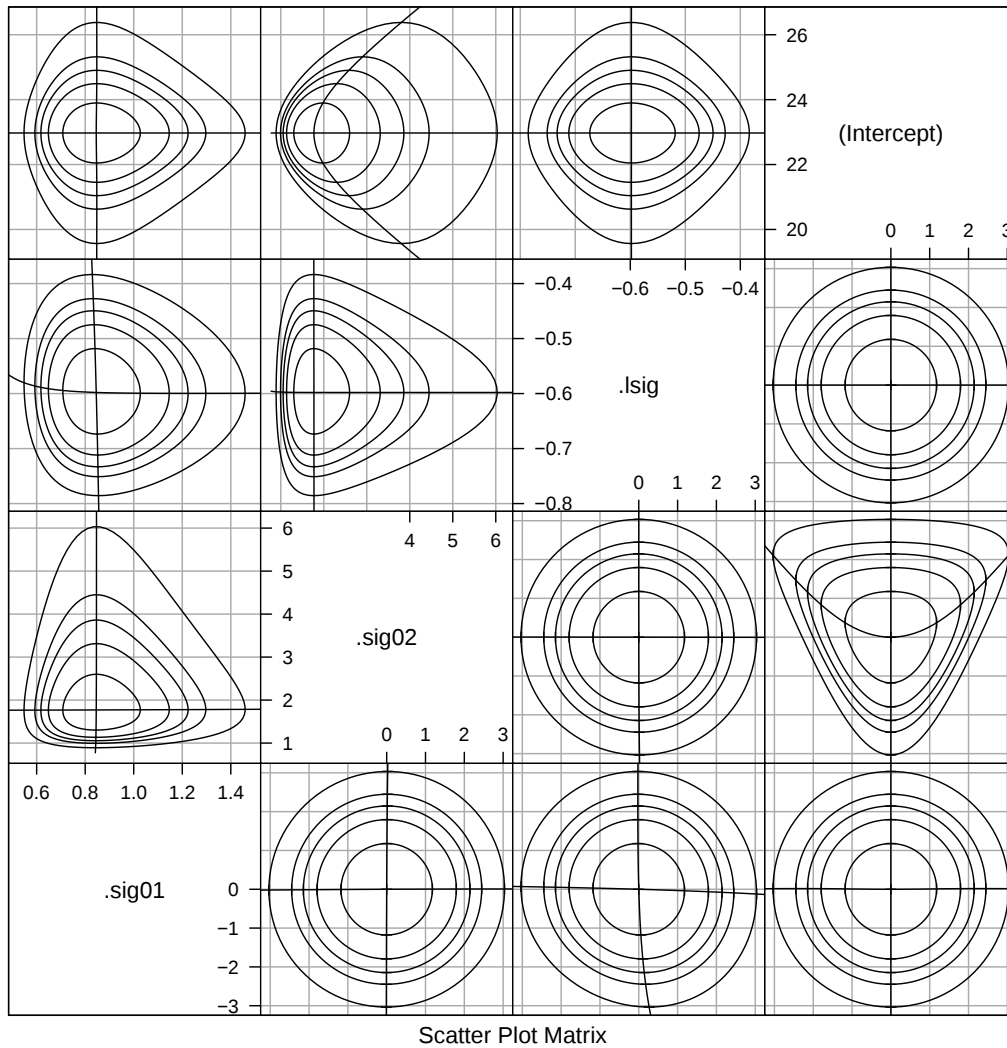
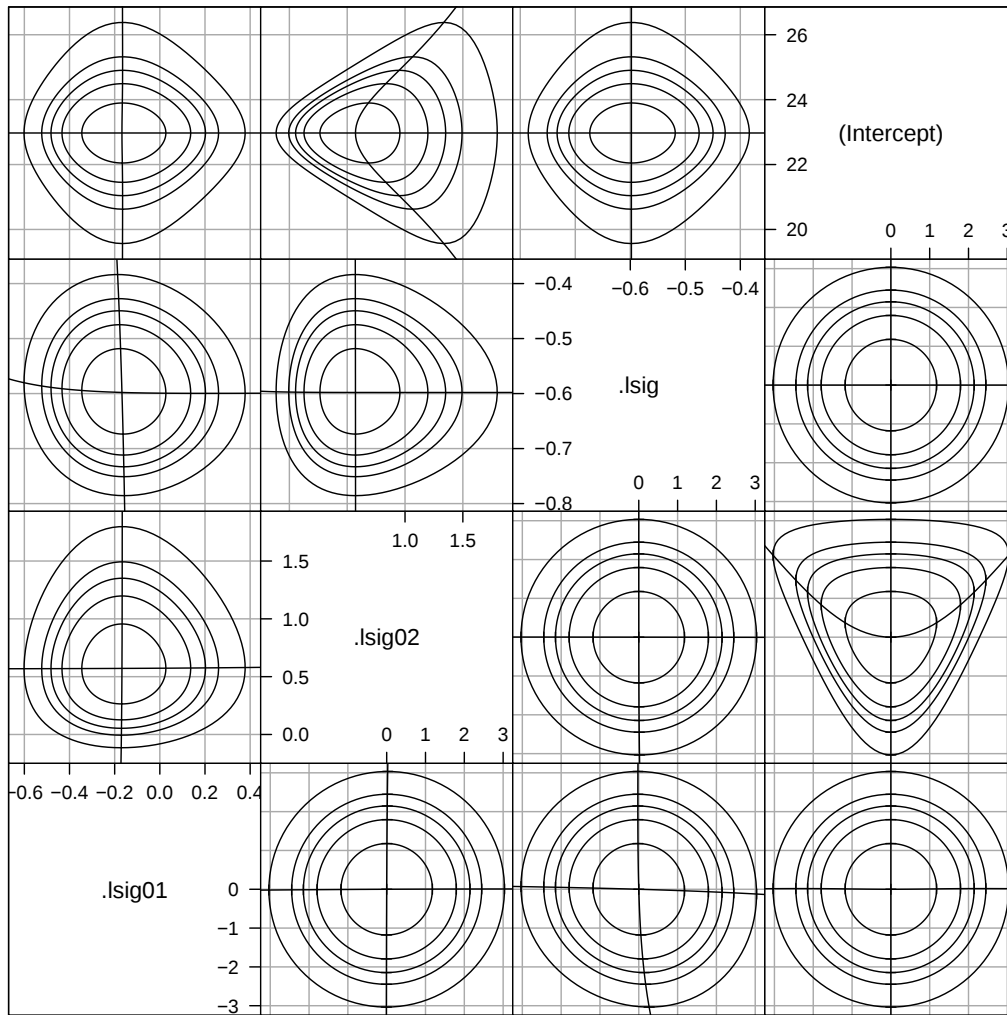


Fig. 2.6 Profile pairs plot for the parameters in model fm2 fit to the Penicillin data.

(panels below the diagonal) the profile traces are nearly straight and orthogonal with the exception of the trace of



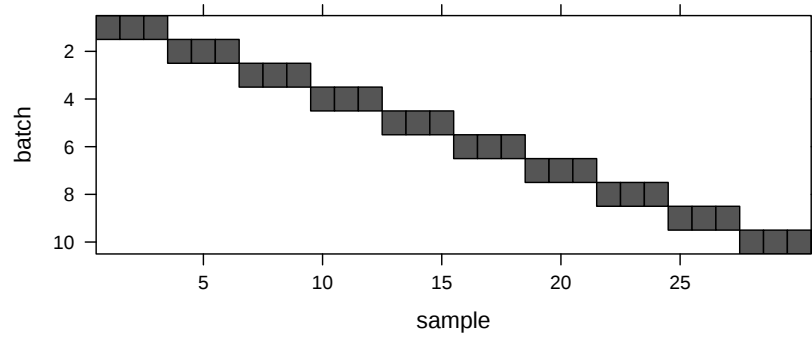
Scatter Plot Matrix

2.2 A Model With Nested Random Effects

In this section we again consider a simple example, this time fitting a model with *nested* grouping factors for the random effects.

2.2.1 *The Pastes Data*

The third example from Davies and Goldsmith [1972, Table 6.5, p. 138] is described as coming from



2.2.1.1 Nested Factors

Because each level of `sample` occurs with one and only one level of `batch` we say that `sample` is *nested within* `batch`. Some presentations of mixed-effects models, especially those related to *multilevel modeling* [Rasbash et al., 2000] or

we get the impression that the

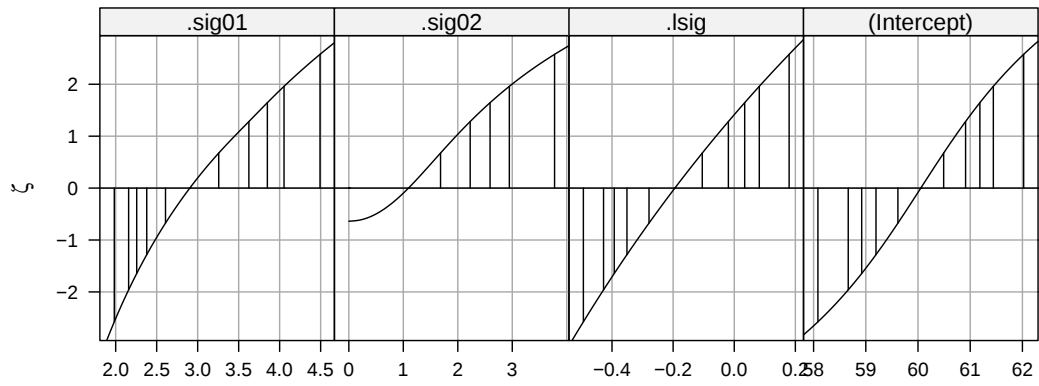


Fig. 2.12 Profile zeta plots for the parameters in model fm3.

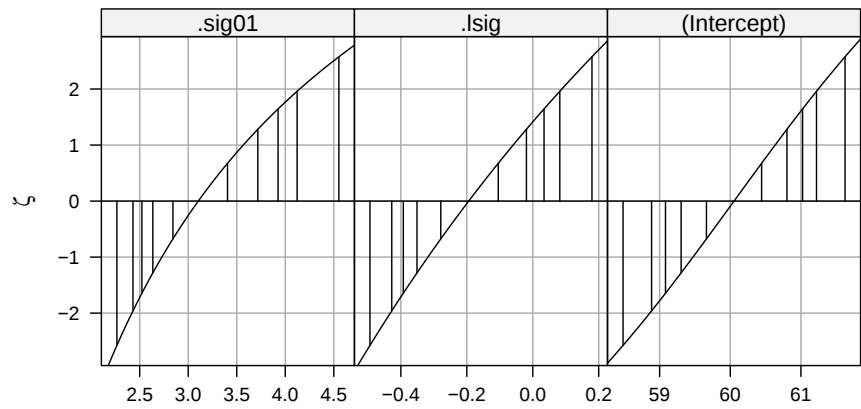


Fig. 2.13 Profile zeta plots for the parameters in model fm3a.

2.2.5 Assessing the Reduced Model, fm3a

The profile zeta plots for the remaining parameters in model fm3a

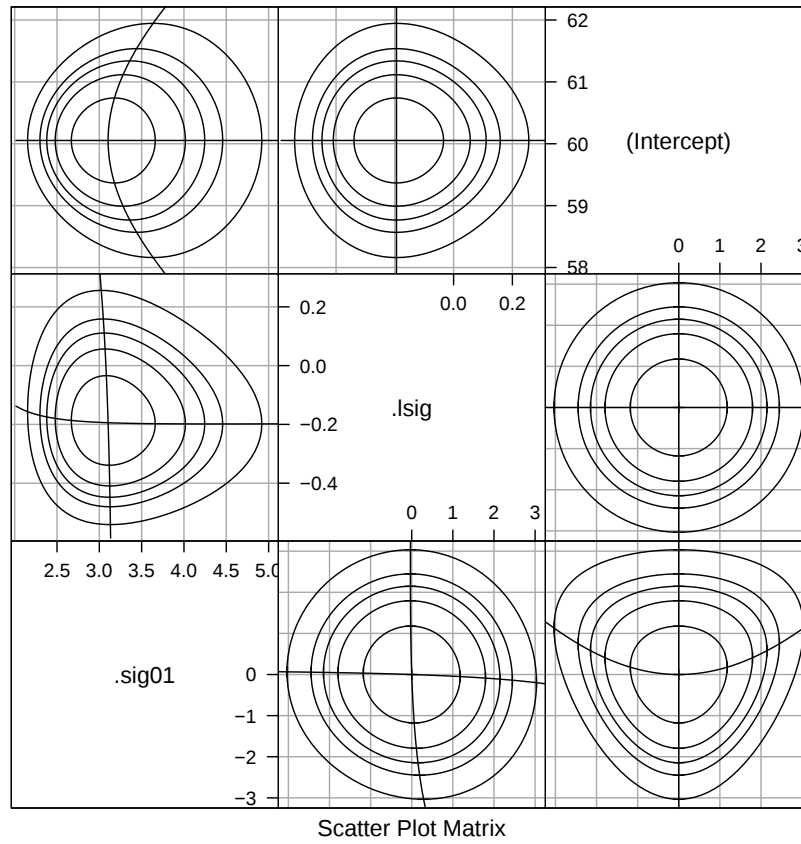


Fig. 2.14 Profile pairs plot for the parameters in model

2.3.1 *The InstEval Data*

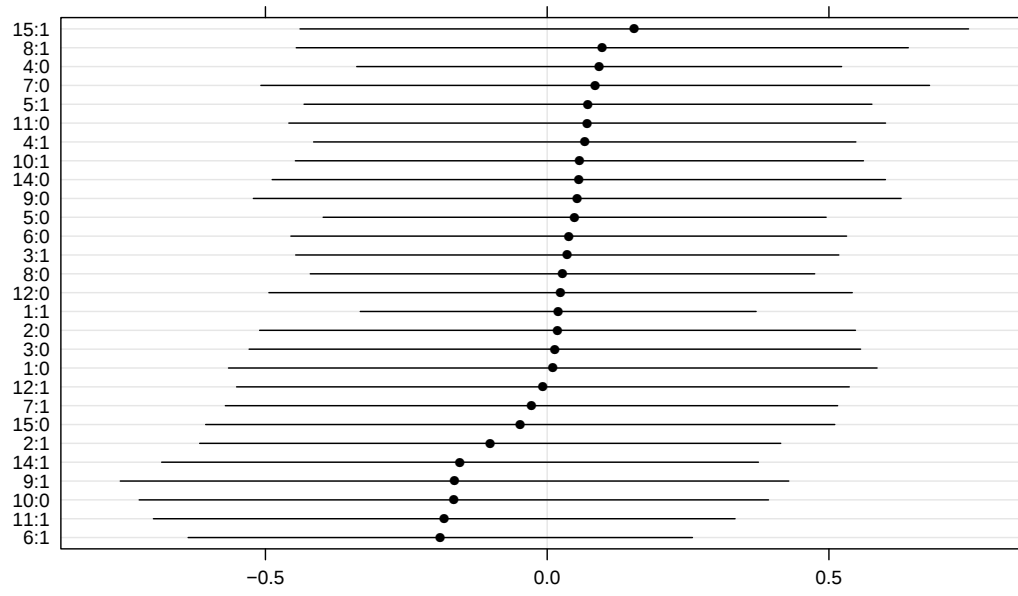


Fig. 2.15

Because simple, scalar random-effects terms can differ only in the descrip-

for the standard deviations of random effects (σ_1 , σ_2 , etc.) are symmetric on a logarithmic scale except for those that could be zero.

2.5. Profile the fitted model and construct 95% profile-based confidence intervals on the parameters. (Note that you will get the same profile object whether you start with the REML fit or the ML fit. There is a slight advan-

2.15. Refit the model without random effects for `Block`. Perform a likelihood ratio test of $H_0 : \sigma_3 = 0$ versus $H_a : \sigma_3 > 0$. Would you reject H_0 in favor of H_a or fail to reject H_0 ? Would you reach the same conclusion if you adjusted the p-value for the test by halving it, to take into account the fact that 0 is on the boundary of the parameter region?

2.16. Profile the reduced model (i.e. the one without random effects for `Block`)