

# Chapter 9

## Conclusions

### 9.1 Introduction

In Chapter 1 I introduced the chestnut leaf blight example and presented some preliminary analyses. None of these were correct since they did not accommodate the correlation introduced by the donor and recipient clones. A feature of the leaf blight example is the presence of crossed random effects. This eliminates the ability to use simpler models and/or longitudinal data approaches like GEEs. I now return to the example and illustrate the Monte Carlo ML approaches of Chapter 7.

### 9.2 Chestnut leaf blight revisited

I focus on selected portions of the model; those interested in the full analysis can consult Cortesi et al. (2001). Recall that the model, given in (5.1) and (5.2), was for the binary outcome of transmission of the virus between two (fungal) individuals and that repeated measurement on clones as either donors or recipients of the virus might introduce correlation. There is no reason to expect that the ability of a particular clone to transmit the virus (donor effect) is the same as its susceptibility to the virus (recipient effect). However, it is possible that the donor effect of a particular clone is correlated with the recipient effect. Accordingly, we fit a bivariate normal random effect distribution for the joint donor and recipient random effects associated with a clone.

The model was fit using a bivariate version of the MCNR algorithm described in Section 7.3. Standard errors were estimated by a similar simulation scheme applied to the information matrix and the values of the log likelihood were estimated by simulation using the method of Geyer and Thompson (1992). The estimate of the covariance between the donor and recipient random effects was almost zero and contributed negligibly to the likelihood. Also, the fourth putatively contributing gene had no effects (main, asymmetry or even third order effects) and hence that gene and the covariance were dropped and the model was refit with independent donor and recipient random effects. For that model the estimate of the donor variance component was  $\sigma_d^2 = 0.28$  and the recipient variance component was  $\sigma_r^2 = 1.24$  with standard errors (respectively) of 0.09 and 0.34.