

Chapter 6

Early research

6.1 Introduction

Early approaches to the accommodation of correlation in non-normal data tended to focus on techniques that were easier to compute, which is not surprising given the computational hurdles identified in previous chapters. Their main drawback was that they tended to be ad hoc and could not easily accommodate more complicated situations.

6.2 Beta-binomial model

One of the earliest models for binary data was the beta-binomial model, which hypothesizes a mixture distribution directly on the probability scale. Since the random “factor” does not enter through a linear predictor, strictly speaking it is not a generalized linear mixed model. As motivation, consider a hypothetical teratology experiment in which lead is administered in the drinking water of pregnant rats, perhaps at different doses and including a control group with no lead. The response we record on all members of a litter is the absence of a birth defect in animal k from mom (and litter) j in treatment group i . Since the response is binary, the outcome must have a marginal Bernoulli distribution. We might hypothesize the following model:

$$(6.1) \quad \begin{aligned} Y_{ijk} &= 1 \text{ if animal } k \text{ from mom } j \text{ in treatment } i \\ &\quad \text{has a birth defect and } 0 \text{ otherwise,} \\ Y_{ijk} | p_{ij} &\sim \text{indep. Bernoulli}(p_{ij}), \\ p_{ij} &\sim \text{indep. Beta}(\alpha_i, \beta_i). \end{aligned}$$

Under this model, Y_{ijk} has a marginal Bernoulli distribution with mean $\mu_i = \alpha_i / (\alpha_i + \beta_i)$. Data that share a value of p_{ij} are modeled as correlated, but observations from different litters are regarded as independent. Temporarily dropping the subscripts i and j , and using $B(\cdot, \cdot)$ to represent the beta function and $Y = \sum_k Y_k$,