6. A HIERARCHICAL MODEL

Applications of hierarchical models of the kind introduced by Lindley and Smith (1972) abound in fields as diverse as educational testing (Rubin 1981), cancer studies (DuMouchel and Harris 1983), and biological growth curves (Strenio, Weisberg, and Bryk 1983). However, both Bayesian and empirical Bayesian models are typically forced to invoke a number of approximations, whose consequences are often unclear under the multiparameter likelihoods induced by the modelling. See, for example, Morris (1983), Racine-Poon (1985), and Racine-Poon and Smith (1990) for details of some approaches to to implementing hierarchical model analysis. By contrast, a full implementation of the Bayesian approach is easily achieved using the Gibbs sampler, at least for the widely used normal hierarchical model structure.

For illustration, we focus on the following population grown problem. In a study conducted by the CIBA-GEIGY company, the weights of 30 young rats in a control group were meassured weekly for five weeks. The data are given in Table 3, with weight measurements available for all five weeks. Later we discuss the substantive problem of comparison with data from a treatment group. Initially, however, we shall focus attention on the control group in order to illustrate the Gibbs sampling methodology.

| Table 3. Rat Popu | lation Growth | Data: C | Control | Group |
|-------------------|---------------|---------|---------|-------|
|-------------------|---------------|---------|---------|-------|

| Rat Week | 1 | 2 | 3 | 4 | 5 | Rat Week | 1 | 2 | 3 | 4 | 5 |
|----------|-----|-----|-----|-----|-----|----------|-----|-----|-----|-----|-----|
| 1 | 151 | 199 | 246 | 283 | 320 | 16 | 160 | 207 | 248 | 288 | 324 |
| 2 | 145 | 199 | 249 | 293 | 354 | 17 | 142 | 187 | 234 | 280 | 316 |
| 3 | 147 | 214 | 263 | 312 | 328 | 18 | 156 | 203 | 243 | 283 | 317 |
| 4 | 155 | 200 | 237 | 272 | 297 | 19 | 157 | 212 | 259 | 307 | 336 |
| 5 | 135 | 188 | 230 | 280 | 323 | 20 | 152 | 203 | 246 | 286 | 321 |
| 6 | 159 | 210 | 252 | 298 | 331 | 21 | 154 | 205 | 253 | 298 | 334 |
| 7 | 141 | 189 | 231 | 275 | 305 | 22 | 139 | 190 | 225 | 267 | 302 |
| 8 | 159 | 201 | 248 | 297 | 338 | 23 | 146 | 191 | 229 | 272 | 302 |
| 9 | 177 | 236 | 285 | 340 | 376 | 24 | 157 | 211 | 250 | 285 | 323 |
| 10 | 134 | 182 | 220 | 260 | 296 | 25 | 132 | 185 | 237 | 286 | 331 |
| 11 | 160 | 208 | 261 | 313 | 352 | 26 | 160 | 207 | 257 | 303 | 345 |
| 12 | 143 | 188 | 220 | 273 | 314 | 27 | 169 | 216 | 261 | 295 | 333 |
| 13 | 154 | 200 | 244 | 289 | 325 | 28 | 157 | 205 | 248 | 289 | 316 |
| 14 | 171 | 221 | 270 | 326 | 358 | 29 | 137 | 180 | 219 | 258 | 291 |
| 15 | 163 | 216 | 242 | 281 | 312 | 30 | 153 | 200 | 244 | 286 | 324 |
| | | | | | | | | | | | |

NOTE: $x_{i1} = 8$, $x_{i2} = 15$, $x_{i3} = 22$, $x_{i4} = 29$, $x_{i5} = 36$ days; i = 1, ..., 30.

For the time period considered, it is reasonable to assume individual straightline growth curves, although non-linear curves can be handled as well. We also assume homoscedastic normal measurement errors (nonhomogeneous varianes can be accommodated as in the previous section), so that

 $Y_{ij} \sim N(\alpha_i + \beta_i x_{ij}, \sigma_c^2), \ i = 1, ..., k; \ j = 1, ..., n_i,$

provides the full measurement model (with k = 30, $n_i = 5$, and x_{ij} denoting the age in days of the *i*th rate when measurement *j* was taken). The population structure is modeled as

$$\left(\begin{array}{c} \alpha_i\\ \beta_i \end{array}\right) \sim N\left\{ \left(\begin{array}{c} \alpha_c\\ \beta_c \end{array}\right), \Sigma_c \right\}, \qquad i=1,...,k,$$

assuming independence throughout. A full Bayesian analysis now requires the specification of a prior for σ_c^2 , $\mu_c = (\alpha_c, \beta_c)^T$, and Σ_c . Typical inferences of interest in such studies include marginal posteriors for the population parameters (α_c, β_c) and predictive intervals for individual future growth given the first-week measurement. We shall see that these are easily obtained using the Gibbs sampler.

For the prior specification, we assume independence, as is customary, taking

$$[\mu_c, \Sigma_c^{-1}, \sigma_c^2] = [\mu_c] [\Sigma_c^{-1}] [\sigma_c^2]$$

to have a normal-Wishart-inverse-gamma form:

$$\begin{split} [\mu_c] &= N(\eta, C), \\ [\Sigma_c^{-1}] &= W((\rho R)^{-1}, \rho), \\ [\sigma_c^2] &= IG\left(\frac{\nu_0}{2}, \frac{\nu_0 \tau_0^2}{2}\right) \end{split}$$

.

Rewriting the measurement model for the *i*th individual as $Y_i \sim N(X_i\theta, \sigma_c^2 I_{n_i})$ where $\theta_i = (\alpha_i, \beta_i)^T$ and X_i denotes the appropriate design matrix and defining

$$Y = (Y_1, ..., Y_k)^T, \quad \overline{\theta} = k^{-1} \sum_{i=1}^k \theta_i, \quad n = \sum_{i=1}^k n_i,$$
$$D_i = \sigma_c^{-1} X_i^T X_i + \Sigma_c^{-1},$$
$$V = (k \Sigma_c^{-1} + C^{-1})^{-1},$$

the Gibbs sampler for $\theta = (\theta_1, ..., \theta_k)$, Σ_c , and σ_c^2 (a total of 66 parameters in the above example) is straightforwardly seen to be specified by the conditional distributions

$$\begin{bmatrix} \theta_i \, | \, Y, \mu_c, \Sigma_c^{-1}, \sigma_c^2 \end{bmatrix} = N \{ D_i (\sigma_c^{-2} X_i^T Y_i + \Sigma_c^{-1} \mu_c), \ D_i \}, \quad i = 1, ..., k \\ \begin{bmatrix} \mu_c \, | \, Y, \{\theta\}, \Sigma_c^{-1}, \sigma_c^2 \end{bmatrix} = N \{ V(k \Sigma_c^{-1} \overline{\theta} + C^{-1} \eta), \ V \}, \\ \begin{bmatrix} \Sigma_c^{-1} \, | \, Y, \{\theta\}, \mu_c, \sigma_c^2 \end{bmatrix} = W \left\{ \left[\sum_i (\theta_i - \mu_c) (\theta_i - \mu_c)^T + \rho R \right]^{-1}, \ k + \rho \right\}, \\ \begin{bmatrix} \sigma_c^2 \, | \, Y, \{\theta\}, \mu_c, \Sigma_c^{-1} \end{bmatrix} = IG \left(\frac{n + \nu_0}{2}, \ \frac{1}{2} \left[\sum_i (Y_i - X_i \theta_i)^T (Y_i - X_i \theta_i) + \nu_0 \tau_0^2 \right] \right) (5)$$

For the analysis of the rat growth data given above, the hyperparameter specification was defined by

$$C^{-1} = 0, \quad \nu_0 = 0, \quad p = 2, \quad R = \begin{pmatrix} 100 & 0 \\ 0 & 0.1 \end{pmatrix}$$

[because $C^{-1} = 0$ the value of η disappears entirely from the full conditionals] reflecting rather vague initial information relative to that to be provided by the data. Simulation from the Wishart distribution for the 2 × 2 matrix Σ_c^{-1} is easily accomplished using the algorithm of Odell and Feiveson (1966): with $G(\cdot, \cdot)$ denoting gamma distributions, draw independently from

$$[U_1] = G\left(\frac{\nu}{2}, \frac{1}{2}\right),$$
$$[U_2] = G\left(\frac{\nu - 1}{2}, \frac{1}{2}\right),$$

and

$$[N]=N(0,1);$$

 set

$$W = \left[\begin{array}{cc} U_1 & N\sqrt{U_1} \\ N\sqrt{U_1} & U_2 + N^2 \end{array} \right];$$

then if $S^{-1} = (H^{1/2})^T (H^{1/2}),$

$$\Sigma_c^{-1} = (H^{1/2})^T W(H^{1/2}) \sim W(S^{-1}, \nu).$$

The iterative process was monitored by observing empirical Q-Q plots for successive samples from α_c , β_c , σ_c^2 , and the eigenvalues of Σ_c^{-1} . Though the α_i and β_i are of less interest, spot checking revealed satisfactory convergence, not surprising in view of (5), which suggests that convergence for the θ_i is comparable to that of μ_c . For the data set summarized in Table 3, convergence was achieved with about 35 cycles of m = 50 drawings.

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