Fall 16 – AMS276 Project 1

Due: Tuesday November 15.

The project is to reproduce part of results given in ICS Example 4.3 (page 109). We consider the kidney infection data given in Example 1.4. Please read Example 1.4 and the paper by McGilchrist and Aisbett (1991) (posted on our course website) for detailed description of the data. The data text file is separately posted.

We consider the shared frailty model;

$$h(y_{ij} \mid w_i, \boldsymbol{x}_{ij}) = h_0(y_{ij}) w_i \exp(\boldsymbol{x}_{ij}' \boldsymbol{\beta}).$$

We include two covariates ($p = 2$): age of the patient at the time of each infection and sex of the patient. We consider the following two models for $h_0(t)$;

- **Model II** Fit the Weibull baseline hazard with multiplicative gamma frailties. That is, we assume the Weibull baseline hazard function

  $$h_0(y_{ij}) = \gamma \alpha y_{ij}^{\alpha - 1},$$

  where (γ, α) are the parameters of the Weibull distribution. We use the gamma frailty model, $w_i \overset{iid}{\sim} \text{Gamma}(\kappa^{-1}, \kappa^{-1})$. Priors for $\eta = \kappa^{-1}$, $\boldsymbol{\beta}$, γ and α are specified as follows;

  $$\eta \sim \text{Gamma}(\phi_1, \phi_2), \quad \boldsymbol{\beta} \sim \text{N}_2(\bar{\boldsymbol{\beta}}, \Sigma), \quad \gamma \sim \text{Gamma}(\rho_1, \rho_2), \text{ and } \alpha \sim \text{Gamma}(a_1, a_2).$$

  (The book has a typo in line 1 below eq (4.1.13). κ should be κ^{-1}.)

  The hyperparameter values used in Example 4.3 are $\phi_1 = \phi_2 = 0.001$, $\bar{\boldsymbol{\beta}} = \mathbf{0}$, $\Sigma = \text{diag}(10^3, 2)$, $\rho_1 = \rho_2 = 0.001$, $a_1 = a_2 = 0.001$.

  (There is another typo in line 6 of paragraph 2. "…. For Models II (not III) and IV ….").

  The posterior is estimated and summarized in Tables 4.3 and 4.4. In Table 4.4, there is μ in the first column. That is γ under Model II (i.e., their posterior mean estimate of γ is 0.016).

1. Derive the full conditionals and implement the model. Check mixing of your MCMC chain and provide some evidence of showing good convergence.

   (There is a typo in full conditional derivation in 4.1.1. Please derive the full conditionals carefully.)

2. Summarize your posterior and compare to the results given in the tables. You can also check with my results that will be illustrated in class.

3. Interpret your posterior estimates.

4. Fit a comparable frequentiest model and compare the inferences.