Vouglas DanDerwerken is a forgetful researcher. While trying to fit a hierarchical model for hemoglobin levels using R, he accidentally forgot to save his most recent version of the code. His advisor wants to know the probability that a new patient will have a slope exceeding 0.5. Here is the model Voug was trying to fit. The code he has left is attached, along with the relevant data set.

For patient *i*, on day *j*, the hemoglobin response can be modeled as:

$$Y_{ij} = \beta_{0i} + \beta_{1i}x_i + \epsilon_{ij}$$

where  $\beta_{0i} \sim N(\mu_0, \tau_0)$ ,  $\beta_{1i} \sim N(\mu_1, \tau_1)$ , and  $\epsilon_{ij} \sim N(0, \tau)$ ; and  $x_j = j - 5.5$ , for j = 1, 2, ..., 10, is the mean-centered day number.

Suppose we have Inverse-Gamma priors on all variance parameters ( $\tau$  parameters). For simplicity, we'll assume *a priori* that each  $\tau$  follows the same  $IG(a=5,\lambda=4)$  distribution, with probability density function

$$f(\tau|a,\lambda) = \frac{\lambda^a}{\Gamma(a)} \tau^{-(a+1)} \exp\left\{-\frac{\lambda}{\tau}\right\}.$$

Furthermore, let  $\mu_0 \sim N(m_0 = 12, s_0^2 = 1)$  and  $\mu_1 \sim N(m_1 = 1, s_1^2 = 1)$ .

Notice that all full conditionals are available in closed-form because of conjugacy, which means Gibbs sampling can be used to obtain the posterior distribution.

Derive the full conditionals for  $\beta_{0i}$  and  $\beta_{1i}$  for all i (the form for each should be the same for all i). Then complete Voug's code using these full conditionals. (The current version of the code will give some hint as to the full conditionals). After obtaining at least 1000 post-burnin draws, find the approximate probability that a new patient will have a slope exceeding 0.5.

For a bonus, which parameter has high autocorrelation in the current implementation of the Gibbs sampler and what could you do to get less correlated draws? You must get both parts to get the bonus.

Note: This problem is an adaptation of Exercise 4.1 in Bayesian Methods for Data Analysis by Carlin and Louis. The full data set is available at: http://www.biostat.umn.edu/~brad/data/HGB\_data.txt.