Stat238: Lab 7

October 14

- This lab continues to explore MCMC-based computations using the NIMBLE package in R. The code in the Unit 6 demo (*unit6-comp.R*) can serve as a template.

- If you get stuck with any of the NIMBLE coding or error messages, let me know.

Problems

1. I'll talk a bit about how NIMBLE determines what samplers to use in an overall Gibbs sampling context (i.e., cycling through the parameters, with each parameter assigned a sampler such as a conjugate sampler, Metropolis sampler, or slice sampler). I'll also talk a bit about user-defined distributions in NIMBLE.

2. We'll continue with the rats random effects linear growth curve model for which you wrote BUGS code in Lab 6. Consider the following statistical model for the data from Gelfand et al. (1990, JASA 85:972) (in the file *ratsy.dat*). The data are weights of rats measured over time at five time points: 8, 15, 22, 29, and 36 days.

$$
\begin{aligned}
Y_{ij} &\sim N(\alpha_i + \beta_i(t_j - \bar{t}), \sigma_y^2) \\
\alpha_i &\sim N(\mu_\alpha, \sigma_\alpha^2) \\
\beta_i &\sim N(\mu_\beta, \sigma_\beta^2) \\
\sigma_y &\sim U(0, c) \\
\sigma_\alpha &\sim U(0, c) \\
\sigma_\beta &\sim U(0, c) \\
p(\mu_\alpha, \mu_\beta) &\propto 1
\end{aligned}
$$

Think about starting values for the MCMC. How could you get some very rough starting values without putting too much effort in? We'll talk about this as a group.

3. Set up a default sampler in NIMBLE. What samplers are being used? Run the sampler for 2000 iterations

4. Consider the performance of the MCMC based on the traceplots of the hyperparameters and a few of the process values (the αs and βs). How long should the burn-in period be? Is the MCMC mixing well once the burn-in is over?

5. Try putting in starting values that you know are wildly unreasonable. Can you get the MCMC to perform really badly, either in terms of a long burn-in or highly auto-correlated values even once the burn-in period is over?

6. Finally consider using different samplers. Try using Metropolis-Hastings or slice sampling for some or all of the parameters (see *help(samplers)* for more information). You could also consider sampling the variance components on the log-scale (see the information in the RW sampler in help(samplers) so the MCMC doesn't propose negative values. Do your various changes help or hurt the mixing?

7. Assess the different MCMC approaches using the formal diagnostics discussed in BDA and in class.