

STA 590, Statistical Computing, Spring 2005

HW4 Due date: March 24, 2005

1. For the Poisson change point model discussed in class and in Tanner's book page 147 assume Inverse Gamma prior distributions on b_1 and b_2 . This is $b_1 \sim IG(c_1, d_1)$ and $b_2 \sim IG(c_2, d_2)$.
 - Derive the full conditional distributions for b_1 and b_2
 - Modify the R code that is available through the web page ("code class March 2") and incorporate the full conditionals for b_1 and b_2 into this code. If you wish to write your own code in Matlab or something else, feel free to do so.
 - Redo Carlin, Gelfand and Smith (1992) analysis by taking $a_1 = a_2 = 0.5$, $c_1 = c_2 = 0$ and $d_1 = d_2 = 1$. In particular, show trace plots and histograms for all the parameters of interest in the model. Remember that k is a key parameter in this model. Also obtain posterior mean estimates and the 2.5% and 97.5% quantiles for the parameters of this model.
 - **Note** You may need to change the parameterization for the Gamma priors on θ and λ . According to Tanner, $G(a, b)$ denotes the Gamma density proportional to $\theta^{a-1}e^{-\theta/b}$
2. For the genetic linkage model of Tanner's book Section 5.1.
 - For the data $Y = (125, 18, 20, 34)$, implement the Gibbs sampler algorithm. Use a flat prior on θ Show expressions for the full conditionals distributions of relevance for this exercise.
 - Plot θ^i versus iteration i . How long a chain did you use?
 - Compute the posterior mean and posterior variance of θ based on your chain and produce a plot of the ergodic means for θ .
 - Run 5 chains of the same length with independent (different) starting values. Compute the averages of the θ 's in each chain. Calculate the standard deviation of the 5 averages. Now compute the standard deviation of the θ 's in each chain. Divide each SD by the square root of the number of iterations. Average these "standard errors" and compare this average to the standard deviation of the averages. Would you expect these numbers to be similar or different? (These calculations are the basis of the Gelman and Rubin convergence diagnostic).