STA 290 Fall 2003 Final Project Due Noon December 9

Researchers conducted a field trial to evaluate early height growth potential of 16 genetic crosses of loblolly pine. The data are in the course web site at

http://www.isds.duke.edu/courses/Fall02/sta290/final/progeny.dat.

The first column is the genetic cross and the second column is the height growth (in inches) during the first year. Because of porcupines, several trees have missing heights, and have values recorded as NA.

The researchers are interested in solutions to the following questions:

- 1. Which crosses are expected to grow at least 24 inches in the first year? (These crosses would be able to out-compete grasses and other vegetation)
- 2. Which cross is best?
- 3. For the best cross, what can the researchers expect typical first year height growth to be?

For question one, they are not really sure whether to use confidence intervals for expected growth or prediction intervals or some other approach. For the meaning of "best" in question 2, they think that expected growth might be a good measure, but are willing to look at other summaries. The researchers have some training in classical methods, but were interested in seeing how a Bayesian approach might answer their questions, and how the results would compare. They were told it is possible to estimate the probability that a given cross is number one (say in expected height growth), and would like to see how that can be carried out from a Bayesian perspective. They were worried about assumptions of equal variances used in some classical methods, and wondered if that really is important or could be relaxed. Carry out an appropriate statistical analysis (exploratory, classical, Bayesian) to answer the researchers questions to the best of your ability. Present a typed report with important supporting equations, figures and tables in the text (maximum of 5 pages) to answer the above questions. For the Bayesian analysis, include in an appendix all full conditionals or proposal distributions/acceptance ratios used for drawing samples from the joint posterior distribution. Please submit programs (with minimal documentation) for your analysis via email. You may build on the R- code from Gelman et al., otherwise all work should be your own. If you have any questions regarding the researchers questions or other points, please see me.