1. Consider again the Bayesian approach to finite population sampling, as described in the class notes by Prof. Banerjee that were covered in class by Prof. Hodges.

(a) A simple random sample of 30 households was drawn from a township containing 576 households. The numbers of persons per household in the sample (available online at www.biostat.umn.edu/~brad/7440/BayesianFinitePopSurveySamplingData.txt) were as follows:

5, 6, 3, 3, 2, 3, 3, 4, 4, 3, 2, 7, 4, 3, 5, 4, 3, 3, 3, 3, 4, 3, 4, 1, 1

Use a non-informative Bayesian analysis to estimate the total number of people in the area and compute the posterior probability that the population total lies within 10% of the sample estimate.

(b) From a list of 468 small 2-year colleges in the northeastern United States, a simple sample of 100 colleges was drawn. Data for the number of students \(y\) and the number of teachers \(x\) for these colleges were summarized as follows:

- The total number of students in the sample was: 44,987
- The total number of teachers in the sample was: 2,079
- Also given are the sample sums of squares: \(\sum_{i=1}^{n} y_i^2 = 29,881,219\) and \(\sum_{i=1}^{n} x_i^2 = 111,090\).

Assuming a non-informative Bayesian setting and where the population of students and teachers are independent, find the posterior mean and 95% credible interval for the student-teacher ratio in the population (i.e., all 468 colleges combined).

2. Spiegelhalter et al. (1995b) analyze the flour beetle mortality data in Table 3.3 (also available online at www.biostat.umn.edu/~brad/data/beetle_data.txt) using BUGS. These authors use only the usual, two-parameter parametrization for \(p_i \equiv P(\text{death}|w_i)\), but compare the logit, probit, and complementary log-log link functions using the centered covariate \(z_i = w_i - \bar{w}\). That is, in the logit case we have

\[
\logit(p_i) = \alpha + \beta(w_i - \bar{w}) = \alpha + \beta z_i,
\]

with similar expressions for the probit and complementary log-log.

(a) The full conditional distributions for \(\alpha\) and \(\beta\) have no closed form, but BUGS does recognize them as being log-concave, and thus capable of being sampled using the Gilks and Wild (1992) adaptive rejection algorithm. Prove this log-concavity under the logit model.
(b) Following the model of Example 4.4, actually carry out the data analysis in **BUGS** (the program above, along with properly formatted data and initial value lists, are included in the “examples” section of the help materials, or on the course webpages associated with the “binary dugongs” example). Do the estimated posteriors for the dosage effect $\beta$ substantially differ for different link functions?

(c) Finally, return to Example 3.7 and consider the generalized logit model,

$$p_i = \left\{\frac{\exp(\alpha + \beta z_i)}{1 + \exp(\alpha + \beta z_i)}\right\}^{m_1}.$$  

Using the same priors you used in part (b) and adding a vague $\text{Gamma}(0.1, 0.1)$ prior for the power parameter $m_1$, find the posterior distribution for this parameter, and check whether it is significantly different from its “null” value, $m_1 = 1$. [**Hint:** You may write your own Metropolis code in **R** (again following the model in Example 3.7), or just use **BUGS** (though this will require use of the “ones” or “zeros” trick to handle the nonstandard model).]