# STA 6352, Report 9.3

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*9.1.3 Example: Multiple logistic regression*

- We next extend Example 9.1.1 to the case where there are two treatments and a placebo with a binary response. The model is

$$y_i \sim \text{Bernoulli}(p_i); \quad \text{logit}(p_i) = \beta_0 + \beta_1 x_1 + \beta_2 x_2,$$

and $x_i$ is an indicator for treatment $i = 1, 2$. So $\beta_1$ represents the log-odds ratio comparing treatment 1 and placebo while $\beta_2$ represents the log-odds ratio comparing treatment 2 and placebo. We can compare the effectiveness of the two treatments by looking at the difference $\beta_2 - \beta_1$. For this example we use $\text{N}(0, 10^2)$ priors for each of the $\beta_i$'s.

- No closed form is available for the joint posterior of $(\beta_0, \beta_1, \beta_2)$ so we use JAGS to perform posterior inferences. Consequently, the algorithm is slightly different from the one in the first example. Since MCMC is used, more inputs are required.

**Algorithm:**

1. Select values for $(\beta_0, \beta_1, \beta_2)$, the sample sizes of interest, the number of replications, $(B)$, the number of MCMC iterations, number of iterations for the burn-in, and initial values for the MCMC chain.
2. For each replication in the simulation, generate data with the selected parameter values.
3. Call JAGS from R.
4. For each data set, keep track of the posterior quantities of interest, for instance, $\Pr(\beta_1 > 0 \mid \text{data})$. If this probability exceeds $1 - \alpha$ then that particular hypothesis is rejected. Keeping track of whether the "true" parameter is contained in the 95% credible interval may also be of interest.
5. Compute the empirical average of the power/Type I error, coverage, etc., across replications.

- Suppose in this example we are interested in comparing each of the treatments against the placebo ($H_0 : \beta_1 = 0$, vs. $H_1 : \beta_1 > 0$ and $H_0 : \beta_2 = 0$ vs. $H_1 : \beta_2 > 0$) along with testing that treatment 2 is better than treatment 1 ($H_0 : \beta_2 = \beta_1$ vs. $H_1 : \beta_2 > \beta_1$).
- We generated 1000 data sets of size 150 (50 observations from each treatment) with the model

$$\text{logit}(p_i) = -0.5 + 0.9x_1 + 1.3x_2.$$

We repeated the simulation under the null model with $\beta_1 = \beta_2 = 0$. Using a Bonferroni correction and rejecting if posterior probabilities exceed 0.983 instead of 0.95 we found an overall Type I error rate of 0.05. For the test of Treatment 1 against placebo the power was 0.57. For Treatment 2 versus placebo the power was 0.89. For the Treatment 1 versus Treatment 2 comparison the power was 0.13.

**Report 9.3.**

*(a)*

Write an R script to produce a simulation like that in the last example. Do so with the Bonferroni correction, then again without it. Report the same simulation summaries and discuss. See the code in Section O.15.

Below is an R script containing the powers for the hypothesis test.

| | |
|---|---|
| With_Bonferroni.Power_Treatment1_vs_Placebo | 0.540 |
| With_Bonferroni.Power_Treatment2_vs_Placebo | 0.850 |
| With_Bonferroni.Power_Treatment2_vs_Treatment1 | 0.126 |
| Without_Bonferroni.Power_Treatment1_vs_Placebo | 0.740 |
| Without_Bonferroni.Power_Treatment2_vs_Placebo | 0.933 |
| Without_Bonferroni.Power_Treatment2_vs_Treatment1 | 0.248 |

*(b)*

Write an R script to produce a graphical summary like that in Figure A.12 and apply it to the credible set constructed for the difference $\beta_2 - \beta_1$ for choices of sample sizes 25, 50, and 75 for each arm. Use the true value $\beta_2 - \beta_1 = 0.5$.