

Assignment 3

Part 1

The data in *wtp_data.csv* represent the amounts two groups of participants (A and B) are willing to pay for snack food items. Each individual placed bids to buy 60 different foods. All participants saw the same 60 foods. They were given an endowment of 5 CHF per food item to use in purchasing the foods from the experimenter. Thus, the maximum bid was 5, even if the participant might have been willing to pay more than 5 CHF.

Test whether Group A and Group B differ in terms of the amount that they bid to purchase snack food items using a standard normal model and a normal model including censor limits at 0 and 5 CHF. Both the standard normal and censored normal models should be hierarchical. They should allow for different mean bids for each participant under a general normal distribution for each of the two groups. The group-level distributions should be separate and not inform one another. However, you should write JAGS models that loops over a group index variable rather than running the same models separately for the two groups. This will require you to extrapolate from the single group hierarchical models we have discussed so far. Hint: if you start from the model in *censoredMeans.txt*, and call the group-level mean parameter *mu.mu*, you can index it such that *mu.mu[1]* is the mean for Group A, and *mu.mu[2]* is the mean for Group B. Monitor the group-level mean and standard deviation parameters for each model (i.e. *mu.mu* and *sigma.mu*).

Details of what to do/turn in:

1. Create a histogram or density plot of the bids with each group shown in a different color. (5% of points)
2. Summary tables and posterior chain correlation plots for the standard normal and censored normal models. (15% of points)
3. Plot the density functions for the normal distributions generated by the group-level mean and standard deviations for groups A and B from each set of model fits. Generate 1000 samples from the parameters (i.e. means of the posterior chains) using the function *rnorm* to use in making these plots. Plot Group A and B in the same plot using different colors for each model. So there will be two separate plots (standard normal, censored normal) that each contain two density functions (Group A, Group B). (15% of points)
4. Test whether the means and standard deviations for Groups A and B differ when estimated from the standard normal and censored normal models. Plot histograms of the differences in the chains and include vertical lines for the 95% HDIs. This will be four plots in total. What can you conclude about the differences between the groups based on the standard normal versus censored normal models (15% of points). To be clear the contrasts are as follows:
 - a. *muA_standard* - *muB_standard*,
 - b. *sigA_standard* - *sigB_standard*,
 - c. *muA_censored* - *muB_censored*,
 - d. *sigA_censored* - *sigB_censored*,

5. All R/Matlab/Python code and the JAGS models used to estimate the models and generate the summaries and plots.

Part 2

The data in *ratings_data.csv* represent ratings on the desire to eat a food from a Likert scale (“Strong No”, “No”, “Neutral”, “Yes”, “Strong Yes”). These categorical responses are recorded as the numbers -2:2 in the data file. Once again there are groups of participants (A and B). Each individual rated 60 different foods in terms of the desire to eat on the Likert scale above, as well as two different attributes (x1 and x2) of the foods on a visual analog scale. We will assume that these visual analog ratings are continuous and censored by the endpoints of the scale. All participants saw the same 60 foods.

Test whether Group A and Group B differ in terms of how x1 and x2 influence their members’ desire to eat the snack food items according to the formula, $\text{Rating} \sim B_0 + B_1 \cdot x_1 + B_2 \cdot x_2 + \text{error}$, using a hierarchical linear regression model (i.e. treating the scale as metric) and an hierarchical ordinal regression model. Both models should allow for different beta parameters for each participant under general normal distributions for each of the two groups. The group-level distributions should be separate and not inform one another. However, you should write JAGS models that loops over a group index variable rather than running the same models separately for the two groups. Monitor the group-level beta parameters and standard deviation parameters for the linear model and the group-level beta parameters and standard deviation, and estimated thresholds for the ordinal model.

Turn in:

1. Plot histograms of the ratings with each group shown in a different color, pool the data from all participants together. (5% of points)
2. Summary tables and posterior chain correlation plots for the linear and ordinal regression models. (15% of points)
3. Test whether x1 or x2 has a stronger influence on ratings in Groups A and B based on the estimates from the linear and ordinal models. Report the results in the form of plots of the beta parameter differences and statements about the posterior probability that beta1 is greater than beta2 in each model. What can you conclude about the differences between the groups based on the metric versus ordinal models? (15% of points). To be clear the contrasts are as follows:
 - a. Metric model
 - i. $\text{beta1.mu}[1] - \text{beta2.mu}[1]$
 - ii. $\text{beta1.mu}[2] - \text{beta2.mu}[2]$
 - b. Ordinal model
 - i. $\text{beta1.mu}[1] - \text{beta2.mu}[1]$
 - ii. $\text{beta1.mu}[2] - \text{beta2.mu}[2]$
4. Test whether the beta parameters for x1 and x2 differ within groups across the two models. Test both the individual beta parameters and the difference between beta1 and beta2 (15% of points). To be clear the contrasts are as follows:
 - c. $\text{beta1.mu}[1] \text{ from met} - \text{beta1.mu}[1] \text{ from ordinal}$,
 - d. $\text{beta2.mu}[1] \text{ from met} - \text{beta2.mu}[1] \text{ from ordinal}$,

- e. $\text{beta1.mu}[2]$ from met – $\text{beta1.mu}[2]$ from ordinal,
 - f. $\text{beta2.mu}[2]$ from met – $\text{beta2.mu}[2]$ from ordinal,
 - g. $(\text{beta1.mu}[1] - \text{beta2.mu}[1] \text{ from met}) - (\text{beta1.mu}[1] - \text{beta2.mu}[1] \text{ from ordinal})$,
 - h. $(\text{beta1.mu}[2] - \text{beta2.mu}[2] \text{ from met}) - (\text{beta1.mu}[2] - \text{beta2.mu}[2] \text{ from ordinal})$,
5. All R/Matlab/Python code and the JAGS models used to estimate the models and generate the summaries and plots.

See example JAGS models on the next page ->

JAGS model starting points:

Standard normal hierarchical means for one group:

```
model {  
  
    mu.mu ~ dnorm(0, 0.0000001) # prior group mean  
    mu.sig ~ dunif(0.0001, 100) # prior for the standard deviation across  
individuals  
    sigma.mu ~ dunif(0.0001, 100) # prior for the standard deviation across trials  
  
    for (s in 1:Nsubj) {  
        mu.s[s] ~ dnorm(mu.mu, 1/mu.sig^2)  
    }  
  
    for (i in 1:Ntotal) {  
        y[i] ~ norm(mu.s[subldx[i]], 1/sigma.mu^2)  
    }  
}
```

Standard linear hierarchical for one group:

```
model {  
  
    beta0.mu ~ dnorm(0, 0.0000001) # prior intercept  
    beta1.mu ~ dnorm(0, 0.0000001) # prior slope  
  
    beta0.sig ~ dunif(0.0001, 100) # prior intercept variability  
    beta1.sig ~ dunif(0.0001, 100) # prior slope variability  
  
    sigma.mu ~ dunif(0.0001, 100) # prior for the regression error  
  
    for (s in 1:Nsubj) {  
  
        beta0.s[s] ~ dnorm(beta0.mu, 1/beta0.sig^2)  
        beta1.s[s] ~ dnorm(beta1.mu, 1/beta1.sig^2)  
  
    }  
  
    for (i in 1:Ntotal) {  
  
        y[i] ~ dnorm(mu[i], 1/sigma.mu^2)  
        mu[i] <- beta0.s[subldx[i]] + beta1.s[subldx[i]]*x[i]  
  
    }  
}
```