Lesson 11 Part B

Тест, 6 вопроса

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1.

We have seen an example of extending a normal linear model to a hierarchical model. We will now explore extending a non-normal linear model. Consider again the OME data in the `MASS` package in R, which we explored in the quiz from Lesson 9. The data consist of experimental results from tests of auditory perception in children. Under varying conditions and for multiple trials under each condition, children either correctly or incorrectly identified the source of changing signals.

One variable we did not use in the model was the child ID number. It turns out that there are multiple (ranging from eight to 20) observations for each child. For example, the first 20 rows of the data are all results from Child 1. Why is it reasonable to consider fitting a hierarchical model in this scenario?

- ○ Observations are independent, within and between different children. Separate tests were conducted, so there's no reason to believe the data are correlated.

- ● Observations from a single child are likely correlated. For example, two results from one child are more likely to be similar than two results from two different children.

- ○ The children may be grouped in a hierarchical fashion, for example, classes in a school.

- ○ Some of the children in the study may be siblings, and their results may be more correlated than for unrelated children.

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2.

Recall that the original model looked like this:

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$$y_i \mid \phi_i \stackrel{\text{ind}}{\sim} \text{Binomial}(n_i, \phi_i), \quad i = 1, \ldots, 712,$$

$$\text{logit}(\phi_i) = \beta_0 + \beta_1 \text{Age}_i + \beta_2 I_{(\text{OME}_i = \text{low})} + \beta_3 \text{Loud}_i + \beta_4 I_{(\text{Noise}_i = \text{incoherent})}$$

$$\beta_0 \sim \text{N}(0, 5^2)$$

$$\beta_k \stackrel{\text{iid}}{\sim} \text{N}(0, 4^2), \quad k = 1, 2, 3.$$

As with other models, we will extend the intercept (and rename it) so that the linear part of the model looks like this:

$$\text{logit}(\phi_i) = \alpha_{\text{ID}_i} + \beta_1 \text{Age}_i + \beta_2 I_{(\text{OME}_i = \text{low})} + \beta_3 \text{Loud}_i + \beta_4 I_{(\text{Noise}_i = \text{incoherent})}$$

where ID_i is an index identifying the child for observation i. The hierarchical prior for the intercepts would then look like this:

$$\alpha_j \stackrel{\text{iid}}{\sim} \text{N}(\mu, \tau^2), \quad j = 1, \ldots, 63 \text{ (there are 63 children)},$$

followed by priors for μ and τ^2:

$$\mu \sim \text{N}(0, 10^2)$$

$$\tau^2 \sim \text{IG}(1/2, 1/2).$$

What does τ^2 indicate in the context of this model?

○   The variability in the number of correct responses across tests for one child.

○   The variability of the intercept across all observations in the data.

◉   The variability of the intercept between children.

○   The variability in proportion of correct responses across tests for one child.

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3.

Fit the hierarchical model proposed in Question 2 with JAGS by adjusting the code given in the quiz from

Lesson 11 (Part B)

Lesson 11 (below). The following R code will be necessary to reproduce the results.

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```
1   library("MASS")
2   data("OME")
3
4   dat = subset(OME, OME != "N/A")
5   dat$OME = factor(dat$OME) # relabel OME
6   dat$ID = as.numeric(factor(dat$ID)) # relabel ID so there are no gaps in
        numbers (they now go from 1 to 63)
7
8   ## Original reference model and covariate matrix
9   mod_glm = glm(Correct/Trials ~ Age + OME + Loud + Noise, data=dat, weights
        =Trials, family="binomial")
10  X = model.matrix(mod_glm)[,-1]
11
12  ## Original model (that needs to be extended)
13  mod_string = " model {
14    for (i in 1:length(y)) {
15      y[i] ~ dbin(phi[i], n[i])
16      logit(phi[i]) = b0 + b[1]*Age[i] + b[2]*OMElow[i] + b[3]*Loud[i] + b[4]
                *Noiseincoherent[i]
17    }
18
19    b0 ~ dnorm(0.0, 1.0/5.0^2)
20    for (j in 1:4) {
21      b[j] ~ dnorm(0.0, 1.0/4.0^2)
22    }
23
24  } "
25
26  data_jags = as.list(as.data.frame(X))
27  data_jags$y = dat$Correct
28  data_jags$n = dat$Trials
29  data_jags$ID = dat$ID
```

How do the convergence diagnostics look?

○ Autocorrelation is quite strong in the chains. This model would require a large number of MCMC iterations before we would use the results to make solid conclusions.

○ Convergence diagnostics look great. There are no concerns.

○ Different chains from different initial values fail to explore the same space. Advanced MCMC techniques will be required to explore this multimodal (many-peaked) posterior.

○ The chains suddenly jump from exploring one space to exploring another, as though the parameters are switching labels. The parameters do not appear to be uniquely identified by the data.

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4.

The DIC value for the original model fit in the quiz for logistic regression is about 1264. Calculate a DIC value for this new hierarchical model. What do you conclude?

◯ The DIC value for this new model is **lower**, indicating a preference for the **new model**.

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Тест, 6 вопроса ◯ The DIC value for this new model is **lower**, indicating a preference for the **original model**.

⦿ The DIC value for this new model is **higher**, indicating a preference for the **original model**.

◯ The DIC value for this new model is **higher**, indicating a preference for the **new model**.

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5.

The actual number of parameters in this hierarchical model is 69 (63 random intercepts, four regression coefficients, and two hyperparameters). What is the effective number of parameters? Round your answer to one decimal place.

28.0

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6.

In the hierarchical model with random intercepts, we assumed that the common distribution for the intercepts is normal. What could we examine to assess whether this is a reasonable assumption?

⦿ We could look at the second-level residuals calculated from $\alpha_j - \mu$ and evaluate how they are distributed.

◯ We could look at the data-level residuals calculated from $(y_i - \phi_i)$ and evaluate how they are distributed.

◯ We could look at the data-level residuals calculated from $(y_i/n_i - \phi_i)$ and evaluate how they are distributed.

◯ We could look at the posterior distribution of μ.

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