

Coursera | Online Courses From Top Universities. Join for Free The DIC is lower for the new model, indicating preference for the model with separate variances across groups. Lesson 8 8/8 points (100%) The DIC is lower for the original model, indicating preference for the model Quiz, 8 questions with one common variance across groups. Correct This suggests we should stay with the original model (if our objective is good prediction). The DIC is higher for the new model, indicating preference for the model with separate variances across groups. Use the original model (single variance) to calculate a 95% interval of highest posterior density (HPD) for $\mu_3-\mu_1$. Which of the following is closest to this interval? (-0.14, 1.13) points The interval contains 0, indicating that the data lack strong (at least at the 95% level) evidence for $\mu_3 eq \mu_1$. In the lesson, the posterior probability that $\mu_3 > \mu_1$ was 0.94. (-0.20, 1.19) (0.22, 1.49) (-1.01, 0.25) **7** What is the correct interpretation of $\mu_3 - \mu_1$ in the context of the plant growth analysis? It is the difference in plant weight between treatment 2 and control. points It is the effect (change) of treatment 2 with respect to the control in mean plant weight. Correct This also equivalent to the β_2 parameter in the baseline and effect model (default in R) that was fit in the lesson. It is the effect (change) of treatment 2 with respect to the control in plant weight. It is the mean range of plant weight across the three treatment groups. The linear model with a baseline mean and group effects is the default in R. However, we can also fit the cell means model in R using the following code: $\label{eq:mod_cm} \begin{array}{lll} \text{mod_cm} &= & \text{lm(weight} \sim \text{-1 + group, data=PlantGrowth)} \\ \text{summary(mod_cm)} \end{array}$ points where the $-\mathbf{1}$ in the model formula tells R to drop the intercept. Because we used fairly noninformative priors for the μ parameters in the analysis with JAGS, the results are very similar. In addition to allowing different prior specifications, what is one advantage of posterior sampling with JAGS over fitting the reference model in R? We can obtain posterior standard deviations (standard errors) for each mean (or coefficient). We can use the posterior samples to obtain simulated posterior distributions of any function of the parameters that may interest us (e.g., $\mu_3-\mu_1$). Correct

Posterior distributions provide a rich tool for characterizing our uncertainty and

We can obtain posterior mode estimates for each mean (or coefficient).

We can estimate the proportion of the variation in plant weight attributable to

updated beliefs about parameters.

the treatment group assignment.

 $Lesson \ 8 \\ Quiz, 8 \ questions \\$