

STAT 700
Homework 7 Problems
due Wed. Nov. 2

2 Problems. Please follow the Lab report directions off the homework web page and work in HW Groups.

1. **Dyestuff Data:** (Ref: Davies, 1960) The variation of the strength of (coloring powder) of a dyestuff from one manufacturing batch to another was studied. Strength was measured by dyeing a square of cloth with a standard concentration of dyestuff and visually comparing the result with a standard. The result was numerically scored as the percentage strength of the dyestuff. Large samples were taken from six batches and from each batch six subsamples were taken. The 36 subsamples were submitted to the laboratory in a random order for testing as described above. There are two sources of variability: batch-to-batch variability and measurement error.

To get the data, the file off the class web page:

<http://www.rohan.sdsu.edu/~babailey/stat700/dye.dat>

and you can use the `read.table` command with option `header=T`.

We will ignore the Subsample and make the Batch a factor by,

```
> dye$Batch <- as.factor(dye$Batch)
```

We now return to the one-way ANOVA model,

$$Y_{ij} = \mu + \alpha_i + \varepsilon_{ij}$$

where μ is the overall mean level, α_i is the random effect of the i th batch and they are iid $N(0, \sigma_\alpha^2)$ and ε_{ij} are iid $N(0, \sigma^2)$.

(a) We can use the R function `lme` to fit the random-effects model using REML (restricted maximum likelihood, the default). Your call should look like,

```
> fit <- lme(Strength~1, data=dye, random=~1 | Batch)
```

Use the summary function to get the REML estimates for the σ^2 and σ_α^2 . How do these estimates compare with your estimates from Homework 6, Problem 2 (c)?

(b) The plot function will give you a diagnostic plot for your fit. From this plot, how well does the model fit the data?

(c) Test the hypothesis $H_0 : \sigma_\alpha^2 = 0$ vs $H_1 : \sigma_\alpha^2 \neq 0$, using a LRT. What do you conclude?

2. The concentrations (in nanograms per milliliter) of plasma epinephrine were measured for ten dogs under: (1) isofluorane, (2) halothane, and (3) cyclopropane anesthesia. (Ref: Perry et al, 1974).

We will study **blocking** and we will use data available off the class web page:

<http://www.rohan.sdsu.edu/~babailey/stat700/dog.dat>

You can use the header information already in the file. Consider the 10 dogs as blocks and the different anesthesia as treatments.

(a) Plot the data using strip charts. Describe any differences that you see.

(b) We will consider the blocks as random effects, so the two-way mixed effects model is:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, \quad i = 1, \dots, I; j = 1, \dots, J. \quad (1)$$

where α_i are independent $N(0, \sigma_\alpha^2)$ random variables, ε_{ij} are independent $N(0, \sigma^2)$ random variables, and β_j are constants subject to $\sum_{j=1}^J \beta_j = 0$. The α_i and ε_{ij} are independent.

Fit a linear mixed effects model with `lme`. Give summary and diagnostics plots of the residuals. What do you conclude? Make sure that a factor is a factor! You can use the `as.factor` function inside of `lme`.

(c) Test the hypothesis $H_0 : \sigma_\alpha^2 = 0$ vs $H_1 : \sigma_\alpha^2 \neq 0$, using a LRT. (Use the `gls` function). What do you conclude?

(d) The default method with `lme` is REML. Repeat (c) using ML for BOTH fits. How do the p -values of the LRT using REML and ML compare?