

1. Pages 3 and 4 of part 3 of the notes describe a study of temperature and catalyst effects on fermentation of dry distillers grain. In that experiment, there are 36 observations (6 tubes in each of 6 growth chambers). Consider a smaller version of that study with only 2 temperatures, 4 growth chambers (2 at each temperature), and 4 tubes per growth chamber (2 at each level of the catalyst). This reduced study uses 4 growth chambers and has 16 tubes.
 - (a) Write out the model using greek letters with subscripts (where needed). Define your subscripts and give the distribution for all random effects.
 - (b) Write out the \mathbf{Z} matrix for this study.
 - (c) Write out the variance-covariance matrix, $\mathbf{\Sigma}$ of the observations, as a 16 x 16 matrix using the appropriate model parameters. If the VC matrix is block diagonal, you may tell me 'block diagonal with XX blocks like' and just provide XX (the number of blocks) and the contents of one block.
 - (d) Write out the full (16 x 16) variance-covariance matrix using Kronecker product notation.
2. Page 5 of part 3 of the notes describes a Gauge Repeatability and Reproducibility study. Consider a smaller version of that study using 2 parts, each measured twice by 2 operators. There are a total of 8 observations. To simplify grading your answers, please use the following order for the 8 observations:

Part	Operator	Measurement
1	1	1
1	1	2
1	2	1
1	2	2
2	1	1
2	1	2
2	2	1
2	2	2

- (a) Write out the model using greek letters with subscripts (where needed). Define your subscripts and give the distribution for all random effects.
 - (b) Write out the \mathbf{Z} matrix for this study.
 - (c) Write out $\mathbf{\Sigma}$, the variance-covariance matrix of the observations, as a 8 x 8 matrix using the appropriate model parameters.
 - (d) Write $\mathbf{\Sigma}$ using Kronecker product notation
3. The data in plankton.txt are one small part of a survey of plankton (small aquatic invertebrates) in a single lake. Plankton are often sampled by towing a net through the water, then collecting, sorting to species, and counting the animals caught in the net. These data are from 12 separate tows of the net, taken in randomly chosen places in the lake. plankton.txt contains data on four species, reported as number caught per tow. The investigators want to

estimate the abundance of each species and quantify the relationship between the four species. The total number of animals caught in each tow varies because plankton are more abundant in some parts of the lake. The investigators propose to treat tow as a blocking variable. In case you're wondering about the ecology, these 12 tows are samples of the same plankton community, so blocking is reasonable.

The first parts of this problem concern diagnostics; treat blocks as fixed effects.

For parts a - c, use an additive block model (tow + species).

- (a) Test whether the four species are equally abundant. Report your test statistic and p-value. Conclusion not necessary.
- (b) The investigators are especially interested in the difference between species 1 and species 2. Estimate that difference and test whether it equals 0. Report the estimate, standard error and p-value. Note: Use all data to estimate the pooled standard deviation.
- (c) The investigators are surprised by the result from part b, because it isn't what they expected. They ask you to check assumptions of the block model. Plot the abundances against the block means and plot residuals against predicted values. Do the additivity and equal variance assumptions seem reasonable? Explain why or why not.
- (d) A friend suggests a log transformation. That is, analyze $\log(\text{count})$ using an additive block model. This is equivalent to assuming that blocks have multiplicative effects on the original values. Fit this model and check the assumptions of additivity and equal variances. Do additivity and equal variances seem reasonable after transformation? Explain why or why not.
- (e) Estimate and test the difference in log abundance between species 1 and 2. Report the estimate (on log scale), standard error and p-value.
- (f) Estimate the log abundance of species 1 in these 12 tows. Report the estimate (on log scale) and its standard error.

For subsequent parts, consider blocks (tows) to be a random effect and use $\log(\text{count})$ as the response.

- (g) Estimate and test the difference in log abundance between species 1 and 2. Report the estimate (on log scale), standard error and p-value.
 - (h) Estimate the log abundance of species 1 in a new set of 12 randomly located tows. Report the estimate (on log scale) and its standard error.
 - (i) Explain why the results for parts (3e) and (3g) are identical but the results for parts (3f) and (3h) are not.
4. Last week, I helped Bob Stephenson design a sensory evaluation study. The researchers wanted to compare 8 treatments, a complete factorial treatment design with 2 levels of each of 3 factors. If you care, the study is comparing flavorfulness of pork loin and the three factors are the genetic background of the pig (2 levels), the state where the pigs were raised (2 levels), and the temperature at which the pork loin was stored (2 levels). I will label those factors A, B, and C with levels of 1 and 2 for each. Flavorfulness is assessed by recruiting participants

to taste samples (in randomized order) and record their evaluation (usually on a continuous 0 - 15 scale).

If each participant scored all 8 items, this study would be an RCDB, with participants as blocks. It is very clear and very common for some individual participants to record flavorfulness consistently lower, and some consistently higher than the average response. Blocking by participant removes this consistent difference among participants.

The food scientists running the study complained that participants get tired and don't give reliable results when tasting more than 4 items. So, Bob devised and I validated an incomplete block design where each participant only evaluates 4 of the 8 treatments. I have made up data (in `bibd.csv`) that might be generated by a study like this, because the actual study hasn't been done yet. For all parts, I suggest you use a model with main effects and interactions of all treatment factors but only the additive effect of blocks (i.e. no `block*something` interaction).

- (a) Consider blocks as an additive fixed effect. Estimate the main effect of factor A and its standard error. You only need to report the estimate and its se.
- (b) Consider blocks as an additive random effect. Estimate the main effect of factor A and its standard error. You only need to report the estimate and its se.
- (c) Explain why the estimated main effects of factor A are not the same. Your explanation can be in terms of general characteristics of the two estimators and does not have to refer to specific numerical aspects of this data set.
- (d) Explain why the standard errors of the main effect of factor A are not the same. Again, your explanation can be in terms of general characteristics of the two estimators and does not have to refer to specific numerical aspects of this data set.
- (e) One standard way to compare experimental designs or estimators is to compute their efficiency. The efficiency of the random blocks analysis relative to the fixed blocks analysis is the variance of an estimate from the fixed blocks analysis divided by the variance of an estimate from the random blocks analysis. Calculate this efficiency for this data set.
- (f) One way to interpret efficiency is in terms of relative sample size. What sample size (per treatment) is needed in the fixed blocks analysis (less precise) to reduce the variance (or se) of an estimate to that in the random blocks analysis (the more precise one). Calculate that sample size for this data set. Do not round.