

1. *Echinaceae* variance components

(a) Source	df
Plant	24
Tissue	2
Plant*Tissue	48
Extract(P*T)	75
Clarify(E*P*T)	150
error	300

Notes: Tissues and plants are crossed. Each combination is a biological sample. Extracts are nested in Samples, Clarifications are nested in Extracts, and Measurements are nested in Clarification

(b)  $AIC = -2\ln L + 2k$ . For REML,  $k$  is the number of variance components: that is either 5 or 4, depending on whether you include the random error or not. I accepted either. So,  $\ln L = (105.1 - 8)/(-2) = -48.55$

(c) The set of 8 models where Plants are a random factor give you the best understanding of which variance components should be included in a model. Model 2 has the lowest AIC among that set.

Note: You can NOT compare models 9 and 10 to the other 8 because they have different fixed effects (plants are fixed in 9 and 10, but not in 1-8). I took off points if you tried to compare the two sets.

(d) Model 1 is also possible because it has an AIC value within 2 of the best model

## 2. Ratio of reaction times

(a) (0.89, 1.312) or perhaps adjacent values in the sorted lists.

There is no correlation between the estimate and its se, so use an ordinary bootstrap. For a 99% ci, want the 0.005 and 0.995 quantiles. Those are given by the 5'th and 995'th values in the sorted vector of bootstrap values. Those are (0.89, 1.312)

(b) The observed value, 1.091 is somewhere in the middle of the randomization distribution. There are at least 20 values more extreme than the observed value, so you CAN tell me that  $p > (20 + 1)/(999 + 1)$ , i.e. that  $p > 0.021$ .

(c) No. The proposed method does not respect the design of the study. The study is paired (treatment and control are measured on the same subject). The proposed bootstrap treats the two measurements as independent.

## 3. Reaction times, part 2

- (a) There are 80 df in the table, so there are  $119 - 80 = 39$  missing observations  
 There are  $1 + 2 + 2 + 41 = 46$  df for the main plot (subjects) part of the ANOVA table (sex + age + sex\*age + subject(sex\*age)). So there are  $59 - 46 = 13$  missing subjects.  
 Notes: A lot of folks missed the second part because they computed  $59 - \text{subject}(\text{sex*age})$ . That ignores the additional df associated with groups (treatments) of subjects.

(b)

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix}$$

Notes: there are three subjects included in this snippet of data: two 60yr old males and one 18yr old female. The first subject has 1 obs., the other two provide 2 obs.

(c)  $\Sigma = \mathbf{ZGZ}' + \mathbf{R} =$ 

$$\begin{bmatrix} \sigma_m^2 + \sigma_s^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_m^2 + \sigma_s^2 & \sigma_m^2 & 0 & 0 \\ 0 & \sigma_m^2 & \sigma_m^2 + \sigma_s^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_m^2 + \sigma_s^2 & \sigma_m^2 \\ 0 & 0 & 0 & \sigma_m^2 & \sigma_m^2 + \sigma_s^2 \end{bmatrix}$$

(d)  $\hat{\sigma}_m^2 = 1.92$ MS for error = 1.30 =  $\hat{\sigma}_s^2$ MS for subjects = 4.53 =  $1.30 + 1.683 \sigma_m^2$  $\hat{\sigma}_m^2 = (4.53 - 1.30) / 1.683 = 1.92$ (e)  $F = \text{MS}(\text{trt*age}) / \text{MS}(\text{error}) = 3.508 / 1.297 = 2.7$ 

Notes: MS for Trt\*Age =  $7.016 / 2 = 3.508$ . The appropriate denominator is MS error =  $36.327 / 28 = 1.297$ . You can see this either by reasoning that trt\*age is a split plot or within-subject factor or by noticing that the E MS for trt\*age only include  $\sigma_e^2$

(f) No need for C-S. numerator 2 df, denominator 28 df.

(g) The MS for sex =  $4.157 / 1 = 4.157$ . The appropriate denominator is  $\sigma_s^2 + 1.529\sigma_m^2$ . This can be calculated either by plugging in the estimates  $\hat{\sigma}_s^2$  and  $\hat{\sigma}_m^2$  to get  $1.30 + 1.529 \times 1.92 = 4.24$ , or by figuring out that  $E(0.9085MS_{\text{subject}(\text{sex*age})} + 0.0915MS_{\text{error}}) = MS_{\text{error}} + 1.529MS_{\text{subject}(\text{sex*age})}$ . If you use the latter approach, you get the same denominator MS:  $0.9085 \times 4.53 + 0.0915 \times 1.30 = 4.23$ . Hence,  $F = 4.157 / 4.23 = 0.98$

- (h) numerator df = 1. denominator df requires C-S: The MS used as the denominator is  $0.908 MS_m + 0.092 MS_s$ . The C-S calculations are:

$$\begin{aligned} \sum a_i MS_i &= 4.24 \quad \text{Note: already have this \#} \\ \sum a_i^2 MS_i^2 / df_i &= \frac{0.908^2 4.53^2}{41} + \frac{0.092^2 1.30^2}{28} \\ &= 0.413 + 0.001 \\ &= 0.413 \\ \nu_{cs} &= 4.24^2 / 0.413 \\ &= 43.51 \end{aligned}$$

There are many opportunities for rounding errors that lead to slightly different answers. Anything close to this and derived in a reasonable way was accepted.

#### 4. Curvature of wings

(a)	Source	df
	Curvature	2
	Wing(Curv.)	3
	subsampling	54
	<u>total</u>	<u>59</u>

Explanation: You are told that the curvature is randomly assigned to a wing. So wings are the eu. There are 6 of these. Wings are nested within curvature levels; a single wing has one and only one curvature. The 10 observations made on each wing are subsamples. If you wrote out a model, the ANOVA table above corresponds to

$$\begin{aligned} Y_{ijk} &= \mu + \alpha_i + \omega_{ij} + \epsilon_{ijk} \\ \omega_{ij} &\sim N(0, \sigma_{wing}^2) \\ \epsilon_{ijk} &\sim N(0, \sigma_{obs}^2) \end{aligned}$$

where  $i$  indexes curvature level,  $j$  indexes wing, and  $k$  indexes observation. The E MS for this model are

Source	E MS
Curvature	$\sigma_{obs}^2 + 10\sigma_{wing}^2 + Q(\text{curvature})$
Wing(Curv.)	$\sigma_{obs}^2 + 10\sigma_{wing}^2$
subsampling	$\sigma_{obs}^2$

- (b) Wing(curv.) is the appropriate denominator for to test differences among curvatures. This follows from the 'use the eu variability to test effects assigned to eu's. Or, it follows directly from the E MS for subsampling.

## 5. Biorenewables

(a)	Source	df
	Expt	2
	Block(Expt.)	12
	Temp	2
	Expt*Temp	4
	w/i Expt	24
	<hr/>	
	,total	59

I also accepted for full credit the model with blocks crossed with experiments, i.e.

	Source	df
	Expt	2
	Block	4
	Expt*Block	8
	Temp	2
	Expt*Temp	4
	w/i Expt	24
	<hr/>	
	,total	59

Explanation: This is a repeated experiment. Each of the three experiments is an RCBD. The experiments are likely to give different (perhaps only slightly different) results because each experiment uses a different batch of corn stalks. All the eu's within experiment 1 use the same batch of corn stalks. I tell you that batches of corn stalks have different composition.

Experiment\*Temp is included because we are concerned about the consistency of the treatment effects across experiments.

Other common answers that got partial credit (some more than others) and why they are not appropriate:

RCBD with only blocks, no mention of experiment: does not separate the variability between experiments from the variability within an experiment (the w/i Expt = block(expt)\*temp error)

Some form of split plot design with experiment as the split plot factor: You could view this as a split plot with corn stalk batch = experiment "assigned" to a main plot eu that is not replicated. Temp is clearly assigned to a smaller size eu. If you want to think of this as a split plot design, temp is the split factor, not experiment.

Only 2 df for blocks: I presume you misread the picture and thought there were 3 blocks, instead of 5.

- (b) If we want broad sense inference, expt\*temp is the appropriate error for temp.

I gave partial credit to block\*temp. The residual got no credit (that would be narrow sense inference).