Math 484 Final is Friday, Dec. 16, 10:15-12:15. You are allowed 15 sheets of notes and a calculator. Any needed tables will be provided. CHECK FORMULAS: YOU ARE RESPONSIBLE FOR ANY ERRORS ON THIS HANDOUT!

The final covers ch. 1, 2, 3, 5, 6, and section 7.1, but not ch. 4. Points 1)-6), 8), 9), 14), 19, 28)-35), and 42)-47) from the last 3 exam reviews are especially important, as are the points below.

For DOE, assume that the residual degrees of freedom are large enough for testing. Then the response and residual plots contain much information. Linearity and constant variance may be reasonable if the p dot plots have roughly the same shape and spread, and the dot plots scatter about the identity line. The p dot plots of the residuals should have similar shape and spread, and the dot plots scatter about the $r = 0$ line. It is easier to check linearity with the response plot and constant variance with the residual plot. Curvature is often easier to see in a residual plot, but the response plot can be used to check whether the curvature is monotone or not. The response plot is more effective for determining whether the signal to noise ratio is strong or weak, and for detecting outliers or influential cases.

The fixed effects two way Anova model has two factors A and B plus a response Y. Factor A has a levels and factor B has b levels. There are ab treatments. The cell means model is $Y_{ijk} = \mu_{ij} + e_{ijk}$ where $i = 1, ..., a$; $j = 1, ..., b$; and $k = 1, ..., m$. The sample size $n = abm$. The μ_{ij} are constants and the e_{ijk} are iid with mean 0 and variance σ^2. Hence the $Y_{ijk} \sim f(y - \mu_{ij})$ come from a location family with location parameter μ_{ij}. The fitted values are $\hat{Y}_{ijk} = \overline{Y}_{ijo} = \hat{\mu}_{ij}$ while the residuals $r_{ijk} = Y_{ijk} - \hat{Y}_{ijk}$.

53) **Know that the 4 step test for AB interaction** is
i) Ho no interaction H_A there is an interaction
ii) F_{AB} is obtained from output.
iii) The pvalue is obtained from output.
iv) If pvalue $< \delta$ reject Ho, and conclude that there is an interaction between A and B, otherwise fail to reject Ho, and conclude that there is no interaction between A and B.

54) Keep A and B in the model if there is an AB interaction.

55) **Know that the 4 step test for A main effects** is
i) Ho $\mu_{10} = \cdots = \mu_{a0}$ H_A not Ho
ii) F_A is obtained from output.
iii) The p–value is obtained from output.
iv) If pvalue $< \delta$ reject Ho and conclude that the mean response depends on the level of A, otherwise fail to reject Ho and conclude that the mean response does not depend on the level of A.

56) **Know that the 4 step test for B main effects** is
i) Ho $\mu_{01} = \cdots = \mu_{0b}$ H_A not Ho
ii) F_B is obtained from output.
iii) The pvalue is obtained from output.
iv) If p–value $< \delta$ reject Ho and conclude that the mean response depends on the level of B, otherwise fail to reject Ho and conclude that the mean response does not depend on the level of B.

The tests for main effects (points 48) and 49)) do not always make sense if the test

for interactions is rejected.

Shown is an ANOVA table for the two way Anova model given in symbols. Sometimes "Error" is replaced by "Residual," or "Within Groups." A and B are the main effects while AB is the interaction. Sometimes "p-value" is replaced by "P", "$Pr(>F)$" or "PR > F." The p-value corresponding to F_A is for Ho: $\mu_{10} = \cdots = \mu_{a0}$. The p-value corresponding to F_B is for Ho: $\mu_{01} = \cdots = \mu_{0b}$. The p-value corresponding to F_{AB} is for Ho: there is no interaction.

Source	df	SS	MS	F	p-value
A	a-1	SSA	MSA	F_A=MSA/MSE	pval
B	b-1	SSB	MSB	F_B=MSB/MSE	pval
AB	$(a-1)(b-1)$	SSAB	MSAB	F_{AB}=MSAB/MSE	pval
Error	$n - ab = ab(m-1)$	SSE	MSE		

An **interaction plot** is made by plotting the levels of one factor (either $1, ..., a$ or $1, ..., b$) versus the cell sample means $\overline{Y}_{ij0}$. Typically the factor with more levels (eg A if $a > b$) is used on the horizontal axis. If the levels of A are on the horizontal axis, use line segments to join the a means that have the same j. There will be b curves on the plot. If the levels of B are on the horizontal axis, use line segments to join the b means that have the same i. There will be a curves on the plot. If **no interaction** is present, then the curves should be roughly parallel.

The interaction plot is rather hard to use, especially if the $n_{ij} = m$ are small. For small m, the curves could be far from parallel even if there is no interaction, but the further the curves are from being parallel, the greater the evidence of interaction. Intersection of curves suggests interaction unless the two curves are nearly the same. The two curves may be nearly the same if two levels of one factor give nearly the same mean response for each level of the other factor. Then the curves could cross several times even though there is no interaction. Software fills space. So the vertical axis needs to be checked to see whether the sample means for two curves are "close" with respect to the standard error $\sqrt{MSE/m}$ for the means.

57) The interaction plot is the most useful if the conclusions for the plot agree with the conclusions for the F test for no interaction.

If A and B are factors, then there are 5 possible models.

i) The two way Anova model has terms A, B and AB.

ii) The additive model or main effects model has terms A and B.

iii) The one way Anova model that uses factor A.

iv) The one way Anova model that uses factor B.

v) The null model does not use any of the three terms A, B or AB. If the null model holds, then $Y_{ijk} \sim f(y - \mu_{00})$ so the Y_{ijk} form a random sample of size n from a location family and the factors have no effect on the response.

A two way Anova model could be fit as a one way Anova model with $k = ab$ treatments, but for balanced models where $n_{ij} \equiv m$, this procedure loses information about A, B and the interaction AB.

58) Response, residual and transformation plots are used in the same way for the two

way (and k way) Anova models as for the one way Anova model.

The μ_{ij} of the cell means model can be parameterized as $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j + (\alpha\beta)_{ij}$ for $i = 1, ..., a$ and $j = 1, ..., b$. Here the α_i are the A main effects and $\sum_i \alpha_i = 0$. The β_i are the B main effects and $\sum_j \beta_j = 0$. The $(\alpha\beta)_{ij}$ are the interaction effects and satisfy $\sum_i (\alpha\beta)_{ij} = 0$, $\sum_j (\alpha\beta)_{ij} = 0$ and $\sum_i \sum_j (\alpha\beta)_{ij} = 0$. The interaction effect $(\alpha\beta)_{ij} = \mu_{ij} - \mu_{i0} - \mu_{0j} + \mu_{00}$. Here the *row factor means* $\mu_{i0} = \sum_j \mu_{ij}/b$, the *column factor means* $\mu_{0j} = \sum_i \mu_{ij}/a$ and $\mu_{00} = \sum_i \sum_j \mu_{ij}/(ab)$.

If there is no interaction, then the factor effects are additive: $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j$.

Use **factorial crossing** to compare the effects (main effects, pairwise interactions, ..., k-fold interaction if there are k factors) of two or more factors. If $A_1, ..., A_k$ are the factors with l_i levels for $i = 1, ..., k$; then there are $l_1 l_2 \cdots l_k$ treatments where each treatment uses exactly one level from each factor.

Below is a partial Anova table for a k way Anova design with the degrees of freedom left blank. For A, use $H_0 : \mu_{10\cdots0} = \cdots = \mu_{l_10\cdots0}$. The other main effect have similar null hypotheses. For interaction, use H_0 : no interaction.

Source	df	SS MS	F	p-value
k main effects		eg SSA = MSA	F_A	p_A
$\binom{k}{2}$ 2 factor interactions		eg SSAB = MSAB	F_{AB}	p_{AB}
$\binom{k}{3}$ 3 factor interactions		eg SSABC = MSABC	F_{ABC}	p_{ABC}
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$\binom{k}{k-1}$ $k-1$ factor interactions				
the k factor interaction		SSA$\cdots$L = MSA$\cdots$L	$F_{A\cdots L}$	$p_{A\cdots L}$
Error		SSE MSE		

These models get complex rapidly as k and the number of levels l_i increase. As k increases, there are a large number of models to consider. For experiments, usually the 3 way and higher order interactions are not significant. Hence a **full model** that includes all k main effects and $\binom{k}{2}$ 2 way interactions is a useful starting point for response, residual and transformation plots. The higher order interactions can be treated as potential terms and checked for significance. As a rule of thumb, significant interactions tend to involve significant main effects.

The sample size $n = m \prod_{i=1}^{k} l_i \geq m \, 2^k$ is minimized by taking $l_i = 2$ for $i = 1, ..., k$. Hence the sample size grows exponentially fast with k.

A **block** is a group of similar (homogeneous) units in that the units in a block are expected to give similar values of the response if given the same treatment.

In agriculture, adjacent plots of land are often used as blocks since adjacent plots tend to give similar yields. Litter mates, siblings, twins, time periods (eg different days) and batches of material are often used as blocks.

The *completely randomized block design* (CRBD) with k treatments and b blocks of k units uses randomization within each block to assign exactly one of the block's k units to each of the k treatments. This design is a generalization of the matched pairs procedure.

59) The **Anova F test for the completely randomized block design** with k treatments and b blocks is nearly the same as the fixed effects one way Anova F test.

i) Ho: $\mu_1 = \mu_2 = \cdots = \mu_k$ and H_A: not Ho.

ii) Fo = MSTR/MSE is usually given by output.

iii) The p-value = $P(F_{k-1,(k-1)(b-1)} > F_o)$ is usually given by output.

iv) If the p–value $< \delta$, reject Ho and conclude that the mean response depends on the level of the factor. Otherwise fail to reject Ho and conclude that the mean response does not depend on the level of the factor. Give a nontechnical sentence.

Shown below is an ANOVA table for the completely randomized block design.

Source	df	SS	MS	F	p-value
Blocks	b-1	SSB	MSB	"F_{block}"	"p_{block}"
Treatment	k-1	SSTR	MSTR	F_0=MSTR/MSE	pval for Ho
Error	$(k-1)(b-1)$	SSE	MSE		

60) Rule of thumb: If $p_{block} \geq 0.1$, then blocking was not useful. If $0.05 \leq p_{block} < 0.1$, then the usefulness was borderline. If $p_{block} < 0.05$, then blocking was useful.

61) The response, residual and transformation plots for CRBD are used almost in the same way as for multiple linear regression when all of the $n_{ij} \equiv m = 1$. Look for the plotted points falling in roughly evenly populated bands about the identity line and $r = 0$ line.

62) The **block response scatterplot** plots blocks versus the response. The plot will have b dot plots of size k with a symbol corresponding to the treatment. Dot plots with clearly different means suggest that blocking was useful. A symbol pattern within the blocks suggests that the response depends on the factor.

The **three basic principles of DOE** (design of experiments) are

i) use **randomization** to assign units to treatments.

ii) Use **factorial crossing** to compare the effects (main effects, pairwise interactions, ..., J-fold interaction) for $J \geq 2$ factors. If $A_1, ..., A_J$ are the factors with l_i levels for $i = 1, ..., J$; then there are $l_1 l_2 \cdots l_J$ treatments where each treatment uses exactly one level from each factor.

iii) **Blocking** is used to divide units into blocks of similar units where "similar" means the units are likely to have similar values of the response when given the same treatment. Within each block randomly assign units to treatments.