

1. Please provide answers to the following questions about checking the assumptions of the single-factor ANOVA model.

a) Explain what a residual plot is, and give the main reason for examining a residual plot. Be specific.

A residual plot is a scatterplot of residuals vs. estimated mean values. A residual is the difference between an observation and its estimated mean. If variation in residuals is not constant across different estimated mean values, this indicates a violation of the constant variance assumption. Checking the constant variance assumption is the main reason for examining a residual plot. (8 points)

b) Sketch a residual plot that indicates some violation of a model assumption. State what assumption appears to be violated and describe a course of action that may correct the problem.

The most common answer was to sketch a residual plot in which the variation in the residuals increased as the estimated mean increased (see Figure 4.2 on page 128). In such cases, a log transformation of the response variable may correct the problem. The log won't work if the variation in residuals decreases as the estimated mean increases or if variation is greatest in the middle. (8 points)

2. Researchers conducted a study of the effects of a potentially toxic compound on weight gain in rats. A total of fifty rats were randomly assigned to five dose groups using a completely randomized, balanced design. The dose groups were defined by the amount of the compound each rat received. The doses considered were 0, 100, 200, 500, and 750 mg/kg body weight. The researchers measured the amount of weight gained (or lost if negative) by each rat during the test period. The weight gain means for each treatment along with the mean square error from the fit of the single-factor analysis of variance model are provided below.

Dose (mg/kg)	0	100	200	500	750	MSE
Weight Gain Mean (g)	10.40	10.33	8.48	4.43	-4.50	9.63

a) After seeing the estimated treatment means provided above, one of the researchers remarked, "The mean for the 750 mg/kg dose appears to be significantly less than each of the other means. Is that true?". What method would you use to address this question? Assume that you should keep the probability of one or more type I errors below 0.05. Circle the best answer below.

ANOVA F -test Bonferroni Dunnett Hsu Tukey Contrast Sum of Squares

This calls for comparing each treatment mean to the lowest observed mean using Hsu's "test for the worst." This method will give a list of treatments that could have the lowest mean, thereby allowing us to determine the answer to the question. The Tukey method could be used, but that would overcorrect since this method is designed for all possible pairwise comparisons of treatment means. That is overkill for this problem because we only want to make four comparisons rather than all ten pairwise comparisons. (7 points)

b) Prior to collecting the data, one of the researchers said that there would be evidence of toxicity if any one of the nonzero doses had a mean weight gain that was significantly less than the mean for the 0 dose treatment. If the researchers want to keep the probability of making one or more type I errors below 0.05, what method would be best for testing for toxicity using this criterion? Circle the best answer below.

ANOVA F -test Bonferroni Dunnett Hsu Tukey Linear Combination of Means

This calls for Dunnett's method for comparing all treatments to a single treatment that has been designated prior to observing the data. From the statement of the problem, the Dunnett 95% one-sided confidence limits produced by SAS would be appropriate. (7 points)

c) Another researcher said that there would be evidence of toxicity if weight gain tended to decrease as the dose increased. She decided to use Tukey's method for making all pairwise comparisons of treatment means. She obtained the table below by issuing the SAS command `lsmeans dose / adjust=Tukey pdiff;`

i / j	0	100	200	500	750
0		1. 0000	0. 6412	0. 0008	<. 0001
100	1. 0000		0. 6724	0. 0010	<. 0001
200	0. 6412	0. 6724		0. 0415	<. 0001
500	0. 0008	0. 0010	0. 0415		<. 0001
750	<. 0001	<. 0001	<. 0001	<. 0001	

Based on this output, list all pairs of means that are significantly different from one another. Again assume that the researchers want to keep the probability of making one or more type I errors below 0.05.

By noting which p-values in the table are less than 0.05, we can see that dose 500 was significantly different from all other treatments. Likewise dose 750 was significantly different from all other treatments.

0 vs. 500, 100 vs. 500, 200 vs. 500, 0 vs. 750, 100 vs. 750, 200 vs. 750, 500 vs. 750

No other differences were significant. (8 points)

d) A researcher claims that the results of the Tukey analysis prove that the compound is safe (i.e., nontoxic) at low doses but toxic at the higher doses. Explain why you agree or disagree with this claim.

We do have evidence that weight gain tended to decrease as the dose increased. Dose 500 had a significantly lower weight gain than all lower dose treatments. Likewise, dose 750 had a significantly lower weight gain than all lower dose treatments. Insofar as reduced weight gain is associated with toxicity, we have established evidence of toxicity for higher doses. We have NOT established that the compound is nontoxic or safe at lower doses. The observed decreases in weight gain means were not statistically significant for doses of 100 and 200. That does not imply that those doses have no effect on weight gain. Failing to reject the null hypothesis simply means that we cannot rule out the possibility of no effect. An adverse effect is still a very real possibility. (8 points)

e) Suppose another researcher wants to get simultaneous confidence intervals for the mean weight gains associated with each of the five treatments. The researcher wants all five intervals to contain the parameters they are estimating with simultaneous confidence level 95%. Each of these confidence intervals has the form

$$\text{estimate} + \text{or} - t^*SE(\text{estimate})$$

Because the data are balanced, the $t^*SE(\text{estimate})$ part will be the same for all intervals. Compute the appropriate value of $t^*SE(\text{estimate})$. Recall that $MSE=9.63$ for this data.

We need to use the Bonferroni method here. Because we want 5 simultaneous confidence intervals (one for each treatment mean), we divide alpha by 5. Thus we need to look up $t_{0.025/5, 45}=t_{0.005, 45}$ which is approximately equal to 2.7. Note the 45 d.f. come from the fact that we have 5 treatments and 10 reps per treatment so that $N-t=50-5=45$. The standard error for a treatment mean is simply $\sqrt{MSE[(1^2)/r]}=\sqrt{9.63[1/10]}=\sqrt{0.963}$. Note that a treatment mean is just a very simple linear combination of treatment means (weight of 1 on one of the means and 0 on the others), so you could use the linear combinations of means formulas to get the standard error if you forgot how to compute the standard error of a treatment mean. The answer is approximately $2.7\sqrt{0.963}=2.65$. (8 points)*

3. Researchers were interested in studying the effect of temperature and light level on the growth of bacterial colonies on potato leaflets. Bacteria were inoculated onto a total of 48 leaflets. The leaflets were randomly assigned to treatment with one of four temperatures (10, 15, 20, or 25°C) and one of three light levels (A=low, B=medium, or C=high). Four weeks after inoculation, the log of the area of the bacterial colony on each leaflet was measured as the response variable. A completely randomized design was used with four leaflets for each combination of temperature and light intensity. Use the SAS code and output on the last page of your exam to answer the following questions.

a) Were there significant differences among the 12 treatment means? Give an appropriate test statistic, its degrees of freedom, a p -value, and a simple "yes" or "no" for a conclusion.

From SAS output: $F=8.50$, $d.f.=11$ and 36 , $p\text{-value}<0.0001$, yes (7 points)

b) Were there any significant differences among the temperature lsmeans? Give an appropriate test statistic, its degrees of freedom, a p -value, and a simple "yes" or "no" for a conclusion.

From SAS output: $F=5.68$, $d.f.=3$ and 36 , $p\text{-value}=0.0027$, yes (7 points)

c) Two models have been fit to the data. Does the second model fit the data adequately? Give an appropriate test statistic, its degrees of freedom, a p -value, and a brief conclusion.

$F = \frac{(1128.67 - 932.13) / (42 - 36)}{932.13 / 36} = 1.27$ Compared to an F -distribution with $42 - 36 = 6$ and 36 $d.f.$, the $p\text{-value} > 0.05$.
Thus there is no evidence of lack of fit for the second model. It may fit adequately.
(8 points)

Now, for each of the three light intensities, suppose there is a linear relationship between the mean of the response variable and temperature.

d) For low light level A, provide the estimated linear regression equation relating mean response to temperature.

$Mean(Y) = b_0 + b_1(Light\ A) + b_2(Light\ B) + b_3(Temp) + b_4(Light\ A)(Temp) + b_5(Light\ B)(Temp)$ Just like city/sludge example.

When light level is A, $(Light\ A) = 1$ and $(Light\ B) = 0$. Thus by substituting accordingly in the above equation, we have

$Mean(Y) = (b_0 + b_1) + (b_3 + b_4)(Temp)$ which is estimated by $(2.0445 - 2.3075) + (0.2766 + 0.808)(Temp)$ which simplifies to

$Y_{hat} = -0.263 + 1.0846(Temp)$ (8 points)

e) For high light level C, give an approximate 95% confidence interval for the slope of the linear regression equation. Based on this confidence interval, is there evidence that temperature affected bacterial colony growth at high light level C? Explain.

For light level C, both $(Light\ A)$ and $(Light\ B)$ are equal to zero. Thus the equation for C is simply

$Mean(Y) = b_0 + b_3(Temp)$ (Substitute 0 for $(Light\ A)$ and $(Light\ B)$ in the first equation in the answer to part d)

From the SAS output we see that the estimate for b_3 is 0.2766. The standard error is 0.23183211. The error $d.f.$ are 42, so the relevant t -value from the table is approximately 2.021. The 95% confidence interval is

$0.2766 + \text{or} - (2.021) * (0.23183211) \quad <====> \quad -0.192 \text{ to } 0.745$

This interval contains zero, so it may be that temperature has no effect on bacteria growth when the light level is high.
(8 points)

f) Estimate the difference between the slope for low light level A and the slope for high light level C, and determine if that difference is significantly different from 0. Provide the estimated difference, a test statistic, its degrees of freedom, a p -value, and a brief conclusion.

From parts (d) and (e), it should be clear that the difference between the slope for A and the slope for C is simply b_4 . Directly from the SAS output we have Estimate = 0.808, $t\text{-stat} = 2.46$, $p\text{-value} = 0.0179$. The error $d.f.$ are 42, so the $t\text{-stat}$ has 42 $d.f.$ We can conclude that the slope for light level A is significantly greater than the slope for light level C. (8 points)

```

proc glm;
  class light temp;
  model y=light temp light*temp;
run;

```

Class Level Information

Class	Levels	Values
light	3	A B C
temp	4	10 15 20 25
Number of observations 48		

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	2420.799306	220.072664	8.50	<.0001
Error	36	932.134425	25.892623		
Corrected Total	47	3352.933731			

Source	DF	Type I SS	Mean Square	F Value	Pr > F
light	2	1588.672888	794.336444	30.68	<.0001
temp	3	441.252123	147.084041	5.68	0.0027
light*temp	6	390.874296	65.145716	2.52	0.0389

Source	DF	Type III SS	Mean Square	F Value	Pr > F
light	2	1588.672887	794.336444	30.68	<.0001
temp	3	441.252123	147.084041	5.68	0.0027
light*temp	6	390.874296	65.145716	2.52	0.0389

```

proc glm;
  class light;
  model y=light temp light*temp / solution;
run;

```

Class Level Information

Class	Levels	Values
light	3	A B C
Number of observations 48		

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	2224.265059	444.853012	16.55	<.0001
Error	42	1128.668673	26.873064		
Corrected Total	47	3352.933731			

Source	DF	Type I SS	Mean Square	F Value	Pr > F
light	2	1588.672888	794.336444	29.56	<.0001
temp	1	373.276984	373.276984	13.89	0.0006
temp*light	2	262.315188	131.157594	4.88	0.0124

Source	DF	Type III SS	Mean Square	F Value	Pr > F
light	2	12.3292407	6.1646204	0.23	0.7960
temp	1	373.2769837	373.2769837	13.89	0.0006
temp*light	2	262.3151875	131.1575938	4.88	0.0124

Parameter	Estimate	Standard Error	t Value	Pr > t
Intercept	2.044500000	4.25902782	0.48	0.6337
light A	-2.307500000	6.02317490	-0.38	0.7036
light B	1.760000000	6.02317490	0.29	0.7716
light C	0.000000000	.	.	.
temp	0.276600000	0.23183211	1.19	0.2395
temp*light A	0.808000000	0.32786011	2.46	0.0179
temp*light B	-0.141250000	0.32786011	-0.43	0.6688
temp*light C	0.000000000	.	.	.