Statistics 5301 — Exam 1 Sketched Solutions NAME _____
February 6, 1998
Gary W. Oehlert ID# _____

For questions 1-6, please also refer to sample analyses of the data attached at the back of these solutions.
1. Describe how you checked assumptions and what you decided. Tell me about nonnormality, nonconstant variance, outliers, and so on. Were there any problems that required fixing?

We have to use the 3 factor interaction as error, though we may wish to pool nonsignificant two factor interactions (e.g., source by temperature) into error. The residuals plots seem OK, though with very few df for error it is difficult to draw strong conclusions about the errors. In fact, residuals look OK on the log scale too.

2. Were all the starch sources equivalent? If not, which ones differed from the others?

No, starch source 4 was different from the other 3 starch sources. This can be seen from paired comparisons on the starch main effects, or by the fact that the starch source effect is nonsignificant when starch 4 data are eliminated from the analysis.
3. Describe the effect of starch concentration on gel strength. Is it consistent across the levels of starch source?

Gel strength increases significantly with concentration for all starch sources. The size of the increase is about the same for the first 3 starches, but is much smaller for the last starch. Thus the source by concentration interaction is essentially a one cell interaction. This can be determined from contrasts in concentration separate for each source, or by fitting an indicator term for the starch 4/concentration 2 combination, or by reanalyzing the data without the source 4 data.
4. Describe how you checked assumptions and what you decided. Tell me about nonnormality, nonconstant variance, outliers, and so on. Were there any problems that required fixing?

Yes, the data showed nonconstant variance. Box-Cox suggests power -.5, but a log is nearly as good. On the log scale, constant variance is improved, but still not perfect. There were no other problems.
5. Protein concentration is a quantitative effect. Was its effect linear, or were there nonlinear (quadratic or cubic) effects?

Leucine increases linearly with concentration of protein. There was no evidence for significant quadratic or cubic terms.
6. Is there evidence of a protein by source interaction? If so, describe this interaction.

Yes, the relationship between response and protein concentration is linear, but the slope is different in each source group. Actually, the slope is not significantly different for sources 1 and 2, but source 3 has a larger slope.
7. Suppose that in a certain experimental situation I expect treatment effects of (-2, -1, 3), an error variance of 7, and I will test at the .05 level. For replication of n=6, my power is .81. What does it mean to have power .81?

Power is the probability of rejecting the null hypothesis when the null hypothesis is incorrect. In this case, if we actually have the supposed treatment effects, error variance, and replication, then we have probability .81 of rejecting the null hypothesis at the .05 level (that is, of declaring significant treatment effects).
8. Suppose that we compute the total effects for an unreplicated 2^4 factorial design ....

It appears that effects, 2, 4, and 6 are large, and the others are negligible. These are the B, C, and BC interactions. Thus we would conclude that factors B and C have significant effects and a significant interaction, but there is no evidence for any other effects or interactions.

Statistics 5301
Winter 1998

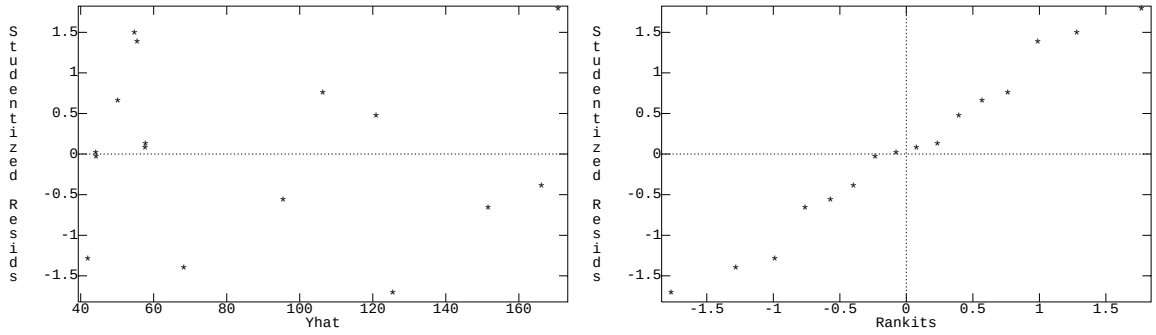
Exam #1 Data Analysis Solutions

1) **Summary.** Starch source, concentration, and temperature all affect gel strength, with concentration having the largest effect. All effects starch are due to starch 4. At the low level of concentration, the four starches have approximately the same gel strength. At the high level of concentration, the gels are 70 to 100 g stronger for starches 1, 2, and 3, and only about 24 g stronger for starch 4. Overall, temperature and concentration act multiplicatively. On starches 1, 2, and 3, concentration 2 is about 2.8 times as strong as concentration 1, and temperature 2 is about 1.28 times as strong as temperature 1.

Analysis. This is a 4x2x2 factorial with no df for error. To begin, we will use the 3-factor interaction as error. After an initial ANOVA, there is not sign of nonconstant variance. The initial ANOVA indicates that the source by temperature interaction is not significant (F=1.1), so we will pool this two factor interaction into error to get a 6 df error term. The resulting ANOVA follows:

	DF	SS	MS	F	P-value
CONSTANT	1	1.2449e+05	1.2449e+05	1461.20081	2.1404e-08
source	3	4057.9	1352.6	15.87727	0.0029314
pct	1	19789	19789	232.28708	5.0367e-06
source.pct	3	3363.5	1121.2	13.16000	0.0047673
temp	1	3460.4	3460.4	40.61768	0.00070116
pct.temp	1	1009.7	1009.7	11.85120	0.013758
ERROR1	6	511.16	85.194		

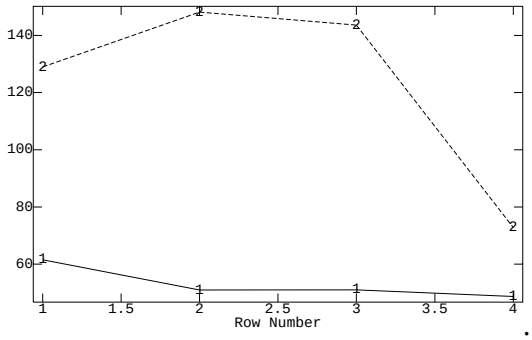
Residual plots do not indicate any problems,



and Box-Cox does not indicate any transformation is necessary.

Some understanding of the source and concentration effects can be obtained by looking at the table of marginal means

(1,1)	61.5	128.95
(2,1)	50.95	148.15
(3,1)	51	143.6
(4,1)	48.7	72.8

or the interaction plot 

. The means at the first concentration are about the same for all starches, while the means at the second concentration are about the same for the first three starches, but the starch 4 mean is lower. The 95% HSD for comparing 4 means of samples of size 2 (across starches within a concentration) is $\sqrt{85.194/2}q_{.05}(4,6) = 6.53 \times 4.90 = 32$, while that for comparing 8 means of samples of size 2 (across all 8 starch concentration combinations) is about 40. Thus the three highest means form a common group separated from all the others, the four starches at low concentration always group, and starch 4 at high concentration is either by itself or grouped with the low concentration starches depending on whether we compare only within level of concentration or across all 8 starch by concentration combinations. Starch 4 is the source of the signifcant starch effect and starch by combination interaction. If we redo the ANOVA using only starches 1, 2, and 3, then starch has no significant effects or interactions.

	DF	SS	MS	P-value
CONSTANT	1	1.1374e+05	1.1374e+05	3.1019e-06
source	2	37.432	18.716	0.80559
pct	1	22059	22059	8.0854e-05
source.pct	2	512.91	256.46	0.15209
temp	1	2360.4	2360.4	0.0058234
pct.temp	1	1146.6	1146.6	0.020124
ERROR1	4	327.92	81.98	

The temperature by concentration means follow

(1,1)	46.275	100.72
(2,1)	59.8	146.02

Increasing the concentration leads to slightly more than a doubling, while changing from temperature 1 to 2 leads to somewhat less than a 50% increase. This seems to be a multiplicative structure, and indeed, analysis on the log scale shows no concentration by temperature interaction.

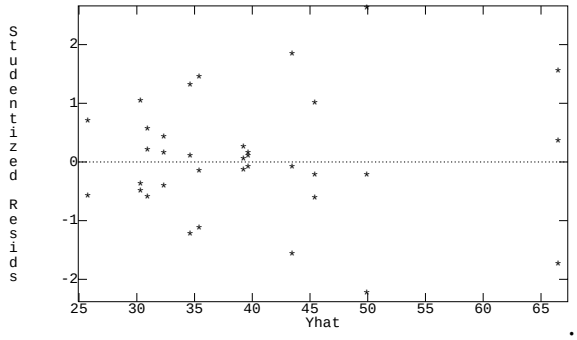
	DF	SS	MS	P-value
CONSTANT	1	303.35	303.35	2.4182e-11
source	3	0.51066	0.17022	0.016619
pct	1	2.6057	2.6057	3.3631e-05
source.pct	3	0.27483	0.091609	0.062423
temp	1	0.44883	0.44883	0.003837
pct.temp	1	0.012273	0.012273	0.47904
ERROR1	6	0.12931	0.021552	

However, residuals show nonconstant variance on the log scale.

2) **Summary.** Leucine concentration depends on both the protein source and the concentration. On the log scale, serum leucine increases linearly with protein concentration, but with a different slope and intercept for each source of protein. The fitted equation is

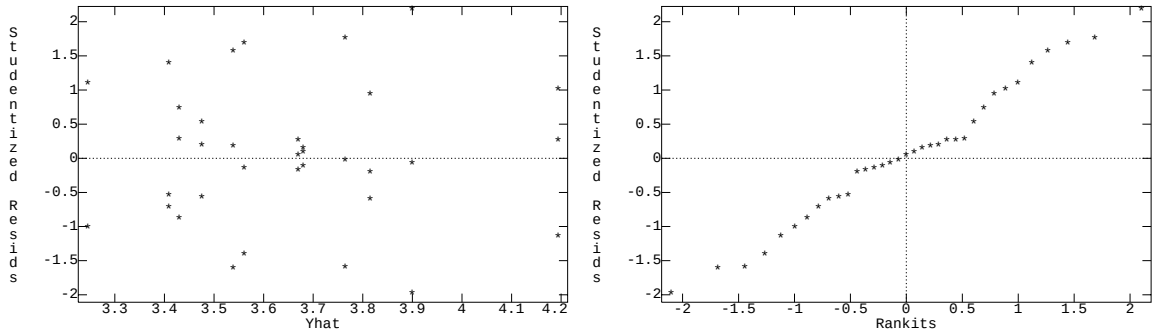
$$\log \text{leucine} = \left\{ \begin{array}{c} 3.1197 \\ 3.3073 \\ 2.9387 \end{array} \right\} + \left\{ \begin{array}{c} 0.020365 \\ 0.027279 \\ 0.067863 \end{array} \right\} \text{concentration}$$

Analysis. These data are from an unbalanced 4x3 factorial. The source factor is qualitative, the percent factor is quantitative with levels 9, 12, 15, and 18 percent. Residuals from an initial 4x3 ANOVA show nonconstant variance.



Box-Cox analysis indicates that a reciprocal square root is best, though the log is almost as good. Future analysis is on the log scale.

After transforming to the log scale, residuals look improved, though still not perfect.



Since percent is quantitative, we analyze using a polynomial fit in percent. Also, since the data are unbalanced, we do our ANOVA models in two orders.

	DF	SS	MS	F	P-value
CONSTANT	1	466.63	466.63	41038.50220	0
p	1	0.51208	0.51208	45.03530	7.6012e-07
p2	1	0.00078144	0.00078144	0.06872	0.79554
p3	1	0.028267	0.028267	2.48600	0.12852
source	2	1.2763	0.63816	56.12348	1.4187e-09
p.source	2	0.1671	0.083552	7.34806	0.0034077
p2.source	2	0.015363	0.0076813	0.67554	0.51869
p3.source	2	0.00051956	0.00025978	0.02285	0.97743
ERROR1	23	0.26152	0.011371		

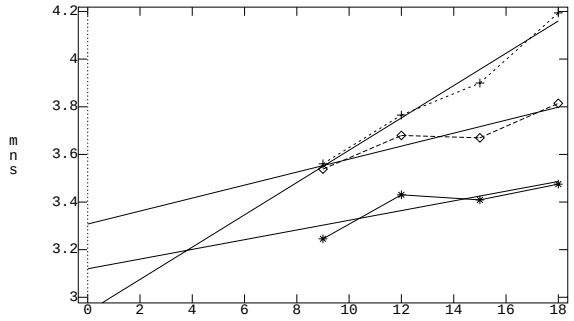
	DF	SS	MS	F	P-value
CONSTANT	1	466.63	466.63	41038.50220	0
source	2	1.1824	0.59119	51.99272	2.9289e-09
p	1	0.5989	0.5989	52.67141	2.1872e-07
p2	1	0.00033685	0.00033685	0.02962	0.86485
p3	1	0.035823	0.035823	3.15052	0.08914
source.p	2	0.1671	0.083552	7.34806	0.0034077
source.p2	2	0.015363	0.0076813	0.67554	0.51869
source.p3	2	0.00051956	0.00025978	0.02285	0.97743
ERROR1	23	0.26152	0.011371		

It appears that the source by quadratic in percent and source by cubic in percent interactions are not signficant, and neither are the quadratic and cubic main effects of percent.

The significant terms are source, linear in percent, and source by linear in percent interaction. This corresponds to a separate slope (in percent) and intercept for each source. Refitting with this model, we get the following coefficients:

```
component: source
(1)       3.1197       3.3073       2.9387
component: source.p
(1,1)     0.020365
(2,1)     0.027279
(3,1)     0.067863
```

This figure illustrates the model fit



This plot suggests the possibility that sources 1 and 2 have the same slope. We check this by making a new factor (s2) that has only two levels, 1 for source 1 and 2, and 2 for source 3.

	DF	SS	MS	P-value
source	3	467.81	155.94	0
s2.p	2	0.76607	0.38303	1.4833e-08
source.p	1	0.002939	0.002939	0.60435
ERROR1	29	0.31056	0.010709	

We see that there is no significant difference between the source 1 and 2 slopes (the source.p term after s2.p). However, there is a significant difference between the source 1 and 2 intercepts:

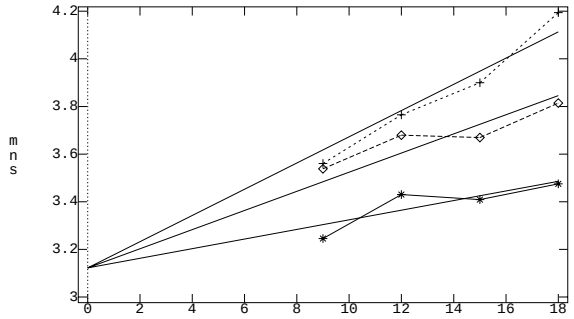
	DF	SS	MS	P-value
s2	2	467.39	233.69	0

s2.p	2	0.7364	0.3682	1.3379e-08
source	1	0.45599	0.45599	2.6007e-07
ERROR1	30	0.3135	0.01045	

One additional model to consider is a model where all sources have the same intercept, but there are different slopes. We check this by looking at source adjusted for source.p (not our usual way of procedure).

	DF	SS	MS	P-value
CONSTANT	1	466.63	466.63	0
p.source	3	1.904	0.63466	1.7504e-12
source	2	0.047397	0.023699	0.12752
ERROR1	29	0.31056	0.010709	

This shows that the common intercept model is not significantly worse than the separate lines model. The common intercept model is illustrated here:



The common intercept is 3.122 and the slopes are (0.020206, 0.040201, 0.055069). However, the residuals from this model show a slight curved pattern that would lead me to reject it, even though the F-test says it is not worse than the separate lines model: