

Analysis of Val Spicer's sensory data involving %free, judge and %protein  
for GRAPE flavoring

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March, 2002

The design involved  $N = 120$  observations on each of two responses: aroma intensity and taste. There was one experimental factor: PPROTEIN and a block: JUDGE. There were 4 levels of PPROTEIN and 10 judges. The main questions of interest were whether or not mean aroma and taste varied by PPROTEIN and whether this association corresponds with that seen in the first experiment.

After averaging over days for each judge, the experiment forms a completely randomized block design with 10 blocks. The averaged intensity measurements then conform well to the assumptions of normality and homoscedasticity underlying ANOVA.

For the TASTE intensities, the PPROTEIN effect is significant ( $p = 0.0150$ ) and the variability among the judges is not statistically significant ( $p > 0.10$ ). Of the six pairwise comparisons among the four protein means only the one comparing the highest and lowest levels of PPROTEIN is statistically significant using Tukey's adjustment for multiplicity of comparisons. Simultaneous 95% confidence intervals are given below as are the Tukey-adjusted  $P$ -values.

The GLM Procedure  
ANOVA table for TASTE

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	32.45555556	10.81851852	4.17	0.0150
judge	9	10.77777778	1.19753086	0.46	0.8873
Error	27	70.04444444	2.5942387		
Corrected Total	39	113.2777778			

pprotein	tastem LSMEAN	LSMEAN Number
0	6.06666667	1
2	5.00000000	2
4	4.30000000	3
6	3.63333333	4

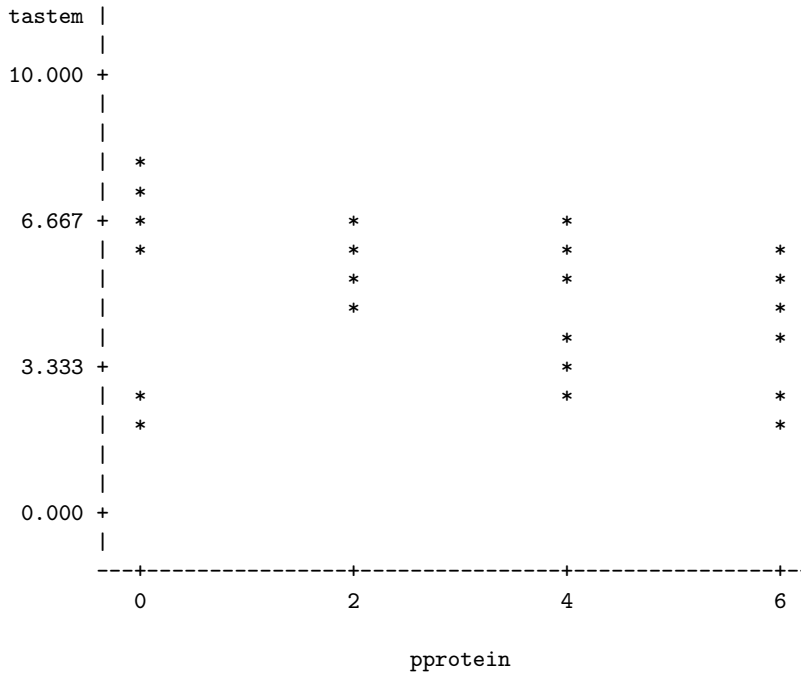
pvalues: Pr > |t| for H0: LSMean(i)=LSMean(j)

i/j	1	2	3	4
1		0.4625	0.0910	0.0113
2	0.4625		0.7664	0.2529
3	0.0910	0.7664		0.7915
4	0.0113	0.2529	0.7915	

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
1	2	1.066667	-0.904511	3.037844
1	3	1.766667	-0.204511	3.737844
1	4	2.433333	0.462156	4.404511
2	3	0.700000	-1.271177	2.671177
2	4	1.366667	-0.604511	3.337844
3	4	0.666667	-1.304511	2.637844

The figure below plots the mean for each judge-by-pprotein combination. This plot, together with the protein means given above, indicates that mean taste measurement decreases as pprotein increases.

Figure 1: plot of mean taste by pprotein.



A lack-of-fit test can be carried out to test a hypothesis that mean taste is linear-decreasing in pprotein. The lack-of-fit F-ratio,  $F = 0.09$  shown in the ANOVA table below, is not statistically significant, indicating that a model in which taste is linear-decreasing in pprotein is plausible. The estimated slope of a simple linear regression of taste on pprotein is  $\hat{\beta} = -0.4$  with a standard error of 0.10. The output is on the following page.

Source	DF	Type I SS	Mean Square	F Value	Pr > F
pprotein	1	32.00000000	32.00000000	12.34	0.0016
judge	9	10.77777778	1.19753086	0.46	0.8873
proteinc (lack-of-fit)	2	0.45555556	0.22777778	0.09	0.9162
Error	27	70.04444444	2.5942387		
Corrected Total	39	113.2777778			

For the aroma intensities, the PPROTEIN effect is highly significant ( $p < 0.0001$ ) and the variability among the judges is not statistically significant ( $p > 0.10$ ). All of the comparisons of mean aroma by protein level are statistically significant except the one comparing the 2nd and 3rd levels. Simultaneous 95% confidence intervals and adjusted  $p$ -values based on Tukey's procedure follow the ANOVA table below:

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	83.76388889	27.92129630	39.13	<.0001
judge	9	11.30277778	1.25586420	1.76	0.1234
Error	27	19.2638889	0.7134774		
Corrected Total	39	114.3305556			

Least Squares Means  
Adjustment for Multiple Comparisons: Tukey

pprotein	aromam LSMEAN	LSMEAN Number
0	6.90000000	1
2	4.76666667	2
4	4.46666667	3
6	2.83333333	4

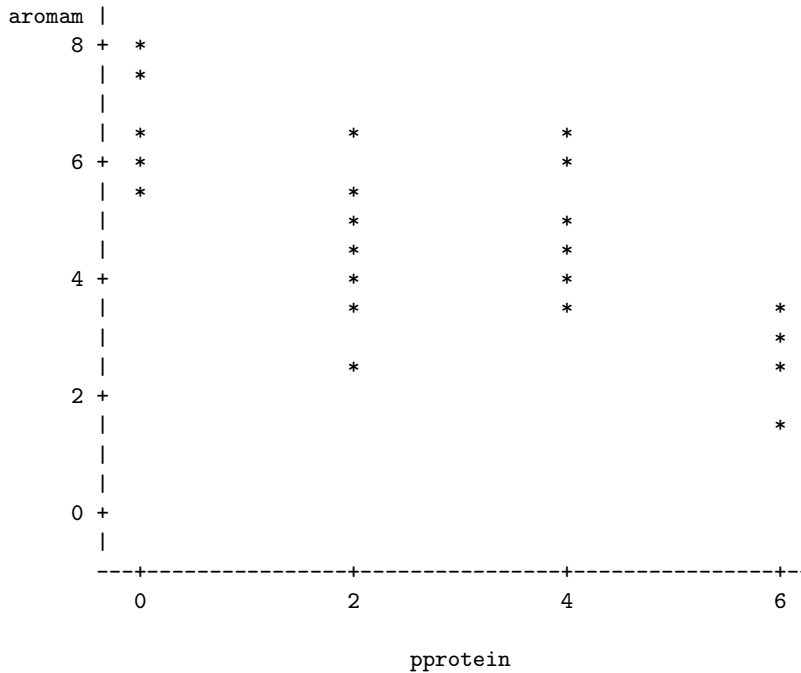
pvalues: Pr > |t| for H0: LSMean(i)=LSMean(j)

i/j	1	2	3	4
1		<.0001	<.0001	<.0001
2	<.0001		0.8564	0.0001
3	<.0001	0.8564		0.0010
4	<.0001	0.0001	0.0010	

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
			Lower	Upper
1	2	2.133333	1.099594	3.167072
1	3	2.433333	1.399594	3.467072
1	4	4.066667	3.032928	5.100406
2	3	0.300000	-0.733739	1.333739
2	4	1.933333	0.899594	2.967072
3	4	1.633333	0.599594	2.667072

The figure below plots mean aroma measurement by level of PPROTEIN. It appears that mean aroma decreases nonlinearly as PPROTEIN increases. The lack-of-fit  $F$ -ratio  $F = 3.95$  is significant ( $p = 0.03$ ), confirming the suspicion of nonlinearity. The output appears below the plot. This negative association between aroma and pprotein for grape flavoring does not appear to correspond with the associations between %FREE and PPROTEIN at various temperature levels (plotting symbols) observed in the other experiment. Residual plots did not indicate any violations of model assumptions underlying the ANOVA and are omitted from this writeup.

Figure 2: plot of mean aroma by pprotein.



Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	1	78.12500000	78.12500000	109.50	<.0001
judge	9	11.30277778	1.25586420	1.76	0.1234
protein <sub>c</sub> (lack-of-fit)	2	5.63888889	2.81944444	3.95	0.0312
Error	27	19.2638889	0.7134774		
Corrected Total	39	114.3305556			

Figure 3: plot of mean %FREE by pprotein.  
(from previous experiment)

