

Follow-up analysis of Val Spicer's data involving %free, judge and %protein

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The second 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 (there were 3 in the first experiment) 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 of 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 highly significant ( $p < 0.0001$ ) and there is substantial variability among the judges as well. All six pairwise differences among the four protein means are statistically significant except the one involving the two highest levels of PPROTEIN. Means and Tukey's simultaneous 95% confidence intervals are given below.  $P$ -values for the difference based on Tukey's procedure are given as well.

ANOVA table for mean tastes

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	91.94444444	30.64814815	23.49	<.0001
judge	9	50.95555556	5.66172840	4.34	0.0014
Error	27	35.2222222	1.3045267		
Corrected Total	39	178.1222222			

Adjustment for Multiple Comparisons: Tukey

pprotein	tastem LSMEAN	LSMEAN Number
0	6.70000000	1
2	4.76666667	2
4	2.90000000	3
6	3.16666667	4

Least Squares Means for effect pprotein  
 Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: tastem

i/j	1	2	3	4
1		0.0041	<.0001	<.0001
2	0.0041		0.0057	0.0203
3	<.0001	0.0057		0.9530
4	<.0001	0.0203	0.9530	

Least Squares Means for Effect pprotein

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
1	2	1.933333	0.535526	3.331140
1	3	3.800000	2.402193	5.197807
1	4	3.533333	2.135526	4.931140
2	3	1.866667	0.468860	3.264474
2	4	1.600000	0.202193	2.997807
3	4	-0.266667	-1.664474	1.131140

For the aroma intensities, the PPROTEIN effect is highly significant ( $p < 0.0001$ ) but the variability among the judges is not statistically significant. The only statistically significant differences were those involving the lowest level of PPROTEIN. That is, the mean aroma measurement at 0 PPROTEIN differs significantly from all three other means and there were no significant differences among the other three means. Simultaneous 95% confidence intervals and adjusted  $p$ -values based on Tukey's procedure follow the ANOVA table below:

ANOVA table for mean aroma intensities

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	76.27500000	25.42500000	15.83	<.0001
judge	9	24.24722222	2.69413580	1.68	0.1436
Error	27	43.3638889	1.6060700		
Corrected Total	39	143.8861111			

Adjustment for Multiple Comparisons: Tukey

pprotein	aromam LSMEAN	LSMEAN Number
0	6.73333333	1
2	4.13333333	2
4	3.53333333	3
6	3.23333333	4

Least Squares Means for effect pprotein  
 Pr > |t| for H0: LSMean(i)=LSMean(j)

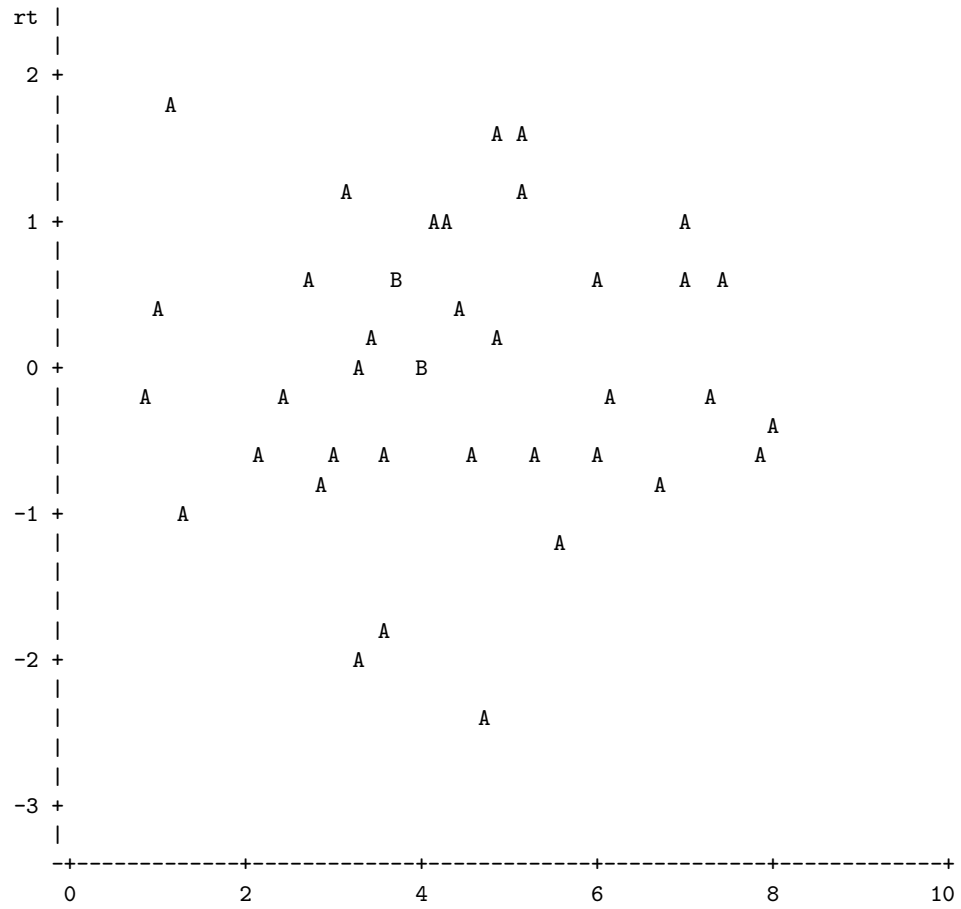
Dependent Variable: aromam

i/j	1	2	3	4
1		0.0005	<.0001	<.0001
2	0.0005		0.7170	0.4020
3	<.0001	0.7170		0.9512
4	<.0001	0.4020	0.9512	

Least Squares Means for Effect pprotein

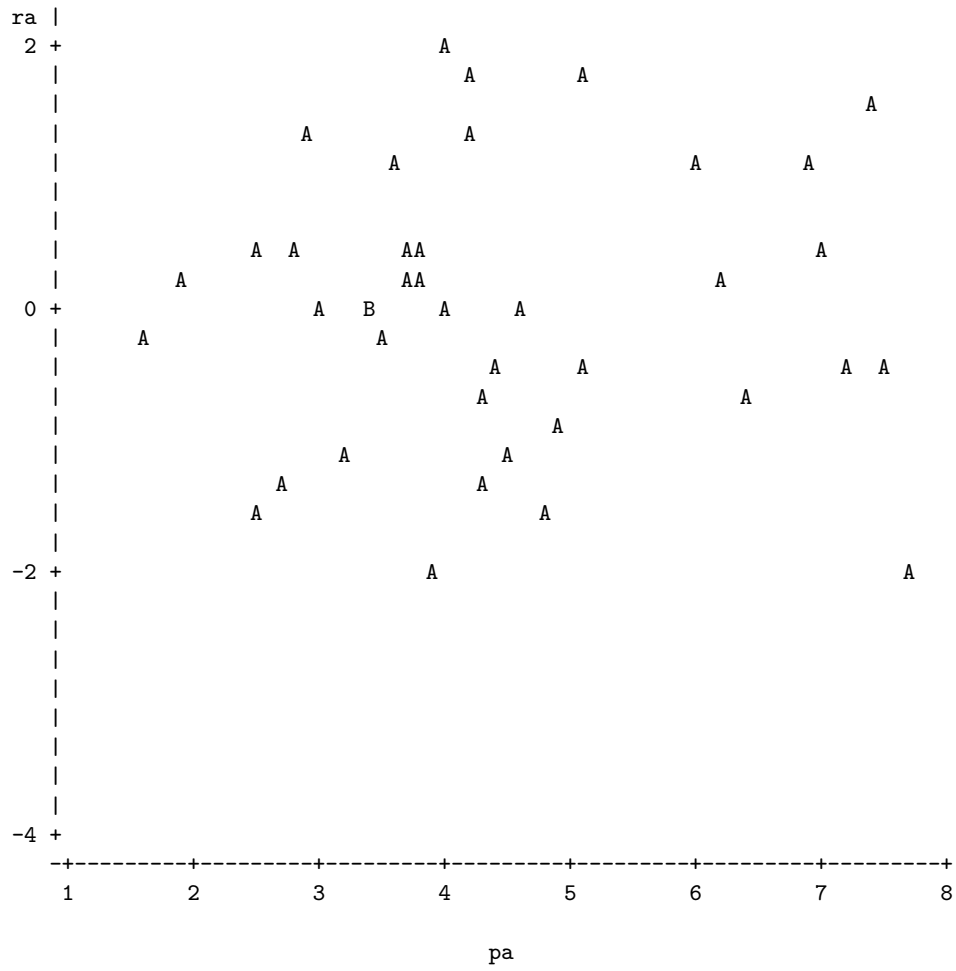
i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
1	2	2.600000	1.049031	4.150969
1	3	3.200000	1.649031	4.750969
1	4	3.500000	1.949031	5.050969
2	3	0.600000	-0.950969	2.150969
2	4	0.900000	-0.650969	2.450969
3	4	0.300000	-1.250969	1.850969

Residuals by predicted tastes. Legend: A = 1 obs, B = 2 obs, etc.

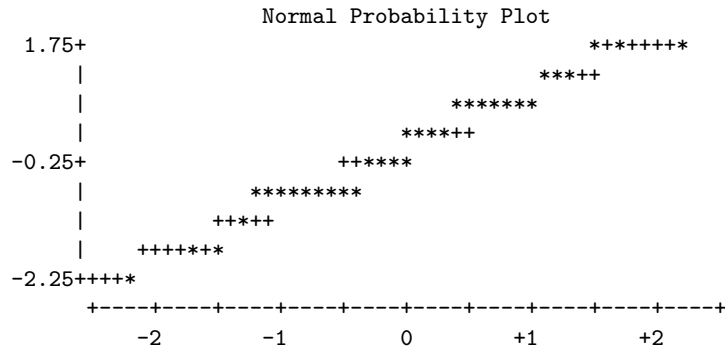


pt

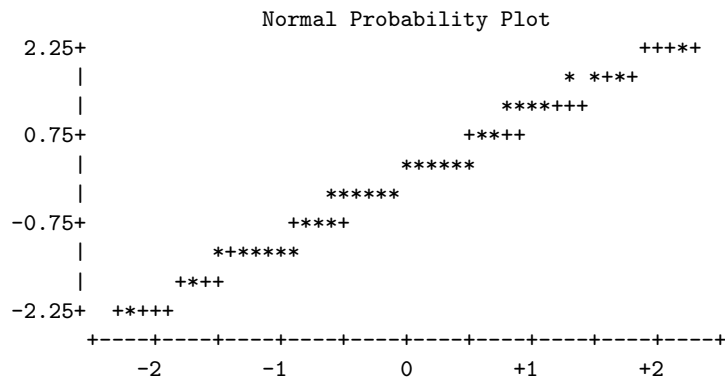
Residuals by predicted aromas. Legend: A = 1 obs, B = 2 obs, etc.



Variable: taste residuals



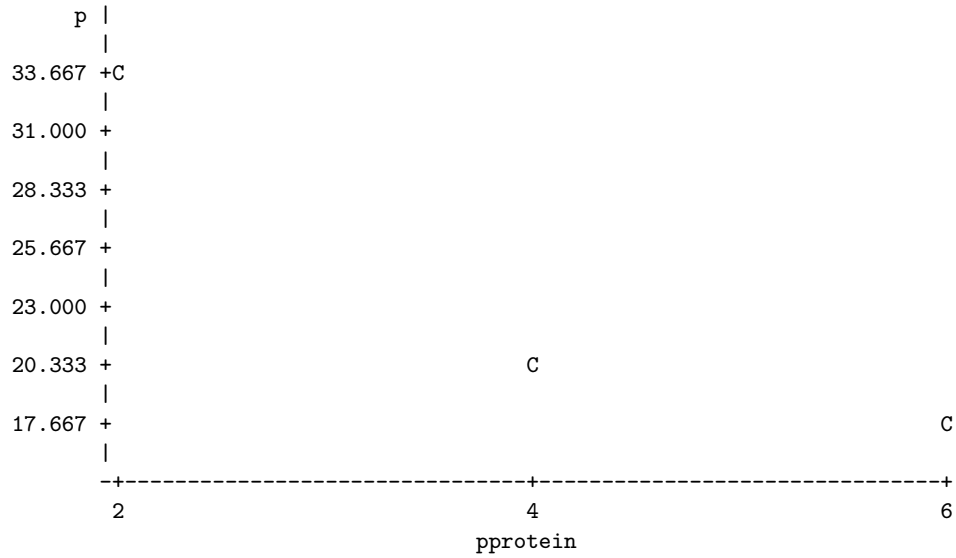
Variable: aroma residuals



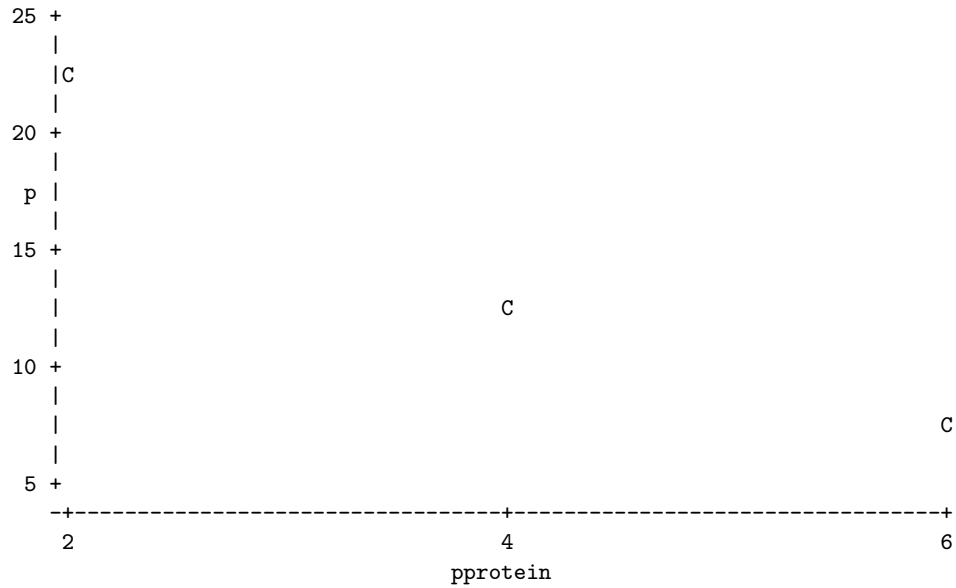
To address the issue of correspondence between PFREE and aroma and taste judgements, plots of mean PFREE vs PPROTEIN appear on this page and the next. They are followed by plots of mean aroma judgement and mean taste judgement vs PPROTEIN.

----- temp=45 -----

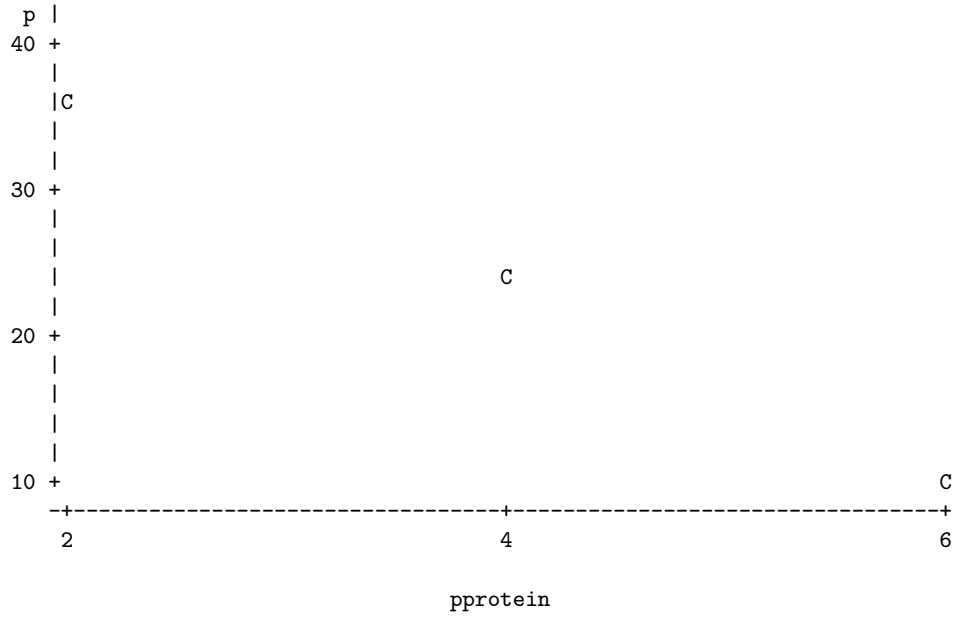
Plots of p\*pprotein. Legend: A = 1 obs, B = 2 obs, etc.



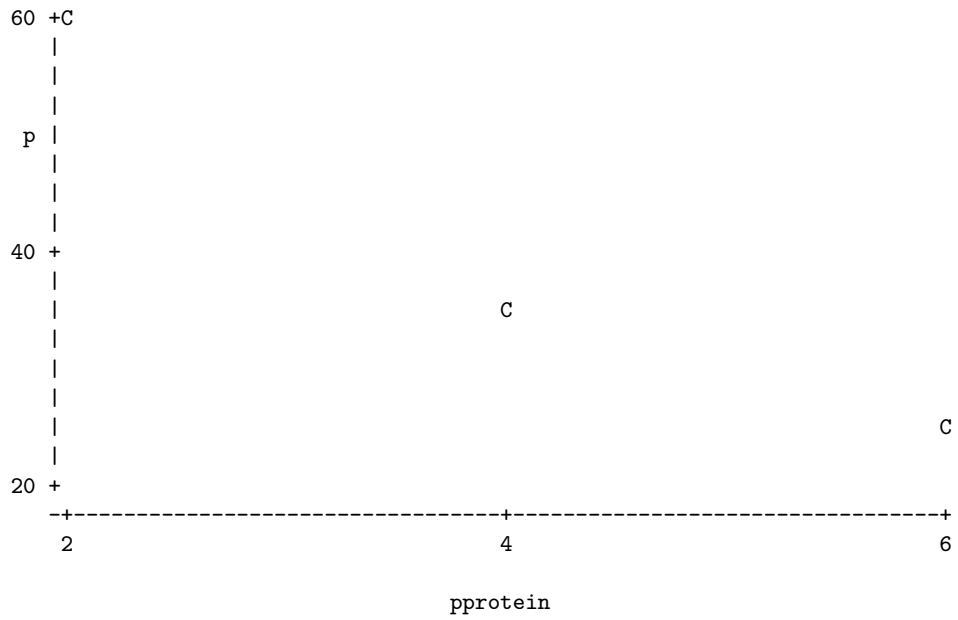
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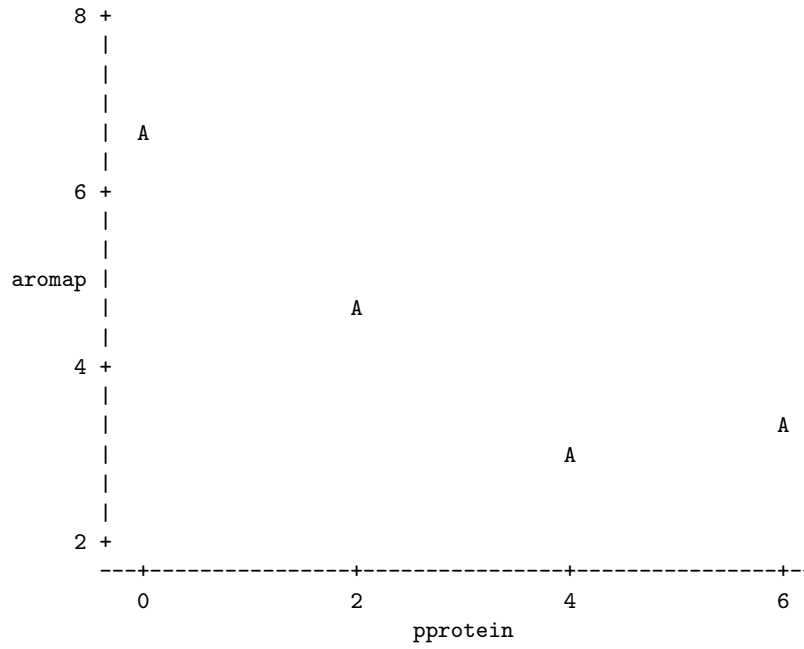
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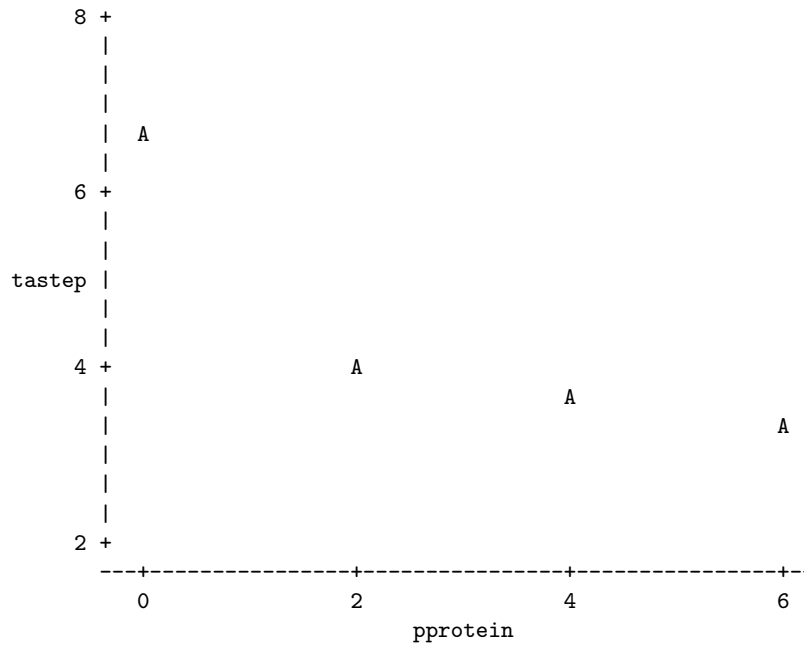
----- temp=75 -----



Plot of aromap\*pprotein. Legend: A = 1 obs, B = 2 obs, etc.



Plot of tastep\*pprotein. Legend: A = 1 obs, B = 2 obs, etc.



While no test of significance is proposed, the agreement of these six plots indicates a general decrease in %free, taste and aroma with increasing values of %protein over the range 0 – 6% considered here. Some SAS code follows:

```

option ls=75 ps=100;

data aroma; /* aroma denotes intensity */
  input pprotein judge day aroma @@;
  cards;
0 1 1 8 0 1 2 6 0 1 3 8
0 2 1 7 0 2 2 8 0 2 3 9
. . .
6 10 1 0 6 10 2 4 6 10 3 2
;
run;

data taste; /* taste denotes intensity */
  input pprotein judge day taste @@;
  cards;
0 1 1 6 0 1 2 6 0 1 3 6
0 2 1 3 0 2 2 4 0 2 3 0
. . .
6 10 1 3 6 10 2 2 6 10 3 2
;
run;

data one;
  merge aroma taste;
  by pprotein judge day;
run;
proc sort; by judge pprotein day; run;
proc means noprint;
  by judge pprotein;
  var aroma taste;
  output out=onemeans mean=aromam tastem;
run;
proc glm noprint;
  class judge pprotein;
  model tastem aromam=pprotein judge;
  output out=two p=pt pa=r=rt ra;
run;
options ps=40;
proc plot;
  plot rt*pt;
  plot ra*pa;
run;
proc univariate normal plot;
  var rt ra;
run;

```