

Analysis of Val Spicer's volatility data  
for CHERRY flavor

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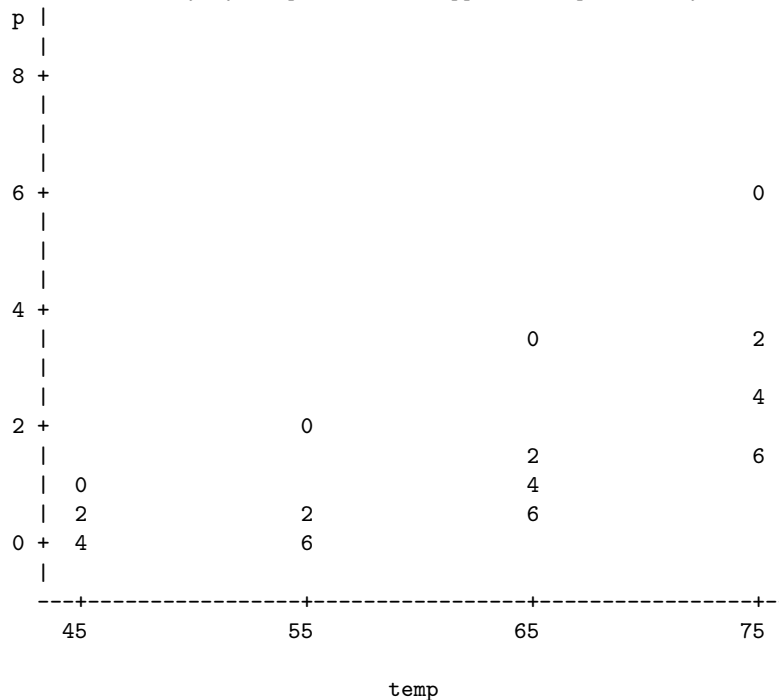
March, 2002

The design involved  $N = 48$  observations and two experimental factors: TEMP and PPROTEIN. There were 4 levels of the TEMP factor and 4 levels of the PPROTEIN factor. The response variable considered was  $y$  =volatility. There was very little variability in the response relative to the observed treatment means in the experiment (observed coefficient of variation was  $CV = \sqrt{MSE}/\bar{y} = 9\%$ ). All of the effects in the full factorial model were highly significant ( $p < 0.0001$ ). Mean volatility is increasing in temperature and decreasing in % protein and the temperature profiles are not the same across levels of % protein (see figure #1 below.) That is, the interaction between temperature and % protein is highly significant. The ANOVA table and plot of the observed treatment means (Figure #1) appear as below:

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	52.22416667	17.40805556	870.40	<.0001
temp	3	65.74750000	21.91583333	1095.79	<.0001
pprotein*temp	9	14.50083333	1.61120370	80.56	<.0001
Error	32	0.64000000	0.02000000		
Corrected Total	47	133.11250000			

Figure #1

Mean volatility by temperature and pprotein (plotted symbol)



The treatment means and their standard errors are given in the table below.

The GLM Procedure  
Least Squares Means

pprotein	temp	Volatility LSMEAN	Standard Error	LSMEAN Number
0	45	1.0666667	0.08164966	1
0	55	2.1000000	0.08164966	2
0	65	3.7333333	0.08164966	3
0	75	6.2333333	0.08164966	4
2	45	0.3666667	0.08164966	5
2	55	0.4666667	0.08164966	6
2	65	1.3000000	0.08164966	7
2	75	3.7333333	0.08164966	8
4	45	0.2000000	0.08164966	9
4	55	0.3000000	0.08164966	10
4	65	0.9000000	0.08164966	11
4	75	2.3000000	0.08164966	12
6	45	0.1666667	0.08164966	13
6	55	0.1666667	0.08164966	14
6	65	0.4000000	0.08164966	15
6	75	1.5666667	0.08164966	16

For pairwise comparisons among these treatment means, Tukey-adjusted p-values are given below and are followed by Tukey-adjusted confidence limits for pairwise differences:

Least Squares Means for effect pprotein\*temp  
Pr > |t| for H0: LSmean(i)=LSmean(j)  
Adjustment for Multiple Comparisons: Tukey

i/j	1	2	3	4	5	6
1		<.0001	<.0001	<.0001	<.0001	0.0010
2	<.0001		<.0001	<.0001	<.0001	<.0001
3	<.0001	<.0001		<.0001	<.0001	<.0001
4	<.0001	<.0001	<.0001		<.0001	<.0001
5	<.0001	<.0001	<.0001	<.0001		0.9999
6	0.0010	<.0001	<.0001	<.0001	0.9999	
7	0.7971	<.0001	<.0001	<.0001	<.0001	<.0001
8	<.0001	<.0001	1.0000	<.0001	<.0001	<.0001
9	<.0001	<.0001	<.0001	<.0001	0.9816	0.6202
10	<.0001	<.0001	<.0001	<.0001	1.0000	0.9816
11	0.9816	<.0001	<.0001	<.0001	0.0049	0.0450
12	<.0001	0.9222	<.0001	<.0001	<.0001	<.0001
13	<.0001	<.0001	<.0001	<.0001	0.9222	0.4334
14	<.0001	<.0001	<.0001	<.0001	0.9222	0.4334
15	0.0002	<.0001	<.0001	<.0001	1.0000	1.0000
16	0.0106	0.0049	<.0001	<.0001	<.0001	<.0001

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

Dependent Variable: y

i/j	7	8	9	10	11	12
1	0.7971	<.0001	<.0001	<.0001	0.9816	<.0001
2	<.0001	<.0001	<.0001	<.0001	<.0001	0.9222
3	<.0001	1.0000	<.0001	<.0001	<.0001	<.0001
4	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
5	<.0001	<.0001	0.9816	1.0000	0.0049	<.0001
6	<.0001	<.0001	0.6202	0.9816	0.0450	<.0001
7		<.0001	<.0001	<.0001	0.0873	<.0001
8	<.0001		<.0001	<.0001	<.0001	<.0001
9	<.0001	<.0001		0.9999	<.0001	<.0001
10	<.0001	<.0001	0.9999		0.0010	<.0001
11	0.0873	<.0001	<.0001	0.0010		<.0001
12	<.0001	<.0001	<.0001	<.0001	<.0001	
13	<.0001	<.0001	1.0000	0.9979	<.0001	<.0001
14	<.0001	<.0001	1.0000	0.9979	<.0001	<.0001
15	<.0001	<.0001	0.9222	0.9999	0.0106	<.0001
16	0.6202	<.0001	<.0001	<.0001	0.0002	<.0001

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

Dependent Variable: y

i/j	13	14	15	16
1	<.0001	<.0001	0.0002	0.0106
2	<.0001	<.0001	<.0001	0.0049
3	<.0001	<.0001	<.0001	<.0001
4	<.0001	<.0001	<.0001	<.0001
5	0.9222	0.9222	1.0000	<.0001
6	0.4334	0.4334	1.0000	<.0001
7	<.0001	<.0001	<.0001	0.6202
8	<.0001	<.0001	<.0001	<.0001
9	1.0000	1.0000	0.9222	<.0001
10	0.9979	0.9979	0.9999	<.0001
11	<.0001	<.0001	0.0106	0.0002
12	<.0001	<.0001	<.0001	<.0001
13		1.0000	0.7971	<.0001
14	1.0000		0.7971	<.0001
15	0.7971	0.7971		<.0001
16	<.0001	<.0001	<.0001	

Least Squares Means for Effect pprotein\*temp

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
1	2	-1.033333	-1.461507	-0.605160
1	3	-2.666667	-3.094840	-2.238493
1	4	-5.166667	-5.594840	-4.738493
1	5	0.700000	0.271827	1.128173
1	6	0.600000	0.171827	1.028173
1	7	-0.233333	-0.661507	0.194840
1	8	-2.666667	-3.094840	-2.238493
1	9	0.866667	0.438493	1.294840
1	10	0.766667	0.338493	1.194840
1	11	0.166667	-0.261507	0.594840
1	12	-1.233333	-1.661507	-0.805160
1	13	0.900000	0.471827	1.328173
1	14	0.900000	0.471827	1.328173
1	15	0.666667	0.238493	1.094840
1	16	-0.500000	-0.928173	-0.071827
2	3	-1.633333	-2.061507	-1.205160
2	4	-4.133333	-4.561507	-3.705160
2	5	1.733333	1.305160	2.161507
2	6	1.633333	1.205160	2.061507
2	7	0.800000	0.371827	1.228173
2	8	-1.633333	-2.061507	-1.205160
2	9	1.900000	1.471827	2.328173
2	10	1.800000	1.371827	2.228173
2	11	1.200000	0.771827	1.628173
2	12	-0.200000	-0.628173	0.228173
2	13	1.933333	1.505160	2.361507
2	14	1.933333	1.505160	2.361507
2	15	1.700000	1.271827	2.128173
2	16	0.533333	0.105160	0.961507
3	4	-2.500000	-2.928173	-2.071827
3	5	3.366667	2.938493	3.794840
3	6	3.266667	2.838493	3.694840
3	7	2.433333	2.005160	2.861507
3	8	-1.33227E-15	-0.428173	0.428173
3	9	3.533333	3.105160	3.961507
3	10	3.433333	3.005160	3.861507
3	11	2.833333	2.405160	3.261507
3	12	1.433333	1.005160	1.861507
3	13	3.566667	3.138493	3.994840
3	14	3.566667	3.138493	3.994840
3	15	3.333333	2.905160	3.761507
3	16	2.166667	1.738493	2.594840

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
4	5	5.866667	5.438493	6.294840
4	6	5.766667	5.338493	6.194840
4	7	4.933333	4.505160	5.361507
4	8	2.500000	2.071827	2.928173
4	9	6.033333	5.605160	6.461507
4	10	5.933333	5.505160	6.361507
4	11	5.333333	4.905160	5.761507
4	12	3.933333	3.505160	4.361507
4	13	6.066667	5.638493	6.494840
4	14	6.066667	5.638493	6.494840
4	15	5.833333	5.405160	6.261507
4	16	4.666667	4.238493	5.094840
5	6	-0.100000	-0.528173	0.328173
5	7	-0.933333	-1.361507	-0.505160
5	8	-3.366667	-3.794840	-2.938493
5	9	0.166667	-0.261507	0.594840
5	10	0.066667	-0.361507	0.494840
5	11	-0.533333	-0.961507	-0.105160
5	12	-1.933333	-2.361507	-1.505160
5	13	0.200000	-0.228173	0.628173
5	14	0.200000	-0.228173	0.628173
5	15	-0.033333	-0.461507	0.394840
5	16	-1.200000	-1.628173	-0.771827
6	7	-0.833333	-1.261507	-0.405160
6	8	-3.266667	-3.694840	-2.838493
6	9	0.266667	-0.161507	0.694840
6	10	0.166667	-0.261507	0.594840
6	11	-0.433333	-0.861507	-0.005160
6	12	-1.833333	-2.261507	-1.405160
6	13	0.300000	-0.128173	0.728173
6	14	0.300000	-0.128173	0.728173
6	15	0.066667	-0.361507	0.494840
6	16	-1.100000	-1.528173	-0.671827
7	8	-2.433333	-2.861507	-2.005160
7	9	1.100000	0.671827	1.528173
7	10	1.000000	0.571827	1.428173
7	11	0.400000	-0.028173	0.828173
7	12	-1.000000	-1.428173	-0.571827
7	13	1.133333	0.705160	1.561507
7	14	1.133333	0.705160	1.561507
7	15	0.900000	0.471827	1.328173
7	16	-0.266667	-0.694840	0.161507

i	j	Difference Between Means	Simultaneous 95% Confidence Limits for LSMean(i)-LSMean(j)	
8	9	3.533333	3.105160	3.961507
8	10	3.433333	3.005160	3.861507
8	11	2.833333	2.405160	3.261507
8	12	1.433333	1.005160	1.861507
8	13	3.566667	3.138493	3.994840
8	14	3.566667	3.138493	3.994840
8	15	3.333333	2.905160	3.761507
8	16	2.166667	1.738493	2.594840
9	10	-0.100000	-0.528173	0.328173
9	11	-0.700000	-1.128173	-0.271827
9	12	-2.100000	-2.528173	-1.671827
9	13	0.033333	-0.394840	0.461507
9	14	0.033333	-0.394840	0.461507
9	15	-0.200000	-0.628173	0.228173
9	16	-1.366667	-1.794840	-0.938493
10	11	-0.600000	-1.028173	-0.171827
10	12	-2.000000	-2.428173	-1.571827
10	13	0.133333	-0.294840	0.561507
10	14	0.133333	-0.294840	0.561507
10	15	-0.100000	-0.528173	0.328173
10	16	-1.266667	-1.694840	-0.838493
11	12	-1.400000	-1.828173	-0.971827
11	13	0.733333	0.305160	1.161507
11	14	0.733333	0.305160	1.161507
11	15	0.500000	0.071827	0.928173
11	16	-0.666667	-1.094840	-0.238493
12	13	2.133333	1.705160	2.561507
12	14	2.133333	1.705160	2.561507
12	15	1.900000	1.471827	2.328173
12	16	0.733333	0.305160	1.161507
13	14	1.332268E-15	-0.428173	0.428173
13	15	-0.233333	-0.661507	0.194840
13	16	-1.400000	-1.828173	-0.971827
14	15	-0.233333	-0.661507	0.194840
14	16	-1.400000	-1.828173	-0.971827
15	16	-1.166667	-1.594840	-0.738493

Plots of residuals versus predicted values (Figure #2) and a normal plot (Figure #3) do not indicate any violations of the assumptions underlying the factorial model and analysis.

Figure #2  
Plot of res.\*pred. Legend: A = 1 obs, B = 2 obs, etc.

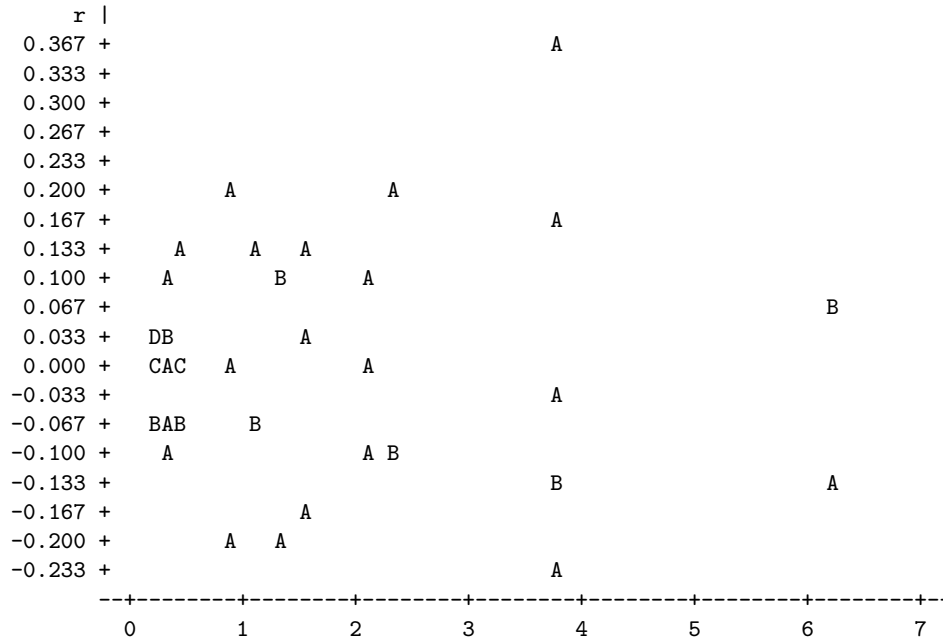
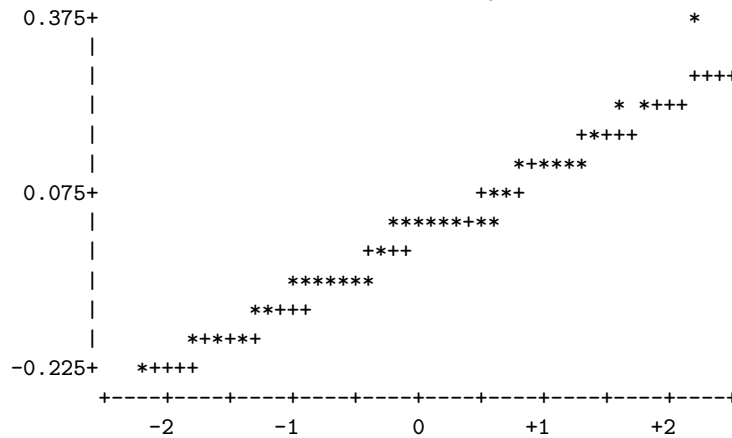


Figure #3  
Normal Probability Plot



Analysis of Val Spicer's volatility data  
for GRAPE flavor

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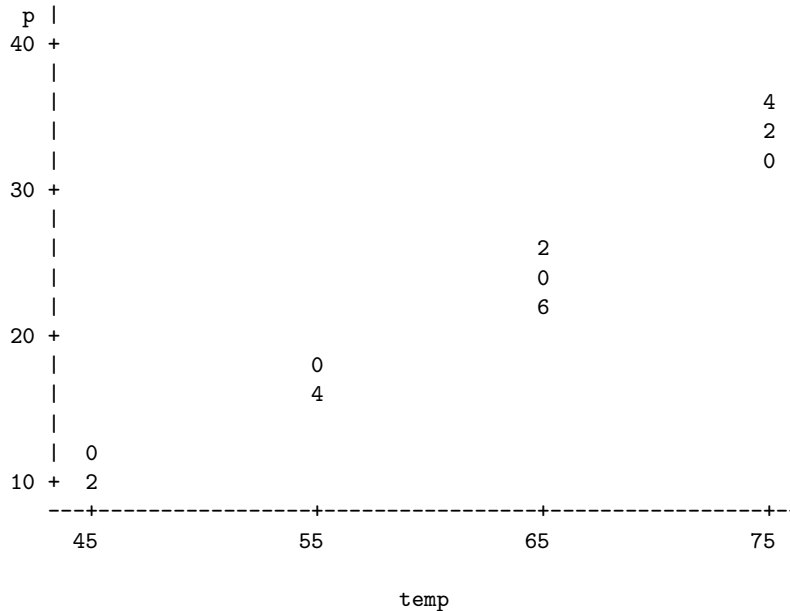
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The experimental design for the GRAPE flavor was the same as that for the CHERRY flavor. The initial analysis proceeds the same way, but yields different conclusions. For the GRAPE data, mean volatility does not differ significantly by level of % protein  $p = 0.087$ , but it does differ by temperature ( $p < 0.0001$ ). Subsequent pairwise comparisons indicate that mean volatilities at all four temperatures differ significantly.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
pprotein	3	23.612292	7.870764	2.39	0.0867
temp	3	3573.845625	1191.281875	362.30	<.0001
pprotein*temp	9	44.820208	4.980023	1.51	0.1851
Error	32	105.220000	3.288125		
Corrected Total	47	3747.498125			

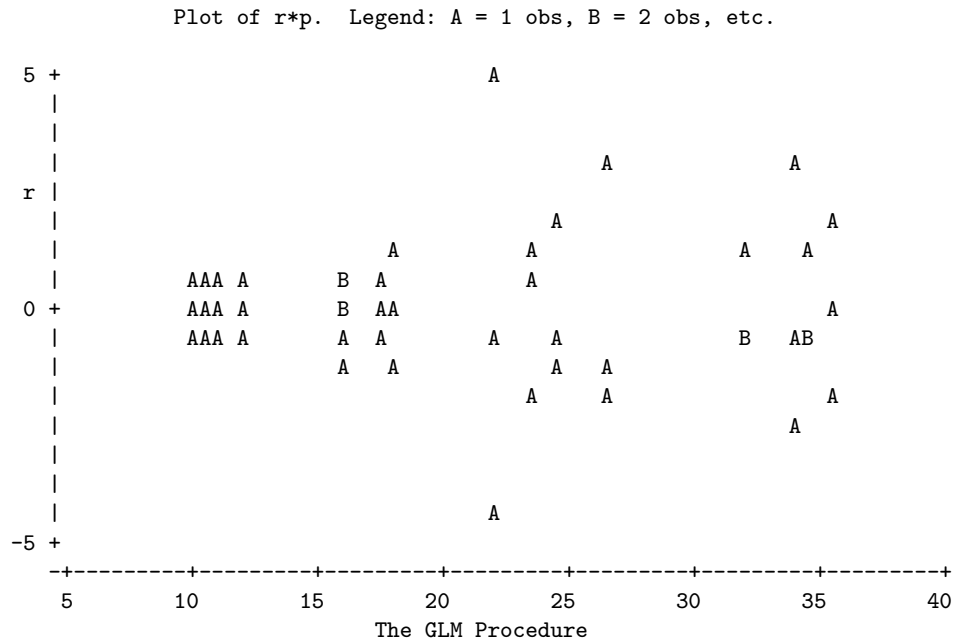
temp	LSMEAN	95% Confidence Limits	
45	10.808333	9.742080	11.874587
55	16.883333	15.817080	17.949587
65	24.183333	23.117080	25.249587
75	33.950000	32.883747	35.016253

Plot1: predicted v. temperature (symbol=protein)



The diagnostic plot of residuals versus predicted values (Figure #4 below) does indicate a heteroscedasticity problem. The variance of the volatility measurements appears to be increasing in the mean. Levene's test for homogeneity of variance on a one-way ANOVA with temperature as the experimental factor confirms this finding:

Figure #4  
residual v. predicted



Levene's Test for Homogeneity of volatility Variance  
ANOVA of Squared Deviations from Group Means

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
temp	3	389.1	129.7	2.96	0.0425
Error	44	1929.2	43.8450		

So, the same analysis was repeated for the log-transformed data and the conclusions turned out differently. The mean log-transformed volatility appears to depend on both temperature ( $p < 0.0001$ ) AND % protein ( $p < 0.01$ ), and the interaction is not statistically significant ( $p = 0.1037$ ). Subsequent comparisons reveal that all temperature means still differ significantly from one another and that there is incomplete separation among the four % protein means. (See output, next page.)

The GLM Procedure

Dependent Variable: log(volatility)

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
temp	3	8.68205716	2.89401905	473.43	<.0001
pprotein	3	0.08947830	0.02982610	4.88	0.0066
temp*pprotein	9	0.09991432	0.01110159	1.82	0.1037
Error	32	0.19561238	0.00611289		
Corrected Total	47	9.06706215			

Tukey's Studentized Range (HSD) Test for log(volatility)

Alpha	0.05
Error Degrees of Freedom	32
Error Mean Square	0.006113
Critical Value of Studentized Range	3.83162
Minimum Significant Difference	0.0865

Means with the same letter are not significantly different.

Tukey Grouping	Mean	N	temp
A	3.52326	12	75
B	3.17829	12	65
C	2.82371	12	55
D	2.37608	12	45

Alpha	0.05
Error Degrees of Freedom	32
Error Mean Square	0.006113
Critical Value of Studentized Range	3.83162
Minimum Significant Difference	0.0865

Tukey Grouping	Mean	N	pprotein
A	3.01781	12	2
A	3.01199	12	0
B A	2.96004	12	4
B	2.91150	12	6

Diagnostic plots of the log-transformed data appear to conform better to the assumptions underlying analysis of variance techniques. (See next page.)

Figure #5  
residual v. predicted

Plot of r\*p. Legend: A = 1 obs, B = 2 obs, etc.

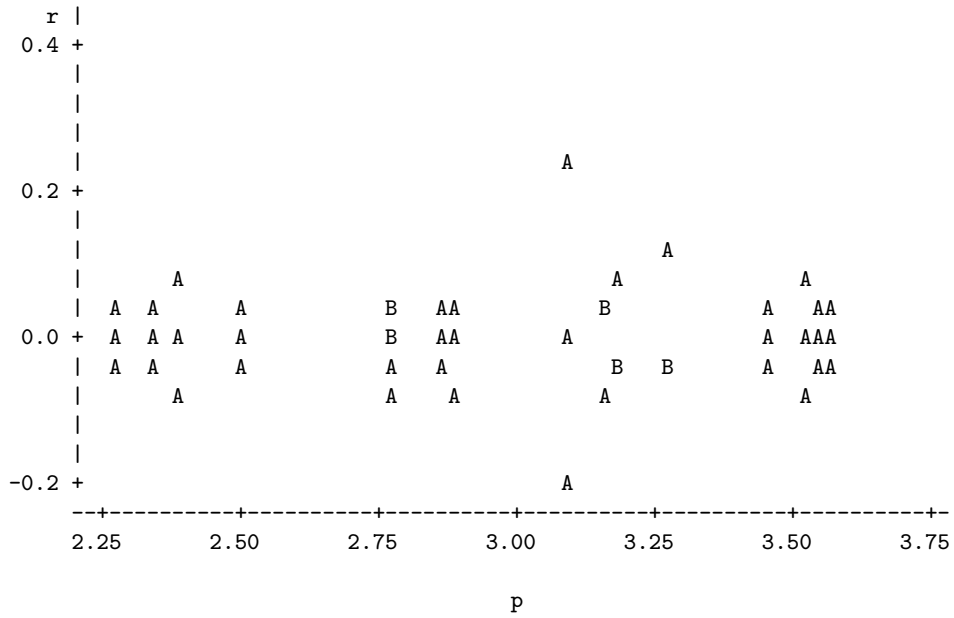


Figure #6

Normal Probability Plot

