The UNIVARIATE Procedure

Variable: DAPI_Stem_cells

Moments			
N	335	Sum Weights	335
Mean	5.84179104	Sum Observations	1957
Std Deviation	2.17952841	Variance	4.75034409
Skewness	-0.0281092	Kurtosis	-0.3865917
Uncorrected SS	13019	Corrected SS	1586.61493
Coeff Variation	37.3092497	Std Error Mean	0.11908036

Basic Statistical Measures			
Location		Variability	
Mean	5.841791	Std Deviation	2.17953
Median	6.000000	Variance	4.75034
Mode	6.000000	Range	11.00000
		Interquartile Range	3.00000

Tests for Location: Mu0=0				
Test	Statistic		p Value	
Student's t	t	49.05755	Pr > |t|	<.0001
Sign	M	167.5	Pr >= |M|	<.0001
Signed Rank	S	28140	Pr >= |S|	<.0001

Tests for Normality				
Test	Statistic		p Value	
Shapiro-Wilk	W	0.97772	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.099445	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.558945	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	3.072594	Pr > A-Sq	<0.0050

Quantiles (Definition 5)	
Quantile	Estimate
100% Max	12
99%	11
95%	9
90%	9
75% Q3	7
50% Median	6
25% Q1	4
10%	3
5%	2
1%	1
0% Min	1

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
1	186	10	333
1	70	11	95

The UNIVARIATE Procedure

Variable: DAPI_Stem_cells

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
1	62	11	145
1	53	11	326
1	29	12	119

The UNIVARIATE Procedure

Variable: RED_Cell_proliferation

Moments			
N	335	Sum Weights	335
Mean	0.82985075	Sum Observations	278
Std Deviation	1.06284768	Variance	1.12964519
Skewness	1.41298238	Kurtosis	2.18159136
Uncorrected SS	608	Corrected SS	377.301493
Coeff Variation	128.076968	Std Error Mean	0.05806957

Basic Statistical Measures			
Location		Variability	
Mean	0.829851	Std Deviation	1.06285
Median	0.000000	Variance	1.12965
Mode	0.000000	Range	6.00000
		Interquartile Range	1.00000

Tests for Location: Mu0=0				
Test	Statistic		p Value	
Student's t	t	14.29063	Pr > |t|	<.0001
Sign	M	82	Pr >= |M|	<.0001
Signed Rank	S	6765	Pr >= |S|	<.0001

Tests for Normality				
Test	Statistic		p Value	
Shapiro-Wilk	W	0.764978	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.292982	Pr > D	<0.0100
Cramer-von Mises	W-Sq	5.062665	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	29.28388	Pr > A-Sq	<0.0050

Quantiles (Definition 5)	
Quantile	Estimate
100% Max	6
99%	4
95%	3
90%	2
75% Q3	1
50% Median	0
25% Q1	0
10%	0
5%	0
1%	0
0% Min	0

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
0	333	4	192
0	332	4	195

The UNIVARIATE Procedure

Variable: RED_Cell_proliferation

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
0	331	4	306
0	329	5	299
0	328	6	179

The UNIVARIATE Procedure

Variable: YELLOW_Apoptosis

Moments			
N	335	Sum Weights	335
Mean	0.03880597	Sum Observations	13
Std Deviation	0.24771726	Variance	0.06136384
Skewness	8.04361367	Kurtosis	76.7214667
Uncorrected SS	21	Corrected SS	20.4955224
Coeff Variation	638.348316	Std Error Mean	0.01353424

Basic Statistical Measures			
Location		Variability	
Mean	0.038806	Std Deviation	0.24772
Median	0.000000	Variance	0.06136
Mode	0.000000	Range	3.00000
		Interquartile Range	0

Tests for Location: Mu0=0				
Test	Statistic		p Value	
Student's t	t	2.867244	Pr > |t|	0.0044
Sign	M	5	Pr >= |M|	0.0020
Signed Rank	S	27.5	Pr >= |S|	0.0020

Tests for Normality				
Test	Statistic		p Value	
Shapiro-Wilk	W	0.145298	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.532391	Pr > D	<0.0100
Cramer-von Mises	W-Sq	26.22112	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	121.5509	Pr > A-Sq	<0.0050

Quantiles (Definition 5)	
Quantile	Estimate
100% Max	3
99%	1
95%	0
90%	0
75% Q3	0
50% Median	0
25% Q1	0
10%	0
5%	0
1%	0
0% Min	0

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
0	335	1	182
0	334	1	192

The UNIVARIATE Procedure

Variable: YELLOW_Apoptosis

Extreme Observations			
Lowest		Highest	
Value	Obs	Value	Obs
0	333	1	195
0	332	2	130
0	331	3	127

The Mixed Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Dependent Variable	DAPI_Stem_cells
Covariance Structure	Diagonal
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Residual

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Dimensions	
Covariance Parameters	1
Columns in X	5
Columns in Z	0
Subjects	1
Max Obs Per Subject	335

Number of Observations	
Number of Observations Read	335
Number of Observations Used	335
Number of Observations Not Used	0

Covariance Parameter Estimates	
Cov Parm	**Estimate**
Residual	4.4710

Fit Statistics	
-2 Res Log Likelihood	1452.5
AIC (smaller is better)	1454.5
AICC (smaller is better)	1454.5
BIC (smaller is better)	1458.3

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Diet	3	331	7.96	<.0001

Least Squares Means						
Effect	**Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**
Diet	CCA	6.0800	0.2442	331	24.90	<.0001
Diet	CCS	6.7941	0.2564	331	26.50	<.0001
Diet	FPA	5.3121	0.1781	331	29.83	<.0001
Diet	FPS	5.6863	0.2961	331	19.20	<.0001

Differences of Least Squares Means									
Effect	**Diet**	**_Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**	**Adjustment**	**Adj P**
Diet	CCA	CCS	-0.7141	0.3541	331	-2.02	0.0445	Tukey-Kramer	0.1838
Diet	CCA	FPA	0.7679	0.3022	331	2.54	0.0115	Tukey-Kramer	0.0556

The Mixed Procedure

Differences of Least Squares Means									
Effect	**Diet**	**_Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**	**Adjustment**	**Adj P**
Diet	CCA	FPS	0.3937	0.3838	331	1.03	0.3057	Tukey-Kramer	0.7344
Diet	CCS	FPA	1.4821	0.3122	331	4.75	<.0001	Tukey-Kramer	<.0001
Diet	CCS	FPS	1.1078	0.3917	331	2.83	0.0050	Tukey-Kramer	0.0255
Diet	FPA	FPS	-0.3742	0.3455	331	-1.08	0.2796	Tukey-Kramer	0.7001

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Distribution	Poisson
Link Function	Log
Dependent Variable	DAPI_Stem_cells

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	275.5060	0.8323
Scaled Deviance	331	275.5060	0.8323
Pearson Chi-Square	331	253.8108	0.7668
Scaled Pearson X2	331	253.8108	0.7668
Log Likelihood		1506.1509	
Full Log Likelihood		-732.1557	
AIC (smaller is better)		1472.3114	
AICC (smaller is better)		1472.4326	
BIC (smaller is better)		1487.5679	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	1.7381	0.0587	1.6230	1.8531	876.04	<.0001
Diet	CCA	1	0.0669	0.0751	-0.0803	0.2142	0.79	0.3727
Diet	CCS	1	0.1780	0.0749	0.0312	0.3248	5.65	0.0175
Diet	FPA	1	-0.0681	0.0692	-0.2036	0.0675	0.97	0.3250
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
Diet	3	17.95	0.0005

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	1.8050	0.04683	38.54	<.0001
CCS	1.9161	0.04652	41.18	<.0001
FPA	1.6700	0.03654	45.70	<.0001
FPS	1.7381	0.05872	29.60	<.0001

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	-0.1111	0.06601	-1.68	0.0925
CCA	FPA	0.1350	0.05940	2.27	0.0230
CCA	FPS	0.06695	0.07511	0.89	0.3727
CCS	FPA	0.2461	0.05916	4.16	<.0001
CCS	FPS	0.1780	0.07492	2.38	0.0175
FPA	FPS	-0.06808	0.06916	-0.98	0.3250

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Distribution	Poisson
Link Function	Log
Dependent Variable	DAPI_Stem_cells

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	275.5060	0.8323
Scaled Deviance	331	331.0000	1.0000
Pearson Chi-Square	331	253.8108	0.7668
Scaled Pearson X2	331	304.9348	0.9213
Log Likelihood		1809.5287	
Full Log Likelihood		-732.1557	
AIC (smaller is better)		1472.3114	
AICC (smaller is better)		1472.4326	
BIC (smaller is better)		1487.5679	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	1.7381	0.0536	1.6331	1.8431	1052.50	<.0001
Diet	CCA	1	0.0669	0.0685	-0.0674	0.2013	0.95	0.3286
Diet	CCS	1	0.1780	0.0684	0.0440	0.3120	6.78	0.0092
Diet	FPA	1	-0.0681	0.0631	-0.1917	0.0556	1.16	0.2806
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	0.9123	0.0000	0.9123	0.9123		

Note: The scale parameter was estimated by the square root of DEVIANCE/DOF

LR Statistics For Type 3 Analysis						
Source	**Num DF**	**Den DF**	**F Value**	**Pr > F**	**Chi-Square**	**Pr > ChiSq**
Diet	3	331	7.19	0.0001	21.56	<.0001

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	1.8050	0.04272	42.25	<.0001
CCS	1.9161	0.04245	45.14	<.0001
FPA	1.6700	0.03334	50.10	<.0001
FPS	1.7381	0.05357	32.44	<.0001

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	-0.1111	0.06022	-1.84	0.0652
CCA	FPA	0.1350	0.05419	2.49	0.0127
CCA	FPS	0.06695	0.06852	0.98	0.3286
CCS	FPA	0.2461	0.05397	4.56	<.0001
CCS	FPS	0.1780	0.06835	2.60	0.0092
FPA	FPS	-0.06808	0.06310	-1.08	0.2806

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Distribution	Poisson
Link Function	Log
Dependent Variable	DAPI_Stem_cells

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	275.5060	0.8323
Scaled Deviance	331	331.0000	1.0000
Pearson Chi-Square	331	253.8108	0.7668
Scaled Pearson X2	331	304.9348	0.9213
Log Likelihood		1809.5287	
Full Log Likelihood		-732.1557	
AIC (smaller is better)		1472.3114	
AICC (smaller is better)		1472.4326	
BIC (smaller is better)		1487.5679	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	1.7381	0.0536	1.6331	1.8431	1052.50	<.0001
Diet	CCA	1	0.0669	0.0685	-0.0674	0.2013	0.95	0.3286
Diet	CCS	1	0.1780	0.0684	0.0440	0.3120	6.78	0.0092
Diet	FPA	1	-0.0681	0.0631	-0.1917	0.0556	1.16	0.2806
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	0.9123	0.0000	0.9123	0.9123		

Note: The scale parameter was estimated by the square root of DEVIANCE/DOF

LR Statistics For Type 3 Analysis						
Source	**Num DF**	**Den DF**	**F Value**	**Pr > F**	**Chi-Square**	**Pr > ChiSq**
Diet	3	331	7.19	0.0001	21.56	<.0001

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	1.8050	0.04272	42.25	<.0001
CCS	1.9161	0.04245	45.14	<.0001
FPA	1.6700	0.03334	50.10	<.0001
FPS	1.7381	0.05357	32.44	<.0001

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	-0.1111	0.06022	-1.84	0.0652
CCA	FPA	0.1350	0.05419	2.49	0.0127
CCA	FPS	0.06695	0.06852	0.98	0.3286
CCS	FPA	0.2461	0.05397	4.56	<.0001
CCS	FPS	0.1780	0.06835	2.60	0.0092
FPA	FPS	-0.06808	0.06310	-1.08	0.2806

The Mixed Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Dependent Variable	RED_Cell_proliferation
Covariance Structure	Diagonal
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Residual

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Dimensions	
Covariance Parameters	1
Columns in X	5
Columns in Z	0
Subjects	1
Max Obs Per Subject	335

Number of Observations	
Number of Observations Read	335
Number of Observations Used	335
Number of Observations Not Used	0

Covariance Parameter Estimates	
Cov Parm	**Estimate**
Residual	1.1292

Fit Statistics	
-2 Res Log Likelihood	997.0
AIC (smaller is better)	999.0
AICC (smaller is better)	999.0
BIC (smaller is better)	1002.8

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Diet	3	331	1.04	0.3750

Least Squares Means						
Effect	**Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**
Diet	CCA	0.8667	0.1227	331	7.06	<.0001
Diet	CCS	0.8676	0.1289	331	6.73	<.0001
Diet	FPA	0.8794	0.08949	331	9.83	<.0001
Diet	FPS	0.5882	0.1488	331	3.95	<.0001

Differences of Least Squares Means									
Effect	**Diet**	**_Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**	**Adjustment**	**Adj P**
Diet	CCA	CCS	-0.00098	0.1779	331	-0.01	0.9956	Tukey-Kramer	1.0000
Diet	CCA	FPA	-0.01277	0.1519	331	-0.08	0.9331	Tukey-Kramer	0.9998

The Mixed Procedure

Differences of Least Squares Means									
Effect	**Diet**	**_Diet**	**Estimate**	**Standard Error**	**DF**	**t Value**	**Pr > |t|**	**Adjustment**	**Adj P**
Diet	CCA	FPS	0.2784	0.1929	331	1.44	0.1498	Tukey-Kramer	0.4731
Diet	CCS	FPA	-0.01179	0.1569	331	-0.08	0.9402	Tukey-Kramer	0.9998
Diet	CCS	FPS	0.2794	0.1968	331	1.42	0.1567	Tukey-Kramer	0.4881
Diet	FPA	FPS	0.2912	0.1736	331	1.68	0.0945	Tukey-Kramer	0.3375

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Distribution	Poisson
Link Function	Log
Dependent Variable	RED_Cell_proliferation

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	462.1992	1.3964
Scaled Deviance	331	462.1992	1.3964
Pearson Chi-Square	331	450.7441	1.3618
Scaled Pearson X2	331	450.7441	1.3618
Log Likelihood		-327.5280	
Full Log Likelihood		-425.1597	
AIC (smaller is better)		858.3195	
AICC (smaller is better)		858.4407	
BIC (smaller is better)		873.5760	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.5306	0.1826	-0.8885	-0.1728	8.45	0.0037
Diet	CCA	1	0.3875	0.2207	-0.0451	0.8201	3.08	0.0791
Diet	CCS	1	0.3887	0.2242	-0.0508	0.8282	3.00	0.0831
Diet	FPA	1	0.4021	0.2035	0.0034	0.8009	3.91	0.0481
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
Diet	3	4.64	0.1999

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	-0.1431	0.1240	-1.15	0.2486
CCS	-0.1420	0.1302	-1.09	0.2755
FPA	-0.1285	0.08980	-1.43	0.1525
FPS	-0.5306	0.1826	-2.91	0.0037

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	-0.00113	0.1798	-0.01	0.9950
CCA	FPA	-0.01462	0.1531	-0.10	0.9239
CCA	FPS	0.3875	0.2207	1.76	0.0791
CCS	FPA	-0.01349	0.1582	-0.09	0.9320
CCS	FPS	0.3887	0.2242	1.73	0.0831
FPA	FPS	0.4021	0.2035	1.98	0.0481

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW
Distribution	Poisson
Link Function	Log
Dependent Variable	RED_Cell_proliferation

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	462.1992	1.3964
Scaled Deviance	331	331.0000	1.0000
Pearson Chi-Square	331	450.7441	1.3618
Scaled Pearson X2	331	322.7965	0.9752
Log Likelihood		-234.5563	
Full Log Likelihood		-425.1597	
AIC (smaller is better)		858.3195	
AICC (smaller is better)		858.4407	
BIC (smaller is better)		873.5760	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.5306	0.2157	-0.9535	-0.1078	6.05	0.0139
Diet	CCA	1	0.3875	0.2608	-0.1237	0.8987	2.21	0.1373
Diet	CCS	1	0.3887	0.2650	-0.1307	0.9080	2.15	0.1424
Diet	FPA	1	0.4021	0.2404	-0.0691	0.8734	2.80	0.0944
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.1817	0.0000	1.1817	1.1817		

Note: The scale parameter was estimated by the square root of DEVIANCE/DOF

LR Statistics For Type 3 Analysis						
Source	**Num DF**	**Den DF**	**F Value**	**Pr > F**	**Chi-Square**	**Pr > ChiSq**
Diet	3	331	1.11	0.3457	3.33	0.3441

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	-0.1431	0.1466	-0.98	0.3289
CCS	-0.1420	0.1538	-0.92	0.3561
FPA	-0.1285	0.1061	-1.21	0.2260
FPS	-0.5306	0.2157	-2.46	0.0139

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	-0.00113	0.2125	-0.01	0.9958
CCA	FPA	-0.01462	0.1810	-0.08	0.9356
CCA	FPS	0.3875	0.2608	1.49	0.1373
CCS	FPA	-0.01349	0.1869	-0.07	0.9424
CCS	FPS	0.3887	0.2650	1.47	0.1424
FPA	FPS	0.4021	0.2404	1.67	0.0944

The GENMOD Procedure

Model Information	
Data Set	WORK.PHENOTYPE_DATANW1
Distribution	Poisson
Link Function	Log
Dependent Variable	YELLOW_Apoptosis

Number of Observations Read	335
Number of Observations Used	335

Class Level Information		
Class	**Levels**	**Values**
Diet	4	CCA CCS FPA FPS

Parameter Information		
Parameter	**Effect**	**Diet**
Prm1	Intercept	
Prm2	Diet	CCA
Prm3	Diet	CCS
Prm4	Diet	FPA
Prm5	Diet	FPS

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Deviance	331	88.8401	0.2684
Scaled Deviance	331	331.0000	1.0000
Pearson Chi-Square	331	403.6000	1.2193
Scaled Pearson X2	331	1503.7302	4.5430
Log Likelihood		-196.4907	
Full Log Likelihood		-55.2228	
AIC (smaller is better)		118.4457	
AICC (smaller is better)		118.5669	
BIC (smaller is better)		133.7022	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-2.3224	0.2317	-2.7765	-1.8683	100.48	<.0001
Diet	CCA	1	-0.8965	0.3783	-1.6380	-0.1549	5.61	0.0178
Diet	CCS	1	-1.8971	0.5675	-3.0094	-0.7848	11.17	0.0008
Diet	FPA	1	-1.2401	0.3475	-1.9212	-0.5589	12.73	0.0004
Diet	FPS	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	0.5181	0.0000	0.5181	0.5181		

Note: The scale parameter was estimated by the square root of DEVIANCE/DOF

LR Statistics For Type 3 Analysis						
Source	**Num DF**	**Den DF**	**F Value**	**Pr > F**	**Chi-Square**	**Pr > ChiSq**
Diet	3	331	6.21	0.0004	18.64	0.0003

The GENMOD Procedure

Diet Least Squares Means				
Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	-3.2189	0.2991	-10.76	<.0001
CCS	-4.2195	0.5181	-8.14	<.0001
FPA	-3.5625	0.2590	-13.75	<.0001
FPS	-2.3224	0.2317	-10.02	<.0001

Differences of Diet Least Squares Means					
Diet	_Diet	Estimate	Standard Error	z Value	Pr > |z|
CCA	CCS	1.0006	0.5982	1.67	0.0944
CCA	FPA	0.3436	0.3957	0.87	0.3852
CCA	FPS	-0.8965	0.3783	-2.37	0.0178
CCS	FPA	-0.6570	0.5792	-1.13	0.2566
CCS	FPS	-1.8971	0.5675	-3.34	0.0008
FPA	FPS	-1.2401	0.3475	-3.57	0.0004