

**ESTIMATE PROP. IMPAIRED PRE- AND POST-INTERVENTION
FOR THIN LIQUID SWALLOW TASKS**

The SURVEYFREQ Procedure

Data Summary

Number of Clusters 30

Number of Observations 360

Table of time_cat by pas_ind

<i>time_cat</i>	<i>pas_ind</i>	<i>Frequency</i>	<i>Percent</i>	<i>Std Err of Percent</i>	<i>95% Confidence Limits for Percent</i>	<i>Row Percent</i>	<i>Std Err of Row Percent</i>	<i>95% Confidence Limits for Row Percent</i>
<i>pre</i>	<i>not impaired</i>	33	9.2958	1.4169	6.3979 12.1936	18.6441	2.8114	12.8942 24.3939
	<i>impaired</i>	144	40.5634	1.3643	37.7731 43.3536	81.3559	2.8114	75.6061 87.1058
	<i>Total</i>	177	49.8592	0.3194	49.2059 50.5124	100.000		
<i>post</i>	<i>not impaired</i>	106	29.8592	3.2343	23.2442 36.4741	59.5506	6.4055	46.4499 72.6513
	<i>impaired</i>	72	20.2817	3.2028	13.7312 26.8321	40.4494	6.4055	27.3487 53.5501
	<i>Total</i>	178	50.1408	0.3194	49.4876 50.7941	100.000		
<i>Total</i>	<i>not impaired</i>	139	39.1549	3.7346	31.5169 46.7930			
	<i>impaired</i>	216	60.8451	3.7346	53.2070 68.4831			
	<i>Total</i>	355	100.000					

Frequency Missing = 5

Rao-Scott Chi-Square Test

Pearson Chi-Square 62.3358

Design Correction 1.8708

Rao-Scott Chi-Square 33.3213

DF 1

Pr > ChiSq <.0001

F Value 33.3213

Num DF 1

Den DF 29

Pr > F <.0001

Sample Size = 355

**ESTIMATE PROP. IMPAIRED PRE- AND POST-INTERVENTION
AT EACH THIN LIQUID VOLUME**

The SURVEYFREQ Procedure

Data Summary

Number of Clusters 30

Number of Observations 360

Table of pas_ind by volume

Controlling for time_cat=pre

<i>pas_ind</i>	<i>volume</i>	<i>Frequency</i>	<i>Percent</i>	<i>Std Err of Percent</i>	<i>95% Confidence Limits for Percent</i>	<i>Row Percent</i>	<i>Std Err of Row Percent</i>	<i>95% Confidence Limits for Row Percent</i>
<i>not impaired</i>	<i>5ml</i>	29	16.3842	2.4660	11.3407 21.4277	87.8788	6.5178	74.5485 100.000
	<i>15ml</i>	3	1.6949	0.9426	0.0000 3.6227	9.0909	4.6040	0.0000 18.5072
	<i>cup sip</i>	1	0.5650	0.5647	0.0000 1.7198	3.0303	2.8817	0.0000 8.9241
	<i>Total</i>	33	18.6441	2.8114	12.8942 24.3939	100.000		
<i>impaired</i>	<i>5ml</i>	31	17.5141	2.5514	12.2958 22.7324	21.5278	2.5089	16.3964 26.6591
	<i>15ml</i>	55	31.0734	1.0743	28.8763 33.2706	38.1944	1.4878	35.1515 41.2374
	<i>cup sip</i>	58	32.7684	0.7342	31.2668 34.2699	40.2778	1.4607	37.2904 43.2652
	<i>Total</i>	144	81.3559	2.8114	75.6061 87.1058	100.000		
<i>Total</i>	<i>5ml</i>	60	33.8983	0.3201	33.2437 34.5529			
	<i>15ml</i>	58	32.7684	0.5680	31.6068 33.9300			
	<i>cup sip</i>	59	33.3333	0.4692	32.3737 34.2929			
	<i>Total</i>	177	100.000					

Rao-Scott Chi-Square Test

Pearson Chi-Square 52.9814

Design Correction 1.1831

Rao-Scott Chi-Square 44.7818

DF 2

Pr > ChiSq <.0001

F Value 22.3909

Num DF 2

Den DF 58

Pr > F <.0001

Sample Size = 355

**ESTIMATE PROP. IMPAIRED PRE- AND POST-INTERVENTION
AT EACH THIN LIQUID VOLUME**

The SURVEYFREQ Procedure

<i>Table of pas_ind by volume</i>										
<i>Controlling for time_cat=post</i>										
<i>pas_ind</i>	<i>volume</i>	<i>Frequency</i>	<i>Percent</i>	<i>Std Err of Percent</i>	<i>95% Confidence Limits for Percent</i>	<i>Row Percent</i>	<i>Std Err of Row Percent</i>	<i>95% Confidence Limits for Row Percent</i>		
<i>not impaired</i>	<i>5ml</i>	50	28.0899	1.8627	24.2803	31.8995	47.1698	3.6139	39.7786	54.5610
	<i>15ml</i>	29	16.2921	2.8217	10.5211	22.0632	27.3585	2.4103	22.4289	32.2881
	<i>cup sip</i>	27	15.1685	2.8458	9.3483	20.9888	25.4717	2.6630	20.0253	30.9180
	<i>Total</i>	106	59.5506	6.4055	46.4499	72.6513	100.000			
<i>impaired</i>	<i>5ml</i>	10	5.6180	1.8700	1.7934	9.4425	13.8889	3.4195	6.8952	20.8825
	<i>15ml</i>	29	16.2921	2.7426	10.6829	21.9014	40.2778	2.6365	34.8855	45.6701
	<i>cup sip</i>	33	18.5393	2.8392	12.7324	24.3462	45.8333	3.2676	39.1503	52.5164
	<i>Total</i>	72	40.4494	6.4055	27.3487	53.5501	100.000			
<i>Total</i>	<i>5ml</i>	60	33.7079	0.2632	33.1697	34.2461				
	<i>15ml</i>	58	32.5843	0.5263	31.5079	33.6607				
	<i>cup sip</i>	60	33.7079	0.2632	33.1697	34.2461				
	<i>Total</i>	178	100.000							

Rao-Scott Chi-Square Test

Pearson Chi-Square 21.5589

Design Correction 0.8399

Rao-Scott Chi-Square 25.6669

DF 2

Pr > ChiSq <.0001

F Value 12.8335

Num DF 2

Den DF 58

Pr > F <.0001

Sample Size = 355

**GEE ANALYSIS FOR THIN LIQUID TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

<i>Model Information</i>	
<i>Data Set</i>	WORK.THINLIQUID
<i>Distribution</i>	Binomial
<i>Link Function</i>	Logit
<i>Dependent Variable</i>	pas_ind Penetration-aspiration impairment indicator

<i>Number of Observations Read</i>	360
<i>Number of Observations Used</i>	355
<i>Number of Events</i>	216
<i>Number of Trials</i>	355
<i>Missing Values</i>	5

<i>Class Level Information</i>			
<i>Class</i>	<i>Value</i>	<i>Design Variables</i>	
<i>time_cat</i>	<i>post</i>	1	
	<i>pre</i>	0	
<i>volume</i>	<i>15ml</i>	1	0
	<i>5ml</i>	0	0
	<i>cup sip</i>	0	1
<i>inst</i>	<i>MUSC</i>	0	
	<i>VA</i>	1	

<i>Response Profile</i>		
<i>Ordered Value</i>	<i>pas_ind</i>	<i>Total Frequency</i>
1	impaired	216
2	not impaired	139

PROC GENMOD is modeling the probability that pas_ind='impaired'. One way to change this to model the probability that pas_ind='not impaired' is to specify the DESCENDING option in the PROC statement.

<i>Parameter Information</i>				
<i>Parameter</i>	<i>Effect</i>	<i>time_cat</i>	<i>volume</i>	<i>inst</i>
<i>Pm1</i>	Intercept			
<i>Pm2</i>	time_cat	post		
<i>Pm3</i>	volume		15ml	
<i>Pm4</i>	volume		cup sip	
<i>Pm5</i>	inst			VA

Algorithm converged.

**GEE ANALYSIS FOR THIN LIQUID TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

Estimated Covariance Matrix

	<i>Prm1</i>	<i>Prm2</i>	<i>Prm3</i>	<i>Prm4</i>	<i>Prm5</i>
<i>Prm1</i>	0.07539	-0.02985	-0.03367	-0.03252	-0.03588
<i>Prm2</i>	-0.02985	0.10214	-0.05160	-0.05525	0.002505
<i>Prm3</i>	-0.03367	-0.05160	0.12970	0.07720	-0.002305
<i>Prm4</i>	-0.03252	-0.05525	0.07720	0.13580	-0.002567
<i>Prm5</i>	-0.03588	0.002505	-0.002305	-0.002567	0.07106

GEE Model Information

<i>Correlation Structure</i>	Exchangeable
<i>Subject Effect</i>	subid (30 levels)
<i>Number of Clusters</i>	30
<i>Clusters With Missing Values</i>	5
<i>Correlation Matrix Dimension</i>	12
<i>Maximum Cluster Size</i>	12
<i>Minimum Cluster Size</i>	11

Covariance Matrix (Model-Based)

	<i>Prm1</i>	<i>Prm2</i>	<i>Prm3</i>	<i>Prm4</i>	<i>Prm5</i>
<i>Prm1</i>	0.12222	-0.02729	-0.02678	-0.02527	-0.08677
<i>Prm2</i>	-0.02729	0.07936	-0.03960	-0.04284	0.0004872
<i>Prm3</i>	-0.02678	-0.03960	0.10263	0.06191	-0.000408
<i>Prm4</i>	-0.02527	-0.04284	0.06191	0.10697	-0.000516
<i>Prm5</i>	-0.08677	0.0004872	-0.000408	-0.000516	0.17345

Algorithm converged.

Working Correlation Matrix

	<i>Col1</i>	<i>Col2</i>	<i>Col3</i>	<i>Col4</i>	<i>Col5</i>	<i>Col6</i>	<i>Col7</i>	<i>Col8</i>	<i>Col9</i>	<i>Col10</i>	<i>Col11</i>	<i>Col12</i>
<i>Row1</i>	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row2</i>	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row3</i>	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row4</i>	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row5</i>	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row6</i>	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row7</i>	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877	0.1877
<i>Row8</i>	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877	0.1877
<i>Row9</i>	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877	0.1877
<i>Row10</i>	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877	0.1877

**GEE ANALYSIS FOR THIN LIQUID TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

Working Correlation Matrix

	Col1	Col2	Col3	Col4	Col5	Col6	Col7	Col8	Col9	Col10	Col11	Col12
Row11	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000	0.1877
Row12	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	0.1877	1.0000

*Exchangeable Working
Correlation*

Correlation 0.1876746038

GEE Fit Criteria

QIC 360.4057

QICu 351.9293

Analysis Of GEE Parameter Estimates

Empirical Standard Error Estimates

<i>Parameter</i>		<i>Estimate</i>	<i>Standard Error</i>	<i>95% Confidence Limits</i>		<i>Z</i>	<i>Pr > Z </i>
<i>Intercept</i>		0.1325	0.3829	-0.6179	0.8830	0.35	0.7293
<i>time_cat</i>	post	-2.3890	0.3817	-3.1372	-1.6409	-6.26	<.0001
<i>volume</i>	15ml	2.1953	0.3574	1.4948	2.8957	6.14	<.0001
<i>volume</i>	cup sip	2.4523	0.3801	1.7074	3.1973	6.45	<.0001
<i>inst</i>	VA	-0.0245	0.4676	-0.9411	0.8920	-0.05	0.9582

*Score Statistics For Type 3 GEE
Analysis*

<i>Source</i>	<i>DF</i>	<i>Chi-Square</i>	<i>Pr > ChiSq</i>
<i>time_cat</i>	1	17.34	<.0001
<i>volume</i>	2	19.20	<.0001
<i>inst</i>	1	0.00	0.9584

Contrast Estimate Results

<i>Label</i>	<i>Mean</i>			<i>L'Beta Estimate</i>	<i>Standard Error</i>	<i>Alpha</i>	<i>L'Beta Confidence Limits</i>		<i>Chi-Square</i>	<i>Pr > ChiSq</i>
	<i>Mean Estimate</i>	<i>Confidence Limits</i>								
<i>treatment effect</i>	0.0840	0.0416	0.1623	-2.3890	0.3817	0.05	-3.1372	-1.6409	39.17	<.0001
<i>Exp(treatment effect)</i>				0.0917	0.0350	0.05	0.0434	0.1938		
<i>15ml vs 5ml</i>	0.8998	0.8168	0.9476	2.1953	0.3574	0.05	1.4948	2.8957	37.73	<.0001
<i>Exp(15ml vs 5ml)</i>				8.9823	3.2100	0.05	4.4585	18.0960		
<i>cupsip vs 5ml</i>	0.9207	0.8465	0.9607	2.4523	0.3801	0.05	1.7074	3.1973	41.63	<.0001
<i>Exp(cupsip vs 5ml)</i>				11.6154	4.4150	0.05	5.5143	24.4665		

**GEE ANALYSIS FOR THIN LIQUID TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

Contrast Estimate Results

<i>Label</i>	<i>Mean</i>			<i>L'Beta Estimate</i>	<i>Standard Error</i>	<i>Alpha</i>	<i>L'Beta</i>		<i>Chi-Square</i>	<i>Pr > ChiSq</i>
	<i>Mean Estimate</i>	<i>Confidence Limits</i>					<i>Confidence Limits</i>			
<i>cupsip vs 15ml</i>	0.5639	0.4682	0.6551	0.2571	0.1962	0.05	-0.1274	0.6416	1.72	0.1900
<i>Exp(cupsip vs 15ml)</i>				1.2931	0.2537	0.05	0.8804	1.8994		

**GEE ANALYSIS FOR FOR ALL SWALLOW TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

<i>Model Information</i>	
<i>Data Set</i>	WORK.SWALLOW
<i>Distribution</i>	Binomial
<i>Link Function</i>	Logit
<i>Dependent Variable</i>	pas_ind Penetration-aspiration impairment indicator

<i>Number of Observations Read</i>	1080
<i>Number of Observations Used</i>	1064
<i>Number of Events</i>	618
<i>Number of Trials</i>	1064
<i>Missing Values</i>	16

<i>Class Level Information</i>			
<i>Class</i>	<i>Value</i>	<i>Design Variables</i>	
<i>time_cat</i>	<i>post</i>	1	
	<i>pre</i>	0	
<i>viscosity</i>	<i>honey</i>	0	0
	<i>nectar</i>	1	0
	<i>thin liquid</i>	0	1
<i>volume</i>	<i>15ml</i>	1	0
	<i>5ml</i>	0	0
	<i>cup sip</i>	0	1
<i>inst</i>	<i>MUSC</i>	0	
	<i>VA</i>	1	

<i>Response Profile</i>		
<i>Ordered Value</i>	<i>pas_ind</i>	<i>Total Frequency</i>
1	impaired	618
2	not impaired	446

PROC GENMOD is modeling the probability that pas_ind='impaired'. One way to change this to model the probability that pas_ind='not impaired' is to specify the DESCENDING option in the PROC statement.

<i>Parameter Information</i>					
<i>Parameter</i>	<i>Effect</i>	<i>time_cat</i>	<i>viscosity</i>	<i>volume</i>	<i>inst</i>
<i>Prm1</i>	Intercept				
<i>Prm2</i>	time_cat	post			
<i>Prm3</i>	viscosity		nectar		
<i>Prm4</i>	viscosity		thin liquid		

**GEE ANALYSIS FOR ALL SWALLOW TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

<i>Parameter Information</i>					
<i>Parameter</i>	<i>Effect</i>	<i>time_cat</i>	<i>viscosity</i>	<i>volume</i>	<i>inst</i>
<i>Prm5</i>	volume			15ml	
<i>Prm6</i>	volume			cup sip	
<i>Prm7</i>	viscosity*volume		nectar	15ml	
<i>Prm8</i>	viscosity*volume		nectar	cup sip	
<i>Prm9</i>	viscosity*volume		thin liquid	15ml	
<i>Prm10</i>	viscosity*volume		thin liquid	cup sip	
<i>Prm11</i>	inst				VA

Algorithm converged.

<i>Estimated Covariance Matrix</i>								
	<i>Prm1</i>	<i>Prm2</i>	<i>Prm3</i>	<i>Prm4</i>	<i>Prm5</i>	<i>Prm6</i>	<i>Prm7</i>	<i>Prm8</i>
<i>Prm1</i>	0.05174	-0.01052	-0.04017	-0.04318	-0.04184	-0.04068	0.04239	0.04100
<i>Prm2</i>	-0.01052	0.02214	-0.003219	0.003072	0.0003976	-0.002096	-0.001425	0.001192
<i>Prm3</i>	-0.04017	-0.003219	0.08513	0.04126	0.04165	0.04201	-0.08446	-0.08484
<i>Prm4</i>	-0.04318	0.003072	0.04126	0.08683	0.04176	0.04142	-0.04191	-0.04154
<i>Prm5</i>	-0.04184	0.0003976	0.04165	0.04176	0.08468	0.04167	-0.08470	-0.04169
<i>Prm6</i>	-0.04068	-0.002096	0.04201	0.04142	0.04167	0.08539	-0.04157	-0.08531
<i>Prm7</i>	0.04239	-0.001425	-0.08446	-0.04191	-0.08470	-0.04157	0.17247	0.08459
<i>Prm8</i>	0.04100	0.001192	-0.08484	-0.04154	-0.04169	-0.08531	0.08459	0.17390
<i>Prm9</i>	0.04597	-0.009040	-0.04039	-0.08766	-0.08483	-0.04085	0.08525	0.04122
<i>Prm10</i>	0.04516	-0.007314	-0.04064	-0.08742	-0.04184	-0.08450	0.04218	0.08480
<i>Prm11</i>	-0.01013	0.0001285	-0.000034	0.0000349	-0.000107	-0.000068	-0.000020	0.0002834

<i>Estimated Covariance Matrix</i>			
	<i>Prm9</i>	<i>Prm10</i>	<i>Prm11</i>
<i>Prm1</i>	0.04597	0.04516	-0.01013
<i>Prm2</i>	-0.009040	-0.007314	0.0001285
<i>Prm3</i>	-0.04039	-0.04064	-0.000034
<i>Prm4</i>	-0.08766	-0.08742	0.0000349
<i>Prm5</i>	-0.08483	-0.04184	-0.000107
<i>Prm6</i>	-0.04085	-0.08450	-0.000068
<i>Prm7</i>	0.08525	0.04218	-0.000020
<i>Prm8</i>	0.04122	0.08480	0.0002834
<i>Prm9</i>	0.18355	0.08939	5.7616E-6
<i>Prm10</i>	0.08939	0.18572	-5.317E-6
<i>Prm11</i>	5.7616E-6	-5.317E-6	0.02014

**GEE ANALYSIS FOR FOR ALL SWALLOW TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

<i>GEE Model Information</i>	
<i>Correlation Structure</i>	Exchangeable
<i>Subject Effect</i>	subid (30 levels)
<i>Number of Clusters</i>	30
<i>Clusters With Missing Values</i>	8
<i>Correlation Matrix Dimension</i>	36
<i>Maximum Cluster Size</i>	36
<i>Minimum Cluster Size</i>	29

<i>Covariance Matrix (Model-Based)</i>							
	<i>Prm1</i>	<i>Prm2</i>	<i>Prm3</i>	<i>Prm4</i>	<i>Prm5</i>	<i>Prm6</i>	<i>Prm7</i>
<i>Prm1</i>	0.10715	-0.006874	-0.03082	-0.03044	-0.03119	-0.03126	0.03157
<i>Prm2</i>	-0.006874	0.01595	-0.002225	0.001842	0.0003051	-0.001221	-0.001042
<i>Prm3</i>	-0.03082	-0.002225	0.06294	0.03119	0.03141	0.03163	-0.06248
<i>Prm4</i>	-0.03044	0.001842	0.03119	0.06722	0.03150	0.03130	-0.03158
<i>Prm5</i>	-0.03119	0.0003051	0.03141	0.03150	0.06426	0.03146	-0.06424
<i>Prm6</i>	-0.03126	-0.001221	0.03163	0.03130	0.03146	0.06355	-0.03138
<i>Prm7</i>	0.03157	-0.001042	-0.06248	-0.03158	-0.06424	-0.03138	0.12755
<i>Prm8</i>	0.03157	0.0005735	-0.06271	-0.03137	-0.03148	-0.06350	0.06260
<i>Prm9</i>	0.03238	-0.006349	-0.03056	-0.06771	-0.06437	-0.03098	0.06464
<i>Prm10</i>	0.03327	-0.005414	-0.03069	-0.06756	-0.03160	-0.06304	0.03182
<i>Prm11</i>	-0.07575	-0.003282	0.0009315	-0.001107	-0.000500	0.0005210	0.0007386

<i>Covariance Matrix (Model-Based)</i>				
	<i>Prm8</i>	<i>Prm9</i>	<i>Prm10</i>	<i>Prm11</i>
<i>Prm1</i>	0.03157	0.03238	0.03327	-0.07575
<i>Prm2</i>	0.0005735	-0.006349	-0.005414	-0.003282
<i>Prm3</i>	-0.06271	-0.03056	-0.03069	0.0009315
<i>Prm4</i>	-0.03137	-0.06771	-0.06756	-0.001107
<i>Prm5</i>	-0.03148	-0.06437	-0.03160	-0.000500
<i>Prm6</i>	-0.06350	-0.03098	-0.06304	0.0005210
<i>Prm7</i>	0.06260	0.06464	0.03182	0.0007386
<i>Prm8</i>	0.12720	0.03125	0.06327	0.0001274
<i>Prm9</i>	0.03125	0.13756	0.06914	0.003522
<i>Prm10</i>	0.06327	0.06914	0.13693	0.002769
<i>Prm11</i>	0.0001274	0.003522	0.002769	0.15330

Algorithm converged.

**GEE ANALYSIS FOR ALL SWALLOW TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

*Exchangeable Working
Correlation*

Correlation 0.2471094745

GEE Fit Criteria

QIC 1266.0636

QICu 1220.6900

Analysis Of GEE Parameter Estimates

Empirical Standard Error Estimates

<i>Parameter</i>		<i>Estimate</i>	<i>Standard Error</i>	<i>95% Confidence Limits</i>		<i>Z</i>	<i>Pr > Z </i>
<i>Intercept</i>		0.4278	0.3923	-0.3411	1.1966	1.09	0.2755
<i>time_cat</i>	post	-1.8543	0.3122	-2.4662	-1.2424	-5.94	<.0001
<i>viscosity</i>	nectar	0.6572	0.2341	0.1984	1.1160	2.81	0.0050
<i>viscosity</i>	thin liquid	-0.6795	0.3312	-1.3287	-0.0302	-2.05	0.0402
<i>volume</i>	15ml	-0.1192	0.1926	-0.4967	0.2584	-0.62	0.5361
<i>volume</i>	cup sip	0.3593	0.2917	-0.2124	0.9310	1.23	0.2180
<i>viscosity*volume</i>	nectar 15ml	0.2973	0.2453	-0.1834	0.7780	1.21	0.2254
<i>viscosity*volume</i>	nectar cup sip	-0.1253	0.3561	-0.8231	0.5726	-0.35	0.7250
<i>viscosity*volume</i>	thin liquid 15ml	2.0923	0.3826	1.3425	2.8422	5.47	<.0001
<i>viscosity*volume</i>	thin liquid cup sip	1.8242	0.4636	0.9156	2.7327	3.94	<.0001
<i>inst</i>	VA	0.2220	0.4902	-0.7388	1.1827	0.45	0.6507

Score Statistics For Joint Tests For GEE

<i>Source</i>	<i>DF</i>	<i>Chi-Square</i>	<i>Pr > ChiSq</i>
<i>time_cat</i>	1	17.94	<.0001
<i>viscosity</i>	2	14.42	0.0007
<i>volume</i>	2	3.61	0.1642
<i>viscosity*volume</i>	4	18.34	0.0011
<i>inst</i>	1	0.18	0.6678

Note: Under full-rank parameterizations, Type 3 effect tests are replaced by joint tests. The joint test for an effect is a test that all the parameters associated with that effect are zero. Such joint tests might not be equivalent to Type 3 effect tests under GLM parameterization.

**GEE ANALYSIS FOR FOR ALL SWALLOW TASKS
CLUSTERED BINARY RESPONSE**

The GENMOD Procedure

Contrast Estimate Results

<i>Label</i>	<i>Mean</i>			<i>L'Beta Estimate</i>	<i>Standard Error</i>	<i>Alpha</i>	<i>L'Beta</i>		<i>Chi-Square</i>	<i>Pr > ChiSq</i>
	<i>Mean Estimate</i>	<i>Confidence Limits</i>					<i>Confidence Limits</i>			
<i>treatment effect</i>	0.1354	0.0783	0.2240	-1.8543	0.3122	0.05	-2.4662	-1.2424	35.28	<.0001
<i>Exp(treatment effect)</i>				0.1566	0.0489	0.05	0.0849	0.2887		
<i>nectar: 15ml vs 5ml</i>	0.5444	0.4415	0.6437	0.1781	0.2108	0.05	-0.2351	0.5914	0.71	0.3981
<i>Exp(nectar: 15ml vs 5ml)</i>				1.1950	0.2519	0.05	0.7905	1.8064		
<i>honey: cupsip vs 15ml</i>	0.6174	0.5003	0.7223	0.4784	0.2435	0.05	0.0012	0.9557	3.86	0.0494
<i>Exp(honey: cupsip vs 15ml)</i>				1.6136	0.3929	0.05	1.0012	2.6006		

**GEE ANALYSIS FOR FOR THIN LIQUID TASKS
CLUSTERED ORDINAL RESPONSE PROPORTIONAL ODDS MODEL**

The GENMOD Procedure

Model Information	
Data Set	WORK.THINLIQUID
Distribution	Multinomial
Link Function	Cumulative Logit
Dependent Variable	pas_class

Number of Observations Read	360
Number of Observations Used	355
Missing Values	5

Class Level Information			
Class	Value	Design Variables	
time_cat	post	1	
	pre	0	
volume	15ml	1	0
	5ml	0	0
	cup sip	0	1
inst	MUSC	0	
	VA	1	

Response Profile		
Ordered Value	pas_class	Total Frequency
1	1	139
2	2	155
3	3	61

PROC GENMOD is modeling the probabilities of levels of pas_class having LOWER Ordered Values in the response profile table. One way to change this to model the probabilities of HIGHER Ordered Values is to specify the DESCENDING option in the PROC statement.

Parameter Information				
Parameter	Effect	time_cat	volume	inst
Prm1	time_cat	post		
Prm2	volume		15ml	
Prm3	volume		cup sip	
Prm4	inst			VA

Algorithm converged.

**GEE ANALYSIS FOR THIN LIQUID TASKS
CLUSTERED ORDINAL RESPONSE PROPORTIONAL ODDS MODEL**

The GENMOD Procedure

Estimated Covariance Matrix

	<i>Intercept1</i>	<i>Intercept2</i>	<i>Prm1</i>	<i>Prm2</i>	<i>Prm3</i>	<i>Prm4</i>
<i>Intercept1</i>	0.05832	0.05072	-0.01889	-0.03539	-0.03569	-0.02220
<i>Intercept2</i>	0.05072	0.07313	-0.009003	-0.04700	-0.04728	-0.02029
<i>Prm1</i>	-0.01889	-0.009003	0.04882	-0.006459	-0.006135	-0.000419
<i>Prm2</i>	-0.03539	-0.04700	-0.006459	0.07555	0.04401	-0.000912
<i>Prm3</i>	-0.03569	-0.04728	-0.006135	0.04401	0.07352	-0.000563
<i>Prm4</i>	-0.02220	-0.02029	-0.000419	-0.000912	-0.000563	0.04411

GEE Model Information

<i>Correlation Structure</i>	Independent
<i>Subject Effect</i>	subid (30 levels)
<i>Number of Clusters</i>	30
<i>Clusters With Missing Values</i>	5
<i>Correlation Matrix Dimension</i>	12
<i>Maximum Cluster Size</i>	12
<i>Minimum Cluster Size</i>	11

Algorithm converged.

GEE Fit Criteria

QIC 678.5553

QICu 660.9725

Analysis Of GEE Parameter Estimates

Empirical Standard Error Estimates

<i>Parameter</i>	<i>Estimate</i>	<i>Standard Error</i>	<i>95% Confidence Limits</i>		<i>Z</i>	<i>Pr > Z </i>
<i>Intercept1</i>	-0.0491	0.3367	-0.7090	0.6108	-0.15	0.8840
<i>Intercept2</i>	2.3409	0.5427	1.2773	3.4046	4.31	<.0001
<i>time_cat</i> post	1.2131	0.3176	0.5907	1.8355	3.82	0.0001
<i>volume</i> 15ml	-1.6590	0.2742	-2.1965	-1.1215	-6.05	<.0001
<i>volume</i> cup sip	-1.6576	0.2900	-2.2259	-1.0893	-5.72	<.0001
<i>inst</i> VA	0.2287	0.4216	-0.5976	1.0551	0.54	0.5874

**GEE ANALYSIS FOR FOR THIN LIQUID TASKS
CLUSTERED ORDINAL RESPONSE PROPORTIONAL ODDS MODEL**

The GENMOD Procedure

Score Statistics For Type 3 GEE
Analysis

Source	DF	Chi-Square	Pr > ChiSq
<i>time_cat</i>	1	12.35	0.0004
<i>volume</i>	2	19.48	<.0001
<i>inst</i>	1	0.29	0.5934

Contrast Estimate Results

Label	Mean			L'Beta Estimate	Standard Error	Alpha	L'Beta		Chi-Square	Pr > ChiSq
	Mean Estimate	Confidence Limits					Confidence Limits			
<i>treatment effect</i>	0.7708	0.6435	0.8624	1.2131	0.3176	0.05	0.5907	1.8355	14.59	0.0001
<i>Exp(treatment effect)</i>				3.3638	1.0682	0.05	1.8052	6.2683		
<i>15ml vs 5ml</i>	0.1599	0.1001	0.2457	-1.6590	0.2742	0.05	-2.1965	-1.1215	36.60	<.0001
<i>Exp(15ml vs 5ml)</i>				0.1903	0.0522	0.05	0.1112	0.3258		
<i>cupsip vs 5ml</i>	0.1601	0.0974	0.2517	-1.6576	0.2900	0.05	-2.2259	-1.0893	32.68	<.0001
<i>Exp(cupsip vs 5ml)</i>				0.1906	0.0553	0.05	0.1080	0.3364		
<i>cupsip vs 15ml</i>	0.5003	0.4105	0.5901	0.0013	0.1853	0.05	-0.3618	0.3644	0.00	0.9943
<i>Exp(cupsip vs 15ml)</i>				1.0013	0.1855	0.05	0.6964	1.4397		
