

The follow code was run:

```
proc genmod data = subjectlevel;  
  class Hypothermia(ref='No')/param = ref;  
  model INDNewIntracranBleed (ref='No')= Hypothermia LastBaselineFibrinogen LastBaselineFibrinogen*Hypothermia / link = logit dist = binomial;  
run;
```

The following appears in the output: PROC GENMOD is modeling the probability that INDNewIntracranBleed='Yes'.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	-0.4666	0.5115	-1.4691	0.5359	0.83	0.3617
Hypothermia	Yes	1	4.0024	2.1521	-0.2156	8.2204	3.46	0.0629
LastBaselineFibrinog		1	-0.0039	0.0023	-0.0083	0.0005	2.97	0.0847
LastBasel*Hypothermi	Yes	1	-0.0140	0.0096	-0.0327	0.0048	2.13	0.1440
Scale		0	1.0000	0.0000	1.0000	1.0000		

Interpret the relationship of fibrinogen to intracranial bleeding. Note that fibrinogen is reported in mg/dL.

PRISM is a measure of illness severity when a child is admitted to an intensive care unit. Age is a categorical (nominal) variable with 4 levels. Interpret the association of PRISM with mortality among neonates. Repeat the interpretation among infants. You may notice that there's really not a lot of interaction here. We'll assume that the analysis was prespecified to include an interaction term, regardless of the amount of interaction observed.

```
proc genmod data = der.subjectlevel descending;
  class PrismAgeCategoryNumeric(ref='Neonate');
  model Dead = PRISMOverallScore PrismAgeCategoryNumeric PRISMOverallScore*PrismAgeCategoryNumeric / dist = binomial link = logit type3;
run;
```

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	-0.6808	0.2389	-1.1490	-0.2127	8.13	0.0044
PRISMOverallScore		1	0.0382	0.0208	-0.0025	0.0788	3.38	0.0661
PrismAgeCategoryNume	Adolescent	1	0.0531	0.6769	-1.2736	1.3798	0.01	0.9374
PrismAgeCategoryNume	Child	1	0.1744	0.4598	-0.7267	1.0756	0.14	0.7044
PrismAgeCategoryNume	Infant	1	0.7604	0.3491	0.0762	1.4446	4.74	0.0294
PrismAgeCategoryNume	Neonate	0	0.0000	0.0000	0.0000	0.0000	.	.
PRISMOver*PrismAgeCa	Adolescent	1	0.0167	0.0565	-0.0941	0.1275	0.09	0.7675
PRISMOver*PrismAgeCa	Child	1	-0.0042	0.0411	-0.0849	0.0764	0.01	0.9181
PRISMOver*PrismAgeCa	Infant	1	-0.0509	0.0355	-0.1205	0.0186	2.06	0.1512
PRISMOver*PrismAgeCa	Neonate	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.0000	0.0000	1.0000	1.0000		

Consider the previous example but use Age as a continuous rather than categorical variable. This is a sad example indeed due to the extremely limited interaction. This is also probably an inappropriate way to model age in a pediatric cohort. But we'll press forward in this academic exercise. Ignore the fact that many parameters could plausibly be zero. What is the association of PRISM with mortality for 3-year-olds? For 17-year-olds?

```
proc genmod data = der.subjectlevel descending;
  class PrismAgeCategoryNumeric(ref='Neonate');
  model Dead = PRISMOverallScore AgeYears PRISMOverallScore*AgeYears / dist = binomial link = logit type3;
run;
```

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	-0.3794	0.1664	-0.7056	-0.0532	5.20	0.0226
PRISMOverallScore	1	0.0185	0.0155	-0.0119	0.0489	1.42	0.2329
AgeYears	1	0.0029	0.0382	-0.0720	0.0778	0.01	0.9392
PRISMOverall*AgeYears	1	0.0006	0.0032	-0.0056	0.0068	0.04	0.8402
Scale	0	1.0000	0.0000	1.0000	1.0000		