

First Five Observations

Obs	RANDID	SEX	AGE	TOTCHOL	CURSMOKE	CIGPDAY	BMI	PERIOD	PREVCHD	CVD	TIMECVD
1	2448	1	39	195	0	0	26.97	1	0	1	6438
2	2448	1	52	209	0	0	.	3	0	1	6438
3	6238	2	46	250	0	0	28.73	1	0	0	8766
4	6238	2	52	260	0	0	29.43	2	0	0	8766
5	6238	2	58	237	0	0	28.50	3	0	0	8766

Number of Study Subjects

distinct_randid
4434

Number of Study Subjects

Examination cycle	distinct_randid
1	4434
2	3930
3	3263

Current Smoking Summary Statistics

The FREQ Procedure

Frequency Percent Row Pct	Table of PERIOD by CURSMOKE			
	PERIOD(Examination cycle)	CURSMOKE(Current Cig Smoker Y/N)		
		0	1	Total
	1	2253 19.38 50.81	2181 18.76 49.19	4434 38.14
	2	2203 18.95 56.06	1727 14.85 43.94	3930 33.80
	3	2142 18.42 65.65	1121 9.64 34.35	3263 28.06
	Total	6598 56.75	5029 43.25	11627 100.00

Prevalent Coronary Heart Disease Summary Statistics

The FREQ Procedure

Frequency Percent Row Pct	Table of PERIOD by PREVCHD			
	PERIOD(Examination cycle)	PREVCHD(Prevalent CHD (MI,AP,CI))		
		0	1	Total
	1	4240 36.47 95.62	194 1.67 4.38	4434 38.14
	2	3642 31.32 92.67	288 2.48 7.33	3930 33.80
	3	2903 24.97 88.97	360 3.10 11.03	3263 28.06
	Total	10785 92.76	842 7.24	11627 100.00

CVD Summary Statistics

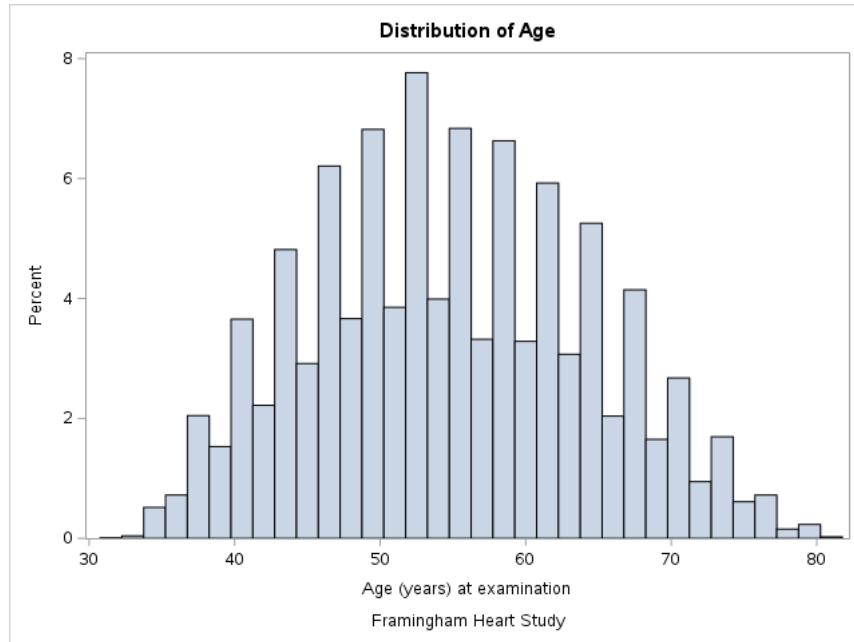
Incident Hosp MI or Stroke, Fatal or Non	distinct_randid
0	3277
1	1157

Sex Summary Statistics

The FREQ Procedure

Frequency Percent Row Pct	Table of PERIOD by SEX			
	PERIOD(Examination cycle)	SEX(SEX)		
		1	2	Total
	1	1944 16.72 43.84	2490 21.42 56.16	4434 38.14
	2	1691	2239	3930

PERIOD(Examination cycle)	SEX(SEX)		
	1	2	Total
	14.54 43.03	19.26 56.97	33.80
3	1387 11.93 42.51	1876 16.13 57.49	3263 28.06
Total	5022 43.19	6605 56.81	11627 100.00



Age Summary Statistics

The MEANS Procedure

Analysis Variable : AGE Age (years) at examination	
Mean	Std Dev
54.79	9.56

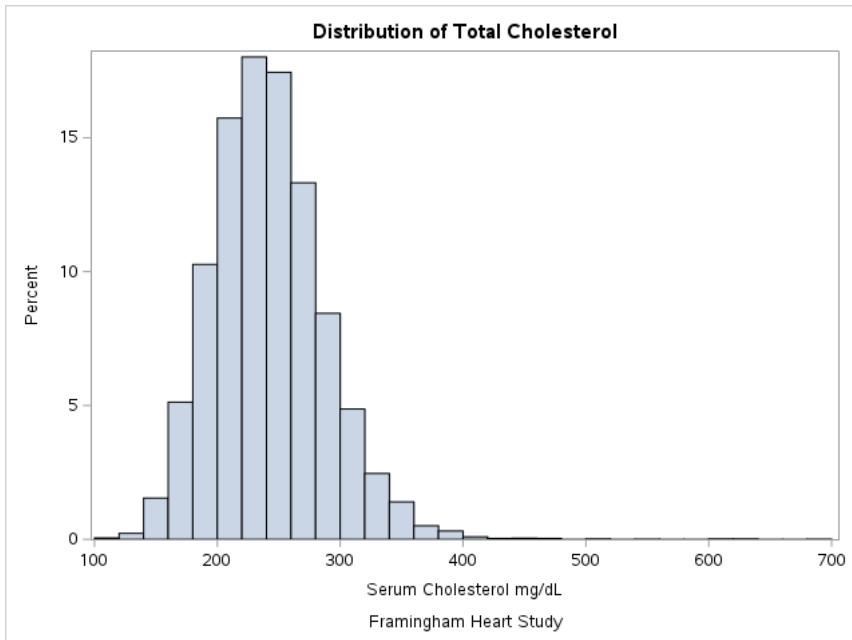
Framingham Heart Study

Age Summary Statistics

The MEANS Procedure

Analysis Variable : AGE Age (years) at examination			
Examination cycle	N Obs	Mean	Std Dev
1	4434	49.93	8.68
2	3930	55.42	8.54
3	3263	60.65	8.30

Framingham Heart Study



Total Cholesterol Summary Statistics

The MEANS Procedure

Analysis Variable : TOTCHOL Serum Cholesterol mg/dL			
	Mean	Std Dev	
241.16	45.37		

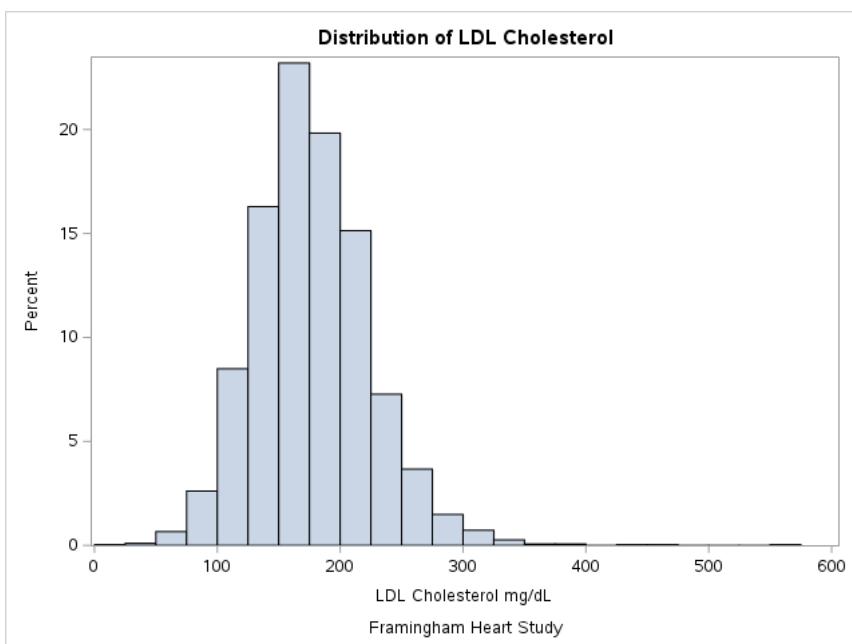
Framingham Heart Study

Total Cholesterol Summary Statistics

The MEANS Procedure

Analysis Variable : TOTCHOL Serum Cholesterol mg/dL			
Examination cycle	N Obs	Mean	Std Dev
1	4434	236.98	44.65
2	3930	249.58	45.75
3	3263	236.71	44.45

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LDL Cholesterol Summary Statistics (Only Measured at Period 3)

The MEANS Procedure

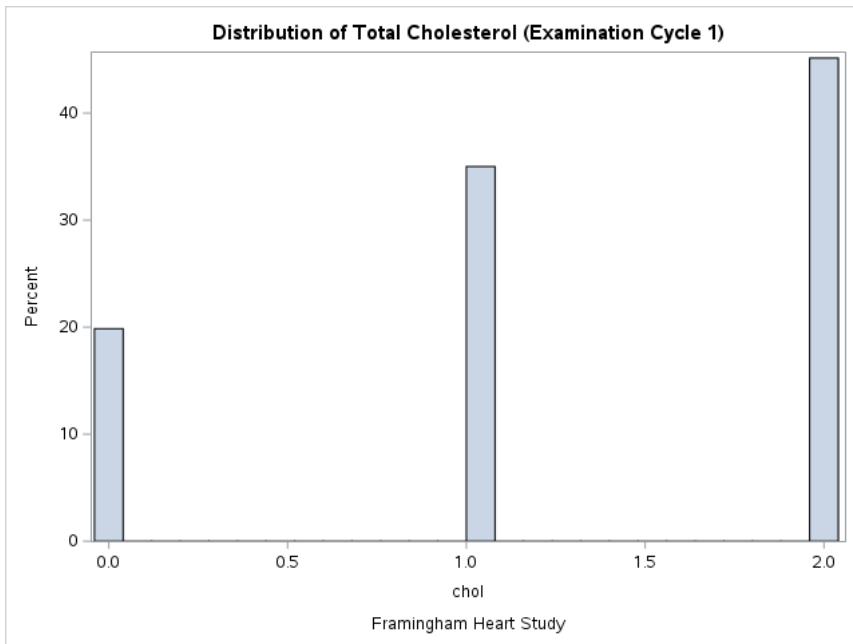
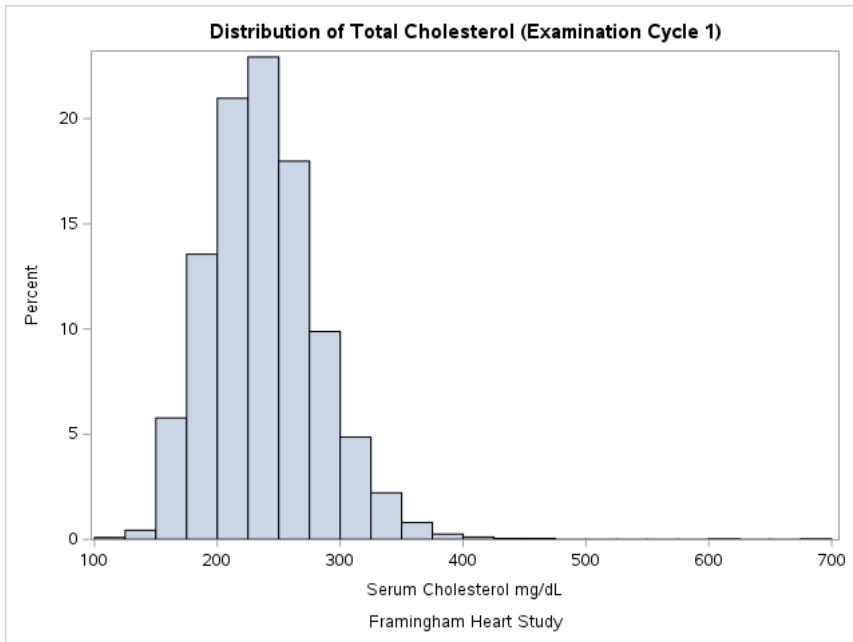
Analysis Variable : LDLC LDL Cholesterol mg/dL	
Mean	Std Dev
176.47	46.86

Framingham Heart Study

LDL Cholesterol Summary Statistics (Only Measured at Period 3)

chol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	Examination cycle	total_count
.	0	0	1	19
.	0	0	2	74
.	0	0	3	121
.	0	1	1	2
.	0	1	2	6
.	0	1	3	15
.	1	0	1	31
.	1	0	2	60
.	1	0	3	65
.	1	1	2	3
.	1	1	3	13
0	0	0	1	393
0	0	0	2	227
0	0	0	3	333
0	0	1	1	15
0	0	1	2	19
0	0	1	3	42
0	1	0	1	438
0	1	0	2	191
0	1	0	3	210
0	1	1	1	24
0	1	1	2	16
0	1	1	3	23
1	0	0	1	741
1	0	0	2	605
1	0	0	3	618
1	0	1	1	32
1	0	1	2	47
1	0	1	3	81
1	1	0	1	737
1	1	0	2	505
1	1	0	3	339
1	1	1	1	24
1	1	1	2	26
1	1	1	3	31
2	0	0	1	992
2	0	0	2	1118
2	0	0	3	814
2	0	1	1	59
2	0	1	2	107
2	0	1	3	118
2	1	0	1	889
2	1	0	2	862
2	1	0	3	403
2	1	1	1	38
2	1	1	2	64
2	1	1	3	37

Framingham Heart Study

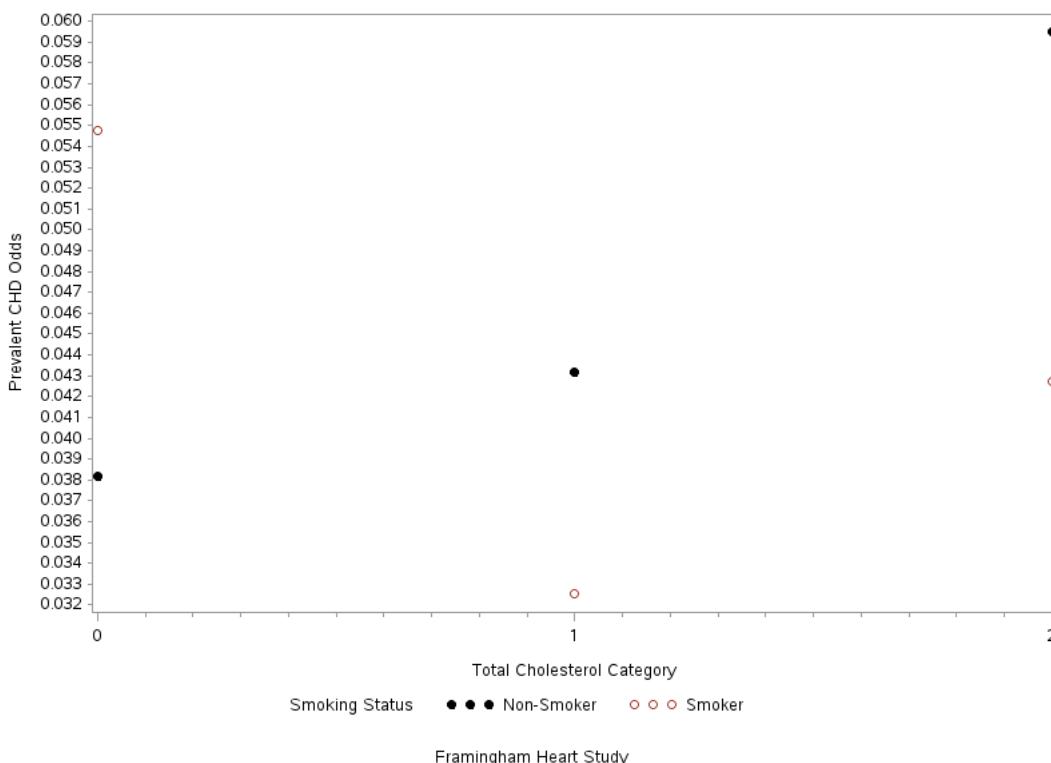


Distribution of Total Cholesterol (Examination Cycle 1)

chol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	total_count
.	0	0	19
.	0	1	2
.	1	0	31
0	0	0	393
0	0	1	15
0	1	0	438
0	1	1	24
1	0	0	741
1	0	1	32
1	1	0	737
1	1	1	24
2	0	0	992
2	0	1	59
2	1	0	889
2	1	1	38

Framingham Heart Study

Odds of Prevalent CHD vs. Total Cholesterol by Current Smoking Status (Examination Cycle 1)



Model 1: Saturated Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	0	0.0000	.
Scaled Deviance	0	0.0000	.
Pearson Chi-Square	.	0.0000	.
Scaled Pearson X2	.	0.0000	.
Log Likelihood		23956.1504	
Full Log Likelihood		-40.6475	
AIC (smaller is better)		105.2950	
AICC (smaller is better)		.	.
BIC (smaller is better)		111.1139	

Framingham Heart Study

Model 2: All Two Way Interactions Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	2	3.3052	1.6526
Scaled Deviance	2	3.3052	1.6526
Pearson Chi-Square	2	3.2829	1.6414
Scaled Pearson X2	2	3.2829	1.6414
Log Likelihood		23954.4978	
Full Log Likelihood		-42.3001	
AIC (smaller is better)		104.6003	
AICC (smaller is better)		324.6003	
BIC (smaller is better)		109.4493	

Framingham Heart Study

Model 3: Conditional Independence of Cholesterol and Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	12.9123	3.2281
Scaled Deviance	4	12.9123	3.2281
Pearson Chi-Square	4	12.9171	3.2293
Scaled Pearson X2	4	12.9171	3.2293

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		23949.6943	
Full Log Likelihood		-47.1037	
AIC (smaller is better)		110.2073	
AICC (smaller is better)		158.2073	
BIC (smaller is better)		114.0866	

Framingham Heart Study

Model 4: Conditional Independence of Cholesterol and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	6.5537	1.6384
Scaled Deviance	4	6.5537	1.6384
Pearson Chi-Square	4	6.5697	1.6424
Scaled Pearson X2	4	6.5697	1.6424
Log Likelihood		23952.8736	
Full Log Likelihood		-43.9244	
AIC (smaller is better)		103.8487	
AICC (smaller is better)		151.8487	
BIC (smaller is better)		107.7280	

Framingham Heart Study

Model 5: Conditional Independence of Smoking and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	3	4.6905	1.5635
Scaled Deviance	3	4.6905	1.5635
Pearson Chi-Square	3	4.6489	1.5496
Scaled Pearson X2	3	4.6489	1.5496
Log Likelihood		23953.8052	
Full Log Likelihood		-42.9928	
AIC (smaller is better)		103.9855	
AICC (smaller is better)		193.9855	
BIC (smaller is better)		108.3497	

Framingham Heart Study

Model 6: Joint Independence of (Cholesterol and Smoking) from CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	8.0237	1.6047
Scaled Deviance	5	8.0237	1.6047
Pearson Chi-Square	5	8.0445	1.6089
Scaled Pearson X2	5	8.0445	1.6089
Log Likelihood		23952.1386	
Full Log Likelihood		-44.6594	
AIC (smaller is better)		103.3187	
AICC (smaller is better)		131.3187	
BIC (smaller is better)		106.7131	

Framingham Heart Study

Model 7: Joint Independence of (Cholesterol and CHD) from Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	14.3823	2.8765
Scaled Deviance	5	14.3823	2.8765
Pearson Chi-Square	5	14.3245	2.8649
Scaled Pearson X2	5	14.3245	2.8649
Log Likelihood		23948.9593	
Full Log Likelihood		-47.8387	
AIC (smaller is better)		109.6773	
AICC (smaller is better)		137.6773	

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
BIC (smaller is better)		113.0717	

Framingham Heart Study

Model 8: Joint Independence of (Smoking and CHD) from Cholesterol

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	6	16.2455	2.7076
Scaled Deviance	6	16.2455	2.7076
Pearson Chi-Square	6	16.3997	2.7333
Scaled Pearson X2	6	16.3997	2.7333
Log Likelihood		23948.0277	
Full Log Likelihood		-48.7703	
AIC (smaller is better)		109.5405	
AICC (smaller is better)		126.3405	
BIC (smaller is better)		112.4500	

Framingham Heart Study

Model 9: Mutual Independence Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	7	17.7155	2.5308
Scaled Deviance	7	17.7155	2.5308
Pearson Chi-Square	7	17.9399	2.5628
Scaled Pearson X2	7	17.9399	2.5628
Log Likelihood		23947.2927	
Full Log Likelihood		-49.5053	
AIC (smaller is better)		109.0105	
AICC (smaller is better)		119.0105	
BIC (smaller is better)		111.4351	

Framingham Heart Study

Compute p-values using Deviance (Examination Cycle 1)

Obs	Model	Deviance	df	pvalue
1	2	3.3052	2	0.19155
2	3	12.9123	4	0.01171
3	4	6.5537	4	0.16144
4	5	4.6905	3	0.19591
5	6	8.0237	5	0.15493
6	7	14.3823	5	0.01335
7	8	16.2455	6	0.01250
8	9	17.7155	7	0.01332

Framingham Heart Study

Final Model: (Model 6) Joint Independence of (Cholesterol and Smoking) from CVD (Examination Cycle 1)

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	8.0237	1.6047
Scaled Deviance	5	8.0237	1.6047
Pearson Chi-Square	5	8.0445	1.6089
Scaled Pearson X2	5	8.0445	1.6089
Log Likelihood		23952.1386	
Full Log Likelihood		-44.6594	
AIC (smaller is better)		103.3187	
AICC (smaller is better)		131.3187	
BIC (smaller is better)		106.7131	

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept		1	3.7042	0.0778	3.5516	3.8567	2264.61 <.0001
chol	0	1	-0.6964	0.0569	-0.8080	-0.5848	149.53 <.0001
chol	1	1	-0.1973	0.0489	-0.2932	-0.1014	16.27 <.0001

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq	
chol	2	0	0.0000	0.0000	0.0000 0.0000	.	.	.
cursmoke	0	1	0.1255	0.0451	0.0372 0.2139	7.76	0.0053	
cursmoke	1	0	0.0000	0.0000	0.0000 0.0000	.	.	.
chol*cursmoke	0	1	-0.2498	0.0815	-0.4096 -0.0901	9.39	0.0022	
chol*cursmoke	0	1	0.0000	0.0000	0.0000 0.0000	.	.	.
chol*cursmoke	1	0	-0.1099	0.0681	-0.2434 0.0236	2.60	0.1066	
chol*cursmoke	1	1	0.0000	0.0000	0.0000 0.0000	.	.	.
chol*cursmoke	2	0	0.0000	0.0000	0.0000 0.0000	.	.	.
chol*cursmoke	2	1	0.0000	0.0000	0.0000 0.0000	.	.	.
CHD	0	1	3.0830	0.0738	2.9383 3.2276	1744.93	<.0001	
CHD	1	0	0.0000	0.0000	0.0000 0.0000	.	.	.
Scale		0	1.0000	0.0000	1.0000 1.0000			

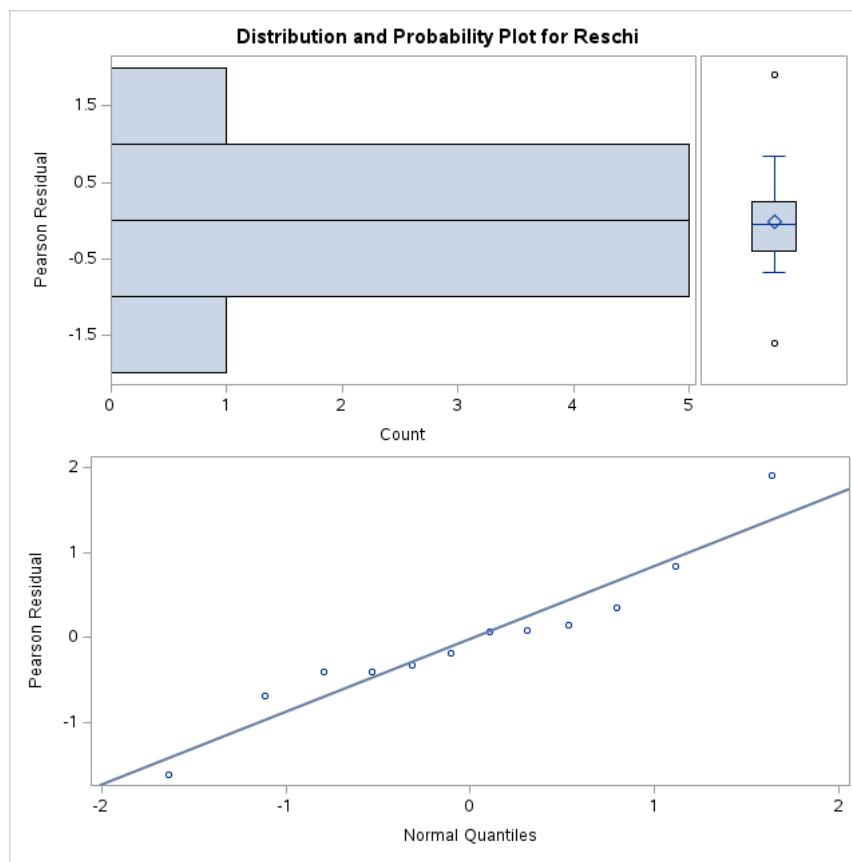
Note: The scale parameter was held fixed.

Observation	Count	chol	cursmoke	CHD	Predicted Value	Linear Predictor	Standard Error of the Linear Predictor	HessWgt	Lower	Upper	Raw Residual	Pearson Residual	Deviance Residual	Std Deviance Residual	Std Pearson Residual	Likelihood Residual	Leverage	CookD	I
1	393	0	0	0	390.12323	5.9664627	0.0496129	390.12323	353.97391	429.96427	2.8767686	0.1456478	0.1454694	0.7297589	0.7306541	0.7306186	0.960264	1.843028	
2	15	0	0	1	17.876769	2.883502	0.0862039	17.876769	15.097748	21.167321	-2.876769	-0.680394	-0.699988	-0.751695	-0.730654	-0.748934	0.1328442	0.0116835	
3	438	0	1	0	441.75719	6.0970604	0.0466365	441.75719	403.16851	484.03933	-3.757188	-0.17876	-0.179015	-0.904206	-0.902921	-0.902972	0.9608039	2.8549201	
4	24	0	1	1	20.242812	3.0077998	0.0845259	20.242812	17.152296	23.89018	3.7571881	0.8350789	0.8110604	0.8769515	0.9029212	0.8807548	0.1446274	0.0196923	
5	741	1	0	0	739.13053	6.6054745	0.0361126	739.13053	688.62385	793.3416	1.869466	0.0687633	0.0687344	0.3618282	0.3619806	0.3619751	0.9639136	0.4999969	
6	32	1	0	1	33.869467	3.5225139	0.0792072	33.869467	28.999267	39.557578	-1.869467	-0.321228	-0.324253	-0.36539	-0.361981	-0.364668	0.2124899	0.0050507	
7	737	1	1	0	727.65632	6.5898289	0.0363939	727.65632	677.55997	781.45661	9.3436787	0.3463815	0.3456442	1.8165056	1.8203807	1.8202406	0.9637936	12.601593	
8	24	1	1	1	33.343679	3.5068682	0.0793359	33.343679	28.541886	38.953311	-9.343679	-1.618122	-1.704191	-1.917209	-1.820381	-1.897297	0.2098714	0.1257424	
9	992	2	0	0	1004.9498	6.9126929	0.031015	1004.9498	945.68026	1067.934	-12.94979	-0.408499	-0.409381	-2.243168	-2.238335	-2.238496	0.9666933	20.773508	
10	59	2	0	1	46.050206	3.8297322	0.0770169	46.050206	39.59813	53.553576	12.949794	1.9080318	1.8279569	2.1440948	2.2383351	2.170243	0.2731515	0.2689749	
11	889	2	1	0	886.38293	6.7871491	0.0330031	886.38293	830.86235	945.61356	2.6170698	0.0879032	0.08786	0.4727035	0.472936	0.4729279	0.9654535	0.892963	
12	38	2	1	1	40.617071	3.7041884	0.0778388	40.617071	34.870013	47.311322	-2.617071	-0.41064	-0.415172	-0.478156	-0.472936	-0.476877	0.2460938	0.0104301	

Framingham Heart Study

Final Model: (Model 6) Joint Independence of (Cholesterol and Smoking) from CVD (Examination Cycle 1)

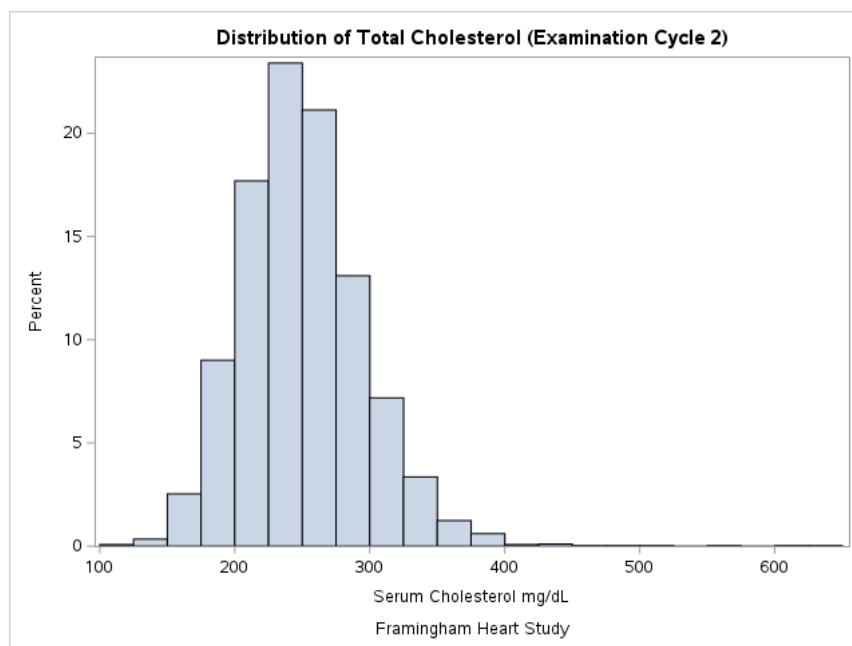
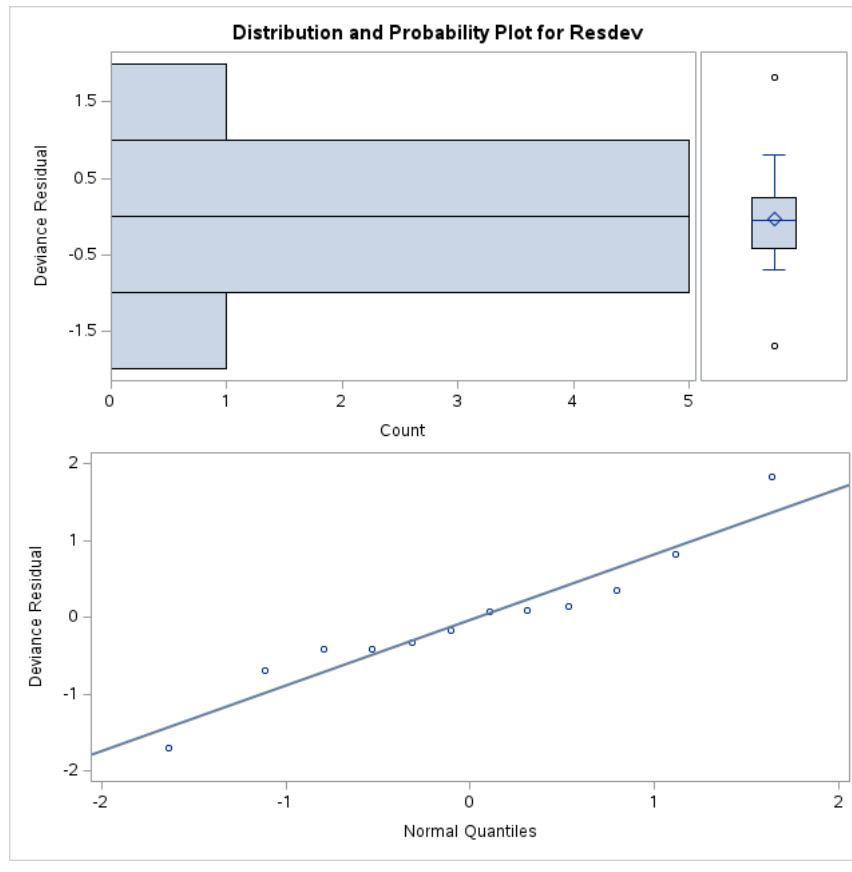
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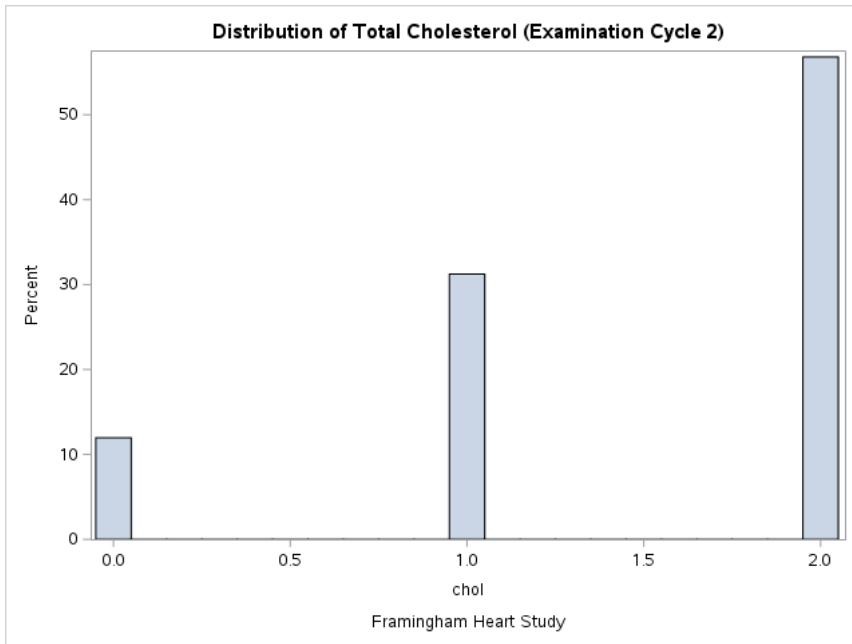


Framingham Heart Study

Final Model: (Model 6) Joint Independence of (Cholesterol and Smoking) from CVD (Examination Cycle 1)

The UNIVARIATE Procedure



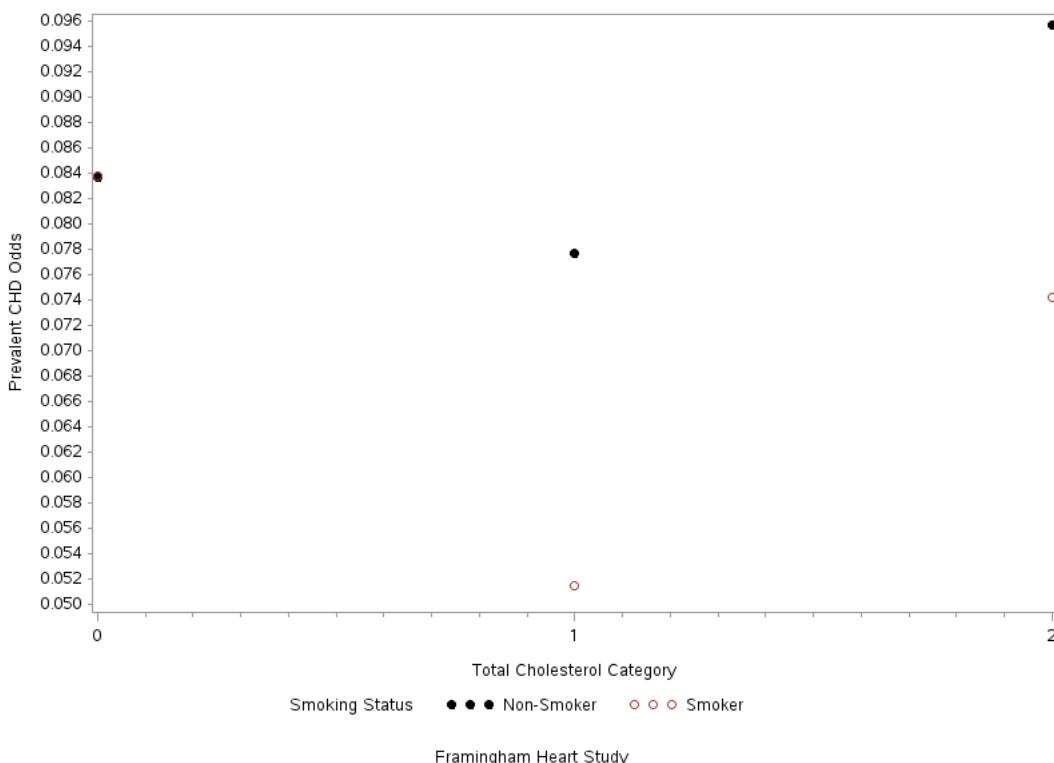


Distribution of Total Cholesterol (Examination Cycle 2)

chol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	total_count
.	0	0	74
.	0	1	6
.	1	0	60
.	1	1	3
0	0	0	227
0	0	1	19
0	1	0	191
0	1	1	16
1	0	0	605
1	0	1	47
1	1	0	505
1	1	1	26
2	0	0	1118
2	0	1	107
2	1	0	862
2	1	1	64

Framingham Heart Study

Odds of Prevalent CHD vs. Total Cholesterol by Current Smoking Status (Examination Cycle 2)



Model 1: Saturated Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	0	0.0000	.
Scaled Deviance	0	0.0000	.
Pearson Chi-Square	.	0.0000	.
Scaled Pearson X2	.	0.0000	.
Log Likelihood		20272.3992	
Full Log Likelihood		-40.4165	
AIC (smaller is better)		104.8329	
AICC (smaller is better)		.	.
BIC (smaller is better)		110.6518	

Framingham Heart Study

Model 2: All Two Way Interactions Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	2	0.9077	0.4539
Scaled Deviance	2	0.9077	0.4539
Pearson Chi-Square	2	0.9113	0.4557
Scaled Pearson X2	2	0.9113	0.4557
Log Likelihood		20271.9454	
Full Log Likelihood		-40.8703	
AIC (smaller is better)		101.7406	
AICC (smaller is better)		321.7406	
BIC (smaller is better)		106.5897	

Framingham Heart Study

Model 3: Conditional Independence of Cholesterol and Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	2.4885	0.6221
Scaled Deviance	4	2.4885	0.6221
Pearson Chi-Square	4	2.5064	0.6266
Scaled Pearson X2	4	2.5064	0.6266

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		20271.1550	
Full Log Likelihood		-41.6607	
AIC (smaller is better)		99.3215	
AICC (smaller is better)		147.3215	
BIC (smaller is better)		103.2007	

Framingham Heart Study

Model 4: Conditional Independence of Cholesterol and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	4.5467	1.1367
Scaled Deviance	4	4.5467	1.1367
Pearson Chi-Square	4	4.4210	1.1053
Scaled Pearson X2	4	4.4210	1.1053
Log Likelihood		20270.1259	
Full Log Likelihood		-42.6898	
AIC (smaller is better)		101.3796	
AICC (smaller is better)		149.3796	
BIC (smaller is better)		105.2589	

Framingham Heart Study

Model 5: Conditional Independence of Smoking and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	3	5.1749	1.7250
Scaled Deviance	3	5.1749	1.7250
Pearson Chi-Square	3	5.0978	1.6993
Scaled Pearson X2	3	5.0978	1.6993
Log Likelihood		20269.8118	
Full Log Likelihood		-43.0039	
AIC (smaller is better)		104.0079	
AICC (smaller is better)		194.0079	
BIC (smaller is better)		108.3720	

Framingham Heart Study

Model 6: Joint Independence of (Cholesterol and Smoking) from CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	8.9204	1.7841
Scaled Deviance	5	8.9204	1.7841
Pearson Chi-Square	5	8.4981	1.6996
Scaled Pearson X2	5	8.4981	1.6996
Log Likelihood		20267.9390	
Full Log Likelihood		-44.8767	
AIC (smaller is better)		103.7533	
AICC (smaller is better)		131.7533	
BIC (smaller is better)		107.1477	

Framingham Heart Study

Model 7: Joint Independence of (Cholesterol and CHD) from Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	6.8622	1.3724
Scaled Deviance	5	6.8622	1.3724
Pearson Chi-Square	5	6.7866	1.3573
Scaled Pearson X2	5	6.7866	1.3573
Log Likelihood		20268.9681	
Full Log Likelihood		-43.8476	
AIC (smaller is better)		101.6952	
AICC (smaller is better)		129.6952	

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
BIC (smaller is better)		105.0895	

Framingham Heart Study

Model 8: Joint Independence of (Smoking and CHD) from Cholesterol

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	6	6.2340	1.0390
Scaled Deviance	6	6.2340	1.0390
Pearson Chi-Square	6	6.1616	1.0269
Scaled Pearson X2	6	6.1616	1.0269
Log Likelihood		20269.2822	
Full Log Likelihood		-43.5335	
AIC (smaller is better)		99.0669	
AICC (smaller is better)		115.8669	
BIC (smaller is better)		101.9764	

Framingham Heart Study

Model 9: Mutual Independence Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	7	10.6077	1.5154
Scaled Deviance	7	10.6077	1.5154
Pearson Chi-Square	7	10.3361	1.4766
Scaled Pearson X2	7	10.3361	1.4766
Log Likelihood		20267.0954	
Full Log Likelihood		-45.7203	
AIC (smaller is better)		101.4406	
AICC (smaller is better)		111.4406	
BIC (smaller is better)		103.8652	

Framingham Heart Study

Compute p-values using Deviance (Examination Cycle 2)

Obs	Model	Deviance	df	pvalue
1	2	0.9077	2	0.63518
2	3	2.4885	4	0.64670
3	4	4.5467	4	0.33705
4	5	5.1749	3	0.15943
5	6	8.9204	5	0.11228
6	7	6.8622	5	0.23109
7	8	6.2340	6	0.39749
8	9	10.6077	7	0.15667

Framingham Heart Study

Final Model: (Model 9) Mutual Independence (Examination Cycle 2)

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	7	10.6077	1.5154
Scaled Deviance	7	10.6077	1.5154
Pearson Chi-Square	7	10.3361	1.4766
Scaled Pearson X2	7	10.3361	1.4766
Log Likelihood		20267.0954	
Full Log Likelihood		-45.7203	
AIC (smaller is better)		101.4406	
AICC (smaller is better)		111.4406	
BIC (smaller is better)		103.8652	

Analysis Of Maximum Likelihood Parameter Estimates						
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept	1	4.2432	0.0642	4.1174	4.3691	4368.04 <.0001
chol	0	-1.5578	0.0517	-1.6591	-1.4565	908.07 <.0001
chol	1	-0.5979	0.0362	-0.6688	-0.5269	272.83 <.0001

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq	
chol	2	0	0.0000	0.0000	0.0000	.0000	.	.
cursmoke	0	1	0.2436	0.0327	0.1794	0.3078	55.36	<.0001
cursmoke	1	0	0.0000	0.0000	0.0000	0.0000	.	.
CHD	0	1	2.5316	0.0622	2.4097	2.6535	1656.36	<.0001
CHD	1	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.0000	0.0000	1.0000	1.0000		

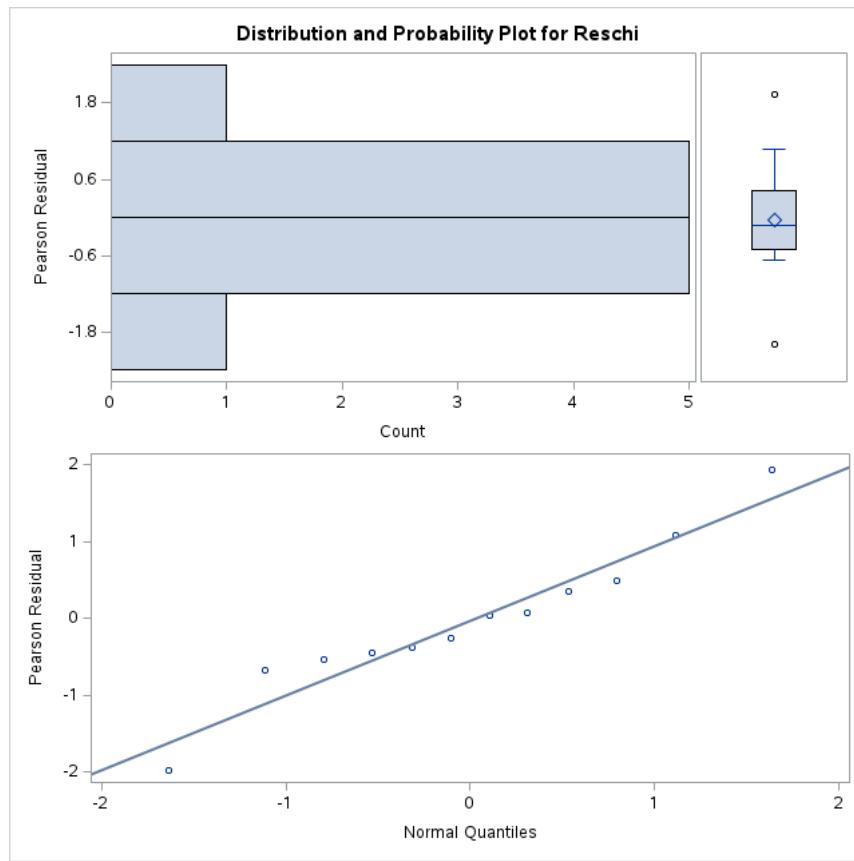
Note: The scale parameter was held fixed.

Observation	Count	chol	cursmoke	CHD	Observation Statistics													
					Predicted Value	Linear Predictor	Standard Error of the Linear Predictor	HessWgt	Lower	Upper	Raw Residual	Pearson Residual	Deviance Residual	Std Deviance Residual	Std Pearson Residual	Likelihood Residual	Leverage	CookD
1	227	0	0	0	235.24325	5.4606201	0.0493506	235.24325	213.55508	259.13402	-8.24325	-0.537452	-0.540638	-0.827288	-0.822413	-0.824499	0.5729296	0.181473
2	19	0	0	1	18.709483	2.9290305	0.0757274	18.709483	16.128816	21.703066	0.2905168	0.0671646	0.0669919	0.0709035	0.0710863	0.0709231	0.1072922	0.0001215
3	191	0	1	0	184.38284	5.2170142	0.0506498	184.38284	166.95801	203.62623	6.6171607	0.4873169	0.4844448	0.6673382	0.6712946	0.6692126	0.4730171	0.0808978
4	16	0	1	1	14.664428	2.6854247	0.0765805	14.664428	12.62059	17.039254	1.3355722	0.3487666	0.3436639	0.3594686	0.3648059	0.3599307	0.0860006	0.0025044
5	605	1	0	0	614.33281	6.4205368	0.032761	614.33281	576.12608	655.07329	-9.332814	-0.37654	-0.377499	-0.646789	-0.645145	-0.645706	0.6593513	0.161122
6	47	1	0	1	48.859423	3.8889473	0.0661245	48.859423	42.920332	55.620334	-1.859423	-0.266014	-0.267728	-0.301913	-0.29998	-0.301501	0.2136352	0.0048895
7	505	1	1	0	481.51192	6.176931	0.0346873	481.51192	449.8639	515.38639	23.488082	1.0703949	1.0618649	1.6372463	1.6503984	1.6448789	0.5793601	0.7503185
8	26	1	1	1	38.295846	3.6453414	0.0670998	38.295846	33.576564	43.678436	-12.29585	-1.98693	-2.110677	-2.320157	-2.184128	-2.297277	0.1724223	0.1987793
9	1118	2	0	0	1117.016	7.0184161	0.0263225	1117.016	1060.8492	1176.1565	0.9840384	0.0294387	0.0619178	0.0619269	0.0619248	0.7739489	0.002626	
10	107	2	0	1	88.839069	4.4868265	0.0631826	88.839069	78.491547	100.5507	18.160931	1.9267976	1.8661815	2.3230356	2.398491	2.3500731	0.354649	0.6322792
11	862	2	1	0	875.51322	6.7748102	0.0286845	875.51322	827.64939	926.14506	-13.51322	-0.456696	-0.457879	-0.865888	-0.863651	-0.864277	0.7203738	0.3843148
12	64	2	1	1	69.631753	4.2432207	0.0642026	69.631753	61.398535	78.969001	-5.631753	-0.674901	-0.684319	-0.810439	-0.799284	-0.807253	0.2870199	0.051436

Framingham Heart Study

Final Model: (Model 9) Mutual Independence (Examination Cycle 2)

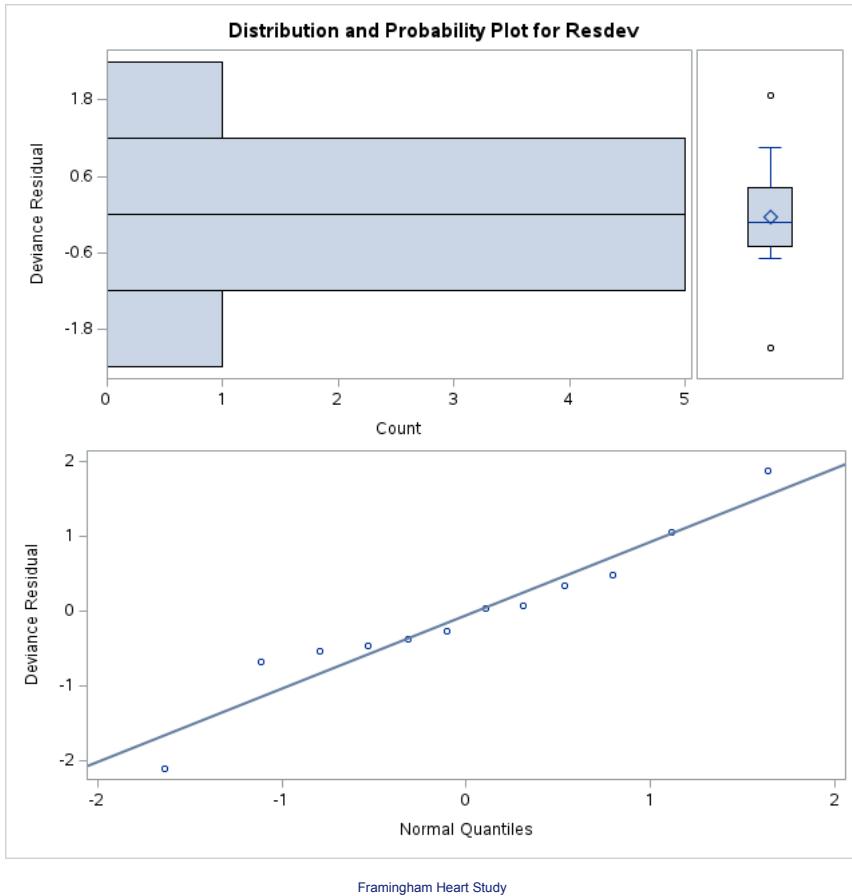
The UNIVARIATE Procedure



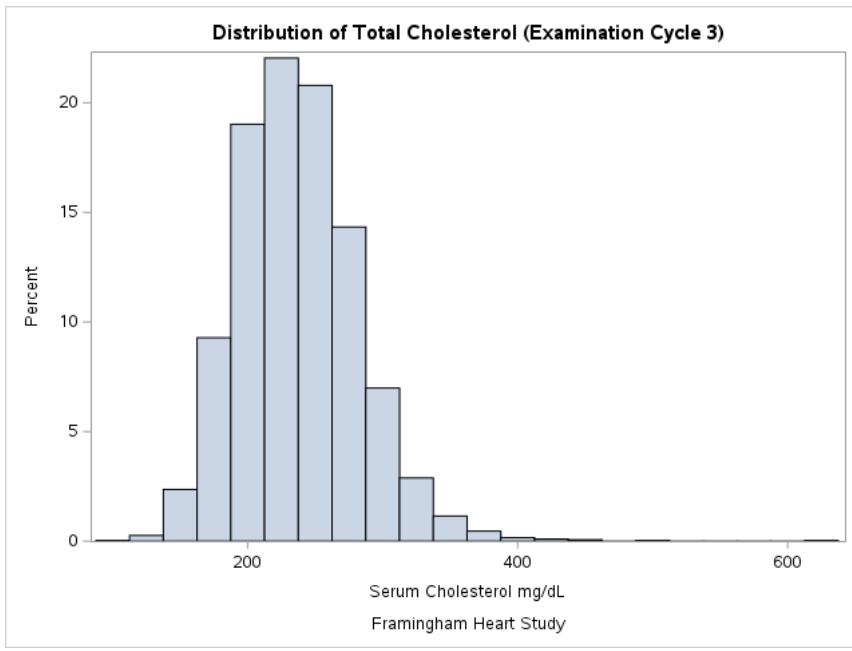
Framingham Heart Study

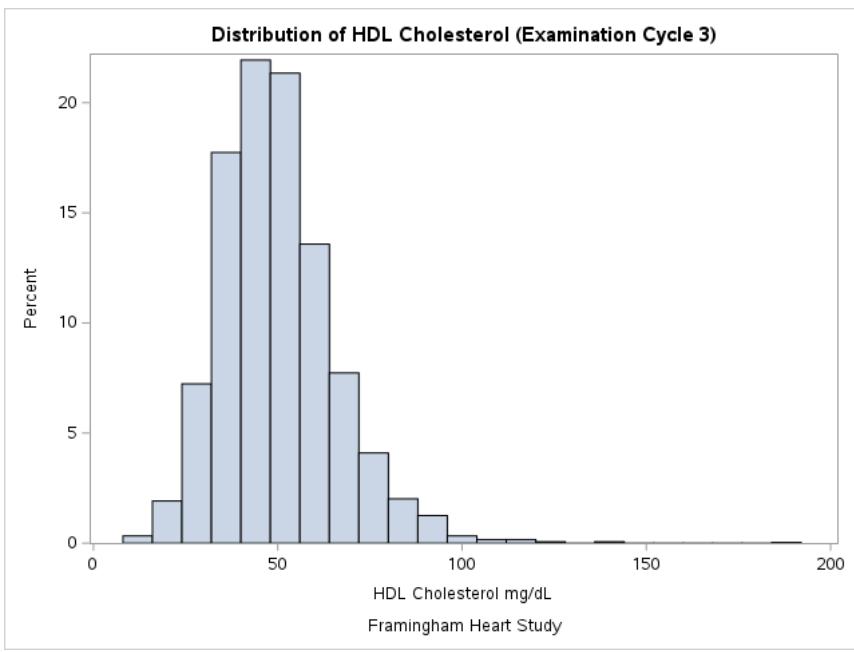
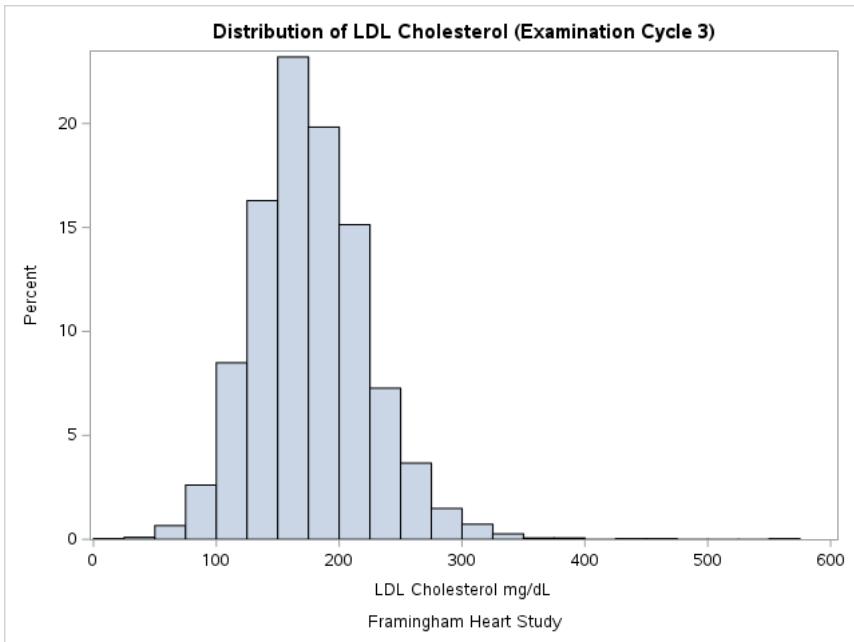
Final Model: (Model 9) Mutual Independence (Examination Cycle 2)

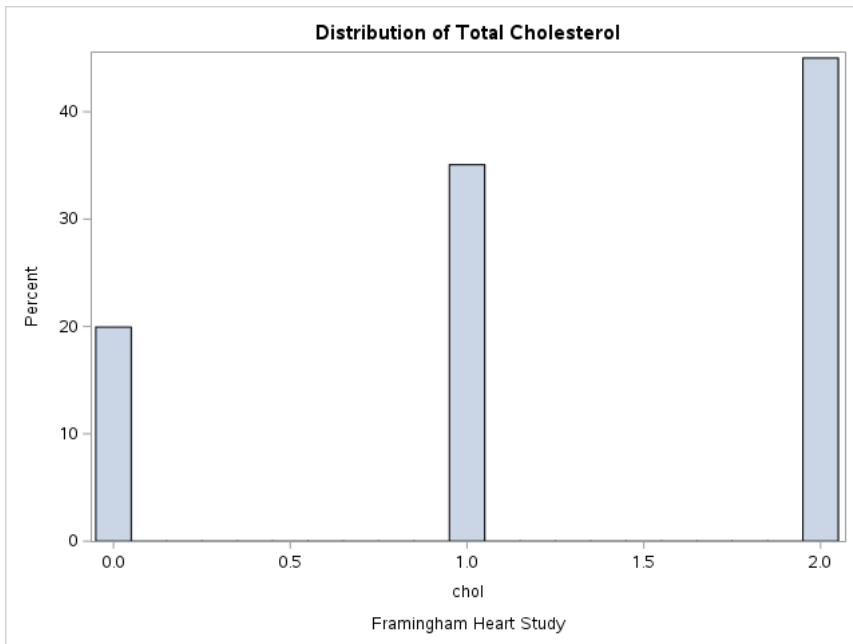
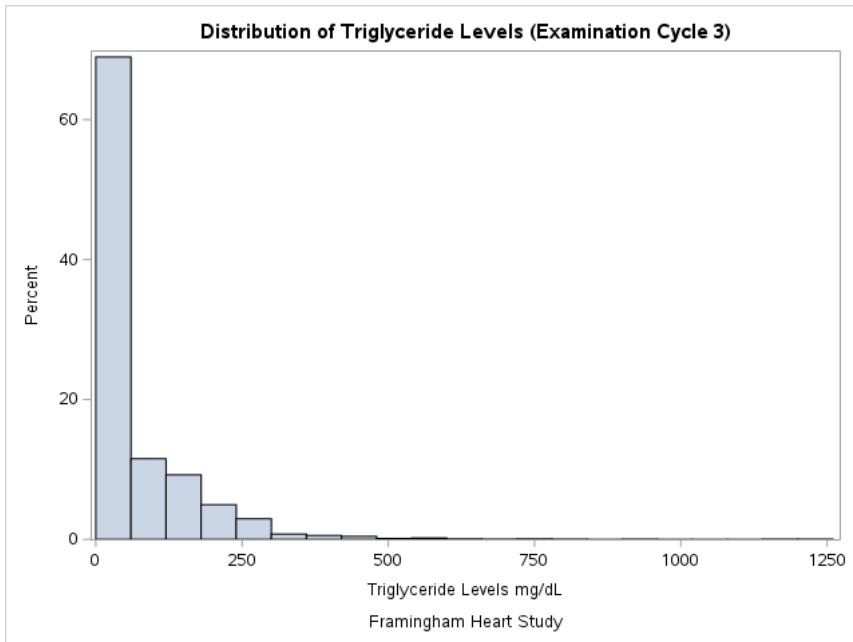
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Framingham Heart Study





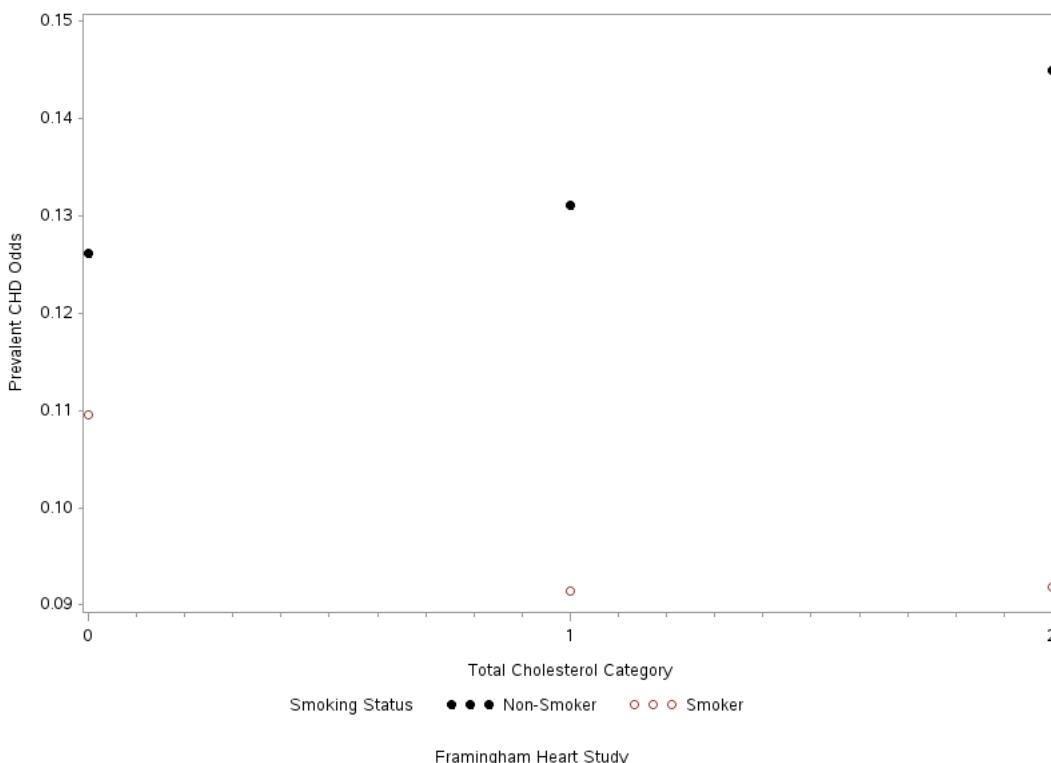


Distribution of Total Cholesterol

chol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	total_count
.	0	0	121
.	0	1	15
.	1	0	65
.	1	1	13
0	0	0	333
0	0	1	42
0	1	0	210
0	1	1	23
1	0	0	618
1	0	1	81
1	1	0	339
1	1	1	31
2	0	0	814
2	0	1	118
2	1	0	403
2	1	1	37

Framingham Heart Study

Odds of Prevalent CHD vs. Total Cholesterol by Current Smoking Status (Examination Cycle 3)



Model 1: Saturated Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	0	0.0000	.
Scaled Deviance	0	0.0000	.
Pearson Chi-Square	.	0.0000	.
Scaled Pearson X2	.	0.0000	.
Log Likelihood		15215.6023	
Full Log Likelihood		-40.6368	
AIC (smaller is better)		105.2736	
AICC (smaller is better)		.	.
BIC (smaller is better)		111.0925	

Framingham Heart Study

Model 2: All Two Way Interactions Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	2	0.8669	0.4334
Scaled Deviance	2	0.8669	0.4334
Pearson Chi-Square	2	0.8757	0.4379
Scaled Pearson X2	2	0.8757	0.4379
Log Likelihood		15215.1689	
Full Log Likelihood		-41.0703	
AIC (smaller is better)		102.1405	
AICC (smaller is better)		322.1405	
BIC (smaller is better)		106.9896	

Framingham Heart Study

Model 3: Conditional Independence of Cholesterol and Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	8.1459	2.0365
Scaled Deviance	4	8.1459	2.0365
Pearson Chi-Square	4	8.2524	2.0631
Scaled Pearson X2	4	8.2524	2.0631

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		15211.5294	
Full Log Likelihood		-44.7098	
AIC (smaller is better)		105.4196	
AICC (smaller is better)		153.4196	
BIC (smaller is better)		109.2988	

Framingham Heart Study

Model 4: Conditional Independence of Cholesterol and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	1.2069	0.3017
Scaled Deviance	4	1.2069	0.3017
Pearson Chi-Square	4	1.2195	0.3049
Scaled Pearson X2	4	1.2195	0.3049
Log Likelihood		15214.9989	
Full Log Likelihood		-41.2402	
AIC (smaller is better)		98.4805	
AICC (smaller is better)		146.4805	
BIC (smaller is better)		102.3598	

Framingham Heart Study

Model 5: Conditional Independence of Smoking and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	3	8.6618	2.8873
Scaled Deviance	3	8.6618	2.8873
Pearson Chi-Square	3	8.3151	2.7717
Scaled Pearson X2	3	8.3151	2.7717
Log Likelihood		15211.2714	
Full Log Likelihood		-44.9677	
AIC (smaller is better)		107.9354	
AICC (smaller is better)		197.9354	
BIC (smaller is better)		112.2995	

Framingham Heart Study

Model 6: Joint Independence of (Cholesterol and Smoking) from CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	9.1088	1.8218
Scaled Deviance	5	9.1088	1.8218
Pearson Chi-Square	5	8.8462	1.7692
Scaled Pearson X2	5	8.8462	1.7692
Log Likelihood		15211.0479	
Full Log Likelihood		-45.1912	
AIC (smaller is better)		104.3824	
AICC (smaller is better)		132.3824	
BIC (smaller is better)		107.7768	

Framingham Heart Study

Model 7: Joint Independence of (Cholesterol and CHD) from Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	16.0479	3.2096
Scaled Deviance	5	16.0479	3.2096
Pearson Chi-Square	5	15.6077	3.1215
Scaled Pearson X2	5	15.6077	3.1215
Log Likelihood		15207.5784	
Full Log Likelihood		-48.6607	
AIC (smaller is better)		111.3215	
AICC (smaller is better)		139.3215	

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
BIC (smaller is better)		114.7158	

Framingham Heart Study

Model 8: Joint Independence of (Smoking and CHD) from Cholesterol

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	6	8.5930	1.4322
Scaled Deviance	6	8.5930	1.4322
Pearson Chi-Square	6	8.6967	1.4494
Scaled Pearson X2	6	8.6967	1.4494
Log Likelihood		15211.3058	
Full Log Likelihood		-44.9333	
AIC (smaller is better)		101.8666	
AICC (smaller is better)		118.6666	
BIC (smaller is better)		104.7760	

Framingham Heart Study

Model 9: Mutual Independence Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	7	16.4949	2.3564
Scaled Deviance	7	16.4949	2.3564
Pearson Chi-Square	7	16.2609	2.3230
Scaled Pearson X2	7	16.2609	2.3230
Log Likelihood		15207.3549	
Full Log Likelihood		-48.8843	
AIC (smaller is better)		107.7685	
AICC (smaller is better)		117.7685	
BIC (smaller is better)		110.1931	

Framingham Heart Study

Compute p-values using Deviance (Examination Cycle 3)

Obs	Model	Deviance	df	pvalue
1	2	0.8669	2	0.64827
2	3	8.1459	4	0.08638
3	4	1.2069	4	0.87696
4	5	8.6618	3	0.03414
5	6	9.1088	5	0.10480
6	7	16.0479	5	0.00671
7	8	8.5930	6	0.19779
8	9	16.4949	7	0.02096

Framingham Heart Study

Final Model: (Model 8) Joint Independence of (Smoking and CHD) from Cholesterol (Examination Cycle 3)

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	6	8.5930	1.4322
Scaled Deviance	6	8.5930	1.4322
Pearson Chi-Square	6	8.6967	1.4494
Scaled Pearson X2	6	8.6967	1.4494
Log Likelihood		15211.3058	
Full Log Likelihood		-44.9333	
AIC (smaller is better)		101.8666	
AICC (smaller is better)		118.6666	
BIC (smaller is better)		104.7760	

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept		1	3.7123	0.1067	3.5031	3.9215	1209.96
cursmoke	0	1	0.9739	0.1230	0.7328	1.2151	62.66
cursmoke	1	0	0.0000	0.0000	0.0000	0.0000	.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
CHD	0	1	2.3477	0.1097	2.1326 2.5628	457.81	<.0001
CHD	1	0	0.0000	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	0 0	1	-0.3566	0.1294	-0.6103 -0.1029	7.59	0.0059
cursmoke*CHD	0 1	0	0.0000	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	1 0	0	0.0000	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	1 1	0	0.0000	0.0000	0.0000 0.0000	.	.
chol	0	1	-0.8138	0.0487	-0.9093 -0.7184	279.05	<.0001
chol	1	1	-0.2495	0.0408	-0.3295 -0.1696	37.42	<.0001
chol	2	0	0.0000	0.0000	0.0000 0.0000	.	.
Scale			0	1.0000	0.0000 1.0000 1.0000		

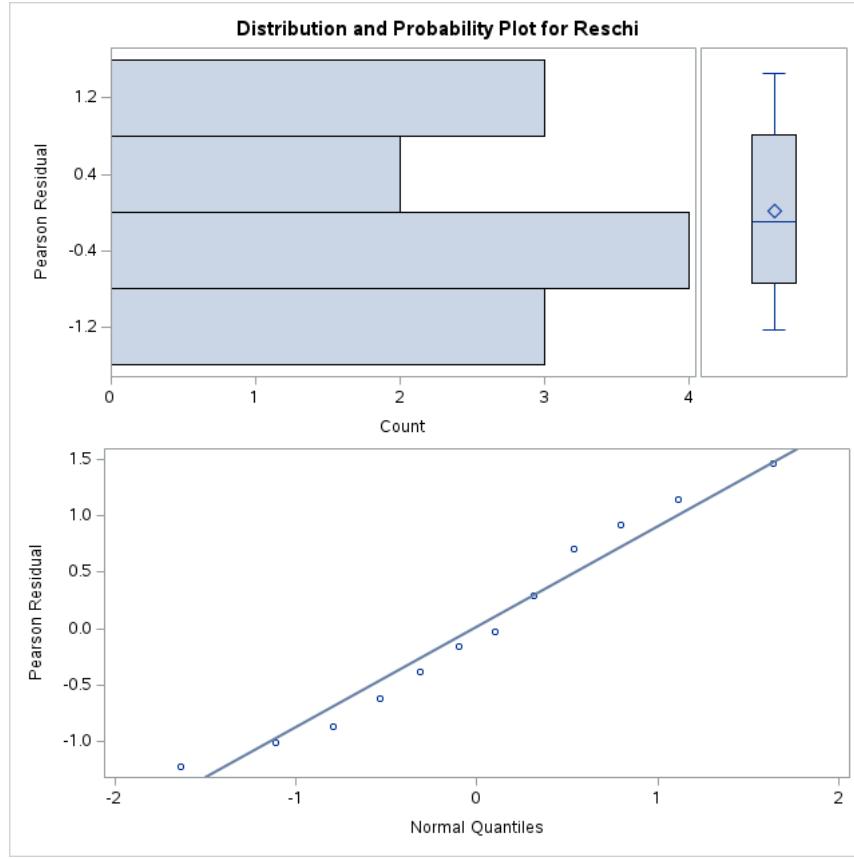
Note: The scale parameter was held fixed.

Observation	Count	chol	cursmoke	CHD	Predicted Value	Linear Predictor	Standard Error of the Linear Predictor	HessWgt	Lower	Upper	Raw Residual	Pearson Residual	Deviance Residual	Std Deviance Residual	Std Pearson Residual	Likelihood Residual	Leverage	CookD
1	333	0	0	0	351.95802	5.8635119	0.0433974	351.95802	323.25924	383.20466	-18.95802	-1.010526	-0.19808	-1.756343	-1.740358	-1.745764	0.662854	0.9924892
2	42	0	0	1	48.057724	3.8724029	0.0739333	48.057724	41.574882	55.551446	-6.057724	-0.873832	-0.893227	-1.040248	-1.01766	-1.034362	0.2626902	0.0614962
3	210	0	1	0	189.83798	5.246171	0.0486537	189.83798	172.57148	208.83207	20.16202	1.4633307	1.4385114	1.9385973	1.972045	1.9536989	0.4493808	0.5289876
4	23	0	1	1	18.146277	2.8984654	0.1109314	18.146277	14.600327	22.553425	4.8537225	1.139413	1.0935623	1.2408463	1.2928723	1.2526513	0.2233039	0.080095
5	618	1	0	0	618.82092	6.4278159	0.0342644	618.82092	578.62751	661.80631	-0.820925	-0.033001	-0.033008	-0.063119	-0.063105	-0.063109	0.7265264	0.0017632
6	81	1	0	1	84.496228	4.4367069	0.06897	84.496228	73.812513	96.726318	-3.496228	-0.380348	-0.383017	-0.495273	-0.491821	-0.493889	0.4019363	0.027094
7	339	1	1	0	333.77763	5.810475	0.0407173	333.77763	308.17586	361.50628	5.222368	0.2858504	0.2851098	0.4266167	0.4277248	0.4272302	0.5533691	0.0377784
8	31	1	1	1	31.905215	3.4627695	0.107687	31.905215	25.834398	39.402612	-0.905215	-0.160258	-0.161025	-0.202871	-0.201905	-0.202514	0.3699885	0.0039901
9	814	2	0	0	794.22106	6.6773618	0.031104	794.22106	747.24948	844.14523	19.778944	0.7018308	0.6989476	1.4522888	1.4582795	1.4568941	0.7683762	1.1757662
10	118	2	0	1	108.44605	4.6862528	0.0674556	108.44605	95.015702	123.77476	9.5539521	0.9174369	0.9044377	1.2707818	1.2890464	1.2798272	0.4934582	0.2697869
11	403	2	1	0	428.38439	6.0600209	0.038096	428.38439	397.56326	461.59493	-25.38439	-1.22645	-1.238872	-2.014272	-1.994075	-2.001739	0.6217172	1.0892011
12	37	2	1	1	40.948508	3.7123154	0.1067235	40.948508	33.219639	50.475573	-3.948508	-0.617041	-0.627378	-0.858858	-0.844706	-0.852287	0.4663993	0.1039446

Framingham Heart Study

Final Model: (Model 8) Joint Independence of (Smoking and CHD) from Cholesterol (Examination Cycle 3)

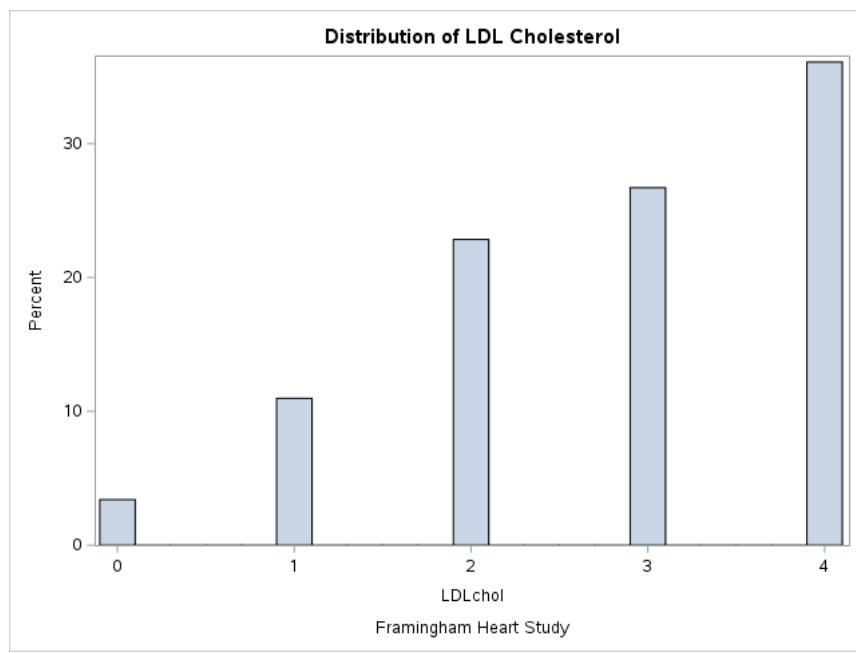
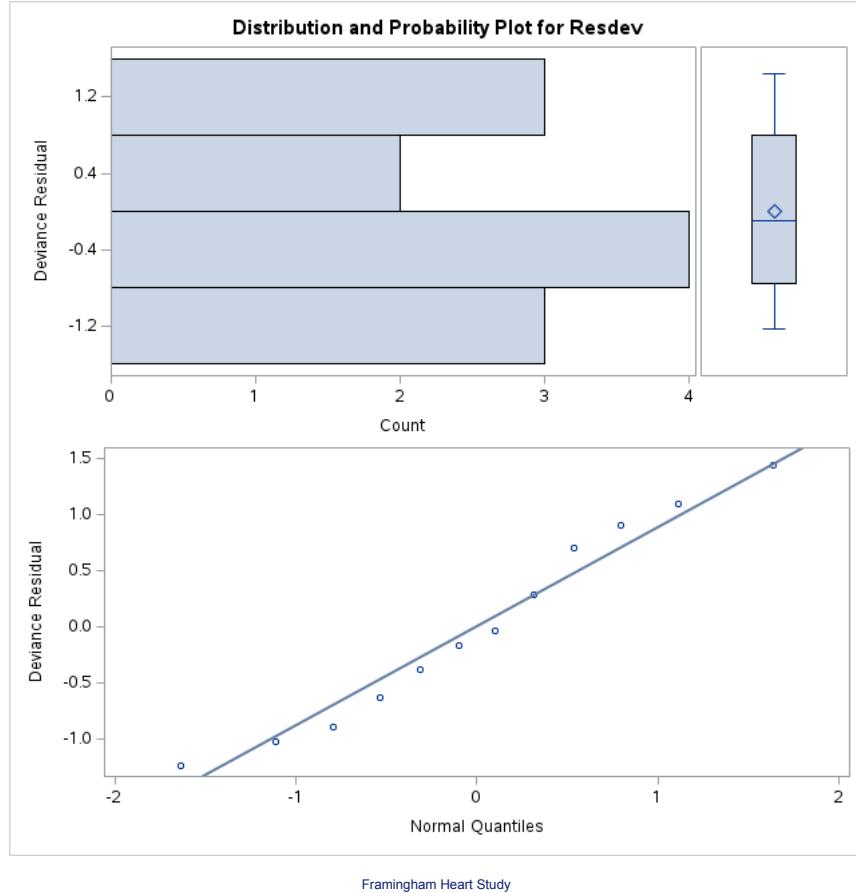
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Framingham Heart Study

Final Model: (Model 8) Joint Independence of (Smoking and CHD) from Cholesterol (Examination Cycle 3)

The UNIVARIATE Procedure

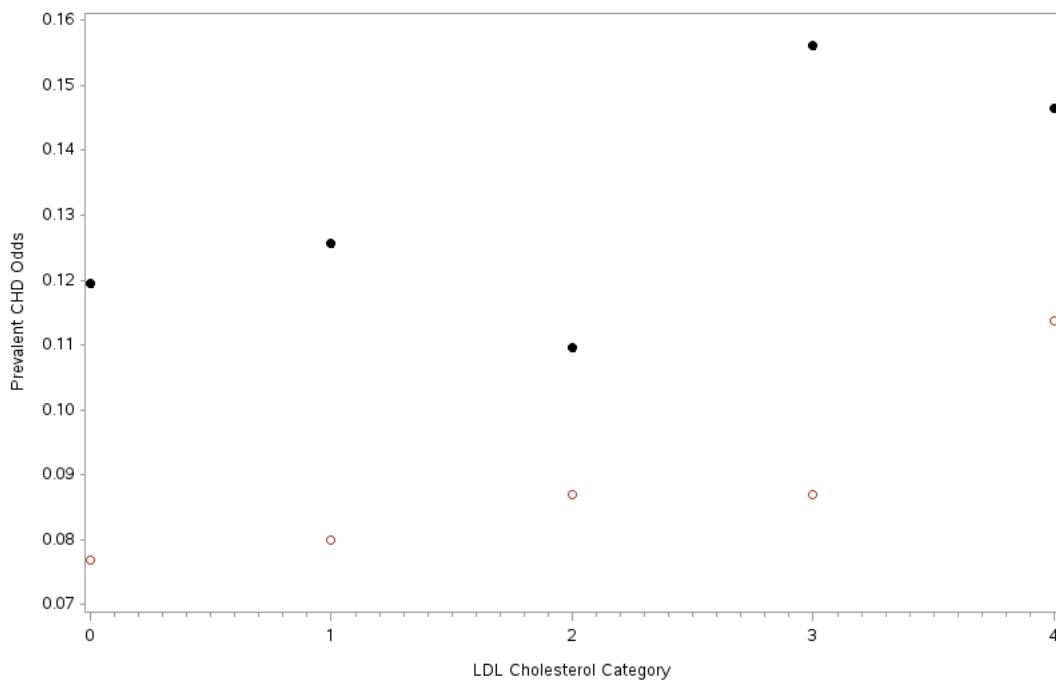


LDLchol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	total_count
.	0	0	135
.	0	1	16
.	1	0	72
.	1	1	14
0	0	0	67
0	0	1	8
0	1	0	26
0	1	1	2
1	0	0	175
1	0	1	22

LDLchol	Current Cig Smoker Y/N	Prevalent CHD (MI,AP,CI)	total_count
1	1	0	125
1	1	1	10
2	0	0	420
2	0	1	46
2	1	0	207
2	1	1	18
3	0	0	461
3	0	1	72
3	1	0	253
3	1	1	22
4	0	0	628
4	0	1	92
4	1	0	334
4	1	1	38

Framingham Heart Study

Odds of Prevalent CHD vs. LDL Cholesterol by Current Smoking Status (Examination Cycle 3)



Framingham Heart Study

Model 1: Saturated Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	0	0.0000	.
Scaled Deviance	0	0.0000	.
Pearson Chi-Square	.	0.0000	.
Scaled Pearson X2	.	0.0000	.
Log Likelihood		13970.2123	
Full Log Likelihood		-60.0450	
AIC (smaller is better)		160.0901	
AICC (smaller is better)		.	.
BIC (smaller is better)		180.0047	

Framingham Heart Study

Model 2: All Two Way Interactions Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	4	1.3305	0.3326
Scaled Deviance	4	1.3305	0.3326

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Pearson Chi-Square	4	1.3169	0.3292
Scaled Pearson X2	4	1.3169	0.3292
Log Likelihood		13969.5471	
Full Log Likelihood		-60.7103	
AIC (smaller is better)		153.4206	
AICC (smaller is better)		334.7539	
BIC (smaller is better)		169.3523	

Framingham Heart Study

Model 3: Conditional Independence of LDL Cholesterol and Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	8	10.5369	1.3171
Scaled Deviance	8	10.5369	1.3171
Pearson Chi-Square	8	10.5641	1.3205
Scaled Pearson X2	8	10.5641	1.3205
Log Likelihood		13964.9439	
Full Log Likelihood		-65.3135	
AIC (smaller is better)		154.6270	
AICC (smaller is better)		199.1984	
BIC (smaller is better)		166.5758	

Framingham Heart Study

Model 4: Conditional Independence of LDL Cholesterol and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	8	5.6112	0.7014
Scaled Deviance	8	5.6112	0.7014
Pearson Chi-Square	8	5.5495	0.6937
Scaled Pearson X2	8	5.5495	0.6937
Log Likelihood		13967.4067	
Full Log Likelihood		-62.8506	
AIC (smaller is better)		149.7012	
AICC (smaller is better)		194.2727	
BIC (smaller is better)		161.6500	

Framingham Heart Study

Model 5: Conditional Independence of Smoking and CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	5	9.5184	1.9037
Scaled Deviance	5	9.5184	1.9037
Pearson Chi-Square	5	9.1117	1.8223
Scaled Pearson X2	5	9.1117	1.8223
Log Likelihood		13965.4531	
Full Log Likelihood		-64.8042	
AIC (smaller is better)		159.6084	
AICC (smaller is better)		279.6084	
BIC (smaller is better)		174.5444	

Framingham Heart Study

Model 6: Joint Independence of (LDL Cholesterol and Smoking) from CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	9	13.7827	1.5314
Scaled Deviance	9	13.7827	1.5314
Pearson Chi-Square	9	13.4807	1.4979
Scaled Pearson X2	9	13.4807	1.4979
Log Likelihood		13963.3210	
Full Log Likelihood		-66.9364	
AIC (smaller is better)		155.8728	

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
AICC (smaller is better)		188.8728	
BIC (smaller is better)		166.8258	

Framingham Heart Study

Model 7: Joint Independence of (LDL Cholesterol and CHD) from Smoking

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	9	18.7085	2.0787
Scaled Deviance	9	18.7085	2.0787
Pearson Chi-Square	9	18.3965	2.0441
Scaled Pearson X2	9	18.3965	2.0441
Log Likelihood		13960.8581	
Full Log Likelihood		-69.3993	
AIC (smaller is better)		160.7986	
AICC (smaller is better)		193.7986	
BIC (smaller is better)		171.7516	

Framingham Heart Study

Model 8: Joint Independence of (Smoking and CHD) from LDL Cholesterol

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	12	14.8013	1.2334
Scaled Deviance	12	14.8013	1.2334
Pearson Chi-Square	12	14.8865	1.2405
Scaled Pearson X2	12	14.8865	1.2405
Log Likelihood		13962.8117	
Full Log Likelihood		-67.4457	
AIC (smaller is better)		150.8913	
AICC (smaller is better)		163.9822	
BIC (smaller is better)		158.8572	

Framingham Heart Study

Model 9: Mutual Independence Model

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	13	22.9728	1.7671
Scaled Deviance	13	22.9728	1.7671
Pearson Chi-Square	13	22.8954	1.7612
Scaled Pearson X2	13	22.8954	1.7612
Log Likelihood		13958.7259	
Full Log Likelihood		-71.5314	
AIC (smaller is better)		157.0629	
AICC (smaller is better)		166.3962	
BIC (smaller is better)		164.0330	

Framingham Heart Study

Model 10: All Two Way Interactions Model with linear and quadratic interaction terms for cLDLchol*cursmoke and cLDLchol*CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	8	11.4424	1.4303
Scaled Deviance	8	11.4424	1.4303
Pearson Chi-Square	8	11.4838	1.4355
Scaled Pearson X2	8	11.4838	1.4355
Log Likelihood		13964.4911	
Full Log Likelihood		-65.7662	
AIC (smaller is better)		155.5325	
AICC (smaller is better)		200.1039	
BIC (smaller is better)		167.4813	

**Model 11: Conditional Independence of Smoking and Heart Disease
with linear and quadratic interaction terms for cLDLchol*cursmoke and cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	9	19.5489	2.1721
Scaled Deviance	9	19.5489	2.1721
Pearson Chi-Square	9	19.4514	2.1613
Scaled Pearson X2	9	19.4514	2.1613
Log Likelihood		13960.4379	
Full Log Likelihood		-69.8195	
AIC (smaller is better)		161.6390	
AICC (smaller is better)		194.6390	
BIC (smaller is better)		172.5921	

Framingham Heart Study

**Model 12: All Two Way Interactions Model
with linear and quadratic interaction terms for cLDLchol*cursmoke and a linear interaction term for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	9	11.5489	1.2832
Scaled Deviance	9	11.5489	1.2832
Pearson Chi-Square	9	11.5831	1.2870
Scaled Pearson X2	9	11.5831	1.2870
Log Likelihood		13964.4379	
Full Log Likelihood		-65.8195	
AIC (smaller is better)		153.6389	
AICC (smaller is better)		186.6389	
BIC (smaller is better)		164.5920	

Framingham Heart Study

**Model 13: Conditional Independence of Smoking and Heart Disease
with linear and quadratic interaction terms for cLDLchol*cursmoke and a linear interaction term for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	10	19.6592	1.9659
Scaled Deviance	10	19.6592	1.9659
Pearson Chi-Square	10	19.5243	1.9524
Scaled Pearson X2	10	19.5243	1.9524
Log Likelihood		13960.3827	
Full Log Likelihood		-69.8746	
AIC (smaller is better)		159.7492	
AICC (smaller is better)		184.1937	
BIC (smaller is better)		169.7065	

Framingham Heart Study

**Model 14: All Two Way Interactions Model
with a linear interaction term for cLDLchol*cursmoke and linear and quadratic interaction terms for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	9	11.4544	1.2727
Scaled Deviance	9	11.4544	1.2727
Pearson Chi-Square	9	11.4805	1.2756
Scaled Pearson X2	9	11.4805	1.2756
Log Likelihood		13964.4851	
Full Log Likelihood		-65.7722	
AIC (smaller is better)		153.5444	
AICC (smaller is better)		186.5444	
BIC (smaller is better)		164.4975	

Framingham Heart Study

Model 15: Conditional Independence of Smoking and Heart Disease

with a linear interaction term for cLDLchol*cursmoke and linear and quadratic interaction terms for cLDLchol*CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	10	19.5657	1.9566
Scaled Deviance	10	19.5657	1.9566
Pearson Chi-Square	10	19.4523	1.9452
Scaled Pearson X2	10	19.4523	1.9452
Log Likelihood		13960.4295	
Full Log Likelihood		-69.8279	
AIC (smaller is better)		159.6557	
AICC (smaller is better)		184.1002	
BIC (smaller is better)		169.6131	

Framingham Heart Study

Model 16: All Two Way Interactions Model
with linear interaction terms for cLDLchol*cursmoke and cLDLchol*CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	10	11.5646	1.1565
Scaled Deviance	10	11.5646	1.1565
Pearson Chi-Square	10	11.5817	1.1582
Scaled Pearson X2	10	11.5817	1.1582
Log Likelihood		13964.4300	
Full Log Likelihood		-65.8273	
AIC (smaller is better)		151.6547	
AICC (smaller is better)		176.0991	
BIC (smaller is better)		161.6120	

Framingham Heart Study

Model 17: Conditional Independence of Smoking and Heart Disease
with linear interaction terms for cLDLchol*cursmoke and cLDLchol*CHD

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	11	19.6759	1.7887
Scaled Deviance	11	19.6759	1.7887
Pearson Chi-Square	11	19.5298	1.7754
Scaled Pearson X2	11	19.5298	1.7754
Log Likelihood		13960.3744	
Full Log Likelihood		-69.8830	
AIC (smaller is better)		157.7659	
AICC (smaller is better)		175.7659	
BIC (smaller is better)		166.7275	

Framingham Heart Study

Model 18: Conditional Independence of LDL Cholesterol and Heart Disease
with linear and quadratic interaction terms for cLDLchol*cursmoke

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	10	14.6389	1.4639
Scaled Deviance	10	14.6389	1.4639
Pearson Chi-Square	10	14.6866	1.4687
Scaled Pearson X2	10	14.6866	1.4687
Log Likelihood		13962.8929	
Full Log Likelihood		-67.3645	
AIC (smaller is better)		154.7290	
AICC (smaller is better)		179.1734	
BIC (smaller is better)		164.6863	

Framingham Heart Study

Model 19: Joint Independence of (LDL Cholesterol and Smoking) from Heart Disease
with linear and quadratic interaction terms for cLDLchol*cursmoke

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	11	22.8104	2.0737
Scaled Deviance	11	22.8104	2.0737
Pearson Chi-Square	11	22.6164	2.0560
Scaled Pearson X2	11	22.6164	2.0560
Log Likelihood		13958.8071	
Full Log Likelihood		-71.4503	
AIC (smaller is better)		160.9005	
AICC (smaller is better)		178.9005	
BIC (smaller is better)		169.8621	

Framingham Heart Study

**Model 20: Conditional Independence of LDL Cholesterol and Smoking
with linear and quadratic interaction terms for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	10	11.5398	1.1540
Scaled Deviance	10	11.5398	1.1540
Pearson Chi-Square	10	11.6175	1.1617
Scaled Pearson X2	10	11.6175	1.1617
Log Likelihood		13964.4424	
Full Log Likelihood		-65.8149	
AIC (smaller is better)		151.6298	
AICC (smaller is better)		176.0743	
BIC (smaller is better)		161.5872	

Framingham Heart Study

**Model 21: Joint Independence of (LDL Cholesterol and Heart Disease) from Smoking
with linear and quadratic interaction terms for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	11	19.7113	1.7919
Scaled Deviance	11	19.7113	1.7919
Pearson Chi-Square	11	19.6711	1.7883
Scaled Pearson X2	11	19.6711	1.7883
Log Likelihood		13960.3567	
Full Log Likelihood		-69.9007	
AIC (smaller is better)		157.8014	
AICC (smaller is better)		175.8014	
BIC (smaller is better)		166.7630	

Framingham Heart Study

**Model 22: Conditional Independence of LDL Cholesterol and Heart Disease
with a linear interaction term for cLDLchol*cursmoke**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	11	14.6556	1.3323
Scaled Deviance	11	14.6556	1.3323
Pearson Chi-Square	11	14.6807	1.3346
Scaled Pearson X2	11	14.6807	1.3346
Log Likelihood		13962.8845	
Full Log Likelihood		-67.3728	
AIC (smaller is better)		152.7457	
AICC (smaller is better)		170.7457	
BIC (smaller is better)		161.7073	

Framingham Heart Study

**Model 23: Joint Independence of (LDL Cholesterol and Smoking) from Heart Disease
with a linear interaction term for cLDLchol*cursmoke**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	12	22.8272	1.9023
Scaled Deviance	12	22.8272	1.9023

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Pearson Chi-Square	12	22.6186	1.8849
Scaled Pearson X2	12	22.6186	1.8849
Log Likelihood		13958.7987	
Full Log Likelihood		-71.4586	
AIC (smaller is better)		158.9172	
AICC (smaller is better)		172.0081	
BIC (smaller is better)		166.8831	

Framingham Heart Study

**Model 24: Conditional Independence of LDL Cholesterol and Smoking
with a linear interaction term for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	11	11.6500	1.0591
Scaled Deviance	11	11.6500	1.0591
Pearson Chi-Square	11	11.7165	1.0651
Scaled Pearson X2	11	11.7165	1.0651
Log Likelihood		13964.3873	
Full Log Likelihood		-65.8700	
AIC (smaller is better)		149.7401	
AICC (smaller is better)		167.7401	
BIC (smaller is better)		158.7017	

Framingham Heart Study

**Model 25: Joint Independence of (LDL Cholesterol and Heart Disease) from Smoking
with a linear interaction term for cLDLchol*CHD**

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	12	19.8215	1.6518
Scaled Deviance	12	19.8215	1.6518
Pearson Chi-Square	12	19.7449	1.6454
Scaled Pearson X2	12	19.7449	1.6454
Log Likelihood		13960.3016	
Full Log Likelihood		-69.9558	
AIC (smaller is better)		155.9116	
AICC (smaller is better)		169.0025	
BIC (smaller is better)		163.8775	

Framingham Heart Study

Compute p-values using Deviance (Examination Cycle 3)

Obs	Model	Deviance	df	pvalue
1	2	1.3305	4	0.85618
2	3	10.5369	8	0.22934
3	4	5.6112	8	0.69069
4	5	9.5184	5	0.09009
5	6	13.7827	9	0.13027
6	7	18.7085	9	0.02779
7	8	14.8013	12	0.25248
8	9	22.9728	13	0.04200
9	10	11.4424	8	0.17787
10	11	19.5489	9	0.02091
11	12	11.5489	9	0.23995
12	13	19.6592	10	0.03265
13	14	11.4544	9	0.24584
14	15	19.5657	10	0.03364
15	16	11.5646	10	0.31525
16	17	19.6759	11	0.04999
17	18	14.6389	10	0.14579
18	19	22.8104	11	0.01880
19	20	11.5398	10	0.31704
20	21	19.7113	11	0.04946
21	22	14.6556	11	0.19881
22	23	22.8272	12	0.02923
23	24	11.6500	11	0.39052

Obs	Model	Deviance	df	pvalue
24	25	19.8215	12	0.07054

Framingham Heart Study

Initial Selected Model: (Model 8) Joint Independence of (Smoking and CHD) from LDL Cholesterol (Examination Cycle 3)

The GENMOD Procedure

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Deviance	12	14.8013	1.2334
Scaled Deviance	12	14.8013	1.2334
Pearson Chi-Square	12	14.8865	1.2405
Scaled Pearson X2	12	14.8865	1.2405
Log Likelihood		13962.8117	
Full Log Likelihood		-67.4457	
AIC (smaller is better)		150.8913	
AICC (smaller is better)		163.9822	
BIC (smaller is better)		158.8572	

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept		1	3.4806	0.1081	3.2686 3.6925	1035.74	<.0001
cursmoke	0	1	0.9808	0.1236	0.7386 1.2231	62.97	<.0001
cursmoke	1	0	0.0000	0.0000	0.0000 0.0000	.	.
CHD	0	1	2.3514	0.1103	2.1352 2.5676	454.34	<.0001
CHD	1	0	0.0000	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	0	0	1	-0.3641	0.1300 -0.6189	-0.1092	7.84 0.0051
cursmoke*CHD	0	1	0	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	1	0	0	0.0000	0.0000 0.0000	.	.
cursmoke*CHD	1	1	0	0.0000	0.0000 0.0000	.	.
LDLchol	0	1	-2.3610	0.1031	-2.5631 -2.1590	524.68	<.0001
LDLchol	1	1	-1.1906	0.0627	-1.3135 -1.0678	360.92	<.0001
LDLchol	2	1	-0.4576	0.0486	-0.5529 -0.3624	88.63	<.0001
LDLchol	3	1	-0.3012	0.0464	-0.3922 -0.2103	42.13	<.0001
LDLchol	4	0	0.0000	0.0000	0.0000 0.0000	.	.
Scale		0	1.0000	0.0000	1.0000 1.0000		

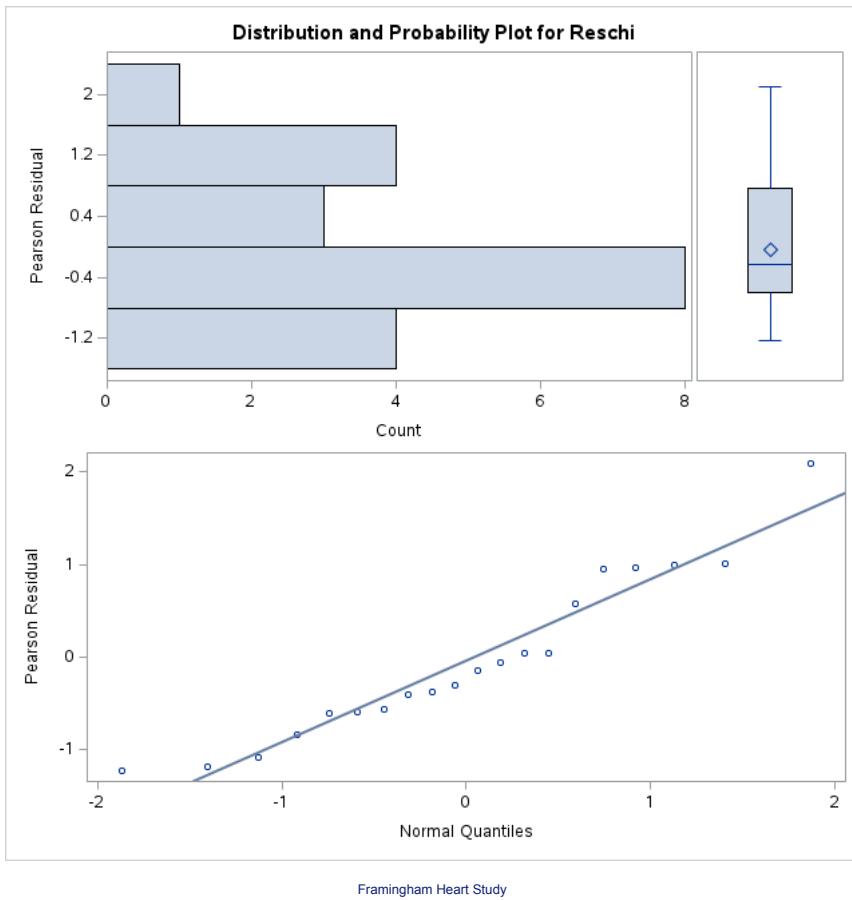
Note: The scale parameter was held fixed.

Observation	Count	LDLchol	cursmoke	CHD	Predicted Value	Linear Predictor	Standard Error of the Linear Predictor	HessWgt	Lower	Upper	Raw Residual	Pearson Residual	Deviance Residual	Std Deviance Residual	Std Pearson Residual	Likelihood Residual	Leverage	CookI
1	67	0	0	0	59.601124	4.0876744	0.0997465	59.601124	49.017375	72.470098	7.3988762	0.9583818	0.9395152	1.4726594	1.5022353	1.4902685	0.5929937	0.410993
2	8	0	0	1	8.1692003	2.100371	0.1163827	8.1692003	6.5030097	10.2623	-0.1692	-0.059199	-0.059405	-0.062992	-0.062773	-0.062968	0.1106513	0.000061
3	26	0	1	0	32.166226	3.470917	0.102159	32.166226	26.329474	39.296878	-6.166226	-1.087225	-1.125072	-1.38038	-1.33945	-1.364968	0.3357018	0.112402
4	2	0	1	1	3.0634501	1.1195418	0.1431411	3.0634501	2.3140294	4.055578	-1.06345	-0.607592	-0.649093	-0.670476	-0.627608	-0.667867	0.0627682	0.003297
5	175	1	0	0	192.11236	5.2580804	0.0570323	192.11236	171.79453	214.83314	-17.11236	-1.234617	-1.253662	-2.046894	-2.015799	-2.027519	0.6248803	0.84611
6	22	1	0	1	26.331791	3.270777	0.0827541	26.331791	22.389271	30.968548	-4.331791	-0.844165	-0.869058	-0.959906	-0.93241	-0.955006	0.1803266	0.02390
7	125	1	1	0	103.68143	4.641323	0.0611537	103.68143	91.970132	116.88402	21.381572	2.0936671	2.0274464	2.5910958	2.6757265	2.624235	0.3877457	0.566772
8	10	1	1	1	9.8744217	2.2899477	0.1174423	9.8744217	7.844127	12.430217	0.1255783	0.0399631	0.0398788	0.0429076	0.0429983	0.04292	0.1361948	0.000036
9	420	2	0	0	399.84831	5.9910853	0.041083	399.84831	368.9142	433.37631	20.151685	1.0077754	0.9994833	1.7528547	1.7673971	1.7626821	0.6748684	0.810472
10	46	2	0	1	54.805023	4.0037819	0.0726868	54.805023	47.527965	63.196279	-8.805023	-1.189379	-1.22357	-1.451656	-1.411092	-1.440028	0.2895555	0.10144
11	207	2	1	0	215.79478	5.3743279	0.0466359	215.79478	196.94473	236.44901	-8.794779	-0.598693	-0.602831	-0.827532	-0.821853	-0.824871	0.4693342	0.074672
12	18	2	1	1	20.551884	3.0229526	0.1105795	20.551884	16.547265	25.525664	-2.551884	-0.562905	-0.575202	-0.664764	-0.650553	-0.661222	0.2513047	0.01775
13	461	3	0	0	467.55056	6.1475075	0.0384481	467.55056	433.6122	504.14524	-6.550562	-0.302945	-0.303657	-0.546407	-0.545127	-0.545522	0.6911598	0.083128
14	72	3	0	1	64.0846	4.1602041	0.0712308	64.0846	55.734222	73.686073	7.9153998	0.9887717	0.9693982	1.1800483	1.2036317	1.1877679	0.3251538	0.087253
15	253	3	1	0	252.33311	5.5307501	0.0443323	252.33311	231.33348	275.23901	0.666887	0.0419822	0.0419637	0.0591053	0.0591313	0.0591182	0.4959243	0.0004
16	22	3	1	1	24.031725	3.1793748	0.1096279	24.031725	19.385167	29.792047	-2.031725	-0.41445	-0.420506	-0.498635	-0.491454	-0.496571	0.2888197	0.012260
17	628	4	0	0	631.88764	6.4487116	0.0340056	631.88764	591.14525	675.43804	-3.88764	-0.154656	-0.154815	-0.298331	-0.298024	-0.298107	0.7307047	0.03012
18	92	4	0	1	86.609385	4.4614082	0.0689344	86.609385	75.663758	99.138423	5.3906146	0.5792363	0.5733783	0.747466	0.7551026	0.7506183	0.4115633	0.049849
19	334	4	1	0	341.02445	5.8319542	0.0405399	341.02445	314.97632	369.22674	-7.024455	-0.380382	-0.381699	-0.575739	-0.573752	-0.574626	0.5604678	0.05247
20	38	4	1	1	32.47852	3.4805789	0.1081499	32.47852	26.274768	40.147042	5.5214804	0.968852	0.9431799	1.1977252	1.2303257	1.210213	0.3798815	0.115910

Framingham Heart Study

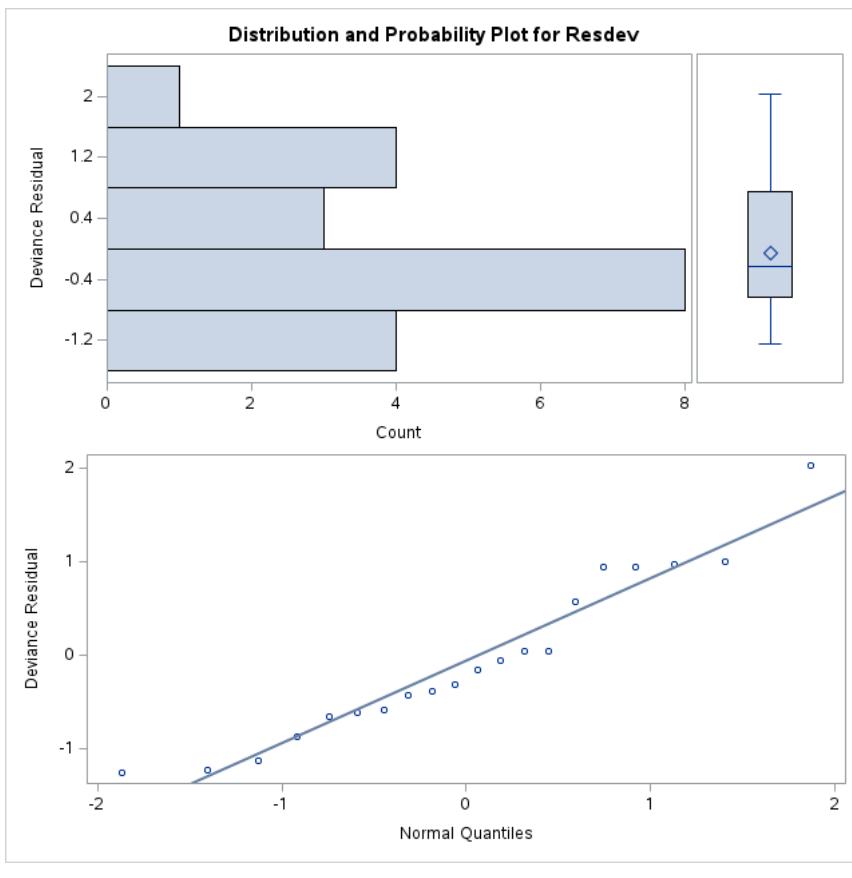
Initial Selected Model: (Model 8) Joint Independence of (Smoking and CHD) from LDL Cholesterol (Examination Cycle 3)

The UNIVARIATE Procedure



Initial Selected Model: (Model 8) Joint Independence of (Smoking and CHD) from LDL Cholesterol (Examination Cycle 3)

The UNIVARIATE Procedure



Model 1: Two Way Interaction Model (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
LDLchol	2	0 1 0 0
	3	0 0 1 0
LDLchol	4	0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124	2091.341	
SC	2093.139	2151.491	
-2 Log L	2085.124	2071.341	

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	13.7827	9	0.1303
Score	13.4807	9	0.1420
Wald	13.2785	9	0.1504

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	0.2850	0.5934
LDLchol	4	3.7745	0.4374
CURSMOKE*LDLchol	4	1.3129	0.8592

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.

Analysis of Maximum Likelihood Estimates					
Parameter		DF	Estimate	Standard Error	Wald Chi-Square
Intercept		1	-2.1253	0.3741	32.2793
CURSMOKE	1	1	-0.4397	0.8236	0.2850
LDLchol	1	1	0.0515	0.4371	0.0139
LDLchol	2	1	-0.0864	0.4050	0.0455
LDLchol	3	1	0.2685	0.3949	0.4622
LDLchol	4	1	0.2045	0.3904	0.2744
CURSMOKE*LDLchol	1 1	1	-0.0123	0.9152	0.0002
CURSMOKE*LDLchol	1 2	1	0.2090	0.8734	0.0572
CURSMOKE*LDLchol	1 3	1	-0.1459	0.8625	0.0286
CURSMOKE*LDLchol	1 4	1	0.1869	0.8486	0.0485

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	47.7	Somers' D	0.120
Percent Discordant	35.7	Gamma	0.144
Percent Tied	16.5	Tau-a	0.023
Pairs	889680	c	0.560

Model 2: Mutual Independence Model (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
	2	0 1 0 0
	3	0 0 1 0
	4	0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2084.672
SC	2093.139		2120.762
-2 Log L	2085.124		2072.672

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	12.4522	5	0.0291
Score	12.0986	5	0.0335
Wald	11.9968	5	0.0348

Type 3 Analysis of Effects			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	7.8568	0.0051
LDLchol	4	4.1787	0.3824

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-2.1410	0.3343	41.0118	<.0001
CURSMOKE	1	-0.3651	0.1303	7.8568	0.0051
LDLchol	1	0.0387	0.3820	0.0102	0.9194
LDLchol	2	-0.0337	0.3581	0.0089	0.9249
LDLchol	3	0.2265	0.3509	0.4166	0.5186
LDLchol	4	0.2528	0.3461	0.5333	0.4652

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.694	0.538	0.896
LDLchol 1 vs 0	1.039	0.492	2.197
LDLchol 2 vs 0	0.967	0.479	1.951
LDLchol 3 vs 0	1.254	0.631	2.495
LDLchol 4 vs 0	1.288	0.653	2.537

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	47.8	Somers' D	0.112
Percent Discordant	36.6	Gamma	0.133
Percent Tied	15.5	Tau-a	0.022
Pairs	889680	c	0.556

Model 3: Two Way Interaction Model (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124	2081.780	
SC	2093.139	2105.840	
-2 Log L	2085.124	2073.780	

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	11.3437	3	0.0100	
Score	10.9347	3	0.0121	
Wald	10.7777	3	0.0130	

Joint Tests				
Effect	DF	Wald		Pr > ChiSq
		Chi-Square	Pr > ChiSq	
CURSMOKE	1	1.5746	0.2095	
LDLchol	1	1.7649	0.1840	
LDLchol*CURSMOKE	1	0.0816	0.7751	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard	Wald	Pr > ChiSq
			Error	Chi-Square	
Intercept	1	-2.2226	0.1923	133.5594	<.0001
CURSMOKE	1	-0.4607	0.3672	1.5746	0.2095
LDLchol	1	0.0824	0.0620	1.7649	0.1840
LDLchol*CURSMOKE	1	0.0337	0.1178	0.0816	0.7751

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	47.7	Somers' D	0.109
Percent Discordant	36.8	Gamma	0.129
Percent Tied	15.5	Tau-a	0.021
Pairs	889680	c	0.554

Model 4: Mutual Independence Model (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	

Model Information		
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2079.862
SC	2093.139		2097.907
-2 Log L	2085.124		2073.862

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	11.2618	2	0.0036
Score	10.9334	2	0.0042
Wald	10.8342	2	0.0044

Type 3 Analysis of Effects			
Effect	DF	Wald	Pr > ChiSq
CURSMOKE	1	7.7723	0.0053
LDLchol	1	3.0277	0.0819

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-2.2497	0.1679	179.4877	<.0001
CURSMOKE	1	-0.3626	0.1301	7.7723	0.0053
LDLchol	1	0.0917	0.0527	3.0277	0.0819

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.696	0.539	0.898
LDLchol	1.096	0.988	1.215

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	47.7	Somers' D	0.109
Percent Discordant	36.8	Gamma	0.129
Percent Tied	15.5	Tau-a	0.021
Pairs	889680	c	0.554

Framingham Heart Study

Compute p-values using -2 log likelihoods (Models Ignoring Age)

Obs	Model	LL	df	pvalue
1	1	2071.34	0	.
2	2	2072.67	4	0.85609
3	3	2073.78	6	0.87523
4	4	2073.86	7	0.92551

Framingham Heart Study

Final Model (NOT Including Age): Mutual Independence Model (LDL Continuous)

The LOGISTIC Procedure

Model Information			
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Model Information		
Data Set	WORK.FRМ	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2079.862
SC	2093.139		2097.907
-2 Log L	2085.124		2073.862

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	11.2618	2	0.0036	
Score	10.9334	2	0.0042	
Wald	10.8342	2	0.0044	

Type 3 Analysis of Effects				
Effect	DF	Wald Chi-Square	Pr > ChiSq	
CURSMOKE	1	7.7723	0.0053	
LDLchol	1	3.0277	0.0819	

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-2.2497	0.1679	179.4877	<.0001
CURSMOKE	1	-0.3626	0.1301	7.7723	0.0053
LDLchol	1	0.0917	0.0527	3.0277	0.0819

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.696	0.539	0.898
LDLchol	1.096	0.988	1.215

Association of Predicted Probabilities and Observed Responses				
Percent Concordant	47.7	Somers' D	0.109	
Percent Discordant	36.8	Gamma	0.129	
Percent Tied	15.5	Tau-a	0.021	
Pairs	889680	c	0.554	

Framingham Heart Study

Model 1: Three Way Interaction Model (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRМ	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
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Number of Observations Used	3026
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Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0 0
	1	1 0 0 0 0
	2	0 1 0 0 0
	3	0 0 1 0 0
4	0 0 0 0 1	

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2009.512
SC	2093.139		2129.812
-2 Log L	2085.124		1969.512

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	115.6117	19	<.0001
Score	115.2223	19	<.0001
Wald	105.7419	19	<.0001

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	0.0090	0.9243
LDLchol	4	1.6232	0.8046
AGE	1	1.6370	0.2007
CURSMOKE*LDLchol	4	3.1723	0.5294
AGE*CURSMOKE	1	0.0194	0.8892
AGE*LDLchol	4	2.0763	0.7217
AGE*CURSMOKE*LDLchol	4	2.7767	0.5959

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.

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-5.7983	2.9676	3.8175	0.0507
CURSMOKE	1	1	0.6639	6.9877	0.0090	0.9243
LDLchol	1	1	1.4708	3.4330	0.1836	0.6683
LDLchol	2	1	0.3715	3.1963	0.0135	0.9075
LDLchol	3	1	-0.2141	3.1404	0.0046	0.9456
LDLchol	4	1	-0.9015	3.1364	0.0826	0.7738
AGE		1	0.0581	0.0454	1.6370	0.2007
CURSMOKE*LDLchol	1 1	1	-6.3122	7.7050	0.6712	0.4126
CURSMOKE*LDLchol	1 2	1	-0.8725	7.3342	0.0142	0.9053
CURSMOKE*LDLchol	1 3	1	-4.5500	7.3195	0.3864	0.5342
CURSMOKE*LDLchol	1 4	1	-1.5864	7.2097	0.0484	0.8258
AGE*CURSMOKE	1	1	-0.0156	0.1121	0.0194	0.8892
AGE*LDLchol	1	1	-0.0226	0.0526	0.1843	0.6677
AGE*LDLchol	2	1	-0.00729	0.0489	0.0222	0.8816
AGE*LDLchol	3	1	0.00722	0.0480	0.0226	0.8806
AGE*LDLchol	4	1	0.0163	0.0479	0.1152	0.7342
AGE*CURSMOKE*LDLchol	1 1	1	0.1012	0.1227	0.6803	0.4095
AGE*CURSMOKE*LDLchol	1 2	1	0.0195	0.1178	0.0273	0.8687
AGE*CURSMOKE*LDLchol	1 3	1	0.0727	0.1171	0.3861	0.5344
AGE*CURSMOKE*LDLchol	1 4	1	0.0326	0.1155	0.0795	0.7779

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.8	Somers' D	0.362
Percent Discordant	31.7	Gamma	0.364
Percent Tied	0.5	Tau-a	0.070

Association of Predicted Probabilities and Observed Responses			
Pairs	889680	c	0.681

Framingham Heart Study

Model 2: All Two Way Interactions Model (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0 0
	1	1 0 0 0 0
	2	0 1 0 0 0
	3	0 0 1 0 0
	4	0 0 0 1 1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2004.335
SC	2093.139		2100.575
-2 Log L	2085.124		1972.335

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	112.7891	15	<.0001	
Score	113.7621	15	<.0001	
Wald	105.1937	15	<.0001	

Joint Tests				
Effect	DF	Wald		Pr > ChiSq
		Chi-Square	Pr > ChiSq	
CURSMOKE	1	2.8955	0.0888	
LDLchol	4	1.6654	0.7970	
AGE	1	1.4919	0.2219	
CURSMOKE*LDLchol	4	1.9005	0.7540	
AGE*CURSMOKE	1	3.5510	0.0595	
AGE*LDLchol	4	2.4865	0.6471	

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.

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-5.2825	2.6689	3.9177	0.0478
CURSMOKE	1	1	-2.3171	1.3617	2.8955	0.0888
LDLchol	1	1	-0.0748	3.0544	0.0006	0.9805
LDLchol	2	1	0.3155	2.8503	0.0122	0.9119
LDLchol	3	1	-1.0945	2.8168	0.1510	0.6976
LDLchol	4	1	-1.1267	2.7976	0.1622	0.6871
AGE		1	0.0501	0.0411	1.4919	0.2219
CURSMOKE*LDLchol	1	1	0.0961	0.9312	0.0106	0.9178
CURSMOKE*LDLchol	1	2	0.3826	0.8889	0.1853	0.6669

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
CURSMOKE*LDLchol	1	3	1	0.0320	0.8774	0.0013
CURSMOKE*LDLchol	1	4	1	0.4473	0.8635	0.2683
AGE*CURSMOKE	1		1	0.0320	0.0170	3.5510
AGE*LDLchol	1		1	0.00127	0.0468	0.0007
AGE*LDLchol	2		1	-0.00642	0.0438	0.0215
AGE*LDLchol	3		1	0.0208	0.0432	0.2309
AGE*LDLchol	4		1	0.0198	0.0430	0.2135
						0.6440

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.7	Somers' D	0.359
Percent Discordant	31.8	Gamma	0.361
Percent Tied	0.5	Tau-a	0.070
Pairs	889680	c	0.679

Framingham Heart Study

Model 3: Conditional Independence of Smoking and LDL Cholesterol (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRМ	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CL)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0 0
	1	1 0 0 0 0
	2	0 1 0 0 0
	3	0 0 1 0 0
	4	0 0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1998.256
SC	2093.139		2070.436
-2 Log L	2085.124		1974.256

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	110.8681	11	<.0001
Score	112.1993	11	<.0001
Wald	103.8547	11	<.0001

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	3.3800	0.0660
LDLchol	4	1.9159	0.7512
AGE	1	1.5582	0.2119
AGE*CURSMOKE	1	3.3191	0.0685
AGE*LDLchol	4	2.6659	0.6152

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-5.4245	2.6614	4.1545	0.0415
CURSMOKE	1	-1.9666	1.0697	3.3800	0.0660
LDLchol	1	-0.1118	3.0264	0.0014	0.9705
LDLchol	2	0.5361	2.8263	0.0360	0.8496
LDLchol	3	1 -1.1545	2.8009	0.1699	0.6802
LDLchol	4	1 -0.8122	2.7746	0.0857	0.7697
AGE	1	0.0514	0.0412	1.5582	0.2119
AGE*CURSMOKE	1	1 0.0307	0.0169	3.3191	0.0685
AGE*LDLchol	1	1 0.00188	0.0468	0.0016	0.9680
AGE*LDLchol	2	1 -0.00847	0.0438	0.0374	0.8467
AGE*LDLchol	3	1 0.0217	0.0433	0.2504	0.6168
AGE*LDLchol	4	1 0.0167	0.0429	0.1506	0.6979

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.5	Somers' D	0.355
Percent Discordant	32.0	Gamma	0.356
Percent Tied	0.5	Tau-a	0.069
Pairs	889680	c	0.677

Framingham Heart Study

Model 4: Conditional Independence of Smoking and Age (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
	2	0 1 0 0
	3	0 0 1 0
	4	0 0 0 1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		2005.911
SC	2093.139		2096.136
-2 Log L	2085.124		1975.911

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	109.2129	14	<.0001
Score	112.5322	14	<.0001
Wald	104.9101	14	<.0001

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq

Joint Tests			
Effect	DF	Chi-Square	Pr > ChiSq
CURSMOKE	1	0.1339	0.7144
LDLchol	4	1.7235	0.7865
AGE	1	1.8083	0.1787
CURSMOKE*LDLchol	4	1.6738	0.7955
AGE*LDLchol	4	2.5274	0.6397

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.

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-5.6306	2.6966	4.3598	0.0368
CURSMOKE	1	1	-0.3064	0.8372	0.1339	0.7144
LDLchol	1	1	-0.3822	3.0944	0.0153	0.9017
LDLchol	2	1	0.1410	2.8876	0.0024	0.9610
LDLchol	3	1	-1.2504	2.8515	0.1923	0.6610
LDLchol	4	1	-1.4081	2.8303	0.2475	0.6188
AGE		1	0.0555	0.0413	1.8083	0.1787
CURSMOKE*LDLchol	1	1	0.1093	0.9343	0.0137	0.9069
CURSMOKE*LDLchol	1	2	0.3326	0.8909	0.1394	0.7088
CURSMOKE*LDLchol	1	3	0.0442	0.8787	0.0025	0.9599
CURSMOKE*LDLchol	1	4	0.4474	0.8651	0.2674	0.6051
AGE*LDLchol	1	1	0.00588	0.0472	0.0155	0.9009
AGE*LDLchol	2	1	-0.00373	0.0442	0.0071	0.9327
AGE*LDLchol	3	1	0.0231	0.0436	0.2798	0.5968
AGE*LDLchol	4	1	0.0240	0.0433	0.3079	0.5790

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.7	Somers' D	0.358
Percent Discordant	31.8	Gamma	0.360
Percent Tied	0.5	Tau-a	0.070
Pairs	889680	c	0.679

Framingham Heart Study

Model 5: Conditional Independence of LDL Cholesterol and Age (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI/AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
	2	0 1 0 0
	3	0 0 1 0
	4	0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	2087.124	1998.813

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
SC	2093.139	2070.993
-2 Log L	2085.124	1974.813

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	110.3109	11	<.0001
Score	108.8546	11	<.0001
Wald	101.2687	11	<.0001

Joint Tests				
Effect	DF	Wald	Chi-Square	Pr > ChiSq
CURSMOKE	1	2.8264	0.0927	
LDLchol	4	3.6486	0.4556	
AGE	1	51.0057	<.0001	
CURSMOKE*LDLchol	4	2.0731	0.7223	
AGE*CURSMOKE	1	3.5877	0.0582	

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.

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-6.0337	0.6778	79.2427	<.0001
CURSMOKE	1	1	-2.2949	1.3651	2.8264	0.0927
LDLchol	1	1	-0.00170	0.4432	0.0000	0.9969
LDLchol	2	1	-0.1038	0.4105	0.0639	0.8004
LDLchol	3	1	0.2551	0.4004	0.4059	0.5241
LDLchol	4	1	0.1636	0.3956	0.1709	0.6793
AGE		1	0.0618	0.00865	51.0057	<.0001
CURSMOKE*LDLchol	1 1	1	0.1066	0.9323	0.0131	0.9089
CURSMOKE*LDLchol	1 2	1	0.4347	0.8900	0.2385	0.6253
CURSMOKE*LDLchol	1 3	1	-0.00827	0.8785	0.0001	0.9925
CURSMOKE*LDLchol	1 4	1	0.3995	0.8645	0.2135	0.6440
AGE*CURSMOKE	1	1	0.0319	0.0169	3.5877	0.0582

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.4	Somers' D	0.352
Percent Discordant	32.1	Gamma	0.354
Percent Tied	0.5	Tau-a	0.069
Pairs	889680	c	0.676

Framingham Heart Study

Model 6: Joint Independence of (Smoking and LDL Cholesterol) from Age (LDL Categorical)

The LOGISTIC Procedure

Model Information			
Data Set	WORK.FRM		
Response Variable	PREVCHD		Prevalent CHD (MI,AP,CI)
Number of Response Levels	2		
Model	binary logit		
Optimization Technique	Fisher's scoring		

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile			
Ordered Value	PREVCHD	Total Frequency	
1	0	2696	
2	1	330	

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information			
Class	Value	Design Variables	
CURSMOKE	0	0	
	1	1	
LDLchol	0	0 0 0 0	
	1	1 0 0 0	
	2	0 1 0 0	
	3	0 0 1 0	

Class Level Information		
Class	Value	Design Variables
	4	0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	2087.124	2000.428
SC	2093.139	2066.593
-2 Log L	2085.124	1978.428

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	106.6957	10	<.0001
Score	107.4410	10	<.0001
Wald	100.8110	10	<.0001

Joint Tests			
Effect	DF	Wald	Chi-Square
		Chi-Square	Pr > ChiSq
CURSMOKE	1	0.1003	0.7514
LDLchol	4	3.6879	0.4499
AGE	1	88.2799	<.0001
CURSMOKE*LDLchol	4	1.8679	0.7600

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.

Analysis of Maximum Likelihood Estimates					
Parameter		DF	Estimate	Standard	Wald
				Error	Chi-Square
Intercept		1	-6.5955	0.6204	113.0046
CURSMOKE	1	1	-0.2640	0.8334	0.1003
LDLchol	1	1	-0.00913	0.4449	0.0004
LDLchol	2	1	-0.1075	0.4121	0.0681
LDLchol	3	1	0.2544	0.4020	0.4006
LDLchol	4	1	0.1609	0.3972	0.1641
AGE		1	0.0704	0.00749	88.2799
CURSMOKE*LDLchol	1	1	0.1052	0.9262	0.0129
CURSMOKE*LDLchol	1	2	0.3905	0.8839	0.1952
CURSMOKE*LDLchol	1	3	-0.0317	0.8727	0.0013
CURSMOKE*LDLchol	1	4	0.3590	0.8586	0.1748

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
		1.057	1.089
AGE	1.073		

Association of Predicted Probabilities and Observed Responses			
Percent Concordant		67.2	Somers' D
Percent Discordant		32.3	Gamma
Percent Tied		0.5	Tau-a
Pairs		889680	c
			0.675

Framingham Heart Study

Model 7: Joint Independence of (Smoking and Age) from LDL Cholesterol (LDL Categorical)

The LOGISTIC Procedure

Model Information			
Data Set	WORK.FRM		
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)	
Number of Response Levels	2		
Model	binary logit		
Optimization Technique	Fisher's scoring		

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
	2	0 1 0 0
	3	0 0 1 0
4	0	0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	2087.124	1992.916
SC	2093.139	2041.036
-2 Log L	2085.124	1976.916

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	108.2082	7	<.0001
Score	106.9241	7	<.0001
Wald	99.6230	7	<.0001

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	3.4477	0.0633
LDLchol	4	3.9438	0.4137
AGE	1	50.9026	<.0001
AGE*CURSMOKE	1	3.3829	0.0659

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.

Analysis of Maximum Likelihood Estimates					
Parameter		DF	Estimate	Standard Error	Wald Chi-Square
Intercept		1	-6.0864	0.6574	85.7120
CURSMOKE	1	1	-1.9781	1.0653	3.4477
LDLchol	1	1	0.00613	0.3876	0.0003
LDLchol	2	1	0.000225	0.3634	0.0000
LDLchol	3	1	0.2427	0.3560	0.4647
LDLchol	4	1	0.2605	0.3511	0.5505
AGE		1	0.0617	0.00865	50.9026
AGE*CURSMOKE	1	1	0.0309	0.0168	3.3829
					0.0659

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
LDLchol 1 vs 0	1.006	0.471	2.151
LDLchol 2 vs 0	1.000	0.491	2.039
LDLchol 3 vs 0	1.275	0.634	2.561
LDLchol 4 vs 0	1.298	0.652	2.582

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.1	Somers' D	0.348
Percent Discordant	32.3	Gamma	0.350
Percent Tied	0.5	Tau-a	0.068
Pairs	889680	c	0.674

Framingham Heart Study

Model 8: Joint Independence of (LDL Cholesterol and Age) from Smoking (LDL Categorical)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0 0 0 0 0
	1	1 0 0 0 0
LDLchol	0	0 0 0 0 0
	1	1 0 0 0 0
	2	0 1 0 0 0
	3	0 0 1 0 0
	4	0 0 0 0 1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1999.599
SC	2093.139		2065.764
-2 Log L	2085.124		1977.599

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	107.5255	10	<.0001
Score	111.0213	10	<.0001
Wald	103.5392	10	<.0001

Joint Tests			
Effect	DF	Wald	Pr > ChiSq
		Chi-Square	
CURSMOKE	1	0.0955	0.7573
LDLchol	4	1.9672	0.7418
AGE	1	1.9595	0.1616
AGE*LDLchol	4	2.7313	0.6037

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-5.8161	2.6546	4.8001	0.0285
CURSMOKE	1	-0.0423	0.1369	0.0955	0.7573
LDLchol	1	-0.3816	3.0188	0.0160	0.8994
LDLchol	2	0.4065	2.8239	0.0207	0.8855
LDLchol	3	-1.2915	2.7982	0.2130	0.6444
LDLchol	4	-0.9708	2.7718	0.1227	0.7262
AGE	1	0.0575	0.0411	1.9595	0.1616
AGE*LDLchol	1	0.00597	0.0467	0.0164	0.8981
AGE*LDLchol	2	-0.00665	0.0438	0.0231	0.8792
AGE*LDLchol	3	0.0237	0.0433	0.2999	0.5839
AGE*LDLchol	4	0.0190	0.0429	0.1954	0.6584

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.959	0.733	1.254

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.5	Somers' D	0.355
Percent Discordant	32.0	Gamma	0.356
Percent Tied	0.5	Tau-a	0.069
Pairs	889680	c	0.677

Framingham Heart Study

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CL)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1
LDLchol	0	0 0 0 0
	1	1 0 0 0
LDLchol	2	0 1 0 0
	3	0 0 1 0
AGE	4	0 0 0 1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1994.322
SC	2093.139		2036.427
-2 Log L	2085.124		1980.322

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	104.8021	6	<.0001
Score	105.5863	6	<.0001
Wald	99.1649	6	<.0001

Type 3 Analysis of Effects			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	0.1015	0.7500
LDLchol	4	3.9390	0.4143
AGE	1	87.7827	<.0001

Analysis of Maximum Likelihood Estimates					
Parameter		DF	Estimate	Standard Error	Wald Chi-Square
Intercept		1	-6.6270	0.5983	122.6915
CURSMOKE	1	1	-0.0436	0.1368	0.1015
LDLchol	1	1	0.00174	0.3876	0.0000
LDLchol	2	1	-0.0117	0.3635	0.0010
LDLchol	3	1	0.2364	0.3561	0.4405
LDLchol	4	1	0.2501	0.3512	0.5072
AGE		1	0.0701	0.00748	87.7827

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.957	0.732	1.252
LDLchol 1 vs 0	1.002	0.469	2.142
LDLchol 2 vs 0	0.988	0.485	2.015
LDLchol 3 vs 0	1.267	0.630	2.546
LDLchol 4 vs 0	1.284	0.645	2.556
AGE	1.073	1.057	1.088

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.0	Somers' D	0.346
Percent Discordant	32.5	Gamma	0.347
Percent Tied	0.5	Tau-a	0.067

Association of Predicted Probabilities and Observed Responses			
Pairs	889680	c	0.673

Framingham Heart Study

Model 10: Three Way Interaction Model (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CL)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1991.817
SC	2093.139		2039.937
-2 Log L	2085.124		1975.817

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	109.3074	7	<.0001	
Score	109.4526	7	<.0001	
Wald	101.4897	7	<.0001	

Joint Tests				
Effect	DF	Wald Chi-Square	Pr > ChiSq	
CURSMOKE	1	1.3708	0.2417	
LDLchol	1	1.2606	0.2615	
AGE	1	2.1971	0.1383	
LDLchol*CURSMOKE	1	0.2731	0.6013	
AGE*CURSMOKE	1	1.1871	0.2759	
LDLchol*AGE	1	1.6460	0.1995	
LDLchol*AGE*CURSMOKE	1	0.1934	0.6601	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-4.3456	1.5007	8.3855	0.0038
CURSMOKE	1	-3.4059	2.9089	1.3708	0.2417
LDLchol	1	-0.5665	0.5046	1.2606	0.2615
AGE	1	0.0341	0.0230	2.1971	0.1383
LDLchol*CURSMOKE	1	0.5011	0.9589	0.2731	0.6013
AGE*CURSMOKE	1	0.0499	0.0458	1.1871	0.2759
LDLchol*AGE	1	0.00988	0.00770	1.6460	0.1995
LDLchol*AGE*CURSMOKE	1	-0.00664	0.0151	0.1934	0.6601

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.4	Somers' D	0.353
Percent Discordant	32.1	Gamma	0.355
Percent Tied	0.5	Tau-a	0.069

Association of Predicted Probabilities and Observed Responses			
Pairs	889680	c	0.676

Framingham Heart Study

Model 11: All Two Way Interactions Model (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CL)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1990.010
SC	2093.139		2032.115
-2 Log L	2085.124		1976.010

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	109.1139	6	<.0001	
Score	109.3474	6	<.0001	
Wald	101.4409	6	<.0001	

Joint Tests				
Effect	DF	Wald		Pr > ChiSq
		Chi-Square	Pr > ChiSq	
CURSMOKE	1	3.9603	0.0466	
LDLchol	1	1.0825	0.2981	
AGE	1	3.6491	0.0561	
LDLchol*CURSMOKE	1	0.4740	0.4911	
AGE*CURSMOKE	1	3.4144	0.0646	
LDLchol*AGE	1	1.5085	0.2194	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard	Wald	Pr > ChiSq
			Error	Chi-Square	
Intercept	1	-4.6557	1.3330	12.1986	0.0005
CURSMOKE	1	-2.2288	1.1200	3.9603	0.0466
LDLchol	1	-0.4543	0.4366	1.0825	0.2981
AGE	1	0.0389	0.0204	3.6491	0.0561
LDLchol*CURSMOKE	1	0.0832	0.1209	0.4740	0.4911
AGE*CURSMOKE	1	0.0312	0.0169	3.4144	0.0646
LDLchol*AGE	1	0.00816	0.00664	1.5085	0.2194

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.4	Somers' D	0.353
Percent Discordant	32.1	Gamma	0.354
Percent Tied	0.5	Tau-a	0.069
Pairs	889680	c	0.676

Model 12: Conditional Independence of Smoking and LDL Cholesterol (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124	1988.488	
SC	2093.139	2024.578	
-2 Log L	2085.124	1976.488	

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	108.6360	5	<.0001	
Score	108.8956	5	<.0001	
Wald	101.1297	5	<.0001	

Joint Tests				
Effect	DF	Wald Chi-Square	Pr > ChiSq	
CURSMOKE	1	3.5096	0.0610	
LDLchol	1	0.8110	0.3678	
AGE	1	4.0376	0.0445	
AGE*CURSMOKE	1	3.4667	0.0626	
LDLchol*AGE	1	1.2742	0.2590	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-4.8486	1.3159	13.5776	0.0002
CURSMOKE	1	-2.0005	1.0678	3.5096	0.0610
LDLchol	1	-0.3826	0.4249	0.8110	0.3678
AGE	1	0.0408	0.0203	4.0376	0.0445
AGE*CURSMOKE	1	0.0314	0.0168	3.4667	0.0626
LDLchol*AGE	1	0.00741	0.00656	1.2742	0.2590

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.3	Somers' D	0.350
Percent Discordant	32.2	Gamma	0.352
Percent Tied	0.5	Tau-a	0.068
Pairs	889680	c	0.675

Model 13: Conditional Independence of Smoking and Age (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRМ	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1991.447
SC	2093.139		2027.537
-2 Log L	2085.124		1979.447

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	105.6768	5	<.0001
Score	108.0270	5	<.0001
Wald	101.0808	5	<.0001

Joint Tests			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	0.5970	0.4397
LDLchol	1	1.1792	0.2775
AGE	1	5.2641	0.0218
LDLchol*CURSMOKE	1	0.5275	0.4677
LDLchol*AGE	1	1.6188	0.2033

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-5.1309	1.3292	14.9000	0.0001
CURSMOKE	1	-0.2928	0.3789	0.5970	0.4397
LDLchol	1	-0.4812	0.4431	1.1792	0.2775
AGE	1	0.0463	0.0202	5.2641	0.0218
LDLchol*CURSMOKE	1	0.0887	0.1222	0.5275	0.4677
LDLchol*AGE	1	0.00853	0.00670	1.6188	0.2033

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.4	Somers' D	0.352
Percent Discordant	32.1	Gamma	0.354
Percent Tied	0.5	Tau-a	0.068
Pairs	889680	c	0.676

Framingham Heart Study

Model 14: Conditional Independence of LDL Cholesterol and Age (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRМ	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	

Model Information	
Optimization Technique	Fisher's scoring

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	2087.124	1989.515
SC	2093.139	2025.605
-2 Log L	2085.124	1977.515

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	107.6096	5	<.0001	
Score	106.2453	5	<.0001	
Wald	98.9057	5	<.0001	

Joint Tests				
Effect	DF	Wald		Pr > ChiSq
		Chi-Square	Pr > ChiSq	
CURSMOKE	1	3.7205	0.0537	
LDLchol	1	1.5420	0.2143	
AGE	1	50.9289	<.0001	
LDLchol*CURSMOKE	1	0.2435	0.6217	
AGE*CURSMOKE	1	3.5203	0.0606	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard	Wald	Pr > ChiSq
			Error	Chi-Square	
Intercept	1	-6.1394	0.5981	105.3521	<.0001
CURSMOKE	1	-2.1876	1.1341	3.7205	0.0537
LDLchol	1	0.0778	0.0627	1.5420	0.2143
AGE	1	0.0617	0.00864	50.9289	<.0001
LDLchol*CURSMOKE	1	0.0590	0.1195	0.2435	0.6217
AGE*CURSMOKE	1	0.0316	0.0168	3.5203	0.0606

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.1	Somers' D	0.347
Percent Discordant	32.4	Gamma	0.349
Percent Tied	0.5	Tau-a	0.067
Pairs	889680	c	0.674

Framingham Heart Study

Model 15: Joint Independence of (Smoking and LDL Cholesterol) from Age (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRM	
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
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Number of Observations Used	3026
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Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	2087.124	1991.061
SC	2093.139	2021.136
-2 Log L	2085.124	1981.061

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	104.0632	4	<.0001
Score	104.8560	4	<.0001
Wald	98.4465	4	<.0001

Joint Tests			
Effect	DF	Wald	
		Chi-Square	Pr > ChiSq
CURSMOKE	1	0.2606	0.6097
LDLchol	1	1.5553	0.2124
AGE	1	88.1012	<.0001
LDLchol*CURSMOKE	1	0.1860	0.6663

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard	Wald	Pr > ChiSq
			Error	Chi-Square	
Intercept	1	-6.7006	0.5306	159.4664	<.0001
CURSMOKE	1	-0.1897	0.3715	0.2606	0.6097
LDLchol	1	0.0784	0.0629	1.5553	0.2124
AGE	1	0.0702	0.00748	88.1012	<.0001
LDLchol*CURSMOKE	1	0.0512	0.1187	0.1860	0.6663

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
AGE	1.073	1.057	1.089

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.0	Somers' D	0.346
Percent Discordant	32.5	Gamma	0.348
Percent Tied	0.5	Tau-a	0.067
Pairs	889680	c	0.673

Framingham Heart Study

Model 16: Joint Independence of (Smoking and Age) from LDL Cholesterol (LDL Continuous)

The LOGISTIC Procedure

Model Information			
Data Set	WORK.FRML		
Response Variable	PREVCHD		Prevalent CHD (MI,AP,CI)
Number of Response Levels	2		
Model	binary logit		
Optimization Technique	Fisher's scoring		

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1987.760
SC	2093.139		2017.835
-2 Log L	2085.124		1977.760

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	107.3640	4	<.0001	
Score	106.1686	4	<.0001	
Wald	98.9271	4	<.0001	

Joint Tests				
Effect	DF	Wald Chi-Square	Pr > ChiSq	
CURSMOKE	1	3.5199	0.0606	
LDLchol	1	3.1206	0.0773	
AGE	1	50.8906	<.0001	
AGE*CURSMOKE	1	3.4639	0.0627	

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.

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-6.1885	0.5910	109.6554	<.0001
CURSMOKE	1	-1.9980	1.0649	3.5199	0.0606
LDLchol	1	0.0943	0.0534	3.1206	0.0773
AGE	1	0.0617	0.00865	50.8906	<.0001
AGE*CURSMOKE	1	0.0313	0.0168	3.4639	0.0627

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
LDLchol	1.099	0.990	1.220

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.1	Somers' D	0.347
Percent Discordant	32.4	Gamma	0.348
Percent Tied	0.5	Tau-a	0.067
Pairs	889680	c	0.673

Framingham Heart Study

Model 17: Joint Independence of (LDL Cholesterol and Age) from Smoking (LDL Continuous)

The LOGISTIC Procedure

Model Information			
Data Set	WORK.FRML		
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)	
Number of Response Levels	2		
Model	binary logit		
Optimization Technique	Fisher's scoring		

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1989.979
SC	2093.139		2020.054
-2 Log L	2085.124		1979.979

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	105.1454	4	<.0001	
Score	107.5840	4	<.0001	
Wald	100.6934	4	<.0001	

Type 3 Analysis of Effects				
Effect	DF	Wald Chi-Square	Pr > ChiSq	
CURSMOKE	1	0.0755	0.7835	
LDLchol	1	0.8111	0.3678	
AGE	1	6.3018	0.0121	
LDLchol*AGE	1	1.2713	0.2595	

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-5.4120	1.2779	17.9370	<.0001
CURSMOKE	1	-0.0376	0.1367	0.0755	0.7835
LDLchol	1	-0.3800	0.4219	0.8111	0.3678
AGE	1	0.0495	0.0197	6.3018	0.0121
LDLchol*AGE	1	0.00735	0.00652	1.2713	0.2595

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.963	0.737	1.259

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	67.2	Somers' D	0.350
Percent Discordant	32.3	Gamma	0.352
Percent Tied	0.5	Tau-a	0.068
Pairs	889680	c	0.675

Framingham Heart Study

Model 18: Mutual Independence of Smoking, LDL Cholesterol, and Age (LDL Continuous)

The LOGISTIC Procedure

Model Information			
Data Set	WORK.FRML		
Response Variable	PREVCHD	Prevalent CHD (MI,AP,CI)	
Number of Response Levels	2		
Model	binary logit		
Optimization Technique	Fisher's scoring		

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status		
Convergence criterion (GCONV=1E-8) satisfied.		

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1989.248
SC	2093.139		2013.308
-2 Log L	2085.124		1981.248

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	103.8761	3	<.0001	
Score	104.7856	3	<.0001	
Wald	98.4320	3	<.0001	

Type 3 Analysis of Effects				
Effect	DF	Wald		Pr > ChiSq
		Chi-Square	Pr > ChiSq	
CURSMOKE	1	0.0911	0.7628	
LDLchol	1	3.0375	0.0814	
AGE	1	88.0033	<.0001	

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-6.7405	0.5231	166.0138	<.0001
CURSMOKE	1	-0.0412	0.1366	0.0911	0.7628
LDLchol	1	0.0930	0.0533	3.0375	0.0814
AGE	1	0.0702	0.00748	88.0033	<.0001

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
		Lower	Upper
CURSMOKE 1 vs 0	0.960	0.734	1.254
LDLchol	1.097	0.988	1.218
AGE	1.073	1.057	1.089

Association of Predicted Probabilities and Observed Responses				
Percent Concordant	67.0	Somers' D	0.345	
Percent Discordant	32.5	Gamma	0.347	
Percent Tied	0.5	Tau-a	0.067	
Pairs	889680	c	0.673	

Framingham Heart Study

Compute p-values using -2 log likelihoods (Models Including Age)

Obs	Model	LL	df	pvalue
1	1	1969.51	0	.
2	2	1972.34	4	0.58787
3	3	1974.26	8	0.78455
4	4	1975.91	5	0.26931
5	5	1974.81	8	0.72497
6	6	1978.43	9	0.44506
7	7	1976.92	12	0.82980
8	8	1977.60	9	0.52540
9	9	1980.32	13	0.62673
10	10	1975.82	12	0.89993
11	11	1976.01	13	0.92614
12	12	1976.49	14	0.93563
13	13	1979.45	14	0.76692
14	14	1977.52	14	0.88917
15	15	1981.06	15	0.71280
16	16	1977.76	15	0.91346
17	17	1979.98	15	0.78938
18	18	1981.25	16	0.76194

Framingham Heart Study

Final Model (Including Age): Mutual Independence of Smoking, LDL Cholesterol, and Age (LDL Continuous)

The LOGISTIC Procedure

Model Information		
Data Set	WORK.FRML	
Response Variable	PREVCHD	Prevalent CHD (MI/AP,CI)
Number of Response Levels	2	
Model	binary logit	
Optimization Technique	Fisher's scoring	

Number of Observations Read	3263
Number of Observations Used	3026

Response Profile		
Ordered Value	PREVCHD	Total Frequency
1	0	2696
2	1	330

Probability modeled is PREVCHD=1.

Note: 237 observations were deleted due to missing values for the response or explanatory variables.

Class Level Information		
Class	Value	Design Variables
CURSMOKE	0	0
	1	1

Model Convergence Status			
Convergence criterion (GCONV=1E-8) satisfied.			

Model Fit Statistics			
Criterion	Intercept Only	Intercept and Covariates	
AIC	2087.124		1989.248
SC	2093.139		2013.308
-2 Log L	2085.124		1981.248

Testing Global Null Hypothesis: BETA=0				
Test	Chi-Square	DF	Pr > ChiSq	
Likelihood Ratio	103.8761	3	<.0001	
Score	104.7856	3	<.0001	
Wald	98.4320	3	<.0001	

Type 3 Analysis of Effects			
Effect	DF	Wald Chi-Square	Pr > ChiSq
CURSMOKE	1	0.0911	0.7628
LDLchol	1	3.0375	0.0814
AGE	1	88.0033	<.0001

Analysis of Maximum Likelihood Estimates					
Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-6.7405	0.5231	166.0138	<.0001
CURSMOKE	1	-0.0412	0.1366	0.0911	0.7628
LDLchol	1	0.0930	0.0533	3.0375	0.0814
AGE	1	0.0702	0.00748	88.0033	<.0001

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
CURSMOKE 1 vs 0	0.960	0.734	1.254
LDLchol	1.097	0.988	1.218
AGE	1.073	1.057	1.089

Association of Predicted Probabilities and Observed Responses				
Percent Concordant	67.0	Somers' D	0.345	
Percent Discordant	32.5	Gamma	0.347	
Percent Tied	0.5	Tau-a	0.067	
Pairs	889680	c	0.673	