

Variables in model	-2 log L
none	36.349
size	29.042
size, index	23.533
size, index, treatment	22.572

1) The data studies the time until death from prostate cancer from the date the patient was randomized to a treatment. The variable *treatment* was a 0 for a placebo and a 1 for DES (a drug). The variable *size* was tumor size, and *index* the Gleason index. Let the full model contain *size*, *index* and *treatment*. Use the table above.

a) If the reduced model uses *size* and *index*, test whether the reduced model is good.

b) If the reduced model uses *size*, test whether the reduced model is good.

	Without	With	Reduced Model
Criterion	Covariates	Covariates	
-2 LOG L	204.801	180.898	
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	23.9034	3	<0.0001

Parameter			Standard		
Variable	DF	Estimate	Error	Chi-Square	Pr > ChiSq
perf	1	-0.05831	0.01309	19.8512	<.0001
type	1	-0.03346	0.40642	0.0068	0.9344
trt	1	0.24725	0.35074	0.4969	0.4809

	Without	With	Full Model
Criterion	Covariates	Covariates	
-2 LOG L	204.801	177.740	
Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	27.0615	6	0.0001

Parameter			Standard		
Variable	DF	Estimate	Error	Chi-Square	Pr > ChiSq
perf	1	-0.11415	0.03909	8.5259	0.0035
type	1	-0.49892	1.09251	0.2086	0.6479
trt	1	-0.34667	0.97596	0.1262	0.7224
perflt	1	0.01633	0.01028	2.5208	0.1124
typelt	1	0.12005	0.28977	0.1716	0.6787
trtlt	1	0.17496	0.24548	0.5080	0.4760

2) The advanced lung cancer data is from Leemis (1995, p. 249). The PH model is the reduced model and has predictors *perf*, *type* and *trt*. The GCR model is the full model and adds *perflt*= *perf**log(time), *typelt* = *type**log(time) and *trtlt* = *trt**log(time) interactions to test whether the PH assumption is reasonable. Test whether the reduced model is good. (The test is the same as if the GCR model is the PH full model.)