

The GENMOD Procedure

Model Information

Data Set	WORK.E
Distribution	Poisson
Link Function	Log
Dependent Variable	matings

Number of Observations Read	41
Number of Observations Used	41

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	39	51.0116	1.3080
Scaled Deviance	39	51.0116	1.3080
Pearson Chi-Square	39	45.1360	1.1573
Scaled Pearson X2	39	45.1360	1.1573
Log Likelihood		10.7400	
Full Log Likelihood		-76.2289	
AIC (smaller is better)		156.4578	
AICC (smaller is better)		156.7736	
BIC (smaller is better)		159.8849	

see notes

Sum of squares of Pearson residuals

Expect this to be if Poisson distribution is appropriate

$$AIC = -2 \log L + 2(p+1)$$

Full log L
p = 1

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept	1	-1.5820	0.5446	-2.6494 -0.5146	8.44	0.0037
age	1	0.0687	0.0137	0.0418 0.0956	24.97	<.0001
Scale	0	1.0000	0.0000	1.0000 1.0000		

NOTE: The scale parameter was held fixed.

at 1

$$BIC = SC = -2 \log L + (p+1) \log N$$

Full log-L
p = 1
N = 41

Bayesian Information Criterion

AICC - correction for finite sample sizes - don't worry about it