The FREQ Procedure

sex	Frequency	Percent	Cumulative Frequency	Cumulative Percent
F	9	100.00	9	100.00

count
0.28125

probability
0.6

The GENMOD Procedure

Bayesian Analysis

Model Information	
Data Set	WORK.WEAPONS
Burn-In Size	2000
MC Sample Size	10000
Thinning	1
Sampling Algorithm	Conjugate
Distribution	Normal
Link Function	Identity
Dependent Variable	an

Number of Observations Read	32
Number of Observations Used	32

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**	
Intercept	1	30.3081	7.5590	15.4928	45.1234
aw	1	-0.3033	0.2284	-0.7509	0.1443
cxen	1	-0.0441	0.2261	-0.4872	0.3991
aw*cxen	1	0.0149	0.0046	0.0059	0.0238
Scale	1	1.2176	0.1522	0.9531	1.5557

Note: The scale parameter was estimated by maximum likelihood.

The GENMOD Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients	
Parameter	**Prior**
Intercept	Constant
aw	Constant
cxen	Constant
awcxen	Constant

Algorithm converged.

Independent Prior Distributions for Model Parameters	
Parameter	**Prior Distribution**
Dispersion	Improper

Initial Values of the Chain						
Chain	**Seed**	**Intercept**	**aw**	**cxen**	**awcxen**	**Dispersion**
1	885251596	30.30807	-0.30328	-0.04405	0.014852	1.395372

Fit Statistics	
DIC (smaller is better)	114.283
pD (effective number of parameters)	5.108

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries						
				Percentiles		
Parameter	N	Mean	Standard Deviation	25%	50%	75%
Intercept	10000	30.2878	8.4458	24.7123	30.3731	35.9524
aw	10000	-0.3025	0.2555	-0.4749	-0.3051	-0.1340
cxen	10000	-0.0447	0.2533	-0.2099	-0.0469	0.1232
awcxen	10000	0.0149	0.00513	0.0115	0.0149	0.0183
Dispersion	10000	1.8268	0.5191	1.4680	1.7418	2.0943

Posterior Intervals					
		Equal-Tail Interval		HPD Interval	
Parameter	Alpha				
Intercept	0.050	13.2292	46.3755	14.1889	47.2866
aw	0.050	-0.7974	0.2081	-0.7965	0.2083
cxen	0.050	-0.5474	0.4577	-0.5603	0.4416
awcxen	0.050	0.00455	0.0247	0.00434	0.0244
Dispersion	0.050	1.0582	3.0544	0.9295	2.8177

Posterior Correlation Matrix					
Parameter	Intercept	aw	cxen	awcxen	Dispersion
Intercept	1.000	-0.842	-0.786	0.973	-0.001
aw	-0.842	1.000	0.345	-0.788	-0.001
cxen	-0.786	0.345	1.000	-0.842	0.002
awcxen	0.973	-0.788	-0.842	1.000	-0.001
Dispersion	-0.001	-0.001	0.002	-0.001	1.000

The GENMOD Procedure

Bayesian Analysis

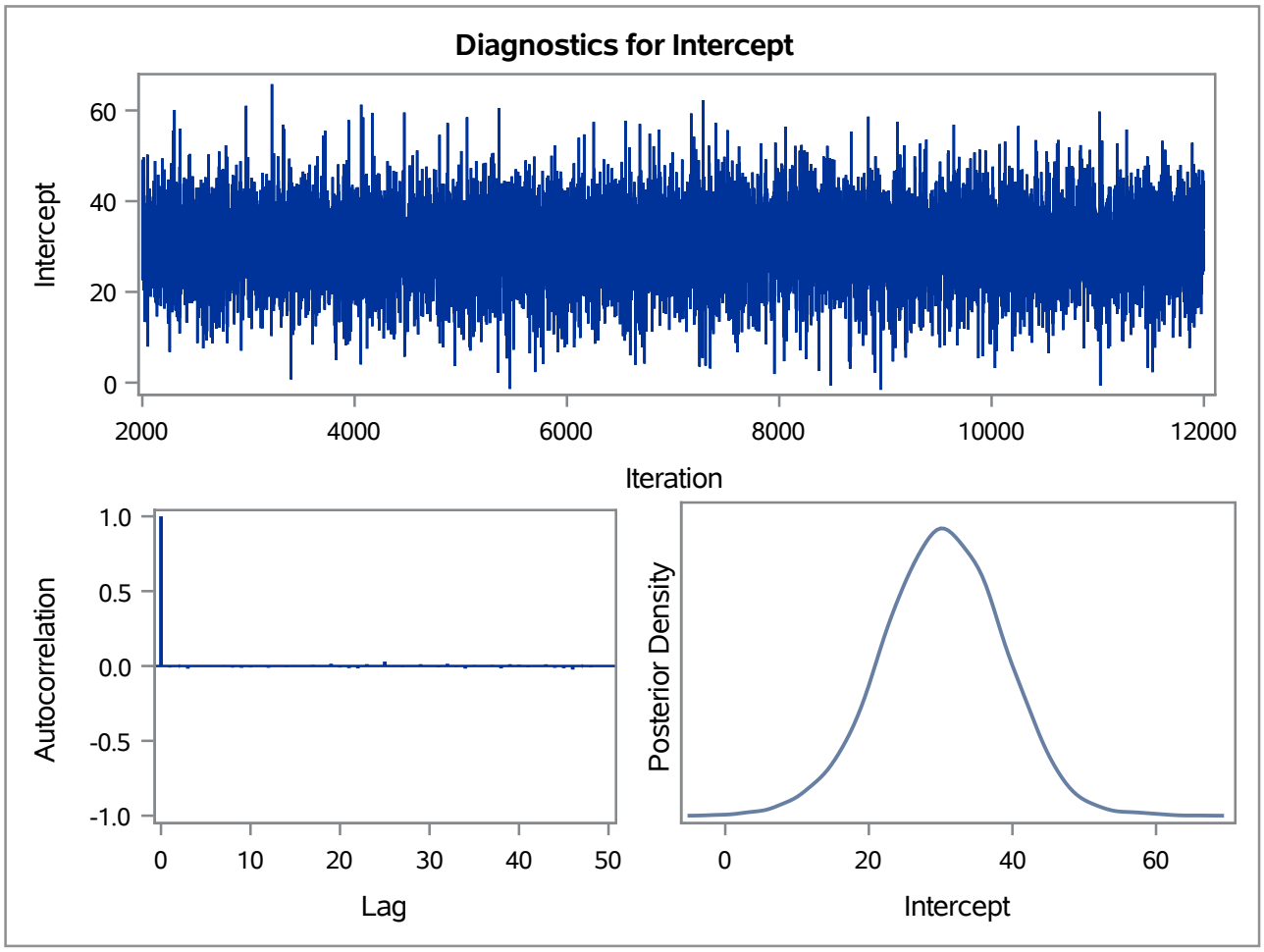
Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	-0.0104	-0.0029	-0.0101	-0.0011
aw	-0.0018	-0.0024	-0.0020	0.0229
cxen	-0.0039	-0.0086	-0.0009	-0.0140
awcxen	-0.0090	-0.0114	-0.0070	-0.0033
Dispersion	-0.0226	0.0009	0.0020	0.0091

Geweke Diagnostics		
Parameter	z	Pr > |z|
Intercept	0.1479	0.8824
aw	0.3875	0.6984
cxen	-0.5315	0.5951
awcxen	0.0303	0.9758
Dispersion	-0.8468	0.3971

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	10213.1	0.9791	1.0213
aw	10000.0	1.0000	1.0000
cxen	10000.0	1.0000	1.0000
awcxen	10000.0	1.0000	1.0000
Dispersion	10474.4	0.9547	1.0474

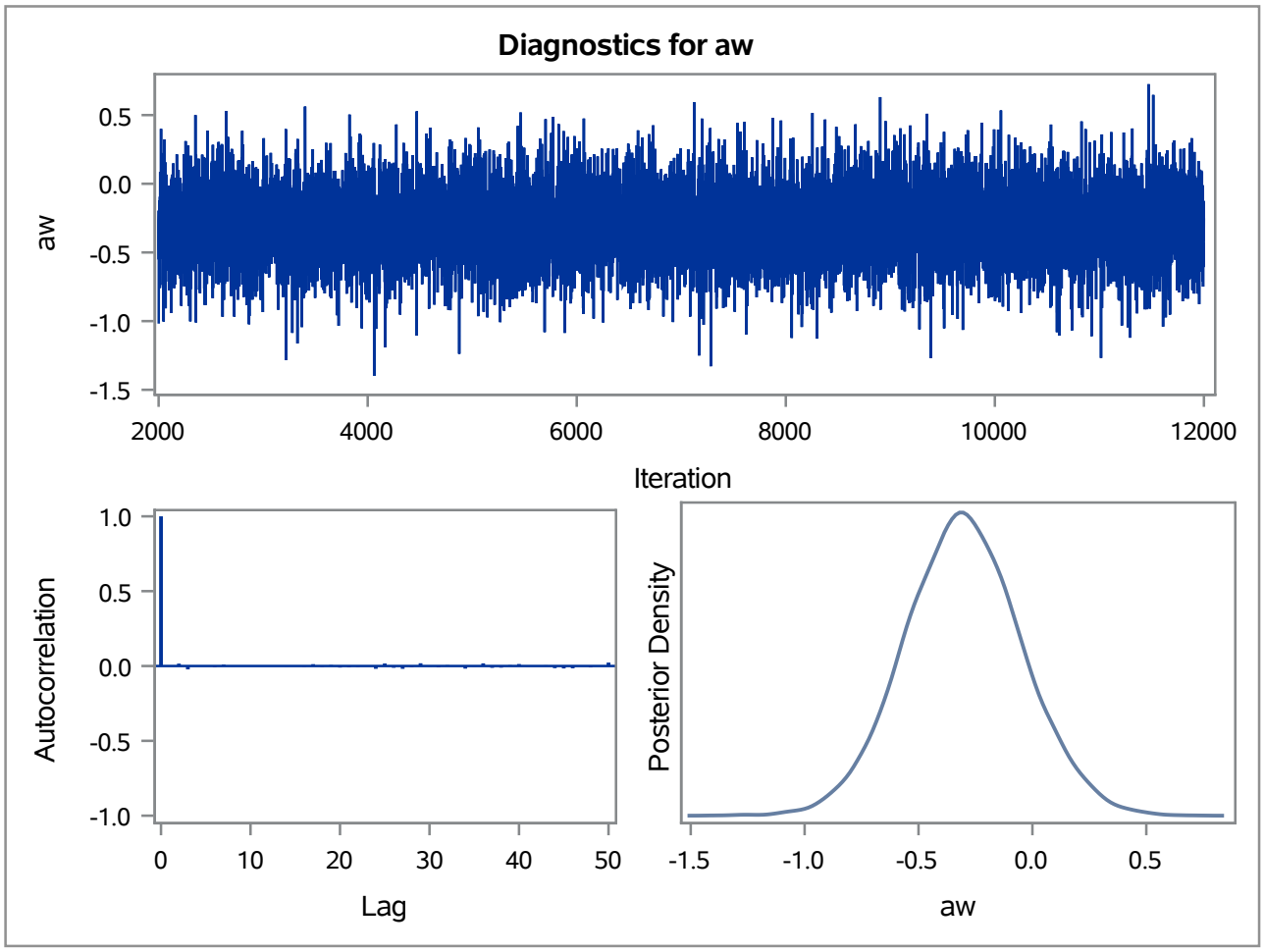
The GENMOD Procedure

Bayesian Analysis



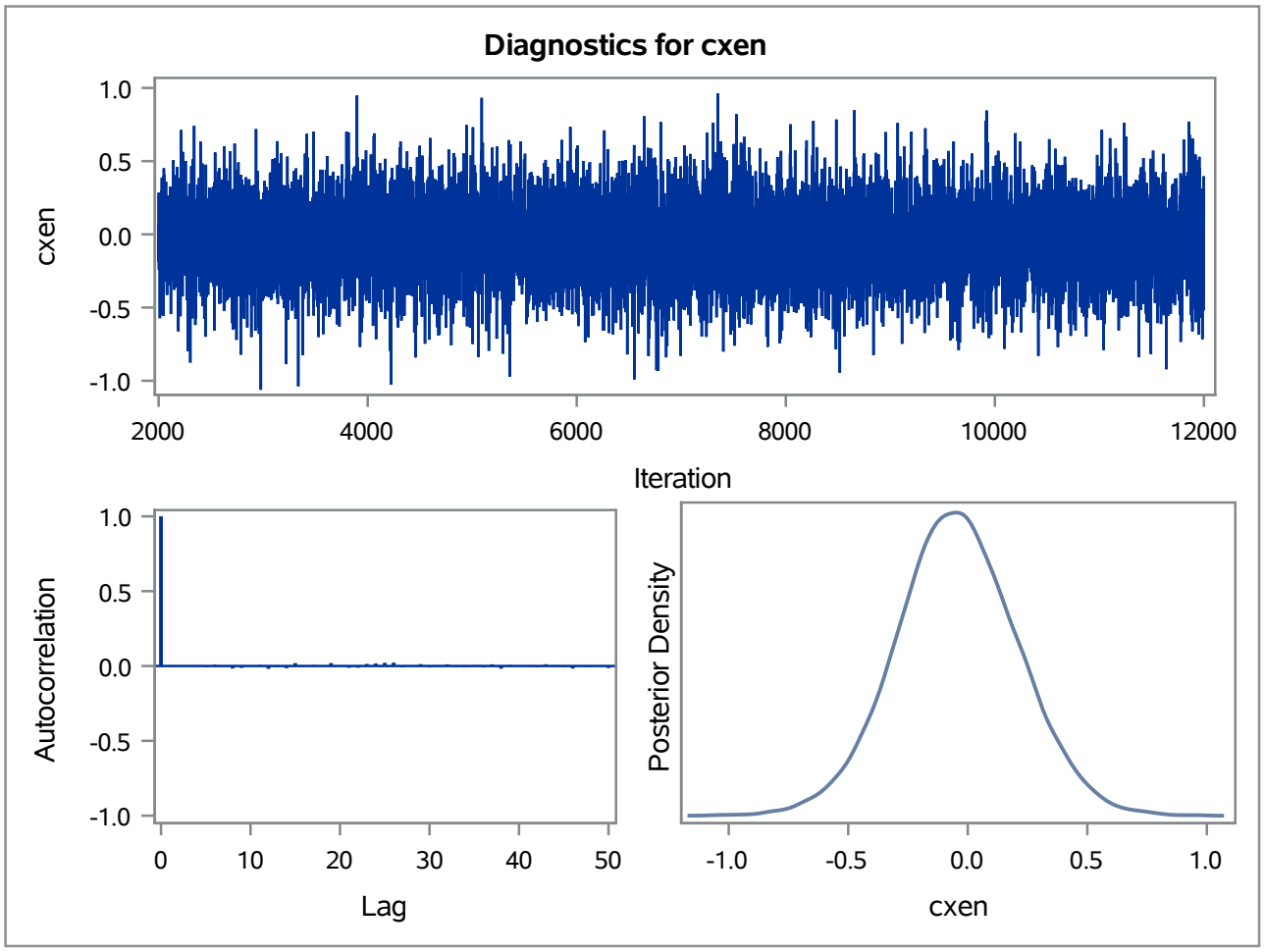
The GENMOD Procedure

Bayesian Analysis



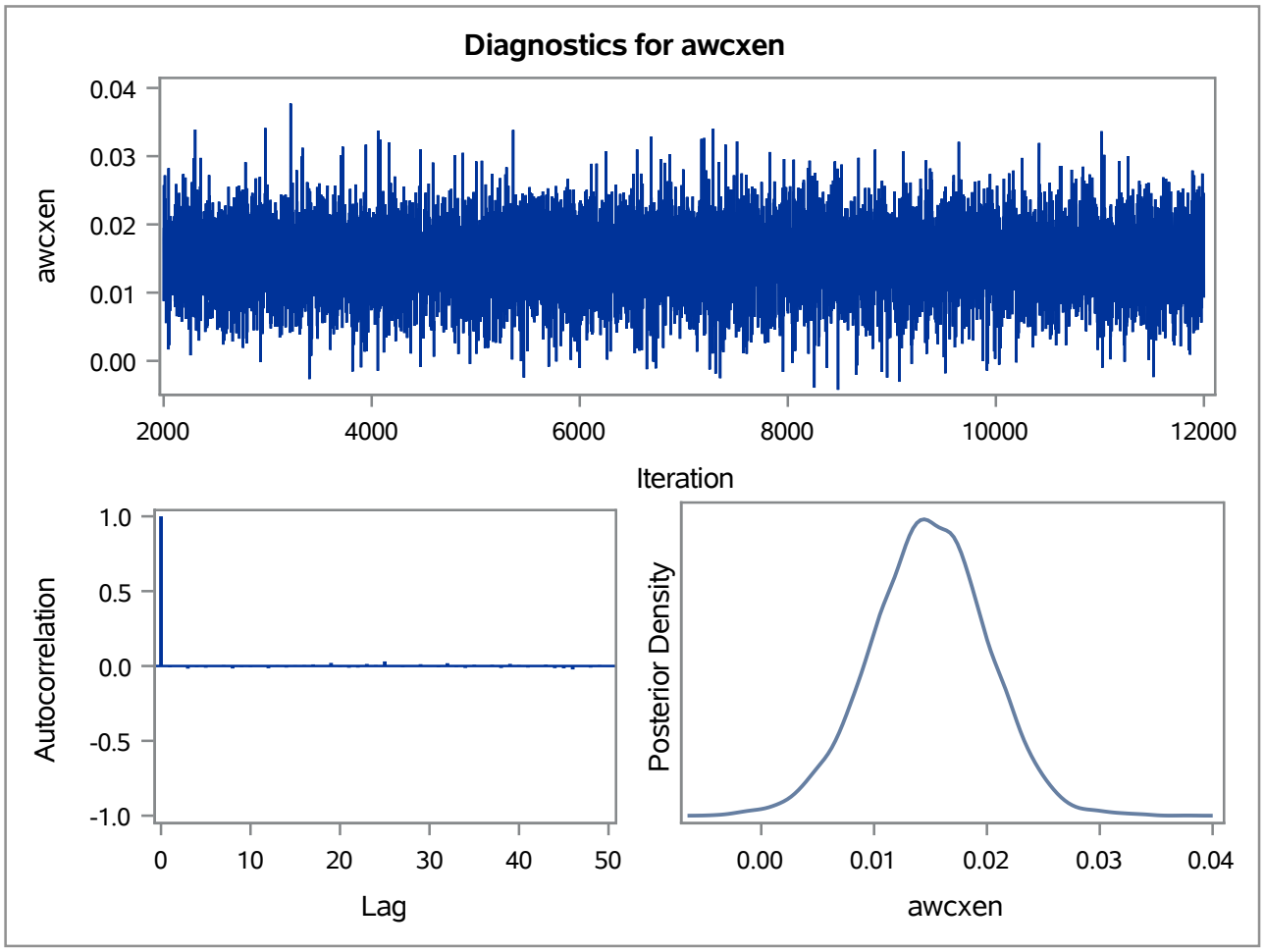
The GENMOD Procedure

Bayesian Analysis



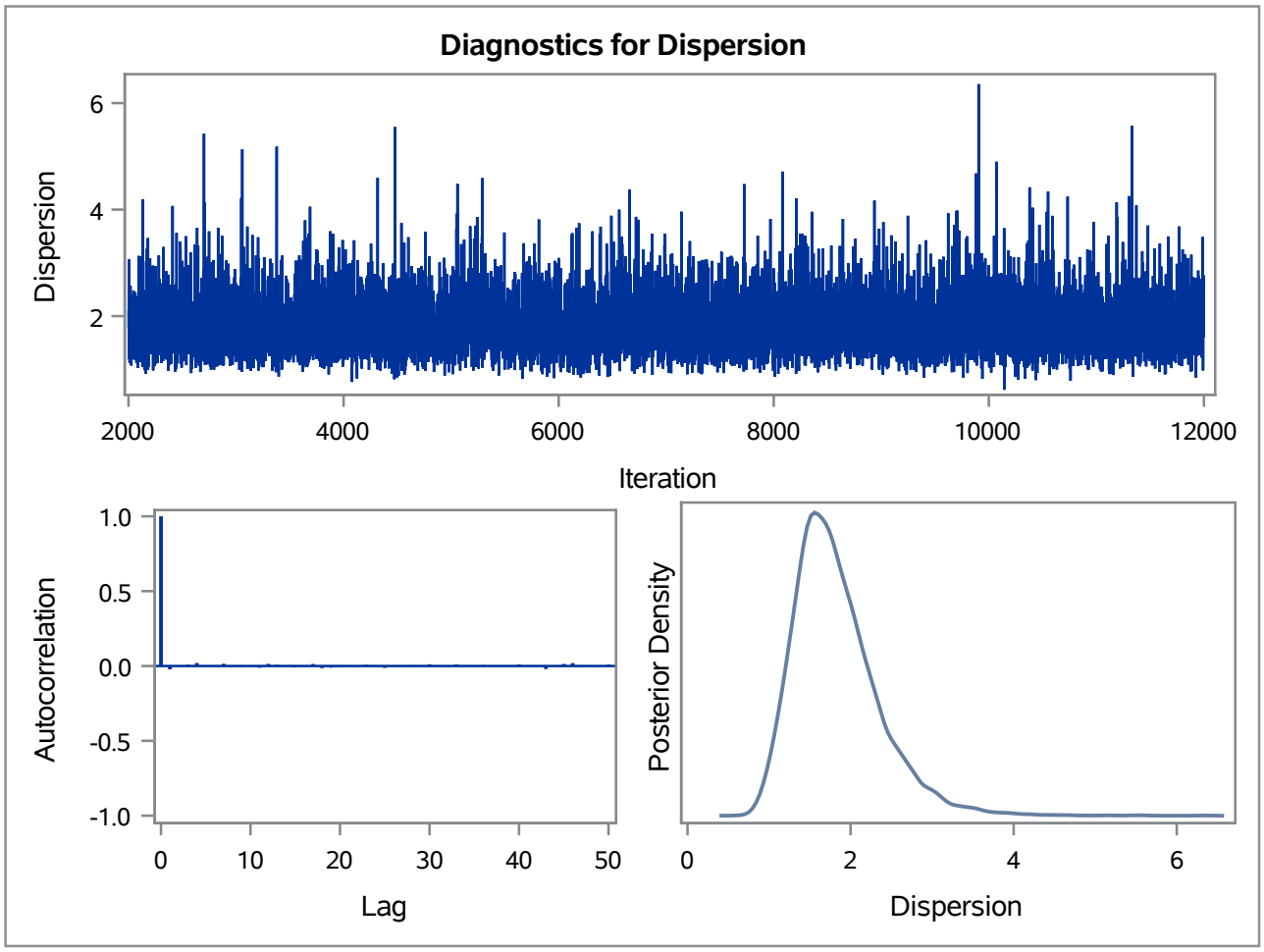
The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis

Model Information	
Data Set	WORK.WEAPONS
Burn-In Size	2000
MC Sample Size	10000
Thinning	1
Sampling Algorithm	Conjugate
Distribution	Normal
Link Function	Identity
Dependent Variable	an

Number of Observations Read	32
Number of Observations Used	32

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**	
Intercept	1	6.5158	2.0347	2.5278	10.5037
aw	1	0.2799	0.1617	-0.0370	0.5968
cxen	1	0.5726	0.1403	0.2976	0.8476
Scale	1	1.4029	0.1754	1.0981	1.7924

Note: The scale parameter was estimated by maximum likelihood.

The GENMOD Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients	
Parameter	**Prior**
Intercept	Constant
aw	Constant
cxen	Constant

Algorithm converged.

Independent Prior Distributions for Model Parameters	
Parameter	**Prior Distribution**
Dispersion	Improper

Initial Values of the Chain					
Chain	**Seed**	**Intercept**	**aw**	**cxen**	**Dispersion**
1	1129948679	6.515785	0.279929	0.572617	1.852319

Fit Statistics	
DIC (smaller is better)	121.078
pD (effective number of parameters)	4.094

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries						
				Percentiles		
Parameter	N	Mean	Standard Deviation	25%	50%	75%
Intercept	10000	6.5343	2.2354	5.0584	6.5294	8.0065
aw	10000	0.2816	0.1779	0.1653	0.2816	0.3981
cxen	10000	0.5706	0.1541	0.4708	0.5691	0.6707
Dispersion	10000	2.3207	0.6457	1.8579	2.2164	2.6622

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	2.1638	11.0269	2.2101	11.0402
aw	0.050	-0.0741	0.6368	-0.0802	0.6224
cxen	0.050	0.2676	0.8807	0.2652	0.8748
Dispersion	0.050	1.3864	3.8424	1.2741	3.6141

Posterior Correlation Matrix				
Parameter	Intercept	aw	cxen	Dispersion
Intercept	1.000	-0.533	0.263	0.008
aw	-0.533	1.000	-0.956	-0.018
cxen	0.263	-0.956	1.000	0.019
Dispersion	0.008	-0.018	0.019	1.000

The GENMOD Procedure

Bayesian Analysis

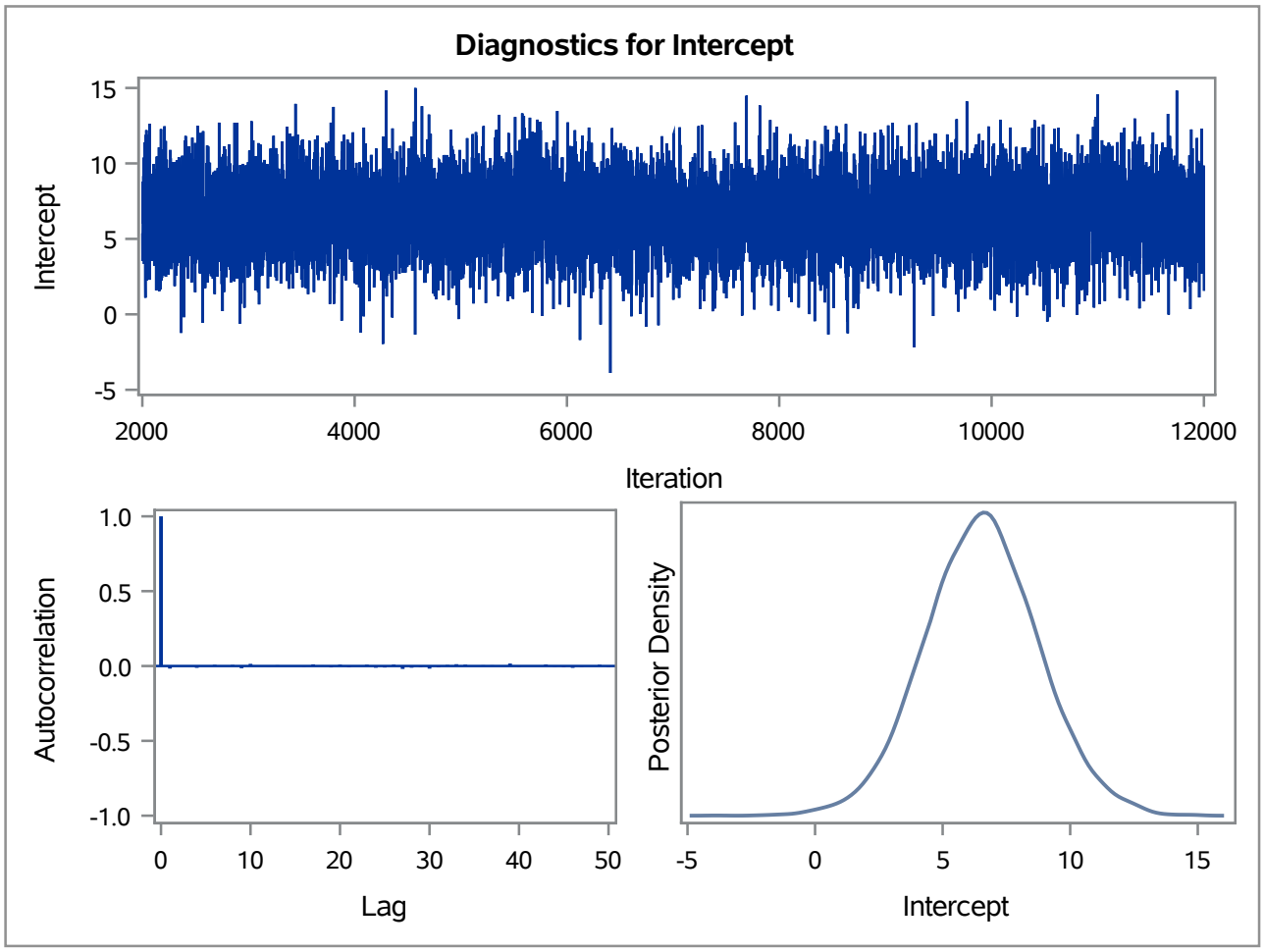
Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	-0.0174	-0.0007	0.0144	-0.0060
aw	-0.0135	-0.0009	0.0217	-0.0032
cxen	-0.0064	0.0005	0.0169	-0.0007
Dispersion	-0.0031	0.0217	-0.0079	-0.0055

Geweke Diagnostics		
Parameter	z	Pr > |z|
Intercept	-0.6472	0.5175
aw	1.1416	0.2536
cxen	-0.8805	0.3786
Dispersion	0.3972	0.6912

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	10360.5	0.9652	1.0361
aw	10276.8	0.9731	1.0277
cxen	10000.0	1.0000	1.0000
Dispersion	10000.0	1.0000	1.0000

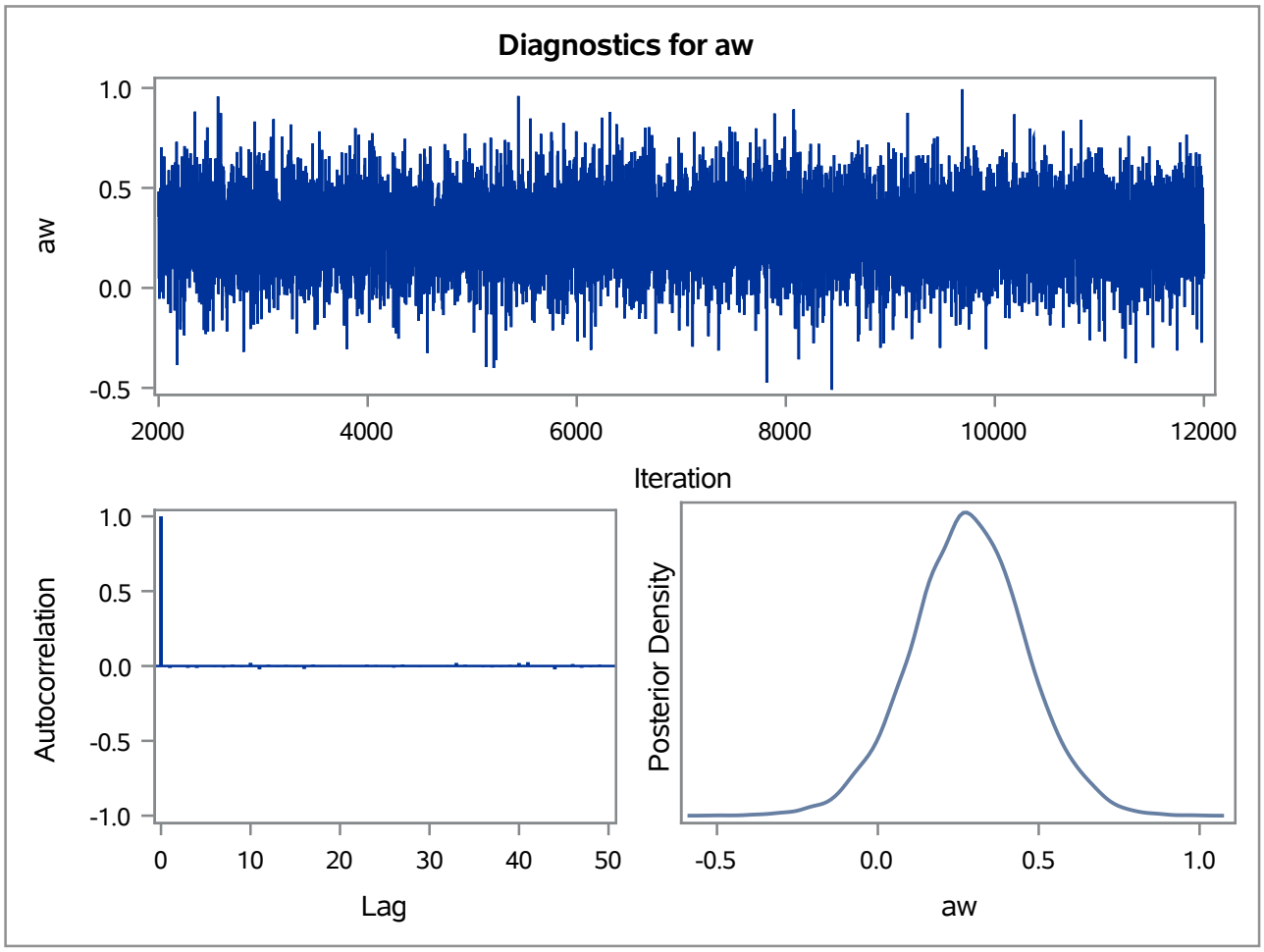
The GENMOD Procedure

Bayesian Analysis



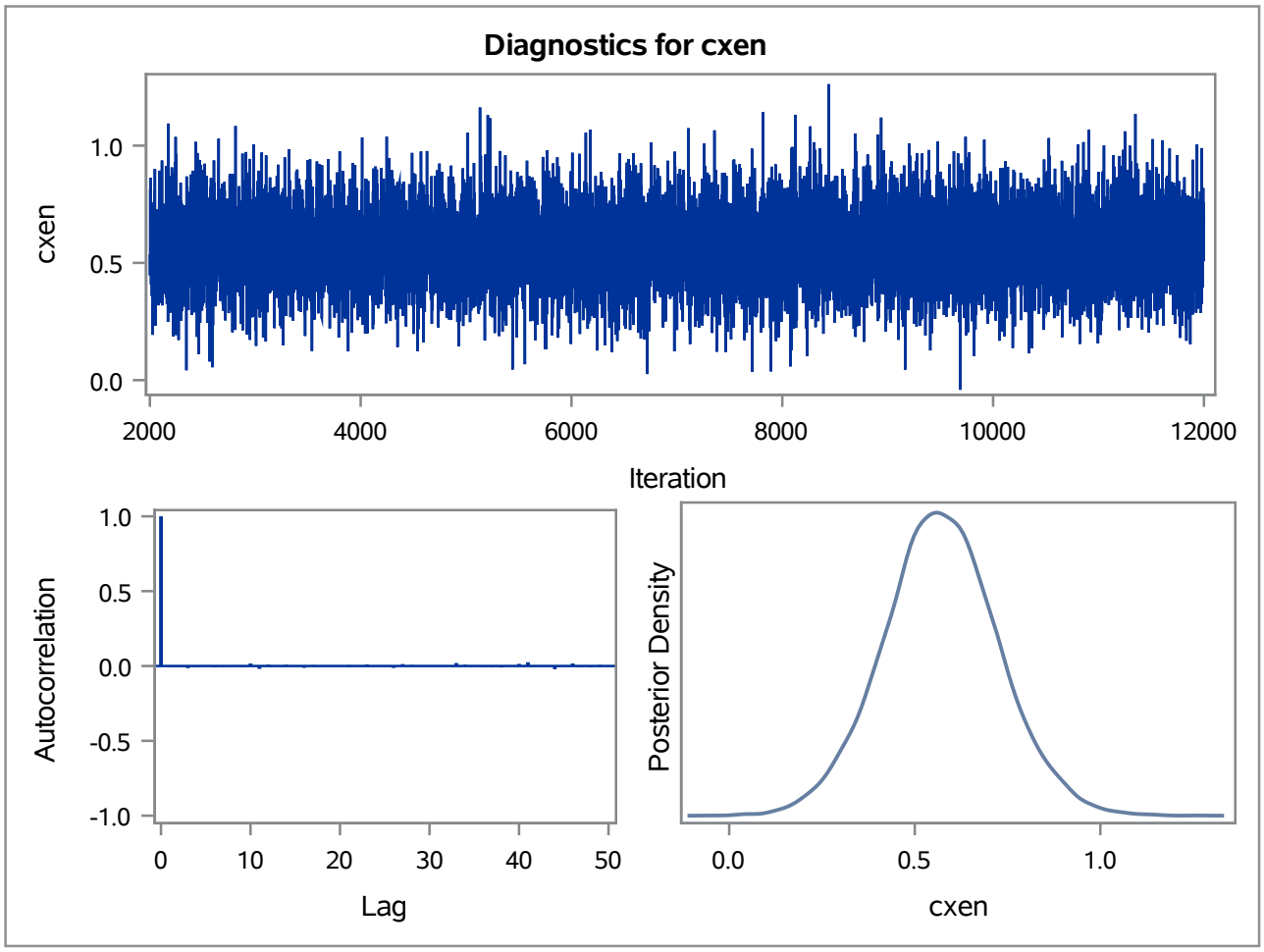
The GENMOD Procedure

Bayesian Analysis



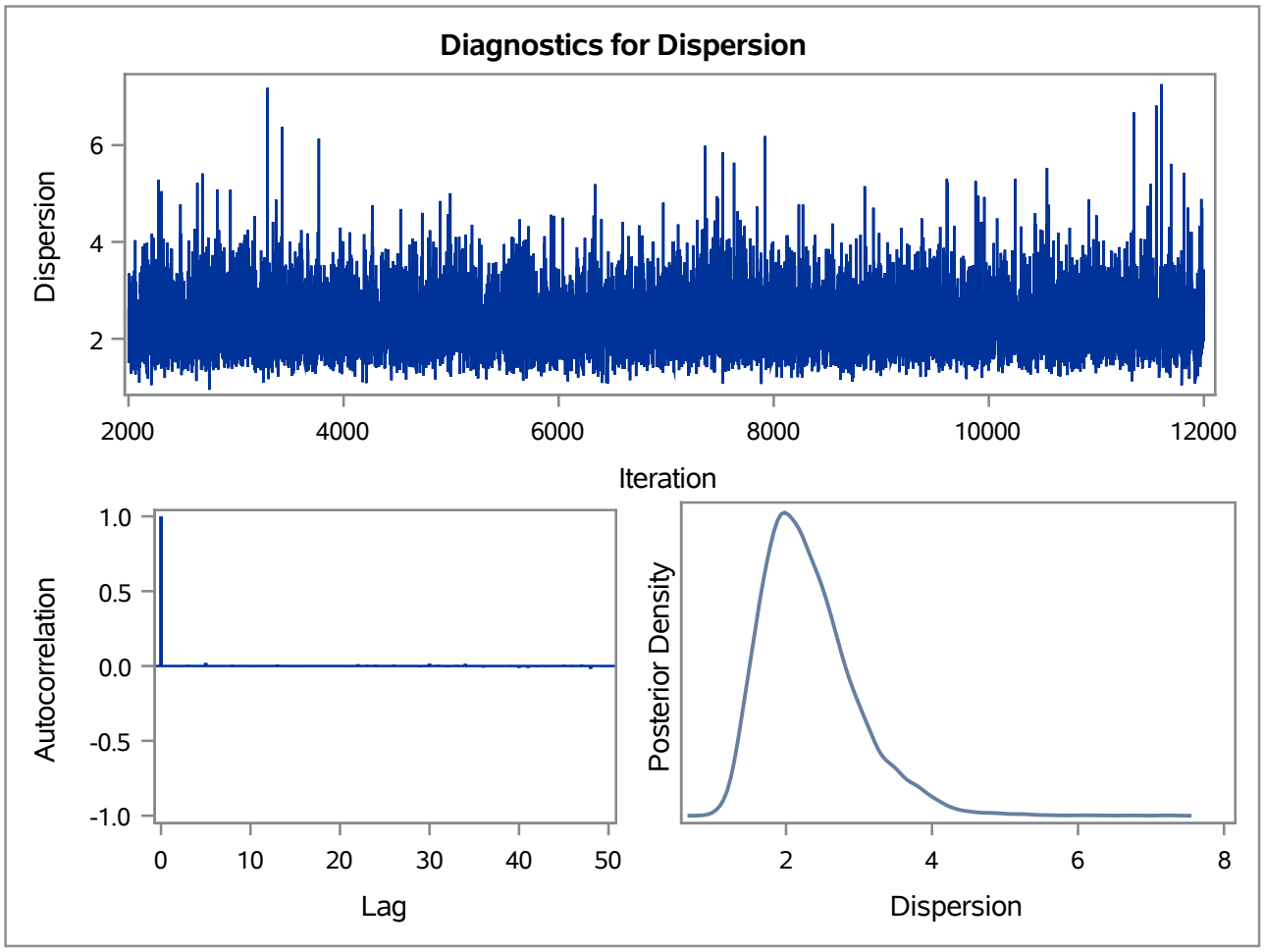
The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis

Model Information	
Data Set	WORK.WEAPONS2
Burn-In Size	2000
MC Sample Size	10000
Thinning	1
Sampling Algorithm	Conjugate
Distribution	Normal
Link Function	Identity
Dependent Variable	an

Number of Observations Read	16
Number of Observations Used	16

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**	
Intercept	1	6.8609	3.8517	-0.6883	14.4102
aw	1	0.4697	0.2624	-0.0447	0.9841
cxen	1	0.3762	0.2346	-0.0837	0.8360
Scale	1	1.6066	0.2840	1.1361	2.2718

Note: The scale parameter was estimated by maximum likelihood.

The GENMOD Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients	
Parameter	**Prior**
Intercept	Constant
aw	Constant
cxen	Constant

Algorithm converged.

Independent Prior Distributions for Model Parameters	
Parameter	**Prior Distribution**
Dispersion	Improper

Initial Values of the Chain					
Chain	**Seed**	**Intercept**	**aw**	**cxen**	**Dispersion**
1	208918630	6.860927	0.469724	0.376169	2.293173

Fit Statistics	
DIC (smaller is better)	69.941
pD (effective number of parameters)	4.198

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries						
				Percentiles		
Parameter	N	Mean	Standard Deviation	25%	50%	75%
Intercept	10000	6.9020	4.6510	3.9683	6.9120	9.8414
aw	10000	0.4736	0.3187	0.2720	0.4747	0.6754
cxen	10000	0.3713	0.2846	0.1901	0.3714	0.5566
Dispersion	10000	3.7337	1.7078	2.5712	3.3403	4.4502

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	-2.3034	16.1227	-2.0398	16.3113
aw	0.050	-0.1522	1.0988	-0.1523	1.0985
cxen	0.050	-0.1918	0.9287	-0.2032	0.9133
Dispersion	0.050	1.6607	8.0133	1.2979	7.0085

Posterior Correlation Matrix				
Parameter	Intercept	aw	cxen	Dispersion
Intercept	1.000	-0.425	0.068	0.016
aw	-0.425	1.000	-0.931	-0.017
cxen	0.068	-0.931	1.000	0.013
Dispersion	0.016	-0.017	0.013	1.000

The GENMOD Procedure

Bayesian Analysis

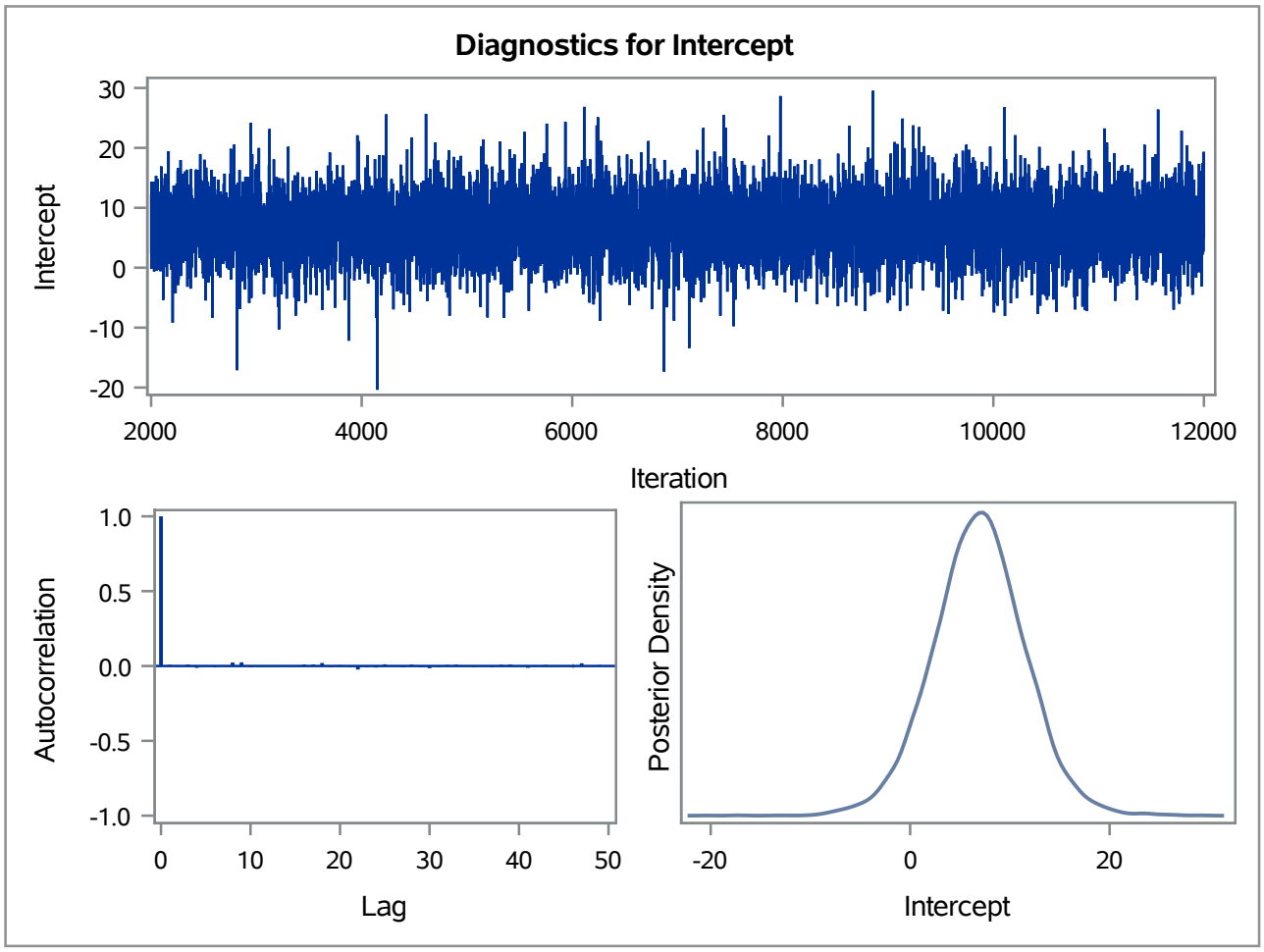
Posterior Autocorrelations				
Parameter	**Lag 1**	**Lag 5**	**Lag 10**	**Lag 50**
Intercept	0.0082	-0.0013	-0.0074	0.0011
aw	0.0002	0.0059	0.0078	0.0065
cxen	0.0033	0.0009	0.0111	0.0007
Dispersion	0.0022	0.0072	0.0057	-0.0012

Geweke Diagnostics		
Parameter	**z**	**Pr > |z|**
Intercept	-1.5125	0.1304
aw	-0.9461	0.3441
cxen	1.7137	0.0866
Dispersion	-1.7247	0.0846

Effective Sample Sizes			
Parameter	**ESS**	**Autocorrelation Time**	**Efficiency**
Intercept	10000.0	1.0000	1.0000
aw	10000.0	1.0000	1.0000
cxen	10000.0	1.0000	1.0000
Dispersion	10000.0	1.0000	1.0000

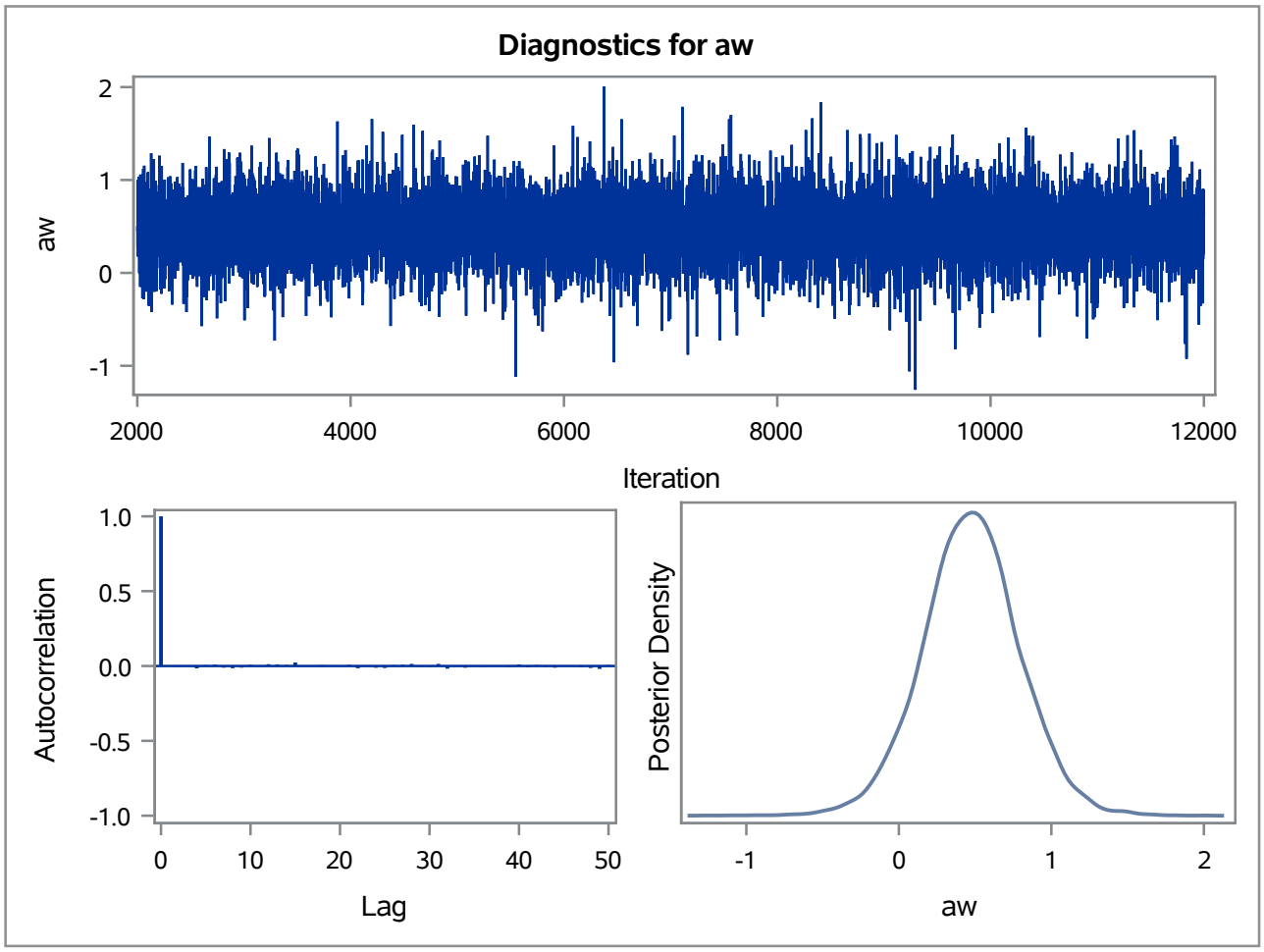
The GENMOD Procedure

Bayesian Analysis



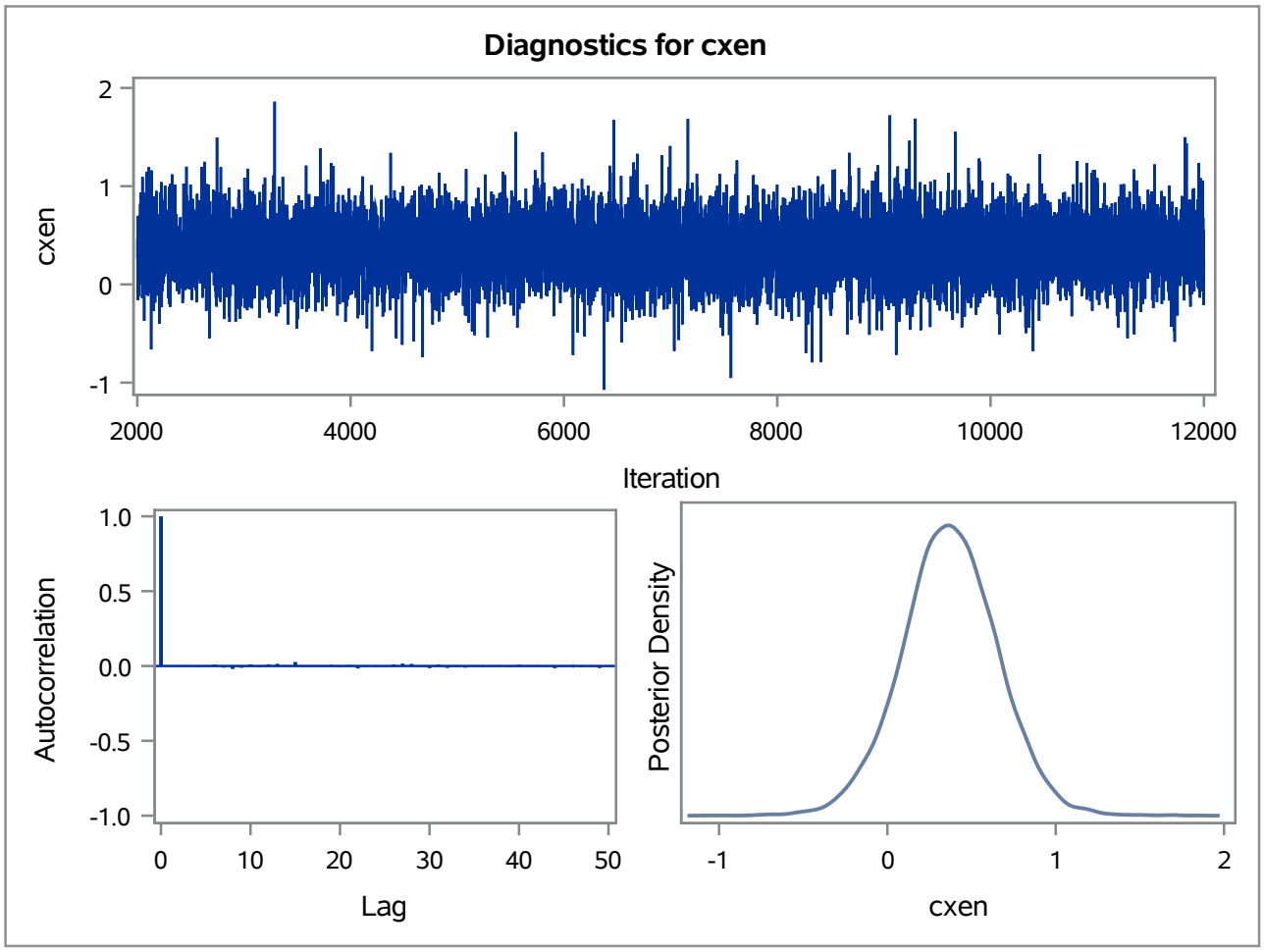
The GENMOD Procedure

Bayesian Analysis



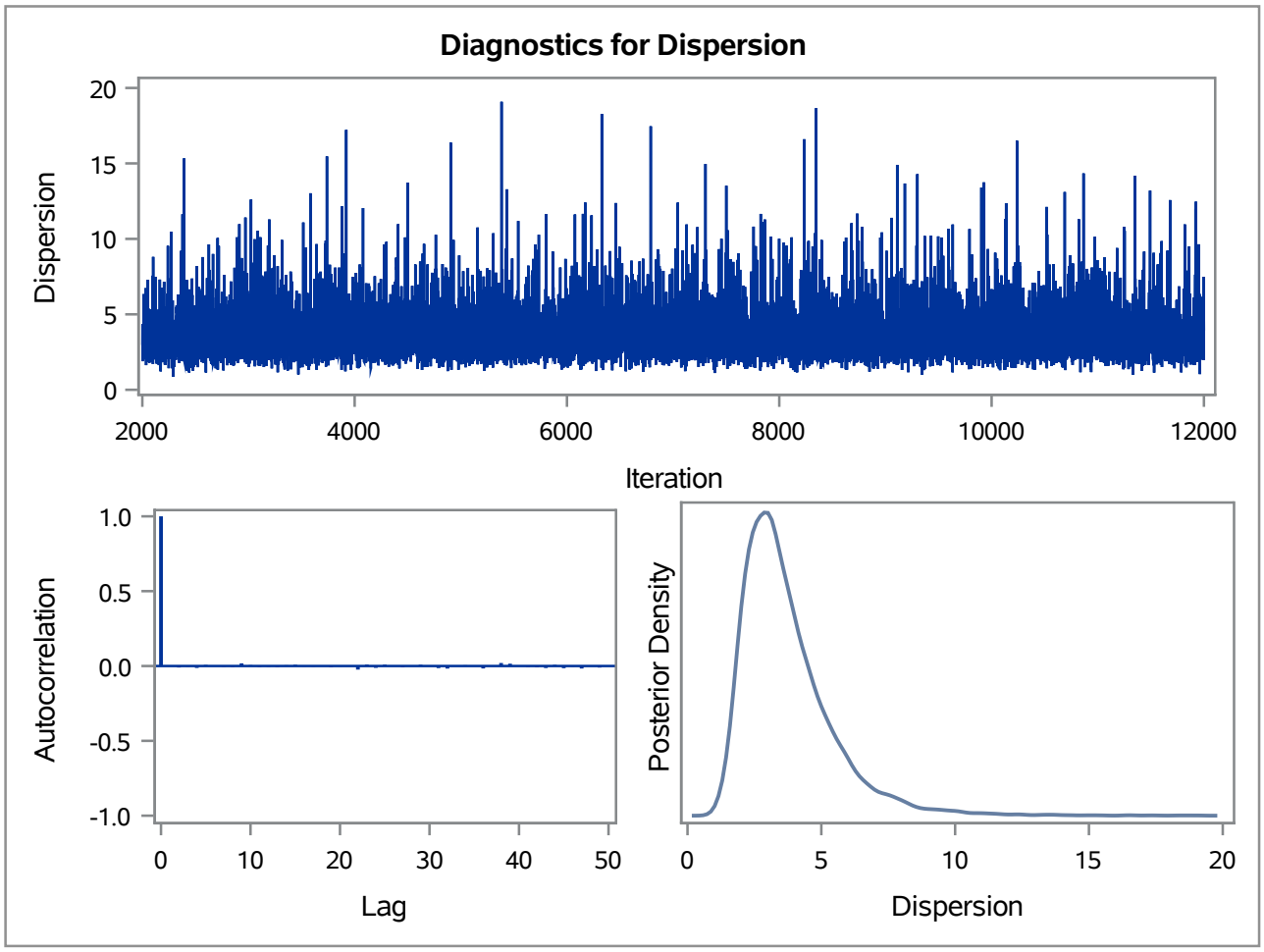
The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis



The REG Procedure
Model: MODEL1
Dependent Variable: an

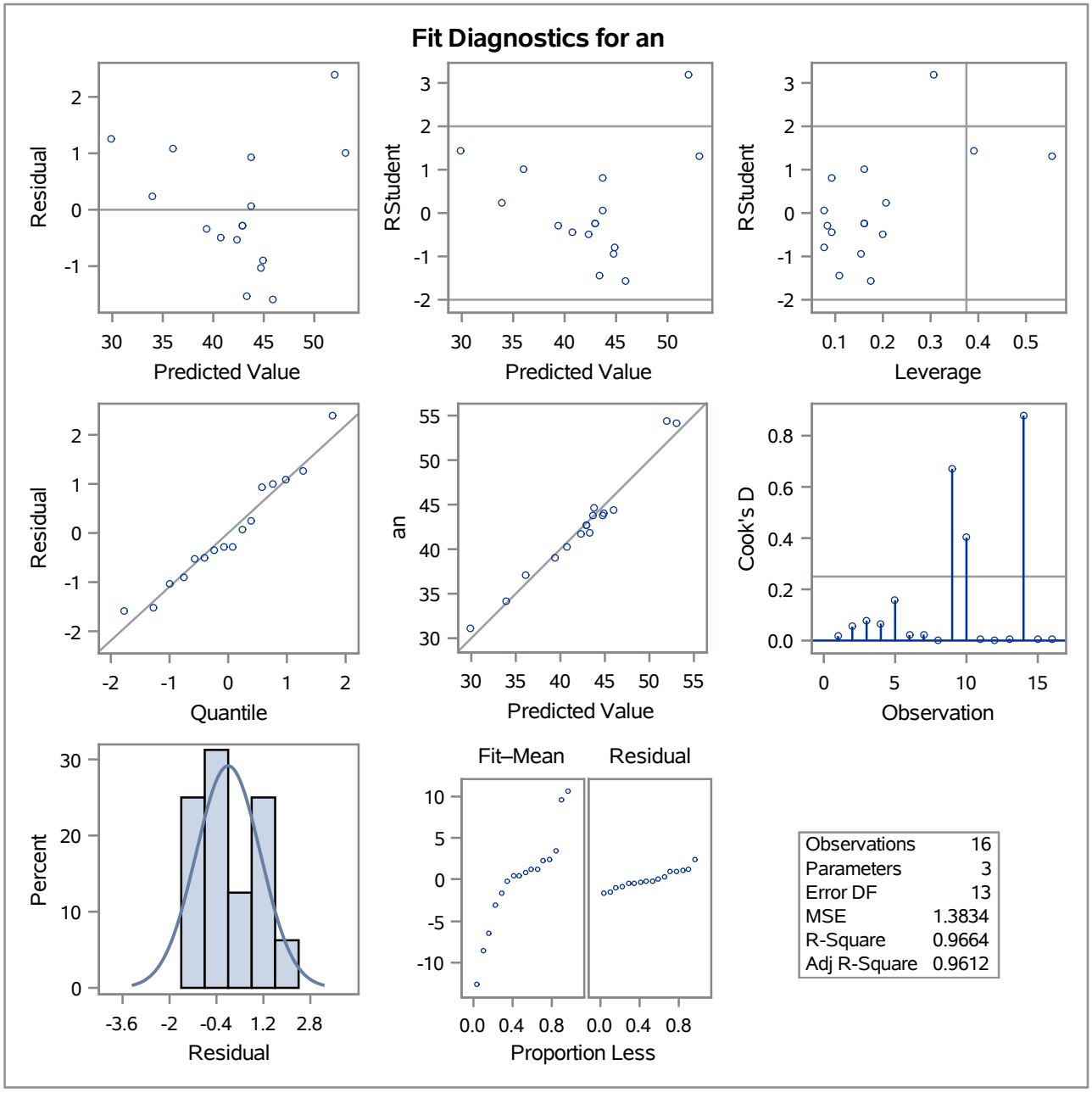
Number of Observations Read	16
Number of Observations Used	16

Analysis of Variance					
Source	**DF**	**Sum of Squares**	**Mean Square**	**F Value**	**Pr > F**
Model	2	516.92607	258.46303	186.84	<.0001
Error	13	17.98381	1.38337		
Corrected Total	15	534.90988			

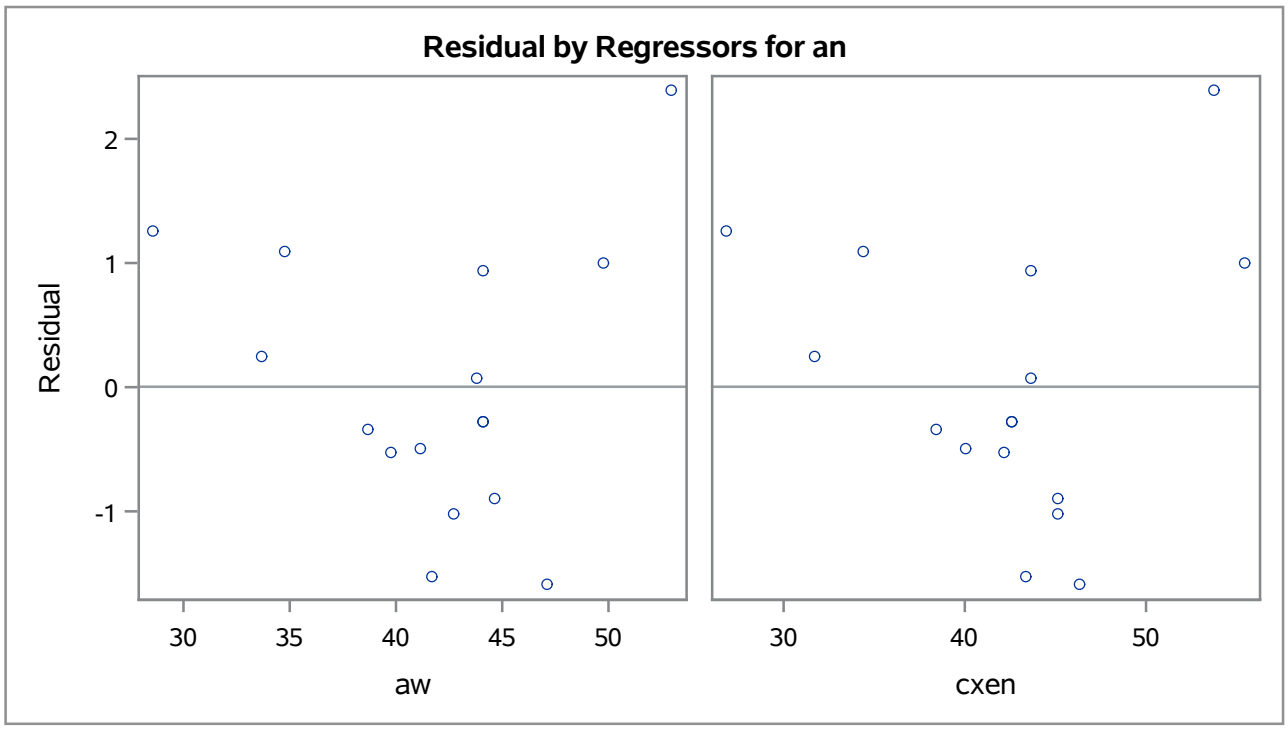
Root MSE	1.17617	**R-Square**	0.9664
Dependent Mean	42.47380	**Adj R-Sq**	0.9612
Coeff Var	2.76916		

Parameter Estimates					
Variable	**DF**	**Parameter Estimate**	**Standard Error**	**t Value**	**Pr > |t|**
Intercept	1	7.50493	2.36379	3.17	0.0073
aw	1	0.06436	0.20170	0.32	0.7547
cxen	1	0.76452	0.16988	4.50	0.0006

The REG Procedure
Model: MODEL1
Dependent Variable: an



The REG Procedure
Model: MODEL1
Dependent Variable: an



The GENMOD Procedure

Bayesian Analysis

Model Information	
Data Set	WORK.WEAPONS2
Burn-In Size	2000
MC Sample Size	10000
Thinning	1
Sampling Algorithm	Conjugate
Distribution	Normal
Link Function	Identity
Dependent Variable	an

Number of Observations Read	16
Number of Observations Used	16

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**	
Intercept	1	6.8609	3.8517	-0.6883	14.4102
aw	1	0.4697	0.2624	-0.0447	0.9841
cxen	1	0.3762	0.2346	-0.0837	0.8360
Scale	1	1.6066	0.2840	1.1361	2.2718

Note: The scale parameter was estimated by maximum likelihood.

The GENMOD Procedure

Bayesian Analysis

Normal Prior for Regression Coefficients				
		Covariance Matrix		
Parameter	Mean	Intercept	aw	cxen
Intercept	.	5.587507	-0.30709	0.175097
aw	.	-0.30709	0.040683	-0.03319
cxen	.	0.175097	-0.03319	0.028861