The GENMOD Procedure

Bayesian Analysis

Model Information		
Data Set	SASUSER.CHWIDE1MAY2012CHICASOLD	chwide1May2012chicasold dataset written by Stat/Transfer Ver. 10.1.1866.0714
Burn-In Size	2000	
MC Sample Size	10000	
Thinning	1	
Sampling Algorithm	Conjugate	
Distribution	Normal	
Link Function	Identity	
Dependent Variable	radfmw3	how much believed family health is affected by radiation NOW

Number of Observations Read	363
Number of Observations Used	363

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**	
Intercept	1	-2.3291	2.5013	-7.2315	2.5734
efradw3	1	0.0420	0.0187	0.0054	0.0786
BSIsoma	1	0.1658	0.1256	-0.0803	0.4120
radfmw2	1	0.9223	0.0380	0.8478	0.9968
radfmw1	1	-0.0964	0.0255	-0.1464	-0.0465
radhlw2	1	0.0377	0.0392	-0.0392	0.1145
kzchorn	1	0.0925	0.0287	0.0362	0.1487
Scale	1	12.9301	0.4799	12.0230	13.9058

Note: The scale parameter was estimated by maximum likelihood.

The GENMOD Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients	
Parameter	**Prior**
Intercept	Constant
efradw3	Constant
BSIsoma	Constant
radfmw2	Constant
radfmw1	Constant
radhlw2	Constant
kzchorn	Constant

Algorithm converged.

Independent Prior Distributions for Model Parameters			
		Hyperparameters	
Parameter	**Prior Distribution**	**Shape**	**Scale**
Dispersion	Inverse Gamma	2.001	0.0001

Initial Values of the Chain									
Chain	**Seed**	**Intercept**	**efradw3**	**BSIsoma**	**radfmw2**	**radfmw1**	**radhlw2**	**kzchorn**	**Dispersion**
1	4	-2.32907	0.042027	0.165847	0.922294	-0.09645	0.037676	0.092464	164.4129
2		29.75438	-0.01355	-0.20776	0.809171	-0.17231	-0.07895	0.007123	131.8382
3		-34.4125	0.097609	0.539457	1.035417	-0.02059	0.154301	0.177805	205.0363

Fit Statistics	
DIC (smaller is better)	2904.597
pD (effective number of parameters)	8.084

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries						
				Percentiles		
Parameter	N	Mean	Standard Deviation	25%	50%	75%
Intercept	10000	-2.3046	2.5423	-4.0325	-2.2905	-0.5810
efradw3	10000	0.0420	0.0189	0.0294	0.0421	0.0549
BSIsoma	10000	0.1657	0.1279	0.0814	0.1655	0.2526
radfmw2	10000	0.9219	0.0384	0.8964	0.9216	0.9478
radfmw1	10000	-0.0968	0.0260	-0.1145	-0.0973	-0.0794
radhlw2	10000	0.0385	0.0393	0.0122	0.0386	0.0646
kzchorn	10000	0.0922	0.0289	0.0726	0.0921	0.1121
Dispersion	10000	169.6	12.7118	160.8	169.0	177.7

Posterior Intervals					
		Equal-Tail Interval		HPD Interval	
Parameter	Alpha				
Intercept	0.050	-7.3386	2.6857	-7.1313	2.8425
efradw3	0.050	0.00488	0.0786	0.00565	0.0791
BSIsoma	0.050	-0.0892	0.4172	-0.0822	0.4232
radfmw2	0.050	0.8469	0.9976	0.8430	0.9932
radfmw1	0.050	-0.1467	-0.0447	-0.1469	-0.0451
radhlw2	0.050	-0.0390	0.1149	-0.0392	0.1143
kzchorn	0.050	0.0351	0.1483	0.0367	0.1493
Dispersion	0.050	146.4	196.0	145.4	194.2

Posterior Correlation Matrix								
Parameter	Intercept	efradw3	BSIsoma	radfmw2	radfmw1	radhlw2	kzchorn	Dispersion
Intercept	1.000	-0.143	-0.474	-0.090	-0.190	0.133	-0.519	0.002
efradw3	-0.143	1.000	0.062	-0.169	-0.022	-0.044	-0.101	-0.012
BSIsoma	-0.474	0.062	1.000	-0.120	0.055	-0.061	-0.112	0.017
radfmw2	-0.090	-0.169	-0.120	1.000	-0.015	-0.647	-0.194	-0.007
radfmw1	-0.190	-0.022	0.055	-0.015	1.000	-0.477	0.004	0.025
radhlw2	0.133	-0.044	-0.061	-0.647	-0.477	1.000	-0.050	0.001

The GENMOD Procedure

Bayesian Analysis

Posterior Correlation Matrix								
Parameter	**Intercept**	**efradw3**	**BSIsoma**	**radfmw2**	**radfmw1**	**radhlw2**	**kzchorn**	**Dispersion**
kzchorn	-0.519	-0.101	-0.112	-0.194	0.004	-0.050	1.000	-0.015
Dispersion	0.002	-0.012	0.017	-0.007	0.025	0.001	-0.015	1.000

The GENMOD Procedure

Bayesian Analysis

Posterior Autocorrelations				
Parameter	**Lag 1**	**Lag 5**	**Lag 10**	**Lag 50**
Intercept	-0.0082	0.0071	-0.0098	-0.0093
efradw3	0.0054	0.0013	0.0154	0.0053
BSIsoma	0.0036	0.0023	0.0121	0.0036
radfmw2	0.0027	0.0071	-0.0089	0.0115
radfmw1	-0.0004	0.0139	-0.0087	0.0037
radhlw2	-0.0088	-0.0035	-0.0016	0.0158
kzchorn	-0.0078	-0.0017	-0.0066	-0.0115
Dispersion	-0.0024	-0.0141	0.0121	-0.0223

Gelman-Rubin Diagnostics		
Parameter	**Estimate**	**97.5% Bound**
Intercept	1.0000	1.0000
efradw3	1.0000	1.0001
BSIsoma	1.0001	1.0004
radfmw2	1.0000	1.0002
radfmw1	1.0003	1.0014
radhlw2	1.0001	1.0005
kzchorn	1.0001	1.0004
Dispersion	0.9999	1.0000

Geweke Diagnostics		
Parameter	**z**	**Pr > |z|**
Intercept	-0.0500	0.9601
efradw3	0.7389	0.4600
BSIsoma	0.7659	0.4437
radfmw2	0.3713	0.7104
radfmw1	-0.4815	0.6302
radhlw2	0.1711	0.8641
kzchorn	-1.3574	0.1747
Dispersion	-0.4245	0.6712

The GENMOD Procedure

Bayesian Analysis

Raftery-Lewis Diagnostics				
Quantile=0.025 Accuracy=+/-0.005 Probability=0.95 Epsilon=0.001				
	Number of Samples			
Parameter	Burn-in	Total	Minimum	Dependence Factor
Intercept	2	3834	3746	1.0235
efradw3	2	3803	3746	1.0152
BSIsoma	.	.	3746	.
radfmw2	.	.	3746	.
radfmw1	2	3866	3746	1.0320
radhlw2	.	.	3746	.
kzchorn	.	.	3746	.
Dispersion	2	3759	3746	1.0035

Heidelberger-Welch Diagnostics								
	Stationarity Test				Half-width Test			
Parameter	Cramer-von-Mises Stat	p	Test Outcome	Iterations Discarded	Half-width	Mean	Relative Half-width	Test Outcome
Intercept	0.0849	0.6640	Passed	0	0.0574	-2.3046	-0.0249	Passed
efradw3	0.0863	0.6565	Passed	0	0.000416	0.0420	0.00991	Passed
BSIsoma	0.0659	0.7768	Passed	0	0.00313	0.1657	0.0189	Passed
radfmw2	0.1447	0.4061	Passed	0	0.000919	0.9219	0.000997	Passed
radfmw1	0.1289	0.4607	Passed	0	0.000448	-0.0968	-0.00463	Passed
radhlw2	0.0729	0.7342	Passed	0	0.000929	0.0385	0.0241	Passed
kzchorn	0.1054	0.5591	Passed	0	0.000517	0.0922	0.00560	Passed
Dispersion	0.0622	0.8002	Passed	0	0.2567	169.6	0.00151	Passed

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	10000.0	1.0000	1.0000
efradw3	10000.0	1.0000	1.0000
BSIsoma	10000.0	1.0000	1.0000
radfmw2	10000.0	1.0000	1.0000

The GENMOD Procedure

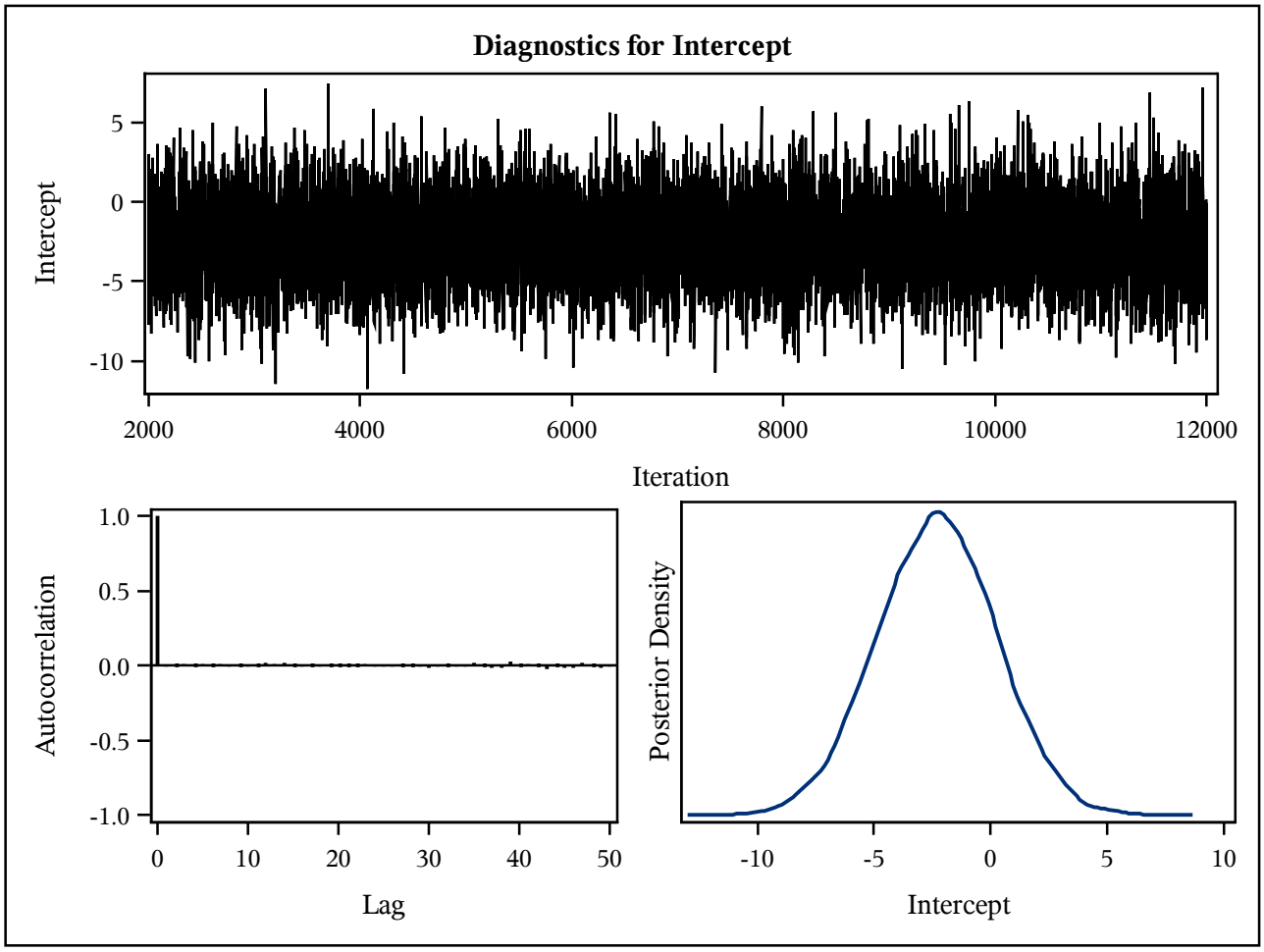
Bayesian Analysis

Effective Sample Sizes			
Parameter	**ESS**	**Autocorrelation Time**	**Efficiency**
radfmw1	10000.0	1.0000	1.0000
radhlw2	10000.0	1.0000	1.0000
kzchorn	10000.0	1.0000	1.0000
Dispersion	10000.0	1.0000	1.0000

Monte Carlo Standard Errors			
Parameter	**MCSE**	**Standard Deviation**	**MCSE/SD**
Intercept	0.0254	2.5423	0.0100
efradw3	0.000189	0.0189	0.0100
BSIsoma	0.00128	0.1279	0.0100
radfmw2	0.000384	0.0384	0.0100
radfmw1	0.000260	0.0260	0.0100
radhlw2	0.000393	0.0393	0.0100
kzchorn	0.000289	0.0289	0.0100
Dispersion	0.1271	12.7118	0.0100

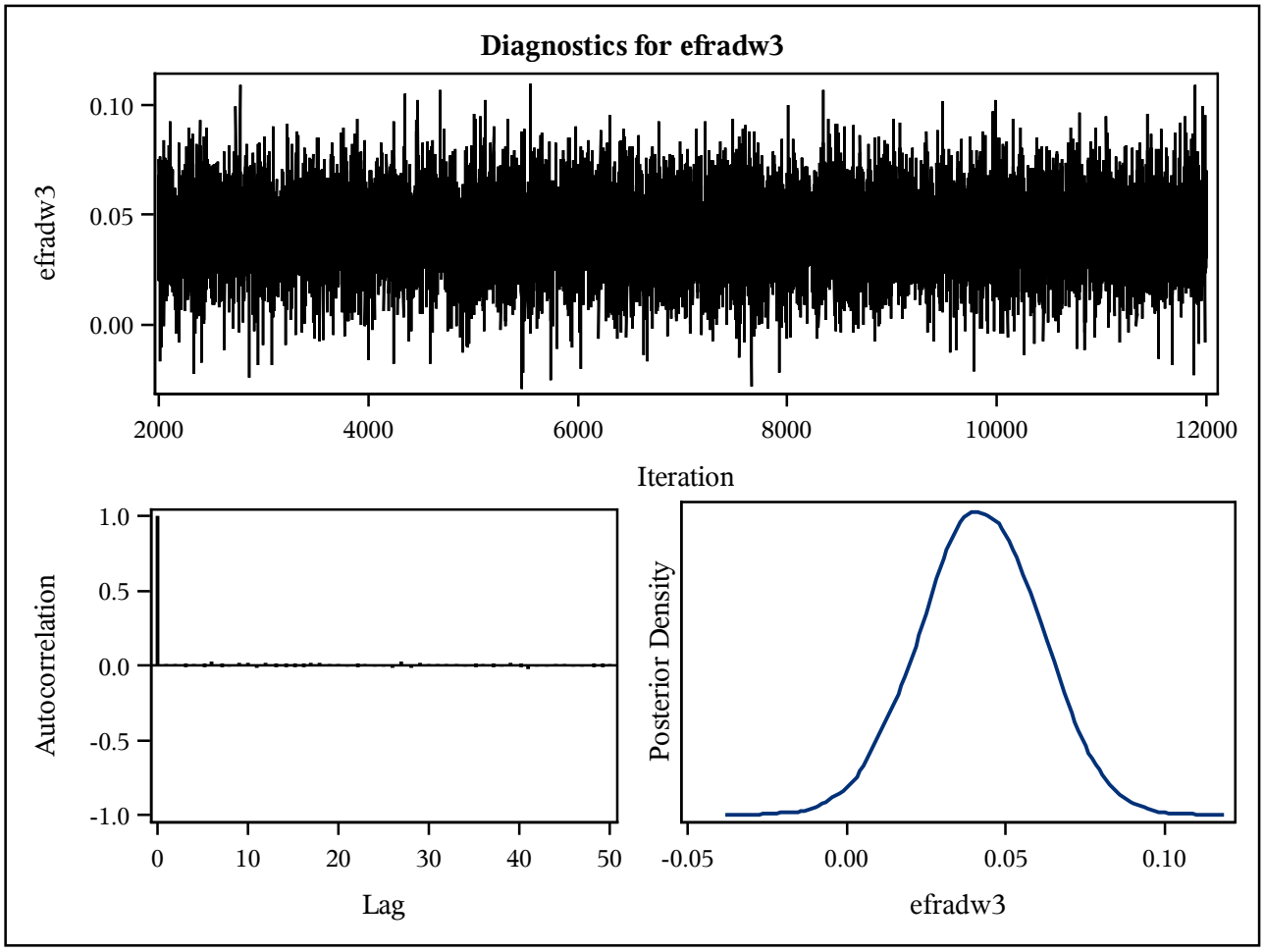
The GENMOD Procedure

Bayesian Analysis



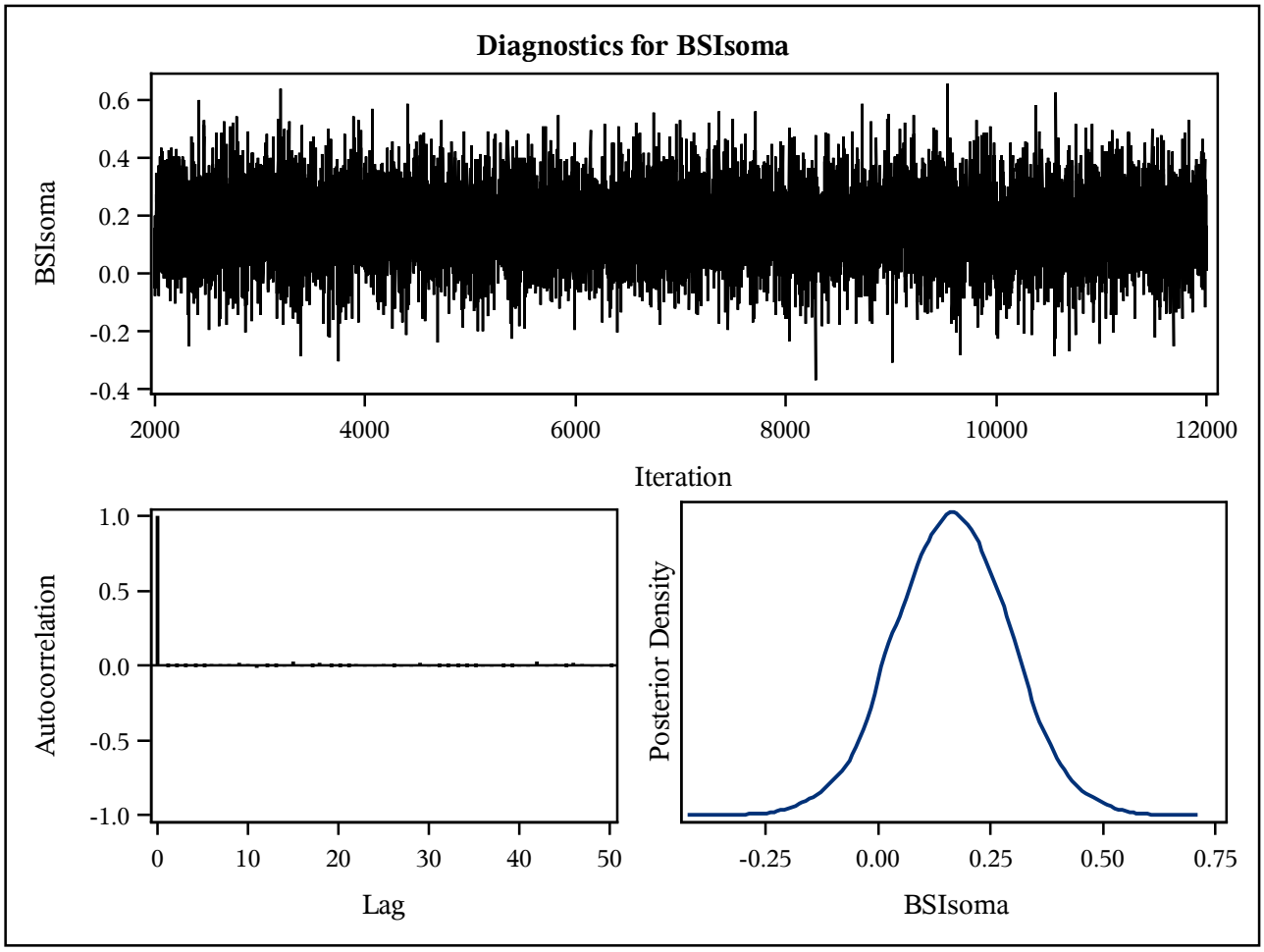
The GENMOD Procedure

Bayesian Analysis



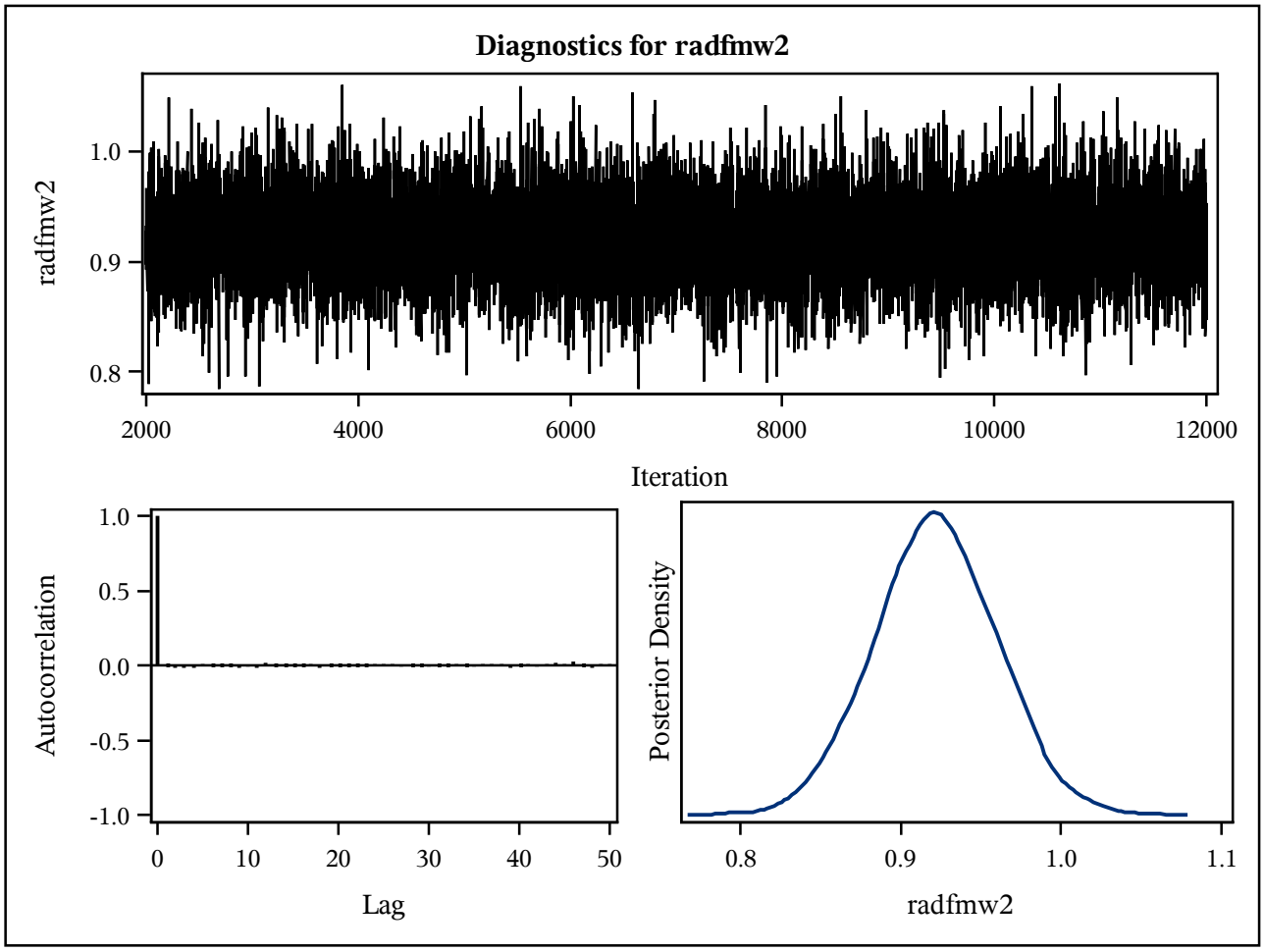
The GENMOD Procedure

Bayesian Analysis



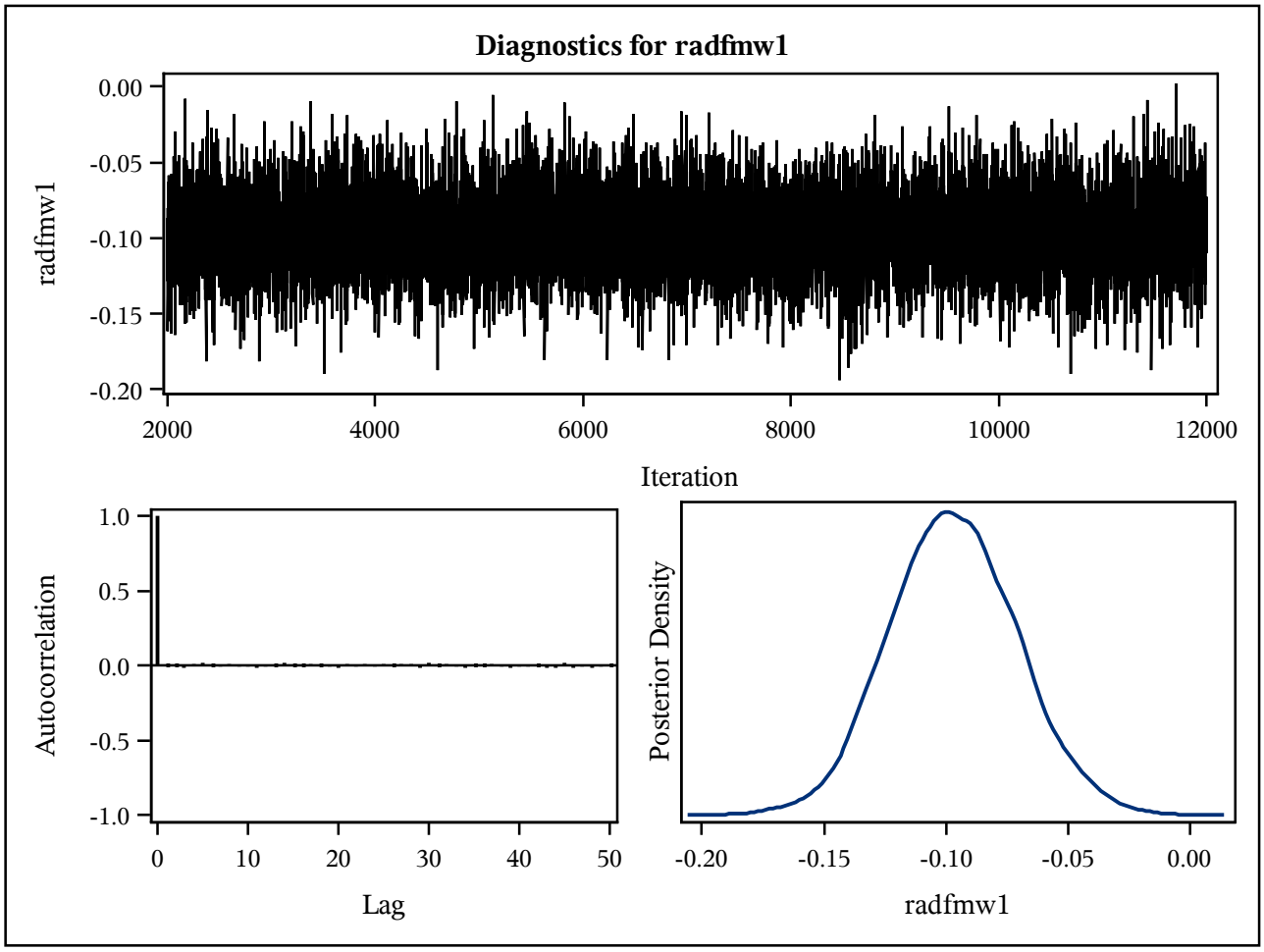
The GENMOD Procedure

Bayesian Analysis



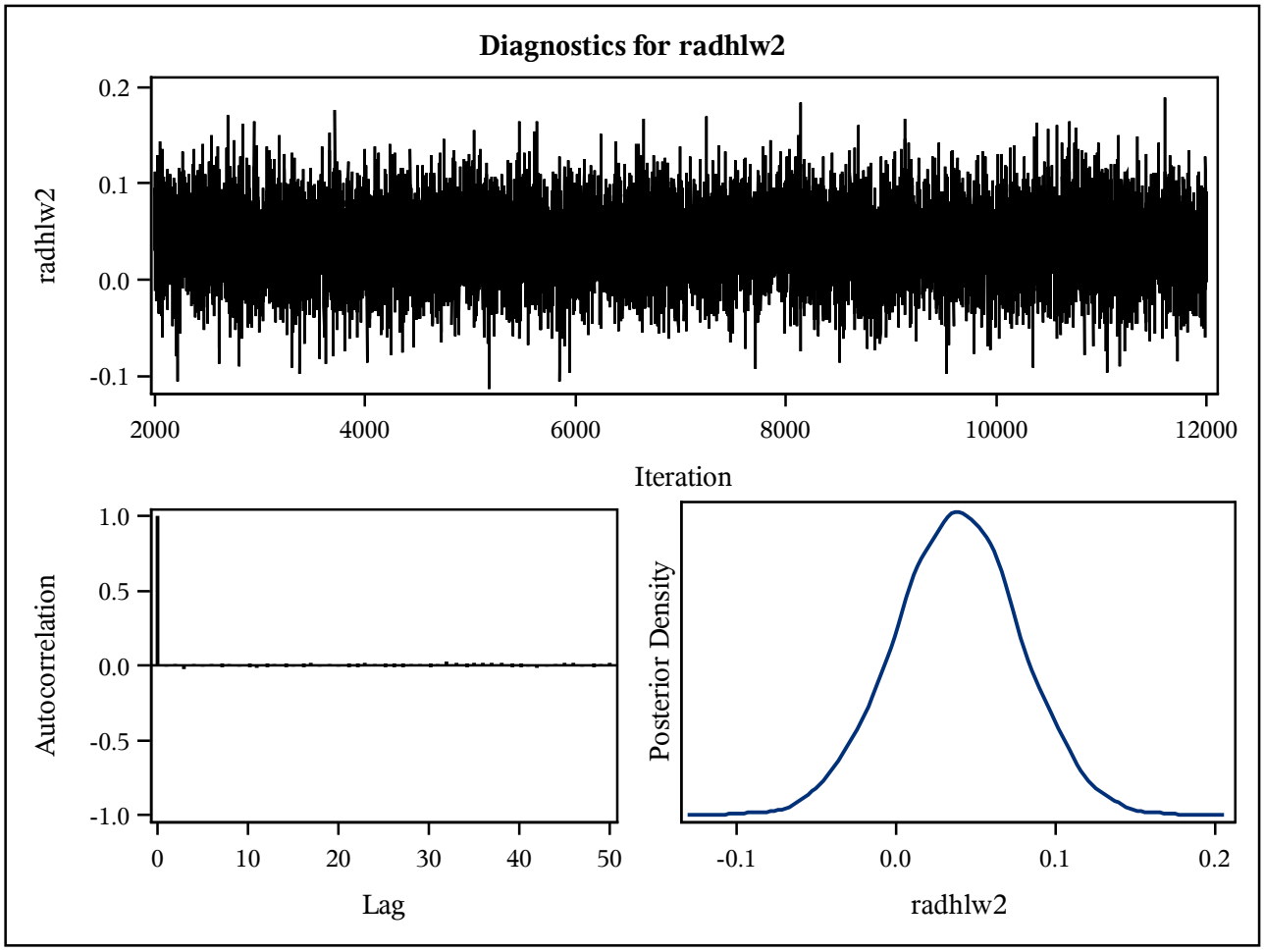
The GENMOD Procedure

Bayesian Analysis



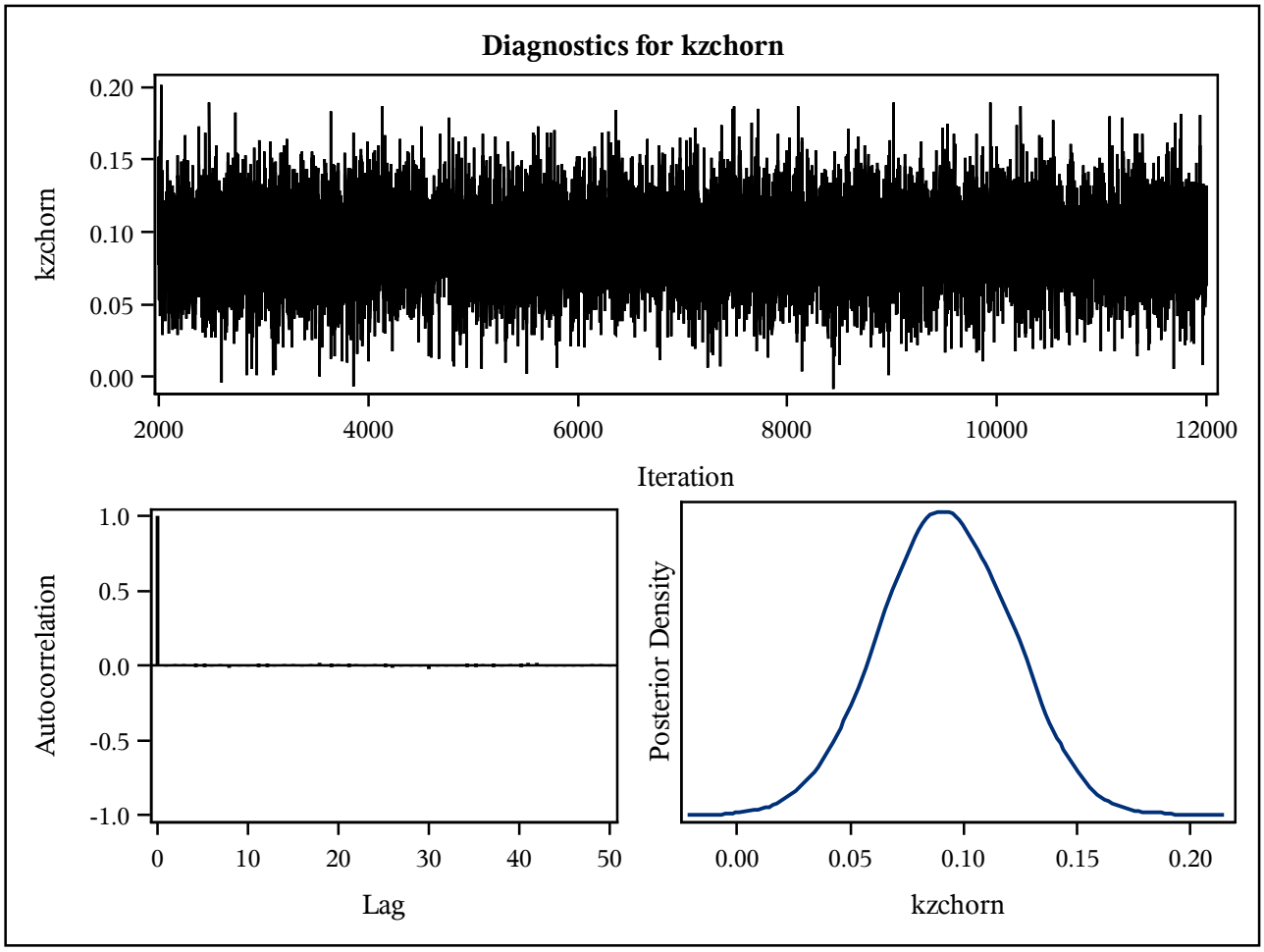
The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis



The GENMOD Procedure

Bayesian Analysis