Example Code using PROC BGLIMM

Simple Linear Regression with Class Variable

In [1]:
```
proc bglimm data=sashelp.class seed=8675309;
   class sex;
   model Weight = Height Age Sex / dist=normal coeffprior=normal(variance=1e6);
run;
```

```
SAS Connection established. Subprocess id is 76633
```

The SAS System

The BGLIMM Procedure

Model Information	
Data Set	SASHELP.CLASS
Response Variable	Weight
Distribution	Normal
Link Function	Identity
Fixed Effects Included	Yes
Random Effects Included	No
Sampling Algorithm	Conjugate
Burn-In Size	500
Simulation Size	5000
Thinning	1
Random Number Seed	8675309
Number of Threads	1

Class Level Information		
Class	Levels	Values
Sex	2	F M

Number of Observations	
Number of Observations Read	19
Number of Observations Used	19

Independent Normal Priors for Fixed Effects		
Parameter	Mean	Variance
Intercept	0	1000000
Height	0	1000000
Age	0	1000000
Sex F	0	1000000

Priors for Scale and Covariance Parameters	
Parameter	Prior
Scale	Inverse Gamma (Shape=2, Scale=2)

Posterior Summaries and Intervals					
Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Intercept	5000	-116.0	33.7405	-186.5	-52.4437
Height	5000	2.8694	0.9448	0.8729	4.6574
Age	5000	3.1130	3.0759	-2.8693	9.3670
Sex F	5000	-8.9601	5.4511	-20.2018	1.1647
Sex M	0	.	.	.	.
Scale	5000	108.8	39.1999	46.6659	186.3

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	5000.0	1.0000	1.0000
Height	4813.2	1.0388	0.9626
Age	5000.0	1.0000	1.0000
Sex F	5000.0	1.0000	1.0000
Sex M	.	.	.
Scale	3488.1	1.4334	0.6976

Toy Example:

Normal Response with Random Effects (MIXED)

In [2]:
```
data work.toy;
   length toy $1;
   input toy $ adhesive $ pressure @@;
datalines;
1 c 67.0 1 b 71.9 1 a 72.2
2 c 67.5 2 b 68.8 2 a 66.4
3 c 76.0 3 b 82.6 3 a 74.5
4 c 72.7 4 b 78.1 4 a 67.3
5 c 73.1 5 b 74.2 5 a 73.2
6 c 65.8 6 b 70.8 6 a 68.7
7 c 75.6 7 b 84.9 7 a 69.0
;
run;
```

```
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59         ods listing close;ods html5 (id=saspy_internal) file=_tomods1 options(bitm
ap_mode='inline') device=svg style=HTMLBlue;
59       ! ods graphics on / outputfmt=png;
NOTE: Writing HTML5(SASPY_INTERNAL) Body file: _TOMODS1
60
61         data work.toy;
62            length toy $1;
63            input toy $ adhesive $ pressure @@;
64         datalines;

NOTE: SAS went to a new line when INPUT statement reached past the end of a line.
NOTE: The data set WORK.TOY has 21 observations and 3 variables.
NOTE: DATA statement used (Total process time):
      real time           0.00 seconds
      cpu time            0.00 seconds


72         ;
73         run;
74
75
76
77         ods html5 (id=saspy_internal) close;ods listing;
78

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79
```

In [3]:
```
proc mixed data=work.toy;
   class adhesive toy;
   model pressure = adhesive / solution ddfm=kr2;
   random toy;
run;
```

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.TOY
Dependent Variable	pressure
Covariance Structure	Variance Components
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Kenward-Roger2
Degrees of Freedom Method	Kenward-Roger2

Class Level Information		
Class	Levels	Values
adhesive	3	a b c
toy	7	1 2 3 4 5 6 7

Dimensions	
Covariance Parameters	2
Columns in X	4
Columns in Z	7
Subjects	1
Max Obs per Subject	21

Number of Observations	
Number of Observations Read	21
Number of Observations Used	21
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	112.40987952	
1	1	107.79020201	0.00000000

Convergence criteria met.

Covariance Parameter Estimates	
Cov Parm	Estimate
toy	11.4478
Residual	10.3716

Fit Statistics	
-2 Res Log Likelihood	107.8
AIC (Smaller is Better)	111.8
AICC (Smaller is Better)	112.6
BIC (Smaller is Better)	111.7

Solution for Fixed Effects						
Effect	adhesive	Estimate	Standard Error	DF	t Value	Pr > |t|
Intercept		71.1000	1.7655	11.6	40.27	<.0001
adhesive	a	-0.9143	1.7214	12	-0.53	0.6050
adhesive	b	4.8000	1.7214	12	2.79	0.0164
adhesive	c	0	.	.	.	.

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
adhesive	2	12	6.36	0.0131

Normal Response with Random Effects (BGLIMM)

In [4]:
```
proc bglimm data=work.toy seed=8675309;
   class adhesive toy;
   model pressure = adhesive / dist=normal coeffprior=normal(variance=1e6);
   random int / subject=toy;
run;
```

The SAS System

The BGLIMM Procedure

Model Information	
Data Set	WORK.TOY
Response Variable	pressure
Distribution	Normal
Link Function	Identity
Fixed Effects Included	Yes
Random Effects Included	Yes
Sampling Algorithm	Conjugate
Burn-In Size	500
Simulation Size	5000
Thinning	1
Random Number Seed	8675309
Number of Threads	1

Class Level Information		
Class	Levels	Values
adhesive	3	a b c
toy	7	1 2 3 4 5 6 7

Number of Observations	
Number of Observations Read	21
Number of Observations Used	21

Independent Normal Priors for Fixed Effects		
Parameter	Mean	Variance
Intercept	0	1000000
adhesive a	0	1000000
adhesive b	0	1000000

Priors for Scale and Covariance Parameters	
Parameter	Prior
Scale	Inverse Gamma (Shape=2, Scale=2)
Random Var	Inverse Gamma (Shape=2, Scale=2)

Posterior Summaries and Intervals					
Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Intercept	5000	71.0953	1.6200	67.9998	74.3500
adhesive a	5000	-0.8956	1.8515	-4.6440	2.8192
adhesive b	5000	4.7668	1.8608	1.0038	8.3715
adhesive c	0	.	.	.	.
Scale	5000	12.2922	5.5328	3.8440	23.0906
Random Var	5000	4.9750	5.1886	0.2362	14.0160

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	1328.1	3.7649	0.2656
adhesive a	5000.0	1.0000	1.0000
adhesive b	5000.0	1.0000	1.0000
adhesive c	.	.	.
Scale	894.9	5.5874	0.1790
Random Var	757.2	6.6036	0.1514

Comparison of Frequentist Estimates and Posterior Means:

Parameter	MIXED Value	BGLIMM Value
Intercept	71.1000	71.0953
Adhesive a	-0.9143	-0.8956
Adhesive b	4.8000	4.7668
Adhesive c	0	0
VC Toy	11.4478	4.9750
VC Residual	10.3716	12.2922

Crab Example:

Poisson Regression with Random Effects (GLIMMIX)

In [5]:
```
data work.crab;
   input color spine width satellites weight site;
   color=color-1;
   weight=weight/1000;
```

```
datalines;
3  3  28.3  8  3050 1
4  3  22.5  0  1550 1
2  1  26.0  9  2300 1
4  3  24.8  0  2100 1
4  3  26.0  4  2600 1
3  3  23.8  0  2100 1
2  1  26.5  0  2350 1
4  2  24.7  0  1900 1
3  1  23.7  0  1950 1
4  3  25.6  0  2150 1
4  3  24.3  0  2150 1
3  3  25.8  0  2650 1
3  3  28.2  11 3050 2
5  2  21.0  0  1850 2
3  1  26.0  14 2300 2
2  1  27.1  8  2950 2
3  3  25.2  1  2000 2
3  3  29.0  1  3000 2
5  3  24.7  0  2200 2
3  3  27.4  5  2700 2
3  2  23.2  4  1950 3
2  2  25.0  3  2300 3
3  1  22.5  1  1600 3
4  3  26.7  2  2600 3
5  3  25.8  3  2000 3
5  3  26.2  0  1300 3
3  3  28.7  3  3150 3
3  1  26.8  5  2700 3
5  3  27.5  0  2600 3
3  3  24.9  0  2100 3
2  1  29.3  4  3200 3
2  3  25.8  0  2600 4
3  2  25.7  0  2000 4
3  1  25.7  8  2000 4
3  1  26.7  5  2700 4
5  3  23.7  0  1850 4
3  3  26.8  0  2650 4
3  3  27.5  6  3150 4
5  3  23.4  0  1900 4
3  3  27.9  6  2800 4
4  3  27.5  3  3100 4
2  1  26.1  5  2800 4
2  1  27.7  6  2500 4
3  1  30.0  5  3300 5
4  1  28.5  9  3250 5
4  3  28.9  4  2800 5
3  3  28.2  6  2600 5
3  3  25.0  4  2100 5
3  3  28.5  3  3000 5
3  1  30.3  3  3600 5
5  3  24.7  5  2100 5
3  3  27.7  5  2900 6
2  1  27.4  6  2700 6
3  3  22.9  4  1600 6
3  1  25.7  5  2000 6
3  3  28.3  15 3000 6
```

```
3  3  27.2  3  2700 6
4  3  26.2  3  2300 6
3  1  27.8  0  2750 6
5  3  25.5  0  2250 6
4  3  27.1  0  2550 6
4  3  24.5  5  2050 6
4  1  27.0  3  2450 6
3  3  26.0  5  2150 6
3  3  28.0  1  2800 7
3  3  30.0  8  3050 7
3  3  29.0  10 3200 7
3  3  26.2  0  2400 7
3  1  26.5  0  1300 7
3  3  26.2  3  2400 7
4  3  25.6  7  2800 7
4  3  23.0  1  1650 7
4  3  23.0  0  1800 7
3  3  25.4  6  2250 7
4  3  24.2  0  1900 7
3  2  22.9  0  1600 7
4  2  26.0  3  2200 7
3  3  25.4  4  2250 7
4  3  25.7  0  1200 8
3  3  25.1  5  2100 8
4  2  24.5  0  2250 8
5  3  27.5  0  2900 8
4  3  23.1  0  1650 8
4  1  25.9  4  2550 8
3  3  25.8  0  2300 8
5  3  27.0  3  2250 8
3  3  28.5  0  3050 8
5  1  25.5  0  2750 8
5  3  23.5  0  1900 8
3  2  24.0  0  1700 8
3  1  29.7  5  3850 8
3  1  26.8  0  2550 8
5  3  26.7  0  2450 9
3  1  28.7  0  3200 9
4  3  23.1  0  1550 9
3  1  29.0  1  2800 9
4  3  25.5  0  2250 9
4  3  26.5  1  1967 9
4  3  24.5  1  2200 9
4  3  28.5  1  3000 9
3  3  28.2  1  2867 9
3  3  24.5  1  1600 9
3  3  27.5  1  2550 9
3  2  24.7  4  2550 9
3  1  25.2  1  2000 9
4  3  27.3  1  2900 10
3  3  26.3  1  2400 10
3  3  29.0  1  3100 10
3  3  25.3  2  1900 10
3  3  26.5  4  2300 10
3  3  27.8  3  3250 10
3  3  27.0  6  2500 10
4  3  25.7  0  2100 10
```

```
3  3  25.0  2  2100 10
3  3  31.9  2  3325 10
5  3  23.7  0  1800 10
5  3  29.3  12 3225 10
4  3  22.0  0  1400 10
3  3  25.0  5  2400 10
4  3  27.0  6  2500 10
4  3  23.8  6  1800 10
2  1  30.2  2  3275 10
4  3  26.2  0  2225 11
3  3  24.2  2  1650 11
3  3  27.4  3  2900 11
3  2  25.4  0  2300 11
4  3  28.4  3  3200 11
5  3  22.5  4  1475 11
3  3  26.2  2  2025 11
3  1  24.9  6  2300 11
2  2  24.5  6  1950 11
3  3  25.1  0  1800 11
3  1  28.0  4  2900 11
5  3  25.8  10 2250 11
3  3  27.9  7  3050 11
3  3  24.9  0  2200 11
3  1  28.4  5  3100 11
4  3  27.2  5  2400 11
3  2  25.0  6  2250 11
3  3  27.5  6  2625 11
3  1  33.5  7  5200 12
3  3  30.5  3  3325 12
4  3  29.0  3  2925 12
3  1  24.3  0  2000 12
3  3  25.8  0  2400 12
5  3  25.0  8  2100 12
3  1  31.7  4  3725 12
3  3  29.5  4  3025 12
4  3  24.0  10 1900 12
3  3  30.0  9  3000 12
3  3  27.6  4  2850 12
3  3  26.2  0  2300 12
3  1  23.1  0  2000 12
3  1  22.9  0  1600 12
5  3  24.5  0  1900 12
3  3  24.7  4  1950 12
3  3  28.3  0  3200 12
3  3  23.9  2  1850 12
4  3  23.8  0  1800 12
4  2  29.8  4  3500 12
3  3  26.5  4  2350 13
3  3  26.0  3  2275 13
3  3  28.2  8  3050 13
5  3  25.7  0  2150 13
3  3  26.5  7  2750 13
3  3  25.8  0  2200 13
4  3  24.1  0  1800 13
4  3  26.2  2  2175 13
4  3  26.1  3  2750 13
4  3  29.0  4  3275 13
```

```
2  1  28.0  0  2625 13
5  3  27.0  0  2625 13
3  2  24.5  0  2000 13
;
run;
```

```
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111        ods listing close;ods html5 (id=saspy_internal) file=_tomods1 options(bitm
ap_mode='inline') device=svg style=HTMLBlue;
111      ! ods graphics on / outputfmt=png;
NOTE: Writing HTML5(SASPY_INTERNAL) Body file: _TOMODS1
112
113        data work.crab;
114           input color spine width satellites weight site;
115           color=color-1;
116           weight=weight/1000;
117        datalines;

NOTE: The data set WORK.CRAB has 173 observations and 6 variables.
NOTE: DATA statement used (Total process time):
      real time           0.00 seconds
      cpu time            0.02 seconds


291        ;
292        run;
293
294
295
296
297        ods html5 (id=saspy_internal) close;ods listing;
298

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```

In [6]:
```
proc glimmix data=work.crab;
   class color spine site;
   model satellites = color spine weight width / dist=poi link=log solution;
   random int / subject=site;
run;
```

The SAS System

The GLIMMIX Procedure

Model Information	
Data Set	WORK.CRAB
Response Variable	satellites
Response Distribution	Poisson
Link Function	Log
Variance Function	Default
Variance Matrix Blocked By	site
Estimation Technique	Residual PL
Degrees of Freedom Method	Containment

Class Level Information		
Class	Levels	Values
color	4	1 2 3 4
spine	3	1 2 3
site	13	1 2 3 4 5 6 7 8 9 10 11 12 13

Number of Observations Read	173
Number of Observations Used	173

Dimensions	
G-side Cov. Parameters	1
Columns in X	10
Columns in Z per Subject	1
Subjects (Blocks in V)	13
Max Obs per Subject	20

Optimization Information	
Optimization Technique	Dual Quasi-Newton
Parameters in Optimization	1
Lower Boundaries	1
Upper Boundaries	0
Fixed Effects	Profiled
Starting From	Data

Iteration History

Iteration	Restarts	Subiterations	Objective Function	Change	Max Gradient
0	0	2	449.40569089	2.00000000	0.000623
1	0	4	614.1159541	2.00000000	0.000098
2	0	4	663.19815369	0.85657396	9.516E-6
3	0	2	666.8508521	0.01462831	1.617E-7
4	0	1	666.88102643	0.00001436	7.644E-9
5	0	0	666.881122	0.00000000	5.635E-6

Convergence criterion (PCONV=1.11022E-8) satisfied.

Fit Statistics

-2 Res Log Pseudo-Likelihood	666.88
Generalized Chi-Square	467.88
Gener. Chi-Square / DF	2.84

Covariance Parameter Estimates

Cov Parm	Subject	Estimate	Standard Error
Intercept	site	0.1494	0.07803

Solutions for Fixed Effects

Effect	color	spine	Estimate	Standard Error	DF	t Value	Pr > |t|
Intercept			-0.6317	1.0019	12	-0.63	0.5402
color	1		0.3829	0.2385	153	1.61	0.1105
color	2		0.1641	0.1702	153	0.96	0.3364
color	3		-0.00907	0.1866	153	-0.05	0.9613
color	4		0	.	.	.	.
spine		1	-0.03307	0.1242	153	-0.27	0.7904
spine		2	-0.1886	0.2022	153	-0.93	0.3525
spine		3	0	.	.	.	.
weight			0.5395	0.1755	153	3.07	0.0025
width			0.006855	0.05181	153	0.13	0.8949

Type III Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
color	3	153	1.48	0.2217
spine	2	153	0.44	0.6447
weight	1	153	9.45	0.0025
width	1	153	0.02	0.8949

Poisson Regression with Random Effects (BGLIMM)

In [7]:
```
proc bglimm data=work.crab seed=8675309 diag=all plots=all;
   class color spine site;
   model satellites = color spine weight width / dist=poisson link=log;
   random int / subject=site;
run;
```

The SAS System

The BGLIMM Procedure

Model Information	
Data Set	WORK.CRAB
Response Variable	satellites
Distribution	Poisson
Link Function	Log
Fixed Effects Included	Yes
Random Effects Included	Yes
Sampling Algorithm	Gamerman, Conjugate
Burn-In Size	500
Simulation Size	5000
Thinning	1
Random Number Seed	8675309
Number of Threads	1

Class Level Information		
Class	Levels	Values
color	4	1 2 3 4
spine	3	1 2 3
site	13	1 2 3 4 5 6 7 8 9 10 11 12 13

Number of Observations	
Number of Observations Read	173
Number of Observations Used	173

Priors for Fixed Effects	
Parameter	Prior
Intercept	Constant
color 1	Constant
color 2	Constant
color 3	Constant
spine 1	Constant
spine 2	Constant
weight	Constant

Priors for Fixed Effects	
Parameter	**Prior**
width	Constant

Priors for Scale and Covariance Parameters	
Parameter	**Prior**
Random Var	Inverse Gamma (Shape=2, Scale=2)

Posterior Summaries and Intervals					
Parameter	**N**	**Mean**	**Standard Deviation**	**95% HPD Interval**	
Intercept	5000	-0.6361	1.0030	-2.5912	1.2345
color 1	5000	0.3608	0.2335	-0.1052	0.8109
color 2	5000	0.1612	0.1720	-0.1633	0.5129
color 3	5000	-0.00556	0.1875	-0.3535	0.3736
color 4	0	.	.	.	.
spine 1	5000	-0.0265	0.1243	-0.2535	0.2281
spine 2	5000	-0.2025	0.2088	-0.6026	0.2103
spine 3	0	.	.	.	.
weight	5000	0.5456	0.1764	0.2051	0.8781
width	5000	0.00533	0.0519	-0.0919	0.1066
Random Var	5000	0.4560	0.1912	0.1827	0.8319

Posterior Autocorrelations				
Parameter	**Lag 1**	**Lag 5**	**Lag 10**	**Lag 50**
Intercept	0.4222	0.0068	-0.0030	-0.0076
color 1	0.4470	0.0430	-0.0167	0.0064
color 2	0.4387	0.0112	-0.0191	-0.0086
color 3	0.4325	-0.0014	-0.0380	-0.0223
color 4	.	.	.	.
spine 1	0.4034	0.0528	0.0077	0.0257
spine 2	0.4475	0.0315	0.0263	0.0058
spine 3	.	.	.	.
weight	0.3996	0.0236	-0.0082	-0.0124
width	0.4106	0.0036	-0.0036	-0.0090
Random Var	0.1051	0.0428	0.0408	0.0231

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	1985.1	2.5188	0.3970
color 1	1729.1	2.8917	0.3458
color 2	1882.4	2.6561	0.3765
color 3	1988.5	2.5144	0.3977
color 4	.	.	.
spine 1	1750.2	2.8568	0.3500
spine 2	1779.7	2.8095	0.3559
spine 3	.	.	.
weight	2101.2	2.3796	0.4202
width	2086.5	2.3963	0.4173
Random Var	2425.5	2.0615	0.4851

Monte Carlo Standard Errors			
Parameter	MCSE	Standard Deviation	MCSE/SD
Intercept	0.0225	1.0030	0.0224
color 1	0.00561	0.2335	0.0240
color 2	0.00396	0.1720	0.0230
color 3	0.00420	0.1875	0.0224
color 4	.	.	.
spine 1	0.00297	0.1243	0.0239
spine 2	0.00495	0.2088	0.0237
spine 3	.	.	.
weight	0.00385	0.1764	0.0218
width	0.00114	0.0519	0.0219
Random Var	0.00388	0.1912	0.0203

Geweke Diagnostics		
Parameter	z	Pr > |z|
Intercept	-0.7959	0.4261
color 1	0.0963	0.9233
color 2	0.3204	0.7487
color 3	0.4559	0.6485
color 4	.	.

Geweke Diagnostics		
Parameter	z	Pr > |z|
spine 1	1.6449	0.1000
spine 2	-1.6347	0.1021
spine 3	.	.
weight	0.4923	0.6225
width	-0.9570	0.3386
Random Var	-0.0642	0.9488

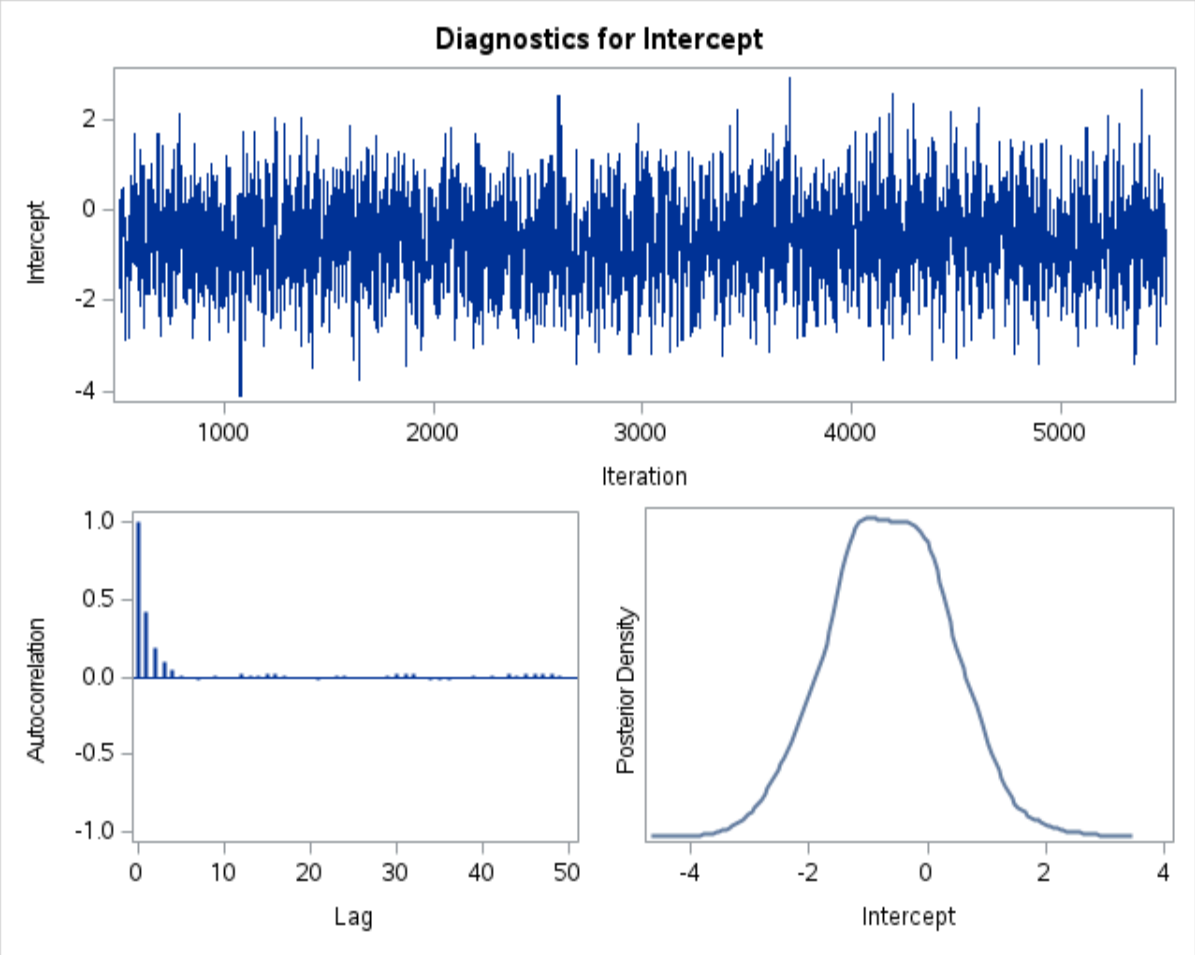
Raftery-Lewis Diagnostics				
Quantile=0.025 Accuracy=+/-0.005 Probability=0.95 Epsilon=0.001				
Parameter	Number of Samples			Dependence Factor
	Burn-In	Total	Minimum	
Intercept	7	7398	3746	1.9749
color 1	8	8927	3746	2.3831
color 2	7	7677	3746	2.0494
color 3	6	7004	3746	1.8697
color 4	.	.	.	.
spine 1	9	9874	3746	2.6359
spine 2	16	16853	3746	4.4989
spine 3	.	.	.	.
weight	8	8600	3746	2.2958
width	7	7677	3746	2.0494
Random Var	2	3742	3746	0.9989

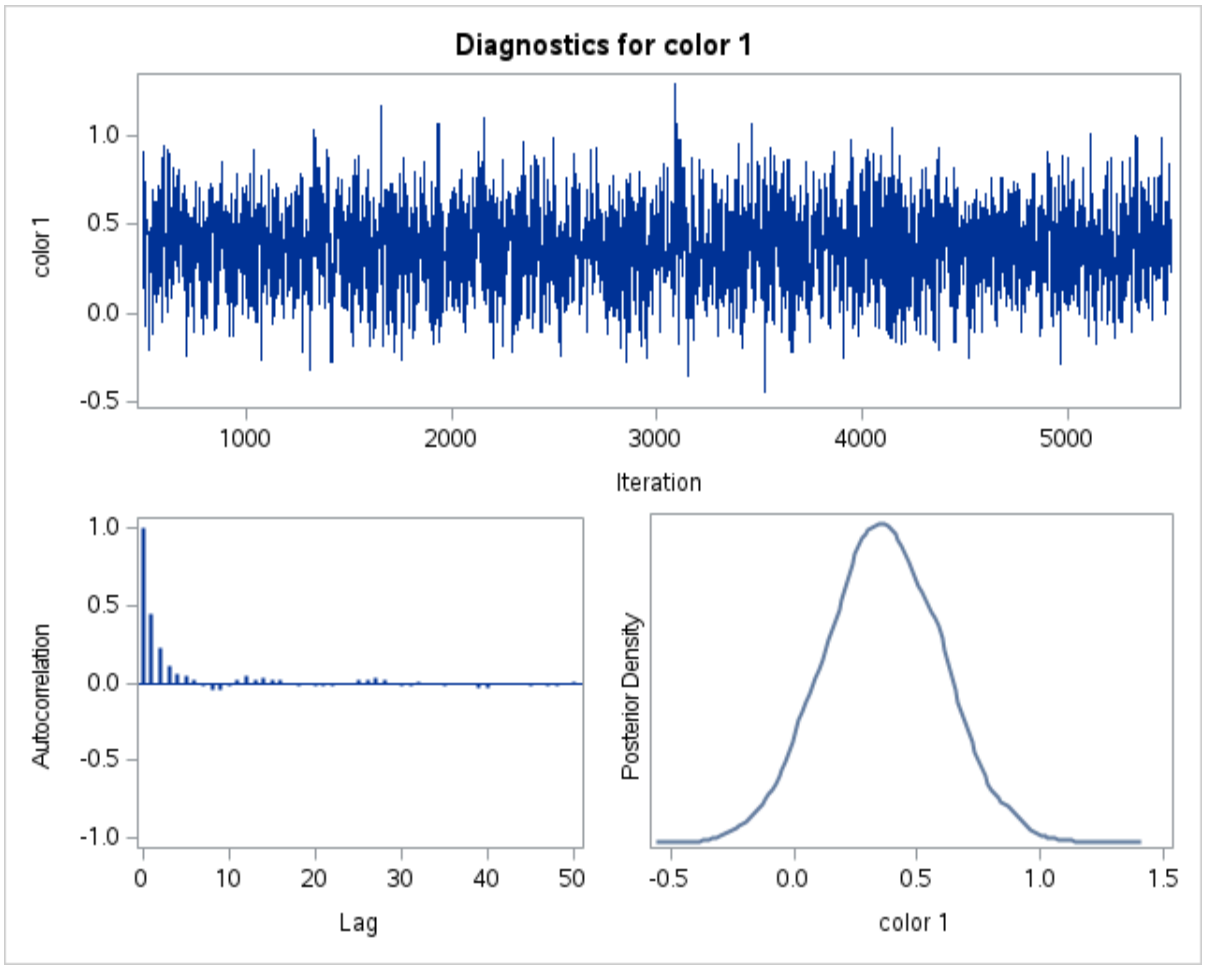
Heidelberger-Welch Diagnostics								
Parameter	Stationarity Test				Half-Width Test			
	Cramer-von Mises Stat	p-Value	Test Outcome	Iterations Discarded	Half-Width	Mean	Relative Half-Width	Test Outcome
Intercept	0.1470	0.3988	Passed	0	0.0478	-0.6361	-0.0751	Passed
color 1	0.0535	0.8549	Passed	0	0.0107	0.3608	0.0295	Passed
color 2	0.2780	0.1562	Passed	0	0.00626	0.1612	0.0388	Passed
color 3	0.1529	0.3808	Passed	0	0.00623	-0.00556	-1.1198	Failed
color 4	.	.		.	.	.	.	
spine 1	0.4039	0.0706	Passed	500	0.00757	-0.0275	-0.2754	Failed
spine 2	0.4229	0.0629	Passed	0	0.00996	-0.2025	-0.0492	Passed

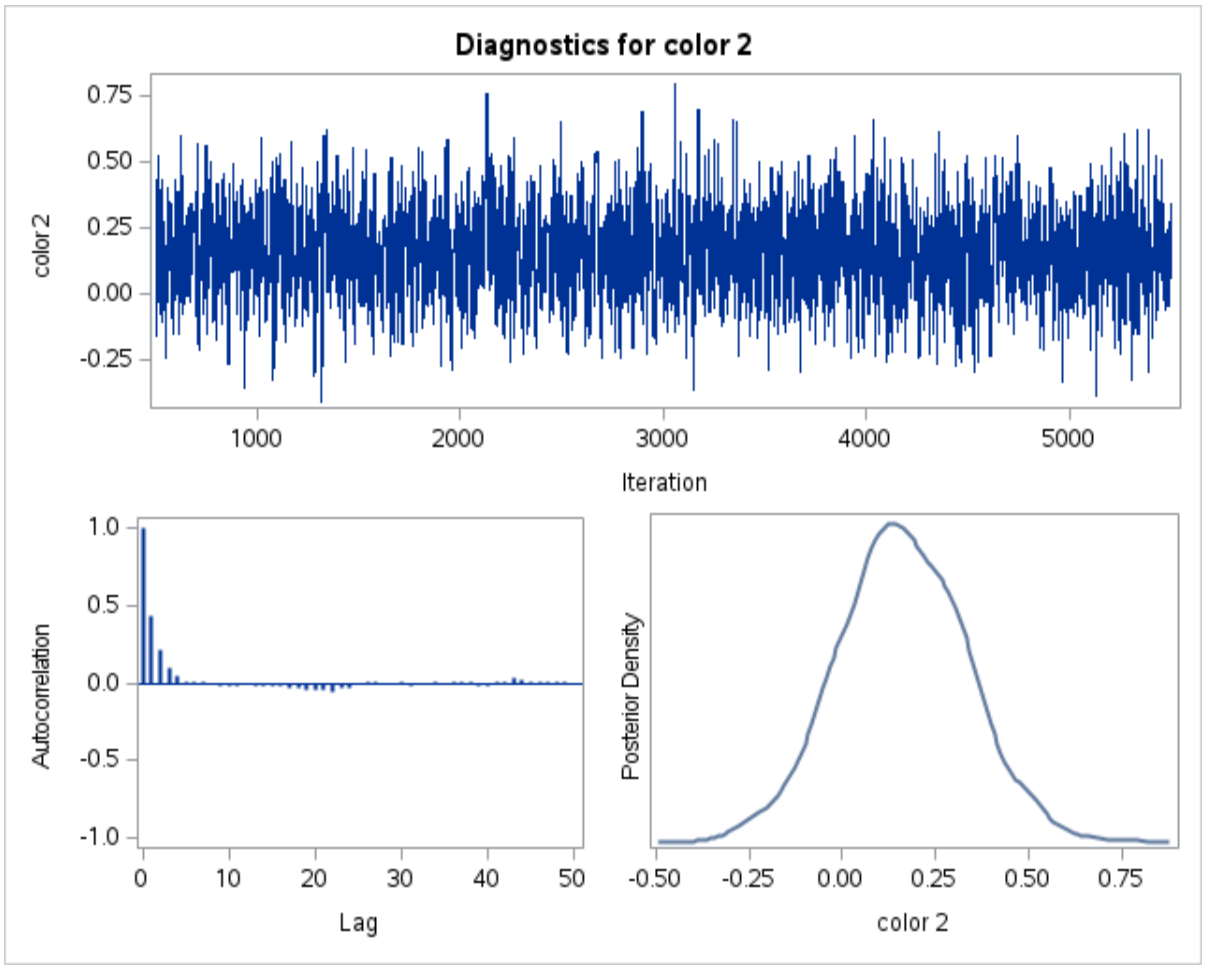
Heidelberger-Welch Diagnostics								
Parameter	Stationarity Test				Half-Width Test			
	Cramer-von Mises Stat	p-Value	Test Outcome	Iterations Discarded	Half-Width	Mean	Relative Half-Width	Test Outcome
spine 3	.	.		.	.	.	.	
weight	0.0343	0.9600	Passed	0	0.00727	0.5456	0.0133	Passed
width	0.2058	0.2565	Passed	0	0.00237	0.00533	0.4451	Failed
Random Var	0.3336	0.1090	Passed	0	0.00944	0.4560	0.0207	Passed

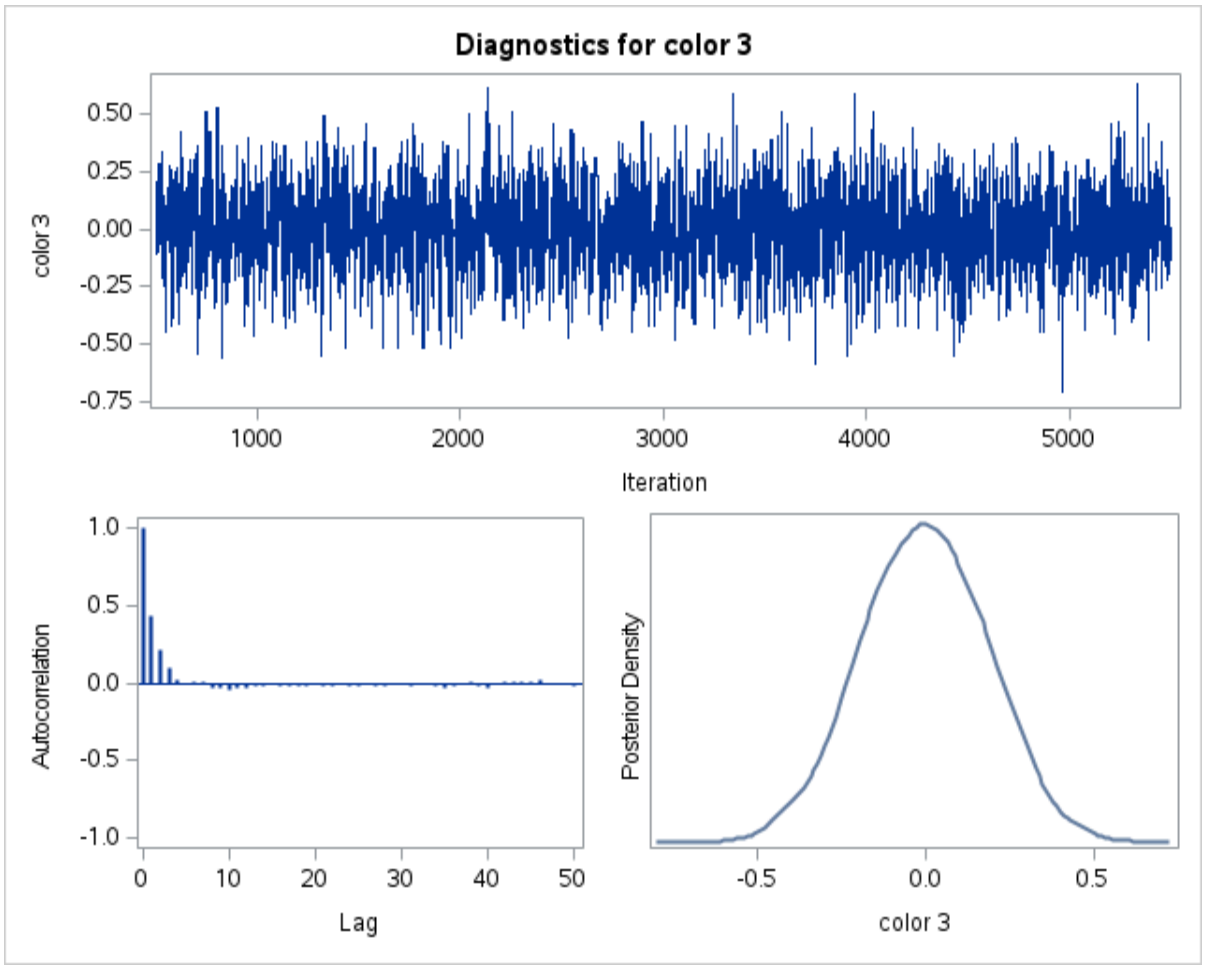
The SAS System

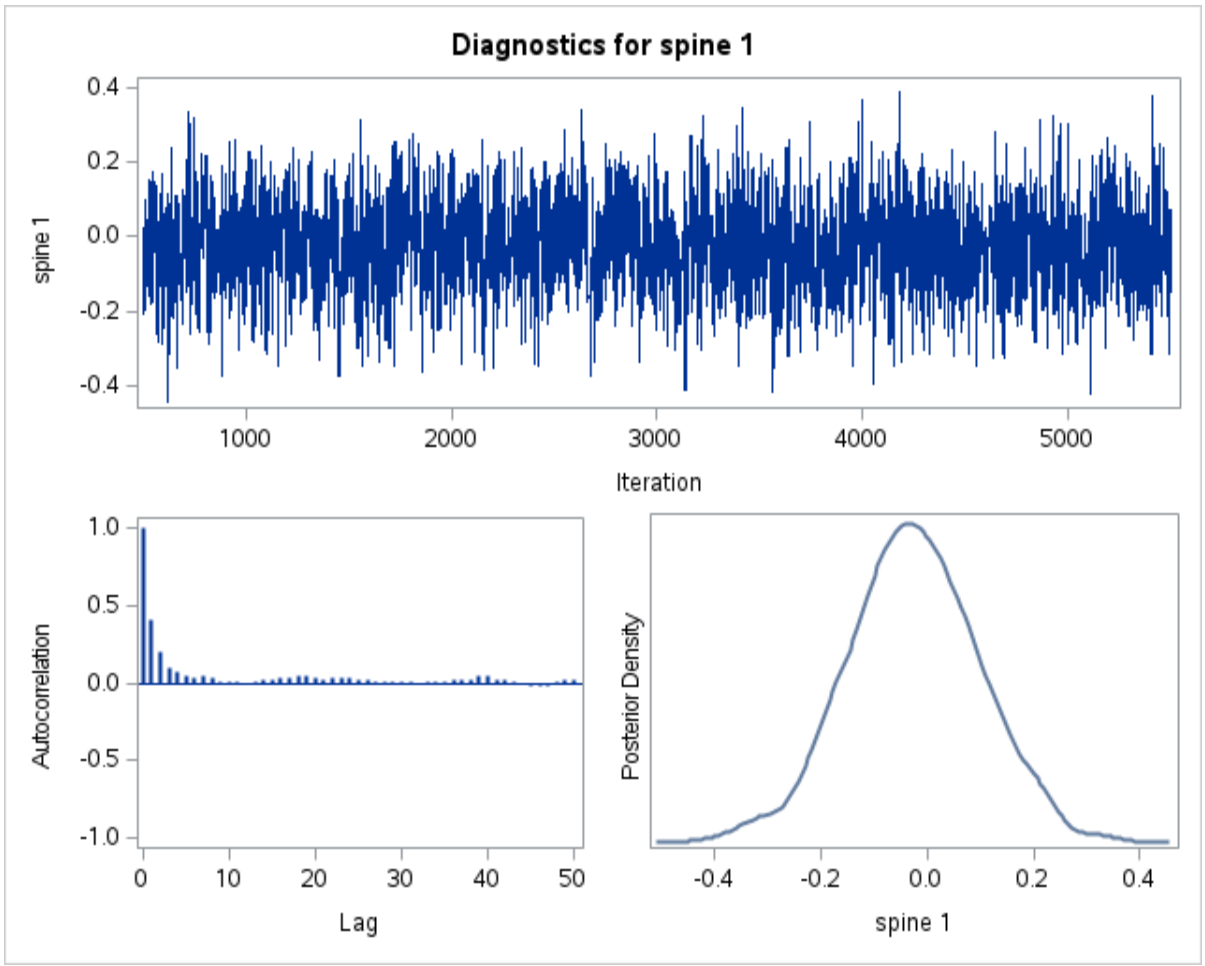
The BGLIMM Procedure

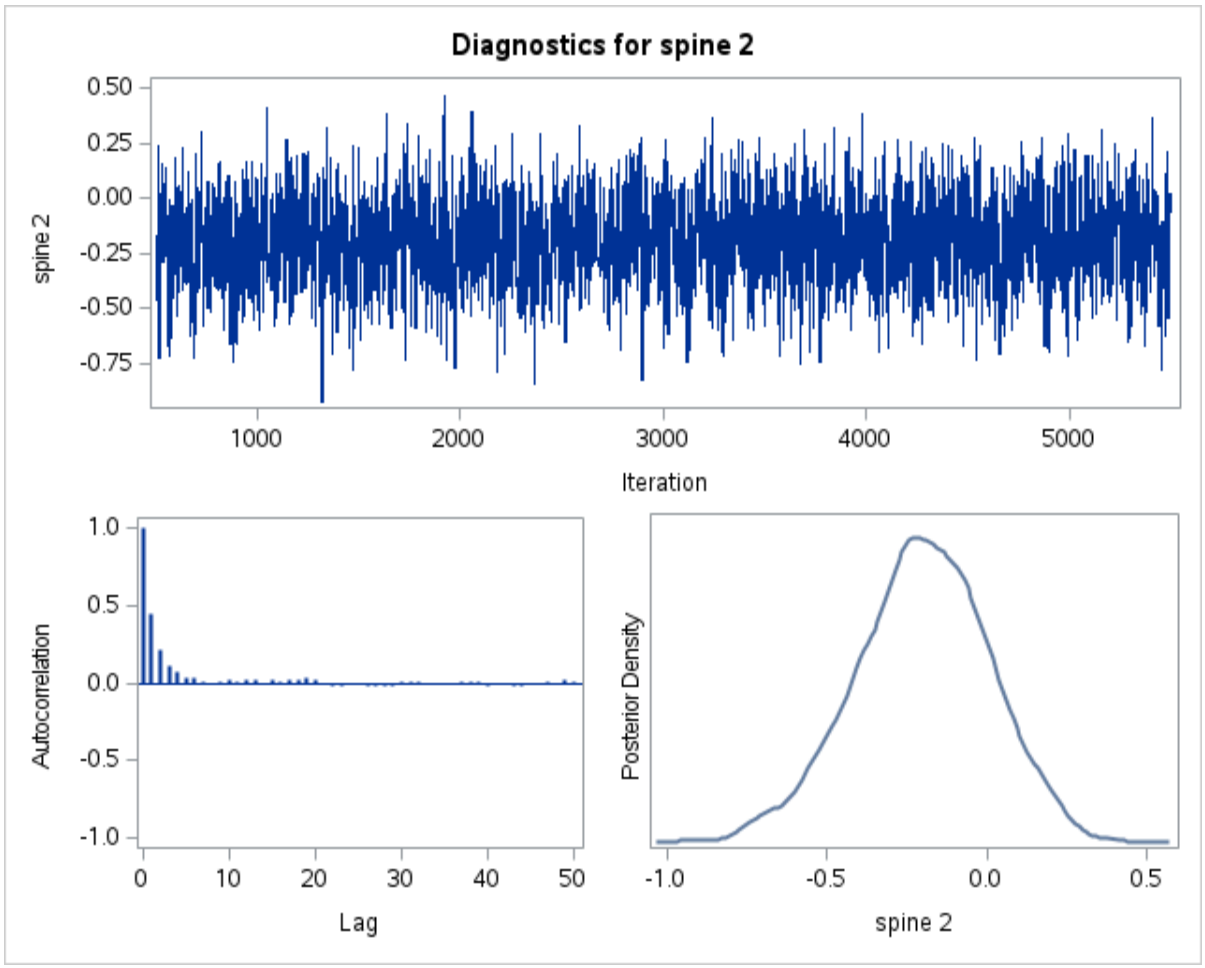


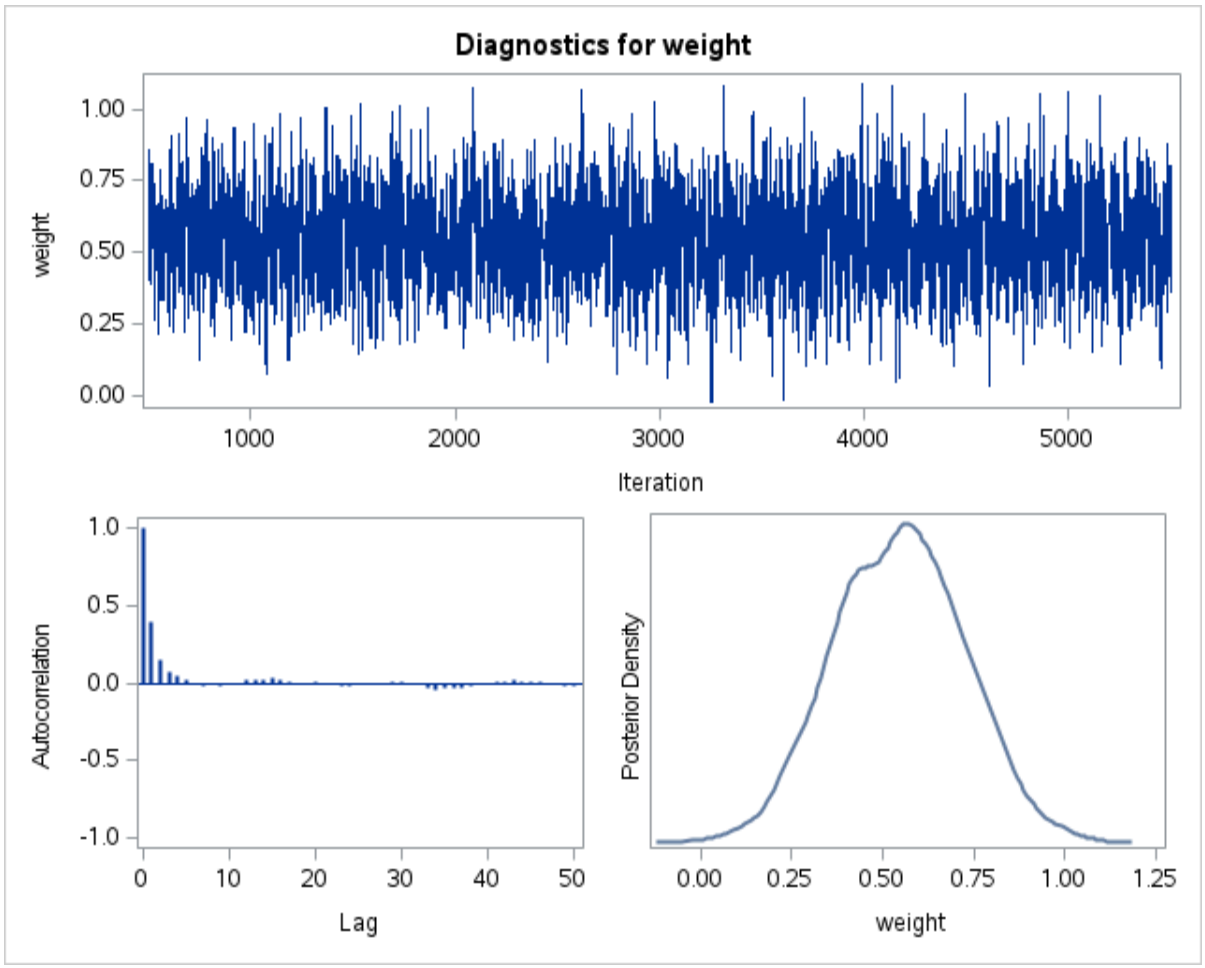

Diagnostics for color 1
color 1
1.0
0.5
0.0
-0.5
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-0.5
0.0
0.5
1.0
1.5
color 1

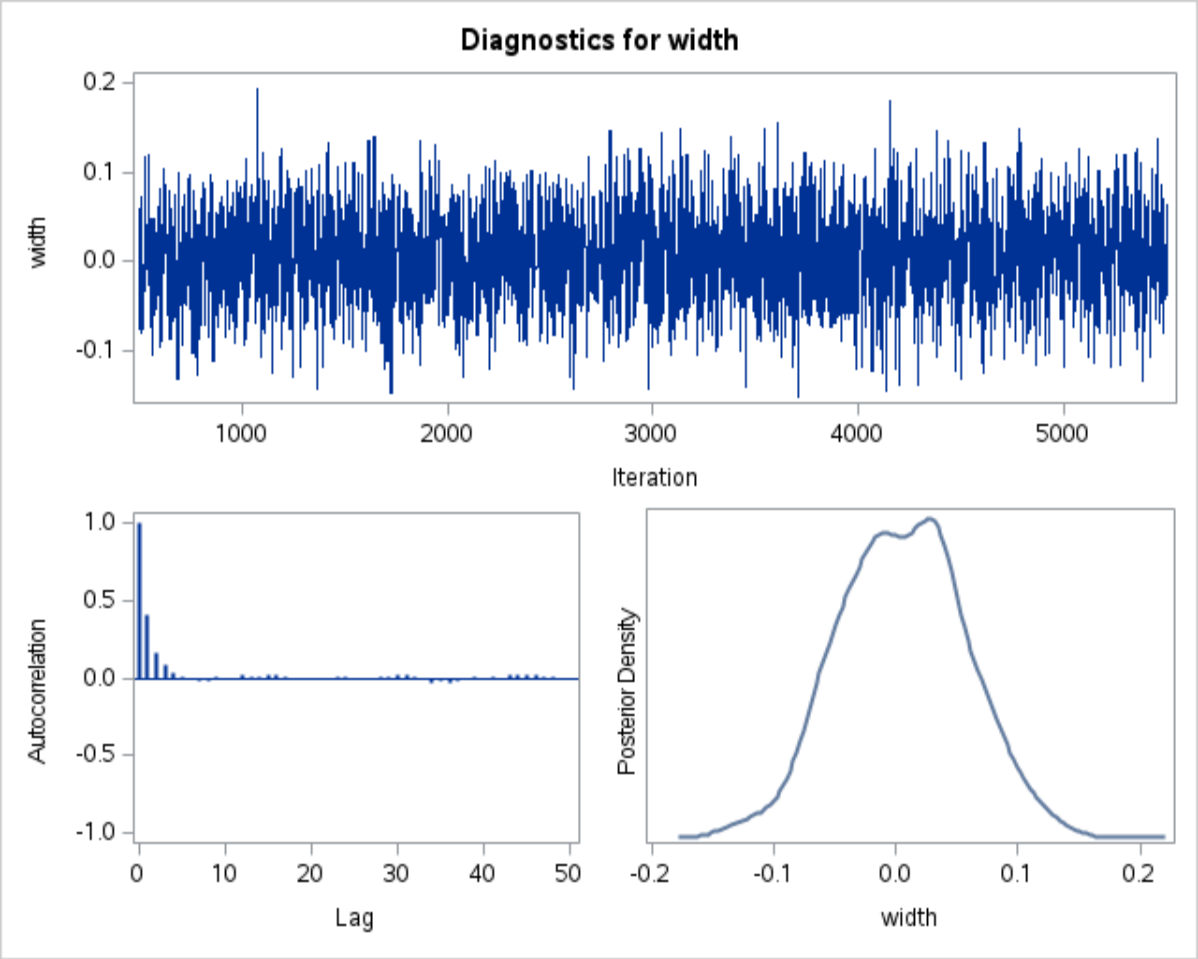

Diagnostics for color 2
color 2
0.75
0.50
0.25
0.00
-0.25
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-0.50
-0.25
0.00
0.25
0.50
0.75
color 2

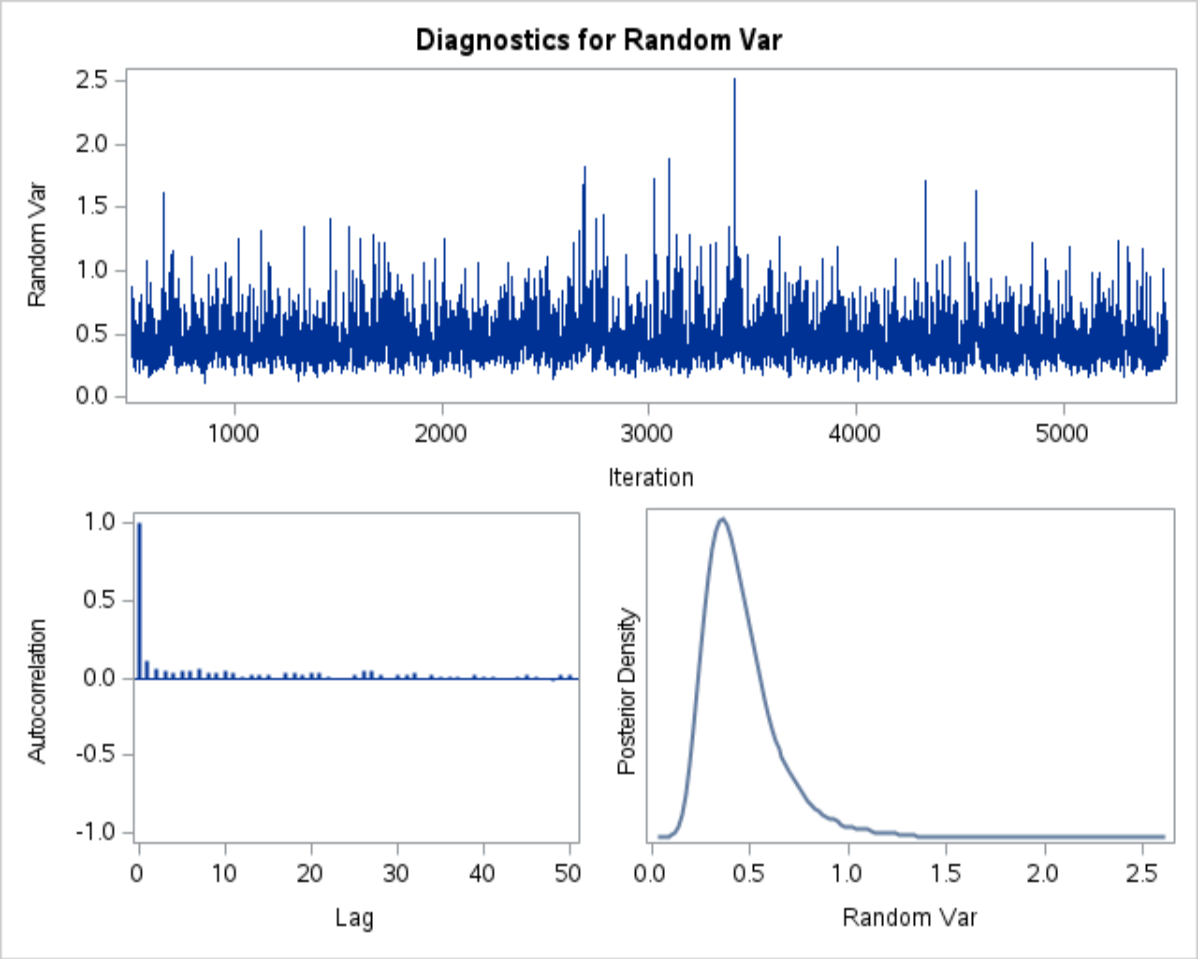

Diagnostics for color 3
color 3
0.50
0.25
0.00
-0.25
-0.50
-0.75
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-0.5
0.0
0.5
color 3


Diagnostics for spine 1
spine 1
0.4
0.2
0.0
-0.2
-0.4
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-0.4
-0.2
0.0
0.2
0.4
spine 1


Diagnostics for spine 2
spine 2
0.50
0.25
0.00
-0.25
-0.50
-0.75
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-1.0
-0.5
0.0
0.5
spine 2


Diagnostics for weight
weight
1.00
0.75
0.50
0.25
0.00
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0.00
0.25
0.50
0.75
1.00
1.25
weight


Diagnostics for width
width
0.2
0.1
0.0
-0.1
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-0.2
-0.1
0.0
0.1
0.2
width



Comparison of Frequentist Estimates and Posterior Means:

Parameter	GLIMMIX	BGLIMM
Intercept	-0.6317	-0.6361
Color1	0.3829	0.3608
Color2	0.1641	0.1612
Color3	-0.00907	-0.00556
Color4	0	0
Spine1	-0.03307	-0.0265
Spine2	-0.1886	-0.2025
Spine3	0	0
Weight	0.5395	0.5456
Width	0.006855	0.00533
VC Site	0.1494	0.4560

Heartrate Example:

Continuous Response (Normal) with Repeated Measures (MIXED)

In [8]:
```
data work.heartrate;
   input patient drug$ baseline hr1 hr5 hr15 hr30 hr1h;
   array hra{5} hr1 hr5 hr15 hr30 hr1h;
   do i = 1 to 5;
      if (i = 1) then hours = 1/60;
      else if (i = 2) then hours = 5/60;
      else if (i = 3) then hours = 15/60;
      else if (i = 4) then hours = 30/60;
      else hours = 1;
      heartrate = hra{i};
      output;
   end;
   drop i hr1 hr5 hr15 hr30 hr1h;
   datalines;
201  p    92   76   84   88   96   84
202  b    54   58   60   60   60   64
203  p    84   86   82   84   86   82
204  a    72   72   68   68   78   72
205  b    80   84   84   96   92   72
206  p    68   72   68   68   64   62
207  a   100  104  100   92   92   68
208  a    60   60   58   56   50   56
209  a    88  104   88   88   78   84
210  b    92   82   82   76   82   80
211  b    88   80   84   80   80   78
212  p   102   86   86   96   86   88
214  a    84   92  100   88   88   80
215  b   104  100   96   88   92   84
216  a    92   80   72   64   68   64
217  p    92   88   84   76   88   84
218  a    72   84   78   80   80   76
219  b    72  100   92   84   88   80
220  p    80   80   80   78   80   78
221  p    72   68   76   72   72   68
222  b    88   88   98   98   96   88
223  b    88   88   96   88   88   80
224  p    88   78   84   64   68   64
232  a    78   72   72   78   80   68
;
run;
```

```
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332        ods listing close;ods html5 (id=saspy_internal) file=_tomods1 options(bitm
ap_mode='inline') device=svg style=HTMLBlue;
332      ! ods graphics on / outputfmt=png;
NOTE: Writing HTML5(SASPY_INTERNAL) Body file: _TOMODS1
333
334        data work.heartrate;
335           input patient drug$ baseline hr1 hr5 hr15 hr30 hr1h;
336           array hra{5} hr1 hr5 hr15 hr30 hr1h;
337           do i = 1 to 5;
338              if (i = 1) then hours = 1/60;
339              else if (i = 2) then hours = 5/60;
340              else if (i = 3) then hours = 15/60;
341              else if (i = 4) then hours = 30/60;
342              else hours = 1;
343              heartrate = hra{i};
344              output;
345           end;
346           drop i hr1 hr5 hr15 hr30 hr1h;
347           datalines;

NOTE: The data set WORK.HEARTRATE has 120 observations and 5 variables.
NOTE: DATA statement used (Total process time):
      real time           0.00 seconds
      cpu time            0.01 seconds


372        ;
373        run;
374
375
376
377
378        ods html5 (id=saspy_internal) close;ods listing;
379

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380
```

In [9]:

```
proc mixed data=work.heartrate;
   class drug hours;
   model heartrate = baseline drug drug*baseline / solution ddfm=kr2;
   repeated hours/ type=un subject=patient;
run;
```

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.HEARTRATE
Dependent Variable	heartrate
Covariance Structure	Unstructured
Subject Effect	patient
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Kenward-Roger2
Degrees of Freedom Method	Kenward-Roger2

Class Level Information		
Class	Levels	Values
drug	3	a b p
hours	5	0.0166666667 0.0833333333 0.25 0.5 1

Dimensions	
Covariance Parameters	15
Columns in X	8
Columns in Z	0
Subjects	24
Max Obs per Subject	5

Number of Observations	
Number of Observations Read	120
Number of Observations Used	120
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	853.84973139	
1	2	780.74069548	0.00157255
2	1	780.22026660	0.00015186
3	1	780.17341828	0.00000304

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
4	1	780.17253674	0.00000000

Convergence criteria met.

Covariance Parameter Estimates		
Cov Parm	Subject	Estimate
UN(1,1)	patient	121.93
UN(2,1)	patient	88.8569
UN(2,2)	patient	94.6168
UN(3,1)	patient	64.1357
UN(3,2)	patient	66.2286
UN(3,3)	patient	92.3397
UN(4,1)	patient	60.5103
UN(4,2)	patient	65.9367
UN(4,3)	patient	75.3812
UN(4,4)	patient	87.2560
UN(5,1)	patient	18.9874
UN(5,2)	patient	17.9136
UN(5,3)	patient	39.6907
UN(5,4)	patient	36.5657
UN(5,5)	patient	61.8748

Fit Statistics	
-2 Res Log Likelihood	780.2
AIC (Smaller is Better)	810.2
AICC (Smaller is Better)	815.1
BIC (Smaller is Better)	827.8

Null Model Likelihood Ratio Test		
DF	Chi-Square	Pr > ChiSq
14	73.68	<.0001

Solution for Fixed Effects						
Effect	drug	Estimate	Standard Error	DF	t Value	Pr > |t|

Solution for Fixed Effects

Effect	drug	Estimate	Standard Error	DF	t Value	Pr > |t|
Intercept		26.3125	24.6028	18	1.07	0.2990
baseline		0.6081	0.2881	18	2.11	0.0491
drug	a	10.3427	32.0594	18	0.32	0.7507
drug	b	15.2890	30.6136	18	0.50	0.6235
drug	p	0	.	.	.	.
baseline*drug	a	-0.1431	0.3826	18	-0.37	0.7128
baseline*drug	b	-0.1327	0.3600	18	-0.37	0.7166
baseline*drug	p	0	.	.	.	.

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
baseline	1	18	12.42	0.0024
drug	2	18	0.12	0.8834
baseline*drug	2	18	0.09	0.9179

In [10]:
```
proc bglimm data=work.heartrate seed=8675309 diag=all plots=all;
   class drug hours patient;
   model heartrate = baseline drug drug*baseline / dist=normal;
   repeated hours/ type=un sub=patient;
run;
```

The SAS System

The BGLIMM Procedure

Model Information	
Data Set	WORK.HEARTRATE
Response Variable	heartrate
Distribution	Normal
Link Function	Identity
Fixed Effects Included	Yes
Random Effects Included	No
Sampling Algorithm	Conjugate
Burn-In Size	500
Simulation Size	5000
Thinning	1
Random Number Seed	8675309
Number of Threads	1

Class Level Information		
Class	Levels	Values
drug	3	a b p
hours	5	0.0166666667 0.0833333333 0.25 0.5 1
patient	24	201 202 203 204 205 206 207 208 209 210 211 212 214 215 216 217 218 219 220 221 222 223 224 232

Number of Observations	
Number of Observations Read	120
Number of Observations Used	120

Priors for Fixed Effects	
Parameter	Prior
Intercept	Constant
baseline	Constant
drug a	Constant
drug b	Constant
baseline*drug a	Constant
baseline*drug b	Constant

Priors for Scale and Covariance Parameters	
Parameter	**Prior**
Residual Cov	Inverse Wishart (DF=8, Scale=8)

Posterior Summaries and Intervals					
Parameter	**N**	**Mean**	**Standard Deviation**	**95% HPD Interval**	
Intercept	5000	26.6251	17.3101	-4.6967	63.0853
baseline	5000	0.6047	0.2011	0.1805	0.9723
drug a	5000	9.5789	26.0936	-43.9401	59.3345
drug b	5000	15.0200	22.0831	-28.4949	58.8145
drug p	0	.	.	.	.
baseline*drug a	5000	-0.1331	0.3239	-0.7473	0.5337
baseline*drug b	5000	-0.1287	0.2630	-0.6272	0.4156
baseline*drug p	0	.	.	.	.
Residual UN(1,1)	5000	113.0	44.8455	42.5884	201.7
Residual UN(2,1)	5000	82.3507	38.2465	24.6172	160.5
Residual UN(2,2)	5000	88.0431	35.8068	33.7373	161.1
Residual UN(3,1)	5000	59.5948	31.5897	9.8821	122.9
Residual UN(3,2)	5000	61.6034	28.5501	16.0573	117.4
Residual UN(3,3)	5000	86.1366	28.0398	39.5599	140.0
Residual UN(4,1)	5000	56.1634	31.6483	5.9291	117.4
Residual UN(4,2)	5000	61.2318	28.9605	16.0253	118.7
Residual UN(4,3)	5000	70.0939	26.3206	27.9061	121.5
Residual UN(4,4)	5000	81.2360	27.9096	38.6838	135.9
Residual UN(5,1)	5000	18.5105	20.0519	-16.7690	61.6879
Residual UN(5,2)	5000	17.6011	17.4506	-13.5262	53.9192
Residual UN(5,3)	5000	37.7513	18.8746	7.6873	75.5229
Residual UN(5,4)	5000	34.8159	17.7153	3.3200	69.5687
Residual UN(5,5)	5000	58.9579	24.8244	24.1370	106.3

Posterior Autocorrelations				
Parameter	**Lag 1**	**Lag 5**	**Lag 10**	**Lag 50**
Intercept	0.0570	0.0249	0.0303	-0.0023
baseline	0.0468	0.0190	0.0304	-0.0071
drug a	0.2796	0.0729	0.0325	0.0239
drug b	0.1112	0.0356	0.0103	0.0046

Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
drug p	.	.	.	.
baseline*drug a	0.3372	0.0879	0.0326	0.0211
baseline*drug b	0.1347	0.0385	0.0095	0.0023
baseline*drug p	.	.	.	.
Residual UN(1,1)	0.4569	0.1225	0.0068	0.0011
Residual UN(2,1)	0.5165	0.1362	0.0258	-0.0009
Residual UN(2,2)	0.4919	0.1267	0.0412	-0.0025
Residual UN(3,1)	0.4491	0.0952	0.0312	0.0084
Residual UN(3,2)	0.4271	0.0820	0.0419	0.0063
Residual UN(3,3)	0.2258	0.0221	0.0276	0.0056
Residual UN(4,1)	0.4933	0.1232	0.0352	0.0093
Residual UN(4,2)	0.4691	0.1074	0.0481	0.0117
Residual UN(4,3)	0.2832	0.0539	0.0417	0.0149
Residual UN(4,4)	0.2911	0.0595	0.0411	0.0229
Residual UN(5,1)	0.3406	0.0470	0.0182	0.0137
Residual UN(5,2)	0.3086	0.0230	0.0172	-0.0060
Residual UN(5,3)	0.2418	0.0068	0.0179	0.0098
Residual UN(5,4)	0.2500	0.0082	0.0169	-0.0028
Residual UN(5,5)	0.4732	0.0959	0.0095	0.0059

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	3761.9	1.3291	0.7524
baseline	4571.9	1.0936	0.9144
drug a	1545.8	3.2346	0.3092
drug b	2928.6	1.7073	0.5857
drug p	.	.	.
baseline*drug a	1392.2	3.5914	0.2784
baseline*drug b	2763.2	1.8095	0.5526
baseline*drug p	.	.	.
Residual UN(1,1)	1236.9	4.0424	0.2474
Residual UN(2,1)	1093.2	4.5738	0.2186
Residual UN(2,2)	1116.7	4.4777	0.2233
Residual UN(3,1)	1278.6	3.9107	0.2557

Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
Residual UN(3,2)	1330.1	3.7591	0.2660
Residual UN(3,3)	2440.9	2.0485	0.4882
Residual UN(4,1)	1138.7	4.3911	0.2277
Residual UN(4,2)	1196.0	4.1807	0.2392
Residual UN(4,3)	1983.0	2.5215	0.3966
Residual UN(4,4)	1696.9	2.9465	0.3394
Residual UN(5,1)	1888.0	2.6483	0.3776
Residual UN(5,2)	2154.7	2.3205	0.4309
Residual UN(5,3)	2710.3	1.8448	0.5421
Residual UN(5,4)	2687.2	1.8607	0.5374
Residual UN(5,5)	1391.4	3.5935	0.2783

Monte Carlo Standard Errors			
Parameter	MCSE	Standard Deviation	MCSE/SD
Intercept	0.2822	17.3101	0.0163
baseline	0.00297	0.2011	0.0148
drug a	0.6637	26.0936	0.0254
drug b	0.4081	22.0831	0.0185
drug p	.	.	.
baseline*drug a	0.00868	0.3239	0.0268
baseline*drug b	0.00500	0.2630	0.0190
baseline*drug p	.	.	.
Residual UN(1,1)	1.2751	44.8455	0.0284
Residual UN(2,1)	1.1568	38.2465	0.0302
Residual UN(2,2)	1.0715	35.8068	0.0299
Residual UN(3,1)	0.8835	31.5897	0.0280
Residual UN(3,2)	0.7828	28.5501	0.0274
Residual UN(3,3)	0.5675	28.0398	0.0202
Residual UN(4,1)	0.9379	31.6483	0.0296
Residual UN(4,2)	0.8374	28.9605	0.0289
Residual UN(4,3)	0.5911	26.3206	0.0225
Residual UN(4,4)	0.6775	27.9096	0.0243
Residual UN(5,1)	0.4615	20.0519	0.0230

Monte Carlo Standard Errors			
Parameter	MCSE	Standard Deviation	MCSE/SD
Residual UN(5,2)	0.3759	17.4506	0.0215
Residual UN(5,3)	0.3625	18.8746	0.0192
Residual UN(5,4)	0.3417	17.7153	0.0193
Residual UN(5,5)	0.6655	24.8244	0.0268

Geweke Diagnostics		
Parameter	z	Pr > |z|
Intercept	0.0394	0.9685
baseline	-0.0675	0.9462
drug a	-0.2494	0.8030
drug b	-0.4477	0.6544
drug p	.	.
baseline*drug a	0.1832	0.8547
baseline*drug b	0.4513	0.6518
baseline*drug p	.	.
Residual UN(1,1)	0.7854	0.4322
Residual UN(2,1)	0.5858	0.5580
Residual UN(2,2)	0.4917	0.6229
Residual UN(3,1)	0.8063	0.4200
Residual UN(3,2)	0.6498	0.5158
Residual UN(3,3)	0.6659	0.5055
Residual UN(4,1)	0.7147	0.4748
Residual UN(4,2)	0.5946	0.5521
Residual UN(4,3)	0.8636	0.3878
Residual UN(4,4)	0.7499	0.4533
Residual UN(5,1)	1.3171	0.1878
Residual UN(5,2)	1.1225	0.2617
Residual UN(5,3)	1.1777	0.2389
Residual UN(5,4)	1.1873	0.2351
Residual UN(5,5)	0.7208	0.4710

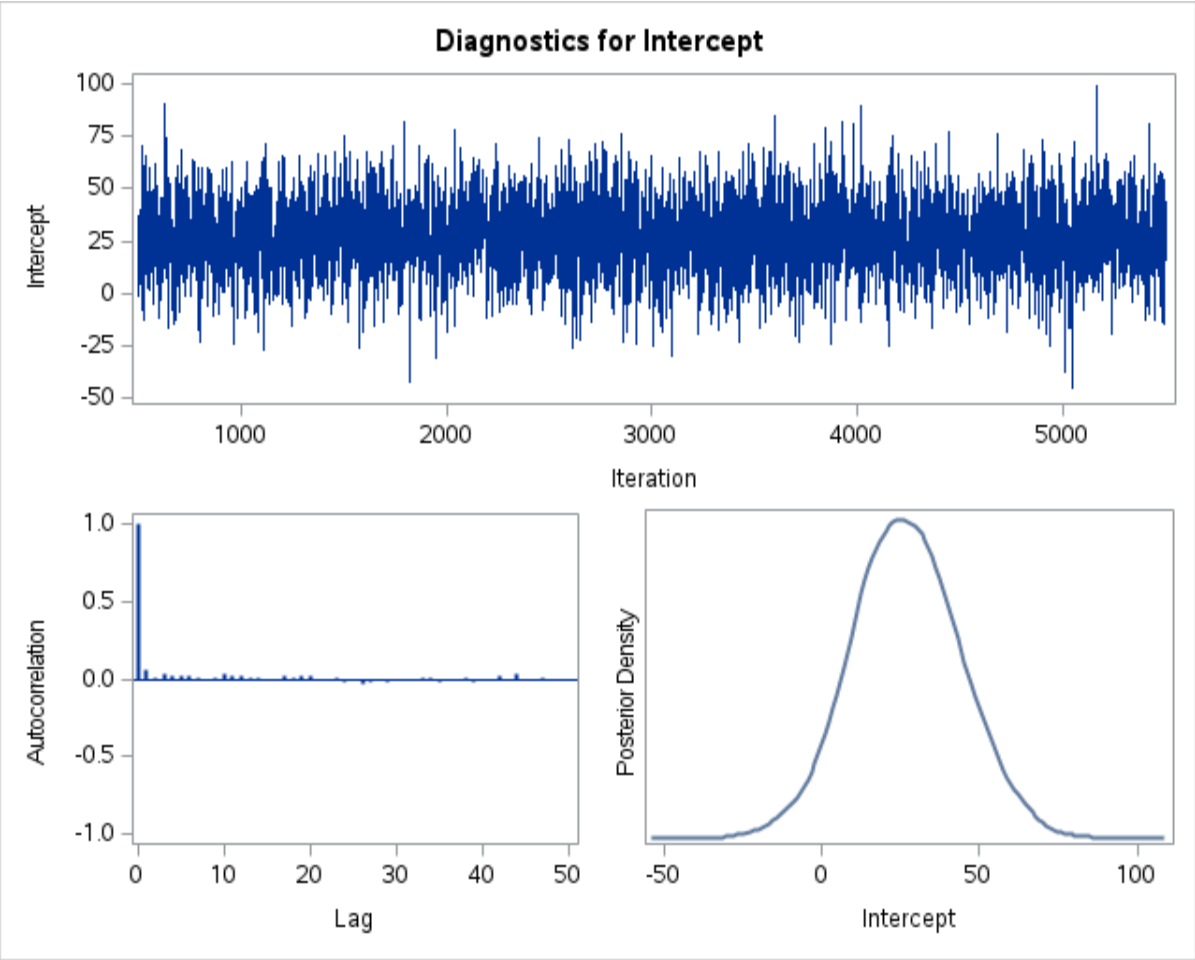
Raftery-Lewis Diagnostics				
Quantile=0.025 Accuracy=+/-0.005 Probability=0.95 Epsilon=0.001				
Parameter	Number of Samples			Dependence Factor
	Burn-In	Total	Minimum	
Intercept	2	3742	3746	0.9989
baseline	2	3995	3746	1.0665
drug a	3	4198	3746	1.1207
drug b	2	3930	3746	1.0491
drug p	.	.	.	.
baseline*drug a	3	4268	3746	1.1393
baseline*drug b	3	4304	3746	1.1490
baseline*drug p	.	.	.	.
Residual UN(1,1)	7	8931	3746	2.3841
Residual UN(2,1)	7	9422	3746	2.5152
Residual UN(2,2)	3	4559	3746	1.2170
Residual UN(3,1)	3	4063	3746	1.0846
Residual UN(3,2)	3	4268	3746	1.1393
Residual UN(3,3)	3	4130	3746	1.1025
Residual UN(4,1)	3	4063	3746	1.0846
Residual UN(4,2)	3	4130	3746	1.1025
Residual UN(4,3)	3	4198	3746	1.1207
Residual UN(4,4)	3	4063	3746	1.0846
Residual UN(5,1)	2	3742	3746	0.9989
Residual UN(5,2)	2	3866	3746	1.0320
Residual UN(5,3)	2	3742	3746	0.9989
Residual UN(5,4)	2	3803	3746	1.0152
Residual UN(5,5)	2	3866	3746	1.0320

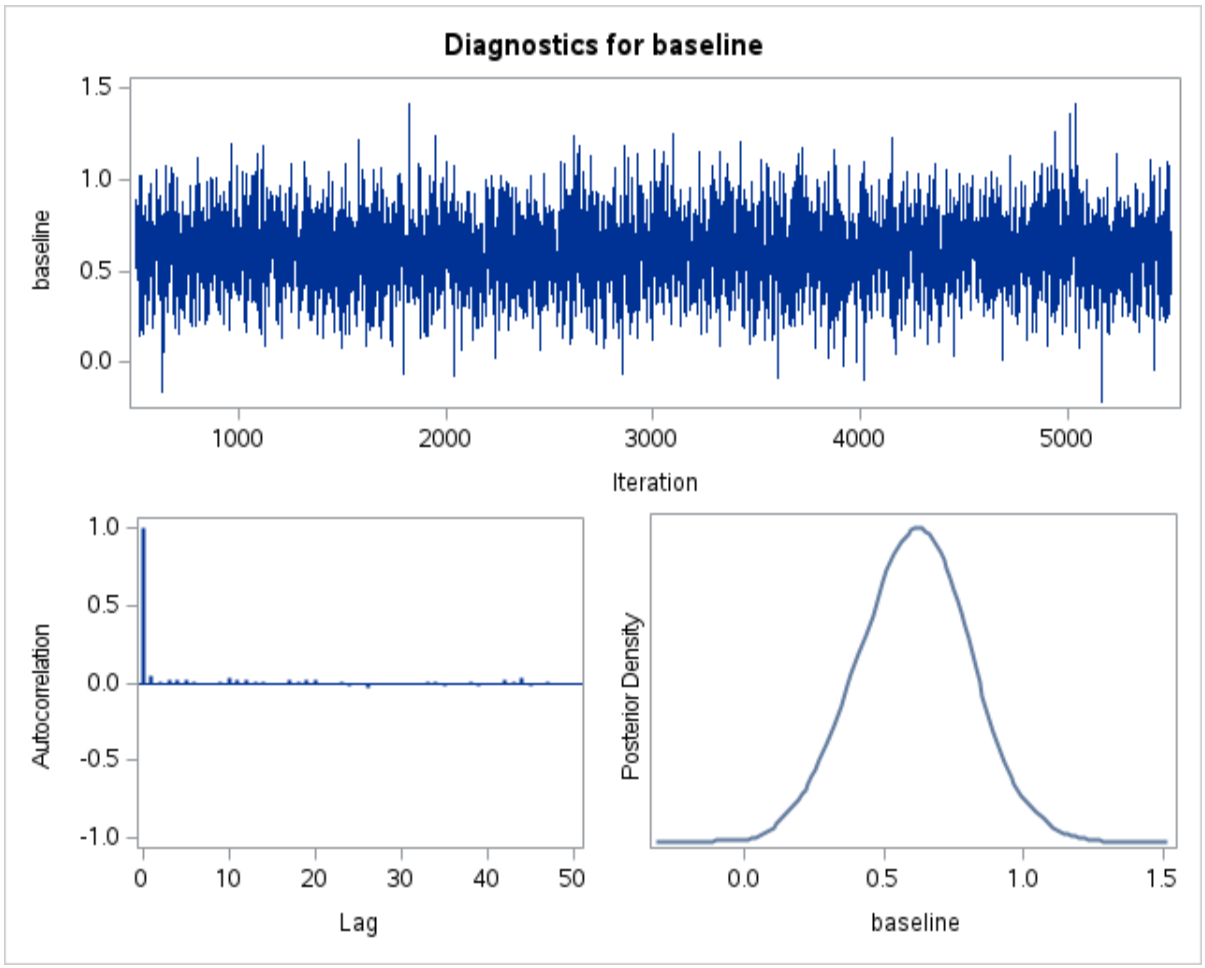
Heidelberger-Welch Diagnostics								
Parameter	Stationarity Test				Half-Width Test			
	Cramer-von Mises Stat	p-Value	Test Outcome	Iterations Discarded	Half-Width	Mean	Relative Half-Width	Test Outcome
Intercept	0.0868	0.6538	Passed	0	0.5825	26.6251	0.0219	Passed
baseline	0.0852	0.6622	Passed	0	0.00636	0.6047	0.0105	Passed
drug a	0.0951	0.6096	Passed	0	1.1968	9.5789	0.1249	Failed

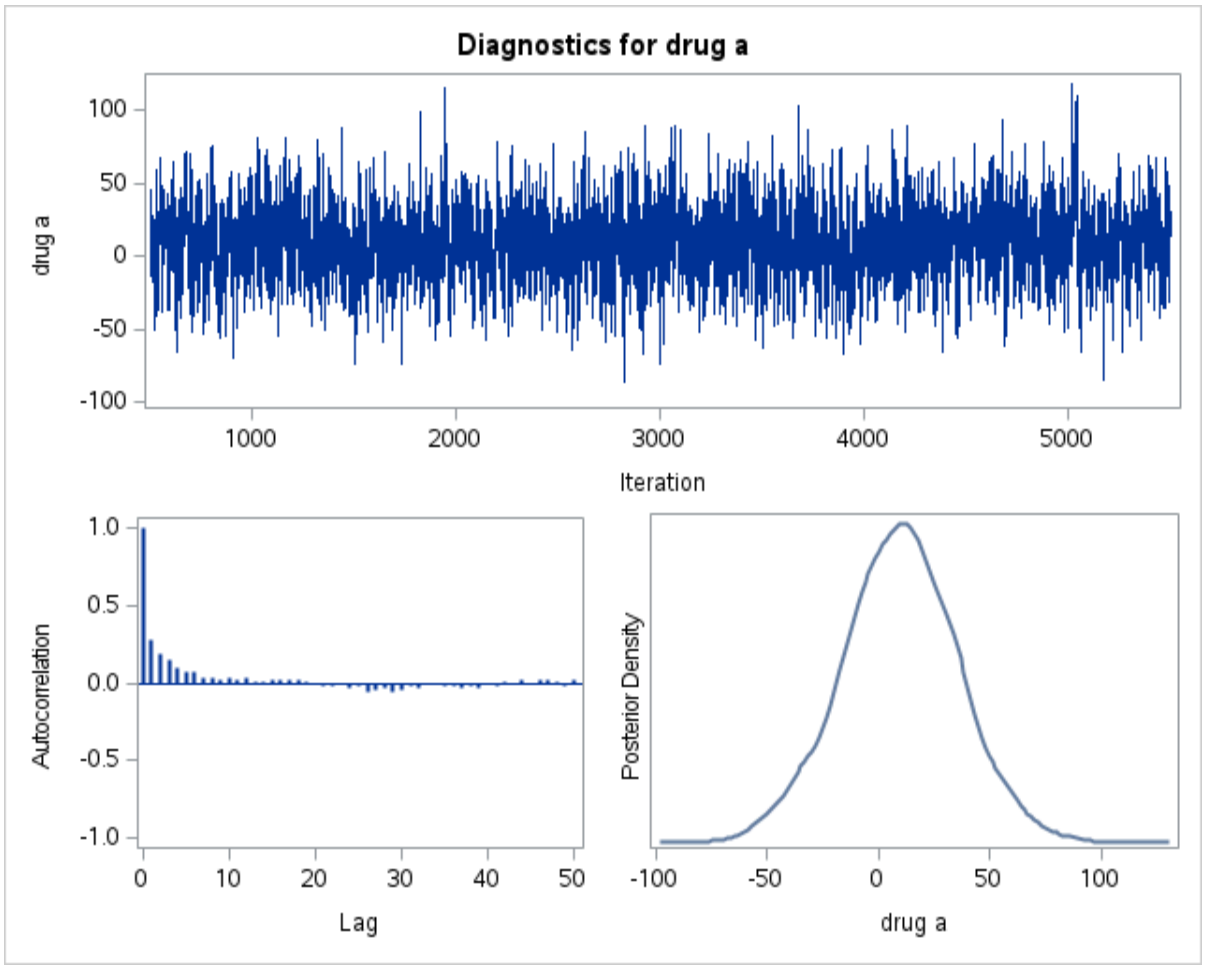
Heidelberger-Welch Diagnostics								
Parameter	Stationarity Test				Half-Width Test			
	Cramer-von Mises Stat	p-Value	Test Outcome	Iterations Discarded	Half-Width	Mean	Relative Half-Width	Test Outcome
drug b	0.1094	0.5407	Passed	0	0.7529	15.0200	0.0501	Passed
drug p	.	.		.	.	.	.	
baseline*drug a	0.0820	0.6804	Passed	0	0.0157	-0.1331	-0.1182	Failed
baseline*drug b	0.1042	0.5644	Passed	0	0.00907	-0.1287	-0.0705	Passed
baseline*drug p	.	.		.	.	.	.	
Residual UN(1,1)	0.0415	0.9251	Passed	0	2.6235	113.0	0.0232	Passed
Residual UN(2,1)	0.0400	0.9334	Passed	0	2.3227	82.3507	0.0282	Passed
Residual UN(2,2)	0.0429	0.9179	Passed	0	2.1136	88.0431	0.0240	Passed
Residual UN(3,1)	0.0575	0.8299	Passed	0	1.7603	59.5948	0.0295	Passed
Residual UN(3,2)	0.0484	0.8858	Passed	0	1.5168	61.6034	0.0246	Passed
Residual UN(3,3)	0.0514	0.8678	Passed	0	1.0813	86.1366	0.0126	Passed
Residual UN(4,1)	0.0518	0.8652	Passed	0	1.8960	56.1634	0.0338	Passed
Residual UN(4,2)	0.0466	0.8968	Passed	0	1.6249	61.2318	0.0265	Passed
Residual UN(4,3)	0.0854	0.6611	Passed	0	1.1964	70.0939	0.0171	Passed
Residual UN(4,4)	0.0772	0.7080	Passed	0	1.3300	81.2360	0.0164	Passed
Residual UN(5,1)	0.0958	0.6057	Passed	0	0.9363	18.5105	0.0506	Passed
Residual UN(5,2)	0.0710	0.7456	Passed	0	0.7735	17.6011	0.0439	Passed
Residual UN(5,3)	0.1089	0.5431	Passed	0	0.7241	37.7513	0.0192	Passed
Residual UN(5,4)	0.0841	0.6685	Passed	0	0.6922	34.8159	0.0199	Passed
Residual UN(5,5)	0.1008	0.5810	Passed	0	1.3200	58.9579	0.0224	Passed

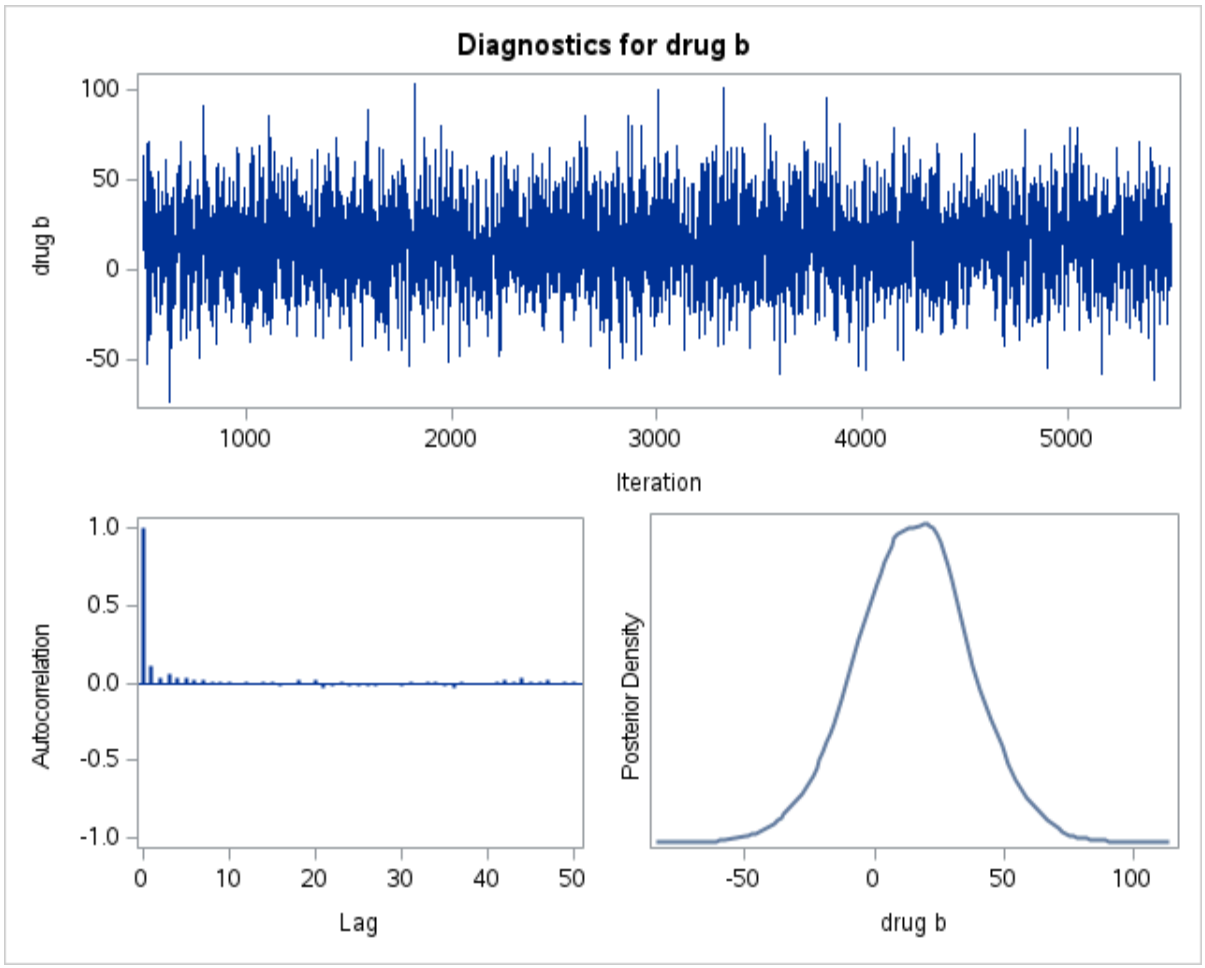
The SAS System

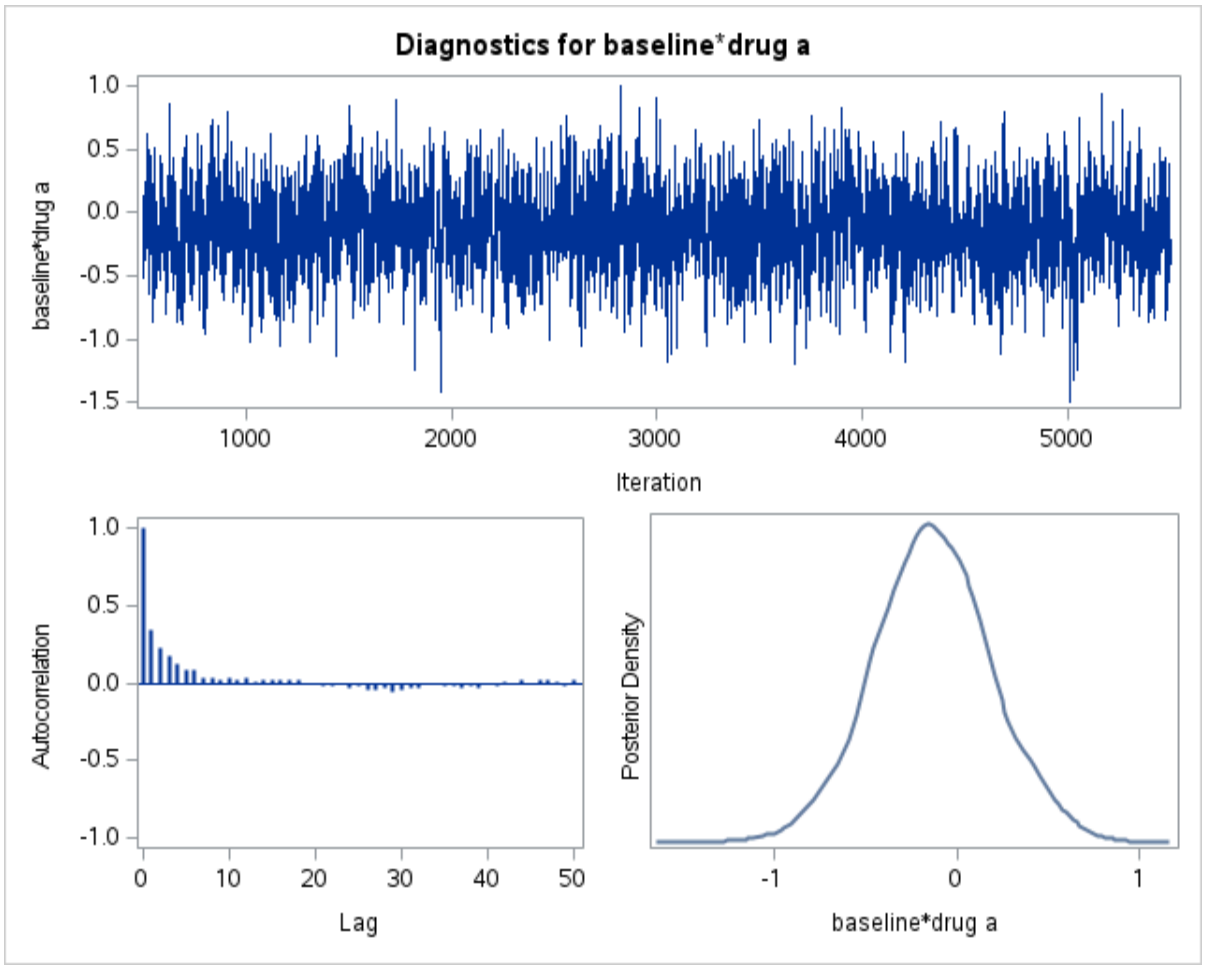
The BGLIMM Procedure

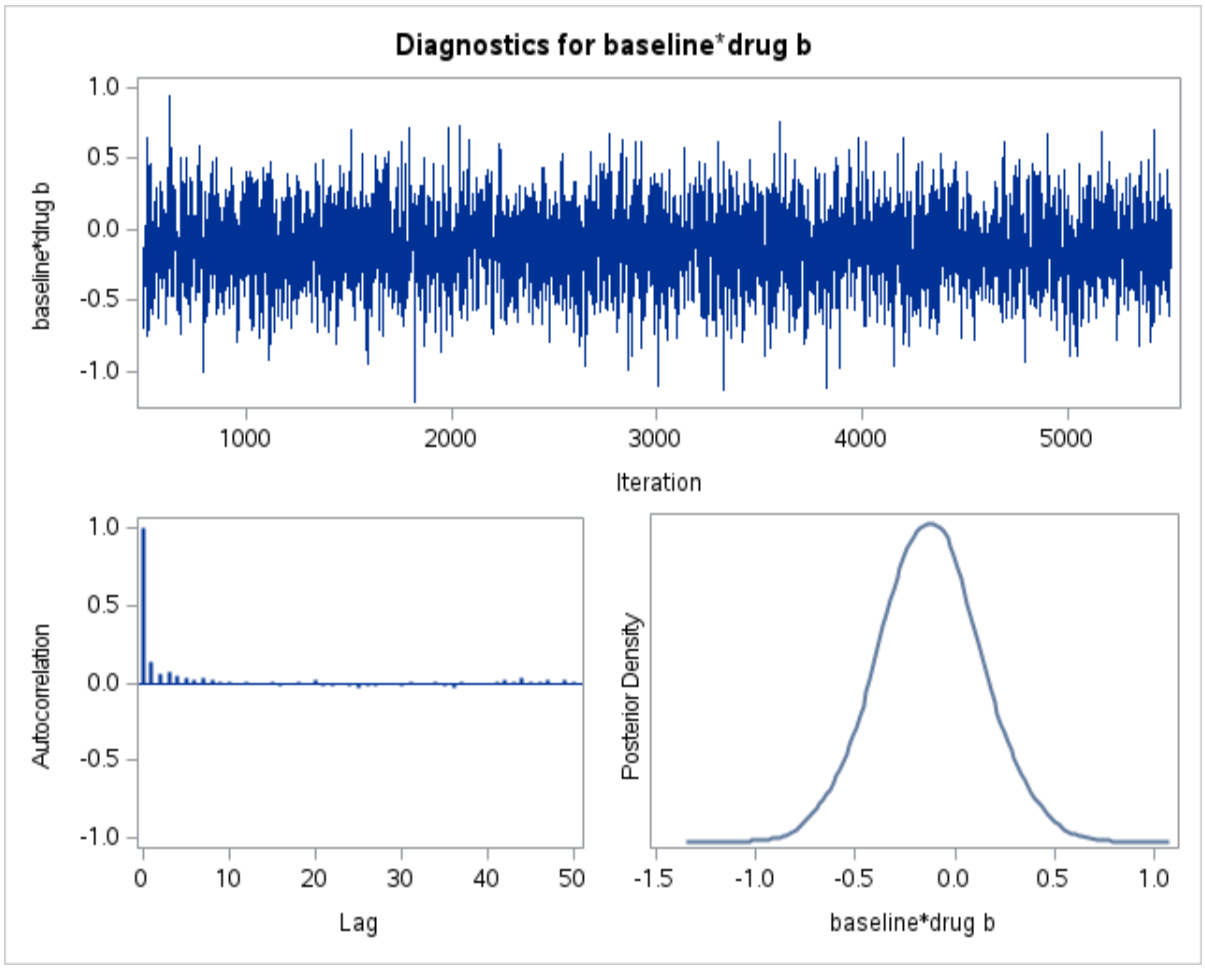


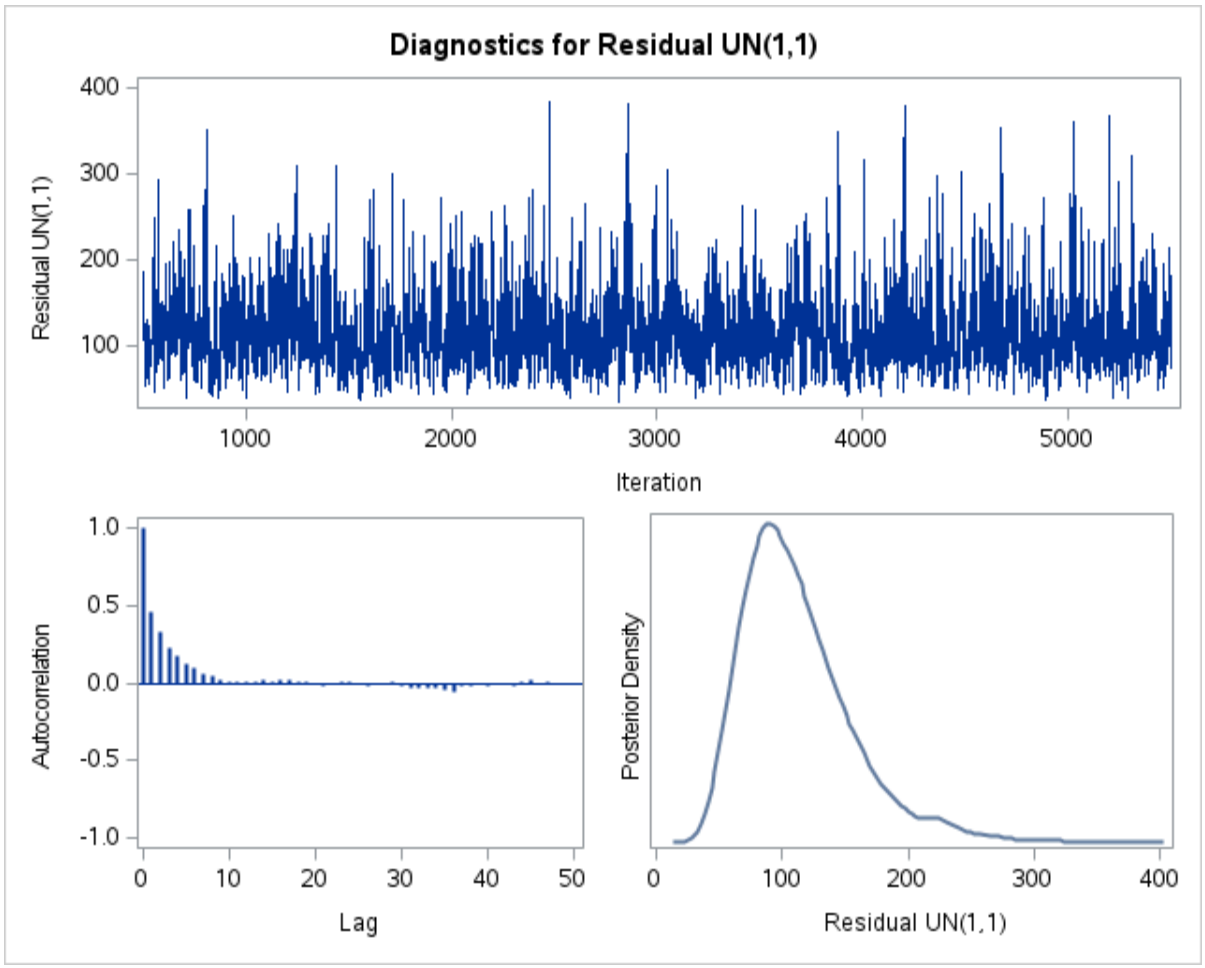

Diagnostics for baseline
baseline
1.5
1.0
0.5
0.0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0.0
0.5
1.0
1.5
baseline

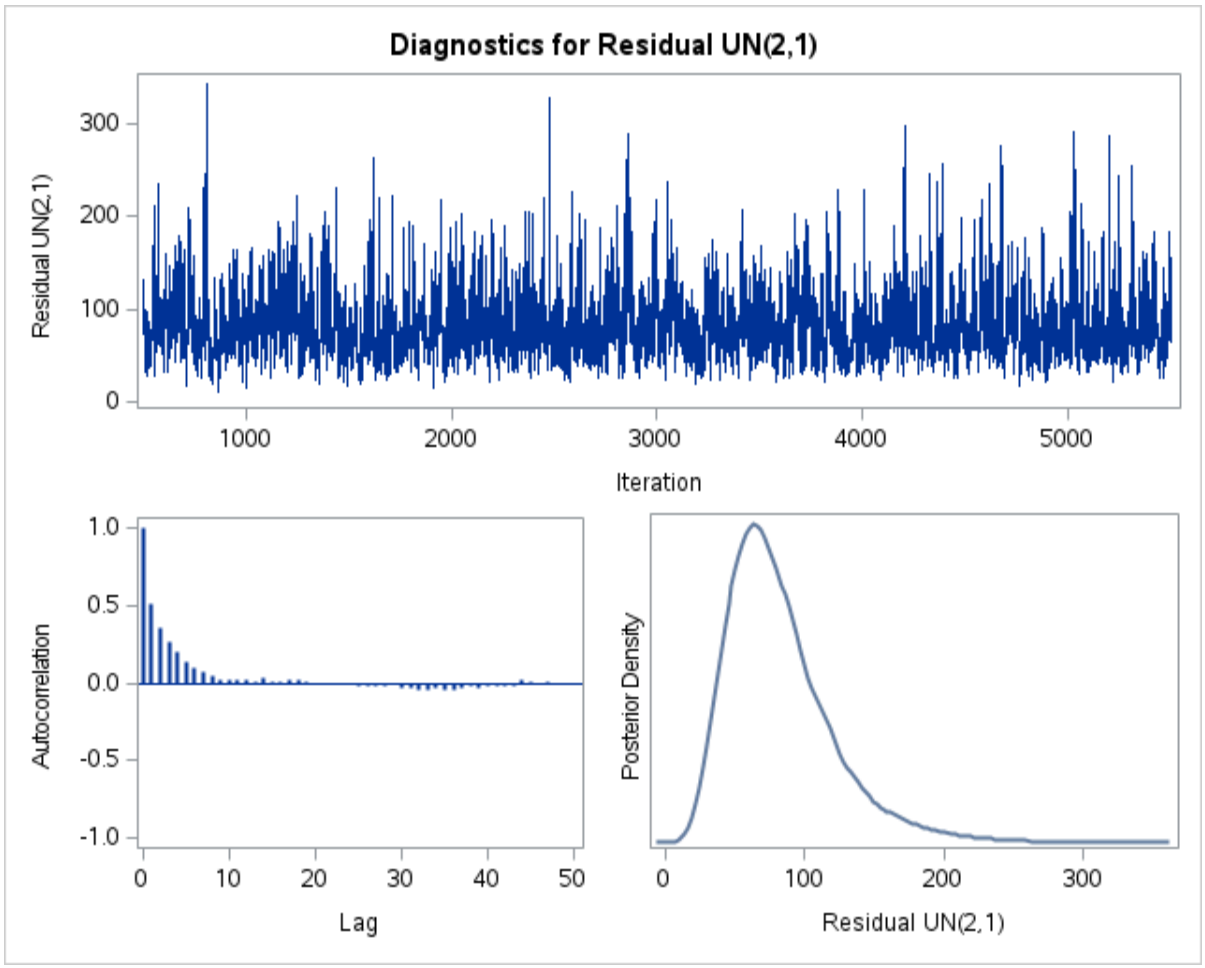

Diagnostics for drug a
drug a
100
50
0
-50
-100
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-100
-50
0
50
100
drug a

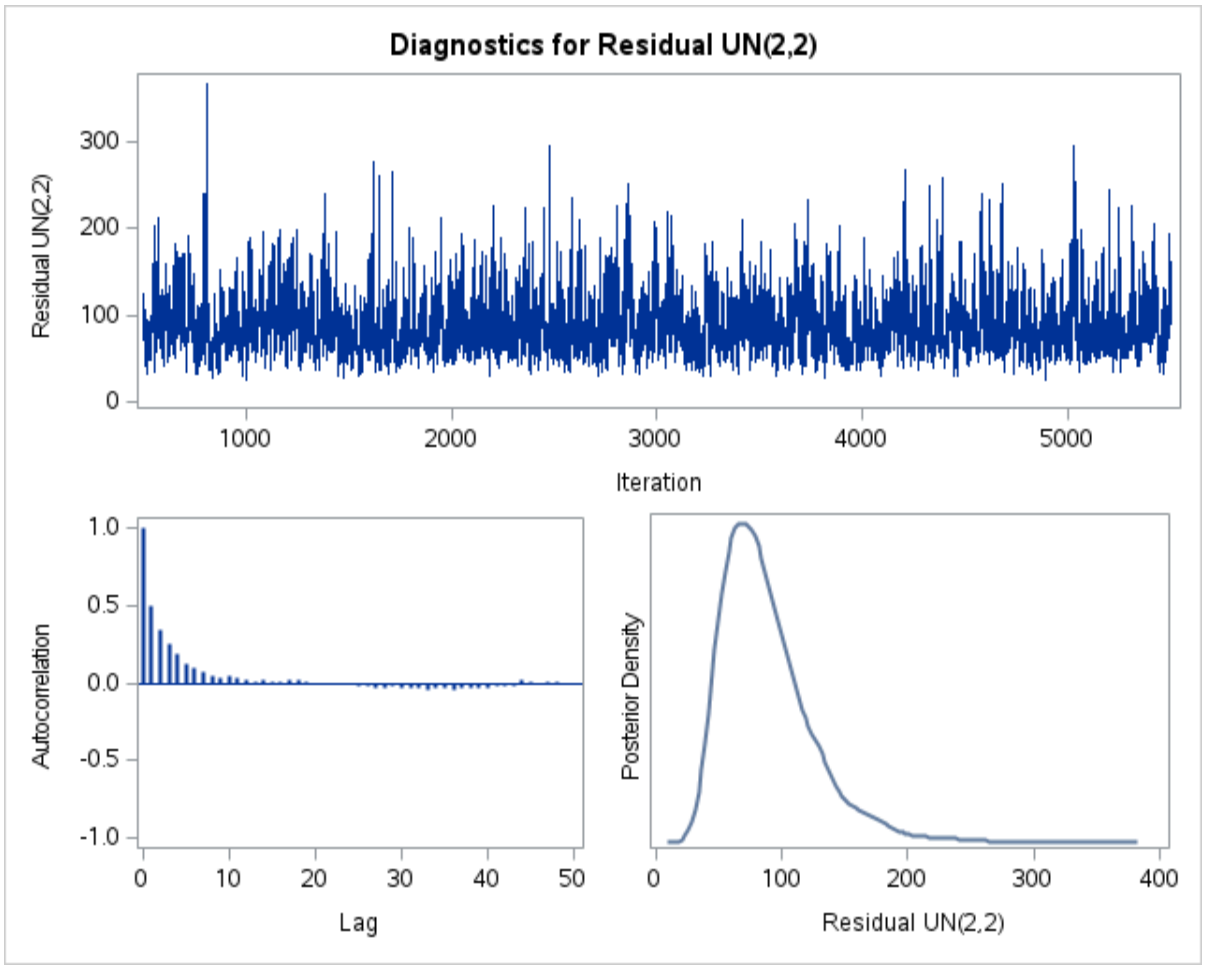

Diagnostics for drug b
drug b
100
50
0
-50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-50
0
50
100
drug b

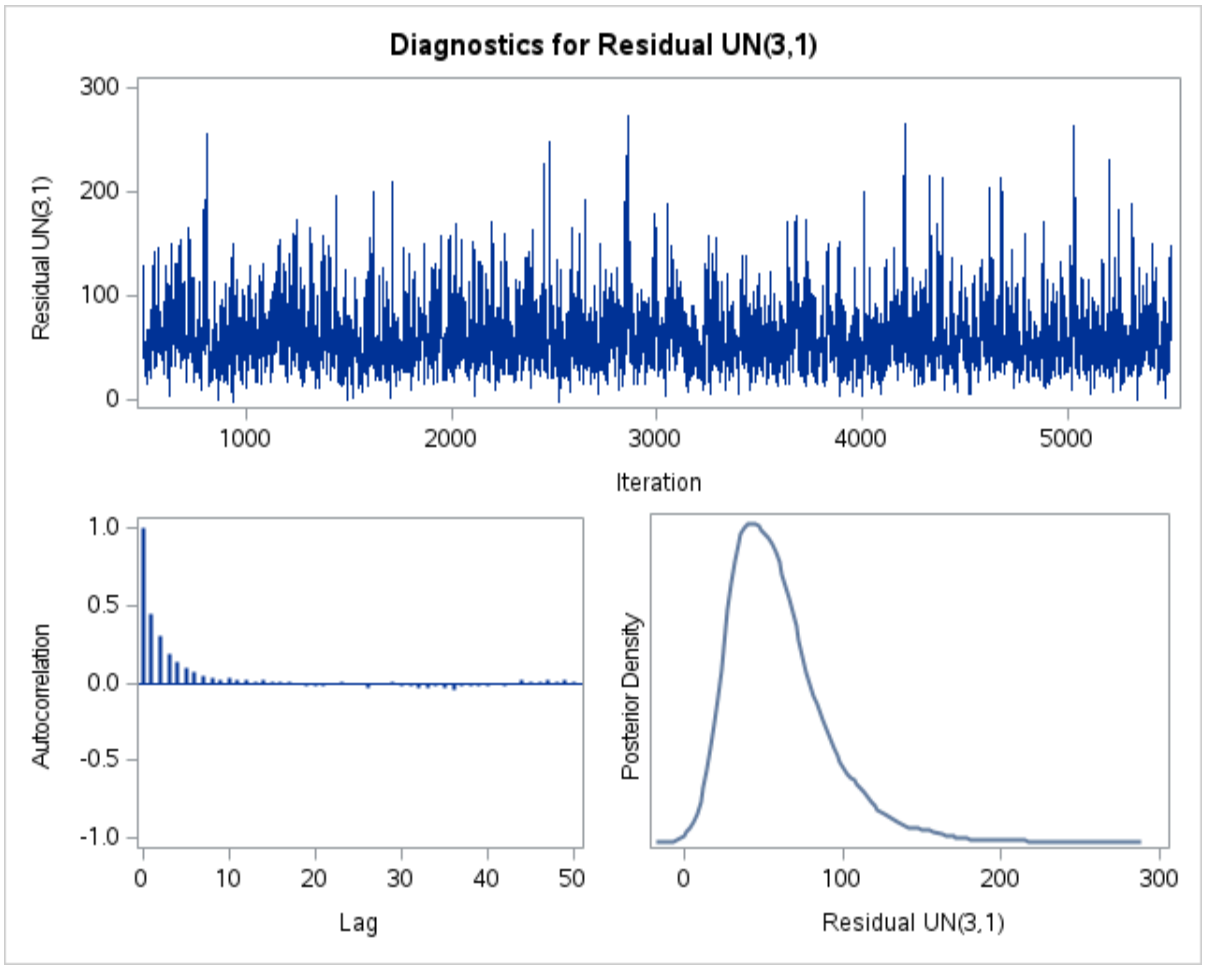

Diagnostics for baseline*drug a
baseline*drug a
1.0
0.5
0.0
-0.5
-1.0
-1.5
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-1
0
1
baseline*drug a

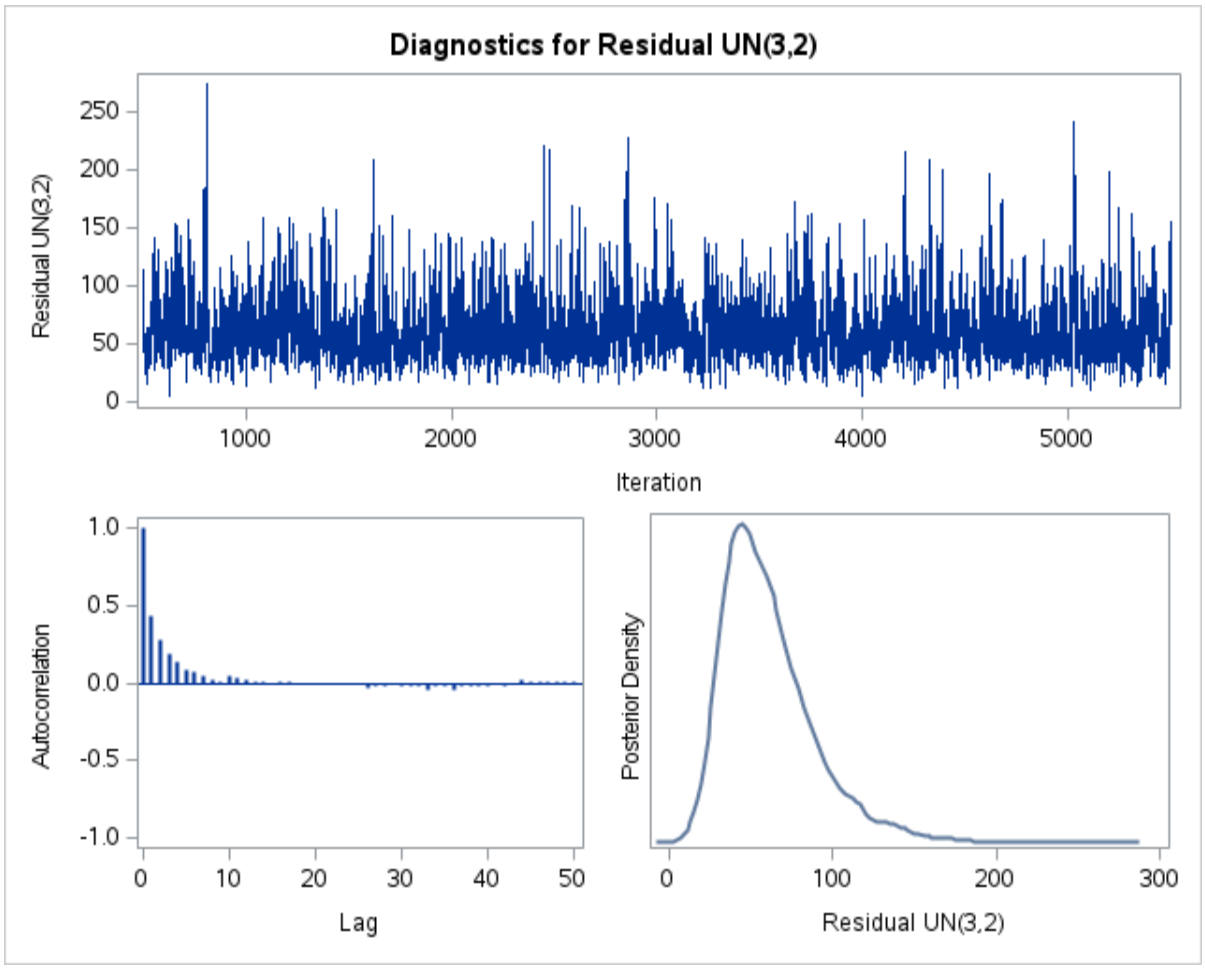

Diagnostics for baseline*drug b
baseline*drug b
1.0
0.5
0.0
-0.5
-1.0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-1.5
-1.0
-0.5
0.0
0.5
1.0
baseline*drug b

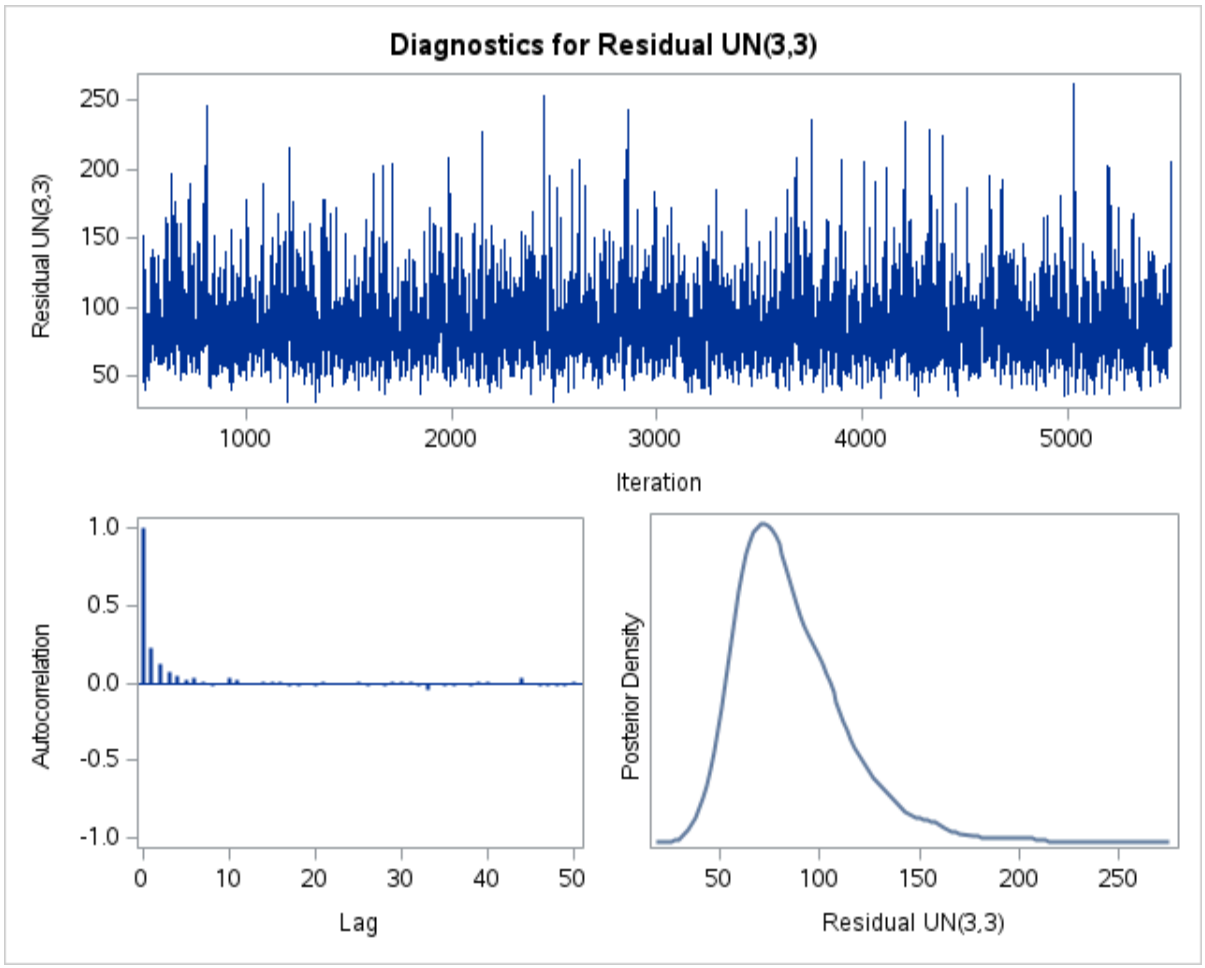

Diagnostics for Residual UN(1,1)
Residual UN(1,1)
400
300
200
100
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
400
Residual UN(1,1)

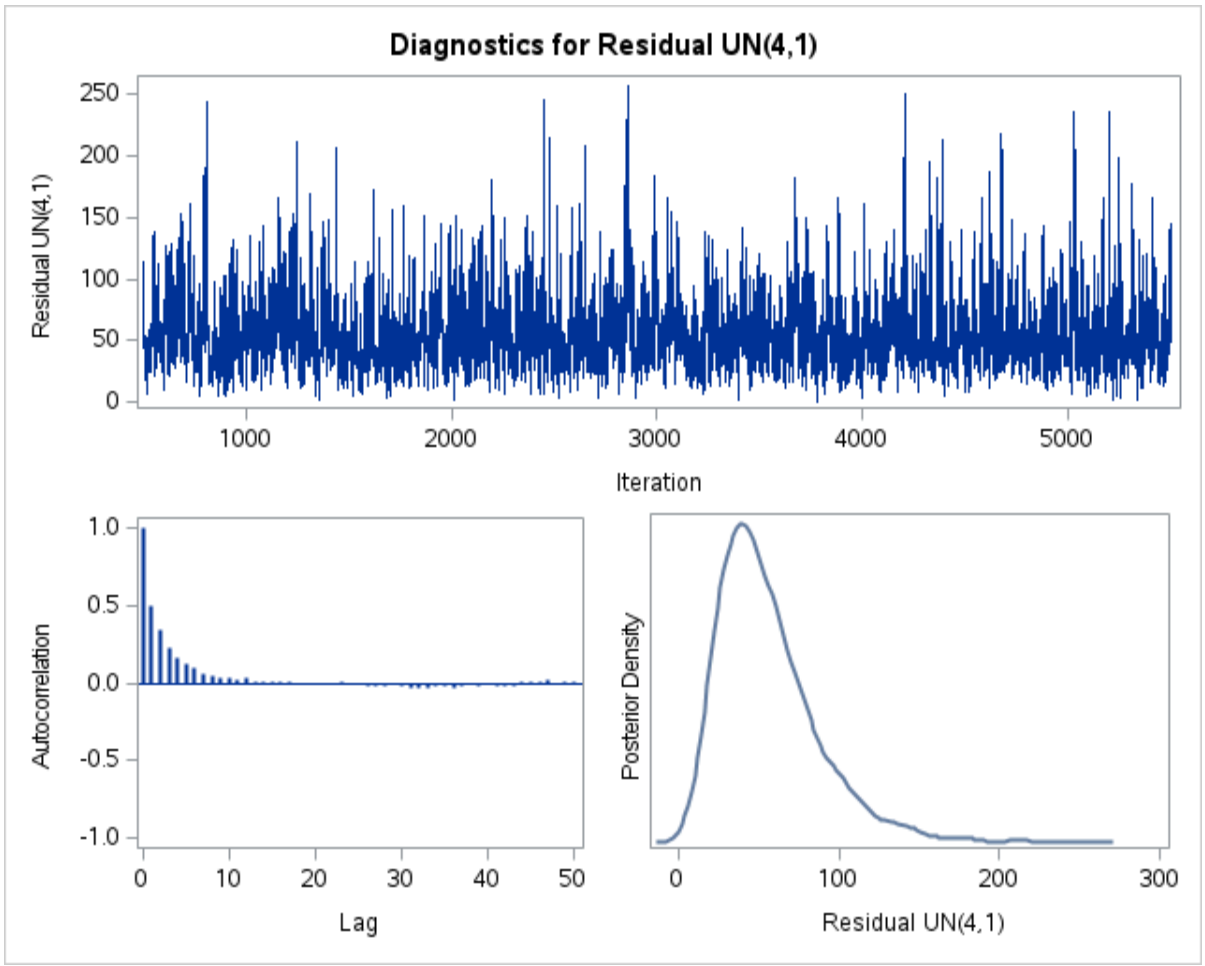

Diagnostics for Residual UN(2,1)
Residual UN(2,1)
300
200
100
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(2,1)

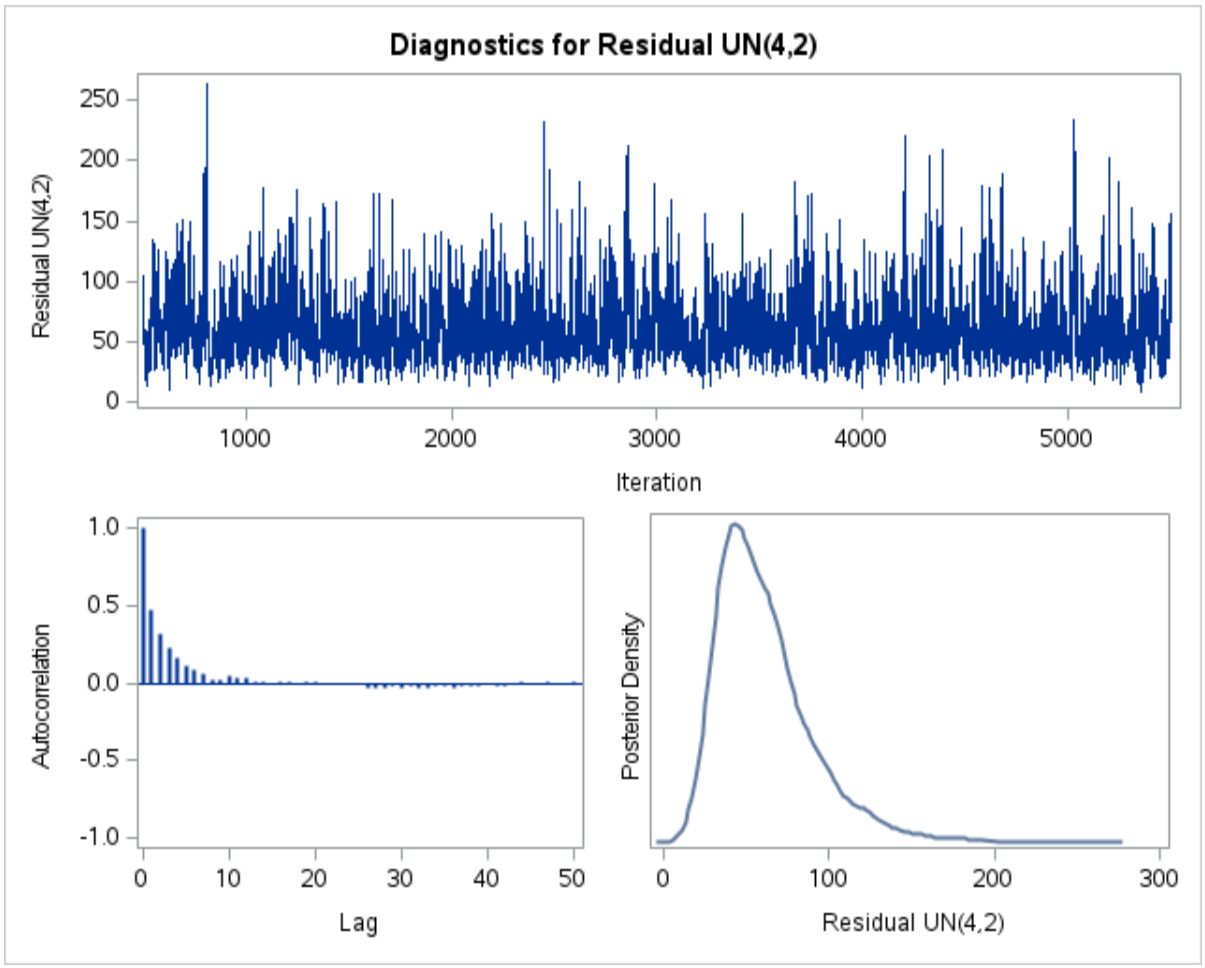

Diagnostics for Residual UN(2,2)
Residual UN(2,2)
300
200
100
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
400
Residual UN(2,2)

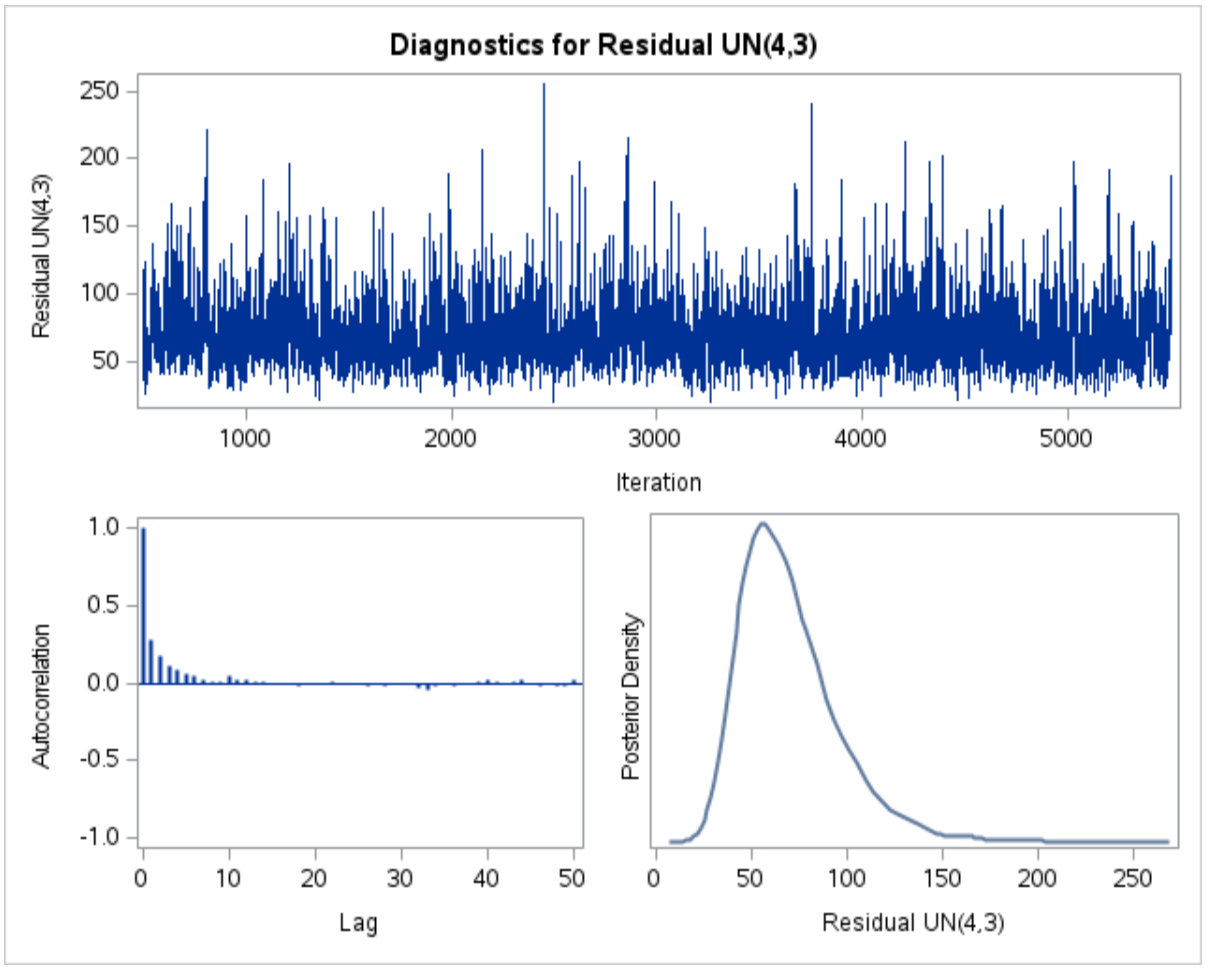

Diagnostics for Residual UN(3,1)
Residual UN(3,1)
300
200
100
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(3,1)

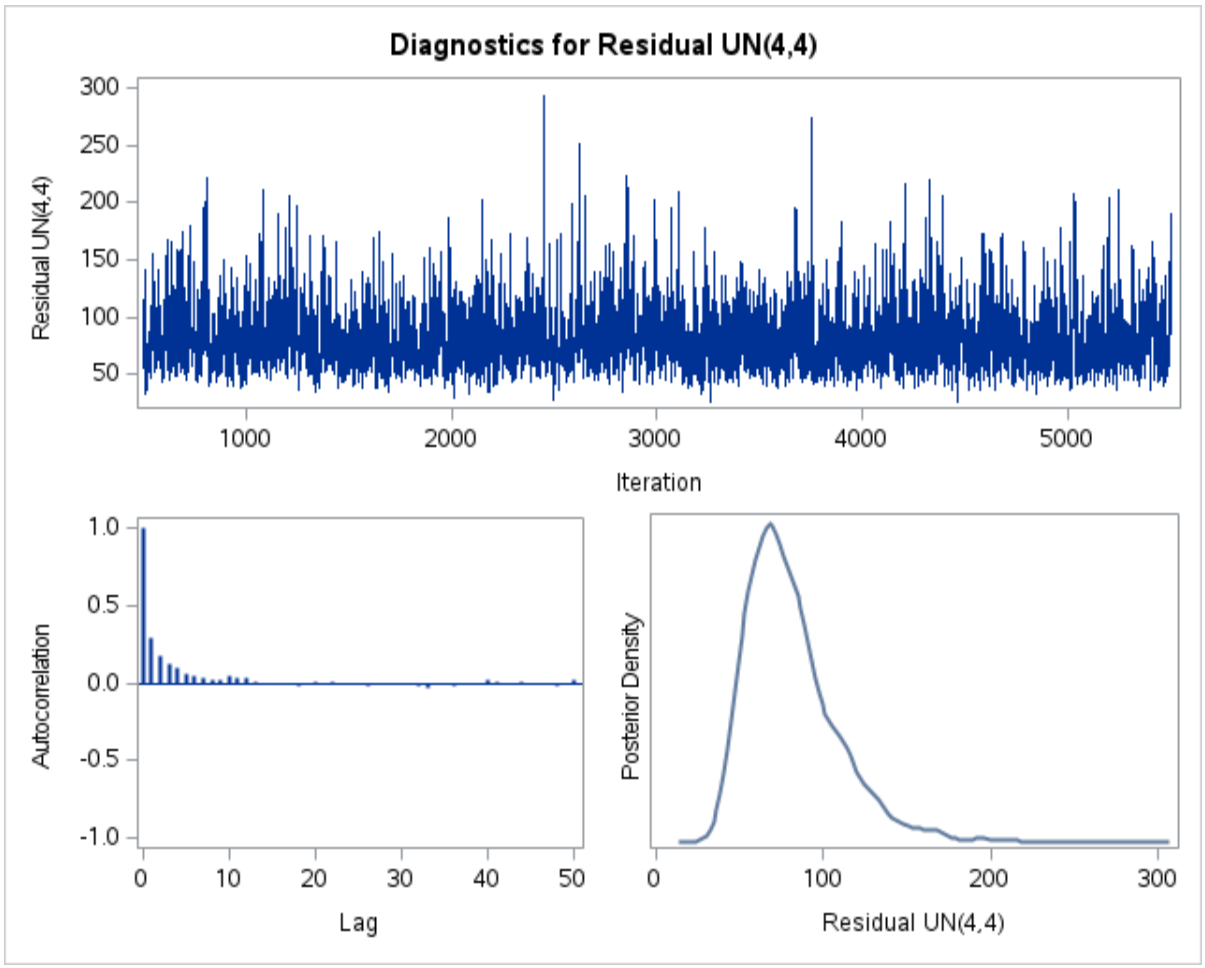

Diagnostics for Residual UN(3,2)
Residual UN(3,2)
250
200
150
100
50
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(3,2)

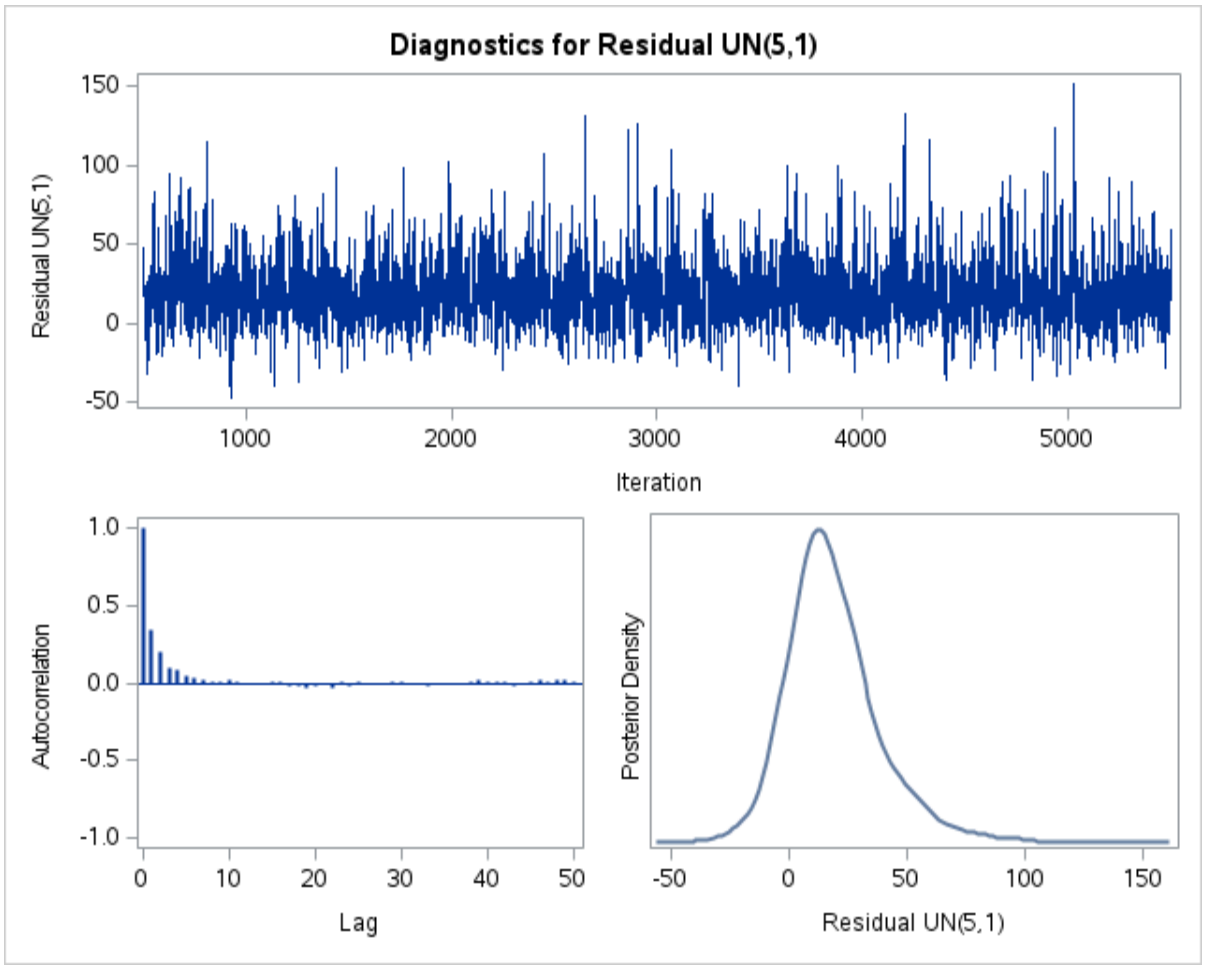

Diagnostics for Residual UN(3,3)
Residual UN(3,3)
250
200
150
100
50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
50
100
150
200
250
Residual UN(3,3)

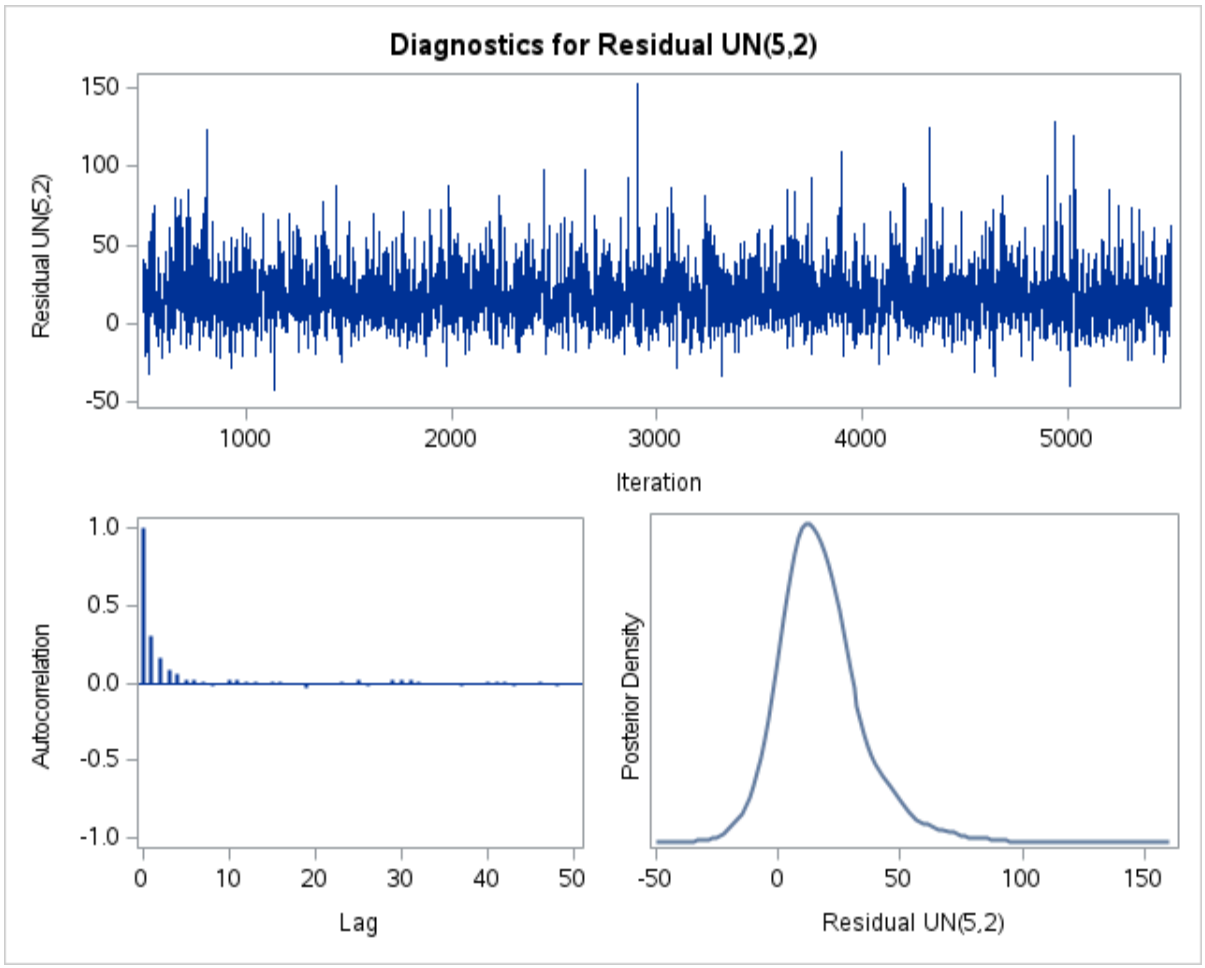

Diagnostics for Residual UN(4,1)
Residual UN(4,1)
250
200
150
100
50
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(4,1)

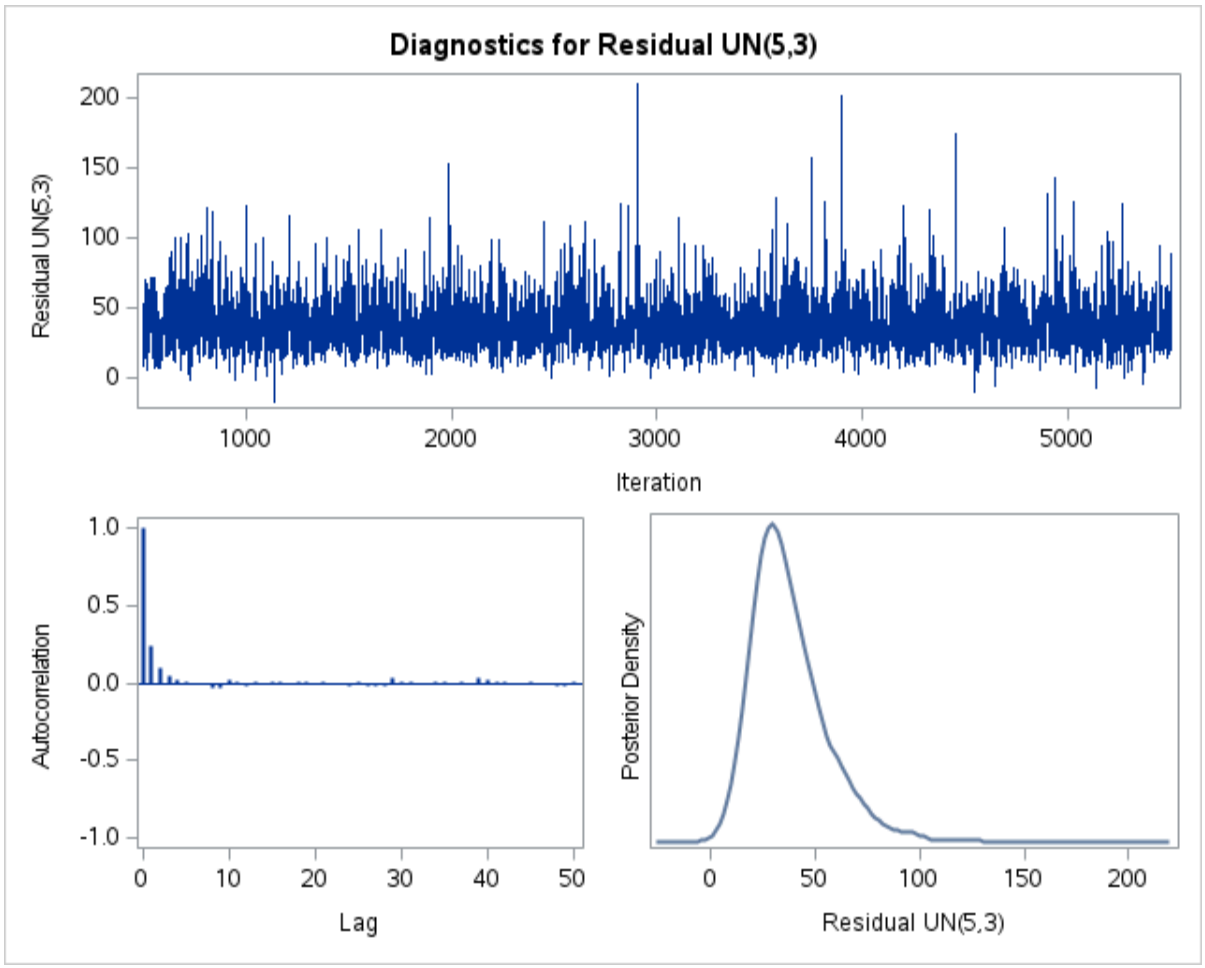

Diagnostics for Residual UN(4,2)
Residual UN(4,2)
250
200
150
100
50
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(4,2)

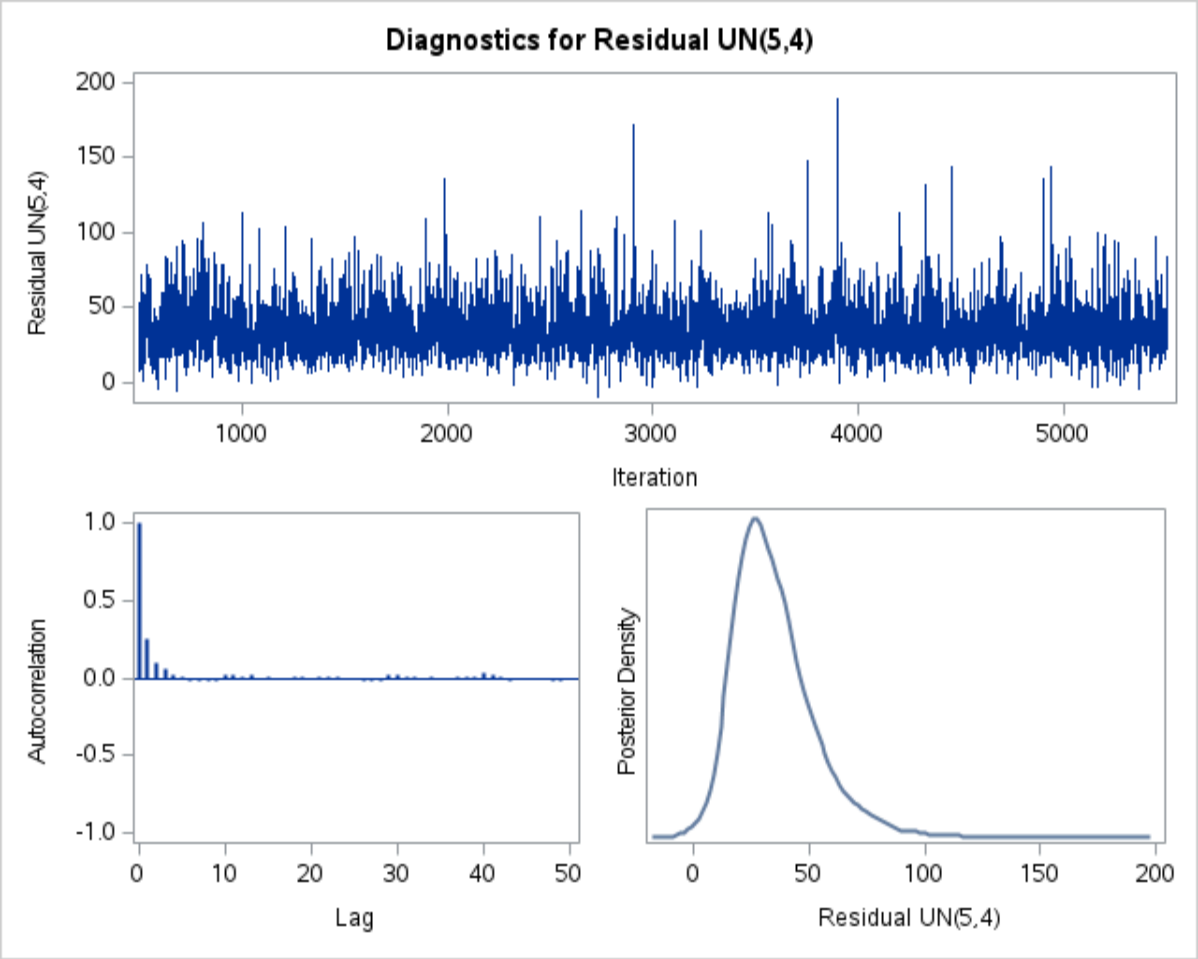

Diagnostics for Residual UN(4,3)
Residual UN(4,3)
250
200
150
100
50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
50
100
150
200
250
Residual UN(4,3)

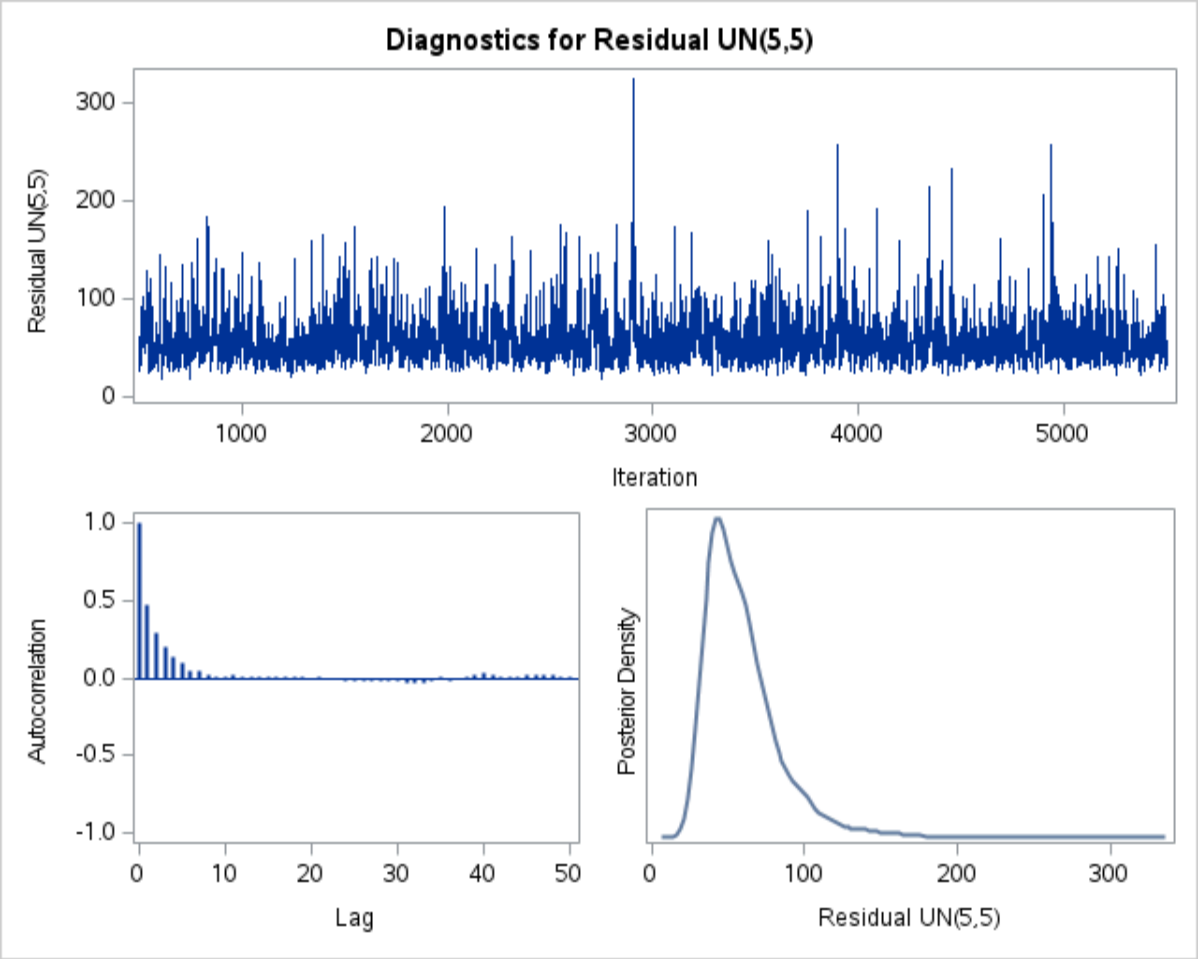

Diagnostics for Residual UN(4,4)
Residual UN(4,4)
300
250
200
150
100
50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(4,4)


Diagnostics for Residual UN(5,1)
Residual UN(5,1)
150
100
50
0
-50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-50
0
50
100
150
Residual UN(5,1)


Diagnostics for Residual UN(5,2)
Residual UN(5,2)
150
100
50
0
-50
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
-50
0
50
100
150
Residual UN(5,2)


Diagnostics for Residual UN(5,3)
Residual UN(5,3)
200
150
100
50
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
50
100
150
200
Residual UN(5,3)


Diagnostics for Residual UN(5,4)
Residual UN(5,4)
200
150
100
50
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
50
100
150
200
Residual UN(5,4)


Diagnostics for Residual UN(5,5)
Residual UN(5,5)
300
200
100
0
1000
2000
3000
4000
5000
Iteration
Autocorrelation
1.0
0.5
0.0
-0.5
-1.0
0
10
20
30
40
50
Lag
Posterior Density
0
100
200
300
Residual UN(5,5)

In [ ]: