All the basic information on the Bayesian model is here. It is always advisable the user to check this part before looking at the rest of the output.

As a first step MLE (frequentist) methods are used to generate the parameter estimates. Then Bayesian methods will be implemented.

## Bayesian analysis of Latent Infection with non-informative priors

The GENMOD Procedure

Bayesian Analysis

| Model Information | |
|---|---|
| Data Set | WORK.ONFIT |
| Burn-In Size | 2000 |
| MC Sample Size | 10000 |
| Thinning | 1 |
| Sampling Algorithm | Gamerman |
| Distribution | Binomial |
| Link Function | Logit |
| Response Variable (Events) | ONFIT |
| Response Variable (Trials) | N |

| | |
|---|---|
| Number of Observations Read | 15 |
| Number of Observations Used | 15 |
| Number of Events | 141 |
| Number of Trials | 1500 |

| Response Profile | | |
|---|---|---|
| Ordered Value | Binary Outcome | Total Frequency |
| 1 | Event | 141 |
| 2 | Nonevent | 1359 |

Algorithm converged.

| Analysis Of Maximum Likelihood Parameter Estimates | | | | | |
|---|---|---|---|---|---|
| Parameter | DF | Estimate | Standard Error | Wald 95% Confidence Limits | |
| Intercept | 1 | -2.2033 | 0.1547 | -2.5065 | -1.9001 |
| CDD | 1 | 0.1071 | 0.0628 | -0.0160 | 0.2302 |
| RAIN | 1 | -0.4264 | 0.1881 | -0.7950 | -0.0577 |
| WW | 1 | -0.0060 | 0.0628 | -0.1292 | 0.1171 |
| Scale | 0 | 1.0000 | 0.0000 | 1.0000 | 1.0000 |

e scale parameter was held fixed.

The MCMC sampling starts with parameters based on (related to) the MLE (frequentist) fit to the data.
To get exact same numerical results each time, put in a seed value.

| Initial Values of the Chain | | | | | |
|---|---|---|---|---|---|
| Chain | Seed | Intercept | CDD | RAIN | WW |
| 1 | 27500 | -2.20328 | 0.107092 | -0.42636 | -0.00604 |

| Fit Statistics | |
|---|---|
| DIC (smaller is better) | 293.078 |
| pD (effective number of parameters) | 4.012 |

## Bayesian analysis of Latent Infection with non-informative priors

The GENMOD Procedure

Bayesian Analysis

**Posterior Summaries**

| Parameter | N | Mean | Standard Deviation | Percentiles | | |
|---|---|---|---|---|---|---|
| | | | | 25% | 50% | 75% |
| Intercept | 10000 | -2.2077 | 0.1555 | -2.3142 | -2.2062 | -2.1004 |
| CDD | 10000 | 0.1063 | 0.0636 | 0.0623 | 0.1065 | 0.1501 |
| RAIN | 10000 | -0.4343 | 0.1911 | -0.5599 | -0.4309 | -0.3036 |
| WW | 10000 | -0.00453 | 0.0631 | -0.0469 | -0.00436 | 0.0376 |

Mean is one central value of the posterior (analogous to a point estimate).
Standard deviation is analogous to the standard error in frequentist analysis.

**Posterior Intervals**

| Parameter | Alpha | Equal-Tail Interval | | HPD Interval | |
|---|---|---|---|---|---|
| Intercept | 0.050 | -2.5109 | -1.9063 | -2.4996 | -1.8987 |
| CDD | 0.050 | -0.0173 | 0.2277 | -0.0172 | 0.2277 |
| RAIN | 0.050 | -0.8237 | -0.0664 | -0.8168 | -0.0617 |
| WW | 0.050 | -0.1278 | 0.1204 | -0.1305 | 0.1154 |

Two ways of getting the 95% credible intervals: percentiles and HPD. (HPD may be more accurate).

**Posterior Correlation Matrix**

| Parameter | Intercept | CDD | RAIN | WW |
|---|---|---|---|---|
| Intercept | 1.000 | 0.261 | -0.512 | -0.240 |
| CDD | 0.261 | 1.000 | -0.583 | -0.796 |
| RAIN | -0.512 | -0.583 | 1.000 | 0.082 |
| WW | -0.240 | -0.796 | 0.082 | 1.000 |

Interpretation is easier when the parameters are not correlated (not required)

## Bayesian analysis of Latent Infection with non-informative priors

The GENMOD Procedure

Bayesian Analysis

**Posterior Autocorrelations**

| Parameter | Lag 1 | Lag 5 | Lag 10 | Lag 50 |
|---|---|---|---|---|
| Intercept | 0.2759 | -0.0108 | 0.0018 | 0.0179 |
| CDD | 0.2816 | -0.0001 | -0.0076 | 0.0007 |
| RAIN | 0.3259 | 0.0161 | -0.0101 | 0.0046 |
| WW | 0.2758 | -0.0104 | 0.0052 | -0.0093 |

**Some diagnostics: Autocorrelations at selected lags (nice to see ~ 0). Geweke statistics should ideally be not significant (Pr > 0.05).**

**Geweke Diagnostics**

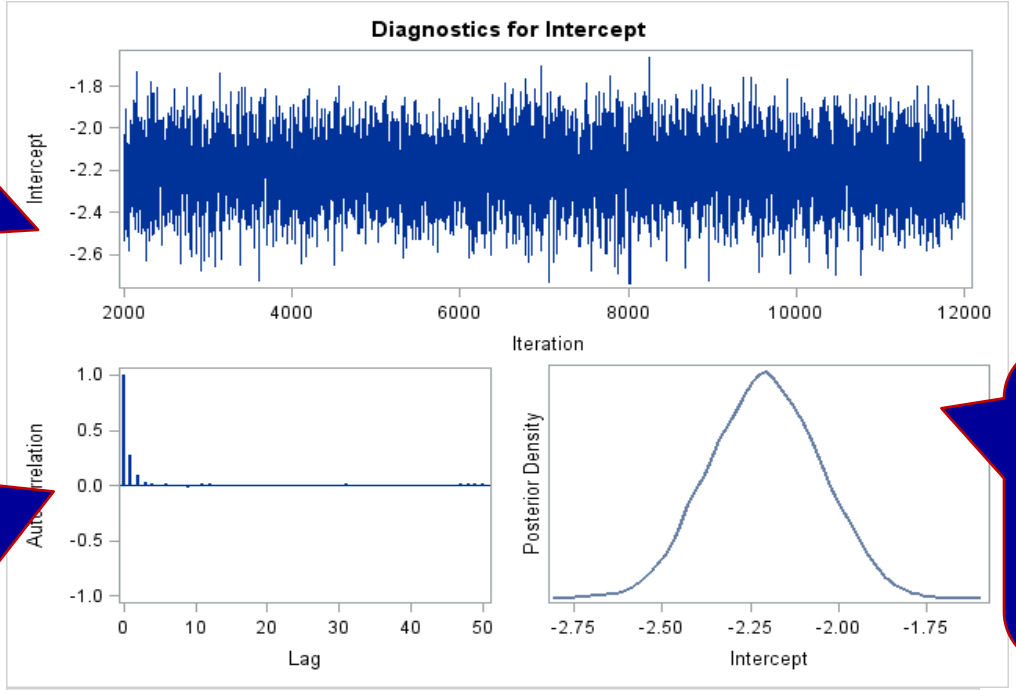
| Parameter | z | Pr > \|z\| |
|---|---|---|
| Intercept | -0.0519 | 0.9586 |
| CDD | -0.5222 | 0.6015 |
| RAIN | 0.9912 | 0.3216 |
| WW | -0.4806 | 0.6308 |

**Effective Sample Sizes**

| Parameter | ESS | Autocorrelation Time | Efficiency |
|---|---|---|---|
| Intercept | 5557.0 | 1.7995 | 0.5557 |
| CDD | 5478.8 | 1.8252 | 0.5479 |
| RAIN | 4660.2 | 2.1458 | 0.4660 |
| WW | 5523.2 | 1.8106 | 0.5523 |

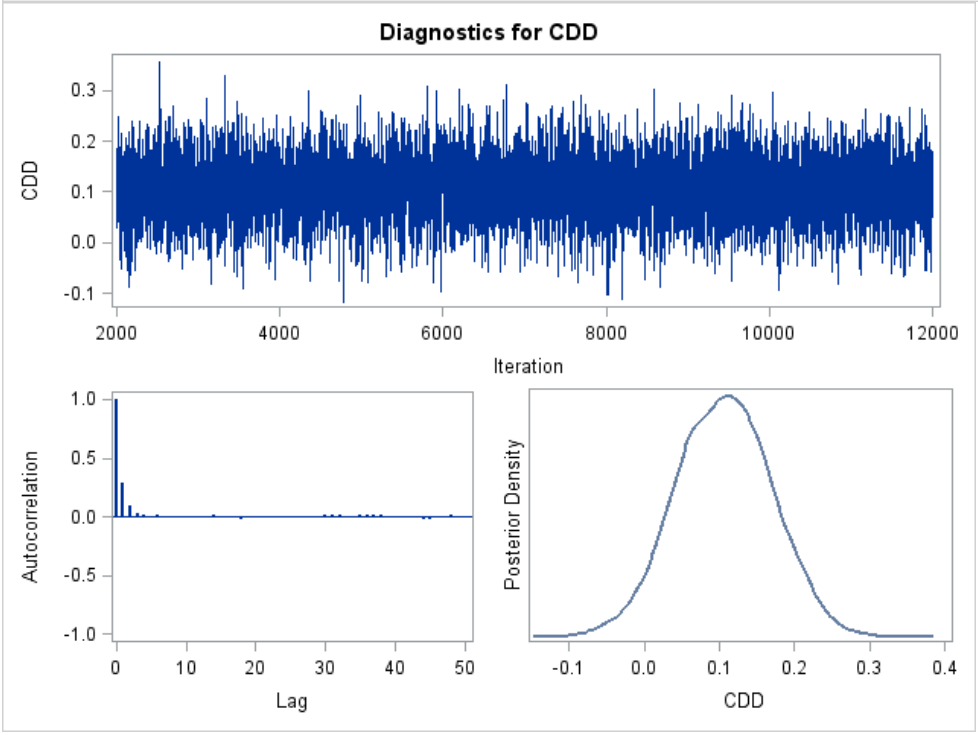
**Effective sample sizes should be similar to the selected *N* for the posterior sampling (a much smaller number means that samples are too highly correlated).**

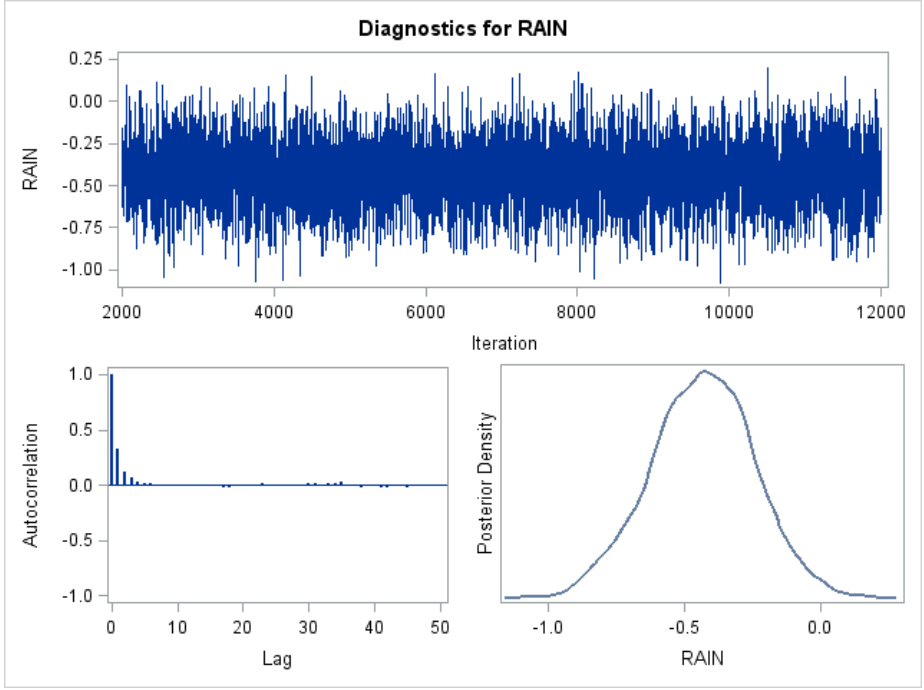
A good trace plot of the N=10000 samples (stable, no trend, frequently crossing the mean line)

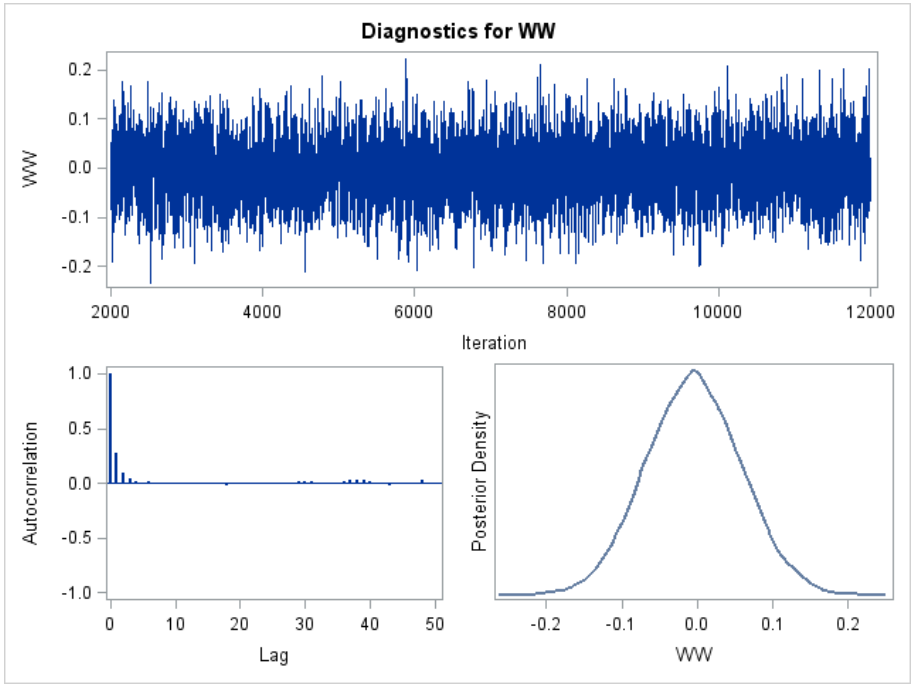



Ideally, the autocorrelation should drop rapidly towards 0 (indicating independence of the MCMC samples)

The estimated posterior density function, determined by a so-called kernel smoothing of the N MCMC samples




Diagnostics for RAIN
RAIN
0.25
0.00
-0.25
-0.50
-0.75
-1.00
2000
4000
6000
8000
10000
12000
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
RAIN


Diagnostics for WW
WW
0.2
0.1
0.0
-0.1
-0.2
2000
4000
6000
8000
10000
12000
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
WW