Bayesian Analysis and Prediction of Acute Bacterial Meningitis

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Abstract

Acute Bacterial Meningitis (ABM) is a rapidly progressing infection that inflames the meninges, the protective membranes surrounding the brain and spinal cord, affecting approximately 3,000 individuals annually in the United States. This study investigates key risk factors associated with the likelihood of ABM and evaluates the predictive performance of a Bayesian logistic regression model. Using the Bayesian model selection, we identify six significant risk factors and implement a Bayesian logistic regression framework with Hamiltonian Monte Carlo (HMC) sampling via the No-U-Turn Sampler (NUTS). Our findings indicate that the Bayesian model offers superior predictive accuracy compared to traditional frequentist logistic regression. Furthermore, we identify CSF/Blood glucose ratio as being strongly associated with the incidence of ABM. These findings can contribute to early screening strategies by identifying individuals at higher risk of ABM, enabling more timely diagnosis and intervention.

1 Introduction

Acute Bacterial Meningitis (ABM) is a severe and rapidly progressing infection that inflames the meninges—the protective membranes surrounding the brain and spinal cord. Despite advancements in medical care, ABM remains a serious health concern due to its high mortality and risk of long-term neurological complications. In the United States alone, approximately 3,000 individuals are diagnosed annually [1], and about 1 in 6 of them die [7].

Early diagnosis is critical to improving outcomes, yet ABM can be difficult to detect in its early stages due to its presence without typical symptoms [4]. Identifying individuals at elevated risk remains a challenge, making predictive modeling an essential tool for improving clinical decision-making and preventive care.

1.1 Literature Review

Researchers at Duke University applied a frequentist logistic regression model to investigate early clinical indicators for predicting the likelihood of bacterial meningitis [6]. Their analysis identified CSF (cerebrospinal fluid) glucose ratio, patient age, and month of onset as significant predictors, emphasizing the value of early clinical and demographic information in guiding timely and appropriate treatment.

In a separate study, Nirajan Budhathoki (2023) at Central Michigan University implemented Bayesian logistic regression with Gibbs sampling on a diabetes dataset, demonstrating the potential of Bayesian inference in medical predictive modeling [2]. This work reflects a growing interest in probabilistic frameworks capable of incorporating uncertainty and prior knowledge into statistical inference.

However, despite these contributions, there remains a notable gap in applying modern Bayesian approaches specifically to the context of acute bacterial meningitis. While Bayesian methods have

been increasingly adopted in medical data analysis, their use in modeling ABM risk remains limited. Addressing this gap is important for improving the identification of relevant clinical risk factors and enhancing predictive performance and early detection.

1.2 Research Question

This study investigates which demographic and clinical risk factors are significantly associated with acute bacterial meningitis (ABM) and evaluates how effectively a Bayesian logistic regression model predicts ABM cases. Using a dataset of 581 patient samples originally compiled by researchers at Duke University, we examine 21 variables to identify meaningful predictors of ABM.

In addition to variable selection, we assess the predictive performance of a Bayesian logistic regression model and compare its results with those of a traditional frequentist approach. The Bayesian framework is particularly well-suited for this type of analysis due to its ability to incorporate prior knowledge, quantify uncertainty in parameter estimates, and perform reliably in moderate sample sizes. Given the clinical importance of early and accurate diagnosis, we aim for a model that is both interpretable and applicable in medical decision-making contexts with potential in aiding in risk detection and early intervention strategies.

2 Data

This study uses a dataset of 581 patient samples originally compiled by the researchers at Duke University in the previously mentioned study [6]. Each sample includes both demographic and clinical information, along with diagnostic outcomes indicating the presence or absence of acute bacterial meningitis (ABM). The dataset contains 22 variables, including ABM status, age, sex, blood and cerebrospinal fluid (CSF) biomarkers, symptom profiles, and other relevant clinical indicators.

2.1 Data Cleaning

To prepare the data for analysis, we first removed columns with a high proportion of missing values, as well as variables deemed irrelevant to the prediction task, such as case number, year and month of onset, and subset classification. Categorical variables were encoded for compatibility with logistic regression models. Additionally, we derived a new variable called the CSF glucose ratio by dividing CSF glucose by blood glucose levels, following its demonstrated usage in the original Duke University study. Lastly, we excluded rows with any missing values in the remaining variables. The final cleaned dataset consisted of 106 patient samples and 16 variables for model development and evaluation.

2.2 Descriptive Statistics and Exploratory Data Analysis

We conducted descriptive statistical analyses and exploratory data analysis to better understand the characteristics of the data and the relationships between predictors and ABM status. Summary statistics for a few continuous variables are provided in Table 1, offering insights into the central tendency, variability, and overall distribution of the data. Additionally, Figure 1 presents box plots for age, cerebrospinal fluid (CSF) glucose ratio, and white blood cell (WBC) count, stratified by ABM status, which illustrate differences in the distribution and variability of these predictors between subjects with and without ABM. Together, these analyses provide preliminary insights into potential associations between certain predictors and ABM.

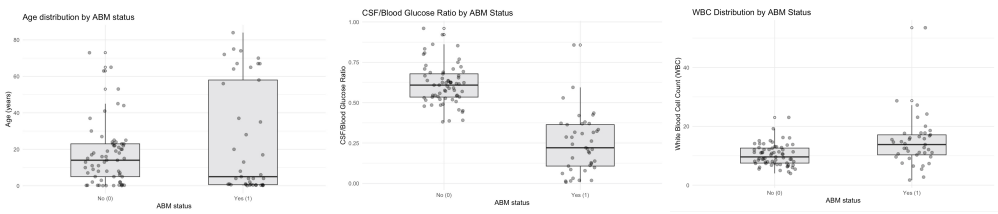

Figure 1: Box Plots for Age, CSF glucose ratio, and WBC count

Table 1: Summary Statistics for 4 select predictors

Variable	Statistic	ABM = 0	ABM = 1
`age`	Mean	16.78	24.73
	SD	16.55	29.95
	Median	14	5
	IQR	18	57.4
`polys`	Mean	39.4	79.27
	SD	35.16	24.97
	Median	33	89
	IQR	69	32
`pr`	Mean	57.15	303.78
	SD	34.22	321.05
	Median	53	194
	IQR	45	227
`reds`	Mean	1763.88	1400.95
	SD	9079.23	4211.56
	Median	9	140
	IQR	79	505

3 Methods

To identify key predictors of acute bacterial meningitis (ABM), we implemented a Bayesian variable selection approach using the Metropolis-Hastings (MH) algorithm, through which we employed the Bayesian Information Criterion (BIC), a model selection criterion that balances model fit with complexity and allowed us to select the most relevant variables for inclusion in our predictive model. To aid in our implementation, we studied the BIC framework outlined by Drton and Plummer [3], which became our guide for using BIC in model selection.

We then applied Bayesian logistic regression to model the probability of ABM, using Hamiltonian Monte Carlo (HMC) sampling through the No-U-Turn Sampler (NUTS) to estimate the posterior distribution of the model parameters. We examined the implementation and advantages of HMC and NUTS through the work of Miller [5]. HMC provides advantages in terms of incorporating prior knowledge, quantifying uncertainty, and offering more robust predictions.

3.1 Model Selection using Bayesian Information Criterion and Metropolis-Hastings

3.1.1 Data Preparation

We partitioned the dataset into 70% training data and 30% testing data. Using the training set, we constructed a full design matrix incorporating all available predictors, including laboratory measures and demographic factors. The binary outcome variable, `abm`, was defined as 0 for no ABM and 1 for ABM.

3.1.2 Model Preparation

Each candidate model was represented by a binary vector z of length p (number of predictors). For example, if $z = (1, 0, 1, 0, ...)$, it means only the 1st and 3rd predictors are included in that model. The Metropolis–Hastings algorithm explores different combinations of predictors by flipping one entry in z_{current} at each iteration to propose a new model.

3.1.3 Bayesian Information Criterion

For Bayesian model comparison, ideally, we want to compute the marginal likelihood of each model for the comparison in Metropolis-Hastings, but in logistic regression this has no closed-form solution. Therefore, we decided to use the Bayesian Information Criterion (BIC), a model scoring rule that balances model fit and complexity, as a fast approximation to the log marginal likelihood.

The formula is typically written as:

$$\text{BIC} = k \log(n) - 2 \log L(\hat{\theta})$$

Where:

- k = number of estimated parameters in the model
- n = number of observations
- $L(\hat{\theta})$ = likelihood of the model evaluated at the MLE

In this case, by definition, models with lower BIC are preferred.

However, in Metropolis-Hastings, we want the quantity to increase when a model is perfomring better so that the comparison is easier. Thus we rearranged the formula by multiplying both sides of the equation by $-\frac{1}{2}$ and we have:

$$-\frac{1}{2}\text{BIC} = \log L(\hat{\theta}) - \frac{k}{2} \log(n)$$

The right hand side is the formula we used to compare the BIC score. So instead of minimizing BIC, we will be maximizing it.

3.1.4 Metropolis–Hastings (MH) Algorithm

To explore all possible models and find out the ones that are best supported by our data, we implemented a Metropolis–Hastings sampler. In this approach, each model is represented by a binary vector z with each entry indicating whether a specific predictor is included (1) or excluded (0).

At each iteration of the algorithm, we propose a new model by randomly flipping one bit in the current model vector, adding or removing one variable at a time. The proposed model is then scored using a BIC-based approximation to the log marginal likelihood, reflecting both how well the model fits the data and how complex it is as it penalizes overly complex models.

To decide whether to accept the new model, we apply the Metropolis-Hastings acceptance rule:

$$\log \alpha = \text{Score}_{\text{proposed}} - \text{Score}_{\text{current}}$$

This corresponds to the probability:

$$\alpha = \min(1, \exp(\text{Score}_{\text{proposed}} - \text{Score}_{\text{current}}))$$

Therefore, the rule is:

- If $\log \alpha > 0$, the proposed model has a higher score than the current model so the new model is always accepted.
- If $\log \alpha < 0$, the proposed model has a lower score but still may be accepted with probability

$$\alpha = \exp(\log \alpha)$$

This rule allows us to favor better-fitting models but still occasionally explore worse ones, preventing the sampler from getting stuck in local optima.

3.1.5 Posterior Inclusion Probabilities (PIP)

After running 10,000 iterations, we used the output z_{chain} to compute the posterior inclusion probability (PIP) for each predictor:

$$\text{PIP}_j = \frac{1}{T} \sum_{t=1}^{T} z_{t,j}$$

where:

- $z_{t,j}$ is the inclusion indicator (0 or 1) for variable j at iteration t,
- T is the total number of MCMC iterations.

Higher PIP shows that the predictor is included in more sampled models so it has greater relevance.

3.1.6 Final Variable Selection Based on PIP

The final output is a ranked list of predictors based on their PIP, which reflects how consistently each feature is selected across high-probability models. In this analysis, variables like CSF glucose ratio (`csf_gluc_ratio`), percentage of polymorphonuclear leukocytes (`polys`), and total leukocytes (`whites`) showed high posterior inclusion probabilities, suggesting they are most predictive of ABM status. Ultimately, we chose the top 6 variables with the highest PIP for our final model: CSF/Blood glucose ratio (`csf_gluc_ratio`), percentage of polymorphonuclear leukocytes (`polys`), total leukocytes in CSF (`whites`), CSF protein (`pr`), sex (`sex`), and white blood cell count (`wbc`) (see Figure 2).

3.2 Bayesian Logistic Regression with Hamiltonian Monte Carlo Sampling

We modeled the binary `abm` outcome using a logistic likelihood, enabling us to quantify the relationship between the predictors and the log-odds of the outcome while incorporating prior beliefs about the regression coefficients. We initially implemented the Metropolis-Hastings (MH) algorithm using a $\mathcal{N}(0, 100)$ prior with 10,000 iterations. However, the resulting chains exhibited high autocorrelation with slow decay and very low effective sample sizes. We also attempted Gibbs sampling with the same prior and number of iterations, but, because the likelihood in logistic regression is not conjugate to the prior, the full conditional distributions are not available in closed form. As a result, Metropolis-Hastings steps were required within the Gibbs sampler, ultimately leading to similar issues with poor mixing and low efficiency.

Given these challenges, we decided to use Hamiltonian Monte Carlo (HMC), which leverages gradient information to more efficiently explore the posterior distribution. HMC substantially improved mixing, reduced autocorrelation, and achieved significantly higher effective sample sizes compared to our earlier approaches.

3.2.1 Hamiltonian Monte Carlo and No U-Turns Sampler

Hamiltonian Monte Carlo (HMC) is a Markov chain Monte Carlo (MCMC) technique that leverages the gradient of the target density to produce more efficient transitions across the posterior distribution by utilizing an approximate Hamiltonian dynamics simulation based on numerical integration which is then corrected by performing a Metropolis acceptance step.

Hamiltonian Monte Carlo (HMC) augments the original parameter space by introducing artificial momentum variables ρ and draws from a joint density:

$$p(\rho, \theta) = p(\rho|\theta)p(\theta).$$

where $\rho \sim MVN(0, M)$ and M is the Euclidean metric, which is a transform of parameter space that makes sampling more efficient.

The joint density $p(\rho, \theta)$ defines the Hamiltonian function:

$$H(\rho, \theta) = T(\rho|\theta) + V(\theta) = -\log p(\rho|\theta) - \log p(\theta)$$

where $T(\rho|\theta)$ is the "kinetic energy" and $V(\theta)$ is the "potential energy".

Starting from the current value of θ, a transition to a new state is generated in two stages before it enters the Metropolis acceptance step.

First, at each iteration, a new momentum ρ is drawn $\rho \sim MVN(0, M)$ which does not persist across iterations.

Next, the joint system (θ, ρ) made up of the current θ and new ρ is evolved via Hamilton's equations:

$$\frac{d\theta}{dt} = \frac{\partial T}{\partial \rho}$$
$$\frac{d\rho}{dt} = -\frac{\partial T}{\partial \theta} - \frac{\partial V}{\partial \theta}.$$

Since $p(\rho|\theta) = p(\rho)$, $\dfrac{\partial T}{\partial \theta} = 0$, yielding the derivatives:

$$\frac{d\theta}{dt} = \frac{\partial T}{\partial \rho} \qquad , \qquad \frac{d\rho}{dt} = -\frac{\partial V}{\partial \theta}.$$

The leapfrog integrator, a numerical integration algorithm that is specifically adapted to provide stable results for Hamiltonian systems of equations, is used to solve these two differential equations.

It takes discrete steps of some small time interval ϵ and begins by drawing a new ρ independently of θ and the previous ρ. It then alternates between updating the momentum with a half-step and updating the position with a full-step.

$$\begin{aligned}
\rho &\leftarrow \rho - \frac{\epsilon}{2}\frac{\partial V}{\partial \theta} \\
\theta &\leftarrow \theta + \epsilon M^{-1}\rho \\
\rho &\leftarrow \rho - \frac{\epsilon}{2}\frac{\partial V}{\partial \theta}.
\end{aligned}$$

The resulting state after L iterations of the above three steps is denoted (ρ^*, θ^*).

Lastly, the Metropolis acceptance step is applied to account for numerical errors during integration. The probability of keeping the proposed (ρ^*, θ^*) is:

$$\min(1, \exp(H(\rho, \theta) - H(\rho^*, \theta^*))).$$

If the proposed (ρ^*, θ^*) is not accepted, the previous θ is retained and used to initialize the next iteration.

We will be using the No U-turn sampler (NUTS) for our model, which is an extension of Hamiltonian Monte Carlo that adaptively tunes M and ϵ during the burn-in phase and adapts L throughout the MCMC run, thereby eliminating the need to select the tuning parameters.

NUTS adaptively determines the trajectory length to avoid inefficient sampling paths that double back toward the starting point. It prevents reversals in direction that would violate detailed balance if stopped too early by dynamically choosing the number of leapfrog steps (L) at each iteration.

The algorithm uses a doubling strategy: it first takes 1 leapfrog step forward or backward, then 2 steps, then 4, and so on, doubling the number of steps each time. This process continues until either the forward or backward trajectory shows signs of turning back. From all points generated during this doubling phase, NUTS samples a final state in a way that ensures detailed balance is preserved.

During burn-in, NUTS also adapts the step size and mass matrix to improve performance; these parameters are fixed after burn-in, but the number of steps (L) continues to be chosen adaptively at each iteration.

3.2.2 Algorithm Implementation

To model the posterior distributions of the parameters associated with acute bacterial meningitis (ABM), we implemented a Bayesian logistic regression framework and NUTS using the `rstanarm` package in R.

The regression model takes the form:

$$P(\text{abm} = 1|X) = \text{logit}^{-1}(\beta_0 + \beta_1 X_1 + \cdots + \beta_p X_p)$$

We specified weakly informative normal priors for all coefficients:

$$\beta_j \sim \mathcal{N}(0, 10^2)$$

This corresponds to specifying `prior = normal(0, 10)` in `rstanarm` with the second argument being the standard deviation, not the variance. These priors reflect uncertainty about the effect sizes while allowing the data to drive posterior estimates.

Model fitting was conducted using four independent Markov chains with 2,000 iterations per chain. A fixed random seed (seed = 123) was used to ensure reproducibility of results. The model employed a logistic likelihood for the probability inference.

3.3 Model Diagnostics

To assess the reliability and convergence of our Bayesian logistic regression model, we conducted standard diagnostics using posterior summary statistics provided by the `rstanarm` package and trace plots of the parameters. These diagnostics help ensure that the Markov chains adequately explored the posterior distribution and that the resulting inferences are valid.

The posterior summary statistics, as shown in Figure 3, focus on three key metrics:

- MCSE (Monte Carlo Standard Error), which quantifies the uncertainty in the estimated posterior mean due to finite sampling. Smaller MCSE values indicate more precise estimates. In our results, MCSE values were close to zero, implying high precision.
- $\hat{R}$, a convergence diagnostic that compares the variance between multiple MCMC chains to the variance within each chain. A value of close to 1.0 indicates that the chains have mixed well and converged to the target distribution. In our model, all parameters had $\hat{R}$ = 1.0, suggesting strong convergence.
- Effective sample size (`n_eff`), which measures the number of independent samples equivalent to the correlated MCMC draws. Larger effective sample sizes imply better sampling efficiency. Across all parameters, the effective sample size was well above 1000, indicating reliable posterior summaries.

The trace plots in Figure 4 show excellent mixing and convergence for all parameters. The chains overlap substantially, display rapid mixing, and remain stable over iterations with no visible trends or drift. This indicates that the chains have reached stationarity, supporting the reliability of the posterior estimates.

4 Discussion

4.1 Posterior Analysis and Model Evaluation

To evaluate the performance of our model, we evaluated the predictions using a confusion matrix, summarizing the agreement between the predicted and actual labels.

	Actual = 1 (ABM)	**Actual = 0 (No ABM)**
Predicted = 1	True Positives (TP) = 11	False Positives (FP) = 0
Predicted = 0	False Negatives (FN) = 1	True Negatives (TN) = 20

Table 2: Confusion Matrix

From this, we derived several key classification metrics:

- **Precision**, the proportion of positive predictions that are correct:
$$\text{Precision} = \frac{\text{TP}}{\text{TP + FP}} = \frac{11}{11+0} = 1.00$$
This indicates perfect reliability in the model's ABM-positive predictions.
- **Recall** (sensitivity), the proportion of actual ABM cases that were detected:
$$\text{Recall} = \frac{\text{TP}}{\text{TP + FN}} = \frac{11}{11+1} \approx 0.917$$
The model captured approximately 91.7% of all true ABM cases.
- **F1 Score**, the harmonic mean of precision and recall, reflecting a balance between false positives and false negatives:
$$\text{F1 Score} = 2 \cdot \frac{1.00 \cdot 0.917}{1.00 + 0.917} \approx 0.9565$$
This high F1 score demonstrates strong overall classification performance.

- **Accuracy**, the proportion of correct predictions overall:

$$\text{Accuracy} = \frac{\text{TP + TN}}{\text{Total}} = \frac{11 + 20}{32} \approx 0.9688$$

The 96.9% accuracy, with a 95% confidence interval of [83.8%, 99.9%], confirms the model's high correctness across both classes.

To provide insight into model performance across all possible thresholds, we evaluated the model using the Receiver Operating Characteristic (ROC) curve and computed the Area Under the Curve (AUC), which summarizes the model's ability to discriminate between ABM-positive and ABM-negative cases. The Youden Index, defined as sensitivity + specificity – 1, identifies the threshold that maximizes the model's overall diagnostic effectiveness. Using this, we selected an optimal probability threshold of 0.455, which maximized the sum of sensitivity and specificity. At this threshold, the model achieved an AUC of 0.954, indicating excellent discriminative performance. The full ROC curve is shown in Appendix Figure 5.

We also examined the posterior distributions of the model coefficients through Posterior density plots that provide a visual summary of the estimated effect sizes and their credible intervals. As shown in Appendix Figure 6, the posterior distributions are smooth and unimodal, with several coefficients centered noticeably away from zero, suggesting that these predictors have a significant association with ABM in the context of the Bayesian model.

Lastly, the posterior predictive check offers a broader evaluation of model fit. In Figure 7, we compare simulated outcomes (light blue) to the observed data (dark blue). The close alignment between the two suggests that the model effectively captures the structure of the observed outcomes, supporting its adequacy for prediction.

4.2 Results

Figure 8 presents the posterior summaries of the regression coefficients. The CSF/blood glucose ratio demonstrates a strong and consistent negative association with ABM status, with its posterior distribution clearly shifted away from zero and concentrated in the negative region. This supports the conclusion made by the Duke University researchers, which identifies low glucose ratios as a key diagnostic marker for bacterial meningitis. Its prominence in the model confirms its robustness as a clinical predictor.

Other variables, such as CSF protein (pr), sex (sex), and percentage of polymorphonuclear leukocytes (polys), also show some deviation from zero in their posterior distributions. However, the deviation is minor and their 95% credible intervals include zero, indicating greater uncertainty in their effects. In contrast, predictors like total leukocytes in CSF (whites) and white blood cell count (wbc) exhibit posterior densities centered close around zero, suggesting weaker associations and limited influence in the classification task.

To evaluate model performance more rigorously, we compared Bayesian logistic regression with a standard frequentist logistic regression using the same variables and training-test data split ratio. The frequentist model performed well, achieving over 90% accuracy, perfect recall, and an F1 score around 0.89 (see Figure 9). These results indicate reliable classification performance.

However, the Bayesian model outperformed slightly, with an F1 score of approximately 0.96 and favorable posterior diagnostics. Beyond predictive accuracy, the Bayesian approach provides important advantages, including full posterior distributions and credible intervals, which allow for richer interpretations and better uncertainty quantification. This is particularly valuable in medical applications to improve crucial understanding of the strength and reliability of predictors.

In summary, while both models show strong classification capabilities, the Bayesian framework offers not only competitive performance but also transparency and interpretability, allowing better understanding of confidence and uncertainty behind each prediction and thus making it a more effective tool in predicting ABM in this dataset. This model can help clinicians prioritize diagnostic tests and treatment decisions based on the most informative clinical and demographic indicators, ultimately contributing to more timely clinical decision-making and improved health outcomes for patients.

References

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A Appendix / supplemental material

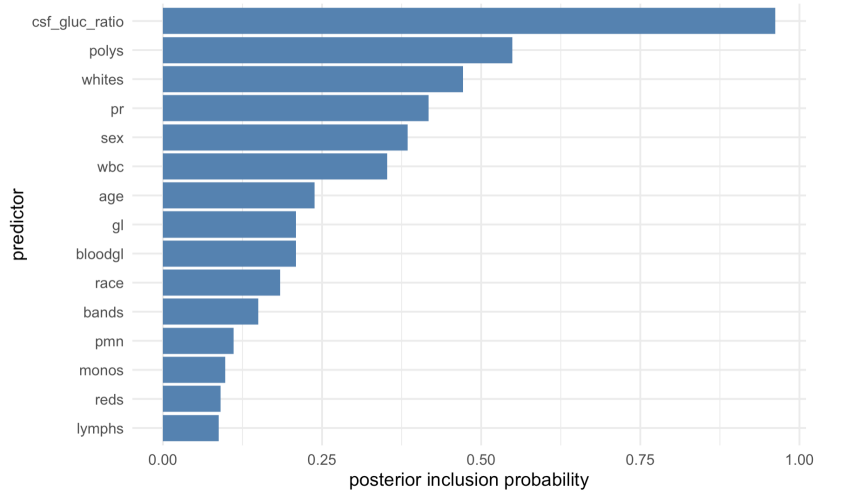

Figure 2: Posterior Inclusion Probabilities of ABM predictors

MCMC diagnostics

	mcse	Rhat	n_eff
(Intercept)	0.1	1.0	1754
csf_gluc_ratio	0.2	1.0	1325
polys	0.0	1.0	1457
whites	0.0	1.0	1070
sex	0.1	1.0	1300
pr	0.0	1.0	1618
wbc	0.0	1.0	1318

Figure 3: Posterior Summary Statistics

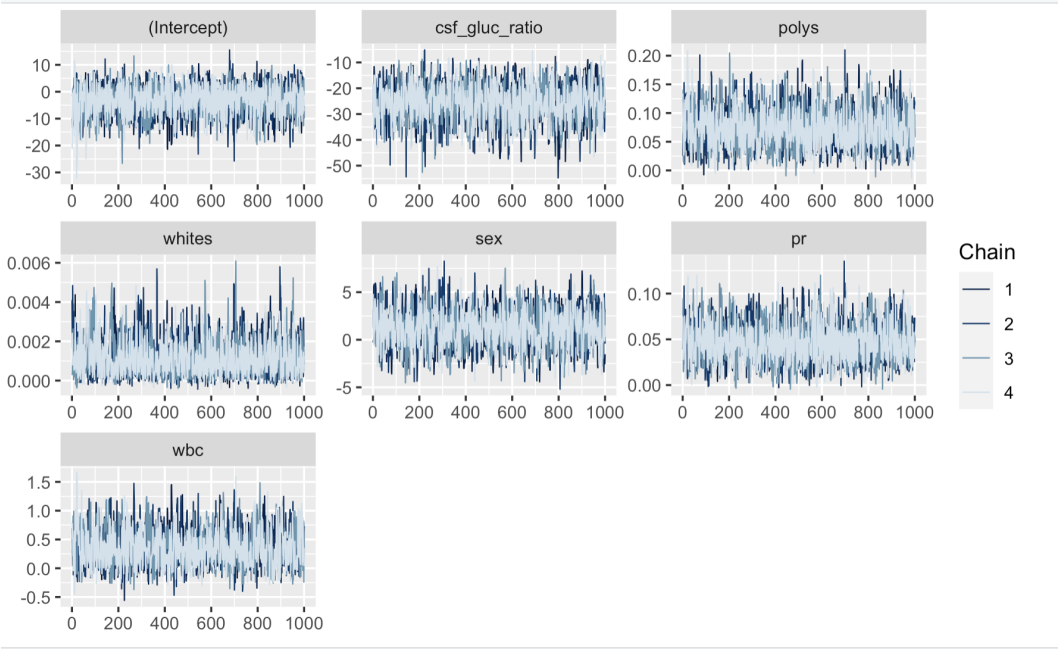

Figure 4: Trace Plots

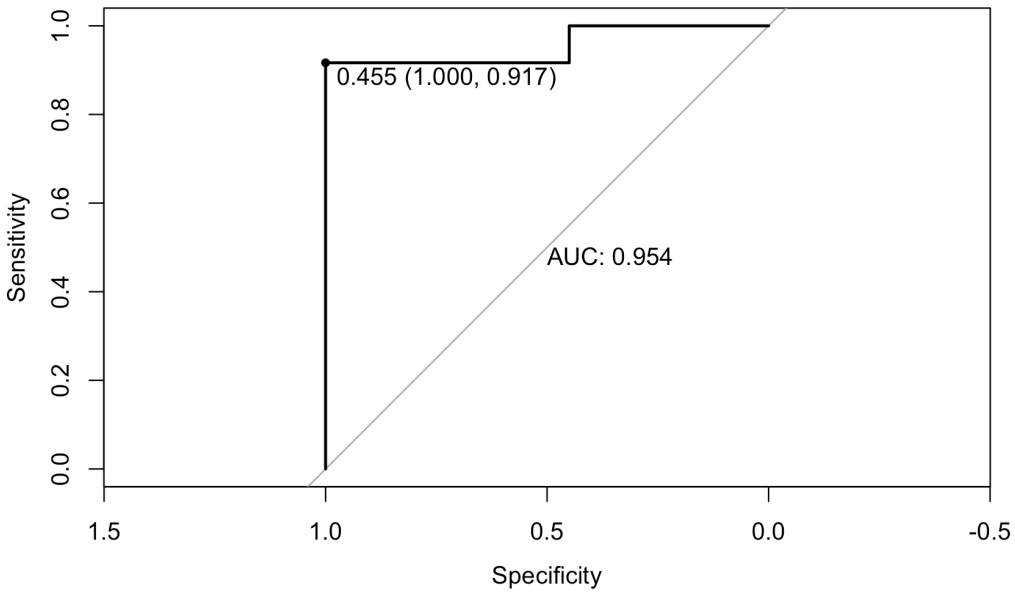

Figure 5: ROC-AUC Curve

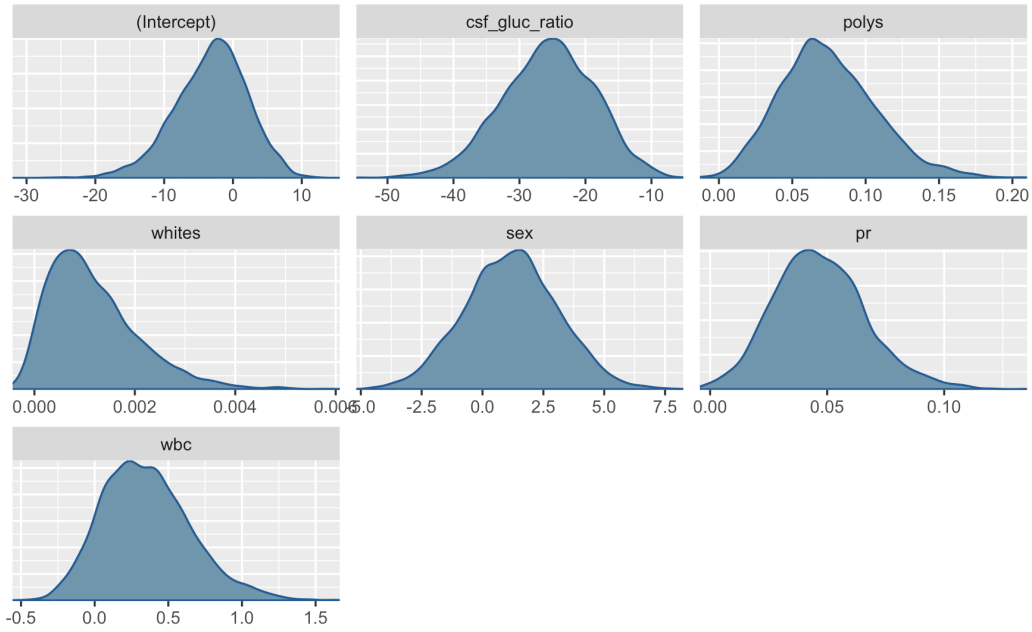

Figure 6: Posterior Density Plots

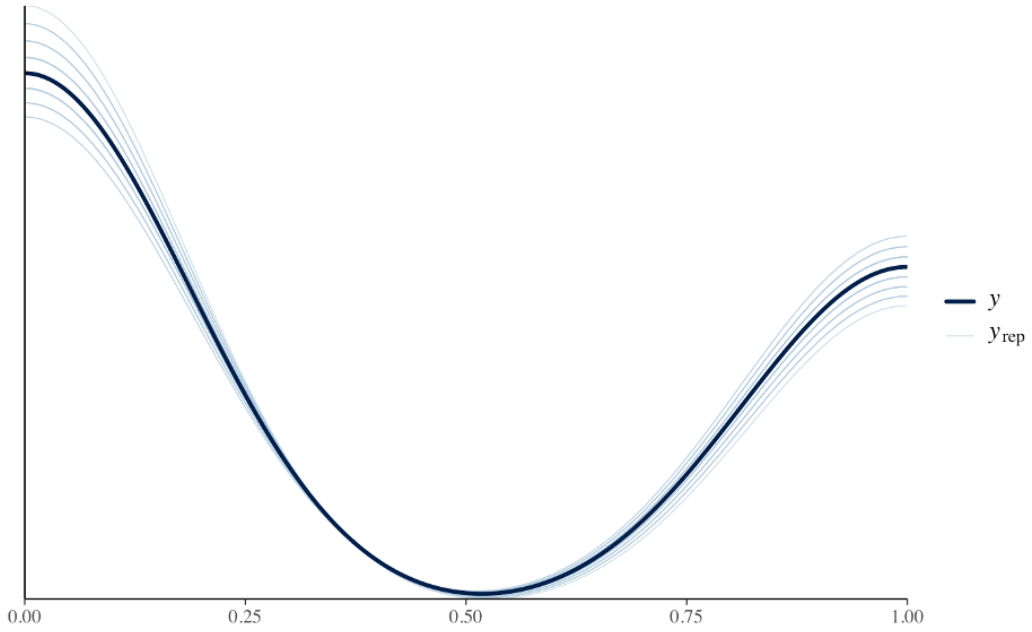

Figure 7: Posterior Predictive Check

```
Estimates:
                 mean   sd    2.5%   97.5%
(Intercept)     -3.2    5.3 -14.8    6.4
csf_gluc_ratio -25.7    7.1 -40.2  -12.5
polys            0.1    0.0   0.0    0.1
whites           0.0    0.0   0.0    0.0
sex              1.2    1.9  -2.5    4.9
pr               0.0    0.0   0.0    0.1
wbc              0.4    0.3  -0.2    1.0
```

Figure 8: Posterior Distribution Summary

```
Prediction  0  1
         0 17  0
         1  3 12

               Accuracy : 0.9062
                 95% CI : (0.7498, 0.9802)
    No Information Rate : 0.625
    P-Value [Acc > NIR] : 0.0003733

                  Kappa : 0.8095

 Mcnemar's Test P-Value : 0.2482131

            Sensitivity : 1.0000
            Specificity : 0.8500
         Pos Pred Value : 0.8000
         Neg Pred Value : 1.0000
             Prevalence : 0.3750
         Detection Rate : 0.3750
   Detection Prevalence : 0.4688
      Balanced Accuracy : 0.9250

       'Positive' Class : 1

Frequentist F1 Score: 0.8889
```

Figure 9: Frequentist Approach