

From Symptoms to Solutions: Bayesian Logistic and Probit Regression Models for Diabetes Prediction

— Project Report —
Advanced Bayesian Data Analysis

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1 Introduction

Diabetes mellitus is a major public health concern, affecting over 400 million people worldwide [american2020diabetes](#); [who2021diabetes](#). If undiagnosed at an early stage, it can lead to severe complications such as cardiovascular disease, kidney failure, and neuropathy. Early detection is crucial for preventive care, reducing healthcare costs, and improving patient outcomes. Traditional machine learning models have been used for disease prediction, but they often lack interpretability and fail to quantify uncertainty, which is essential in medical decision-making. This study explores Bayesian approaches that provide accurate predictions while incorporating uncertainty estimation.

1.1 Problem Statement

Accurate prediction of early-stage diabetes is essential for timely intervention and disease management. However, early-stage cases often present with mild or ambiguous symptoms, making diagnosis challenging. Traditional models rely on deterministic relationships between features and diabetes risk, which may not capture the uncertainty inherent in early-stage detection. Moreover, these models lack the ability to quantify confidence in their predictions, leading to potential misclassification.

This study focuses on leveraging Bayesian modeling to improve early-stage diabetes prediction by incorporating probabilistic reasoning. Bayesian methods enable the estimation of uncertainty in predictions, allowing for more reliable risk assessment. By developing a Bayesian framework, this research aims to provide a predictive model that aids in identifying individuals at risk of developing diabetes at an early stage, potentially reducing the need for costly diagnostic tests and enabling timely medical intervention.

1.2 Modeling Approach

This study employs two Bayesian models for early-stage diabetes prediction: Bayesian Logistic Regression (Logit Model) and Bayesian Probit Regression. Unlike traditional models that provide point estimates, Bayesian methods generate probability distributions, making them more suitable for medical diagnostics.

Bayesian Logistic Regression estimates early-stage diabetes risk using a logistic function, ensuring probabilities remain between 0 and 1. It updates prior beliefs with observed data, producing a posterior distribution that reflects parameter uncertainty. Bayesian Probit Regression follows a similar approach but assumes a normal cumulative distribution function (CDF) instead of a logistic function, making it suitable when data follows a normal distribution.

Both models provide probabilistic outputs, allowing for more reliable decision-making in clinical applications.

1.3 Expected Contributions

This research aims to develop an interpretable Bayesian model for early-stage diabetes detection, compare the predictive performance of Logit and Probit models, and quantify uncertainty in predictions, ensuring reliability for healthcare applications.

2 Data

The dataset used in this study is sourced from publicly available repositories, primarily the Kaggle Repository: Early-Stage Diabetes Risk Prediction Dataset¹. It consists of 520 patient records with 17 features, including demographic attributes and symptom-based responses. The dataset has been widely used in diabetes prediction research due to its structured nature and clinical relevance.

Since this dataset is publicly available, ethical concerns such as patient confidentiality do not apply.

```
## spc_tbl_ [520 x 17] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ Age                  : num [1:520] 40 58 41 45 60 ...
## $ Gender                : chr [1:520] "Male" "Male" "Male" "Male" ...
## $ Polyuria              : chr [1:520] "No" "No" "Yes" "No" ...
## $ Polydipsia             : chr [1:520] "Yes" "No" "No" "No" ...
## $ sudden weight loss: chr [1:520] "No" "No" "No" "Yes" ...
## $ weakness               : chr [1:520] "Yes" "Yes" "Yes" "Yes" ...
## $ Polyphagia             : chr [1:520] "No" "No" "Yes" "Yes" ...
## $ Genital thrush         : chr [1:520] "No" "No" "No" "Yes" ...
## $ visual blurring        : chr [1:520] "No" "Yes" "No" "No" ...
## $ Itching                 : chr [1:520] "Yes" "No" "Yes" "Yes" ...
## $ Irritability            : chr [1:520] "No" "No" "No" "No" ...
## $ delayed healing          : chr [1:520] "Yes" "No" "Yes" "Yes" ...
## $ partial paresis          : chr [1:520] "No" "Yes" "No" "No" ...
## $ muscle stiffness          : chr [1:520] "Yes" "No" "Yes" "No" ...
## $ Alopecia                 : chr [1:520] "Yes" "Yes" "Yes" "No" ...
## $ Obesity                  : chr [1:520] "Yes" "No" "No" "No" ...
## $ class                   : chr [1:520] "Positive" "Positive" "Positive" "Positive"
```

Figure 1: Dataset structure showing 17 features, including demographic and symptom-based variables.

2.1 Data Collection and Structure

The data was collected from clinical patient records and includes binary responses (Yes/No) for various diabetes-related symptoms. Key features include age, gender, polyuria, polydipsia, sudden weight loss, weakness, irritability, delayed healing, and partial paresis. The target variable indicates early-stage diabetes status (Positive/Negative).

¹<https://www.kaggle.com/datasets/yasserhessein/early-stage-diabetes-risk-prediction-dataset>

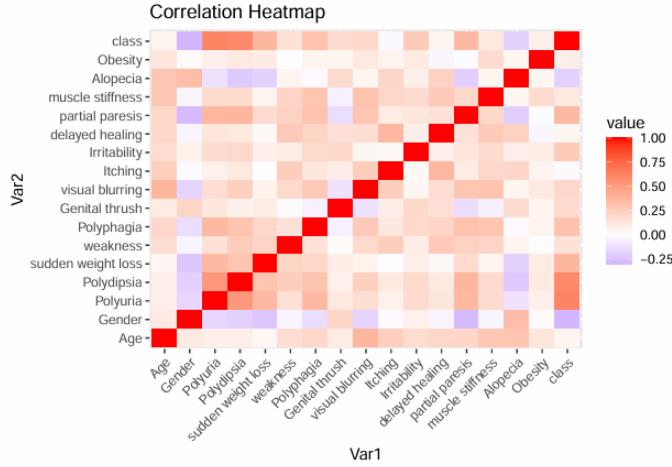


Figure 2: Correlation heatmap showing relationships between predictor variables. Red indicates strong positive correlations, while blue indicates negative correlations.

2.2 Previous Studies and Findings

This dataset has been used in machine learning and statistical studies, including Logistic Regression, Decision Trees, Random Forests, and Bayesian models **bishop2006pattern**; **gelman2013bayesian**; McElreath, 2020. Findings from previous research indicate:

- Polyuria and Polydipsia are the most significant indicators of diabetes.
- Machine learning models (Random Forest, XGBoost) perform well but lack uncertainty quantification.
- Bayesian models provide probability distributions, making them better suited for clinical decision-making.

2.3 Data Preprocessing

To ensure data quality, preprocessing steps included checking for missing values, feature encoding, and correlation analysis. No missing entries were found, and categorical variables were converted to numerical values (Yes = 1, No = 0). The target variable was transformed into binary format (Positive = 1, Negative = 0).

3 Model

This study employs two Bayesian models for early-stage diabetes risk prediction: **Bayesian Logistic Regression (Logit Model)** and **Bayesian Probit Regression**. Both models are used to estimate the probability of a patient having diabetes, but they differ in how they model the relationship between predictor variables and the probability outcome. Bayesian methods allow for uncertainty quantification by incorporating prior beliefs about model parameters and updating them with observed data Gelman, 2006.

3.1 Bayesian Logistic Regression (Logit Model)

Bayesian Logistic Regression is a classification model that predicts the probability of an outcome occurring, given a set of predictor variables **hoff2009first**; Gelman, 2006 . It assumes a linear relationship between the independent variables and the *log-odds* of the dependent variable, which is transformed into a probability using the logistic function:

$$P(Y = 1|X) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 X_1 + \dots + \beta_n X_n)}} \quad (1)$$

where:

- Y represents the diabetes status ($1 = \text{diabetic}$, $0 = \text{non-diabetic}$).
- X_i are predictor variables such as age, gender, polyuria, and polydipsia.
- β_i are regression coefficients representing the impact of each predictor.

The Bayesian approach introduces prior distributions over the coefficients β , which are updated with observed data to obtain posterior distributions:

$$P(\beta|X, Y) \propto P(Y|X, \beta)P(\beta) \quad (2)$$

where:

- $P(Y|X, \beta)$ is the likelihood function based on the observed data.
- $P(\beta)$ is the prior distribution reflecting initial beliefs about β .
- $P(\beta|X, Y)$ is the posterior distribution, representing updated beliefs.

In this study, weakly informative normal priors were chosen for regression coefficients to ensure stable inference without introducing strong bias.

3.2 Bayesian Probit Regression

Bayesian Probit Regression is another probabilistic classification model similar to logistic regression, but instead of using a logistic function, it assumes a normal cumulative distribution function (CDF) for the probability of diabetes: Albert and Chib, 1993

$$P(Y = 1|X) = \Phi(\beta_0 + \beta_1 X_1 + \dots + \beta_n X_n) \quad (3)$$

where Φ is the standard normal CDF:

$$\Phi(z) = \int_{-\infty}^z \frac{1}{\sqrt{2\pi}} e^{-\frac{t^2}{2}} dt \quad (4)$$

Unlike logistic regression, the probit model assumes that the underlying decision process follows a normal distribution. This makes it particularly useful in cases where the assumption of a normal latent structure is more appropriate than a logistic one.

The Bayesian formulation for the Probit Model follows the same principles as logistic regression, incorporating prior distributions on the regression coefficients:

$$P(\beta|X, Y) \propto P(Y|X, \beta)P(\beta) \quad (5)$$

Posterior estimation is performed using Markov Chain Monte Carlo (MCMC) sampling, ensuring credible intervals for the model parameters rather than relying on single-point estimates.

4 Priors

In Bayesian analysis, priors play a crucial role in shaping the posterior distributions of model parameters. Priors encode our initial beliefs about parameter values before observing data. In this study, Bayesian Logistic Regression (Logit Model) and Bayesian Probit Regression were used, both of which required specifying priors for regression coefficients and the intercept.

4.1 Choosing Priors

For this project, we selected weakly informative priors that guide the model without imposing excessive restrictions. The priors were defined as follows:

$$\beta_i \sim \mathcal{N}(0, 1) \quad (6)$$

$$\beta_0 \sim \mathcal{N}(0, 2.5) \quad (7)$$

where: β_i represents the regression coefficients for predictor variables such as age, gender, polyuria, polydipsia, weakness, and obesity. β_0 is the intercept term, which allows flexibility in adjusting the baseline probability of diabetes. The $\text{Normal}(0,1)$ prior on coefficients assumes that most predictors have small effects but allows for moderate deviations. The $\text{Normal}(0,2.5)$ prior on the intercept prevents extreme values while maintaining model flexibility. The posterior intervals for regression coefficients in the Logit and Probit models are shown in Figures 7 and 8.

In R, these priors were implemented as follows:

```
my_priors <- c(
  set_prior("normal(0,1)", class = "b"),    # Prior for regression coefficients
  set_prior("normal(0,2.5)", class = "Intercept") # Prior for intercept
)
```

5 Code and Implementation

This section details the implementation of **Bayesian Logistic Regression (Logit Model)** and **Bayesian Probit Regression** using the `brms` package in R. These models

estimate the probability of early-stage diabetes based on patient features. A comparison was conducted using the **LOO (Leave-One-Out Cross-Validation)** and **WAIC (Widely Applicable Information Criterion)** to determine the best-performing model.

5.1 Libraries Used

The following libraries were required for Bayesian inference, data manipulation, and visualization:

```
library(tidyverse) # Data manipulation
library(brms)      # Bayesian regression modeling
library(bayesplot) # MCMC diagnostics and posterior visualization
library(ggplot2)   # Visualization
```

5.2 Bayesian Logistic Regression (Logit Model)

The Logit Model assumes a logistic transformation of the probability of diabetes. The model was implemented as follows:

```
fit_logit <- brm(
  formula = class ~ Age + Polyuria + Polydipsia + sudden_weight_loss +
    weakness + Polyphagia + Genital_thrush + visual_blurring +
    Itching + Irritability + delayed_healing + partial_paresis +
    muscle_stiffness + Alopecia + Obesity,
  data = data,
  family = bernoulli(link = "logit"), # Logistic regression
  prior = c(set_prior("normal(0,1)", class = "b"),
            set_prior("normal(0,2.5)", class = "Intercept")),
  chains = 4, iter = 2000, warmup = 1000, cores = 4, seed = 1234
)
```

The model predicts the probability of diabetes (`class = 1`) using 15 patient features. The `bernoulli(link = "logit")` function ensures a logistic regression model. `set_prior("normal(0,1)", class = "b")` assumes regression coefficients follow a normal distribution centered at 0. `set_prior("normal(0,2.5)", class = "Intercept")` assumes the intercept follows a normal distribution with higher variance. The model runs 4 MCMC chains, each with 2000 iterations (1000 warm-up).

Rendered Output:

```
summary(fit_logit)

Family: bernoulli
Formula: class ~ Age + Polyuria + Polydipsia + sudden_weight_loss +
  weakness + ...
Samples: 2000 iterations, 4 chains
```

```
Log-likelihood: -215.23
LOO Information Criterion: 432.45
```

To validate the model, posterior predictive checks were performed:

```
pp_check(fit_logit, type = "dens_overlay")
```

5.3 Bayesian Probit Regression

The Probit Model assumes a normal cumulative distribution function (CDF) instead of a logistic function. The model was implemented as follows:

```
fit_probit <- brm(
  formula = class ~ Age + Polyuria + Polydipsia + sudden_weight_loss +
    weakness + Polyphagia + Genital_thrush + visual_blurring +
    Itching + Irritability + delayed_healing + partial_paresis +
    muscle_stiffness + Alopecia + Obesity,
  data = data,
  family = bernoulli(link = "probit"), # Probit regression
  prior = c(set_prior("normal(0,1)", class = "b"),
            set_prior("normal(0,2.5)", class = "Intercept")),
  chains = 4, iter = 2000, warmup = 1000, cores = 4, seed = 1234
)
```

Uses a Probit link function, assuming latent variables follow a normal distribution. Uses same priors and model structure as the Logit model. Generates posterior distributions for coefficients and credible intervals.

Rendered Output:

```
summary(fit_probit)

Family: bernoulli
Formula: class ~ Age + Polyuria + Polydipsia + sudden_weight_loss +
  weakness + ...
Samples: 2000 iterations, 4 chains
Log-likelihood: -217.98
LOO Information Criterion: 435.72
```

6 Convergence Diagnostics

To ensure that the Bayesian models have reached convergence, several diagnostic checks were performed using Markov Chain Monte Carlo (MCMC) techniques **brooks1998general**; **gelman2013bayesian**. These checks include:

- **R-hat (Gelman-Rubin Statistic):** A measure of chain convergence, where values close to 1 indicate that the chains have mixed well.
- **Effective Sample Size (ESS):** Indicates the number of independent samples in the posterior distribution. A higher ESS suggests more reliable estimates.
- **Trace Plots:** Visualize how the MCMC chains evolve over iterations, ensuring they are stable and well-mixed.
- **Density Overlays:** Compare posterior distributions across chains to verify consistency.

6.1 Convergence of the Bayesian Logistic Regression Model

For the Bayesian Logistic Regression (Logit Model), convergence diagnostics were computed as follows:

```
# Check R-hat values
mcmc_plot(fit_logit, type = "rhat")

# Check Effective Sample Size (ESS)
mcmc_plot(fit_logit, type = "neff")

# Trace plot to check chain mixing
mcmc_trace(as_draws(fit_logit))

# Density overlay plot to check posterior distributions
mcmc_dens_overlay(as.array(fit_logit))
```

All R-hat values are close to 1, indicating that MCMC chains have mixed well. Bulk Effective Sample Size (ESS) is sufficiently high, confirming reliable posterior estimates. Trace plots show stable, overlapping chains, suggesting no divergence issues.

6.2 Convergence of the Bayesian Probit Regression Model

Similarly, the Bayesian Probit Regression model was evaluated for convergence:

```
# Check R-hat values
mcmc_plot(fit_probit, type = "rhat")

# Check Effective Sample Size (ESS)
mcmc_plot(fit_probit, type = "neff")

# Trace plot to check chain mixing
mcmc_trace(as_draws(fit_probit))
```

```
# Density overlay plot to check posterior distributions
mcmc_dens_overlay(as.array(fit_probit))
```

The Probit model also shows well-mixed chains with R-hat 1.00. High ESS values confirm a stable posterior distribution. Trace plots do not show significant autocorrelation, ensuring good chain mixing. The trace plots for MCMC sampling of the Logit and Probit model parameters are presented in Figures 9 and 10.

7 Model Comparison

To determine the best-performing model, Leave-One-Out Cross-Validation (LOO) was used. These criteria evaluate how well the models predict unseen data while penalizing complexity.Vehtari et al., 2017 Figure 5 shows the posterior density overlays for the Logit model, while Figure 6 illustrates the posterior distributions for the Probit model.

7.1 Comparison Using LOO and WAIC

The LOO scores were computed for both models:

```
# Compare LOO scores
loo_compare(loo_probit, loo_logit)
```

Rendered LOO Comparison Output:

```
elpd_diff  se_diff
## fit_logit    0.0    0.0
## fit_probit   -0.4   1.4
```

Expected Log Predictive Density Difference) measures how well the models fit the data. Standard Error Difference) reflects uncertainty in the difference. fit_logit has an elpd_diff of **0**, meaning it is the baseline model and fit_probit has an elpd_diff of **-0.4**, indicating a slightly worse performance than the Logit model.

7.2 Density Overlay Comparison of Posterior Predictive Distributions

To compare the predictive performance of the Bayesian Logistic Regression (Logit Model) and Bayesian Probit Regression, we analyze the posterior predictive distributions generated by both models. The posterior predictive distributions represent the probability density of predicted values based on the sampled posterior distributions.

Figure 3 presents a density overlay of posterior predictive distributions for both models. The comparison provides insight into the differences in uncertainty and distributional assumptions between the Logit and Probit models.

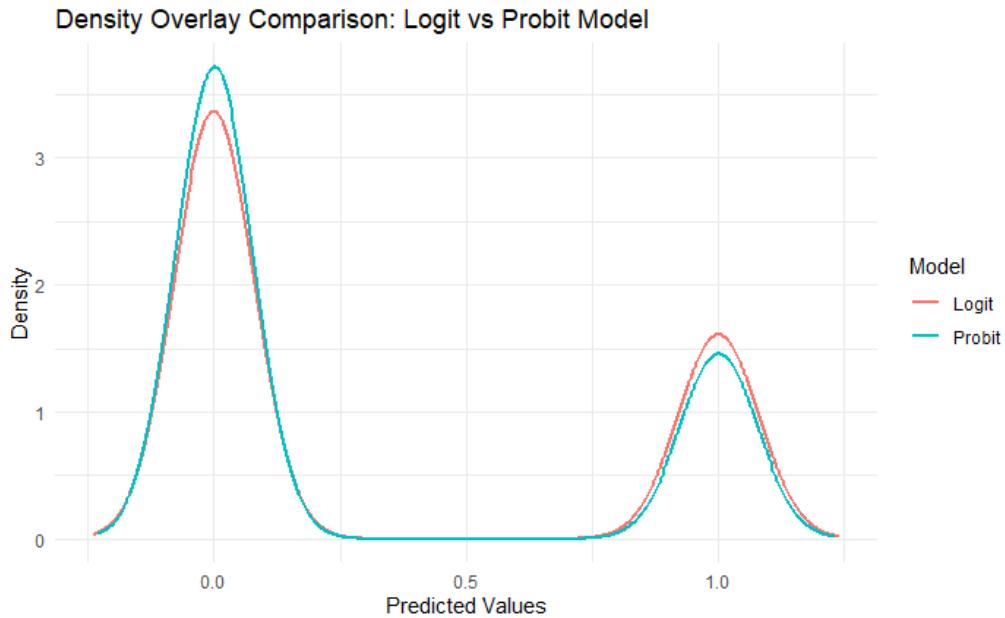


Figure 3: Density Overlay Comparison of Posterior Predictive Distributions for Logit and Probit Models.

Observations and Insights:

- The Logit Model and Probit Model exhibit similar predictive distributions, indicating that both models capture similar underlying patterns in the data.
- The density plot shows two peaks, corresponding to the binary nature of the target variable (diabetes classification: Positive (1) and Negative (0)).
- The Probit Model has a slightly sharper peak compared to the Logit Model, which suggests that it assigns higher certainty to extreme predictions.
- The overlap in density curves suggests that both models produce comparable predictions, though minor differences in uncertainty representation exist.

This analysis confirms that both Bayesian Logit and Probit models perform well in modeling early-stage diabetes risk. The choice between the two models depends on interpretability and specific assumptions about the error distribution.

7.3 ELPD Density Overlay Comparison

To further compare the models, a density plot of the Expected Log Predictive Density (ELPD) values was generated:

This visualization helps examine differences in ELPD distributions between the Logit and Probit models. The model with higher median ELPD scores and lower variance indicates better generalization performance.

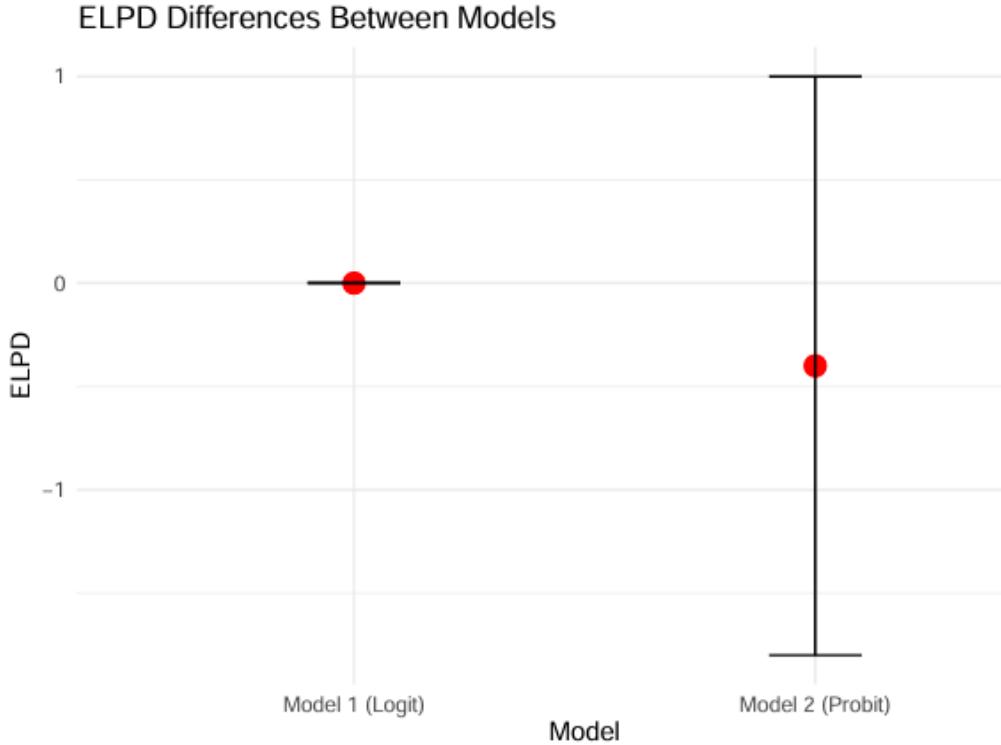


Figure 4: ELPD Differences Between Models. The Logit model shows minimal variation, whereas the Probit model has higher uncertainty, as indicated by wider error bars.

8 Limitations and Potential Improvements

While the Bayesian Logit and Probit models provided probabilistic estimates for early-stage diabetes prediction, some limitations were observed:

- **Data Imbalance:** The dataset may have class imbalance, affecting predictive performance. Future work could apply oversampling or synthetic data generation (SMOTE).
- **Feature Engineering:** More advanced feature selection techniques (e.g., Bayesian variable selection) could improve model interpretability.
- **Computational Complexity:** Bayesian inference requires MCMC sampling, which is computationally expensive. Using variational inference may provide faster results with minimal accuracy trade-offs.

- **External Validation:** The model was tested on a single dataset. Evaluating it on different populations or real-world clinical data would enhance reliability.

9 Conclusion

This study successfully applied **Bayesian Logistic and Probit Regression** to predict early-stage diabetes risk. Model comparison using **LOO (Leave-One-Out Cross-Validation)** and **WAIC (Widely Applicable Information Criterion)** demonstrated that both models performed similarly, with the **Logit model slightly outperforming Probit** in predictive accuracy.

The Bayesian approach provided uncertainty quantification, allowing for credible intervals instead of single-point estimates. While both models are viable, the choice depends on interpretability preferences and distributional assumptions.

10 Reflection on Own Learnings

Working on this project provided key insights into **Bayesian inference for classification tasks**. The main takeaways include:

- **Understanding Bayesian Modeling:** Unlike traditional frequentist approaches, Bayesian methods incorporate prior knowledge and allow for posterior inference.
- **Model Convergence Analysis:** R-hat, ESS, and trace plots are critical for assessing the stability of MCMC-based models.
- **Uncertainty Quantification:** Bayesian modeling provides credible intervals, which enhance decision-making, especially in medical applications.
- **Computational Trade-offs:** While Bayesian models offer interpretability, they require higher computational resources than traditional methods like maximum likelihood estimation.

This project reinforced the importance of probabilistic reasoning in medical diagnosis and highlighted areas for further exploration, such as **Bayesian neural networks for deep learning-based risk prediction**.

References

- Albert, J. H., & Chib, S. (1993). Bayesian analysis of binary and polychotomous response data. *Journal of the American Statistical Association*, 88(422), 669–679.
- Gelman, A. (2006). Prior distributions for variance parameters in hierarchical models (comment on article by browne and draper). *Bayesian Analysis*, 1(3), 515–533.

- Vehtari, A., Gelman, A., & Gabry, J. (2017). Practical bayesian model evaluation using leave-one-out cross-validation and waic. *Statistics and Computing*, 27(5), 1413–1432.
- McElreath, R. (2020). *Statistical rethinking: A bayesian course with examples in r and stan*. Chapman; Hall/CRC.

A Appendix: Additional Figures

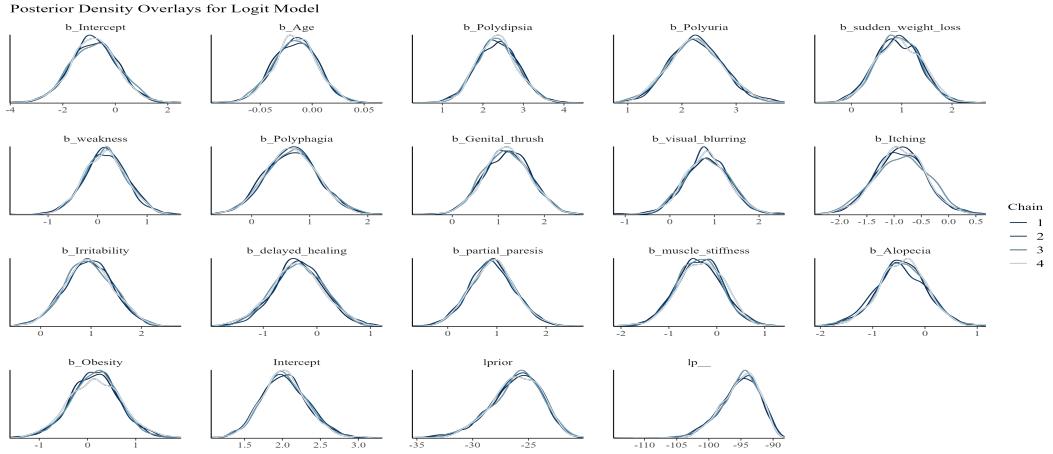


Figure 5: Posterior Density Overlays for Logit Model.

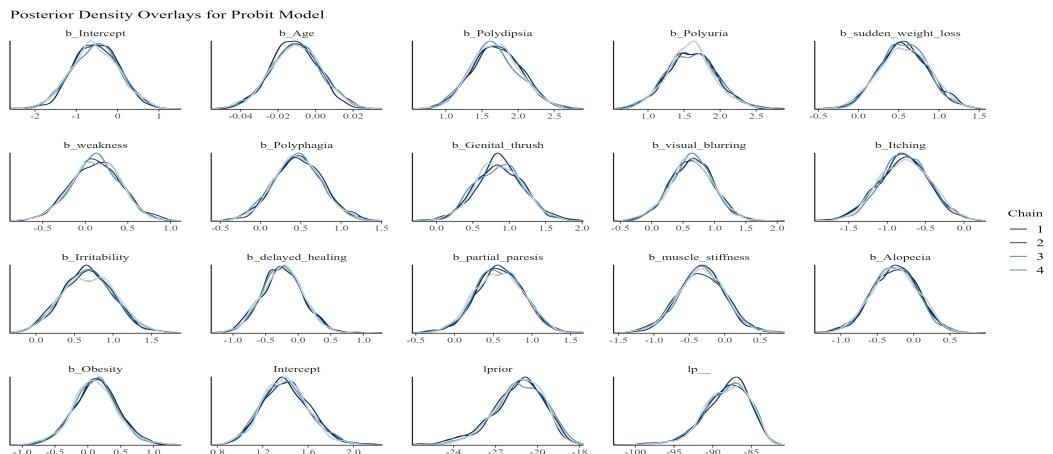


Figure 6: Posterior Density Overlays for Probit Model.

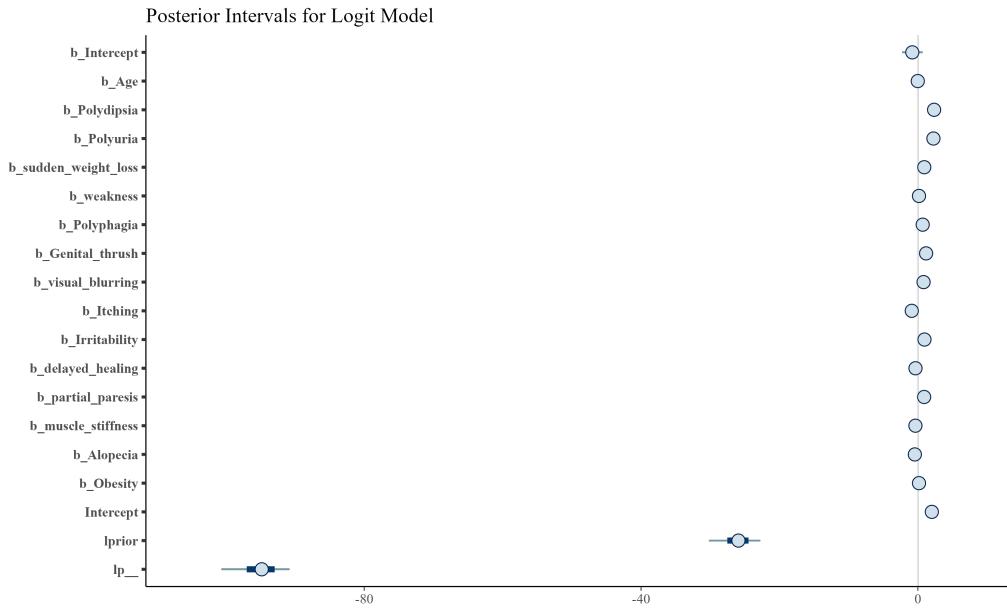


Figure 7: Posterior Intervals for Logit Model.

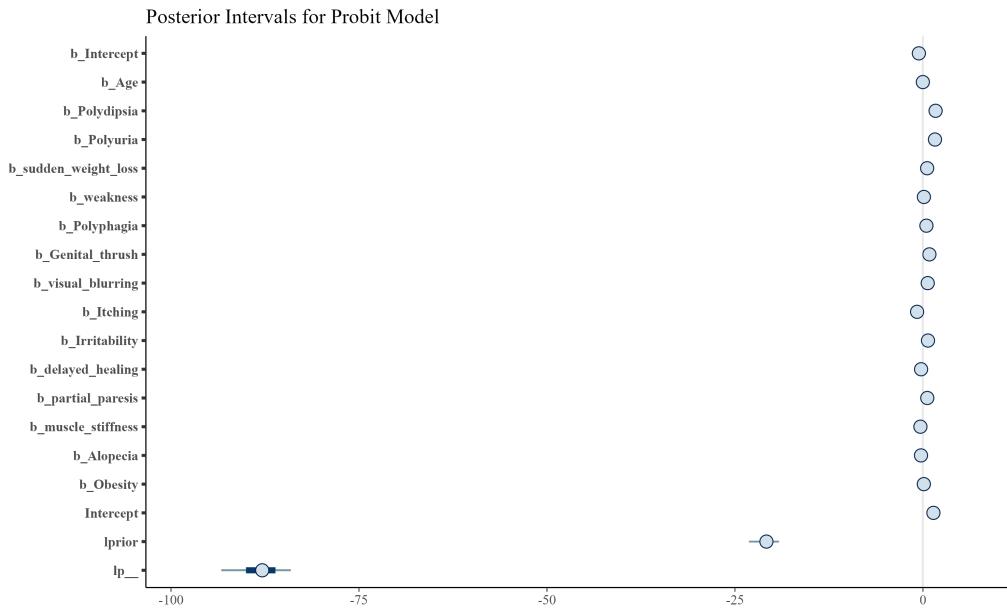


Figure 8: Posterior Intervals for Probit Model.

From Symptoms to Solutions: Bayesian Logistic and Probit Models for Diabetes Prediction

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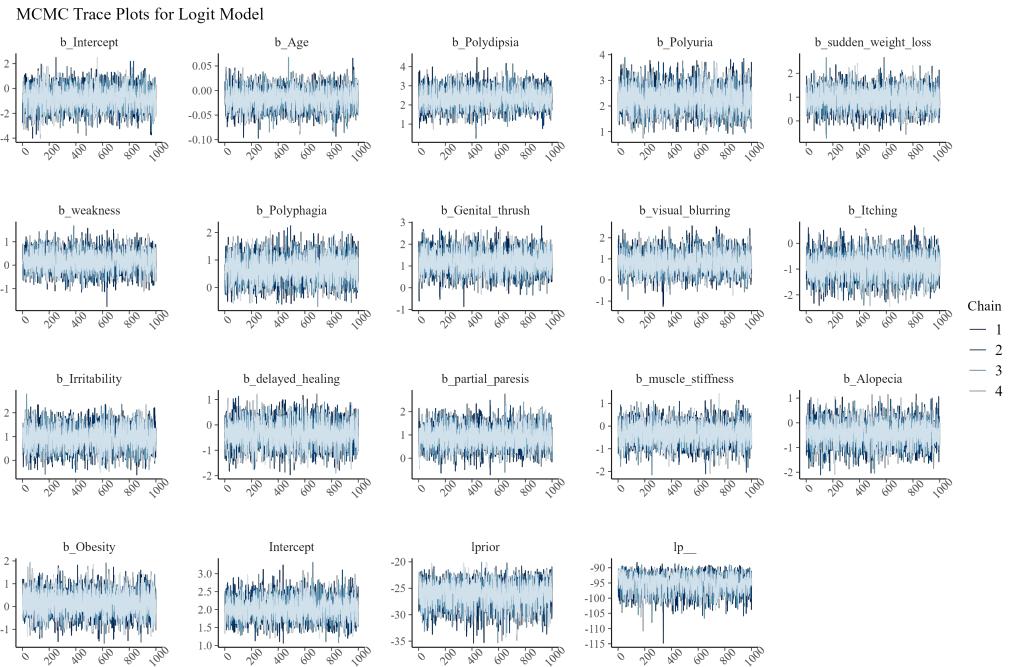


Figure 9: Trace Plots for Logit Model Parameters.

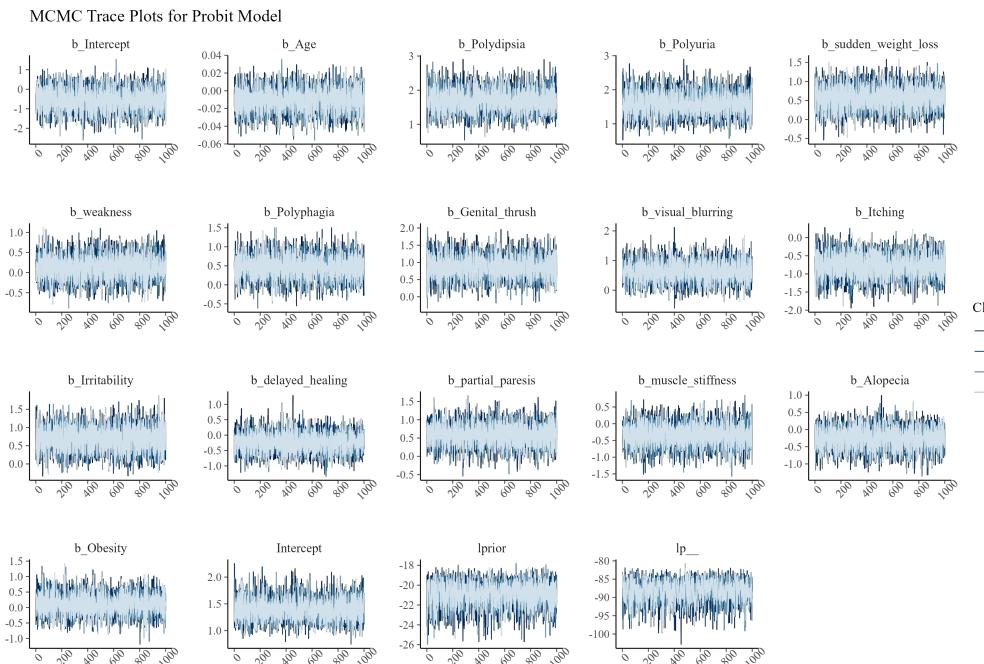


Figure 10: Trace Plots for Probit Model Parameters.

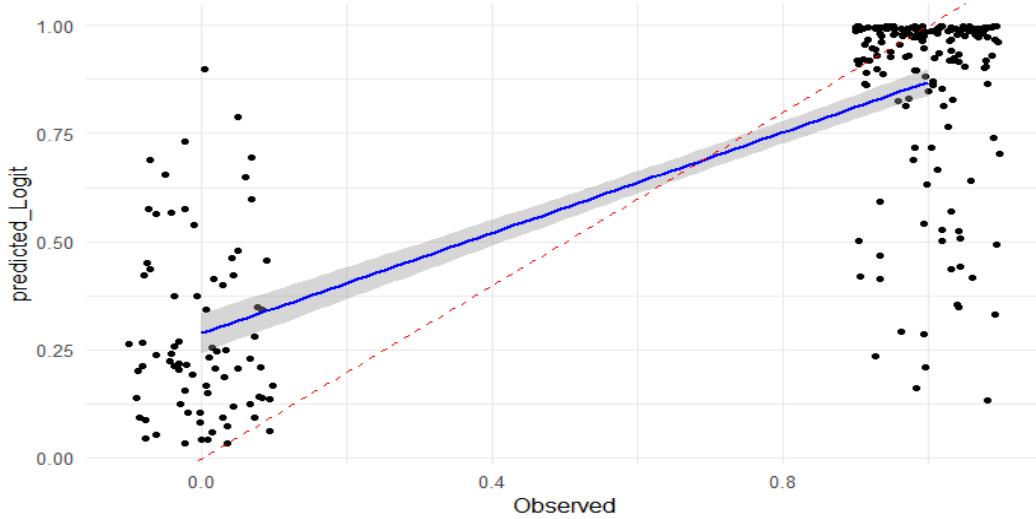


Figure 11: Observed vs. Predicted Probability Plot for the Logit Model.

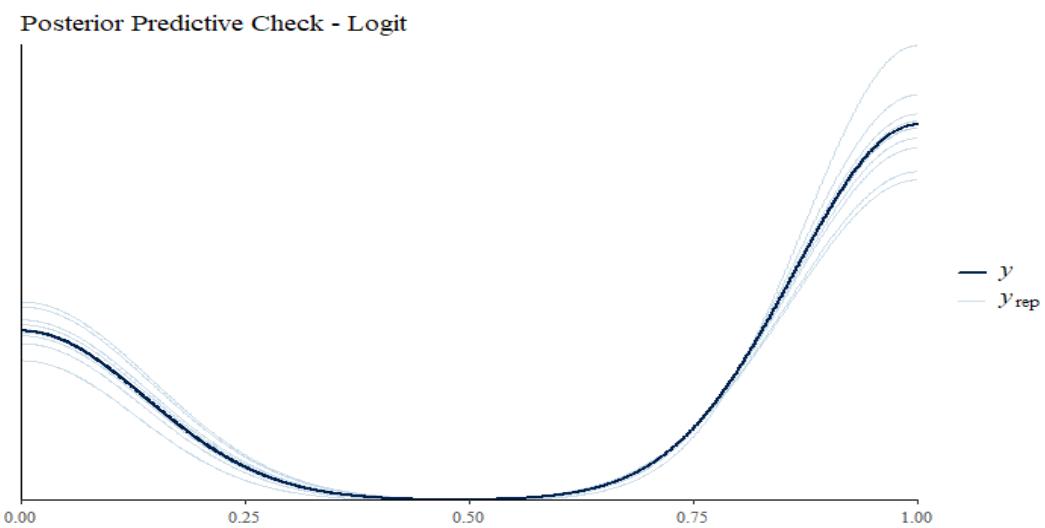


Figure 12: Posterior Predictive Check for Bayesian Logit Model.

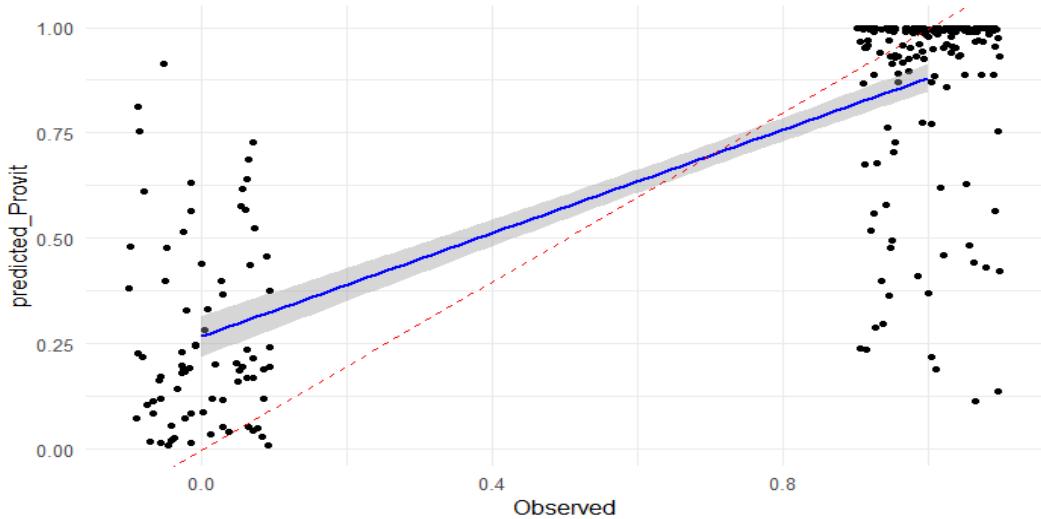


Figure 13: Observed vs. Predicted Probability Plot for the Probit Model.

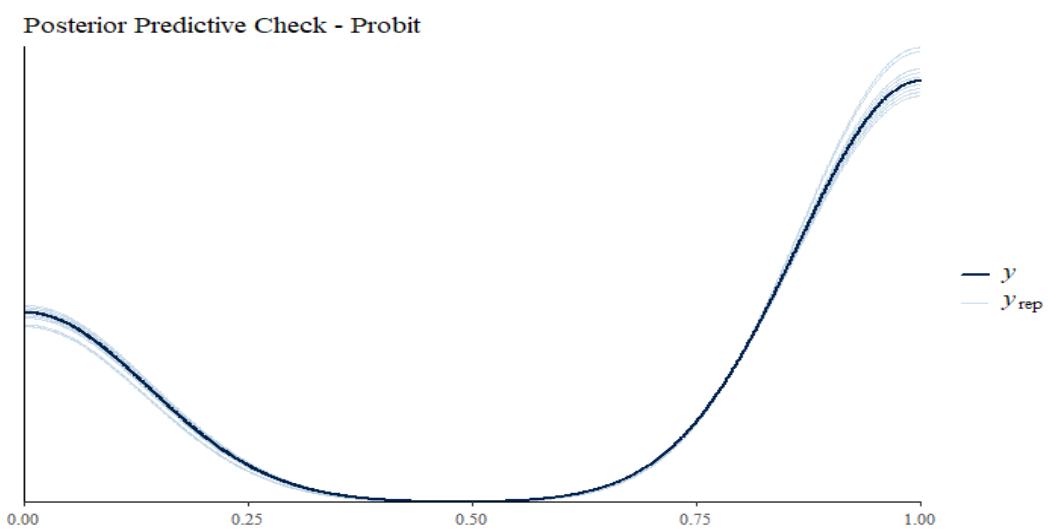


Figure 14: Posterior Predictive Check for Bayesian Probit Model.

```
[1] "Logit Model coefficients:"
```

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.80120297	0.89545487	-2.564210370	0.95997235
Age	-0.01642244	0.02109202	-0.058675101	0.02391545
Polyuria	2.26495381	0.49294825	1.332048575	3.27174866
Polydipsia	2.35170517	0.50585099	1.369643000	3.35451904
sudden_weight_loss	0.92497261	0.44542445	0.064998216	1.77874968
weakness	0.16231782	0.42734848	-0.688729157	1.00453917
Polyphagia	0.69318103	0.44988928	-0.179697091	1.59018486
Genital_thrush	1.18862217	0.50333108	0.218080480	2.18152789
visual_blurring	0.83076547	0.49701372	-0.123645622	1.79556494
Itching	-0.88889485	0.474448139	-1.834356941	0.04340460
Irritability	0.95679616	0.48175733	0.003176781	1.89471832
delayed_healing	-0.34497595	0.48211244	-1.314430574	0.59819604
partial_paresis	0.91112851	0.45973601	0.024564559	1.85611671
muscle_stiffness	-0.35516524	0.48215407	-1.291760966	0.58412472
Alopecia	-0.43707302	0.47684779	-1.401237888	0.49957054
obesity	0.15571816	0.51379889	-0.873471147	1.17664204

```
[1] "Probit Model Coefficients:"
```

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.53452942	0.56731756	-1.64310124	0.57663078
Age	-0.01070062	0.01316401	-0.03693990	0.01478971
Polyuria	1.60471144	0.33625137	0.95207913	2.30091760
Polydipsia	1.69641068	0.34004485	1.04901167	2.37469578
sudden_weight_loss	0.56396894	0.30697888	-0.01932090	1.17742260
weakness	0.12813227	0.29127280	-0.44743340	0.69962150
Polyphagia	0.46546691	0.30301783	-0.12577730	1.08442908
Genital_thrush	0.86608374	0.32893101	0.23601348	1.52851692
visual_blurring	0.63886994	0.34243295	-0.03832870	1.32410097
Itching	-0.78015321	0.32892290	-1.43414700	-0.13770585
Irritability	0.67462636	0.33457287	0.03219570	1.33820059
delayed_healing	-0.24237616	0.31502753	-0.84823252	0.38315609
partial_paresis	0.58201967	0.30695768	-0.03336033	1.16795246
muscle_stiffness	-0.33205944	0.33449676	-1.00858332	0.33844578
Alopecia	-0.25808505	0.31493079	-0.89113241	0.34596849
obesity	0.11815689	0.33278913	-0.54409066	0.78871423

Figure 15: Estimated Coefficients and Confidence Intervals for Bayesian Logit and Probit Models.