

A Bayesian Approach To Modelling Pregnancy Risks Using Latent Gaussian Model

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ABSTRACT

A latent Gaussian model (LGM) that follows a Gaussian Markov random field was developed for pregnancy risk data. Inference was done through INLA. Sensitivity analysis was done to adjust for underweight bias in BMI. Positive maternal Hepatitis B status (HBsAg) was the strongest risk factor, increasing the odds of high-risk pregnancy more than 300-fold (AOR = 313.69, 95% CI: 43.72–39,858.39). Elevated systolic blood pressure independently increased the odds by 4.3% per unit increase (AOR = 1.043, 95% CI: 1.025–1.061). In contrast, a negative blood or urine sugar test reduced the odds by 54.6% (AOR = 0.454, 95% CI: 0.285–0.723), while each unit increase in BMI within the normal-to-overweight range reduced the odds by 31% (AOR = 0.690, 95% CI: 0.634–0.743). LGM was comparable to classical logistic model (AUC $\approx$ 0.734; accuracy 70.54% vs. 70.44%). Prior sensitivity analysis demonstrated the robustness of LGM to prior specifications.

1. Introduction

The early detection of pregnancy risks emerges as a pivotal approach to facilitating timely and targeted interventions by healthcare professionals [1-2]. Identifying high-risk pregnancies is a critical step in ensuring maternal and fetal health, however, it remains an ongoing research area due to the complexity and variability of the factors involved [3-4]. The successful progression of pregnancy and the birth of a healthy baby requires the establishment of remarkably complex maternal-fetal interactions at the interface between the two organisms. Studying these mechanisms is critical for deepening our understanding of human development, uncovering the causes of pregnancy complications, and developing strategies to improve maternal-fetal health [5].

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Efforts have gone into developing models to assess pregnancy risks, Bayesian approaches has seen Amoche et al.[6] fit a Bayesian hierarchical logistic random intercept model for modeling risk of miscarriage during first trimester of subsequent intrauterine pregnancy. Negesse and Abebe[7] binary logistic regression analysis using Brms R-package to assess factors associated with preterm birth at public hospitals in Sidama regional state. Onatunji et al.[8] applied Bayesian Logit model to calculate probabilities of different systolic blood pressure outcomes among pregnant women in LAUTECH Teaching Hospital, Oyo State. In terms of spatial approach to fertility dynamics, Ekong and Olayiwola [9] examined the dynamics of fertility rate across Africa using geographically weighted regression.

Machine learning has seen Pi et al.[10] employed multilayer perceptron (MLP), logistic regression (LR), decision tree (DT), random forest (RF), eXtreme Gradient Boosting (XGBoost), and support vector machine (SVM) to construct predictive models for high-risk pregnancy among expectant mothers. Togunwa et al.[3] applied artificial neural networks (ANN) and random forest (RF) algorithms for risk classification in pregnant women. Mustamin et al.[1] classified maternal health risk using the Naive Bayes method with three models-Gaussian, Multinomial, and Bernoulli. Bosschietter et al.[2] used explainable boosting machine (EBM), a machine learning approach for the prediction and identification of important risk factors in pregnancy. McLachlan et al.[11] used Bayesian network that combined expert elicitation with knowledge from literature and national health statistics for classification of pregnancy complications and outcomes using national health statistics for all births in England and Wales during 2021.

This study presents a latent Gaussian model (LGM) which is a subset of hierarchical Bayesian additive models where the observed responses are conditionally independent based on the likelihood hyperparameters θ and the linear predictor η . Within this framework the joint posterior density and subsequently the marginal posterior densities, can be efficiently and accurately calculated using the integrated nested Laplace approximation (INLA) methodology [12]. INLA has become pervasive in Bayesian statistical inference for hierarchical models in different applications, see [13-17].

2.0 Methodology

2.1 Latent Gaussian model

LGMs are defined by

$$\eta = \beta_0 + \beta X + \sum_{m=1}^M f_m(u_{im}) + \epsilon_i \quad (1)$$

where β represent the linear fixed effects of the covariates X , ϵ is the unstructured random effects and the $\{f_k(\cdot)\}$'s represent unknown (non-linear) functions of the covariates u . A latent field χ is the vector of additive predictor as $\{\beta_0, \beta, \{f_k(\cdot)\}, \eta\}$ with a multivariate Gaussian prior, such that χ forms a Gaussian Markov random field with sparse precision matrix matrix $Q(\theta_2)$, i.e. $\chi \sim N(0, Q^{-1}(\theta_2))$. A prior, $\pi(\theta)$, can then be formulated for the set of hyperparameters $\theta = (\theta_1, \theta_2)$. From this hierarchical Bayesian formulation the joint posterior distribution is then given as follows:

$$\pi(\chi, \theta | y) \propto \pi(\theta) \pi(\chi | \theta) \prod_i \pi(y_i | \chi, \theta) \quad (2)$$

2.2 Hierarchical latent Gaussian model for pregnancy risk

Given a pregnant individual j , then the likelihood of having a high risk pregnancy is given as

$$Y_j \sim \text{Bernoulli}(p_j), \quad (3)$$

and the linear predictor is

$$\eta = \text{logit}(p_j) = \alpha + \mathbf{X}_j^T \boldsymbol{\beta} + u_j \quad (4)$$

where α is intercept, u_j is structured random effects, and $\boldsymbol{\beta}$ is vector of coefficients corresponding to the individual-specific covariate vector $\mathbf{X}$. $\boldsymbol{\chi} = \{\alpha, \boldsymbol{\beta}, \mathbf{u}, \eta\}$ and $\boldsymbol{\chi} \sim N(\mathbf{0}, \mathbf{Q}^{-1}(\boldsymbol{\theta}_2))$ as

$$P(\boldsymbol{\chi}|\boldsymbol{\theta}) = (2\pi)^{pm} |\mathbf{Q}(\boldsymbol{\theta}_2)|^{-\frac{1}{2}} \exp\left(-\frac{1}{2} \boldsymbol{\chi}' \mathbf{Q}(\boldsymbol{\theta}_2) \boldsymbol{\chi}\right). \quad (5)$$

Priors are assumed for the vector of fixed effects as $\boldsymbol{\beta} \sim N(\mathbf{0}, \tau_\beta \mathbf{I})$, $\alpha \sim N(0, \tau_\alpha)$, $\mathbf{u} \sim N(\mathbf{0}, \boldsymbol{\Sigma})$ and $\boldsymbol{\Sigma} \sim \text{PC}(\sigma)$ $p_j \sim \text{Beta}(1, 19)$ where $\boldsymbol{\beta}, \alpha, \mathbf{u} \in \boldsymbol{\chi}$ and $p_j, \tau_\alpha, \tau_\beta, \boldsymbol{\Sigma} \in \boldsymbol{\theta}$.

From this hierarchical Bayesian formulation the joint posterior distribution is then given as:

$$\begin{aligned} p(\boldsymbol{\chi}, \boldsymbol{\theta}|\mathbf{D}) &\propto p(\boldsymbol{\theta}) p(\boldsymbol{\chi}|\boldsymbol{\theta}) \prod_i p(\mathbf{D}_i|\boldsymbol{\chi}, \boldsymbol{\theta}), \\ &\propto p(\boldsymbol{\theta}) |\mathbf{Q}(\boldsymbol{\theta}_2)|^{\frac{1}{2}} \exp\left(-\frac{1}{2} \boldsymbol{\chi}' \mathbf{Q}(\boldsymbol{\theta}_2) \boldsymbol{\chi}\right. \\ &\quad \left. + \sum_{i=1}^n \log(\mathbf{D}_i|\boldsymbol{\chi}_i, \boldsymbol{\theta})\right). \end{aligned} \quad (6)$$

where $\mathbf{D}$ is the observed data. Within this framework the joint posterior density (6) and subsequently the marginal posterior densities, $p(\boldsymbol{\chi}_i|\mathbf{D})$; $i = 1, \dots, n$ and $p(\boldsymbol{\theta}|\mathbf{D})$ can be efficiently and accurately calculated. The marginal posterior densities becomes

$$p(\boldsymbol{\chi}_i|\mathbf{D}) = \int p(\boldsymbol{\chi}_i, \boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta} = \int p(\boldsymbol{\chi}_i, \boldsymbol{\theta}|\mathbf{D}) p(\boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta}, \quad (7)$$

and

$$p(\boldsymbol{\theta}_i|\mathbf{D}) = \int p(\boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta}_{-i}, \quad (8)$$

where $d\boldsymbol{\theta}_{-i}$ denotes all the elements in $\boldsymbol{\theta}$ except the i -th element.

2.3 Posterior Estimation with INLA

The marginal posterior densities of $\boldsymbol{\chi}_i$ becomes

$$p(\boldsymbol{\chi}_i|\mathbf{D}) = \int p(\boldsymbol{\chi}_i, \boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta} = \int p(\boldsymbol{\chi}_i|\boldsymbol{\theta}, \mathbf{D}) p(\boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta} \quad (9)$$

and the marginal posterior of the j -th hyperparameter is

$$p(\boldsymbol{\theta}_i|\mathbf{D}) = \int p(\boldsymbol{\theta}|\mathbf{D}) d\boldsymbol{\theta}_{-j}. \quad (10)$$

First, $p(\boldsymbol{\theta}|\mathbf{D})$ from (10) is evaluated using Laplace approximation as

$$p(\boldsymbol{\theta}|\mathbf{D}) = \frac{p(\boldsymbol{\chi}, \boldsymbol{\theta}|\mathbf{D})}{p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})} = \frac{p(\mathbf{D}|\boldsymbol{\chi}, \boldsymbol{\theta})p(\boldsymbol{\chi}|\boldsymbol{\theta})p(\boldsymbol{\theta})}{p(\mathbf{D}|\boldsymbol{\theta})p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})} \quad (11)$$

based on the second-order Taylor expansion of $\log p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$ centered at the maximum a posteriori (MAP) estimate. $p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$ is given as

$$p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D}) \propto \exp\left(-\frac{1}{2}\boldsymbol{\chi}'\mathbf{Q}(\boldsymbol{\theta})\boldsymbol{\chi} + \sum_{i=1}^n g_i(\boldsymbol{\chi}_i)\right) \quad (12)$$

where $g_i(\boldsymbol{\chi}_i) = \log p(\mathbf{D}_i|\boldsymbol{\chi}_i, \boldsymbol{\theta})$. The approximation locates the posterior mode $\boldsymbol{\chi}^*(\boldsymbol{\theta})$, taking it as the mean of the Gaussian approximation [18]. The Gaussian approximation of $p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$, given as $p_G(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$ is obtained by matching the mode and the curvature at the mode of $p(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$. The mode is computed iteratively by using a Newton Raphson method. Let $\boldsymbol{\mu}^{(0)}$ be the initial value of the mode, and expand $g_i(\boldsymbol{\chi}_i)$ around $\boldsymbol{\mu}_i^{(0)} = (\mu_{i1}^{(0)}, \dots, \mu_{iN}^{(0)})$ to the second order Taylor expansion,

$$g_i(\boldsymbol{\chi}_i) \approx g_i(\boldsymbol{\mu}_i^{(0)}) + \mathbf{b}_i'\boldsymbol{\chi}_i - \frac{1}{2}\mathbf{c}_i'\boldsymbol{\chi}_i\boldsymbol{\chi}_i \quad (13)$$

where $\mathbf{b}_i$ and $\mathbf{c}_i$ depend on $\boldsymbol{\mu}^{(0)}$. Substituting equation (13) into equation (12) yields

$$\begin{aligned} p_G(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D}) &\approx g_i(\boldsymbol{\mu}_i^{(0)}) \exp\left(-\frac{1}{2}\boldsymbol{\chi}'(\mathbf{Q} + \mathbf{c})\boldsymbol{\chi} + \mathbf{b}'\boldsymbol{\chi}\right) \\ &\propto \exp\left(-\frac{1}{2}\boldsymbol{\chi}'(\mathbf{Q} + \mathbf{c})\boldsymbol{\chi} + \mathbf{b}'\boldsymbol{\chi}\right). \end{aligned} \quad (14)$$

The Gaussian approximation of $p_G(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$ is obtained, with the precision matrix $(\mathbf{Q} + \text{diag}(\mathbf{c}))$ and mode $\boldsymbol{\mu}^{(1)}$, which is the solution of $(\mathbf{Q} + \text{diag}(\mathbf{c}))\boldsymbol{\mu}^{(1)} = \mathbf{b}$. The process can then be iterated, with $\boldsymbol{\mu}^{(1)}$ as the new starting value, until it converges to a Gaussian distribution with, say, mean $\boldsymbol{\mu}^{(j)} \rightarrow \boldsymbol{\mu}^{(*)} = \boldsymbol{\chi}^*$ and precision matrix $\mathbf{Q}^{(j)} \rightarrow \mathbf{Q}^{(*)} = \mathbf{Q} + \text{diag}(\mathbf{c}^*)$, $j = 1, 2, \dots$, where an appropriate convergence criterion must be used.

If the mean of $\boldsymbol{\chi}$ is $\boldsymbol{\mu}$, the density of $\boldsymbol{\chi}$ is

$$p(\boldsymbol{\chi}) = (2\pi)^{-n/2}|\mathbf{Q}|^{1/2} \exp\left[-\frac{1}{2}(\boldsymbol{\chi} - \boldsymbol{\mu})^T \mathbf{Q}(\boldsymbol{\chi} - \boldsymbol{\mu})\right] \quad (15)$$

The sparse matrix $\mathbf{Q}$ is factorised as Cholesky triangle product $\mathbf{L}\mathbf{L}^T$, and only non-zero terms are computed due to the Markov property and $L_{ji} = 0$. Let $\mathbf{L}^T \boldsymbol{\chi} = \mathbf{r}$ where $\mathbf{r} \sim N(\mathbf{0}, \mathbf{1})$, then we have that $L_{ii}\chi_i = r_i - \sum_{k=i+1}^n L_{ki}\chi_k$ for $i = n, \dots, 1$. Multiplying each side with $\chi_j, j \geq i$ and taking the expectation yields the recursion

$$\Sigma_{ij} = \frac{\partial_{ij}^2}{L_{ii}} - \frac{1}{L_{ii}} \sum_{k=i+1}^n L_{ki}\Sigma_{kj} \quad j \geq i, \quad i = n, \dots, 1$$

where $\boldsymbol{\Sigma} = \mathbf{Q}^{-1}$ is the covariance matrix and $\partial_{ij} = 1$ if $i = j$ and $\partial_{ij} = 0$ otherwise. These recursion results in Gaussian approximations $\tilde{p}_G(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D})$ with mean $\mu_i(\boldsymbol{\theta})$ and marginal variance $\sigma_i^2(\boldsymbol{\theta})$.

The resulting approximation will then be [19]:

$$\tilde{p}_G(\boldsymbol{\chi}|\boldsymbol{\theta}, \mathbf{D}) \approx \exp\left(-\frac{1}{2}(\boldsymbol{\chi} - \boldsymbol{\chi}^*(\boldsymbol{\theta}))'(\mathbf{Q}(\boldsymbol{\theta}) + \text{diag}(\mathbf{c}))(\boldsymbol{\chi} - \boldsymbol{\chi}^*(\boldsymbol{\theta}))\right), \quad (16)$$

where $\mathbf{c}$ is the second-order term in the Taylor expansion of $\sum_{i=1}^n \log p(\mathbf{D}_i|\boldsymbol{\chi}_i, \boldsymbol{\theta})$ at modal value $\boldsymbol{\chi}^*(\boldsymbol{\theta})$.

2.4 Approximate AIC and BIC from INLA for model comparison

Since pure Bayesian analysis estimates parameters as full probability distributions rather than point estimates, standard maximum likelihood estimation (MLE)-based Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) cannot be directly calculated from generated quantities without adjusting the approach. However, one can approximate BIC directly using the marginal log-likelihood, $\ln(P(D|M))$. Given $\hat{L}$ the maximum likelihood, k the number of estimated parameters, n the sample size, the relationship relies on the Laplace approximation of the posterior [20, 21]:

$$\ln(P(D|M)) \approx \ln(\hat{L}) - \frac{k}{2} \ln(n) + \frac{k}{2} \ln(2\pi) + \frac{k}{2} \ln(\hat{\Sigma}) \quad (17)$$

where $\hat{\Sigma}$ is the inverse Hessian matrix of the negative log-likelihood evaluated at the posterior mode. Dropping the constant terms (a standard practice as it does not affect relative model comparison), the approximated BIC from the marginal log-likelihood becomes

$$BIC \approx -2 \ln(P(D|M)), \quad (18)$$

and the AIC becomes

$$AIC \approx -\ln(P(D|M)) \ln(n), \quad (19)$$

Since standard BIC is defined as $-2 \ln(\hat{L}) + k \ln(n)$ and AIC is defined as $-2 \ln(\hat{L}) + 2k$.

3. Application, Results and Discussion

The approached studied in the paper is applied to a publicly available dataset on maternal health and high-risk pregnancy [22]. This dataset provides a collection of maternal health data, focusing on key health indicators throughout pregnancy. It includes essential details such as the mother's age, gravida (number of pregnancies), weight, height, blood pressure, gestational age, and fetal health status. All categorical variables reported in the results in Table 1 were in reference to the baseline category in each variable, e.g. for gravida, the baseline category is Gravida1 representing 1st gravida. The results for the LGM and classical model fitted to the dataset as presented in Table 1 (OR = odds ratio, CI-lower and CI-upper are 95% credible and confidence intervals for LGM and classical model respectively) showed that both models give similar significant results with decimal places differences in the odd ratios. BMI showed a statistically significant protective association (OR $\approx$ 0.80, 95% CI excludes 1), indicating each unit increase in BMI was associated with about 20% lower odds of high risk pregnancy, showing to be a protective factor. Systolic blood pressure was positively associated with the outcome (OR $\approx$ 1.04, 95% CI excludes 1), suggesting that a unit increase of systolic pressure increased the odds of high risk pregnancy by 4%. UST1 (urine sugar test with negative result) also appeared protective (95% CI = 0.28 - 0.47, CI excludes 1), women with negative urine sugar test are about 54.6% less likely to have high risk pregnancy than those with positive urine sugar test.

Investigating the BMI results, out of 992 total participants, 81% are normal weight, only 11.7% are overweight, and 7.1% are underweight. Since BMI was analyzed as a continuous variable rather than in categories, the mathematical model is heavily weighted by the massive cluster of healthy-weight individuals. To assess the stability of our findings, a sensitivity analysis was performed by excluding underweight participants (N = 71). The protective effect of BMI remained highly robust and increased in magnitude (adjusted OR = 0.69, 95% CI: 0.634, 0.743). This indicates that the observed inverse relationship was not an artifact driven by the higher risk profile of the underweight cohort. Most other predictors had confidence intervals including 1, indicating no statistically significant association.

Hepatitis B Surface Antigen positive status (HBsAg1) emerged as an exceptionally strong, deterministic predictor of high-risk pregnancy status, exhibiting near-complete statistical separation with the outcome. Due to the fact that virtually all HBsAg-positive participants fell within the high-risk cohort, the maximum likelihood estimation yielded an artificially inflated baseline odds ratio

(2.86×10^{14} , 95% CI: 1.75×10^6 – 4.69×10^{22}), confirming its status as a critical independent clinical risk vector alongside systolic blood pressure. The extreme odds ratio and confidence interval for HBsAg1 (Hepatitis B Surface Antigen positive status) indicate a massive statistical anomaly known as complete separation or perfect prediction in your logistic regression model. A Firth's Penalized Logistic Regression (also called penalized likelihood) that applies a mathematical correction specifically designed to handle complete separation was applied to the adjusted data, reducing the astronomical numbers to a realistic Odds Ratio and a narrow, valid 95% Confidence Interval, (AOR = 313.69, 95% CI: 43.72–39,858.39).

In the final model excluding underweight individuals (N=921), four variables were identified as independent, shown in Table 2, statistically significant predictors of high-risk pregnancy status. Hepatitis B Surface Antigen positive status (HBsAg1) emerged as the strongest independent risk factor, with affected women exhibiting a 313-fold increase in the odds of a high-risk pregnancy classification (AOR = 313.69, 95% CI: 43.72–39,858.39). Elevated systolic blood pressure also operated as a significant independent risk vector, increasing odds by 4.3% per unit (AOR = 1.043, 95% CI: 1.025–1.061). Conversely, two powerful independent protective factors were observed. A negative blood or urine sugar test (UST1) reduced the odds of a high-risk pregnancy by 54.6% (AOR = 0.454, 95% CI: 0.285–0.723). Furthermore, incremental increases in continuous BMI within the normal-to-overweight range maintained a highly stable protective effect, with a 31% risk reduction per unit increase (AOR = 0.690, 95% CI: 0.634–0.743).

Table 1: Odd Ratios and 95% Credible and Confidence Intervals

Variable	LGM with Credible Interval			CLASSICAL with Confidence Interval		
	OR	CI-lower	CI-upper	OR	CI-lower	CI-upper
α	4.433	0.138	142.127	4.356	0.136	140.984
Age	0.998	0.957	1.040	1.002	0.961	1.045
Gravida2	1.028	0.690	1.533	1.025	0.690	1.535
Gravida3	0.840	0.101	6.982	0.872	0.091	8.251
BMI	0.800	0.751	0.853	0.805	0.755	0.857
Systolic	1.043	1.025	1.061	1.038	1.021	1.056
Diastolic	1.014	0.995	1.034	1.013	0.994	1.033
Fetal heartbeat	0.996	0.980	1.012	0.999	0.983	1.015
Pregnancy age	1.001	0.972	1.030	1.002	0.973	1.031
Anemia1	0.959	0.529	1.738	0.956	0.531	1.754
Anemia2	1.103	0.601	2.022	1.093	0.602	2.035
Jaundice1	0.633	0.126	3.172	0.618	0.123	3.501
Jaundice2	1.318	0.131	13.257	1.032	0.126	21.408
Baby position1	0.653	0.097	4.400	0.629	0.092	5.210
UAT1	0.749	0.371	1.513	0.749	0.374	1.540
UAT2	1.074	0.541	2.131	1.065	0.542	2.153
UAT3	0.876	0.433	1.769	0.871	0.435	1.791
UST1	0.454	0.285	0.723	0.466	0.289	0.735
VDRL1	0.785	0.575	1.071	0.790	0.578	1.077
HRsAG1	3.95×10^{14}	1.99×10^6	7.84×10^{22}	4.47×10^7	5.39×10^2	3.25×10^{67}

The adjusted BMI component exposes a multifaceted clinical ecosystem driven by four primary anchors: viral hepatitis, glycemic control, cardiovascular stability, and metabolic mass. The profound risk associated with a positive maternal Hepatitis B status (AOR = 313.69) matches stringent global obstetric guidelines, which mandate high-risk classification for chronic viral hepatitis to preempt vertical transmission, maternal hepatic flares, and placental complications. Similarly, elevated systolic blood pressure (AOR = 1.043) follows classic pathophysiological expectations regarding hypertensive risk vectors.

Table 2: Significant risk factors with OR and 95% CI from LGM

variable	OR	CI-lower	CI_upper
bmi	0.69	0.634	0.743
Systolic	1.039	1.02	1.06
UST1	0.428	0.26	0.70
HRsAG1	313.686	43.722	39858.390

The true epidemiological innovation of the model lies in the behaviour of continuous BMI (AOR = 0.690) when adjusting for these dominant parameters. By simultaneously controlling for both chronic viral load (HBsAg1), absolute systolic stress (Systolic BP), and maternal glycemic status (UST1), the model isolates the physiological impact of maternal weight from its most common pathological correlates. In the absolute absence of diabetes, hypertension, and active viral hepatitis, an incremental increase in BMI strictly within the normal-to-overweight spectrum acts as a robust protective asset. This indicates that healthy maternal tissue and calorie reserves provide a distinct physiological buffer that shields the pregnancy from non-glycemic, non-cardiovascular high-risk vulnerabilities. These findings advocate for an updated clinical paradigm: maternal weight should not be evaluated as a standalone hazard if a patient demonstrates excellent glycemic health (UST1) and stable blood pressure vitals.

From Table 3, the classical model achieved lower AIC (1130.7 vs 1333.4), lower BIC (1228.8 vs 1431.5) and higher log-likelihood (-545.3 vs -646.7), indicating better model fit than the LGM model. It should be noted however that LGM with posterior estimation using INLA does not compute AIC and BIC, the values presented in the table were approximated values computed from the marginal log-likelihood of the LGM fit on the dataset as presented in section 2.4. So the comparison using both metrics were a matter of convenience than accuracy and precision. Nevertheless, the predictive performance was nearly identical: AUC was approximately 0.734 for both models and classification accuracy was about 70.54%, and 70.44% for LGM and classical model respectively, indicating moderate discrimination. Thus, both models have similar predictive ability.

Table 3: Comparing LGM with Classical regression

	AIC	BIC	Loglik	AUC	Accuracy
LGM	1333.425	1431.540	-646.713	0.7345	0.705411
CLASSICAL	1130.700	1228.804	-545.345	0.7343	0.704409

Figures 1 showed ROC curves for the LGM and Classical models, both curves indicate moderate discriminatory performance, consistent with the AUC values around 0.73 (AUC < 0.80), but both outperform random classification (AUC = 0.50). The fitted probabilities shows the close similarity supported by the comparable predictive performance reported in Table 3.

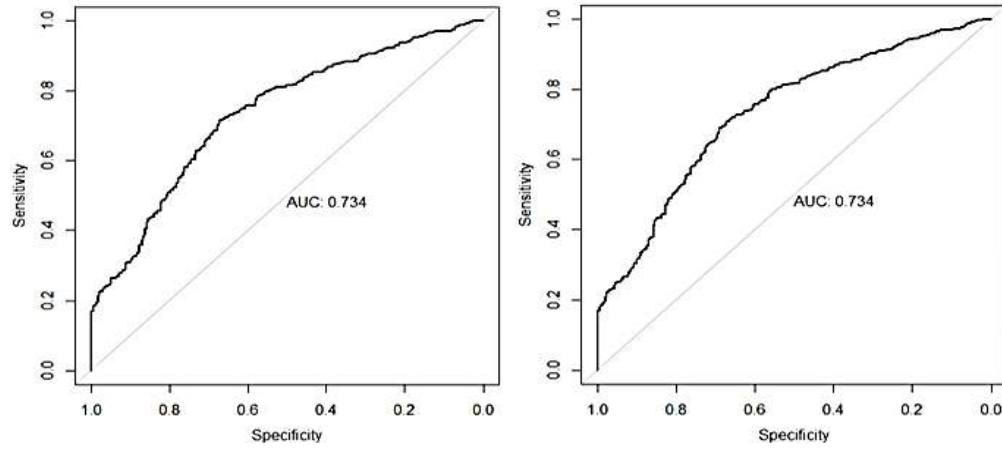


Figure 1: ROC for LGM (Left panel) and classical logistic model (right panel)

4. Sensitivity analyses on Prior specification in the LGM

The question of prior sensitivity is addressed here, given that Bayesian results can be sensitive to priors. Prior specifications for fixed effects was systematically varied across four distinct structural philosophies: Flat (Default), weakly uninformative, Weakly Informative, Moderately Restrictive, and Strongly Regularized. The model fitting computes information criteria deviance information criterion (DIC), Watanabe information criterion (WAIC), log-pseudo marginal likelihood (LPML), conditional predictive ordinate (CPO). Model adequacy is assessed through the stability of posterior estimates across priors, the absence of CPO failures, reasonable PIT distributions, and consistency of DIC, WAIC, and LPML across the sensitivity analysis. The type of prior is defined by the choice of the precision parameter value, from 0.001, 0.01, 0.1, 1, and 2 respectively for each structural philosophies on the Gaussian prior used. The priors were respectively named Normal1000, Normal100, Normal10, Normal1, and Normal0.5. The results is presented in Table 1.

Table 4: Priors sensitivity model diagnostics comparisons

Prior	DIC	WAIC	LPML	Mean CPO	CPO failures	Marginal LogLik	BIC	Eff. Par	Mean PIT
Normal1000	1236.310	1236.361	-618.181	0.572949	0	-647.041	1325.155	4.981	0.786818
Normal100	1236.286	1236.335	-618.168	0.572935	0	-641.307	1313.687	4.968	0.786819
Normal10	1236.101	1236.136	-618.068	0.572810	0	-635.752	1302.576	4.860	0.786825
Normal1	1235.937	1235.930	-617.965	0.572274	0	-631.013	1293.099	4.369	0.786850
Normal0.5	1236.081	1236.064	-618.032	0.572090	0	-629.770	1290.613	4.173	0.786852

From Table 4, five prior specifications were considered for the regression coefficients, ranging from the default vague prior to a strongly regularized prior. Model performance was evaluated using the Deviance Information Criterion (DIC), Widely Applicable Information Criterion (WAIC), Log Pseudo Marginal Likelihood (LPML), Conditional Predictive Ordinate (CPO), marginal log-likelihood, approximate BIC, and the effective number of parameters. Across all prior specifications, DIC ranged from 1235.94 to 1236.31, while WAIC ranged from 1235.93 to 1236.36. These differences are less than one unit, indicating virtually identical model fit regardless of the prior specification. The moderately restrictive prior yielded the smallest DIC (1235.94) and WAIC (1235.93), although the improvement over the other priors was negligible and unlikely to be practically meaningful. Similarly, LPML values varied only slightly from -618.18 to -617.97, with

the moderately restrictive prior producing the highest (least negative) LPML, suggesting marginally better predictive performance. Mean CPO values were almost identical (approximately 0.572), and importantly, no CPO failures were observed for any prior specification, indicating stable numerical estimation and satisfactory predictive performance across all fitted models. The effective number of parameters decreased gradually from approximately 4.98 under the default vague prior to 4.17 under the strongly regularized prior. This reduction reflects the expected shrinkage effect of increasingly informative priors, whereby stronger regularization reduces model complexity without materially affecting model fit. Likewise, the marginal log-likelihood and approximate BIC improved slightly as stronger priors were adopted, although these changes were relatively small compared with the overall similarity in the predictive criteria.

The Conditional Predictive Ordinate (CPO) plot in Figure 2 assesses the leave-one-out predictive performance of the model for each observation. From Figure 1, the CPO values appear stable across all prior specifications, with no evidence of extreme outliers or failed CPO computations. This observation agrees with the summary statistics reported in Table 1, where the number of CPO failures was zero for every model. The similarity of the CPO distributions indicates that predictive performance remains essentially unchanged irrespective of the prior selected. This demonstrates that the fitted logistic INLA model is not sensitive to reasonable changes in the fixed-effect prior specification.

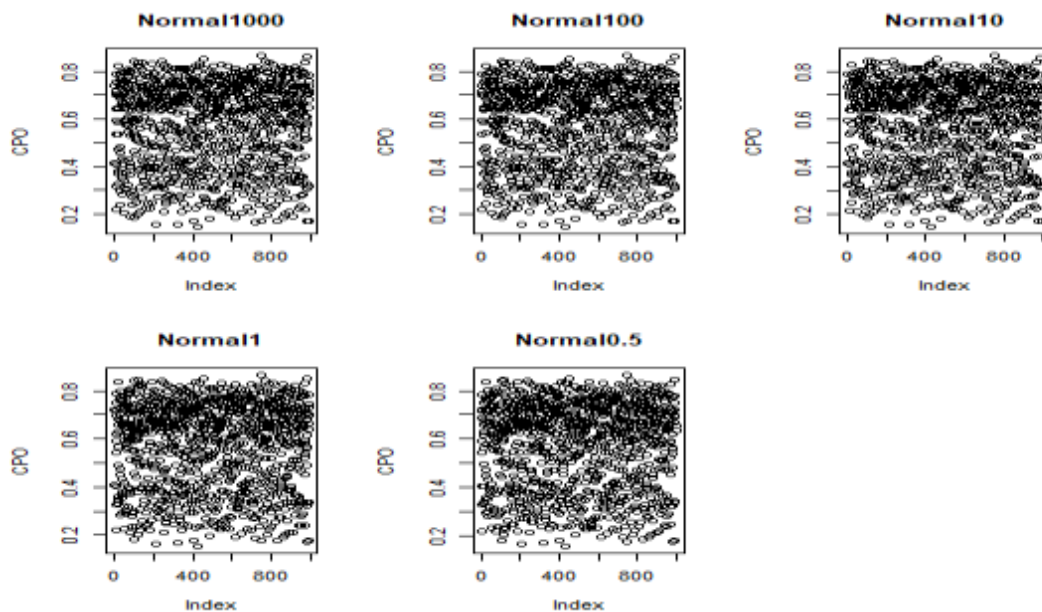


Figure 2: Conditional Predictive Ordinate (CPO) plot

Figure 3 showed the Probability Integral Transform (PIT) histogram used to evaluate calibration of Bayesian predictive distributions. An approximately uniform PIT distribution indicates that predicted probabilities are well calibrated and that the model adequately represents the observed data. The PIT histograms in Figure 3 show no obvious systematic departures from uniformity, such as U-shaped or hump-shaped patterns, suggesting that the model does not exhibit substantial under-dispersion or over-dispersion. The consistency of the PIT distributions across all prior specifications further demonstrates that predictive calibration is insensitive to the choice of prior.

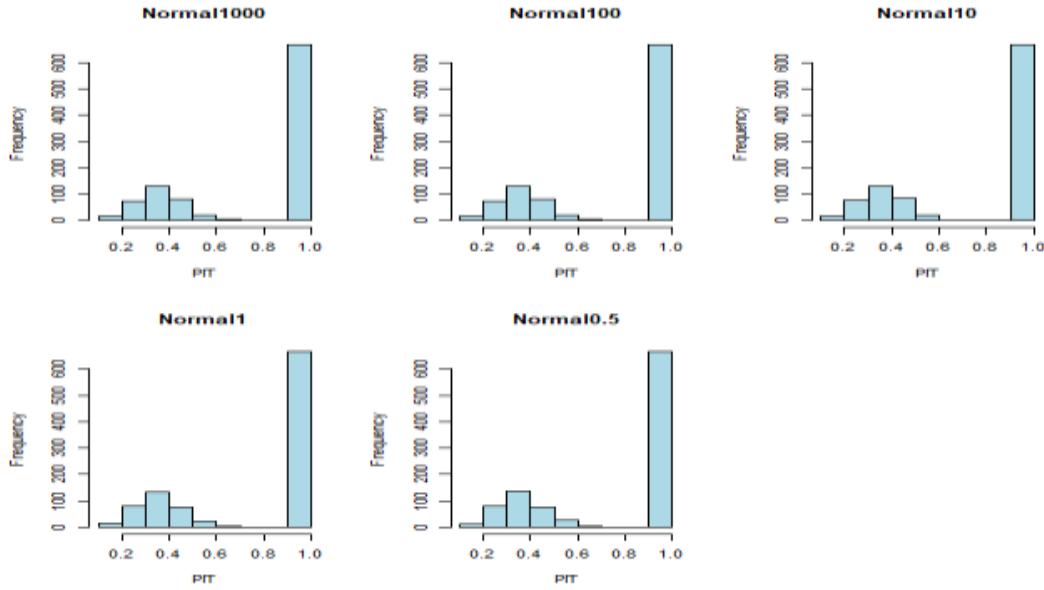


Figure 3: Probability Integral Transform (PIT) histogram

Figure 4 compares posterior estimates of the regression coefficients under different prior distributions. The posterior means and corresponding 95% credible intervals remain remarkably similar across all prior specifications. The overlap of the credible intervals indicates that neither the magnitude nor the direction of the estimated effects changes appreciably when increasingly informative priors are imposed. Minor shrinkage of coefficient estimates under the strongest regularization is expected from Bayesian theory but does not materially alter statistical inference. This consistency indicates that the observed data provide sufficient information to dominate the prior specification, resulting in stable posterior estimates.

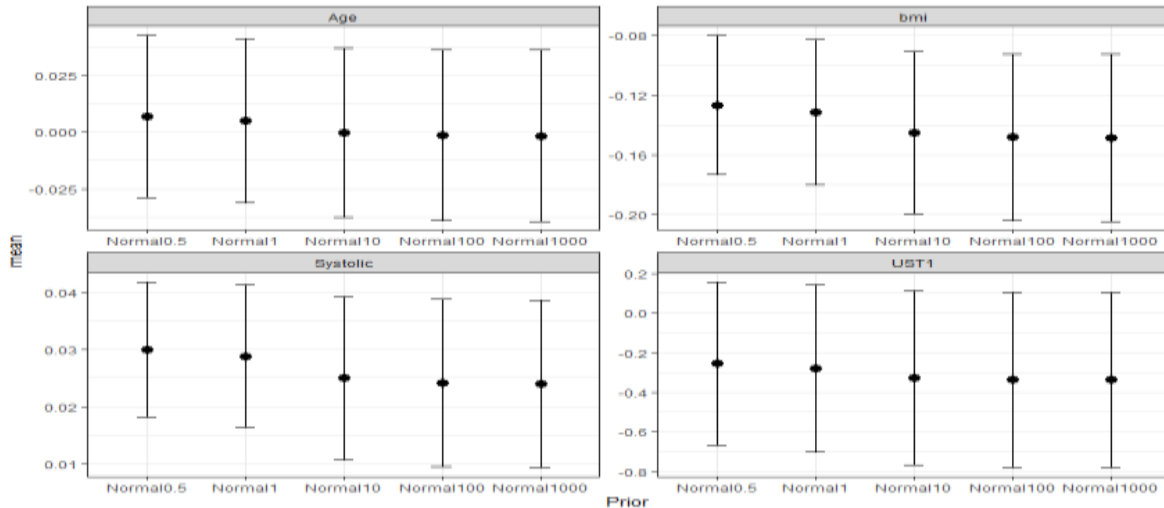


Figure 4: Plot of Posterior estimates across Prior choice

The prior sensitivity analysis provides strong evidence that the LGM fitted was robust to the choice of fixed-effect prior distributions. Despite evaluating priors ranging from vague to strongly regularizing, all measures of model fit and predictive performance remained remarkably stable. The differences in DIC and WAIC were less than one unit, which is substantially below the threshold generally regarded as indicating meaningful differences between competing models. Likewise,

LPML values differed only marginally, suggesting essentially equivalent predictive ability under all prior specifications. The absence of CPO failures across all models further supports the numerical stability of the estimation procedure. Stable CPO values and approximately uniform PIT distributions indicate satisfactory predictive calibration and suggest that the fitted model adequately captures the relationship between high-risk status and the explanatory variables without evidence of systematic predictive bias. Together, these diagnostics demonstrate that the predictive performance of the model is largely unaffected by prior selection. The stability of the posterior coefficient estimates across prior specifications further confirms that inference is primarily driven by the observed data rather than prior assumptions. This finding implies that the dataset contains sufficient information to identify the regression coefficients reliably, thereby reducing dependence on subjective prior choices. Such behaviour is desirable in Bayesian analyses because it increases confidence that the reported associations between Age, BMI, UST, Systolic blood pressure, and the probability of being classified as high risk are robust and reproducible.

5. Conclusion

The computational advantage of LGM posterior estimation using INLA has been discussed in literatures. The similarity in predictive performance between LGM and classical logistic regression does not raise concern of a presumed complexity of Bayesian framework. The first reason is that, researches into theories and applications of Bayesian approaches are active areas. Secondly, it is normal scientific approach to compare existing procedures to new ones for specificity and sensitivity. Limitations are acknowledged, and include that, while sensitivity analysis successfully insulated the data from the confounding baseline risks of maternal underweight status, the data lacked representation of extreme obesity classes. Second, the model detected an exceptionally wide 95% confidence interval for maternal Hepatitis B Surface Antigen positive status (95% CI: 43.72–39,858.39). While the entire interval sits decisively above 1.0—confirming HBsAg1 as an indisputable severe risk vector in this data—the enormous width of the interval indicates a state of near-complete statistical separation. Future multicenter studies with a larger, more evenly distributed sample of viral-positive participants are required to narrow this interval and generate a more precise point estimate for this specific hazard. The study limited comparison to classical model. Future study may consider other distributions of response variables, and possibility of random effects in the generalised modelling approach for pregnancy risk incidence.

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