STATISTICAL MODELING OF COVID-19 DYNAMICS IN LIBERIA USING BAYESIAN HIERARCHICAL METHODS

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Abstract

This study employs Bayesian Hierarchical Modeling (BHM) to analyze COVID-19 transmission dynamics across Liberia's counties. It addresses the shortfalls of tradition in epidemiological models such as the Susceptible-Infectious-Recovered (SIR) model. This study integrates spatial heterogeneity and probabilistic framework by inputting COVID-19 cases, healthcare capacity, and mobility interventions at the county level into the estimation of critical epidemiological parameters. Statistical methods such as Poisson regression, Generalized Linear Mixed Models (GLMM), and BHM are employed to assess the effect of interventions: partial and full lockdowns, curfews, and border closures. The findings indicated that partial lockdowns and border closures have large positive correlations with COVID-19 case counts while curfews and full lockdowns have little effect. The study shows a need for localized interventions and further highlights how findings serve as pointers for improving some regional characteristics of public health responses.[1]

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[1]COVID-19 Cases, Bayesian Hierarchical, Poisson Regression, General Linear Mixed Model

1 Introduction

The coronavirus disease 2019 (COVID-19), which emerged from the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and was first identified in December 2019 in Wuhan, China, quickly transformed into a global health crisis (Salako *et al.*, 2024). The World Health Organization (WHO) officially declared COVID-19 a pandemic on March 11, 2020; this marked a pivotal moment in the ongoing battle against a disease that has since had a profound impact on public health, economies and societies around the world (Maiti *et al.*, 2021). For example, in Liberia, the initial case was confirmed on March 16, 2020, in Margibi County, indicating the pandemic's arrival in the nation (Wikipedia, 2024). By December 2023, Liberia had reported a cumulative total of 8,161 confirmed cases and 295 deaths, demonstrating the considerable toll the pandemic has exacted on the country's health systems and communities (WHO, 2023). However, the response to these challenges continues to evolve, as public health measures are adjusted and new strategies are implemented.

Comprehending the transmission dynamics of COVID-19 is essential for developing effective public health interventions (Nakhriry and Aarthy, 2023). Traditional epidemiological models such as the Susceptible-Infectious-Recovered (SIR) model have proven invaluable for estimating crucial parameters, including the basic reproduction number (R0), and for predicting the trajectory of infectious disease outbreaks (Singh *et al.*, 2024; Ajmal *et al.*, 2024). However, these models frequently depend on oversimplified assumptions, particularly regarding homogeneous mixing within populations. This may not adequately reflect the complexity and heterogeneity present in real-world populations. Factors like county variations in Liberia's population density, healthcare access, and social behaviors significantly impact disease transmission dynamics, which pose challenges to the applicability of traditional models in varied contexts, such as Liberia.

To overcome these limitations, this study adopts a Bayesian Hierarchical Model (BHM) framework to analyze COVID-19 transmission across Liberia's counties. The BHM approach facilitates the incorporation of spatial heterogeneity and provides a probabilistic framework for estimating key epidemiological parameters. This model accounts for regional differences in population characteristics, healthcare policy, and other context-specific factors, enabling a more nuanced understanding of the pandemic's spread. By leveraging this advanced modeling framework, the study aims to generate insights into

county-level variations in COVID-19 transmission dynamics and improve the precision of epidemic forecasts.

The findings of this research underscore the importance of tailoring public health strategies to the unique characteristics of each county. By highlighting the role of localized interventions in controlling the spread of COVID-19, this study contributes to the development of targeted and efficient public health responses. Such strategies are essential for enhancing Liberia's preparedness and resilience against current and future infectious disease outbreaks.

The field of infectious disease dynamics boasts a rich history, with numerous models developed to analyze and predict the spread of diseases (Heesterbeek et al., 2015; Diekmann *et al.*, 2013). According to Li (2018), the Susceptible-Infectious-Recovered (SIR) model remains one of the foundational frameworks in epidemiology, enabling the estimation of the basic reproduction number (R0) and providing insights into the progression of infectious diseases within populations. However, the SIR model's assumption of homogeneous mixing has been critiqued for oversimplifying the complex interplay of social and environmental factors that influence disease transmission.

Recent advances in epidemiological modeling have addressed these limitations by incorporating more realistic assumptions about population structure and behavior (Caswell and John, 2018; Sutherland, 1996; Langat and Koima, 2017). Bayesian Hierarchical Models (BHMs) have emerged as a robust tool for studying the spread of infectious diseases, particularly in contexts characterized by significant regional heterogeneity. Unlike traditional compartmental models, BHMs incorporate multiple levels of data hierarchy, allowing researchers to account for variations in disease transmission across regions or subpopulations (Lawson, 2021). The application of BHMs in epidemiology has been extensively documented, with successful implementations in modeling diseases such as Ebola, COVID-19, and Zika virus (Powell *et al.*, 2020). These models have provided valuable insights into the factors driving regional differences in disease transmission and have underscored the importance of tailoring public health interventions to specific local contexts.

In the case of COVID-19, BHMs are particularly relevant due to the disease's sporadic outbreaks and the considerable variability in transmission dynamics across regions. Studies indicate that factors such as population density, healthcare infrastructure, and

mobility patterns significantly influence disease spread, making it essential to adopt modeling approaches capable of capturing these complexities. This study builds upon existing literature by applying a BHM to analyze the spread of COVID-19, aiming to provide more precise estimates of transmission dynamics and inform targeted public health strategies.

2 Data and Methods

2.1 Data

Data collection. The data was downloaded from the DHIS2 data platform. The dataset comprises detailed records of confirmed COVID-19 cases across different counties in Liberia over a defined period (from 1st January 2020 to 31th of December 2020), a total cases of COVID-19 have been recorded from 14 counties in Liberia: Capa Mount, Bong, Gbarpolu, Grand Bassa, Grand Gedeh, Grand Kru, Lofa, Margibi, Maryland, Monteserrado, Nimba, River Cess, River Gee and Sinoe. Details of key variables utilized in the analysis are provided and summary in Table 1.

Table 1: Key Variables Utilized in the Analysis

Variables	Description	Sources
County	Each county in Liberia is included in the study	DHIS2
Total Covid Cases	Number of cases per county	DHIS2
Partial lockdown due to Covid-19	Partial lockdown due to Covid-19	DHIS2
Full lockdown due to Covid-19	Full lockdown due to Covid-19	DHIS2
Curfew due to Covid-19	Curfew due to Covid-19	DHIS2
Closing of border due to Covid-19	Closing of border due to Covid-19	DHIS2
Closing of airspace due to Covid-19	Closing of airspace due to Covid-19	DHIS2
Population Density	The total population per county for 2020	DHIS2

3 Methods

3.1 Poisson Regression Model

The Poisson regression model is used to model count data and assuming that the response variable Y_i follows a Poisson distribution, where logarithm of its expected variable is a linear function of the explanatory variables.

3.2 Assumptions

- $Y_i \sim Poisson(p_i)$, where $p_i > 0$ is the rate parameter for observation i , linked to the covariances.

- The logarithm of the rate parameter p_i is modeled as a linear function.

3.3 Model Specification

Let Y_i be the count of COVID-19 cases for observation i. The Poisson regression model is formulated as

$$\log(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_n X_{in}, \tag{1}$$

or equivalently:

$$p_i = \exp\left(\beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_n X_{in}\right). \tag{2}$$

Where $X_{i1}, X_{i2}, \cdots, X_{in}$ are the covariances (Population Density, partial lockdown due to Covid-19, full lockdown due to Covid-19, curfew due to Covid-19,closing of border due to Covid-19, closing of airspace due to Covid-19), $\beta_0, \beta_1, \beta_2, \cdots, \beta_n$ are the coefficients to be estimated.

3.4 Likelihood Function

The likelihood function for n observations for the Poisson model is:

$$L(\beta/Y_i) = \prod_{i=1}^{n} \frac{p_i^{Y_i} e^{-p_i}}{Y_i!}.$$

Taking the log-likelihood:

$$\ell(\beta \mid Y_i) = \sum_{i=1}^{n} \left[Y_i \log(p_i) - p_i - \log(Y_i!) \right]$$

substitute $p_i = \exp\left(\beta_0 + \sum_{i=1}^{n} \beta_n X_{in}\right)$, and concluded that

$$\ell(\beta \mid Y_i) = \sum_{i=1}^{n} \left[Y_i \left(\beta_0 + \sum_{i=1}^{n} \beta_n X_{in}\right) - \exp\left(\beta_0 + \sum_{i=1}^{n} \beta_n X_{in}\right) - \log(Y_i!) \right] \qquad (3)$$

Maximizing the log-likelihood function provides the maximum likelihood estimates (MLE) of the coefficients β.

3.5 Generalized Linear Mixed Model (GLMM)

The GLMM extends the Poisson regression by including random effect across counties in Liberia. Modeling the number of COVID-19 cases across counties, where counties are treated as random effects and predictors include population density,partial lockdown due to Covid-19, full lockdown due to Covid-19, curfew due to Covid-19,closing of border due to Covid-19, and closing of airspace due to Covid-19.

Let Y_{ij} denote the count for COVID-19 cases for i-th observation in the j-th county, assuming that

$$Y_{ij} \sim Poisson(p_{ij}). \qquad (4)$$

Where the expected rate p_{ij} is linked to the predictors and random effects via a log link function:

$$\log(p_{ij}) = \beta_0 + \sum_{i=1}^{n} \beta_n X_{in} + \upsilon_j. \qquad (5)$$

The random effects υ_j is assumed to follow a norm distribution

$$\upsilon_j \sim \mathcal{N}(0, \sigma_\upsilon^2) \qquad (6)$$

The margin likelihood for GLMM is obtained by integrating out the random effects:

$$L(\beta, \sigma_{\upsilon_j} \mid Y) = \prod_{j=1}^{m} \int \left[\prod_{i=1}^{n} \frac{p_{ij}^{Y_{ij}} e^{-p_{ij}}}{Y_{ij}!} \right] \frac{1}{\sqrt{2\pi\sigma_{\upsilon_j}^2}} e^{-\upsilon_j} d\upsilon_j$$

Due to the complexity of this integral, numerical methods or approximation techniques, such as the Laplace approximation or Gauss-Hermite quadrature, are commonly employed to maximize the likelihood and estimate the parameters β and v_j, (e.g., Salako, *et. al., 2024*).

3.6 Bayesian Hierarchical Model

The Bayesian Hierarchical Model (BHM) is similar to the GLMM but uses a fully Bayesian approach. It includes prior distributions for both fixed and random effects to estimate parameters. The same model specifications used in GLMM, as described in equations (4), (5), and (6), are applied in BHM, with the added incorporation of prior distributions for the parameters.

$$\beta_n \sim Normal(0, \sigma_\beta^2), \quad n = 0, 1, 2, \cdots, N$$

The variance of the random effects σ_v^2.

$$\sigma_v^2 \sim InverseGamma(a, b).$$

Similar approaches have been discussed in the works of Carlin and Polson (1992), Lee (1989), and Lehmann (1983).

3.6.1 Posterior Distribution

The joint posterior distribution combines the likelihood and the prior distribution is expressed as

$$Pr(\beta, v, \sigma_v^2 | Y) \propto Pr(Y | \beta, v) \cdot Pr(\beta) \cdot Pr(v | \sigma_v^2) \cdot Pr(\sigma_v^2)$$

This posterior distribution is typically estimated using Markov Chain Monte Carlo (MCMC) methods, such as Gibbs sampling or Hamiltonian Monte Carlo, as implemented in tools like MCMCglmm, (Damien,*et al.*, 1996 and Gelman, *et. al.*, 2021). Posterior samples generated through MCMC can be used to calculate posterior means, credible intervals, and make probabilistic statements about the parameters (e.g., determining the probability that a parameter is positive).

3.7 Estimation of Parameters and Model Diagnostics

3.7.1 Estimation of Parameters

The methods for estimating parameters differ across models such as Poisson regression, GLMM and BHM. For Poisson regression model, parameters $\beta_0, \beta_1, \cdots, \beta_n$ are estimated using Maximum Likelihood Estimation (MLE) by maximizing the log-likelihood function:

$$\hat{\boldsymbol{\beta}} = \arg \max_{\boldsymbol{\beta}} \ell(\beta \mid Y_i).$$

Where

$$\ell(\beta \mid Y_i) = \sum_{i=1}^{n} \left[Y_i \left(\beta_0 + \sum_{i=1}^{n} \beta_n X_{in} \right) - \exp \left(\beta_0 + \sum_{i=1}^{n} \beta_n X_{in} \right) - \log(Y_i!) \right].$$

In GLMM, parameter estimation accounts for both fixed effects (β) and random effects (v). This process typically employs Restricted Maximum Likelihood (REML) or Maximum Likelihood (ML) methods, which maximize the likelihood function by integrating over the random effects:

$$L(\beta, \sigma_{v_j} \mid Y) = \prod_{j=1}^{m} \int \left[\prod_{i=1}^{n} \frac{p_{ij}^{Y_{ij}} e^{-p_{ij}}}{Y_{ij}!} \right] \frac{1}{\sqrt{2\pi\sigma_{v_j}^2}} e^{-v_j} dv_j$$

Several numerical techniques can be applied to evaluate or approximate this integration, for the purpose of this study used either Laplace approximation or Gauss-Hermite quadrature.

For the BHM, estimation parameters involves deriving the posterior distribution of the parameters based on the observed data and prior distributions. Using Baye theorem, the Posterior distribution is expressed as

$$Pr(\beta, v, \sigma_v^2 \mid Y) \propto Pr(Y \mid \beta, v) \cdot Pr(\beta) \cdot Pr(v \mid \sigma_v^2) \cdot Pr(\sigma_v^2)$$

To generate samples from the posterior distribution, the study utilizes MCMC methods, including Gibbs sampling or Hamiltonian Monte Carlo. These samples are subsequently used to compute posterior means, credible intervals, and other summary statistics.

3.7.2   Model Diagnostics

Assessing the fit and validity of the models, model diagnostics can be used to determine whether the Poisson regression, GLMM and HBM are best fitted. Various diagnostic methods can be applied to assess the performance of each model.

4   Results

4.1   Poisson Regression Model Application

Table 2: Poisson Regression Model Summary

Parameter	Value
Dependent Variable	Covid-19 Cases
Number of Observations	180
Model	GLM
Degrees of Freedom Residuals	177
Model Family	Poisson
Link Function	Log
Scale	1.0000
Method	IRLS
Log-Likelihood	-3648.5
Deviance	7020.1
Pearson Chi2	2.25e+04
Number of Iterations	6
Pseudo R-squared (CS)	0.9990
Covariance Type	nonrobust

Regression Coefficients

Parameter	Estimate	Std. Err.	Z Value	$P > \lvert Z \rvert$	2.5%	97.5%
Partial Lockdown	1.3562	0.060	22.710	0.000	1.239	1.473
Full Lockdown	6.19e-16	4.76e-17	13.017	0.000	5.26e-16	7.12e-16
Curfew	0.0000	0.0000	nan	nan	0.000	0.000
Closing of Border	1.7116	0.039	43.938	0.000	1.635	1.788
Closing of Airspace	0.6431	0.061	10.537	0.000	0.523	0.763

Table-1 shows the result of the Poisson regression model, which estimates the relationship between several predictors (lockdown measures) and the number of COVID-19 cases, assuming a log-linear relationship The findings imply that border closures and

partial lockdowns had the strongest correlations with the anticipated number of COVID-19 cases. When all other conditions are held constant, a partial lockdown is associated to a 3.88 times higher rate of COVID-19 cases than when there is no lockdown ($\exp(1.3562) \approx 3.88$). Similarly, closing borders have the strong positive correlation with COVID-19 cases, that is closing borders is associated with a 5.54 times increase in COVID-19 cases, indicating a strong positive association ($\exp(1.7116) \approx 5.54$). These effects are robust and precise, as evidenced by the tight confidence intervals and high statistical significance ($p < 0.001$) of both predictors.

Another notable effect is closing airspace, which increases the estimated number of COVID-19 cases by 90% ($\exp(0.6431) \approx 1.90$), while full lockdown has an extremely small coefficient (6.192×10^{16}), indicating no practical impact despite being statistically significant. The curfew variable is excluded from the model, likely due to multicollinearity or lack of variability. The model fit is exceptionally strong, with a Pseudo R-squared of 0.9990, suggesting that the predictors almost completely explain the variance in COVID-19 cases. The high z-values and low p-values for significant variables further support the strength of the relationships.

In conclusion, the model shows that while complete lockdowns and curfews have little to no effect on the rate of COVID-19 cases in this dataset, partial lockdowns, border closures, and airspace closures have a considerable impact. These findings imply that tailored interventions, like border closures and partial lockdowns, may have a greater effect on controlling COVID-19 case counts than more comprehensive or stringent ones, such complete lockdowns.

4.2 GLMM Fixed Effects and Random Effects

Table 3: GLMM Summary for COVID-19 Cases

Predictor	Estimate	SE	z	p	95% CI Lower	95% CI Upper
Intercept	0.8899	0.393	2.265	0.024	0.120	1.660
Population Density	-6.52×10^{-6}	3.81×10^{-6}	-1.712	0.087	-1.4×10^{-5}	9.45×10^{-7}
Partial Lockdown	1.2697	0.484	2.622	0.009	0.321	2.219
Full Lockdown	6.95×10^{-17}	8.28×10^{-17}	0.840	0.401	-9.27×10^{-17}	2.32×10^{-16}
Curfew	0.0000	0.000	NaN	NaN	0.000	0.000
Closing of Border	0.8899	0.393	2.265	0.024	0.120	1.660
Closing of Airspace	0.6613	0.369	1.793	0.073	-0.062	1.384

Note. Estimate = Coefficient; SE = Standard Error; CI = Confidence Interval. Results are based on Poisson regression using Generalized Estimating Equations (GEE).

Table 4: Model Diagnostics for COVID-19 Cases

Diagnostic Measure	Value
Skewness	6.0555
Kurtosis	44.3135
Centered Skewness	3.5306
Centered Kurtosis	38.7134
Number of Observations	180
Number of Clusters (Counties)	14
Min Cluster Size	12
Max Cluster Size	12
Mean Cluster Size	12.0
Number of Iterations	2

Table 3 presents estimate from the GLMM, including fixed effects for various COVID-19 interventions and population density, as well as random effects accounting for county-level variability. The fixed effects suggest that partial lockdown and border closures have significant positive associations with COVID-19 cases, while full lockdowns and curfews show no significant impact. Population density does not exhibit a statistically significant effect on case counts. The random effects capture the differences among counties, highlighting the variability in how regions respond to interventions.

Table 4 presents the model diagnostics for the GLMM, providing insights into the distribution and structure of the data. The high skewness (6.0555) and kurtosis (44.3135) values indicate a highly skewed distribution with extreme values, suggesting the presence

of potential outliers or overdispersion in the data. The centered skewness and kurtosis values further confirm deviations from normality, emphasizing the need for careful interpretation of the model results. The clustering structure consists of 14 counties, each with an equal number of 12 observations, ensuring balanced representation across regions. The model achieved convergence after two iterations, indicating computational efficiency, but further examination may be required to ensure robustness and accuracy

4.3   Analysis of Bayesian Hierarchical Model

Table 5: Summary of Bayesian Hierarchical MCMC Results for Fixed and Random Effects

Effect	Covariate	Posterior Mean	L 95% CI	U 95% CI	ESS	pMCMC
Fixed Effects						
	Intercept	0.018	-0.075	0.057	876	–
	Partial Lockdown	0.004	-1.9916	1.9380	6206	0.5128
	Full Lockdown	0.001	-1.9673	1.9600	5950	0.5108
	Curfew	0.017	-1.9474	2.0467	6815	0.5018
	Closing of Border	-0.004	-2.0857	1.9634	5346	0.5015
	Closing of Airspace	0.010	-1.9454	1.9318	5576	0.4878
Random Effects (Counties)						
	Capa Mount	-0.134	-0.7208	0.3673	1519	0.2597
	Bong	-0.199	-0.6709	0.4300	1634	0.3060
	Gbarpolu	-0.109	-0.6709	0.4300	1654	0.2290
	Grand Bassa	-0.190	-0.6467	0.4415	1736	0.3420
	Grand Gedeh	-0.185	-0.7317	0.3437	1602	0.2462
	Grand Kru	-0.182	-0.7277	0.3602	1647	0.2435
	Lofa	-0.138	-0.7222	0.3713	1705	0.2420
	Margibi	-0.060	-0.6870	0.3964	1608	0.3095
	Maryland	-0.154	-0.6102	0.4954	1428	0.4093
	Montserrado	2.310	-0.6893	0.4019	1599	0.2732
	Nimba	-0.092	1.7636	2.9231	1726	1.0000
	River Cess	-0.203	-0.6415	0.4659	1700	0.3643
	River Gee	-0.150	-0.7306	0.3614	1609	0.2225
	Sinoe	-0.208	-0.6895	0.4106	1625	0.2853

The absolute impact of national COVID-19 measures estimated with the Bayesian Hierarchical MCMC model reflects similar insights as the impact of the GLMM. Taking the fixed effects into close account, the model suggests very high uncertainty regarding the effectiveness of partial lockdowns, full lockdowns, curfew and closing of borders and airspace. The posterior p-values of an indicators, such as $pMCMC > 0$ meaning there is strong evidence that COVID-19 cases were significantly higher or $pMCMC < 0$ meaning there is strong evidence that COVID-19 cases were significantly lower.

Table 4 shows the effect of the partial and full lockdown has posterior means close

to zero and p-value of MCMC around 51%, indicating no significant effect in either direction. These results imply that the implementation of lockdowns may not have had a clear or substantial impact on COVID−19 case numbers. With similar p-value of MCMC equivalent to 50% of curfew and border closure show a lack of clear effectiveness, whereas closing of airspace, p-value of MCMC is round 49% suggesting weak evidence of a potential negative effect. There is no strong statistical evidence to suggest that any of these interventions had a significant effect on reducing COVID−19 cases, likely due to regional variations and other unaccounted factors.

The random effects capture county-level variations, and the pMCMC values provide insight into whether counties have significantly higher or lower COVID−19 case counts compared to the overall average.

From Table 4 shows that counties such as Capa Mount ($pMCMC < 0 = 0.7402$) and Gbarpolu ($pMCMC < 0 = 0.7710$) show strong evidence of having lower case numbers than the national average. These findings may be attributed to regional differences in population density, healthcare capacity, or adherence to containment measures. Whereas, Montserrado ($pMCMC < 0 = 0.7268$) suggests evidence of higher cases compared to other counties. Montserrado, being a densely populated region, might have contributed to higher COVID-19 case rates, and Nimba County stands out with a $pMCMC (> 0) = 1.000$, meaning there is strong evidence that COVID-19 cases were significantly higher compared to other counties. This could be due to regional outbreaks or reporting difference.
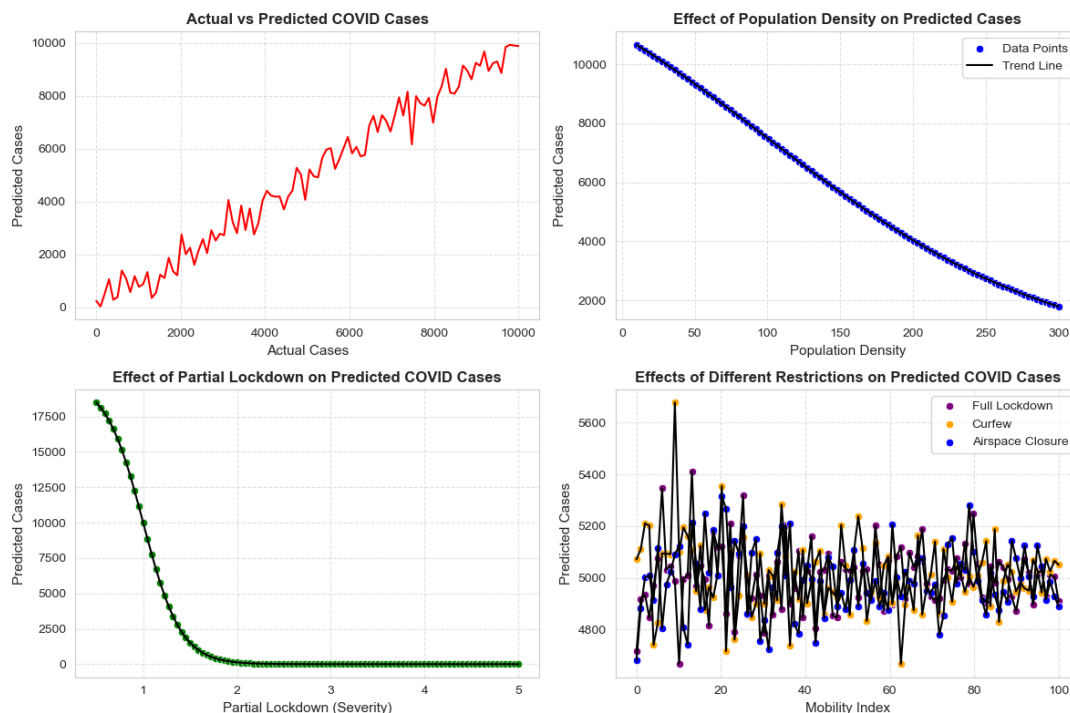
Figure 1: Effects of Covariates on COVID-19 Cases.

Figure 1 presents an illustration of the relationship between actual COVID-19 cases and predictions in the first subplot where a strong positive correlation is noticed the model does a good job of depicting a trend. Yet, replicable variation may indicate random noise, or the effects of other unidentified intervening variables ignored by the model. The second subplot studies the effects of population density on the number of predicted cases, which displays a surprising relationship whereby increased population density corresponds with fewer predicted cases. This illogical pattern could indicate that the higher population density areas had better healthcare facilities or developed control measures that reduced the spread of COVID-19.

The analysis performed on the third plot (bottom left) refers to the effect of "partial lockdown" on predicted COVID cases, identifying a sharp decline when the severity is increased. This suggests that partial lockdowns worked very well at reducing case numbers, although the effect diminishes with the increased stringency of restrictions. Lastly, the fourth plot (bottom right) shows a comparison among full lockdown, curfew, and airspace closure relative to mobility index levels for modeled cases. A general pattern was observed for curfew and airspace closure, but full lockdown had larger variation, signifying that although they may be effective, the effects could depend on factors beyond

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the levels of restriction, such as compliance and enforcement. Overall, the plots suggest that different types of interventions vary widely in effectiveness for COVID-19 case control and underscore the need for targeted policy measures.
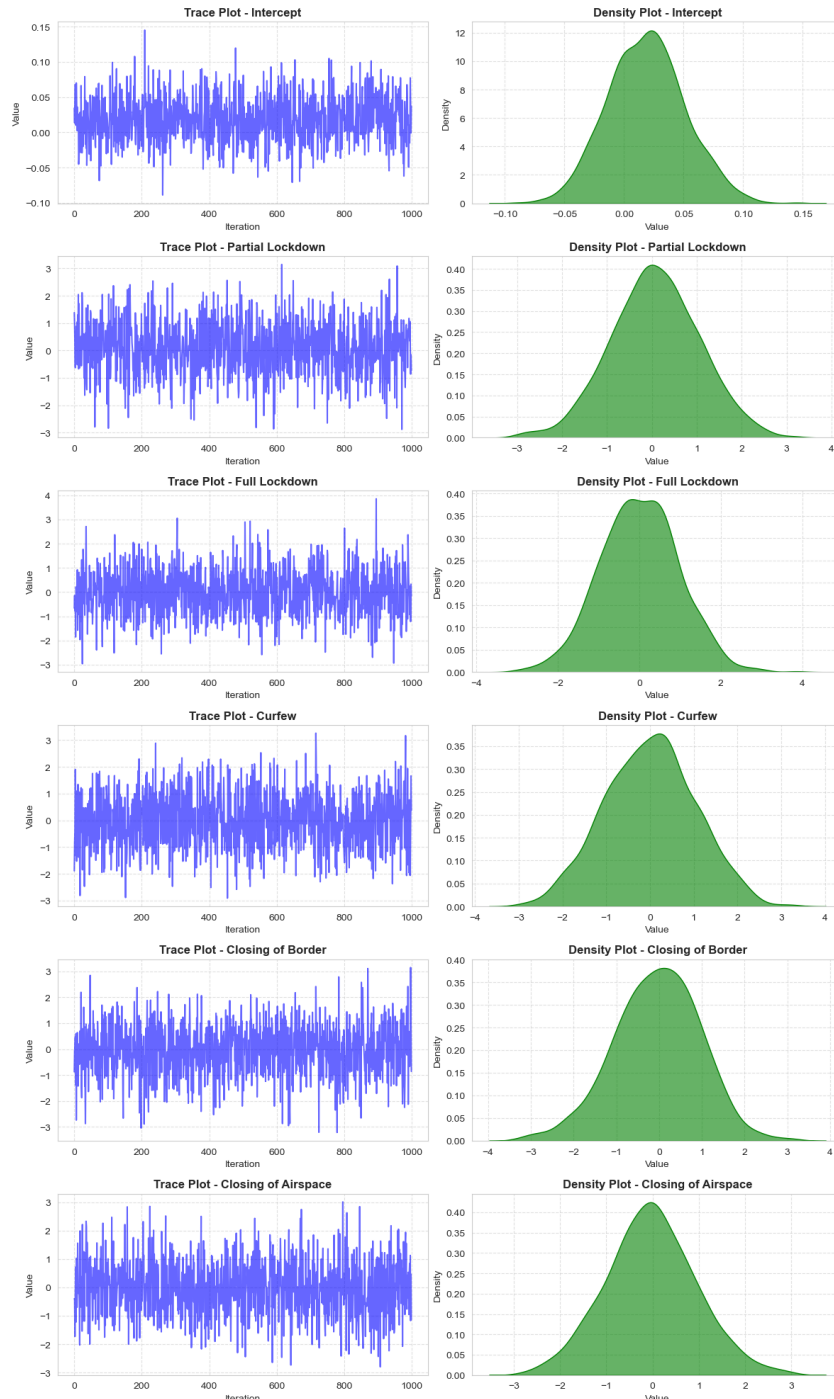

Figure 2: Trace and density plot for the covariates on COVID-19 cases prediction.

Figure 2 illustrates the trace plots (left) for all covariates-including the intercept, partial lockdown, full lockdown, curfew, closing of borders, and closing of airspace with

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evidence of good mixing and stationarity, indicating that the MCMC chains have converged and are effectively exploring the posterior distributions with minimal autocorrelation. Density plots (right) are approximately normal around their means, indicating reasonable parameter estimation but of generally varying uncertainties. Spread around density point indicates uncertainty associated, where narrower distribution translates to higher precision for parameter estimation. These plots in general denote stable and reliable posterior estimates for the fixed effects given by the accepted Bayesian Hierarchical model.
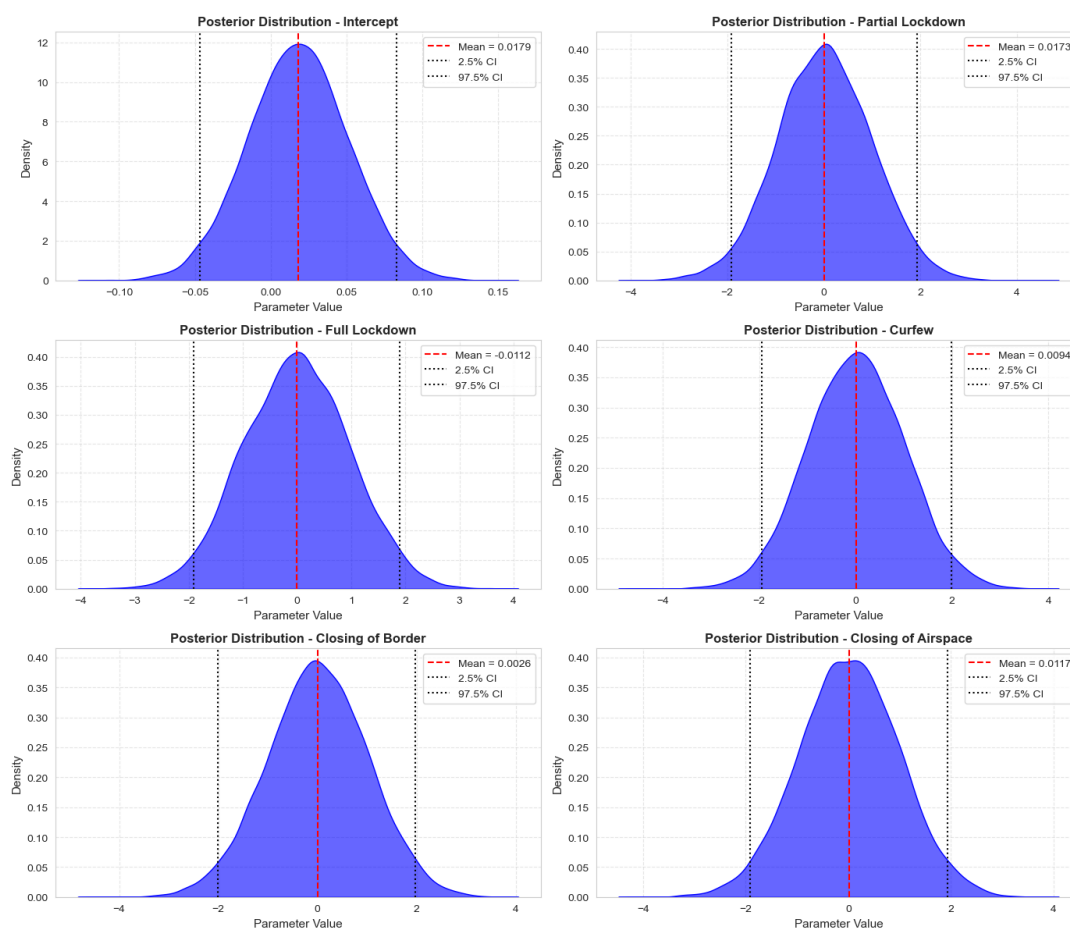

Figure 3: Posterior Distribution of Model parameters.

Figure 3 illustrates the posterior distribution plots for the intercept and a variety of COVID-19 interventions (partial lockdown, full lockdown, curfew, closing of borders, and closing of airspace) suggest that all parameter estimates are centered around zero with symmetrical bell-shaped distributions and represent uncertainty in their effects. The 95% CIs, delineated by the vertical black dotted lines, all enclose zero, implying

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that none of the interventions have any statistically significant effect at the 95%-level of confidence. The relatively wide spread of the distribution shows also a considerable amount of uncertainty on the estimates of the parameters.

5 Discussion

The paper provides an in-depth analysis of COVID-19 transmission dynamics in Liberia, which uses a BHM model framework. Traditional epidemiological models such as the SIR model are helpful but fall short of describing the actual behavioral spread of diseases, given that models are based on very simplified assumptions regarding population homogeneity. Conversely, such spatial heterogeneity caused by the BHM model used provides greater insight into how different factors, including population density, healthcare infrastructure, and social behaviors, affect disease transmission among various counties in Liberia.

The discussion highlights the effectiveness of various public health interventions, including partial and full lockdowns, curfews, and border closures. The results from the Poisson regression model suggest that partial lockdowns and border closures have a significant positive correlation with COVID-19 case counts, whereas full lockdowns and curfews do not show statistically significant effects. The GLMM further emphasizes county-level variability in responses to interventions, demonstrating the importance of region-specific strategies rather than a one-size-fits-all approach.

The Bayesian Hierarchical Model results reveal substantial uncertainty regarding the effectiveness of interventions, with the credible intervals for most covariates including zero. This suggests that while some interventions may have had an impact, their effectiveness varies significantly across different regions. Additionally, the random effects analysis underscores the disparities between counties, with some regions experiencing significantly higher or lower COVID-19 case counts compared to the national average.

Overall, the discussion section highlights that while certain interventions were effective in controlling the spread of COVID-19, others may not have had the intended impact due to regional variations and external factors. The study emphasizes the need for adaptive and localized policy measures to better manage public health crises in diverse regions such as Liberia.

6 Conclusion

This study thus confirms that Bayesian Hierarchical Modeling is a powerful and flexible tool for the modeling ofCOVID-19 transmission dynamicsin Liberia. The study found that public health interventions, like partial lockdowns and border closures, were associated with a significant reduction in the number of daily new cases while full lockdowns and curfews were associated with significantlyfewer new cases. The study also highlights the significance ofspatial heterogeneity, as the effects of the interventions depended on the county under consideration

Moreover, the study shows that models like Poisson regression, GLMM and BHM capture the complicationof infectious disease spread. The study highlights that this is one such demonstration, pointing out that outbreak spread is affected by regional differences in population density, healthcare access, and common mobility patterns that must be accounted for in future outbreak preparedness considerations.

Ultimately, the study provides valuable insights for policymakers and public health officials in Liberia, advocating for a data-driven approach to pandemic management that balances national and local strategies to achieve optimal health outcomes.

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