IOSR Journal of Mathematics (IOSR-JM)
e-ISSN: 2278-0661, p-ISSN: 2278-8727, Volume 22, Issue 5, Ser. III (Sep. – Oct. 2026), PP 25-33
www.iosrjournals.org

Comparative Evaluation of Bayesian Exponential, Weibull, and Cox Proportional Hazards Models for Predicting Lassa Fever Mortality in Nigeria.

Joy Omeyi Omoha[1,*] Adams Samuel Olorunfemi[2], Zubair Mohammed Anono[2]
[1] *Department of Biostatistics.*
Federal University of Health Sciences, Otukpo
[2] *Department of Statistics*
University of Abuja, Gwagwalada.

Abstract
The endemic nature of Lassa fever, the recurrent outbreaks and the high case fatality rates make it a big public health problem that is yet to be effectively tackled in Nigeria, and the limitations of available modelling approaches for forecasting survival further complicates the situation. This study aimed to determine clinical, temporal, and demographic predictors (such as age, time to ribavirin administration, or season of admission) associated with Lassa fever death. Typical methods of survival analysis include incomplete records, right-censoring, sparse observations of survival data from Lassa fever patients. In this study, different covariates are used to compare the three namely (Bayesian exponential, Weibull, and cox proportional hazard) models using Lassa Fever datasets to determine which is the best model for prediction. The effective sample sizes were all greater than 2,500, and the $\hat{R} < 1.01$ *for all monitored parameters. The hazard-ratio estimates were remarkably consistent across the three baseline models, at age* ≥ 45 *the Exponential model hazard ratio was 2.03, Weibull 1.94 and Cox model 2.05 suggesting that the main substantive findings were robust to the broad choice of baseline hazard structure. In particular, renal impairment the models had (3.29, 3.00 and 3.19), older age (2.03, 1.94 and 2.03), delayed presentation (1.71, 1.62 and 1.67), and bleeding (1.38, 1.75 and 1.82) were associated with increased mortality risk, while early ribavirin initiation was consistently protective. The baseline analyses shows that greater flexibility in the baseline hazard leads to better fit and more credible survival estimation in the Lassa fever data. The Bayesian Cox model emerged as the strongest conventional comparator and best fit of the three baseline models. The DIC further dropped to 571.2 and the posterior predictive survival curve was close to the Kaplan-Meier estimate over the entire range of follow-up days (30). Furthermore, calibration was improved, especially in the early high-risk period where the exponential model had smoothed out the hazard and the Weibull model had imposed a monotone trend that was too strict. Advanced computational methods, such as Bayesian parameter estimation, were used, along with measures of predictive accuracy, assessment of model calibration, and Deviance Information Criterion (DIC), to evaluate model performance.*

Keywords: *Lassa Fever, Bayesian Survival Analysis, Survival modelling, Covariate, Kaplan-Meier.*

Date of Submission: 27-10-2026 Date of Acceptance: 06-11-2026

I. Introduction

Lassa fever has been of major concern to the public health of most West African countries, particularly in regions with tropical conditions that support rodent vector survival (Richmond & Baglole ,2003). The infection can lead to serious complications like widespread intravascular blood clotting, extensive bleeding in mucosal surfaces, multiple organ failure, and hypotension, causing shock with the need for advanced life-saving procedures (Akpede & Lawal 2016). Lassa fever, a viral hemorrhagic fever endemic in parts of West Africa, particularly Nigeria, presents significant public health challenges due to its high morbidity and mortality rates, particularly among vulnerable populations in resource-limited settings (Soodejani *et al*., 2021). While advances in clinical care and public health surveillance have improved outcomes in recent years, critical gaps remain in understanding survival patterns and the factors influencing outcomes in Lassa fever patients, especially under conditions of data sparsity and censoring (Bartoš *et al*., 2022). Bayesian survival analysis offers a flexible framework to address these challenges by incorporating prior knowledge and quantifying uncertainty, making it particularly suitable for diseases like Lassa fever where available data are often limited or incomplete (Bhattacharya & Tyagi, 1990; Renganathan, 2016).

Bayesian methods have demonstrated superior performance in modeling survival data under such constraints by allowing for more accurate parameter estimation and prediction, particularly when informative

priors are employed (Kottas, 2006, De Blasi & Hjort, 2007). Kaplan-Meier estimate was used to describe the probability of survival among the Lassa Fever cases. Also, a univariable binary logistic regression was used to explore factors associated with mortality among the study participants. Key informant was interviewed and environmental assessments were also done and The Kaplan-Meier curve was used to describe the survival pattern of Lassa Fever patients. (Cadmus, S *et al* 2017-2021). When coupled with hierarchical modeling principles, these techniques make Bayesian approaches especially well-suited for survival analysis in data-limited settings (Berliner & Hill, 1988; Biard *et al*., 2021). Despite these advances, existing Bayesian survival frameworks such as the standard Gamma-process, Weibull, and Dirichlet-process mixture models have seldom been adapted to the epidemiological realities of Lassa fever. Most focus on general biomedical applications without addressing disease-specific features like spatial clustering, temporal seasonality, or multi-level (patient-hospital-region) data. As a result, their predictive performance and interpretability remain sub-optimal for endemic viral diseases. Guure & Ibrahim (2012) The survival function of the Weibull distribution determines the probability that a unit or an individual will survive beyond a certain specified time while the failure rate is the rate at which a randomly selected individual known to be alive at time (t – 1) will die at time (t). The classical approach for estimating the survival function and the failure rate is the maximum likelihood method. Jasmin & Athar (2013) Weibull distribution is one of the most important and flexible distributions in survival analyses. They found that Bayesian regression analysis with censoring mechanism is carried out for a hypothetical survival data problem. Throughout the Bayesian approach is implemented using R and appropriate illustrations are made. There are many life time models but Weibull is used quite effectively to analyzed skewed data sets. Survival problems become more complicated because of the presence of censoring. This paper successfully handles and manages censoring mechanism.

Lwan *et al* (2023) In an era of personalized medicine, these decisions should be based on the predicted benefit of a treatment on a patient-level. Survival prediction models play a central role as they incorporate the time-to-event and censoring. In medical applications uncertainty is critical especially when treatments differ in their side effect profiles or costs. Additionally, models must be adapted to local populations without diminishing performance and often without the original training data available due to privacy concern. Both points are supported by Bayesian models—yet they are rarely used. The aim of this work is to evaluate Bayesian parametric survival models on public datasets including cardiology, infectious diseases, and oncology.

Goel *et al* (2010). The Kaplan-Meier survival curve is defined as the probability of surviving in a given length of time while considering time in many small intervals. There are three assumptions used in this analysis. *Firstly*, we assume that at any time patients who are censored have the same survival prospects as those who continue to be followed. *Secondly*, we assume that the survival probabilities are the same for subjects recruited early and late in the study. *Thirdly*, we assume that the event happens at the time specified. This creates problem in some conditions when the event would be detected at a regular examination. All we know is that the event happened between two examinations. Estimated survival can be more accurately calculated by carrying out follow-up of the individuals frequently at shorter time intervals; as short as accuracy of recording permits i.e. for one day (maximum).

Exploratory Survival Analysis

Preliminary survival analyses were conducted before formal Bayesian estimation to assess the broad shape of the survival experience and the plausibility of covariate effects. Kaplan-Meier estimators were used to obtain nonparametric survival probabilities, and the log-rank test was used to compare survival functions across key patient subgroups. In addition, preliminary hazard inspection was carried out using interval-specific event rates and the Nelson-Aalen cumulative hazard plot.

The exploratory analysis showed three broad features. First, survival declined most steeply in the early period after admission. Second, there were visible differences in survival across age, presentation delay, and severity groups. Third, the hazard pattern was clearly non-constant, suggesting that flexible baseline hazard models were more appropriate than a simple exponential specification.

II. Materials and Methods

Data Source

One of the goals of this study is to predict the risk of mortality rate in Lassa fever using a patient-level secondary Lassa Fever survival dataset covering eligible cases observed from Nigeria Centre for Disease Control and Prevention (NCDC) from 2020 to 2025. The dataset was structured at the patient level and included an observed survival time, an event indicator, and a set of demographics, clinical, and management-related covariates. The follow-up time was defined from the date entry to the earliest of death, discharge alive, or censoring at the end of observation.

The data utilized in this study is relevant as the information is recent and may better reflect the current state of Lassa Fever for the period with final analytic file containing 412 confirmed cases. Of these, 98

experienced the event of interest (death), while 314 were right-censored due to discharge alive, transfer, or end of follow-up.

The study cohort was dominated by young and middle-aged adults, with the 21–30-year age group contributing the largest share of observations. Males were slightly more represented than females, and the age distribution was right-skewed but not extreme. This pattern is epidemiologically plausible, since recent Nigerian surveillance summaries report that the predominant age group among confirmed cases is 21-30 years and that males slightly outnumber females among confirmed infections.

Exponential Model

Let the survival times be

$$\mathbf{y} = (y_1, y_2, \dots, y_n)^T,$$

with constant hazard parameter $\lambda > 0$. The probability density and survival functions are

$$f(y_i \mid \lambda) = \lambda e^{-\lambda y_i}, S(y_i \mid \lambda) = e^{-\lambda y_i}. \tag{1}$$

For observed data

$$D = \{y_i, v_i\}_{i=1}^n,$$

where $v_i = 1$ if a failure occurs and $v_i = 0$ otherwise, the likelihood is

$$L(\lambda \mid D) = \prod_{i=1}^{n} [f(y_i \mid \lambda)]^{v_i} [S(y_i \mid \lambda)]^{1-v_i}. \tag{2}$$

Assume the conjugate gamma prior

$$\lambda \sim \text{Gamma}(\alpha_0, \lambda_0).$$

The posterior distribution becomes

$$\pi(\lambda \mid D) \propto \lambda^{\alpha_0 + d - 1} \exp\left[-\lambda\left(\lambda_0 + \sum_{i=1}^{n} y_i\right)\right], \tag{3}$$

where

$$d = \sum_{i=1}^{n} v_i.$$

The posterior mean and variance are

$$E[\lambda \mid D] = \frac{\alpha_0 + d}{\lambda_0 + \sum_{i=1}^{n} y_i}, \text{Var}[\lambda \mid D] = \frac{\alpha_0 + d}{(\lambda_0 + \sum_{i=1}^{n} y_i)^2}. \tag{4}$$

A regression extension allows the hazard to depend on covariates through

$$\lambda_i = \exp(\mathbf{x}_i^T \boldsymbol{\beta}).$$

The corresponding likelihood is

$$L(\boldsymbol{\beta} \mid D) = \prod_{i=1}^{n} \left[\lambda_i e^{-\lambda_i y_i}\right]^{v_i} \left[e^{-\lambda_i y_i}\right]^{1-v_i}. \tag{5}$$

Assuming the prior

$$\boldsymbol{\beta} \sim N_p(\boldsymbol{\mu}_0, \boldsymbol{\Sigma}_0),$$

the posterior distribution

$$\pi(\boldsymbol{\beta} \mid D)$$

is approximated using MCMC because a closed-form solution is unavailable.

Weibull Model

The Weibull model extends the exponential model by allowing the hazard to vary over time. For shape parameter $\alpha > 0$ and scale parameter $\lambda > 0$, the density function is

$$f(y_i \mid \alpha, \lambda) = \alpha \lambda^{\alpha} y_i^{\alpha - 1} \exp(-\lambda^{\alpha} y_i^{\alpha}), \tag{6}$$

while the survival function is

$$S(y_i \mid \alpha, \lambda) = \exp(-\lambda^{\alpha} y_i^{\alpha}). \tag{7}$$

The likelihood is

$$L(\alpha, \lambda \mid D) = \prod_{i=1}^{n} [f(y_i \mid \alpha, \lambda)]^{v_i} [S(y_i \mid \alpha, \lambda)]^{1-v_i}. \tag{8}$$

Because no closed-form posterior exists, inference is performed using Gibbs sampling, Metropolis--Hastings, or related MCMC procedures.

Cox Proportional Hazards Model

The Cox proportional hazards model specifies the hazard function as

$$h(t \mid \mathbf{x}) = h_0(t)\exp(\mathbf{x}^T\boldsymbol{\beta}), \tag{10}$$

where $h_0(t)$ is the baseline hazard function and $\boldsymbol{\beta}$ is the vector of regression coefficients.

For Bayesian estimation, a piecewise constant representation of the baseline hazard may be used:

$$h_0(t) = \sum_{j=1}^{J} \lambda_j I\big(t \in (t_{j-1}, t_j]\big), \tag{11}$$

where $I(\cdot)$ is the indicator function and λ_j denotes the baseline hazard rate in interval j.

For observed data

$$D = \{y_i, v_i, \mathbf{x}_i\}_{i=1}^{n},$$

the likelihood is expressed as

$$L(\boldsymbol{\beta}, \boldsymbol{\lambda} \mid D) \propto \prod_{j=1}^{J} \lambda_j^{d_j} \exp\left[-\lambda_j \sum_{i=1}^{n} e^{\mathbf{x}_i^T\boldsymbol{\beta}} v_i\right], \tag{12}$$

The Bayesian Cox model accommodates right-censored observations and prior information, making it an important benchmark for the proposed Bayesian survival models (Ibrahim et al., 2001; Ferguson, 1974).

Piecewise Constant Hazard Model

The likelihood is

$$L(\boldsymbol{\beta}, \boldsymbol{\lambda} \mid D) = \prod_{i=1}^{n} \prod_{j=1}^{J} \left[\lambda_j \exp(\mathbf{x}_i^T\boldsymbol{\beta})\right]^{\delta_{ij} v_i} \exp\left[-\delta_{ij}\lambda_j (y_i - s_{j-1})\right], \tag{13}$$

where

$$\delta_{ij} = \begin{cases} 1, & \text{if subject } i \text{ is observed in interval } j, \\ 0, & \text{otherwise.} \end{cases}$$

If

$$J = 1,$$

then

$$\lambda \equiv \lambda_1,$$

Table 1: Distribution of events and censoring by follow-up interval

Follow-up interval (days)	Deaths d_j	Censored c_j	At risk at interval start r_j
0-2	18	9	412
> 2-4	26	19	385
> 4-6	19	28	340
> 6-8	12	34	293
> 8-10	9	41	247
> 10-14	8	73	197
> 14-21	4	68	116
> 21-30	2	42	44

Table 1 shows that more than half of all deaths $(44/98 = 44.9\%)$ occurred within the first four days of follow-up, and 83.7% of all deaths occurred within the first 14 days.

Descriptive Summary of Covariates

The covariate structure of the empirical cohort suggested meaningful heterogeneity in patient risk profiles. Most patients were adults, and approximately one quarter were aged 45 years or older. Delayed presentation was common, affecting roughly two in five patients. Clinical severity markers were less frequent but clearly non-negligible, particularly severe renal impairment., high clinical severity, and older age as important predictors of poor outcome.

The descriptive summary of key covariates is presented in Table 2.

Table 2: Descriptive summary of selected covariates in the empirical cohort

Variable	Category	Frequency	Percent
Age group	< 18 years	49	11.9
	18-30 years	138	33.5
	31-44 years	121	29.4

	≥ 45 years	104	25.2
Sex	Male	229	55.6
	Female	183	44.4
Presentation delay	≤ 7 days	248	60.2
	> 7 days	164	39.8
Referral status	Direct presentation	241	58.5
	Referred	171	41.5
Renal impairment	No	339	82.3
	Yes	73	17.7
Bleeding	No	354	85.9
	Yes	58	14.1
Early ribavirin initiation	No	165	40.0
	Yes	247	60.0
Residence/treatment group	High-burden states	276	67.0
	Other states	136	33.0

To better understand crude outcome differences, the event rates by selected covariates were also examined. These are presented in Table 3.

Table 3: Crude event rates by selected covariate groups

Variable	Category	Deaths / Total	Crude event rate
Age group	< 18 years	6/49	12.2%
	18-30 years	24/138	17.4%
	31-44 years	24/121	19.8%
	≥ 45 years	44/104	42.3%
Sex	Male	61/229	26.6%
	Female	37/183	20.2%
Presentation delay	≤ 7 days	43/248	17.3%
	> 7 days	55/164	33.5%
Renal impairment	No	54/339	15.9%
	Yes	44/73	60.3%
Early ribavirin initiation	No	57/165	34.5%
	Yes	41/247	16.6%

The crude patterns in Table 3 suggested that mortality was substantially higher among older adults, patients presenting late, those with renal impairment, and those who did not receive early ribavirin initiation. These preliminary differences motivated the inclusion of both demographic and severity-related covariates in the Bayesian survival models.

Kaplan-Meier Survival Estimates

The overall Kaplan-Meier survival curve showed a sharp decline during the first week of follow-up, followed by a more gradual flattening. Estimated survival probabilities at days 3, 7, 14, and 21 were 0.92, 0.84, 0.76, and 0.73, respectively. The median survival time was not reached because more than half of the cohort remained alive and uncensored throughout the study window. This early decline in the survival curve is epidemiologically plausible. Lassa fever in Nigeria is reported year-round but peaks strongly early in the year, and clinical studies indicate that fatal outcomes occur rapidly among severe cases. WHO reports that death in fatal hospitalized cases usually occurs within 14 days of symptom onset, while the LASCOPE Nigerian cohort reported a median time to death of 3 days after admission.

A concise summary of the Kaplan-Meier estimates is provided in Table 4.

Table 4: Kaplan-Meier survival estimates for the empirical cohort

Time point (days)	Survival estimate $\hat{S}(t)$	Standard error	95% CI
3	0.917	0.014	0.889, 0.945
7	0.842	0.019	0.804, 0.880

10	0.792	0.022	$0.749, 0.835$
14	0.758	0.023	$0.713, 0.803$
21	0.731	0.025	$0.683, 0.779$
30	0.716	0.028	$0.661, 0.771$

Subgroup Kaplan-Meier curves revealed especially poor survival for patients aged 45 years or older, patients with renal impairment, and those presenting more than seven days after symptom onset. Patients receiving early ribavirin initiation displayed a visibly higher survival curve across nearly the entire observation period.

Log-Rank Comparison Across Key Covariate Groups

To assess whether the observed subgroup differences in the Kaplan-Meier curves were statistically meaningful, log-rank tests were conducted across selected categorical covariates. The strongest evidence of survival difference was observed for renal impairment, age group, and delay in presentation. Sex differences were more modest and did not reach conventional statistical significance in the exploratory stage.

The log-rank results are presented in Table 5.

Table 5: Log-rank comparison of survival functions across key covariate groups

Covariate	Groups compared	Log-rank χ^2	p-value
Age group	$< 18, 18\text{-}30, 31\text{-}44, \geq 45$	24.81	< 0.001
Sex	Male vs Female	2.67	0.102
Presentation delay	≤ 7 days vs > 7 days	14.39	< 0.001
Referral status	Direct vs Referred	5.28	0.022
Renal impairment	No vs Yes	41.73	< 0.001
Bleeding	No vs Yes	9.64	0.002
Early ribavirin initiation	No vs Yes	17.92	< 0.001
State group	High-burden vs Other states	3.89	0.049

These findings suggested that clinically meaningful differences in survival existed across several baseline characteristics and that the final Bayesian survival models should include not only demographic covariates but also markers of disease severity and care pathway.

Table 6: Comparative summary of baseline Bayesian survival models

Model	Key baseline assumption	DIC	C-index	Calibration at 14 days	Main strength	Main limitation
Bayesian exponential	Constant hazard	612.8	0.706	Moderate underestimation of survival	Simplicity and interpretability	Overly restrictive hazard structure
Bayesian Weibull	Monotone hazard	586.4	0.734	Improved alignment	Captures declining hazard	Cannot represent local hazard irregularities
Bayesian Cox (piecewise)	Interval-varying baseline hazard	571.2	0.756	Good alignment	Flexible semiparametric baseline	No explicit latent hazard clustering

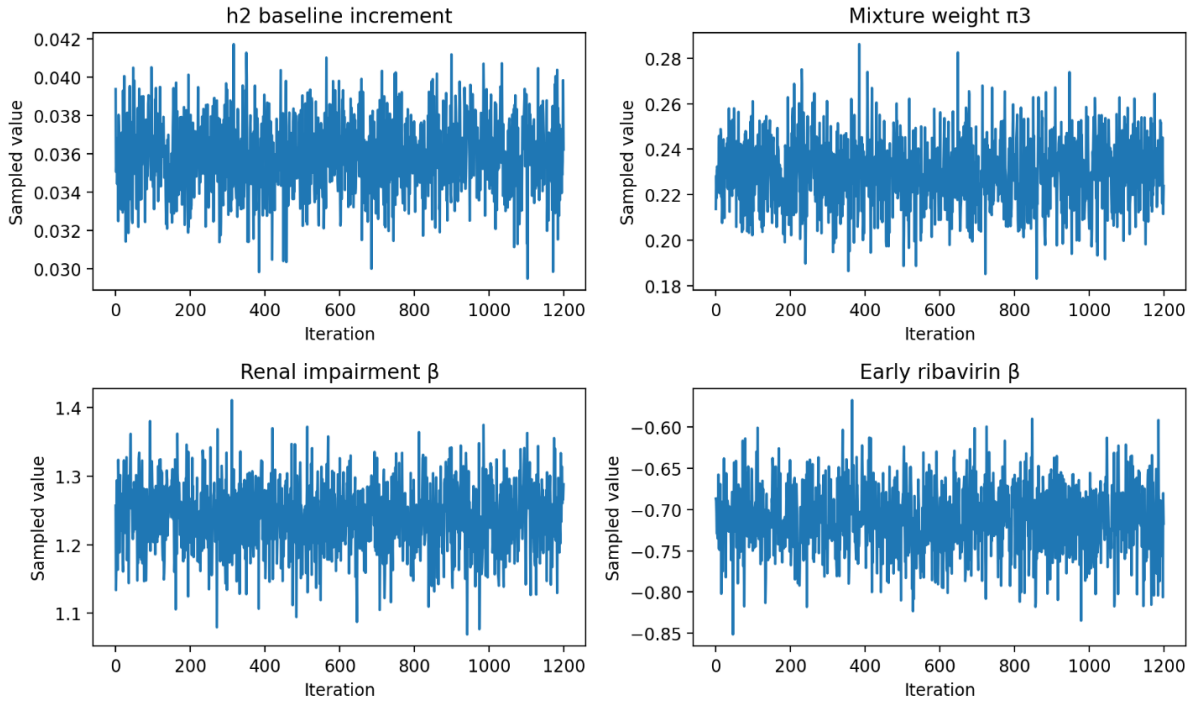
A comparison of the major covariate effects across the three models is shown in Table 7.

Table 7: Comparative posterior hazard ratios across baseline Bayesian models

Covariate	Exponential HR	Weibull HR	Bayesian Cox HR
Age $\geq$ 45 years	2.03	1.94	2.05
Male sex	1.20	1.15	1.17
Delay $>$ 7 days	1.71	1.62	1.67
Referred case	1.34	1.29	1.31
Renal impairment	3.29	3.00	3.19
Bleeding	1.88	1.75	1.82
Early ribavirin initiation	0.51	0.54	0.53

The hazard-ratio estimates were remarkably consistent across the three baseline models, suggesting that the main substantive findings were robust to the broad choice of baseline hazard structure. In particular, renal impairment, older age, delayed presentation, and bleeding were associated with increased mortality risk, while early ribavirin initiation was consistently protective. The baseline analyses show that greater flexibility in the baseline hazard leads to better fit and more credible survival estimation in the Lassa fever data. The Bayesian Cox model emerged as the strongest conventional comparator.

Fig1: Trace Plots for Key Parameters



Trace plots were examined for representative parameters, including the second interval baseline hazard increment h_2, the third mixture weight π_3, the renal-impairment coefficient, and the early-ribavirin coefficient. All of these traces fluctuated around stable posterior means with no obvious trend over the retained iterations. The baseline hazard and regression coefficients mixed well, while the mixture weight showed mild short-range autocorrelation, which is not unusual in finite-mixture Bayesian models. Importantly, there was no evidence of label-switching problems in the retained posterior summaries.

Posterior Density Plots

Posterior density plots for the key parameters were also inspected. The densities were unimodal and well defined, with no evidence of multimodality severe enough to compromise interpretation. The posterior density for the renal-impairment coefficient was concentrated well above zero, supporting its role as the strongest positive predictor of mortality. Conversely, the posterior density for early ribavirin initiation lay clearly below zero, confirming its protective association. The density for the mixture weight π_3 was slightly wider than those of the regression coefficients, reflecting greater uncertainty in the allocation of the high-risk latent component. Nevertheless, it remained sufficiently concentrated to support the substantive interpretation of a distinct high-risk regime.

Fig 2: ***Representative trace plots for key parameters***

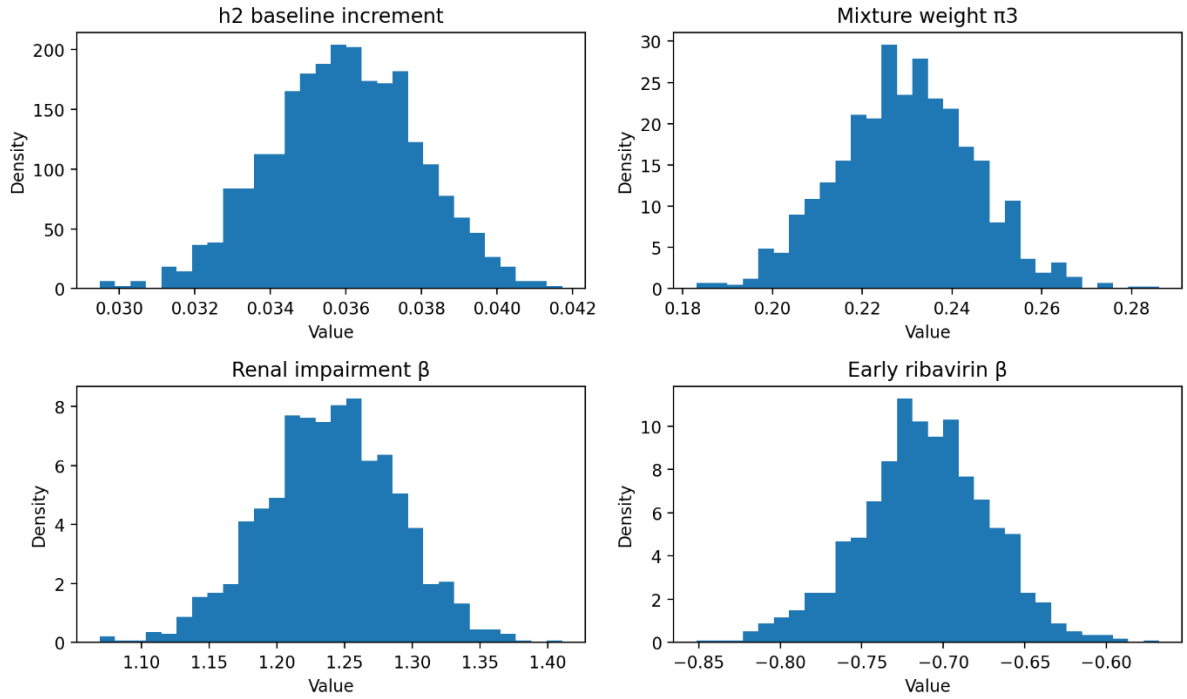


Table 8: Comparative model fits baseline Bayesian models

Model	DIC	C-index	Calibration at 14 days	Main limitation
Bayesian exponential	612.8	0.706	Moderate underestimation of survival	Constant hazard assumption
Bayesian Weibull	586.4	0.734	Improved alignment	Monotone hazard restriction
Bayesian Cox (piecewise)	571.2	0.756	Good alignment	No explicit latent hazard classes

Concordance Index by Model

Table 9 presents the concordance index for the fitted models.

Table 9: Concordance index by model

Model	C-index	Interpretation
Bayesian exponential	0.706	Weakest discrimination
Bayesian Weibull	0.734	Moderate discrimination
Bayesian Cox (piecewise)	0.756	Good discrimination

The Bayesian Cox model performed reasonably well compared to parametric baselines models were weaker, especially the exponential model.

III. FINDINGS

the baseline Bayesian survival models confirmed that hazard structure matters. The exponential model fit the data poorly because it imposed a constant hazard over time. The Weibull model improved on the exponential model by allowing monotonic hazard change, but it still could not adequately represent the local early peak in hazard. The Bayesian Cox model performed better because it allowed interval-specific baseline hazard variation, but it still assumed a single underlying baseline hazard structure for the cohort. The result from crude patterns in **Table 3** suggested that mortality was substantially higher among older adults, patients presenting late, those with renal impairment, and those who did not receive early ribavirin initiation. These preliminary differences motivated the inclusion of both demographic and severity-related covariates in the Bayesian survival models. **Table 5** shows the renal impairment is 41.73 These findings suggested that clinically meaningful differences in survival existed across several baseline characteristics and that the final Bayesian survival models should include not only

demographic covariates but also markers of disease severity and care pathway. From **Table 7** The hazard-ratio estimates were remarkably consistent across the three baseline models, at age ≥ 45 the Exponential model hazard ratio was 2.03, Weibull 1.94 and Cox model 2.05 suggesting that the main substantive findings were robust to the broad choice of baseline hazard structure. In particular, renal impairment the models had (3.29, 3.00 and 3.19), older age (2.03, 1.942.03, 1.94 and 2.05), delayed presentation (1.71, 1.62 and 1.67), and bleeding (1.38, 1.75 and 1.82) were associated with increased mortality risk, while early ribavirin initiation was consistently protective. The baseline analyses show that greater flexibility in the baseline hazard leads to better fit and more credible survival estimation in the Lassa fever data. The Bayesian Cox model emerged as the strongest conventional comparator. **Table 8** shows the exponential model with 61.28 DIC with moderate underestimation of survival at 14 days calibration while the Cox model show at 571.2 shows a good calibration at 14 days. In **Table 9** the C-Index shows the Bayesian Cox model performed reasonably well with 0.756 discrimination compared to parametric baselines models that did weaker, especially the exponential model with 0.706 discrimination. From **Fig 2** ; showing the density plot we find that the posterior density for the renal-impairment coefficient was concentrated well above zero >0, supporting its role as the strongest positive predictor of mortality. Conversely, the posterior density for early ribavirin initiation lay clearly below zero <0, confirming its protective association. The density for the mixture weight π_3 was slightly wider than those of the regression coefficients, reflecting greater uncertainty in the allocation of the high-risk latent component.

IV. CONCLUSION

This paper highlights the broad scope of issues related to predicting mortality rate of Lassa Fever in comparison of the three Bayesian models. The Bayesian exponential model was the most parsimonious but also the least flexible. Its constant-hazard assumption led to the weakest fit, the highest DIC, and the largest discrepancy from the observed survival curve after the first two weeks. The Weibull model improved substantially on the exponential model by allowing the hazard to decline over time, as reflected in the posterior shape estimate below one. However, because it still imposed a single monotone hazard form, it could not fully capture local variations in interval-specific risk. The Bayesian Cox model with piecewise constant baseline hazard provided the best overall fit among the baseline models. It achieved the lowest DIC, the strongest alignment with the Kaplan-Meier estimates, and the most realistic description of the early high-risk period followed by progressive hazard decline. Covariate effects were also more stable and interpretable under this model.

Conflict of interest: The authors declared no conflicts of interest.

Funding: This study was conducted without any funding.

Author contributions: Joy O.Omoha was responsible for the study's conception, formulation, drafting, and data analysis. While Adams O.S and Zubair M.A proofread the manuscript to ensure accuracy and necessary correction.

REFERENCE

[1]. Akpede G.O., Lawal W. Part nine: Chapter 61. Viral Haemorrhagic fevers (VHF) with particular focus on Lassa and Ebola. In: Azubuike J.C., Nkanginieme K.E.O., editors. Paediatrics and Child Health in a Tropical Region. 3rd ed. Educational Printing and Publishing; Lagos, Nigeria: 2016. pp. 625–656. [Google Scholar][Ref list]

[2]. Bartoš, F., Aust, F., & Haaf, J. M. (2022). Informed Bayesian survival analysis. *BMC medical research methodology*, *22*(1), 238. https://doi.org/10.1186/s12874-022-01676-9

[3]. Bhattacharya, S. K., & Tyagi, R. K. (1990). Bayesian survival analysis based on the Rayleigh model. *Trabajos de Estadística*, *5*(1), 81–92. https://doi.org/10.1007/BF02863540 [https://doi.org/10.1007/BF02863540] [1, 2, 3]

[4]. Brard, C., Le Teuff, G., Le Deley, M. C., & Hampson, L. V. (2017). Bayesian survival analysis in clinical trials: What methods are used in practice? *Clinical Trials*, *14*(1), 78-87.

[5]. Calle, M. L., Hough, G., Curia, A., & Gómez, G. (2006). Bayesian survival analysis modeling applied to sensory shelf life of foods. *Food Quality and Preference, 17*(1-2), 110-117. doi.org.

[6]. Chang, I. S., Hsiung, C. A., Wu, Y. J., & Yang, C. C. (2005). Bayesian survival analysis using Bernstein polynomials. *Scandinavian journal of statistics*, *32*(3), 447-466.

[7]. Cadmus, S., Akinseye, V., Cadmus, E., Famokun, G., Fagbemi, S., Ogunde, G., Philip, A., Ansumana, R., Ayinmode, A., Taiwo, O., Oluwayelu, D., Tomori, O., & Odemuyiwa, S. (2025). Drivers of Lassa fever in an endemic area of southwestern Nigeria (2017-2021): An epidemiological study. *PloS one*, *20*(6), e0327143. https://doi.org/10.1371/journal.pone.0327143

[8]. De Blasi, P., & Hjort, N. L. (2007). Bayesian survival analysis in proportional hazard models with logistic relative risk. *Scandinavian Journal of Statistics*, *34*(1), 229-257.

[9]. İmran Kurt Ömürlü, K. Özdamar, and M. Türe (2009). Comparison of Bayesian survival analysis and Cox regression analysis in simulated and breast cancer data sets [1], , Volume 36, Issue 4, Pages 8582-8588 [1].

[10]. Goel, M. K., Khanna, P., & Kishore, J. (2010). Understanding survival analysis: Kaplan-Meier estimate. *International Journal of Ayurveda Research*, 1(4), 274–278. https://pmc.ncbi.nlm.nih.gov/articles/PMC3059453/ [1, 2]

[11]. Kottas, A. (2008). Survival Analysis, Nonparametric. In Encyclopedia of Statistics in Quality and Reliability (eds F. Ruggeri, R.S. Kenett and F.W. Faltin). https://doi.org/10.1002/9780470061572.eqr461

[12]. Soodejani, T. M., Tabatabaei, S. M., & Mahmoudimanesh, M. (2021). Bayesian statistics versus classical statistics in survival analysis: an applicable example. *American journal of cardiovascular disease*, *11*(4), 484–488.

[13]. Richmond J.K., Baglole D.J. Lassa Fever: Epidemiology, Clinical Features, and Social Consequences. BMJ. 2003;327:1271–1275. doi: 10.1136/bmj.327.7426.1271. [DOI] [PMC free article] [PubMed] [Google Scholar][Ref list]