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A Bayesian Perspective on Survival Prediction in Colorectal Cancer Using Accelerated Failure Time Models

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Abstract

Accurate survival prediction in colorectal cancer (CRC) is essential for guiding prognosis and optimizing treatment strategies. This study applies a Bayesian Accelerated Failure Time (AFT) modeling framework using three parametric distributions namely Weibull, log-normal and log-logistic to estimate survival times based on clinical characteristics. The models were evaluated using the Widely Applicable Information Criterion (WAIC), Deviance Information Criterion (DIC) and Log Pseudo Marginal Likelihood (LPML). Among the three, the Bayesian log-normal AFT model achieved the best overall fit and predictive performance. Clinical covariates including age, sex, tumor stage, nodal involvement, metastasis status and tumor histology were incorporated to assess their effects on survival time. The analysis confirmed a strong association between advanced nodal stage (N2) and prolonged survival, while estimates for tumor stages, tumor type and sex showed wider credible intervals, indicating greater uncertainty and highlighting the importance of individualized survival modeling. Posterior trace plots confirmed MCMC convergence and parameter stability, reinforcing the model's reliability. Moreover, The survival probability plots from the Bayesian lognormal AFT model illustrated how age, when combined with key clinical factors impacts the survivability of the patients. This work demonstrates the practical utility of Bayesian AFT models in handling non-proportional hazards and offers a flexible, interpretable framework for individualized survival estimation in CRC. The findings offer a foundation for future studies integrating more complex covariates and advancing personalized oncology.

Keywords: colorectal cancer, Bayesian methods, accelerated failure time model, survival prediction.

1. Introduction

Colorectal cancer (CRC), sometimes referred to as colon cancer or rectal cancer depending on where it is found is the third most common cancer globally (World Health Organization (2023)). It is a slowly spreading disease that starts as an abnormal tissue growth or tumor in the colon or rectum's lining (Yu and Hemminki (2020)) and accounts for around 10% of all cancer diagnoses. It is the third most common cancer in women, after breast and lung

cancer and also the third most common in men, after prostate and lung cancer (Bray, Ferlay, Soerjomataram, Siegel, Torre, and Jemal (2018); Hassan, Suan, Soelar, Mohammed, Ismail, and Ahmad (2016)). Although colon and rectal cancer are anatomically distinct entities, they are often jointly referred to as CRC due to their shared characteristics and overlapping risk factors (Kazemi, Zayeri, Baghestani, Bakhshandeh, and Hafizi (2023)).

There is a concerning upward trend in the incidence of colon cancer worldwide, particularly in developing countries that have embraced a Western lifestyle (Rawla, Sunkara, and Barsouk (2019)).

Colorectal cancer is a complex illness with a significant impact played by a number of factors including hormones, food, physical activity and heredity (Kesse, Clavel Chapelon, and Boutron Ruault (2006)). A number of lifestyle decisions are believed to contribute to the development of colorectal cancer (Rawla *et al.* (2019)) including obesity, sedentary behavior and the use of nicotine, alcohol and red meat.

Patients with colorectal cancer have a highly variable prognosis with 5-year survival rates ranging from 90% to 10% depending on the disease's stage and other relevant variables (Chen, Collins, Wang, and Toh (2021)). Several studies have shown significant relationships between the survival of CRC patients and variables such body mass index (BMI), tumor grade, size, marital status and initial treatment modality (Asghari-Jafarabadi, Hajizadeh, Kazemnejad, and Fatemi (2009); Boyle and Langman (2000); Moghimi-Dehkordi, Safaee, and Zali (2008)). Knowing the stage of the disease helps doctors prescribe the best course of treatment and anticipate the prognosis or chance of recovery for the patient. Even if the literature on the predictive significance of tumor location with regard to overall survival is expanding, more research with sizable patient cohorts is still required (Wang, Shahjehan, Merchea, Li, Bekaii-Saab, Grothey, Colibaseanu, and Kasi (2019)).

Traditionally, survival analysis in oncology has heavily relied on the Cox Proportional Hazards (PH) model, which estimates hazard ratios under the key assumption that covariate effects are constant over time (Kleinbaum and Klein (2012)). While the Cox PH model provides a well-established and interpretable framework for exploring the relationship between covariates and survival outcomes, its strict proportional hazards assumption can limit its applicability in clinical datasets where effects may vary over time (Alvares, Haneuse, Lee, and Lee (2019)). Such violations can lead to biased estimates and compromised predictive performance, particularly in heterogeneous diseases like colorectal cancer. Although the Bayesian paradigm extends the Cox PH model by incorporating prior information and offering a coherent approach to uncertainty quantification, it still inherits this proportional hazards limitation (Pan, Sun, and Carroll (2017)). This underscores the need for alternative approaches that can accommodate more complex survival dynamics. Bayesian Accelerated Failure Time (AFT) models address these challenges by directly modeling survival times, thus relaxing the proportional hazards assumption (Zhou, Hanson, and Zhang (2022)). By explicitly specifying the survival time distribution, Bayesian AFT models allow for customized analyses that better capture the unique characteristics of colorectal cancer data. Commonly employed distributions within this framework include the Weibull, log-normal and log-logistic, each offering distinct advantages in modeling various hazard shapes and survival patterns (Renganathan (2016)). This flexibility makes Bayesian AFT models particularly suited for developing individualized prognostic tools in oncology.

Thus, to overcome the limitations posed by the proportional hazards assumption inherent in traditional Cox PH models, this study employs Bayesian survival modeling within the AFT framework to predict survival outcomes for CRC patients. By explicitly modeling survival times and incorporating distributions such as Weibull, log-normal and log-logistic, the Bayesian AFT approach allows for greater flexibility in capturing complex survival dynamics. This framework enables the integration of critical clinical and demographic factors, including tumor stage, site, and other prognostic covariates, providing a comprehensive basis for understanding survival patterns. Such an approach offers valuable insights that can inform personalized treatment strategies and ultimately enhance clinical decision-making in colorectal cancer care.

2. Review of literature

In recent years, there has been a consistent rise in the popularity of Bayesian statistics. The smooth integration of outside knowledge, the ability to continuously track evidence and the ability to accept uncertainty regarding the data-generating process are just a few advantages that Bayesian approaches bring to parametric survival analysis (Van de Schoot, Depaoli, King, Kramer, Märtens, Tadesse, Vannucci, Gelman, Veen, Willemsen *et al.* (2021)). Through prior distributions, Bayesian estimation enables us to easily integrate outside knowledge into statistical models (Gronau, Ly, and Wagenmakers (2020); Rhodes, Turner, and Higgins (2015); Stefan, Evans, and Wagenmakers (2022); Bartoš, Gronau, Timmers, Otte, Ly, and Wagenmakers (2021)). The idea of incorporating expert opinions or historical data is not new. It was first suggested in medicine around forty-five years ago (Pocock (1976)) and has since been promoted on numerous occasions (Berry (2006); Hobbs and Carlin (2007); Cope, Ayers, Zhang, Batt, and Jansen (2019); Thirard, Ascione, Blazeby, and Rogers (2020)). Such outside information can increase the accuracy of survival predictions, reduce error rates and provide superior sample characteristics (Cope *et al.* (2019); Brard, Hampson, Gaspar, Le Deley, and Le Teuff (2019); Hampson, Whitehead, Eleftheriou, and Brogan (2014); Molinares (2011); Omurlu, Ture, and Ozdamar (2015); Van Rosmalen, Dejardin, Van Norden, Löwenberg, and Lesaffre (2018); Viele, Berry, Neuenschwander, Amzal, Chen, Enas, Hobbs, Ibrahim, Kinnersley, Lindborg *et al.* (2014)). There are precautions against the negative effects of external knowledge, even though incorrect integration of external knowledge could skew estimates and raise the error rate (Cuffe (2011)). For instance, to account for differences from earlier research, researchers can employ meta-analytic prediction priors (Van Rosmalen *et al.* (2018)) that take into account the data regarding between-study heterogeneity (Neuenschwander, Capkun-Niggli, Branson, and Spiegelhalter (2010).

Mahmoudi, Fallah, Roshanaei, and Asghari-Jafarabadi (2022) examined CRC mortality and recurrence using Bayesian semi-competing hazards models, finding important variables including treatment frequency and tumor stage. The significance of Bayesian approaches in survival prediction was highlighted by their findings, which showed how well Bayesian frameworks could handle complex survival data and integrate various covariates. In a similar vein, Alinia, Asghari-Jafarabadi, Mahmoudi, Roshanaei, and Safari (2024) evaluated survival outcomes in CRC patients classified by tumor site using Bayesian log-normal models. Significant differences between colon and rectal cancer were found in their analysis, highlighting how well Bayesian techniques capture complex survival dynamics. To determine the comorbidities influencing the survival outcomes of colorectal cancer, Rubio, Alvares, Redondo-Sanchez, Marcos-Gragera, Sánchez, and Luque-Fernandez (2022) used Bayesian variable selection techniques. Their research demonstrated how flexible Bayesian methods are for managing huge clinical datasets and choosing pertinent predictors for survival analysis. Furthermore, Carroll and Zhao (2019) expanded the use of Bayesian techniques to spatiotemporal survival analyses, showcasing their capacity to capture regional variations in survival patterns and offering insights into the models' wider usefulness. Bayesian approaches for parametric survival models were investigated by Zhou, Liu, Zhang, Li, and Cao (2020b) and Bartoš, Aust, and Haaf (2022) with an emphasis on computational effectiveness and the incorporation of historical data. However, there is a knowledge vacuum regarding their relative predictive powers because their work did not primarily focus on CRC and did not directly compare these AFT distributions. A generalized log-logistic AFT model for laryngeal cancer data was presented by Muse, Mwalili, Ngesa, Alshanbari, Khosa, and Hussam (2022) using the Bayesian framework. They emphasized how the log-logistic distribution may be used to accommodate both monotone and non-monotone hazard functions. A variational Bayesian technique was presented by Xian, de Souza, He, Rodrigues, and Tian (2024) for AFT models which achieved accuracy and computing efficiency. Although this invention holds promise for managing huge datasets, it has not yet been particularly implemented for CRC survival analysis. Although Dasgupta, Cramb, Aitken, Turrell, and Baade (2014) and Siddique, Baum, Deziel, Kelly, Warren, and Ma (2024) highlighted differences in CRC survival according to demographic

and regional characteristics, their research did not apply Bayesian AFT models to account for these differences, providing a chance to investigate their potential in this area.
Bayesian estimate and inference for an AFT model has become a desirable substitute for likelihood-based techniques (Ibrahim, Chen, and Sinha (2001)). The AFT model has been implemented in several contexts using the Bayesian survival analysis framework; for instance, Lambert, Collett, Kimber, and Johnson (2004), Komárek and Lesaffre (2008), Zhang and Lawson (2011) and Tang, Song, and Yi (2022). The majority of current research either concentrates on other malignancies or general Bayesian parametric models, which leaves a void in applications specific to colorectal cancer. Moreover, thorough comparisons of these distributions' prediction abilities with clinical data are not yet available. Filling up these gaps will help us understand the usefulness of Bayesian AFT models and how they might help improve CRC patient survival estimates.

3. Methodology

The approach used in this chapter is presented in this section, detailing the procedures from data collection and preprocessing to survival prediction. As the proportional hazards (PH) assumption was not satisfied, the Cox PH model was deemed unsuitable. Therefore, we employed Bayesian AFT models, which directly model survival time without requiring the PH assumption.

3.1. Data source and variables

The clinical dataset used in this study was obtained from cBioPortal. The dataset comprises patient-specific survival data, demographic information and tumor characteristics, as summarized in Table 1. The primary variable of interest in this study is time to death, measured as Overall Survival Months.

Table 1: Overview of clinical data variables used in the study

Variable	Description
Overall Survival Months	The duration (in months) from diagnosis or treatment until death or the last follow-up.
Overall Survival Status	Indicates whether the patient is alive or deceased at the time of follow-up (1 = Death, 0 = Censored).
Diagnosis Age	The age of the patient at the time of initial diagnosis.
Metastasis Stage	Represents the extent of metastasis: M0 (No metastasis), M1 (Metastasis present), MX (Unknown status).
Node Stage	Describes the extent of lymph node involvement: N0 (No lymph node involvement), N1 (Nearby lymph nodes involved), N2 (Distant lymph nodes involved).
Tumor Stage	Classification of the tumor based on size and invasion: T1 (Small, localized tumor), T2 (Larger tumor without spread), T3 (Tumor invading nearby tissues), T4 (Tumor invading adjacent structures).
Sex	The biological sex of the patient (Male or Female).
Tumor Type	The classification of the tumor subtype (Colon Adenocarcinoma, Rectal Adenocarcinoma).

3.2. Bayesian AFT model and posterior estimation

The Bayesian Accelerated Failure Time (AFT) model is a parametric survival model that directly relates the logarithm of survival time T_i to a linear function of covariates. Mathematically, it is given by

$$\log(T_i) = \beta_0 + x_i^\top \beta + \epsilon_i. \tag{1}$$

Here, β_0 represents the intercept, x_i is the vector of covariates for the i^{th} individual, β denotes the corresponding regression coefficient vector and ϵ_i is an error term that follows a specific distribution, which defines the survival distribution and thus determines the type of AFT model. In this study, we consider Weibull, log-normal and log-logistic distributions for ϵ_i, as these are among the most commonly employed models due to their flexibility in capturing various survival time patterns (Muse *et al.* (2022)).

Weibull distribution

The Weibull AFT model assumes that the error term follows an Extreme Value distribution, leading to a Weibull survival distribution. The probability density function (PDF) is given by

$$f(T_i) = p\lambda T_i^{p-1} e^{-\lambda T_i^p}, \quad T_i > 0, \tag{2}$$

where p is the shape parameter and $\lambda = e^{-(x_i^\top \beta)}$ is the scale parameter.
The cumulative distribution function (CDF) is given by

$$F(T_i) = \int_0^{T_i} p\lambda u^{p-1} e^{-\lambda u^p}\, du = 1 - e^{-\lambda T_i^p}. \tag{3}$$

The survival function is given by

$$S(T_i) = 1 - F(T_i) = e^{-\lambda T_i^p}. \tag{4}$$

Log-normal distribution

If the error term follows a Normal distribution, the resulting survival time follows a log-normal distribution. The probability density function (PDF) of the log-normal distribution is given by

$$f(T_i) = \frac{1}{T_i \sigma \sqrt{2\pi}} \exp\left(-\frac{(\log T_i - \mu)^2}{2\sigma^2}\right), \tag{5}$$

where, $\mu = x_i^\top \beta$ and σ is the standard deviation.
The cumulative distribution function (CDF) is given by

$$F(T_i) = \int_0^{T_i} \frac{1}{u\sigma\sqrt{2\pi}} \exp\left(-\frac{(\log u - \mu)^2}{2\sigma^2}\right) du = \Phi\left(\frac{\log T_i - \mu}{\sigma}\right). \tag{6}$$

The survival function is given by

$$S(T_i) = 1 - F(T_i) = 1 - \Phi\left(\frac{\log T_i - \mu}{\sigma}\right). \tag{7}$$

Log-logistic distribution

If the error term follows a Logistic distribution, the survival time follows a log-logistic distribution. The probability density function (PDF) of the log-logistic distribution is given by

$$f(T_i) = \frac{(T_i^{\gamma-1}) e^{-\frac{T_i^\gamma}{\lambda}}}{\lambda^{\frac{1}{\gamma}} \left(1 + e^{-\frac{T_i^\gamma}{\lambda}}\right)^2}, \tag{8}$$

where γ is the shape parameter.
The cumulative distribution function (CDF) is given by

$$F(T_i) = \int_0^{T_i} \frac{(u^{\gamma-1})e^{-\frac{u^\gamma}{\lambda}}}{\lambda^{\frac{1}{\gamma}}\left(1+e^{-\frac{u^\gamma}{\lambda}}\right)^2} du = \frac{1}{1+e^{-(\log T_i-\mu)/\sigma}}. \tag{9}$$

The survival function is given by

$$S(T_i) = 1 - F(T_i) = \frac{1}{1+e^{(\log T_i-\mu)/\sigma}}. \tag{10}$$

Prior distributions

In Bayesian analysis, prior distributions formally encode existing beliefs or knowledge about model parameters before observing the current data (Gelman (2006)). To incorporate prior knowledge and ensure numerical stability, the regression coefficients β are assigned a normal prior $\beta \sim \mathcal{N}(0, \tau^2 I)$, allowing regularization and the scale parameter σ^2 follows an Inverse-Gamma prior $\sigma^2 \sim \text{IG}(a, b)$, ensuring positivity.

Bayesian posterior estimation

Using Bayes' Theorem, the posterior distribution of the parameters is estimated by combining the likelihood function of the observed survival times with the prior distributions of the model parameters. This posterior distribution represents updated beliefs about the parameters after taking the data into account. Mathematically, it is given by

$$p(\beta, \sigma^2, \gamma \mid T, X) \propto L(\beta, \sigma^2, \gamma) p(\beta) p(\sigma^2) p(\gamma). \tag{11}$$

Substituting the prior distributions that we have considered, we get

$$\begin{aligned} p(\beta, \sigma^2, \gamma \mid T, X) \propto & \left[\prod_{i=1}^{n} f(T_i \mid \beta, \sigma^2, \gamma)\right] \times \exp\left(-\frac{1}{2\tau^2}\beta^\top \beta\right) \\ & \times (\sigma^2)^{-(a+1)} \exp\left(-\frac{b}{\sigma^2}\right) \\ & \times \gamma^{c_0-1} \exp(-d_0\gamma). \end{aligned} \tag{12}$$

The likelihood function of the posterior is obtained by

$$\begin{aligned} L_{\text{posterior}}(\beta, \sigma^2, \gamma) = & \left[\prod_{i=1}^{n} f(T_i \mid \beta, \sigma^2, \gamma)\right] \times \exp\left(-\frac{1}{2\tau^2}\beta^\top \beta\right) \\ & \times (\sigma^2)^{-(a+1)} \exp\left(-\frac{b}{\sigma^2}\right) \\ & \times \gamma^{c_0-1} \exp(-d_0\gamma). \end{aligned} \tag{13}$$

Taking the logarithm, the log-likelihood of the posterior is given by

$$\begin{aligned} \log L_{\text{posterior}}(\beta, \sigma^2, \gamma) = & \sum_{i=1}^{n} \log f(T_i \mid \beta, \sigma^2, \gamma) - \frac{1}{2\tau^2}\beta^\top \beta \\ & - (a+1)\log \sigma^2 - \frac{b}{\sigma^2} \\ & + (c_0 - 1)\log \gamma - d_0\gamma. \end{aligned} \tag{14}$$

The posterior distribution of the parameters differs based on the assumed survival distribution.
For the Weibull AFT model, the likelihood function is given by

$$L(\beta, p) = \prod_{i=1}^{n} p T_i^{p-1} e^{\left[-e^{-x_i^\top \beta} T_i^p\right]}. \tag{15}$$

Substituting the priors, the posterior distribution is given by

$$\begin{aligned} p(\beta, p \mid T, X) \propto & \left[\prod_{i=1}^{n} p T_i^{p-1} e^{-e^{-(x_i^\top \beta)} T_i^p}\right] \times \exp\left(-\frac{1}{2\tau^2}\beta^\top \beta\right) \\ & \times p^{c_0 - 1} e^{-d_0 p}. \end{aligned} \tag{16}$$

Taking the logarithm, we get

$$\begin{aligned} \log p(\beta, p \mid T, X) = & \sum_{i=1}^{n} \left[\log p + (p-1)\log T_i - e^{-(x_i^\top \beta)} T_i^p\right] - \frac{1}{2\tau^2}\beta^\top \beta \\ & + (c_0 - 1)\log p - d_0 p. \end{aligned} \tag{17}$$

For the log-normal AFT model, the likelihood function is given by

$$L(\beta, \sigma^2) = \prod_{i=1}^{n} \frac{1}{T_i \sigma \sqrt{2\pi}} \exp\left(-\frac{(\log T_i - x_i^\top \beta)^2}{2\sigma^2}\right). \tag{18}$$

Substituting the priors, the posterior distribution is given by

$$\begin{aligned} p(\beta, \sigma^2 \mid T, X) \propto & \left[\prod_{i=1}^{n} \frac{1}{T_i \sigma \sqrt{2\pi}} \exp\left(-\frac{(\log T_i - x_i^\top \beta)^2}{2\sigma^2}\right)\right] \\ & \times \exp\left(-\frac{1}{2\tau^2}\beta^\top \beta\right) \\ & \times (\sigma^2)^{-(a+1)} \exp\left(-\frac{b}{\sigma^2}\right). \end{aligned} \tag{19}$$

Taking the logarithm, we get

$$\begin{aligned} \log p(\beta, \sigma^2 \mid T, X) = & \sum_{i=1}^{n} \left[-\log T_i - \log \sigma - \frac{1}{2}\log(2\pi) - \frac{(\log T_i - x_i^\top \beta)^2}{2\sigma^2}\right] \\ & - \frac{1}{2\tau^2}\beta^\top \beta \\ & - (a+1)\log \sigma^2 - \frac{b}{\sigma^2}. \end{aligned} \tag{20}$$

For the log-logistic AFT model, the likelihood function is given by

$$L(\beta, \gamma) = \prod_{i=1}^{n} \frac{(T_i^{\gamma-1}) e^{-\frac{T_i^\gamma}{e^{x_i^\top \beta}}}}{e^{(x_i^\top \beta)} \left(1 + e^{-(\log T_i - x_i^\top \beta)/\sigma}\right)^2}. \tag{21}$$

Substituting the priors, the posterior distribution is given by

$$\begin{aligned} p(\beta, \gamma \mid T, X) \propto & \left[\prod_{i=1}^{n} \frac{(T_i^{\gamma-1}) e^{-\frac{T_i^\gamma}{e^{x_i^\top \beta}}}}{e^{(x_i^\top \beta)} \left(1 + e^{-(\log T_i - x_i^\top \beta)/\sigma}\right)^2}\right] \\ & \times \exp\left(-\frac{1}{2\tau^2}\beta^\top \beta\right) \\ & \times \gamma^{c_0 - 1} \exp(-d_0 \gamma). \end{aligned} \tag{22}$$

Taking the logarithm, we get

$$\begin{aligned}\log p(\beta,\gamma \mid T,X) = &\sum_{i=1}^{n}\left[(\gamma-1)\log T_i - \frac{T_i^{\gamma}}{e^{x_i^{\top}\beta}} - 2\log\left(1+e^{-(\log T_i - x_i^{\top}\beta)/\sigma}\right)\right] \\ &- \frac{1}{2\tau^2}\beta^{\top}\beta \\ &+ (c_0-1)\log\gamma - d_0\gamma. \end{aligned} \tag{23}$$

Since the posterior distribution involves high-dimensional integrals that do not have closed-form solutions, *Markov Chain Monte Carlo (MCMC)* methods are employed for posterior estimation. MCMC refers to a class of iterative algorithms that generate samples by constructing a Markov chain, which is a sequence of random variables where each subsequent state depends only on the current state. These algorithms are specifically designed so that the stationary distribution of the chain corresponds to the target posterior distribution, thereby enabling efficient sampling from it. This approach allows for the estimation of model parameters and the quantification of their associated uncertainties (Gelman, Carlin, Stern, Dunson, Vehtari, and Rubin (2013)). In this study, the implementation was carried out in `R` using the `spBayesSurv` (Zhou, Hanson, and Zhang (2020a)) package, with 5000 MCMC iterations performed to ensure adequate posterior convergence.

Model evaluation

To assess the performance of the Bayesian AFT models with different error term distributions, several statistical criteria were employed. Specifically, the Deviance Information Criterion (DIC), Watanabe-Akaike Information Criterion (WAIC) and Log Pseudo Marginal Likelihood (LPML) were selected for model comparison. These metrics are widely recommended for Bayesian hierarchical models because they simultaneously evaluate model fit and penalize complexity using the full posterior distribution (Gelman, Hwang, and Vehtari (2014); Vehtari, Gelman, and Gabry (2017)). In particular, WAIC and LPML are asymptotically equivalent to Bayesian leave-one-out cross-validation (LOO-CV) but are computationally more stable and efficient for MCMC estimated models, as they avoid repeated refitting (Vehtari *et al.* (2017)). Traditional measures such as R^2 are not well-defined in the presence of censored data or within fully Bayesian survival frameworks, making them less appropriate for this context (Gelman (2006)). Therefore, DIC, WAIC and LPML were chosen to provide robust, fully Bayesian assessments of predictive performance. Each of these metrics balances goodness-of-fit and model complexity, with lower values of DIC and WAIC and higher values of LPML indicating better model adequacy.

Deviance Information Criterion (DIC) is a generalization of the Akaike Information Criterion (AIC) for Bayesian models, defined as

$$\text{DIC} = 2\overline{D(\theta)} - D(\bar{\theta}), \tag{24}$$

where $D(\theta) = -2\log p(\text{data} \mid \theta)$ is the deviance, $\overline{D(\theta)}$ is the posterior mean of the deviance, and $D(\bar{\theta})$ is the deviance evaluated at the posterior mean of the parameters.

Watanabe-Akaike Information Criterion (WAIC) is a fully Bayesian metric that estimates predictive accuracy by summing pointwise log-likelihoods:

$$\text{WAIC} = -2\sum_{i=1}^{n}\log\left(\frac{1}{S}\sum_{s=1}^{S}p(y_i \mid \theta^{(s)})\right) + 2\text{Var}\left(\sum_{s=1}^{S}\log p(y_i \mid \theta^{(s)})\right), \tag{25}$$

where n is the number of observations, S the number of posterior samples, and $p(y_i \mid \theta^{(s)})$ the likelihood under posterior sample $\theta^{(s)}$.

Log Pseudo Marginal Likelihood (LPML) evaluates predictive adequacy via the conditional predictive ordinate (CPO), defined as

$$\text{LPML} = \sum_{i=1}^{n} \log \text{CPO}_i, \tag{26}$$

where

$$\text{CPO}_i = \left(\frac{1}{S} \sum_{s=1}^{S} \frac{1}{p(y_i \mid \theta^{(-i,s)})} \right)^{-1}, \tag{27}$$

with $p(y_i \mid \theta^{(-i,s)})$ denoting the leave-one-out predictive density for observation i based on posterior sample $\theta^{(-i,s)}$.

The best-fitting model, identified by its superior performance across these criteria, was selected for further analysis and survival predictions.

4. Results and discussions

The results of the Bayesian Accelerated Failure Time (AFT) model analysis are presented in this part with an emphasis on two main goals: figuring out which model best fits the dataset and identifying important factors that affect survival probabilities.
With the highest LPML value and the lowest WAIC and DIC values, the log-normal model performed the best. The log-normal model was therefore chosen for additional examination and survival forecasting. The following Table 2 provides a summary of the findings.

Table 2: Model comparison with WAIC, DIC, and LPML

Model	**WAIC**	**DIC**	**LPML**
log-normal	613.4227	609.2702	-306.7114
log-logistic	614.599	610.3965	-307.2995
Weibull	615.1233	611.5729	-307.5616

The substantial relationships between variables and survival outcomes are revealed by the posterior estimates (see Table 3) of the regression coefficients derived from the Bayesian log-normal AFT model. It uses Metastasis Stage M0, Node Stage N0, Tumor Stage T1, Sex Female and Tumor Type Colon Adenocarcinoma as reference categories, serving as baselines for comparison. Here, the interpretation of results is guided by the concept of credible intervals, which represent the range within which the true parameter value lies with a specified posterior probability given the observed data and prior assumptions. Specifically, a 95% credible interval indicates that there is a 95% probability the true effect size falls within this range, directly quantifying uncertainty in a manner particularly meaningful for clinical inference Gelman (2006); Gelman *et al.* (2014).
Compared to the reference category of M0 (no detected metastasis), patients classified as M1 show a positive posterior estimate with 95% credible interval (0.34 to 1.60), suggesting longer expected survival times, which may reflect the impact of aggressive treatments and therapies often administered upon detection of metastasis (Wang *et al.* (2019)). However, the estimate for MX (unknown metastasis status) has a credible interval that contains zero, meaning there is no clear evidence of a difference from M0. This likely reflects uncertainty due to unclear staging, which limits the ability to draw firm conclusions for this group. Node Stage N2 demonstrated a clear positive association with survival times, suggesting that more advanced nodal involvement might trigger intensified treatment regimens that extend survival, whereas Node Stage N1's interval included zero, indicating less certainty about its effect. The tumor stages (T2, T3, T4) exhibited wide credible intervals crossing zero, reflecting considerable uncertainty about their direct impact on survival in this cohort, possibly due to biological

heterogeneity or differences in treatment response. Similarly, while male patients and those with rectal adenocarcinoma showed posterior means suggesting shorter survival compared to their respective reference groups, their credible intervals included zero, underscoring uncertainty.

Our approach directly estimated how covariates accelerate or decelerate survival times, avoiding the proportional hazards assumption often questioned in colorectal cancer (Moghimi-Dehkordi *et al.* (2008)). Similar applications in gastrointestinal cancers by Pan *et al.* (2017) have highlighted the robustness of Bayesian approaches under non-proportional hazards. Our findings reinforce the value of this methodology for CRC, providing more flexible insights into patient prognosis.

Table 3: Results of Bayesian log-normal AFT model

Variable	**Mean**	**Median**	**Standard Deviation**	**Lower Credible Value**	**Upper Credible Value**
Diagnosis Age	0.04990	0.04985	0.01062	0.03029	0.07144
Metastasis Stage M0 (Ref)	-	-	-	-	-
Metastasis Stage M1	0.94491	0.93623	0.32472	0.34014	1.60179
Metastasis Stage MX	-0.08408	-0.08755	0.38978	-0.81690	0.68820
Node Stage N0 (Ref)	-	-	-	-	-
Node Stage N1	0.63745	0.64938	0.3752	-0.11267	1.32906
Node Stage N2	1.10589	1.1232	0.40092	0.30063	1.87753
Tumor Stage T1 (Ref)	-	-	-	-	-
Tumor Stage T2	-0.98246	-1.03121	1.24171	-3.18225	1.65979
Tumor Stage T3	-0.05041	-0.17991	1.11505	-1.88578	2.50217
Tumor Stage T4	0.94262	0.81063	1.12369	-0.93958	3.48228
Sex Female (Ref)	-	-	-	-	-
Sex Male	-0.12942	-0.18650	0.29242	-0.79837	0.34287
Tumor Type Colon Adenocarcinoma (Ref)	-	-	-	-	-
Tumor Type Rectal Adenocarcinoma	-0.79420	-0.78546	0.44375	-1.70052	0.04909

The trace plots for the Bayesian log-normal AFT model, displayed in Figure 1, show good mixing and convergence across all covariates. Each MCMC chain was run for 11,000 iterations, with the first 6,000 iterations discarded as burn-in, leaving 5,000 iterations used for posterior inference. No thinning was applied. The plots demonstrate that most parameters

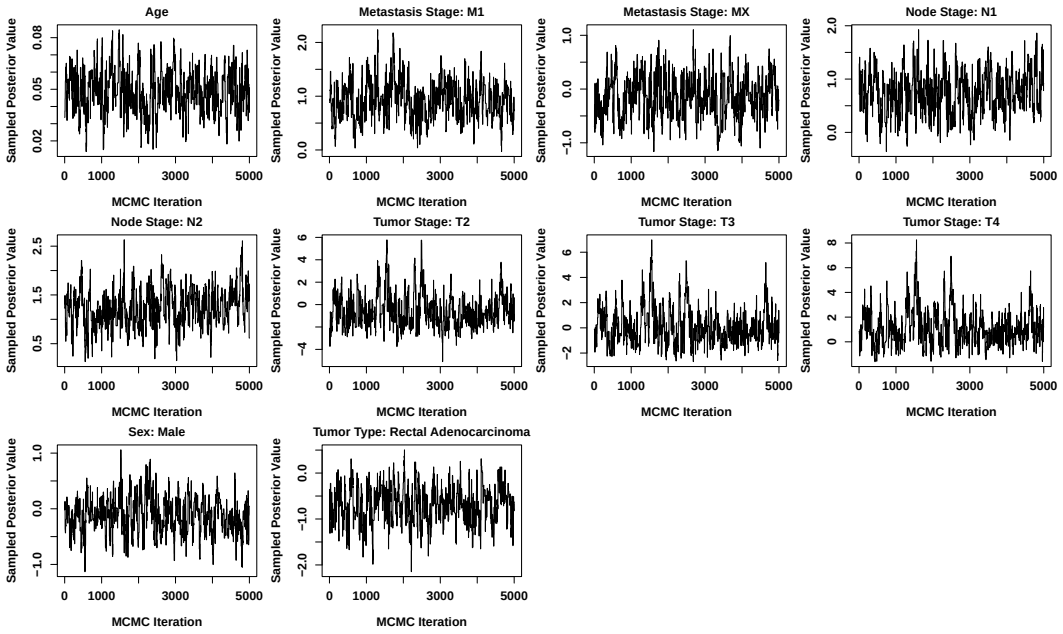


Figure 1: Trace plots of posterior samples for each parameter in the Bayesian log-normal AFT model across MCMC iterations. The x-axis represents the MCMC iteration number and the y-axis shows the sampled posterior values for each parameter.

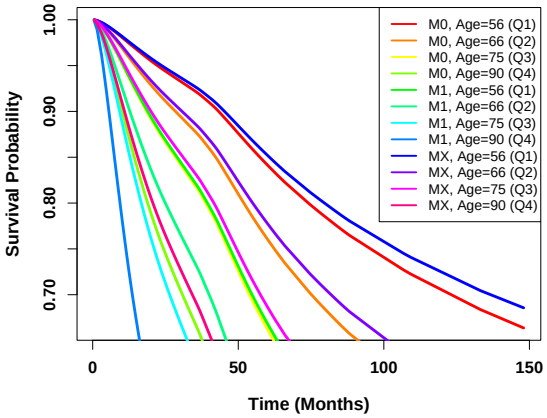
stabilize after initial fluctuations, with no systematic drifts, indicating that the chains have reached stationarity. This is particularly evident for key covariates such as tumor and node stages, where the sampled posterior values fluctuate consistently around a stable mean. The absence of significant trends or autocorrelation across iterations supports the adequacy of the sampling process, making the posterior estimates reliable for subsequent colorectal cancer survival analysis.

The Bayesian lognormal AFT model's survival probability curves (see Figure 2) demonstrate the influence of different clinical factors on survival over time. Across all examined categories, younger patients (Q1: 56 years) consistently show higher survival probabilities, while older patients (Q4: 90 years) exhibit a more pronounced decline, highlighting the effect of age on disease progression and treatment outcomes. The observed patterns further reveal substantially lower survival probabilities for advanced tumor stages, emphasizing the critical role of early detection and staging in colorectal cancer prognosis.These findings provide valuable insights into identifying patient subgroups at increased risk who may require closer follow-up or adjusted therapeutic approaches.

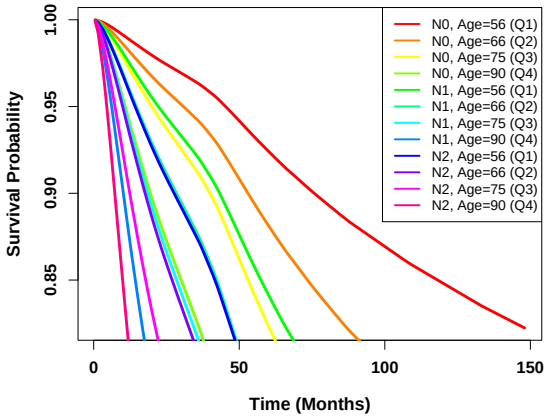
These findings hold practical significance for healthcare practitioners and policymakers by facilitating more precise stratification of colorectal cancer patients based on clinical risk factors. By identifying subgroups with poorer survival probabilities—such as older patients, those with advanced tumor or nodal stages, or rectal adenocarcinomas—the Bayesian AFT framework supports informed decisions on intensifying follow-up schedules or tailoring treatment regimens. This targeted approach aligns with precision medicine objectives and may aid in optimizing resource allocation and improving patient outcomes in routine oncology practice.

This study also has certain limitations. The analysis was conducted using retrospective data obtained from the cBioPortal platform, which, although comprehensive and widely used, may still introduce selection or information biases inherent in aggregated multi-institutional datasets. Some clinical subgroups had relatively small sample sizes, potentially limiting the ability to detect modest associations. Additionally, because the data primarily represent patients treated at contributing institutions with varying clinical practices, the generalizability of these findings to broader or different healthcare settings may be constrained. Further validation using prospective multicenter cohorts and integration of additional molecular features

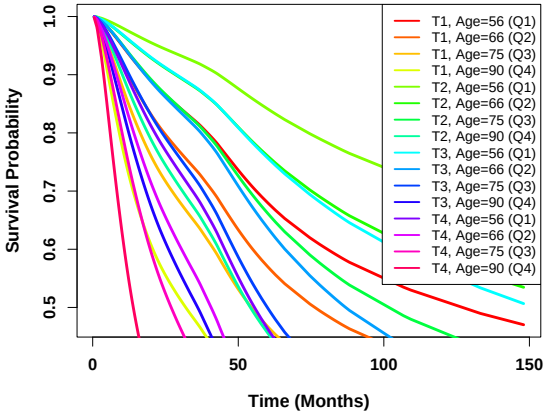
could help strengthen and expand these observations.



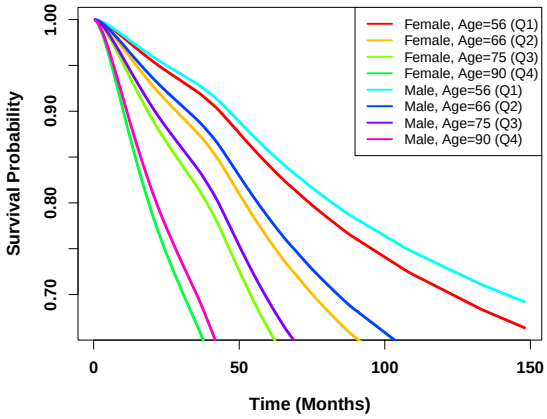
(i) Metastasis stage



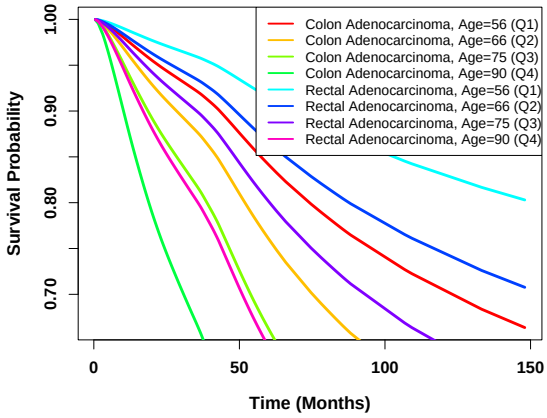
(ii) Node stage



(iii) Tumor stage



(iv) Sex



(v) Tumor type

Figure 2: Estimated survival probability curves under the Bayesian log-normal AFT model across varying covariate groups and predefined age quartiles. Each curve represents a specific combination of covariate levels and age group.

5. Conclusion

In this study, Bayesian survival models were systematically compared using WAIC, DIC, and LPML, with the log-normal AFT model emerging as the best fit, outperforming the log-logistic and Weibull models in predictive accuracy. The analysis identified tumor stage, nodal stage, metastasis status, gender, tumor type, and age as significant predictors of colorectal cancer survival. Advanced tumor (T3, T4) and nodal stages (N2) were associated with reduced survival, while Metastasis Stage M1 showed longer survival, likely reflecting the benefits of aggressive treatments upon early metastasis detection. Rectal adenocarcinoma also indicated a poorer prognosis than colon adenocarcinoma, especially among older patients. The MCMC trace plots validated convergence, supporting the robustness of the posterior estimates.
Importantly, the proposed Bayesian AFT framework offers practical value for real-world clinical applications by enabling direct estimation of survival times and accommodating uncertainties inherent in patient data. This facilitates the stratification of patients into distinct risk categories, supporting more informed decisions on monitoring intensity and treatment planning. Such an approach aligns with precision oncology initiatives, where tailoring interventions to individual risk profiles is critical. Future work can extend this framework by incorporating molecular biomarkers and evaluating time-dependent effects, thereby enhancing its potential to guide personalized therapeutic strategies in colorectal cancer management.

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