



Bayesian Models in Biostatistics

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ABSTRACT

Bayesian models constitute a fundamental theoretical and methodological framework in biostatistics, offering a coherent probabilistic approach for statistical inference under uncertainty. Grounded in probability theory and Bayes' theorem, Bayesian methods systematically update prior knowledge with observed data and represent uncertainty through posterior distributions. This paper presents a comprehensive theoretical and methodological overview of Bayesian models in biostatistics, with emphasis on their mathematical foundations, inferential principles, and practical applicability in biomedical research. Key concepts discussed include the axiomatic basis of probability, prior and posterior distributions, likelihood functions, credibility intervals, conjugate Bayesian models, and Bayesian parameter estimation. The study further examines the role of numerical methods, particularly Monte Carlo and Markov Chain Monte Carlo (MCMC) algorithms, in approximating posterior distributions when analytical solutions are unavailable. Illustrative examples, including the Poisson-Gamma conjugate model and MCMC-based inference, are used to demonstrate the practical implementation of Bayesian reasoning in biostatistical contexts. The paper highlights the advantages of Bayesian models in handling complex data structures, small sample sizes, uncertainty, and the integration of prior information, while also discussing key methodological challenges such as prior specification and computational demands. In all, the study underscores the relevance and robustness of Bayesian models as a powerful framework for contemporary biostatistical analysis and biomedical decision-making.

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Introduction

Biostatistics is a key discipline in the biomedical sciences, providing mathematical and statistical tools for the analysis, interpretation, and modeling of biological and health data. With the increasing complexity of clinical, genomic, and epidemiological data, traditional frequentist methods often face limitations, especially in the presence of small samples, incomplete data, or hierarchical structures. In this context, Bayesian models have emerged as a powerful and flexible alternative for statistical inference in biostatistics (Lesaffre & Lawson, 2022).

The Bayesian approach is based on Bayes' theorem, which provides a mathematical framework for updating probabilistic beliefs about parameters of interest in light of new data. In contrast to the frequentist approach, which treats parameters as fixed and unknown values, Bayesian statistics considers parameters as random variables, allowing uncertainty to be described through prior and posterior distributions (Gelman et al., 2020). This probabilistic formalization is particularly useful in biostatistical applications, where prior knowledge from previous studies or clinical expertise can be directly integrated into the analysis. Bayes' theorem constitutes the theoretical foundation of Bayesian statistics and provides a formal probabilistic framework for updating knowledge about unknown parameters based on observed data. Mathematically, it expresses the relationship between the prior distribution, the likelihood function, and the posterior distribution, enabling the coherent integration of prior information with empirical evidence. In the context of biostatistics, this approach is particularly important as it allows the inclusion of clinical knowledge or results from previous studies in the process of statistical inference, more realistically reflecting the uncertainty that characterizes biological data (Gelman et al., 2020). Through Bayes' theorem, parameters are treated as random variables, which enables probabilistic inference and intuitive interpretation of results, especially in studies with small samples or incomplete data, common in modern biomedical research (Rosner et al., 2021; van de Schoot et al., 2021).

In Bayesian statistics:

$$\pi(\theta | D)$$

represents the posterior distribution of the parameter θ given the data D . The formula is:

$$\pi(\theta | D) = \frac{L(D | \theta) \pi(\theta)}{\int_{\theta} L(D | \theta) \pi(\theta) d\theta}$$

Where:

$\pi(\theta | D)$ = posterior probability of θ after observing the data D

$L(D | \theta)$ = likelihood of the data given θ

$\pi(\theta)$ = prior probability of θ before observing data

$\int_{\theta} L(D | \theta) \pi(\theta) d\theta$ = normalizing constant (ensures the posterior sums/integrates to 1)

In simple words:

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior}$$

This formula emphasizes the central idea of Bayesian inference: prior knowledge is updated by empirical data to produce complete and interpretive statistical inference. In recent years, the use of Bayesian models in biostatistics has grown significantly, driven by developments in computational power and advances in numerical algorithms, such as Markov Chain Monte Carlo (MCMC) and Hamiltonian Monte Carlo. These methods have made it possible to estimate complex models, including hierarchical and non-parametric models, which are common in modern clinical and epidemiological studies (McElreath, 2020; van de Schoot et al., 2021). In the field of survival analysis and clinical trials, Bayesian models have demonstrated significant advantages over classical methods, providing more robust risk estimates and more interpretable confidence intervals. Furthermore, they allow for the natural handling of censoring and missing data, which are inevitable in biomedical research (Zhao et al., 2023). In epidemiology, these models have been widely used for predicting the spread of diseases and for assessing uncertainty in health decision-making. The contribution of this paper lies in providing an integrated theoretical and applied overview of Bayesian models, with particular emphasis on their mathematical interpretation and use in contemporary biostatistical contexts. This study focuses primarily on the theoretical and methodological aspects of

Bayesian models and does not aim to exhaustively address specific software implementations. Thus, the paper aims to present a theoretical and practical overview of Bayesian models in biostatistics, highlighting their mathematical foundations, main advantages, and contemporary applications in biomedical data analysis. This study aims to contribute to a deeper understanding of the role of Bayesian statistics in modern scientific research and to promote its use in biostatistical analytical practices.

Problem Identification

In contemporary biomedical analyses, data are often presented with significant uncertainty, complex structures, and limited sample sizes, making statistical inference particularly challenging. Traditional frequentist approaches, which focus primarily on the probability of observed data rather than on hypotheses or parameters of interest, often result in limitations in probabilistic interpretation of results and in managing uncertainty (Fornacon-Wood et al., 2022). A significant problem relates to the inability of these methods to systematically integrate prior information, which in the biostatistical context is often available through previous studies or clinical trials. This lack of integration becomes particularly problematic in situations with small samples or rare events, where statistical estimates may be inconsistent or uninformative (Hong et al., 2021). Furthermore, the growing interest in more flexible analyses and more realistic models has highlighted the need for approaches that can handle uncertainty explicitly and interpretively. Recent studies have shown that Bayesian methods offer significant advantages over classical approaches, especially in contexts where combining different sources of information and assessing uncertainty in clinical decision-making is required (Hong & Carlin, 2023). However, despite the widespread adoption of Bayesian methods in biostatistics, a significant gap remains in the literature regarding the clear and integrated exposition of their mathematical foundations alongside their inferential implications in biomedical research. Existing studies and textbooks often adopt one of two approaches: highly technical treatments that emphasize advanced theory with limited connection to applied biostatistical contexts, or application-focused reviews that rely heavily on software implementations while providing minimal insight into the underlying probabilistic structure of Bayesian inference. As a result, there is limited clarity on how fundamental Bayesian principles, such as the interaction between prior distributions and likelihood functions, the interpretation of posterior distributions, and the role of numerical approximation methods, collectively support robust inference in biostatistical practice.

Furthermore, while Bayesian models are frequently promoted for their flexibility in handling uncertainty, hierarchical structures, and small sample sizes, the mathematical mechanisms through which these advantages arise are often insufficiently articulated in the biostatistics literature. In particular, the conceptual linkage between probability axioms, Bayes' theorem, conjugate modeling, and Markov Chain Monte Carlo (MCMC) methods is rarely presented in a unified framework accessible to both methodologically oriented researchers and applied biostatisticians. This lack of integration can hinder informed methodological choices and limit the effective application of Bayesian inference in biomedical decision-making.

Purpose of the Study

In response to these gaps, the purpose of this study is to provide a structured and mathematically grounded overview of Bayesian models in biostatistics, explicitly linking their theoretical foundations to their inferential and practical relevance. The paper aims to clarify the core probabilistic principles underlying Bayesian inference, with particular emphasis on the formulation of prior and posterior distributions, Bayesian parameter estimation, and the role of conjugate models in analytical inference. In addition, it highlights the importance of numerical methods, especially MCMC algorithms, as essential tools for implementing Bayesian models in complex biostatistical settings. By integrating mathematical theory, methodological discussion, and illustrative examples within a single coherent framework, this study addresses the need for a clearer conceptual understanding of Bayesian inference in biostatistics. The paper seeks to support researchers and practitioners in making informed methodological decisions and to promote the rigorous and transparent use of Bayesian models in contemporary biomedical and epidemiological research.

Literature Review

Bayesian Models in Biostatistics

The contemporary literature in biostatistics highlights the growing use of Bayesian models as a flexible and interpretive alternative to traditional statistical approaches. Various studies have argued that Bayesian inference provides a coherent probabilistic framework for estimating parameters and uncertainty, especially in situations where data are limited or complex (Ashby, 2020). This approach has been widely used in clinical, epidemiological, and health risk analyses, enabling more intuitive interpretation of statistical results. In particular, Bayesian models are effective in dealing with hierarchical data and inter-individual variability, which are characteristic of biomedical studies. Methodological reviews have emphasized that these models allow the incorporation of different sources of information, increasing the robustness of estimates and the quality of inference (Camara et al., 2025).

Computational Advances and MCMC Methods

One of the main factors that has driven the spread of Bayesian methods in biostatistics is the development of computational techniques, especially Markov Chain Monte Carlo (MCMC) algorithms. These methods enable numerical estimation of posterior distributions even for complex models, where analytical solutions are impossible (Jones & Qin, 2022). MCMC has become a standard tool for Bayesian inference in biomedical applications, including Bayesian regression, survival analysis, and spatial models. Recent studies have highlighted the importance of diagnosing the convergence and efficiency of Markov chains, emphasizing the need for good computational practices in Bayesian analyses (Craiu & Rosenthal, 2021). These developments have contributed to increasing the reliability and usability of Bayesian models in practical biostatistical contexts.

Clinical and Epidemiological Applications

In the clinical and epidemiological fields, Bayesian models have been widely used for survival data analysis, chronic disease modeling, and health risk assessment. Narrative reviews have shown that the Bayesian approach offers significant advantages in interpreting results and supporting clinical decision-making under uncertainty (Hong & Carlin, 2023). These models are particularly useful in contexts with censored data or rare events. Spatial and spatiotemporal Bayesian models have also been used for disease distribution analysis and epidemiological risk assessment. Recent studies have demonstrated that these approaches offer greater flexibility compared to traditional methods, improving the understanding of health dynamics in populations (Wang et al., 2024). Similarly, the study by Spahiu (2025) highlights numerical analysis as a transformative tool for modern scientific research, supporting advances in technology, healthcare, and engineering. The findings highlight its role in enabling accurate simulations, increasing algorithmic efficiency, and driving technological progress across a range of scientific disciplines.

Methodological Comparison with Traditional Approaches

The methodological literature suggests that, although frequentist methods remain important in biostatistical analyses, they often provide less intuitive interpretations of statistical uncertainty. In contrast, the Bayesian approach allows for direct probabilistic parameter estimates, which are particularly important in clinical and decision-making contexts (Fornacon-Wood et al., 2022). However, some authors emphasize that the choice of prior distributions and computational requirements remain methodological challenges that require careful handling. Also, the study by Kamberi et al. (2022) examines the Weibull distribution for real data and also compares it with several subdistributions (models) such as the Exponential-Weibull and Weibull-Rayleigh distributions to show its performance. Therefore, the distributions considered offer a very good opportunity in practice for data analysis.

Mathematical Foundations of Bayesian Models

The axiomatic framework of probability

Bayesian inference is built on the axiomatic theory of probability, where probability is interpreted as a measure of subjective belief about unknown events and parameters. Let $(\Omega, \mathcal{F}, P)$ be a probability space and $D = (X_1, \dots, X_n)$ a sample of independent observations, with $X_i \sim f(x | \theta)$, where $\theta \in \Theta \subset \mathbb{R}^k$. In the Bayesian framework, the parameter θ is treated as a random variable with a prior distribution $\pi(\theta)$, which constitutes the fundamental difference from frequentist inference (Bernardo, 2006; Watanabe, 2018).

Credibility function and prior

The reliability function is defined as

$$L(\theta | D) = \prod_{i=1}^n f(X_i | \theta)$$

and represents the connecting mechanism between the statistical model and the observed data. The choice of the prior distribution $\pi(\theta)$ plays a crucial role in the construction of the Bayesian model, as it summarizes the prior information on the parameters. Theoretical studies have shown that the prior cannot be estimated in isolation, but only in interaction with the likelihood function, as it is this interaction that determines the shape of the posterior distribution (Gelman, Simpson, & Betancourt, 2017).

Bayes' Theorem and the Posterior Distribution

The central relation of Bayesian inference is given by Bayes' theorem:

$$\pi(\theta | D) = \frac{L(\theta | D) \pi(\theta)}{m(D)}$$

where,

$$m(D) = \int_{\Theta} L(\theta | D) \pi(\theta) d\theta$$

is the marginal probability of the data (evidence). The posterior distribution constitutes a well-defined probabilistic measure over the parameter space and serves as a basis for inference and prediction. According to Bernardo (2006), the posterior contains all the necessary inferential information about the parameters after observing the data.

Bayesian inference and parameter estimation

Bayesian inference is performed through posterior distribution functions. Bayesian parameter estimation is usually based on the posterior mean:

$$\hat{\theta}_{BAYES} = E[\theta | D] = \int_{\Theta} \theta \pi(\theta | D) d\theta$$

or in the Maximum A Posteriori (MAP) assessment:

$$\hat{\theta}_{MAP} = \underset{\theta \in \Theta}{\operatorname{arg\,max}} \pi(\theta | D)$$

In the case of uniform priors, the MAP estimate coincides with the Maximum Likelihood estimate, which shows the theoretical connection between the two inferential paradigms (Watanabe, 2018).

Conjugate Bayesian models

If the prior distribution belongs to the same functional family as the posterior distribution, then the prior is called a conjugate. These models allow for closed analytical inference. A classic example in biostatistics is the Poisson-Gamma model:

$$X_i | \lambda \sim \text{Poisson}(\lambda), \quad \lambda \sim \text{Gamma}(\alpha, \beta)$$

which leads to the posterior distribution:

$$\lambda | D \sim \text{Gamma}\left(\alpha + \sum_{i=1}^n X_i, \beta + n\right)$$

Conjugate models have been widely used in epidemiological analyses due to their mathematical simplicity (Ashby, 2020).

Numerical methods and Markov chains (MCMC)

In most cases, the posterior distribution does not have a closed analytical form, necessitating the use of numerical methods. Markov Chain Monte Carlo (MCMC) algorithms construct a Markov chain with a stationary distribution. $\pi(\theta|D)$. For the Metropolis-Hastings algorithm, the acceptance probability is given by:

$$\alpha(\theta, \theta') = \min\left(1, \frac{\pi(\theta' | D) q(\theta | \theta')}{\pi(\theta | D) q(\theta' | \theta)}\right)$$

This can be shown differently. Suppose:

Current state: $\theta^{(t)}$

Proposed state: θ^* (sampled from a proposal distribution $q(\theta^* | \theta^{(t)})$)

The acceptance probability α , is:

$$\alpha = \min\left(1, \frac{\pi(\theta^* | D) q(\theta^{(t)} | \theta^*)}{\pi(\theta^{(t)} | D) q(\theta^* | \theta^{(t)})}\right)$$

Where:

$\pi(\theta | D)$ = posterior of θ (as we discussed earlier)

$q(\theta^* | \theta^{(t)})$ = proposal distribution probability

The ratio compares how “good” the proposed state is relative to the current state, adjusted by how likely the proposal is in both directions.

If $q(\theta^* | \theta^{(t)}) = q(\theta^{(t)} | \theta^*)$ (like in the original Metropolis algorithm), then it simplifies to:

$$\alpha = \min\left(1, \frac{\pi(\theta^* | D)}{\pi(\theta^{(t)} | D)}\right)$$

In the limit, the empirical mean converges towards the posterior expected value, according to the ergodic law of Markov chains (Craiu & Rosenthal, 2021). The mathematical foundations presented in this chapter constitute the theoretical framework upon which the interpretation and discussion of Bayesian models in the biostatistical context are based.

Illustrative example of a Bayesian model (Poisson-Gamma)

To concretely illustrate the functioning of Bayesian inference presented in the theoretical chapter, a simple Poisson-Gamma model is considered, which is widely used in biostatistics for modeling the number of events, such as disease incidence or the number of cases in a given time interval.

Model formulation

Let there be $X_1, \dots, X_n$ independent observations, where:

$$X_i | \lambda \sim \text{Poisson}(\lambda), \quad i = 1, \dots, n$$

and $\lambda > 0$ represents the average intensity of events.

Prior knowledge of the parameter is assumed, λ , represented by a Gamma prior distribution:

$$\lambda \sim \text{Gamma}(\alpha, \beta)$$

with density:

$$\pi(\lambda) = \frac{\beta^\alpha}{\Gamma(\alpha)} \lambda^{\alpha-1} e^{-\beta\lambda}$$

Posterior distribution

By combining the Gamma prior with the Poisson likelihood, the resulting posterior distribution is also Gamma:

$$\lambda | D \sim \text{Gamma}\left(\alpha + \sum_{i=1}^n X_i, \beta + n\right)$$

This result demonstrates the conjugacy property, which allows closed analytical inference without the use of numerical methods.

Illustrative numerical example

In this illustration, the following data are considered:

$$D = \{3, 2, 4, 3, 5\}$$

with prior:

$$\lambda \sim \text{Gamma}(2, 1)$$

then:

$$\sum_{i=1}^n X_i = 17, \quad n = 5$$

and the posterior distribution is given by:

$$\lambda | D \sim \text{Gamma}(19, 6)$$

The figure below shows the density of the prior and posterior distributions for the parameter λ . The shifting and narrowing of the posterior distribution reflect how empirical data updates the prior information, reducing the uncertainty about the parameters.

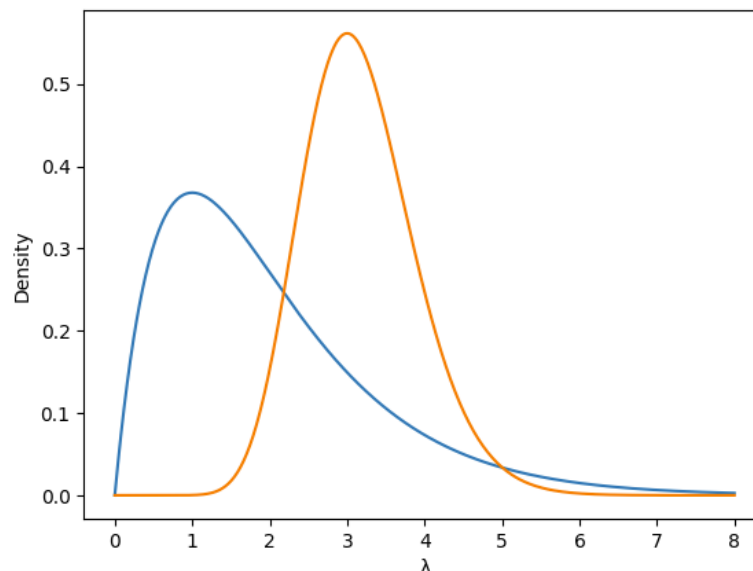


Figure 1. Prior and Posterior for the Poisson-Gamma model

This visualization clearly shows the essence of Bayesian inference:

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior}$$

This illustrative example shows how Bayesian models formally combine prior information with observed data to produce coherent statistical inference. In the biostatistical context, this formalization is particularly useful in situations with small samples or when prior knowledge from previous studies exists. Although the presented model is simple, it serves as a conceptual basis for building more complex Bayesian models, including hierarchical and spatiotemporal models.

Illustration of Bayesian inference through the Monte Carlo (MCMC) method

In many Bayesian models used in biostatistics, the posterior distribution does not have a closed analytical form, making it impossible to draw inferences directly. In these cases, inference is performed through Monte Carlo methods, particularly Markov Chain Monte Carlo (MCMC) algorithms, which generate samples from the posterior distribution without the need for its explicit normalization.

The mathematical formulation of MCMC

Let $\pi(\theta | D)$ be the posterior distribution of interest. The goal of MCMC is to construct a Markov chain.

$$\{\theta^{(t)}\}_{t=1}^T$$

with a stationary distribution $\pi(\theta | D)$. For any integrable function $h(\theta)$, it holds:

$$\frac{1}{T} \sum_{t=1}^T h(\theta^{(t)}) \xrightarrow{T \rightarrow \infty} E_{\pi(\theta|D)}[h(\theta)]$$

This result constitutes the theoretical basis for the use of MCMC in Bayesian inference.

The Metropolis-Hastings algorithm

One of the most widely used MCMC algorithms is Metropolis-Hastings. Assuming a proposal distribution $q(\theta' | \theta)$, the transition from the current state θ to a new state θ' is accepted with probability:

$$\alpha(\theta, \theta') = \min \left(1, \frac{\pi(\theta' | D) q(\theta | \theta')}{\pi(\theta | D) q(\theta' | \theta)} \right)$$

This mechanism ensures that the Markov chain has the desired posterior as its boundary distribution.
Numerical illustration for the Poisson-Gamma model

Although the Poisson-Gamma model has analytical solutions, it serves as an illustrative example for MCMC. By constructing a Metropolis-Hastings chain for the parameter λ , samples are generated that approximate the posterior distribution:

$$\lambda | D \sim \text{Gamma}(19, 6)$$

The figure below shows a histogram of samples generated through MCMC, which approximates the density of the posterior distribution. The agreement of this approximation with the theoretical form of the posterior demonstrates the validity of Monte Carlo methods for Bayesian inference, even in cases where an analytical solution is not available.

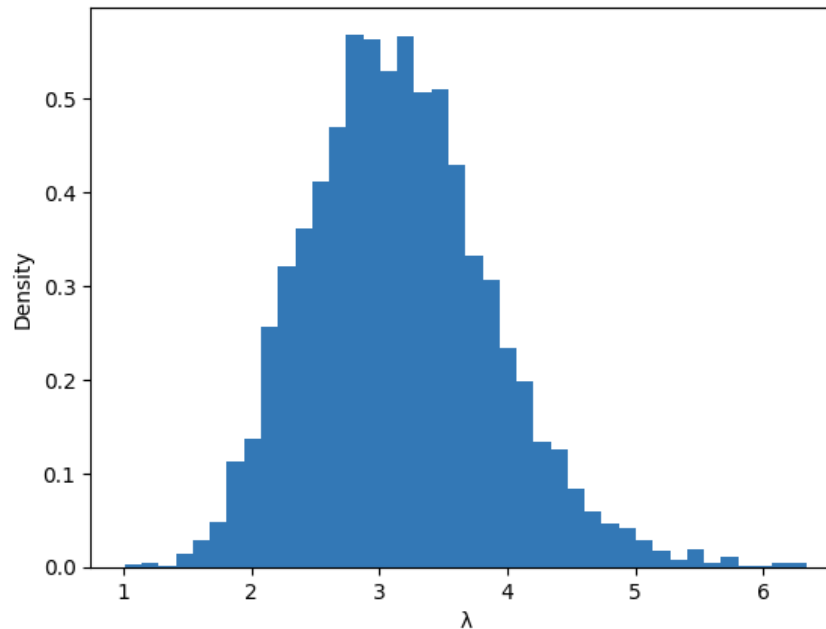


Figure 2. MCMC Sampling from the Poisson-Gamma Posterior

In real-world biostatistical applications, such as hierarchical models, survival analyses, or spatiotemporal models, MCMC constitutes the main tool for the practical realization of Bayesian inference. This illustration shows that, although Bayesian theory is built on rigorous mathematical foundations, Monte Carlo methods are essential for its application to complex real-world problems. In all, the illustrative examples and the Monte Carlo approach demonstrate that Bayesian models are not only theoretically powerful but also practically applicable in complex biostatistical analyses.

DISCUSSION

This section aims to interpret and critically analyze the mathematical foundations of Bayesian inference presented in the previous chapter, placing them in the context of biostatistical applications and highlighting the methodological implications of this approach. The discussion focuses on the theoretical advantages of Bayesian models, their limitations, and the relationship with traditional frequentist approaches. One of the main mathematical implications of Bayesian inference is the treatment of parameters as random variables and the description of uncertainty through the posterior distribution. This probabilistic formalization allows for direct probabilistic inferences on the parameters of interest, which is a substantial advantage over frequentist confidence intervals, which have an indirect interpretation. As argued in the literature, this feature makes Bayesian inference particularly suitable for biomedical analyses, where uncertainty is unavoidable and must be addressed explicitly (Bernardo, 2006; Ashby, 2020).

From a methodological point of view, Bayesian models offer great flexibility for building complex models, including hierarchical models and multilevel structures, which are common in biostatistical studies. Integrating prior information through prior distributions can improve the stability of estimates, especially in situations with small samples or sparse data. Various studies have highlighted that this approach contributes to more informed decision-making in clinical and epidemiological contexts (Lesaffre & Lawson, 2022; Dunson, 2001). Despite their advantages, Bayesian models also present important limitations. One of the main challenges is related to the choice of prior distributions, which can significantly affect the inference results, especially in cases with limited data. As Gelman, Simpson, and Betancourt (2017) point out, the prior should always be evaluated relative to the credibility function to avoid unstable inference. Furthermore, the computational requirements of Bayesian methods, especially in complex models, remain a practical obstacle in some applications. Compared to the

frequentist approach, Bayesian inference offers a more straightforward interpretation of uncertainty and a more coherent framework for updating knowledge in light of new data. However, the literature suggests that the two approaches are not necessarily competitive, but often complementary, depending on the context of application. In biostatistics, the choice between these paradigms should be based on the nature of the data, the purpose of the analysis, and the inferential requirements of the study (Breslow, 1990; Ashby, 2020).

Conclusion

This paper presented a theoretical and methodological treatment of Bayesian models in biostatistics, with a particular focus on their mathematical foundations and inferential implications in biomedical data analysis. Drawing on probability theory and the formalization of Bayes' theorem, it was shown that the Bayesian approach provides a coherent and flexible framework for dealing with statistical uncertainty and for integrating prior information into the inference process. Through a literature review and the development of mathematical foundations, it was emphasized that Bayesian models represent a powerful alternative to traditional frequentist approaches, especially in situations with small samples, hierarchical structures, and incomplete data. The formalization of prior and posterior distributions, as well as the use of conjugate models, showed that Bayesian inference allows for direct probabilistic conclusions on the parameters of interest, which is particularly important in the biostatistical context. The illustrative examples presented in the discussion chapter demonstrated concretely how Bayesian theory is applied in practice. The Poisson-Gamma model served to illustrate the analytical mechanism of updating information through the posterior distribution, while the illustration of Monte Carlo and Markov Chain Monte Carlo methods showed how Bayesian inference can be performed even in cases where analytical solutions are not available. These methods constitute an essential component of modern biostatistics, enabling the treatment of complex and realistic models. Although Bayesian models offer considerable theoretical and practical advantages, important limitations were also identified, especially regarding the choice of prior distributions and the computational requirements of numerical methods. These aspects require careful handling and emphasize the need for in-depth theoretical and practical knowledge in the application of Bayesian inference. In conclusion, this study demonstrates that Bayesian models constitute a robust and suitable mathematical framework for contemporary biostatistical analysis. Future work could focus on concrete empirical applications, extending to more complex hierarchical models, or integrating Bayesian methods into advanced survival and epidemiology analyses. This paper aims to serve as a theoretical basis for these further developments and for the informed use of Bayesian statistics in biomedical research.

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