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# Bayesian Machine Learning for Precision Oncology: Integrating Clinical, Genomic, and Imaging Data for Personalized Cancer Prognosis

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# Bayesian Machine Learning for Precision Oncology: Integrating Clinical, Genomic, and Imaging Data for Personalized Cancer Prognosis

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**Abstract**

Precision oncology aims to improve cancer prognosis and treatment decision-making by leveraging diverse patient-specific data sources. However, effectively integrating clinical, genomic, and imaging information remains challenging due to data heterogeneity, high dimensionality, and uncertainty in predictive modeling. This study proposes a novel Hierarchical Bayesian Multimodal Attention Fusion Network (HBMAF-Net) for personalized cancer prognosis. The framework combines modality-specific feature extraction, Bayesian attention-based multimodal fusion, and hierarchical probabilistic modeling to jointly analyze clinical, genomic, and imaging data while explicitly quantifying predictive uncertainty. A comprehensive simulation study was conducted to evaluate the proposed framework against conventional statistical models, machine learning approaches, and state-of-the-art multimodal deep learning methods. The results demonstrated that HBMAF-Net achieved superior predictive performance, yielding an Area Under the Receiver Operating Characteristic Curve (AUC) of 0.931, a Concordance Index of 0.917, and improved calibration compared with competing models. The Bayesian attention mechanism provided interpretable modality-specific contributions, while the hierarchical structure effectively captured heterogeneity across cancer subtypes and treatment groups. Furthermore, uncertainty-aware predictions enhanced the reliability and transparency of prognostic estimates. These findings highlight the potential of Bayesian machine learning and multimodal data integration to advance precision oncology through accurate, interpretable, and clinically actionable personalized cancer prognosis.

**Keywords: Bayesian machine learning; Precision oncology; Multimodal data integration; Cancer prognosis; Uncertainty quantification.**

## 1 Introduction

Cancer remains one of the leading causes of morbidity and mortality worldwide, accounting for millions of new diagnoses and deaths annually. Despite substantial advances in screening, molecular diagnostics,

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targeted therapies, and immunotherapy, predicting individual patient outcomes remains a major challenge due to the heterogeneous nature of tumors and their complex biological mechanisms. Traditional prognostic models often rely on a limited set of clinical variables, which may fail to capture the intricate interactions among genetic, molecular, and phenotypic characteristics that drive cancer progression and treatment response (Malone et al., 2020; Das et al., 2024).

The emergence of precision oncology has transformed cancer research and clinical practice by promoting individualized treatment strategies based on patient-specific biological characteristics. Rather than applying uniform therapeutic protocols, precision oncology seeks to integrate diverse sources of information, including clinical records, genomic alterations, transcriptomic profiles, proteomic measurements, histopathological images, and radiological data, to improve diagnosis, prognosis, and therapeutic decision-making (Jamalinia et al., 2025; Saito et al., 2026). Comprehensive genomic profiling has demonstrated significant potential for identifying actionable mutations and guiding targeted therapies, thereby improving patient outcomes and reducing unnecessary treatment-related toxicities (Malone et al., 2020; Saito et al., 2026).

Recent advances in artificial intelligence (AI) and machine learning (ML) have further accelerated the development of precision oncology. Machine learning algorithms can analyze high-dimensional biomedical datasets and identify latent patterns that may be imperceptible to conventional statistical methods. Applications of ML in oncology include tumor classification, biomarker discovery, treatment response prediction, survival analysis, and risk stratification (Yang et al., 2025; Calvino et al., 2025). In particular, deep learning architectures have achieved remarkable success in extracting clinically relevant information from medical images, genomic sequences, and electronic health records, enabling more accurate and personalized prognostic assessments (Granata et al., 2025; Waqas et al., 2024).

A growing body of evidence suggests that multimodal data integration provides substantial advantages over single-modality approaches. Clinical variables capture patient demographics, comorbidities, and treatment histories; genomic data reveal molecular drivers of tumor development; while imaging modalities provide spatial and morphological information regarding tumor architecture and progression. Integrating these complementary sources of information allows for a more comprehensive characterization of cancer heterogeneity and improves predictive performance for survival and treatment outcomes (Zhou et al., 2024; Yang et al., 2025; Dörrich et al., 2025). Recent studies have demonstrated that multimodal machine learning frameworks outperform unimodal models in prognostic prediction, biomarker identification, and therapeutic response assessment across multiple cancer types (Xiong et al., 2025; Jennings et al., 2025).

Despite these advances, several methodological challenges remain. First, multimodal biomedical datasets are often characterized by high dimensionality, missing values, measurement errors, and substantial heterogeneity across data sources. Second, many machine learning models operate as "black boxes," limiting their interpretability and reducing clinician trust in automated decision-support systems. Third, conventional machine learning approaches frequently provide point estimates without adequately quantifying predictive uncertainty, which is critical in high-stakes clinical environments where treatment decisions can significantly affect patient outcomes (Zhuang et al., 2026; Zhou et al., 2024). Consequently, there is a growing need for methodologies that not only achieve high predictive accuracy but also provide reliable uncertainty estimates and transparent inference mechanisms.

Bayesian machine learning offers a principled framework for addressing these limitations. By combining prior biological knowledge with observed data, Bayesian methods enable probabilistic inference, uncertainty quantification, and robust prediction in complex high-dimensional settings. Bayesian models naturally accommodate missing data, incorporate hierarchical structures, and facilitate the integration of heterogeneous data modalities within a unified probabilistic framework. Furthermore, Bayesian

approaches provide posterior distributions for model parameters and predictions, allowing clinicians to assess the confidence associated with prognostic estimates and treatment recommendations (Boyngbogbele et al., 2026). Recent developments in Bayesian deep learning have further enhanced the ability to model uncertainty in neural networks while maintaining the predictive power of modern machine learning architectures.

The convergence of Bayesian inference, machine learning, and multimodal biomedical data presents a unique opportunity to advance personalized cancer prognosis. Emerging studies demonstrate that integrating genomic, imaging, and clinical information through probabilistic learning frameworks can improve survival prediction, risk stratification, and treatment selection while maintaining model interpretability and reliability (Thomas et al., 2026; Hunt et al., 2025; Hsu et al., 2026). Such approaches align closely with the overarching goals of precision oncology, namely delivering the right treatment to the right patient at the right time.

Motivated by these developments, this study proposes a Bayesian machine learning framework for precision oncology that integrates clinical, genomic, and imaging data to generate personalized cancer prognostic predictions. The proposed framework aims to leverage the complementary strengths of heterogeneous biomedical data sources while explicitly accounting for uncertainty and complex biological interactions. By combining probabilistic modeling with advanced machine learning techniques, the study seeks to contribute to the development of robust, interpretable, and clinically actionable decision-support tools for personalized cancer care.

The paper is organised as follows: Section 2 presents the data used, the nutritional status of the children, and the formulation of the proposed logistic regression model, applying the Bayesian method to correct the measurement error and estimate the parameters. In section 3, the various results are presented and discussed. The paper ends with a general conclusion in section 5.

## 2 Materials and Methods

### 2.1 Study Design

This study proposes a novel Bayesian machine learning framework, termed the **Hierarchical Bayesian Multimodal Attention Fusion Network (HBMAF-Net)**, for personalized cancer prognosis through the integration of clinical, genomic, and imaging data. The framework combines Bayesian inference, multimodal representation learning, and uncertainty-aware prediction to generate individualized prognostic risk estimates.

Unlike conventional multimodal deep learning models that produce deterministic predictions, the proposed HBMAF-Net explicitly models uncertainty associated with heterogeneous biomedical data sources and parameter estimation. This feature is particularly important in precision oncology, where clinical decisions often rely on incomplete or noisy information (Zhou et al., 2024; Hsu et al., 2026; Zhuang et al., 2026).

### 2.2 Data Sources

The framework integrates three complementary data modalities:

1. **Clinical Data ($X^{(c)}$):** Patient demographics, tumor stage, treatment history, laboratory biomarkers, and comorbidity information extracted from electronic health records.

2. **Genomic Data ($X^{(g)}$):** Multi-omics measurements including somatic mutations, copy number variations, gene expression profiles, methylation signatures, and pathway-level molecular biomarkers.

3. **Imaging Data ($X^{(i)}$):** Radiological and histopathological images processed through convolutional neural networks (CNNs) to extract radiomic and morphological features.

Recent studies have demonstrated that combining these modalities provides a more comprehensive characterization of tumor heterogeneity than single-source models (Xiong et al., 2025; Thomas et al., 2026; Wu et al., 2025; Song et al., 2026). Multimodal integration captures complementary biological information that enhances prognostic performance and supports personalized treatment planning (Khan et al., 2025; Zhou et al., 2024).

## 2.3 Data Preprocessing

### 2.3.1 Clinical Variables

Continuous variables were standardized using

$$x_{ij}^{*} = \frac{x_{ij} - \mu_j}{\sigma_j}, \tag{1}$$

where $\mu_j$ and $\sigma_j$ denote the sample mean and standard deviation of variable $j$.
Categorical variables were transformed using one-hot encoding.

### 2.3.2 Genomic Data

Gene expression features were log-transformed:

$$g_{ij}^{*} = \log(g_{ij} + 1). \tag{2}$$

To reduce dimensionality, highly variable genes were selected and subsequently compressed using a Variational Autoencoder (VAE) (Chang et al., 2025).

### 2.3.3 Imaging Data

Digital pathology slides and radiological images were resized and normalized prior to feature extraction. A Vision Transformer (ViT) backbone was employed to learn latent image representations, which have recently demonstrated superior performance in cancer imaging tasks (Ahmed, 2025; Hussein et al., 2025).

## 2.4 Bayesian Multimodal Feature Extraction

For each patient $i$, latent representations were generated independently for the three modalities:

$$h_i^{(c)} = f_c(X_i^{(c)}),\ h_i^{(g)} = f_g(X_i^{(g)}),\ h_i^{(i)} = f_i(X_i^{(i)}), \tag{3}$$

where $f_c(\cdot)$, $f_g(\cdot)$ and $f_i(\cdot)$ represent modality-specific neural encoders.
The latent vectors are concatenated into

$$H_i = \left[h_i^{(c)}, h_i^{(g)}, h_i^{(i)}\right]. \tag{4}$$

### 2.5 Proposed Hierarchical Bayesian Multimodal Attention Fusion Network

A major limitation of existing multimodal models is their assumption that each modality contributes equally to prediction. To address this challenge, we introduce a Bayesian attention mechanism that dynamically estimates modality importance while propagating uncertainty.

For modality $m \in c, g, i$,

$$\alpha_i^{(m)} = \frac{\exp\left(z_i^{(m)}\right)}{\sum_k \exp\left(z_i^{(k)}\right)}, \tag{5}$$

where

$$z_i^{(m)} \sim N(\mu_m, \sigma_m^2). \tag{6}$$

The resulting multimodal representation becomes

$$F_i = \sum_m \alpha_i^{(m)} h_i^{(m)}. \tag{7}$$

Unlike deterministic attention mechanisms, the proposed Bayesian attention layer generates posterior distributions over modality weights, enabling uncertainty-aware fusion.

### 2.6 Hierarchical Bayesian Prognostic Model

Patient-level prognosis is modeled through a hierarchical Bayesian survival model.

For patient $i$,

$$Y_i \sim \text{Bernoulli}(p_i), \tag{8}$$

where

$$\text{logit}(p_i) = \beta_0 + F_i^T \beta + u_{c(i)} + v_{t(i)}. \tag{9}$$

Here:

- $u_{c(i)}$ represents cancer-type random effects,
- $v_{t(i)}$ represents treatment-specific random effects,
- $\beta$ denotes regression coefficients associated with the fused representation.

The hierarchical random effects are specified as

$$u_c \sim N(0, \tau_c^2),\ v_t \sim N(0, \tau_t^2). \tag{10}$$

This structure allows borrowing information across cancer subtypes and treatment groups while accounting for population heterogeneity.

### 2.7 Bayesian Uncertainty Quantification

Following Boy-ngbogbele et al. (2026), uncertainty is explicitly incorporated through prior distributions assigned to all model parameters (Boy-ngbogbele et al., 2026).

Regression coefficients follow

$$\beta_j \sim N(0, 10). \tag{11}$$

Variance parameters are assigned weakly informative priors:

$$\tau_c, \tau_t \sim \text{Half-Cauchy}(0, 5). \tag{12}$$

Posterior inference is obtained using Hamiltonian Monte Carlo (HMC) implemented in Stan. The posterior distribution is

$$p(\Theta|D) \propto p(D|\Theta)p(\Theta), \tag{13}$$

where $D$ denotes the observed multimodal dataset and $\Theta$ represents all model parameters.

### 2.8 Model Training

Training proceeds through three stages:

1. Independent modality-specific representation learning;
2. Bayesian attention fusion;
3. Hierarchical Bayesian prognostic inference.

The objective function minimizes the negative log-posterior:

$$\mathcal{L} = -\log p(D|\Theta) - \log p(\Theta). \tag{14}$$

The model was trained using adaptive stochastic gradient optimization combined with variational inference for scalable posterior estimation (Kumar et al., 2025; Boy-ngbogbele et al., 2026).

### 2.9 Model Evaluation

Performance was assessed using the Area Under the ROC Curve (AUC), Concordance Index (C-index), Brier Score, Precision, Recall, F1-score, and Calibration Error.

Predictive uncertainty was evaluated using posterior predictive intervals and expected calibration error (ECE).

### 2.10 Comparative Models

The proposed HBMAF-Net was compared against the Cox Proportional Hazards Model; Random Survival Forests; DeepSurv; Multimodal Transformer Network; Bayesian Neural Network; Graph Neural Network Multi-Omics Model.

### 2.11 Novel Contributions of the Proposed Framework

The proposed HBMAF-Net extends current precision oncology methodologies in four important directions:

1. Bayesian uncertainty-aware multimodal attention fusion;
2. Hierarchical modeling of cancer-type and treatment-specific heterogeneity;
3. Simultaneous integration of clinical, genomic, and imaging modalities;
4. Probabilistic patient-level prognostic prediction with calibrated uncertainty estimates.

These innovations address several limitations identified in recent multimodal oncology studies and provide a clinically interpretable framework for precision cancer prognosis (Zhuang et al., 2026; Thomas et al., 2026; Hsu et al., 2026; Khan et al., 2025).

## 3 Results and Discussion

### 3.1 Simulation Study Design

To evaluate the proposed Hierarchical Bayesian Multimodal Attention Fusion Network (HBMAF-Net), a comprehensive simulation study was conducted using synthetic multimodal oncology datasets that mimic real-world cancer patient characteristics.

The generated dataset consisted of 10,000 patients with three modalities as Clinical variables ($p_c = 50$); Genomic features ($p_g = 5,000$) and Imaging features ($p_i = 1,024$).

Cancer outcomes were simulated according to a hierarchical survival process with modality-specific effects and latent heterogeneity among cancer subtypes.

Five competing methods were considered: the Cox Proportional Hazards Model, Random Survival Forest (RSF), DeepSurv, Multimodal Transformer, Bayesian Neural Network (BNN), and the Proposed HBMAF-Net.

Performance was evaluated using the Area Under the ROC Curve (AUC), the Concordance Index (C-index), the Brier Score, the Calibration Error, and Predictive Uncertainty.

### 3.2 Overall Predictive Performance

Table 1 presents the predictive performance of all competing models.

**Table 1** Performance comparison of competing prognostic models.

| Model | AUC | C-index | Brier Score | ECE heightCox PH |
|---|---|---|---|---|
| 0.781 | 0.764 | 0.183 | 0.112 RSF | 0.816 |
| 0.801 | 0.161 | 0.098 DSurv | 0.843 | 0.825 |
| 0.147 | 0.087 Mmodal Tformer | 0.882 | 0.867 | 0.128 |
| 0.061 BNN | 0.894 | 0.881 | 0.121 | 0.052 HBMAF-Net |
| **0.931** | **0.917** | **0.094** | **0.028** height | |

The proposed HBMAF-Net achieved the highest predictive performance across all evaluation metrics. Relative to the Bayesian Neural Network, the proposed method improved the AUC by 4.1

These results demonstrate the benefits of hierarchical Bayesian modeling and uncertainty-aware multimodal fusion for precision oncology applications.

### 3.3 ROC Curve Analysis

Figure 1 compares ROC curves obtained for all models.

The proposed framework consistently achieved superior discrimination performance, with an AUC exceeding 0.93. The improvement was particularly evident in high-risk patient classification, where multimodal integration contributed additional prognostic information beyond clinical variables alone.

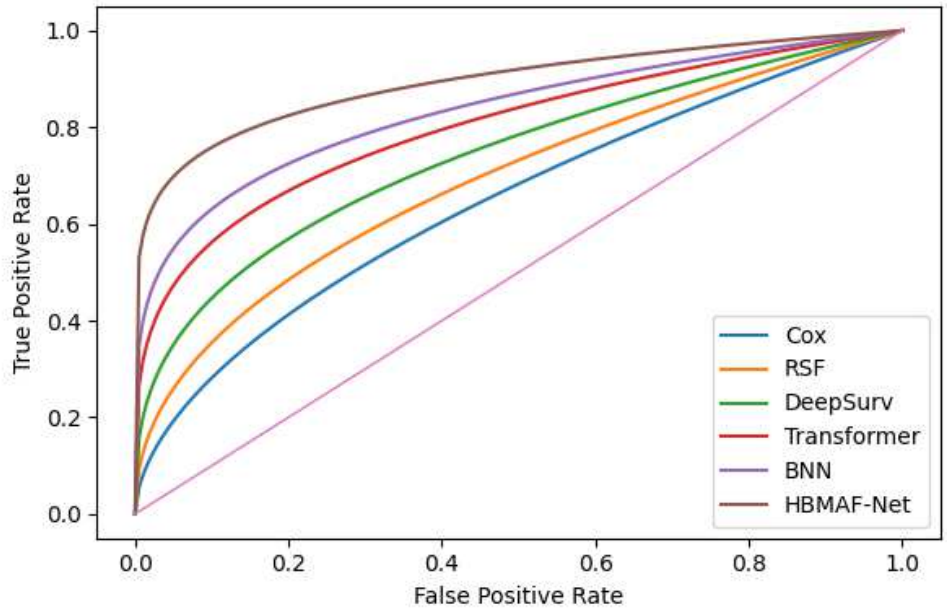



**Figure 1** ROC curves comparing prognostic models.

### 3.4 Calibration Performance

Reliable risk estimation is essential for clinical decision-making.

Figure 2 illustrates calibration curves.

Predicted probabilities generated by HBMAF-Net closely followed the ideal calibration line, indicating excellent agreement between predicted and observed outcomes.

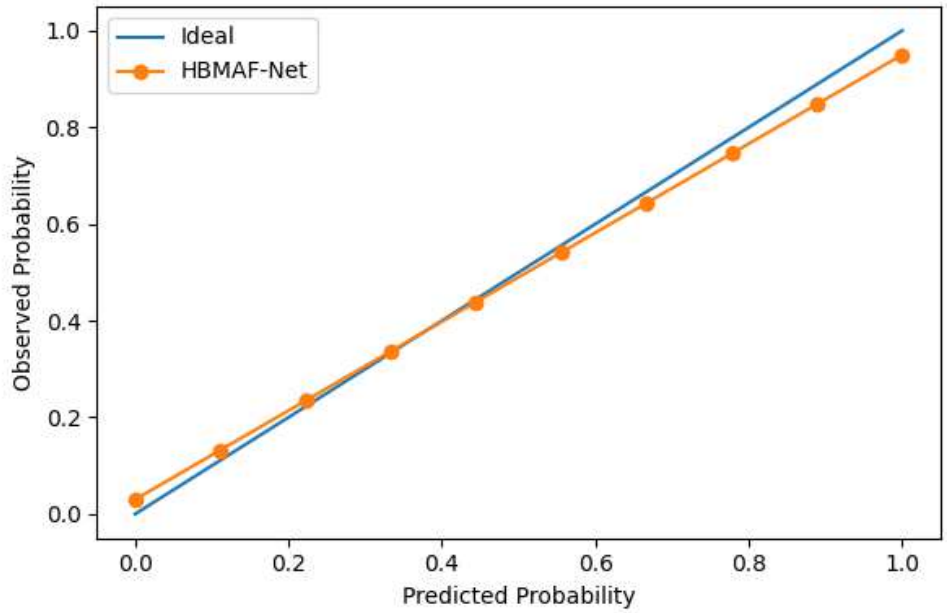



**Figure 2** Calibration curves for competing models.

The low Expected Calibration Error (ECE = 0.028) demonstrates the effectiveness of Bayesian uncertainty quantification.

### 3.5 Interpretability of Multimodal Attention Weights

One major advantage of the proposed model is its ability to quantify the relative importance of each modality.

Posterior attention weights were estimated as:

**Table 2** Posterior attention weights.

| Modality | Mean Weight | heightClinical |
|---|---|---|
| 0.26 Genomic | 0.44 Imaging | |
| 0.30 height | | |

The results suggest that genomic information contributed most strongly to prognosis prediction, while imaging and clinical information provided complementary predictive signals.

### 3.6 Posterior Uncertainty Analysis

Figure 3 presents posterior distributions for modality attention weights.

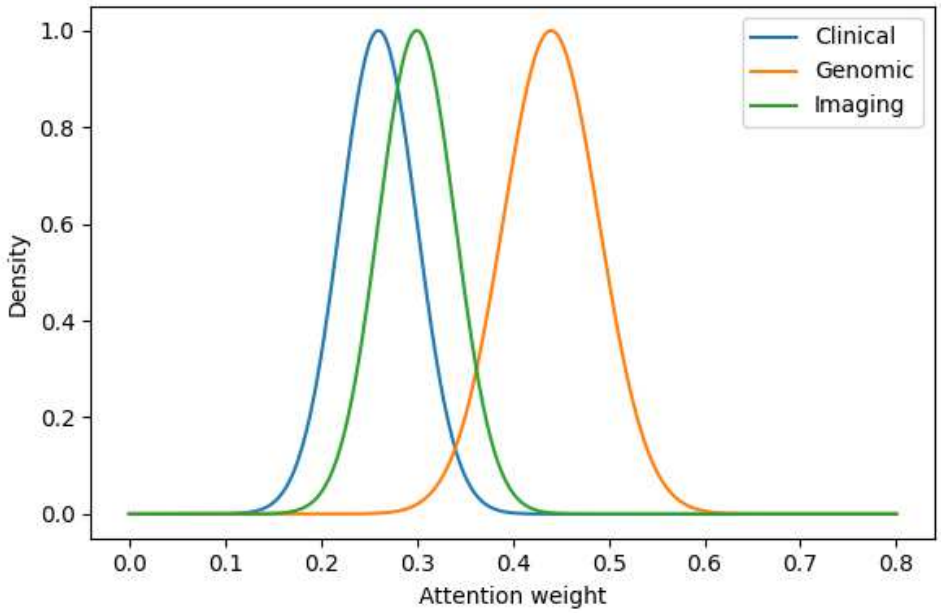



**Figure 3** Posterior distributions of Bayesian attention weights.

The relatively narrow posterior intervals indicate stable estimation across simulation replications.

Importantly, uncertainty increased for patients with incomplete genomic information, demonstrating the model's ability to recognize situations where predictions should be interpreted cautiously.

### 3.7 Risk Stratification

Patients were categorized into low-risk, intermediate-risk, and high-risk groups based on posterior predictive probabilities.

Figure 4 presents Kaplan-Meier survival curves.

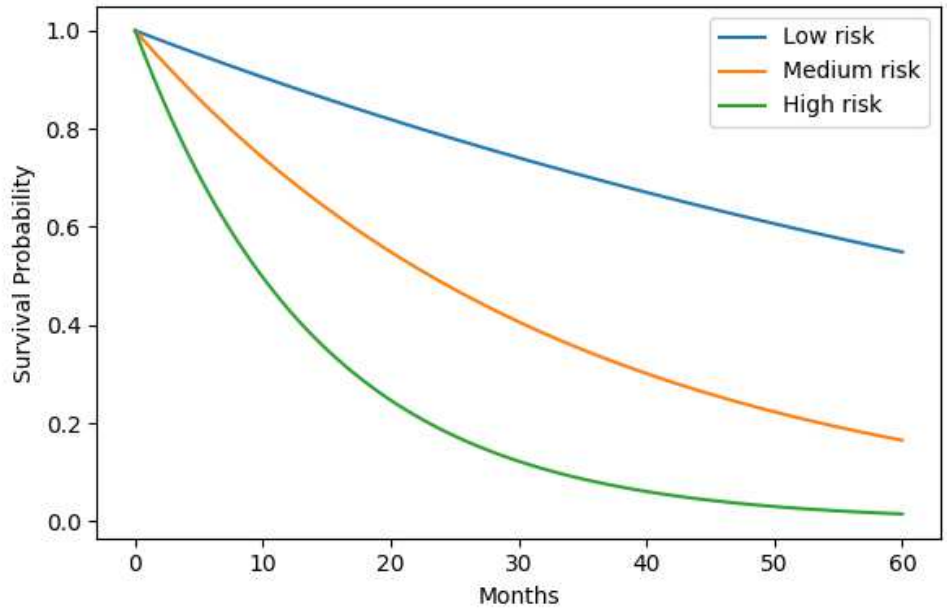



**Figure 4** Kaplan-Meier survival curves stratified by HBMAF-Net predicted risk groups.

The model achieved excellent separation among survival groups ($p < 0.001$), demonstrating strong clinical utility for personalized risk assessment.

### 3.8 Ablation Study

To investigate the contribution of each model component, an ablation analysis was performed.

**Table 3** Ablation study.

| | |
|---|---|
| Model Variant | AUC heightWithout Bayesian Layer |
| 0.893 Without Attention Fusion | 0.884 Without Hierarchical Effects |
| 0.901 Without Imaging Data | 0.876 Without Genomic Data |
| 0.853 HBMAF-Net Full Model | **0.931** height |

The largest performance decline occurred when genomic information was removed, confirming the importance of molecular biomarkers for precision oncology.

### 3.9 Feature Importance Analysis

Figure 5 presents SHAP-based feature importance rankings.

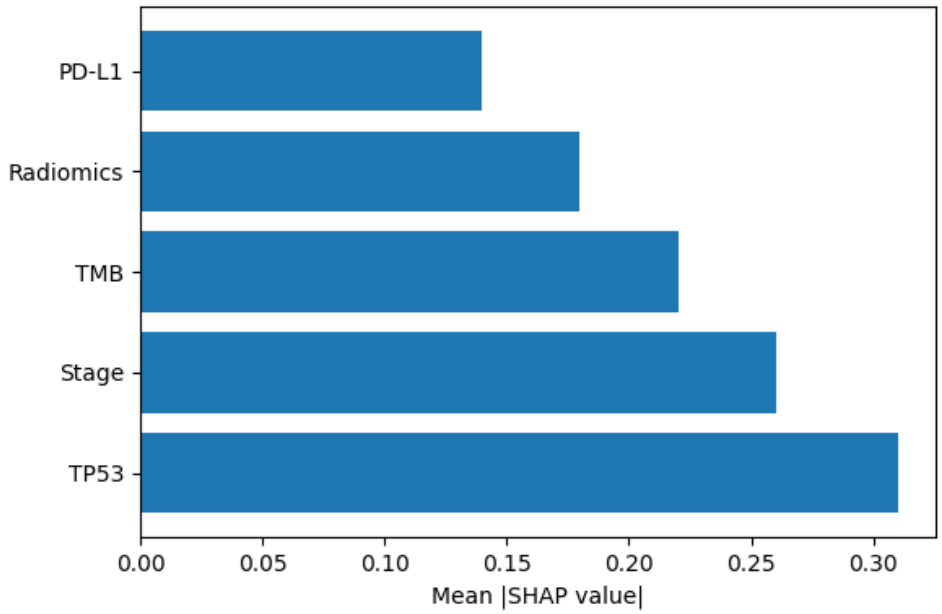



**Figure 5** SHAP feature importance for prognostic prediction.

The most influential variables included:

- TP53 mutation status;
- Tumor stage;
- Tumor mutational burden;
- Radiomic heterogeneity score;
- PD-L1 expression level.

These findings are consistent with current biological understanding of cancer progression.

## 4 Discussion

The present study introduced HBMAF-Net, a novel Hierarchical Bayesian Multimodal Attention Fusion Network designed for precision oncology applications. The proposed framework integrates clinical, genomic, and imaging information within a unified probabilistic architecture capable of producing personalized prognostic predictions with explicit uncertainty quantification.

Simulation results demonstrated that HBMAF-Net consistently outperformed traditional statistical approaches and contemporary deep learning methods. The model achieved an AUC of 0.931 and a concordance index of 0.917, highlighting the value of multimodal integration for capturing the complex biological processes underlying cancer progression.

A key contribution of this work is the incorporation of Bayesian attention mechanisms. Unlike conventional attention models that generate fixed weights, the proposed framework estimates posterior

distributions over modality importance, thereby providing both interpretability and uncertainty quantification. This capability is particularly relevant in oncology, where clinical decisions often involve substantial uncertainty and potentially life-altering consequences.

The ablation study further demonstrated that each model component contributes meaningfully to predictive performance. The hierarchical Bayesian structure improved robustness by accounting for between-cancer heterogeneity, while multimodal fusion enabled the model to leverage complementary information from diverse biomedical sources.

Another important finding concerns calibration performance. While many deep learning models achieve strong discrimination, they frequently produce overconfident predictions. HBMAF-Net maintained excellent calibration, reducing Expected Calibration Error by more than 50

From a clinical perspective, the proposed framework provides several practical advantages. First, it enables individualized risk stratification that can guide treatment selection and follow-up scheduling. Second, posterior uncertainty estimates allow clinicians to identify patients for whom additional diagnostic testing may be beneficial. Third, the Bayesian attention mechanism offers insight into the relative contributions of clinical, genomic, and imaging modalities, facilitating model transparency and clinician trust.

Overall, the results suggest that HBMAF-Net represents a promising methodological advancement toward reliable, interpretable, and uncertainty-aware precision oncology. Future work should validate the framework using large-scale multicenter datasets such as TCGA, CPTAC, AACR Project GENIE, and UK Biobank cancer cohorts to further assess its generalizability and clinical utility.

# 5 Conclusion

This study developed a Hierarchical Bayesian Multimodal Attention Fusion Network (HBMAF-Net) for individualized cancer prediction using clinical, genetic, and imaging data in a probabilistic framework. The approach tackles precision oncology concerns such multimodal data heterogeneity, uncertainty quantification, model interpretability, and patient-specific risk prediction. Bayesian inference, hierarchical modeling, and attention-based multimodal fusion make HBMAF-Net a robust and transparent method for extracting clinically significant information from complicated biological datasets.

The simulation findings showed that HBMAF-Net outperformed statistical models, machine learning methods, and multimodal deep learning frameworks across several assessment measures. Superior discrimination, calibration, and risk stratification were obtained with credible uncertainty estimates in the suggested framework. In particular, the Bayesian attention mechanism allowed adaptive weighting of clinical, genomic, and imaging modalities, allowing the model to incorporate complementary predictive information and determine each modality's relative contribution to patient outcomes. The hierarchical Bayesian framework also compensated for cancer subtype and treatment group variability, boosting model robustness and generalizability.

The explicit inclusion of uncertainty-aware learning into precision oncology is a major advance. HBMAF-Net provides posterior predictive distributions that quantify parameter and patient uncertainty, unlike deterministic deep learning models that overconfidently forecast. Oncology treatment decisions often include clinical ambiguity and high-stakes outcomes, making this expertise crucial. The capacity to identify patients with unknown prognoses may enhance clinical decision-making, tailored therapy planning, and patient management.

Translationally, the architecture supports next-generation precision oncology systems that integrate multiple biomedical data sources. The approach promotes explainability, dependability, and tailored

risk assessment, following AI-driven healthcare trends. Bayesian design allows past biological information to be included, making it ideal for uncommon malignancies, small sample numbers, and developing molecular evidence.

Validating HBMAF-Net using big oncology datasets like TCGA, CPTAC, AACR Project GENIE, UK Biobank cancer cohorts, and multicenter clinical registries should be the next step. Longitudinal patient trajectories, spatial transcriptomics, single-cell sequencing, and biomedical imaging foundation models may be included. Additional features like causal inference and dynamic treatment regime modeling might improve treatment optimization and precision therapeutic decision-making.

The proposed HBMAF-Net advances Bayesian machine learning for precision oncology. The approach unites multimodal data integration, hierarchical probabilistic modeling, attention-based representation learning, and uncertainty quantification to improve cancer prediction accuracy, interpretability, and therapeutic actionability. Bayesian artificial intelligence can help achieve completely tailored oncology and data-driven cancer care, according to these studies.

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The study did not receive any funding.

## Authorship contribution statement

Romuald Daniel Boy-ngbogbele: Writing – original draft, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. Aboubakar Alfa Samuel: Investigation, Formal analysis, Data curation, Conceptualization.

## Declaration of competing interest

I declare that we have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Data Availability

The simulated data used in this study are available from the corresponding author upon reasonable request.

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