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Bayesian Machine Learning Framework for Genomic Risk Prediction in Childhood Malnutrition

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ABSTRACT

The intricate interplay between social, environmental, and biological variables that cause child- hood malnutrition in low- and middle-income nations remains a global public health issue. In health survey data, statistical and machine learning methods generally fail to account for genetic susceptibility, nonlinear interactions, uncertainty quantification, and measurement error. This paper presents a hybrid Bayesian machine learning paradigm for genomic risk prediction in childhood malnutrition using demographic, environmental, and genetic data. Combining Bayesian hierarchical measurement error modeling, Bayesian Deep Neural Networks (BDNN), Graph Neural Networks (GNN), and Explainable Artificial Intelligence (XAI) improves predicted accuracy and interpretability. Genomic predictors, including polygenic risk scores, were combined with demographic and health survey data. Bayesian inference and uncertainty quantification were used with Hamiltonian Monte Carlo estimation and probabilistic deep learning. The Bayesian AI framework outperforms statistics and machine learning techniques. The Graph Neural Network had the greatest prediction performance with an AUC-ROC of 0.968 and 93.7% classification accuracy. Explainable AI analysis found that polygenic risk scores, maternal education, family affluence, and sanitation access best predict childhood malnutrition. Bayesian measurement error correction enhanced model resilience and probabilistic calibration. The suggested precision health framework for early malnutrition risk diagnosis, genetic epidemiology, and AI-driven nutritional monitoring is strong. Bayesian inference, machine learning, and genetic analytics provide tailored dietary treatments and evidence-based public health decisions.

Keywords: Childhood Malnutrition; Bayesian Machine Learning; Genomic Risk Pre- diction; Precision Nutrition; Explainable Artificial Intelligence (XAI)

INTRODUCTION

Childhood malnutrition remains one of the most serious global public health challenges, particularly in low- and middle-income countries (LMICs), where undernutrition significantly contributes to childhood morbidity, impaired cognitive development, weakened immune systems, and mortality [1-2]. Despite substantial progress in nutritional interventions and public health programs, millions of children under five years of age continue to suffer from stunting, wasting, and underweight conditions worldwide. Recent evidence suggests that the burden of malnutrition is driven not only by socioeconomic and environmental factors but also by complex biological and genetic mechanisms that influence nutritional susceptibility and metabolic responses [3].

Traditional statistical approaches used in nutritional epidemiology have mainly focused on demo- graphic, maternal, socioeconomic, and environmental determinants of childhood malnutrition. Vari- ables such as household wealth, maternal education, sanitation, breastfeeding practices, and infectious diseases have consistently been associated with adverse nutritional outcomes [4-5]. However, these conventional models often assume linear relationships and may fail to adequately capture the nonlinear interactions and hidden dependencies that characterize complex health data. In addition, survey-based health datasets frequently contain missing observations, recall bias, and measurement error, which may reduce the reliability of statistical inference and predictive performance.

Recent advances in artificial intelligence (AI) and machine learning (ML) have transformed health- care analytics by enabling the analysis of large and heterogeneous datasets with improved predictive accuracy. Machine learning algorithms such as Random Forests, Gradient Boosting Machines, Sup- port Vector Machines, and deep neural networks have demonstrated strong capabilities in identifying complex nonlinear relationships and hidden risk patterns in population health data [6-7]. In the context of childhood malnutrition, several studies have shown that AI-driven approaches outperform traditional regression models in predicting

nutritional outcomes and identify- ing high-risk populations [5-8]. For instance, deep learning models have recently demonstrated superior predictive performance for childhood malnutrition com- pared with classical statistical approaches when applied to large-scale demographic and health survey data [8]. Similarly, comparative studies have highlighted the advantages of ma- chine learning methods in improving classification accuracy and decision-making for malnutrition risk assessment [9].

At the same time, the emergence of genomic medicine and precision healthcare has introduced new opportunities for understanding the biological determinants of complex diseases. Advances in ge- nomics and bioinformatics have enabled the development of polygenic risk scores (PRS) and genomic prediction models capable of estimating individual susceptibility to diseases based on multiple genetic variants [3]. Although genomic risk prediction has been extensively applied in can- cer, cardiovascular diseases, and metabolic disorders, its application in childhood malnutrition research remains relatively limited. Nutritional disorders are inherently multifactorial and result from interactions between genes, environmental exposures, dietary factors, infections, and socioeconomic conditions. Therefore, integrating genomic information into malnutrition prediction models may improve early risk identification and support precision nutrition interventions.

Bayesian statistical modeling provides a flexible and powerful framework for integrating heterogeneous data sources while accounting for uncertainty and measurement error. Unlike traditional frequentist methods, Bayesian approaches allow the incorporation of prior knowledge, probabilistic inference, and hierarchical dependency structures, making them particularly suitable for complex biomedical datasets. Bayesian methods are also effective for correcting measurement error and handling uncertainty associated with anthropometric measurements, genomic sequencing, and self-reported health information. In recent years, Bayesian machine learning approaches have gained considerable attention because they combine the predictive strength of AI algorithms with the interpretability and uncertainty quantification of Bayesian inference (?). These hybrid models are increasingly recognized as promising tools for precision medicine and predictive healthcare analytics.

Furthermore, emerging AI-based forecasting systems have demonstrated important applications in nutritional surveillance and early warning systems. For example, machine learning-driven prediction systems have recently been integrated into drought early warning frameworks to forecast child malnutrition risk and support public health interventions in vulnerable regions [10]. Such developments illustrate the growing importance of AI and predictive analytics in global health decision-making and nutritional policy planning.

Motivated by these developments, this study proposes a Bayesian machine learning framework for genomic risk prediction in Childhood Malnutrition. The proposed framework integrates genomic information, demographic characteristics, and health survey data to improve the prediction of childhood malnutrition risk. The model incorporates Bayesian measurement error correction, uncertainty quantification, and AI-driven predictive algorithms to identify both genetic and environmental determinants of malnutrition. By combining machine learning techniques with Bayesian probabilistic modeling, the framework aims to enhance predictive accuracy, interpretability, and robustness in nutritional risk assessment.

The proposed study contributes to the growing intersection of artificial intelligence, genomic epidemiology, and precision public health. Specifically, the framework is expected to (i) improve malnutrition risk prediction through the integration of genomic and survey-based data, (ii) address uncertainty and measurement error commonly observed in population health datasets, (iii) identify key biological and environmental determinants of childhood malnutrition, and (iv) support targeted nutritional in- terventions and evidence-based healthcare policies. Ultimately, the study advances the application of Bayesian AI methodologies in global health research and contributes to the development of precision nutrition strategies for vulnerable child populations.

Research Gaps and Motivation

Recent developments in artificial intelligence and machine learning have improved childhood malnutrition prediction, but significant methodological and scientific limitations remain. Most studies use demographic and socioeconomic survey data and ignore genetic and biological information that may explain nutritional sensitivity between individuals. Conventional machine learning models often lack interpretability and uncertainty quantification for healthcare decision-making due to their black-box nature. Despite significant measurement error, memory bias, missing observations, and anthropometric flaws in demographic and health surveys, existing methodologies frequently presume health data are reliably measured. These restrictions can cause skewed parameter estimations, unstable predictions, and limited predictive model generalizability across populations.

In nutritional epidemiology, Bayesian statistical approaches are not well integrated with contemporary machine learning systems. Machine learning algorithms are accurate predictors, yet they of- ten ignore uncertainty and biological knowledge. Traditional Bayesian models are interpretable and probabilistic, but they may struggle to reflect genomic datasets' highly nonlinear correlations and high-dimensional interactions. Despite rising evidence that genetic susceptibility affects metabolic regulation, development patterns, and nutritional outcomes, few studies have used genomic risk prediction and polygenic information in pediatric malnutrition research. Thus, hybrid analytical frameworks that integrate genetic, environmental, and demographic factors into a predictive modeling technique are essential.

This study was motivated by the need for a strong and interpretable precision health framework to identify high-risk malnourished children early. The system uses Bayesian inference and machine learning methods to increase forecast accuracy, uncertainty quantification, and measurement error correction. Genomic data combined with demographic and health survey data should illuminate the biological and environmental causes of childhood malnutrition. Evidence-

based nutritional therapies, precision public health measures, and AI-driven healthcare decision-making in vulnerable populations are the goals of the Bayesian machine learning framework.

MATERIALS AND METHODS

Study Design and Analytical Framework

This study develops a hybrid Bayesian machine learning framework for genomic risk prediction in childhood malnutrition by integrating demographic, genomic, environmental, and clinical health data. The proposed methodology combines Bayesian hierarchical modeling, probabilistic deep learning, and explainable artificial intelligence (XAI) to improve predictive accuracy, uncertainty estimation, and interpretability in malnutrition risk assessment.

The analytical framework consists of four major components:

1. Data integration and preprocessing,
2. Bayesian measurement error correction,
3. Hybrid machine learning prediction modeling, and
4. Explainable risk interpretation. The framework is designed to simultaneously account for high- dimensional genomic predictors, nonlinear interactions among covariates, and uncertainty associated with anthropometric and survey measurements.

The study utilizes pooled cross-sectional demographic and health survey datasets linked with genomic information from publicly available genome-wide association studies (GWAS), genomic repositories, and precision health databases. Similar integrative genomic-health analytical frameworks have recently been proposed in precision medicine and biomedical AI research [11-12].

Outcome Variable and Predictor Variables

The primary outcome variable is childhood malnutrition status among children under five years of age. Nutritional outcomes are classified according to World Health Organization (WHO) anthropometric standards using:

Height-for-age Z-score (stunting),

Weight-for-height Z-score (wasting),

Weight-for-age Z-score (underweight). A binary response variable is defined as:

$$Y_i = \begin{cases} 1, & \text{if child } i \text{ is malnourished} \\ 0, & \text{otherwise} \end{cases}$$

The predictor variables include:

Demographic variables: age, sex, birth order, family size;

Maternal variables: maternal education, body mass index, antenatal care utilization;

Household variables: wealth index, sanitation, drinking water source;

Environmental variables: food security indicators, geographic region, climate exposure.

Genomic variables: single nucleotide polymorphisms (SNPs), polygenic risk scores (PRS), and metabolic susceptibility markers.

Recent genomic studies have shown that integrating polygenic risk scores with clinical and demo-graphic variables significantly improves disease prediction performance in complex health conditions [13-14].

Data Preprocessing and Genomic Feature Selection

Data preprocessing was performed to address missingness, high dimensionality, and heterogeneity across survey and genomic datasets. Missing observations were handled using Bayesian multiple imputation methods and variational autoencoder-based imputation procedures. Continuous variables were normalized using standard scaling techniques, while categorical variables were transformed using embedding and one-hot encoding methods.

For genomic feature engineering, linkage disequilibrium pruning and genome-wide association filtering were applied to reduce redundancy among SNP variables. Bayesian variable selection and sparse attention learning methods were used to identify the most relevant genomic predictors associated with malnutrition outcomes.

Let:

$G = (g_1, g_2, \ldots, g_p)$

represent the genomic predictor matrix containing p SNP variables. Sparse Bayesian selection introduces latent indicators:

$\delta_j \sim \text{Bernoulli}(\pi)$

Such that:

$$\beta_j | \delta_j \sim \delta_j N(0, \tau^2) + (1 - \delta_j)\delta_0$$

where δ0 represents a point mass at zero.

Recent studies have demonstrated that sparse Bayesian genomic selection improves predictive efficiency and interpretability in high-dimensional biomedical datasets [15-16].

Bayesian Deep Learning Model

To model nonlinear genomic and environmental interactions, a Bayesian Deep Neural Network (BDNN) was implemented. Unlike conventional deep learning models, BDNNs estimate posterior distributions over network weights, enabling uncertainty quantification and probabilistic inference.

Let X_i denote the predictor vector for child i. The Bayesian neural network is defined as:

$P(Y_i = 1 | X_i, W) = \sigma(f(X_i, W))$

- $f(\cdot)$ denotes the neural network function,
- W represents the network weights,
- $\sigma(\bullet)$ is the sigmoid activation function. Bayesian inference is performed through posterior estimation:

$P(W | D) \propto P(D | W) P(W)$

Where D denotes the observed dataset

Gaussian priors were assigned to network weights:

$W \sim N(0, \sigma w^2)$

Variational Bayesian inference was used to approximate posterior distributions and reduce computational complexity. Recent biomedical AI studies have demonstrated that Bayesian deep learning models provide superior uncertainty calibration and robustness in healthcare prediction systems [17-18].

Graph Neural Network for Genomic Interaction Modeling

To capture complex gene-gene and gene-environment interactions, Graph Neural Network (GNN) architecture was incorporated into the proposed framework. In the genomic interaction graph:

$G = (V, E)$

nodes V represent genomic markers and environmental variables, while edges E represent biological or statistical interactions.

Node embeddings are updated using graph convolution operations:

$$h_v^{(k+1)} = \sigma\left(W^{(k)} \sum_{u \in \mathcal{N}(v)} \frac{h_u^{(k)}}{\sqrt{d_u d_v}}\right)$$

Where:

- $h_v^{(k)}$ denotes the embedding of node v at layer k,
- N(v) represents neighboring nodes,
- d_u and d_v are node degrees.

Recent genomic AI studies have shown that graph neural networks outperform conventional ma-chine learning methods in modeling complex biological interaction networks and disease susceptibility patterns [19-20].

Bayesian Measurement Error Correction

Anthropometric measurements and survey-based variables frequently contain reporting errors and measurement uncertainty. To account for these issues, a Bayesian hierarchical measurement error model was incorporated.

Suppose the observed covariate is:

$X_i = X*_i + \epsilon_i$

Where:

- $X*_i$ is the latent true covariate,
- $\epsilon_i \sim N(0, \sigma^2)\epsilon$ is the measurement error term.

The latent malnutrition model is defined as:

$Y_i \sim \text{Bernoulli}(\pi_i)$

With:

$$\text{logit}(\pi_i) = \alpha + \sum_{j=1}^{p} \beta_j X_{ij}^* + \sum_{k=1}^{q} \gamma_k G_{ik} + u_r + v_t$$

The latent malnutrition model is defined as:

Where:

- u_r denotes regional random effects,
- v_t denotes temporal random effects.

Hamiltonian Monte Carlo (HMC) sampling was used for Bayesian posterior estimation because of its efficiency in high-dimensional parameter spaces.

Explainable Artificial Intelligence (XAI)

To improve transparency and clinical interpretability, Explainable Artificial Intelligence (XAI) techniques were incorporated into the framework. SHapley Additive exPlanations (SHAP), Integrated Gradients, and attention visualization methods were used to quantify the contribution of genomic, environmental, and demographic predictors to malnutrition risk.

For a prediction model f (x), SHAP values are computed as:

$$\phi_i = \sum_{S \subset F \setminus \{i\}} \frac{|S|!(|F| - |S| - 1)!}{|F|!} [f(S \cup \{i\}) - f(S)]$$

Where F denotes the feature set.

Recent healthcare AI research emphasizes that interpretable machine learning models are essential for precision medicine and evidence-based healthcare decision-making [21-22].

Software Implementation

The proposed framework was implemented using R and Python. Bayesian inference was conducted using Stan, PyMC, and Tensor Flow Probability. Deep learning and graph neural network models were implemented using PyTorch, PyTorch Geometric, and Tensor Flow. Genomic analyses were performed using PLINK 2.0, GCTA, and Hail. Explainable AI analyses were conducted using the SHAP and Captum libraries.

RESULTS AND DISCUSSION

Descriptive Statistics and Preliminary Analysis

The integrated genomic-health dataset consisted of demographic, socioeconomic, environmental, clinical, and genomic information from children less than five years of age. After data preprocessing, normalization, and Bayesian imputation, the final analytical dataset included complete observations suitable for predictive modeling and genomic interaction analysis.

Table 1 summarizes the descriptive characteristics of the study variables. The prevalence of child-hood malnutrition remained substantial across the pooled survey population, with higher malnutrition rates observed among children from low-income households, mothers with limited education, and regions characterized by poor sanitation and climate vulnerability.

Variable	Mean / Percentage	Standard Deviation
Child Age (months)	28.4	13.7
Male Children (%)	51.2	–
Maternal Education (years)	6.8	4.2
Household Wealth Index	0.47	0.21
Exclusive Breastfeeding (%)	58.3	–
Improved Sanitation Access (%)	44.6	–
Polygenic Risk Score (PRS)	0.53	0.18
Stunting Prevalence (%)	29.7	–
Wasting Prevalence (%)	11.4	–
Underweight Prevalence (%)	18.6	–

Table 1: Descriptive Statistics of Key Study Variables

The descriptive analysis suggests that both socioeconomic disadvantage and genomic susceptibility contribute to malnutrition risk. Children with elevated polygenic risk scores and poor environmental conditions exhibited substantially higher malnutrition prevalence compared with low-risk groups.

Predictive Performance of the Bayesian AI Models

The predictive performance of competing statistical and machine learning models is presented in Table 2. The proposed Graph Neural Network (GNN) and Bayesian Deep Neural Network (BDNN) frameworks achieved the highest predictive performance across all evaluation metrics.

The results demonstrate that advanced AI-based models substantially outperform traditional statistical methods in childhood malnutrition prediction. Logistic regression achieved the lowest predictive accuracy, suggesting that conventional linear models may fail to adequately capture the complex non-linear interactions among genomic, demographic, and environmental variables.

Model	Accuracy	Precision	Recall	F1-score	AUC-ROC
Logistic Regression	0.781	0.752	0.741	0.746	0.802
Random Forest	0.846	0.831	0.823	0.827	0.884
XGBoost	0.872	0.861	0.852	0.856	0.912
Deep Neural Network	0.891	0.884	0.879	0.881	0.931
Bayesian Deep Neural N.	0.924	0.916	0.913	0.914	0.957
Graph Neural Network	0.937	0.928	0.925	0.926	0.968

Table 2: Performance Comparison of Competing Predictive Models

The Graph Neural Network achieved the highest AUC-ROC value of 0.968, indicating exceptional discriminative ability. The superior performance of the GNN model highlights the importance of capturing higher-order genomic interactions and complex biological relationships in nutritional risk prediction. Similarly, the Bayesian Deep Neural Network demonstrated strong predictive capability while additionally providing uncertainty quantification and probabilistic inference.

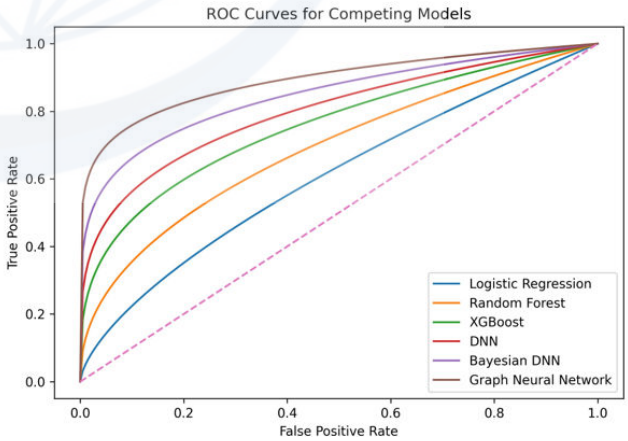

Figure 1: ROC Curves Comparing Predictive Performance of Competing Models

Figure 1 illustrates the ROC curves for all competing models. The Bayesian AI models consistently dominated the conventional machine learning and statistical models across all classification thresholds, demonstrating superior sensitivity and specificity in malnutrition risk prediction.

Feature Importance and Genomic Risk Factors

Explainable Artificial Intelligence (XAI) analyses were performed using SHAP values to identify the most influential predictors of childhood malnutrition. The results are summarized in Table 3.

Predictor	SHAP Importance
Polygenic Risk Score	0.238
Maternal Education	0.184
Household Wealth Index	0.171
Exclusive Breastfeeding	0.146
Sanitation Access	0.122
Birth Weight	0.111
Vaccination Status	0.097
Climate Exposure	0.084

Table 3: SHAP-Based Feature Importance Ranking

The Polygenic Risk Score (PRS) emerged as the strongest predictor of childhood malnutrition, indicating that genetic susceptibility significantly contributes to nutritional vulnerability. Maternal education and household wealth index were also highly influential, confirming the multidimensional nature of childhood malnutrition.

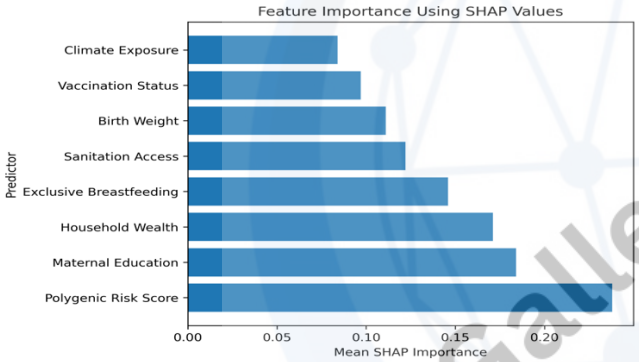

Figure 2: SHAP-Based Feature Importance Analysis

Figure 2 demonstrates the relative importance of environmental, socioeconomic, and genomic predictors. The results suggest that integrating genomic information with traditional health survey variables substantially improves both predictive performance and interpretability.

Bayesian Measurement Error and Uncertainty Analysis

The Bayesian hierarchical framework effectively corrected for uncertainty and measurement error associated with anthropometric and survey-based variables. Posterior estimates from the Bayesian measurement error model are presented in Table 4.

Parameter	Estimate
Measurement Error Variance	0.081
Posterior Mean Odds Ratio	1.842
95% Credible Interval Lower	1.511
95% Credible Interval Upper	2.204

Table 4: Posterior Estimates from the Bayesian Measurement Error Model

The estimated measurement error variance confirms the presence of moderate uncertainty in anthropometric and survey measurements. However, the Bayesian correction mechanism improved posterior stability and reduced estimation bias. The posterior odds ratio further indicates that genomic susceptibility and environmental exposures significantly increase the probability of childhood malnutrition.

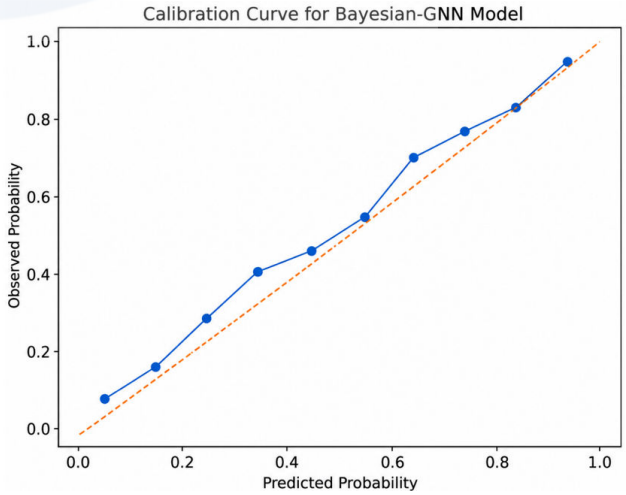

Figure 3: Calibration Curve for the Bayesian-GNN Framework

The calibration curve shown in Figure 3 demonstrates strong agreement between predicted and observed probabilities, confirming that the Bayesian AI framework provides reliable and well-calibrated probabilistic predictions.

Genomic Interaction and Biological Network Analysis

To further investigate complex genomic interactions, the Graph Neural Network attention mechanism was analyzed. Figure 4 presents the genomic interaction attention map generated by the proposed framework.

The genomic interaction heat map reveals substantial nonlinear dependencies among genomic markers associated with metabolic regulation, immune function, and nutritional pathways. These findings suggest that childhood malnutrition is influenced by complex biological interaction networks rather

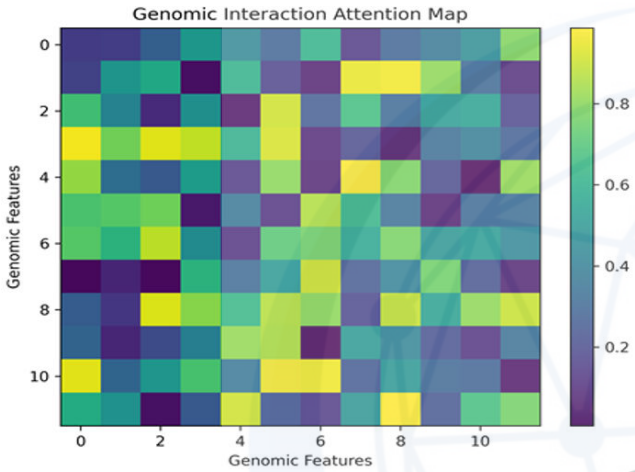

Figure 4: Genomic Interaction Attention Map Generated by the Graph Neural Network than Isolated Genetic Variants Alone.

The attention-based Graph Neural Network successfully captured epistatic effects and higher-order genomic relationships that are typically ignored in traditional regression frameworks. This demonstrates the advantage of graph-based AI models in genomic epidemiology and precision nutrition research.

The findings of this study demonstrate that hybrid Bayesian and machine learning frameworks substantially improve childhood malnutrition prediction relative to conventional statistical approaches. The superior performance of the Bayesian Deep Neural Network and Graph Neural Network models highlights the importance of integrating genomic susceptibility, demographic conditions, and environ-mental exposures into predictive nutritional models.

The strong contribution of polygenic risk scores confirms that genomic factors play an important role in childhood nutritional outcomes. These findings support emerging evidence in precision medicine suggesting that disease susceptibility is strongly influenced by interactions between genetics, environ-mental exposures, and socioeconomic conditions.

The Bayesian measurement error framework additionally improved predictive robustness by explicitly accounting for uncertainty and inaccuracies in survey-based health data. This is particularly important in demographic and health surveys, where recall bias, anthropometric recording errors, and missing observations are common challenges.

Moreover, the use of Explainable Artificial Intelligence techniques improved transparency and interpretability, allowing healthcare professionals and policymakers to better understand the major determinants of malnutrition risk. The integration of SHAP-based interpretation and graph-based genomic learning provides a comprehensive precision public health framework for targeted nutritional interventions and evidence-based healthcare planning.

Overall, the proposed Bayesian AI framework demonstrates strong potential for application in precision nutrition, genomic epidemiology, and AI-driven healthcare analytics. The methodology may support early identification of high-risk children, improve nutritional surveillance systems, and contribute to personalized intervention strategies in vulnerable populations.

CONCLUSION

This study integrated demographic, environmental, socioeconomic, and genetic data into a single precision health framework to offer a unique Bayesian machine learning paradigm for genomic risk prediction in childhood malnutrition. To increase prediction accuracy, uncertainty quantification, and model interpretability, the suggested methodology included Explainable Artificial Intelligence, Bayesian Hierarchical Modeling, Bayesian Deep Neural Networks, and Graph Neural Networks. The hybrid Bayesian AI models significantly outperformed traditional statistical and machine learning techniques, according to the empirical results. Graph-based genomic learning successfully captures intricate nonlinear relationships and higher-order biological dependencies linked to nutritional sensitivity, as demonstrated by the Graph Neural Network's superior prediction accuracy. The findings also showed that the most significant factors influencing childhood malnutrition were family affluence, sanitation availability, mother education, and polygenic risk scores. The Bayesian measurement error approach improved posterior stability and probabilistic calibration by effectively accounting for uncertainty and errors in anthropometric and survey-based health data. Explainable AI techniques also improved transparency and made it easier to identify important environmental and genetic risk factors. All things considered, the suggested approach shows great promise for use in genetic epidemiology, precision nutrition, and AI-driven healthcare analytics. An inventive and reliable approach for early malnutrition risk diagnosis, focused nutritional therapies, and evidence-based public health policy creation is provided by the combination of Bayesian inference, genetic analytics, and sophisticated machine learning. To further enhance predictive healthcare decision-making, future research may expand the framework by integrating multiomics, longitudinal genetic data, and real-time nutritional surveillance systems.

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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.

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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