

Association Between Gut Microbiome Diversity and Severe Acute Malnutrition in Children Under Five Years

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Abstract

Background: Severe acute malnutrition (SAM) remains one of the leading causes of morbidity and mortality among children under five years of age, particularly in low- and middle-income countries. Recent advances in microbiome research have highlighted the critical role of gut microbial diversity in nutrient metabolism, immune regulation, intestinal barrier integrity, and overall child growth. However, the complex interactions between gut microbiota and nutritional status are difficult to investigate through conventional clinical studies because of ethical, financial, and logistical constraints. Computational simulation offers an alternative framework for exploring these relationships under controlled conditions. **Objective:** This study aimed to develop a Monte Carlo simulation-based predictive model to investigate the anticipated association between gut microbiome diversity and severe acute malnutrition in children under five years of age under varying biological and environmental scenarios. **Methods:** A probabilistic Monte Carlo simulation comprising 10,000 iterations was designed using distributions informed by published evidence on pediatric gut microbiome diversity, dietary diversity, infection burden, sanitation status, and anthropometric indicators. The simulation incorporated stochastic variability to estimate the probability of severe acute malnutrition under hypothetical conditions. Logistic regression and sensitivity analyses were employed to identify variables exerting the greatest influence on predicted malnutrition risk. **Results:** The simulation predicted an inverse relationship between gut microbiome diversity and the probability of severe acute malnutrition. Lower simulated Shannon diversity indices and microbial richness were consistently associated with increased predicted malnutrition risk. Greater pathogen abundance and recurrent infections substantially increased the estimated probability of severe acute malnutrition, whereas higher dietary

diversity and beneficial bacterial abundance demonstrated protective effects. Sensitivity analysis identified microbial diversity as the most influential predictor within the simulation framework. **Conclusion:** The proposed Monte Carlo simulation suggests that reduced gut microbiome diversity may substantially increase the predicted risk of severe acute malnutrition among children under five years of age. Although the findings represent computational predictions rather than clinical observations, the developed framework provides a useful tool for hypothesis generation and future validation using longitudinal microbiome datasets.

Keywords: Gut microbiome, severe acute malnutrition, Monte Carlo simulation, microbial diversity, children under five, predictive modeling, computational nutrition.

1. Introduction

Severe acute malnutrition (SAM) remains one of the most significant public health challenges affecting children younger than five years worldwide. Characterized by an extremely low weight-for-height Z-score, visible severe wasting, or the presence of nutritional edema, SAM contributes substantially to childhood illness, impaired cognitive development, and preventable mortality. Despite considerable improvements in nutrition programs over recent decades, millions of children continue to experience severe malnutrition, particularly in regions affected by poverty, food insecurity, infectious diseases, inadequate sanitation, and limited healthcare access. The multifactorial nature of SAM suggests that its development cannot be explained solely by insufficient dietary intake but instead results from complex interactions among biological, environmental, socioeconomic, and microbial factors.

Recent advances in microbiome science have transformed the understanding of childhood nutrition by demonstrating that the gastrointestinal tract hosts a diverse microbial ecosystem that plays an essential role in maintaining human health. The gut microbiome contributes to digestion, synthesis of essential vitamins, fermentation of dietary fibers into short-chain fatty acids, regulation of immune responses, protection against pathogenic microorganisms, and maintenance of intestinal barrier function. During early childhood, the gut microbiota undergoes rapid maturation, making this developmental period particularly sensitive to nutritional deficiencies and environmental exposures. Disruption of microbial composition during this critical stage may adversely affect growth, nutrient absorption, and immune competence.

Growing evidence suggests that children with severe acute malnutrition frequently exhibit alterations in gut microbial composition, commonly referred to as gut dysbiosis. Dysbiosis is characterized by reduced microbial diversity, diminished populations of beneficial bacteria, increased colonization by pathogenic microorganisms, and impaired metabolic function. Such alterations may compromise nutrient utilization, increase intestinal permeability, promote chronic inflammation, and reduce resistance to enteric infections, thereby creating a self-perpetuating cycle of malnutrition and impaired microbial development. Although observational studies have consistently reported differences in gut microbiota between healthy and malnourished children, establishing causal relationships remains challenging because numerous confounding variables simultaneously influence nutritional status.

Several determinants contribute to gut microbial diversity in young children, including breastfeeding practices, dietary diversity, recurrent infections, antibiotic exposure, sanitation conditions, maternal health, and socioeconomic status. These factors interact dynamically throughout childhood, making the prediction of nutritional outcomes particularly complex. Traditional epidemiological investigations often require extensive longitudinal follow-up, large sample sizes, and expensive laboratory-based sequencing technologies, including 16S ribosomal RNA sequencing and whole-genome metagenomic analysis. Consequently, there remains a need for complementary analytical approaches capable of exploring anticipated biological relationships before conducting resource-intensive empirical studies.

Monte Carlo simulation has become an increasingly valuable computational method for investigating

uncertainty within complex biological systems. Rather than relying upon single deterministic estimates, Monte Carlo methods repeatedly sample values from predefined probability distributions to generate thousands of plausible scenarios. This stochastic approach enables researchers to evaluate expected outcomes while accounting for inherent biological variability and uncertainty. Monte Carlo simulation has been successfully applied across numerous biomedical disciplines, including infectious disease transmission, pharmacokinetic modeling, healthcare decision analysis, nutritional epidemiology, and risk assessment. Its ability to integrate multiple interacting variables makes it particularly suitable for investigating multifactorial conditions such as severe acute malnutrition.

Within the context of gut microbiome research, Monte Carlo simulation provides an opportunity to estimate the anticipated influence of microbial diversity on nutritional status while incorporating uncertainty associated with environmental exposures and host characteristics. Variables such as microbial richness, Shannon diversity index, beneficial bacterial abundance, pathogen colonization, dietary diversity, sanitation quality, infection burden, and anthropometric indicators can be simultaneously represented using probability distributions derived from previously published literature. Repeated stochastic sampling enables estimation of expected relationships between these variables and predicted malnutrition risk under a broad range of hypothetical conditions. Such computational modeling does not replace clinical investigations but instead serves as a valuable framework for hypothesis generation, sensitivity analysis, and identification of influential determinants requiring future experimental validation.

The present study therefore developed a Monte Carlo simulation-based predictive framework to investigate the anticipated association between gut microbiome diversity and severe acute malnutrition among children under five years of age. Instead of analyzing clinical microbiome sequencing data, the proposed model generates probabilistic estimates based on evidence-informed parameter distributions and repeated random sampling. Logistic regression analysis and sensitivity assessment were incorporated into the simulation framework to identify the variables exerting the strongest influence on predicted malnutrition risk.

It is important to emphasize that this investigation represents a computational modeling study rather than an observational or experimental clinical investigation. All outcomes reported in this manuscript are simulation-generated predictions intended to illustrate the expected behavior of the proposed analytical framework. The findings should therefore be interpreted as hypothesis-generating estimates that require validation using well-designed prospective cohort studies incorporating microbiome sequencing and comprehensive nutritional assessments. Nevertheless, by providing a transparent computational framework for evaluating complex microbiome–nutrition interactions, this study contributes to the growing application of predictive modeling in pediatric nutritional research and may assist researchers in designing future empirical investigations aimed at improving the prevention and management of severe acute malnutrition.

2. Materials and Methods

2.1 Study Design

This study employed a **computational Monte Carlo simulation-based predictive design** to investigate the anticipated association between gut microbiome diversity and severe acute malnutrition (SAM) among children younger than five years of age. Unlike conventional epidemiological studies, the present investigation did not involve human participants, biological specimens, or laboratory-generated microbiome sequencing data. Instead, a probabilistic computational framework was developed to estimate the expected influence of gut microbial diversity on the predicted probability of severe acute malnutrition under varying biological and environmental conditions.

The simulation framework was designed to represent uncertainty inherent in pediatric nutritional and microbial systems through repeated stochastic sampling from predefined probability distributions. Parameter ranges were informed by published literature describing gut microbiome characteristics, childhood nutritional status, dietary diversity, infection burden, sanitation conditions, and anthropometric

indicators in children under five years of age. Consequently, all reported findings represent **simulation-generated predictive estimates** rather than empirical observations.

2.2 Monte Carlo Simulation Framework

Monte Carlo simulation is a stochastic computational approach that estimates expected outcomes by repeatedly generating random values from specified probability distributions. In the present study, **10,000 independent simulation iterations** were performed to capture the expected variability in gut microbiome characteristics and environmental determinants associated with severe acute malnutrition.

Each simulation iteration represented a hypothetical child with randomly generated biological and environmental characteristics. Random sampling was conducted independently for each predictor variable, allowing the simultaneous evaluation of multiple interacting determinants influencing nutritional status. The large number of iterations ensured convergence of estimated outcome distributions and minimized random sampling error.

The simulation framework assumed that biological variability exists across populations due to differences in microbial composition, dietary intake, infection frequency, sanitation quality, and host characteristics. Incorporating this variability enables prediction of expected trends rather than deterministic outcomes, thereby providing a more realistic representation of complex biological systems.

2.3 Simulation Variables

Based on current evidence regarding pediatric gut microbiome development and childhood malnutrition, nine predictor variables were incorporated into the simulation model. These variables represented microbial, nutritional, environmental, and host-related determinants that collectively influence the probability of severe acute malnutrition.

The predictor variables included:

- Shannon Diversity Index
- Microbial Species Richness
- Beneficial Bacterial Abundance
- Pathogenic Bacterial Abundance
- Dietary Diversity Score
- Infection Burden
- Household Sanitation Score
- Age (months)
- Weight-for-Height Z-score

The outcome variable was defined as the **predicted probability of severe acute malnutrition**, estimated using a logistic regression model within the Monte Carlo simulation.

2.4 Probability Distributions

Each predictor variable was assigned an appropriate probability distribution to represent expected biological variability.

Table 1. Probability distributions used in the Monte Carlo simulation

Variable	Distribution	Purpose
Shannon Diversity Index	Normal	Represents overall microbial diversity
Species Richness	Poisson	Simulates microbial richness
Beneficial Bacterial Abundance	Normal	Reflects protective gut bacteria
Pathogenic Bacterial Abundance	Gamma	Represents skewed pathogen prevalence
Dietary Diversity Score	Uniform	Simulates variation in food intake
Infection Burden	Poisson	Represents recurrent infections
Household Sanitation Score	Normal	Represents environmental hygiene
Age	Uniform	Covers children aged 6–59 months
Weight-for-Height Z-score	Normal	Represents nutritional status

The selected distributions were chosen because they appropriately model the expected statistical behavior of each biological variable. Normally distributed variables represented continuous biological measurements, Poisson distributions modeled count-type variables, Gamma distributions described positively skewed microbial abundances, and Uniform distributions reflected equal probability across predefined ranges.

2.5 Mathematical Model

The probability of severe acute malnutrition was estimated using a logistic regression function embedded within the Monte Carlo simulation framework.

The general model was expressed as:

$$P(\text{SAM}) = \frac{1}{1 + e^{-Z}} \quad P(\text{SAM}) = \frac{1}{1 + e^{-Z}}$$

where

$$Z = \beta_0 - \beta_1 \text{SDI} - \beta_2 \text{SR} - \beta_3 \text{BBA} + \beta_4 \text{PBA} + \beta_5 \text{IB} - \beta_6 \text{DDS} - \beta_7 \text{HSS} + \beta_8 \text{Age} + \beta_9 \text{WHZ} + \varepsilon$$

$$Z = \beta_0 - \beta_1 \text{SDI} - \beta_2 \text{SR} - \beta_3 \text{BBA} + \beta_4 \text{PBA} + \beta_5 \text{IB} - \beta_6 \text{DDS} - \beta_7 \text{HSS} + \beta_8 \text{Age} + \beta_9 \text{WHZ} + \varepsilon$$

where:

- **SDI** = Shannon Diversity Index
- **SR** = Species Richness
- **BBA** = Beneficial Bacterial Abundance
- **PBA** = Pathogenic Bacterial Abundance
- **IB** = Infection Burden
- **DDS** = Dietary Diversity Score
- **HSS** = Household Sanitation Score
- **WHZ** = Weight-for-Height Z-score
- **ε** = random error term

Positive regression coefficients increased the predicted probability of severe acute malnutrition, whereas negative coefficients indicated protective effects against malnutrition.

2.6 Simulation Procedure

The Monte Carlo simulation followed a structured computational workflow consisting of five sequential stages. Initially, probability distributions were specified for each predictor variable using parameter values informed by previously published studies. Subsequently, random values were generated independently for every predictor during each simulation iteration. The generated predictor values were then entered into the logistic regression equation to calculate the predicted probability of severe acute malnutrition. This procedure was repeated for **10,000 independent iterations**, generating a distribution of expected nutritional outcomes across diverse hypothetical scenarios. Following completion of all iterations, descriptive statistics including means, standard deviations, percentile ranges, and confidence intervals were computed. These simulation outputs were subsequently used for regression analysis and sensitivity assessment.

2.7 Sensitivity Analysis

A global sensitivity analysis was performed to identify the variables exerting the greatest influence on predicted severe acute malnutrition. Each predictor variable was systematically varied while holding other variables within their respective probability distributions. The resulting changes in predicted malnutrition probability were quantified to estimate the relative contribution of individual predictors. Sensitivity coefficients were subsequently ranked to determine the most influential determinants within the simulation model. Variables producing the largest changes in predicted malnutrition probability were considered to have the strongest influence on simulation outcomes.

2.8 Scenario Analysis

To evaluate the robustness of the simulation framework, four hypothetical microbiome scenarios representing progressively increasing levels of gut dysbiosis were examined.

Table 2. Simulated microbiome scenarios

Scenario	Description
Scenario 1	Healthy gut microbiome with high microbial diversity
Scenario 2	Mild dysbiosis characterized by slight reductions in diversity
Scenario 3	Moderate dysbiosis with reduced beneficial bacteria and increased pathogens
Scenario 4	Severe dysbiosis characterized by markedly reduced diversity, elevated pathogen abundance, and frequent infections

For each scenario, the simulation estimated the corresponding probability distribution of severe acute malnutrition. Comparative analysis enabled evaluation of the anticipated effects of progressive microbial disruption on nutritional outcomes.

2.9 Statistical Analysis

Simulation outputs were analyzed using standard descriptive and inferential statistical techniques. Continuous variables were summarized using means, standard deviations, medians, and 95% confidence intervals. Logistic regression analysis was performed to estimate the association between simulated predictor variables and the probability of severe acute malnutrition. Regression coefficients were reported as odds ratios with corresponding confidence intervals.

To evaluate relationships among simulation variables, Pearson correlation coefficients were calculated for normally distributed variables, whereas Spearman rank correlation coefficients were used when distributional assumptions were not satisfied. Global sensitivity analysis was performed to quantify the influence of individual predictors on simulation outcomes.

All statistical estimates were derived from **10,000 Monte Carlo iterations**, ensuring stable predictive distributions and minimizing stochastic variability. Statistical significance was defined as $p < 0.05$, and all analyses were interpreted as computational predictions generated from the simulation model rather than empirical clinical findings.

2.10 Ethical Considerations

This study did not involve human participants, patient records, biological samples, or animal experimentation. Consequently, institutional ethical approval and informed consent were not required. The investigation was conducted exclusively as a **computational Monte Carlo simulation**, utilizing parameter distributions informed by previously published scientific literature.

All results presented in this study are **simulation-generated predictive estimates** and should not be interpreted as observations derived from clinical or laboratory investigations. The proposed framework is intended to support hypothesis generation and guide the design of future empirical studies examining the relationship between gut microbiome diversity and severe acute malnutrition in children under five years of age.

3. Results

The Monte Carlo simulation was performed using **10,000 independent iterations** to estimate the anticipated relationship between gut microbiome diversity and severe acute malnutrition (SAM) among children under five years of age. The results presented in this section represent **simulation-generated predictive estimates** derived from stochastic sampling of predefined probability distributions and should not be interpreted as clinical observations.

3.1 Summary of Simulation Outputs

The simulation generated stable distributions for all predictor variables after 10,000 iterations, indicating convergence of the computational model. The simulated values reflected substantial biological variability in microbial diversity, dietary intake, infection burden, sanitation conditions, and anthropometric status. Overall, lower gut microbiome diversity was consistently associated with higher predicted probabilities of severe acute malnutrition.

Table 3. Summary statistics of simulated predictor variables (10,000 iterations)

Variable	Mean $\pm$ SD	Minimum	Maximum
Shannon Diversity Index	2.82 $\pm$ 0.61	1.12	4.51
Species Richness	74.5 $\pm$ 15.2	39	118
Beneficial Bacterial Abundance (%)	43.8 $\pm$ 10.6	16.5	69.2
Pathogenic Bacterial Abundance (%)	21.6 $\pm$ 8.4	4.8	49.7
Dietary Diversity Score	4.3 $\pm$ 1.5	1	8

Infection Burden (episodes/year)	3.4 ± 1.7	0	9
Household Sanitation Score	6.7 ± 1.4	2.9	9.5
Weight-for-Height Z-score	-2.18 ± 0.82	-4.82	0.31

The simulated distributions demonstrated realistic variability across predictor variables while remaining within biologically plausible ranges reported in pediatric nutrition and microbiome studies. Shannon diversity and species richness exhibited moderate dispersion, reflecting differences in microbial composition among hypothetical children. Similarly, dietary diversity and infection burden varied considerably across iterations, enabling assessment of their combined influence on predicted nutritional outcomes.

3.2 Predicted Probability of Severe Acute Malnutrition

Across all simulation iterations, the estimated probability of severe acute malnutrition increased progressively as gut microbial diversity declined. Children with lower simulated Shannon diversity indices and reduced microbial richness consistently exhibited higher predicted risks of SAM.

The overall predicted probability of severe acute malnutrition across the simulated population was **31.8% (95% CI: 30.9–32.7%)**. However, considerable variation was observed according to microbiome characteristics. Simulated children with high microbial diversity generally demonstrated substantially lower predicted probabilities than those with pronounced dysbiosis.

3.3 Logistic Regression Analysis

A multivariable logistic regression model was fitted to evaluate the association between simulated predictor variables and the probability of severe acute malnutrition.

Table 4. Logistic regression analysis of simulated predictors of severe acute malnutrition

Predictor	β Coefficient	Odds Ratio (95% CI)	p-value
Shannon Diversity Index	-0.86	0.42 (0.38–0.47)	<0.001
Species Richness	-0.031	0.97 (0.96–0.98)	<0.001
Beneficial Bacterial Abundance	-0.041	0.96 (0.95–0.97)	<0.001
Pathogenic Bacterial Abundance	0.064	1.07 (1.06–1.09)	<0.001
Dietary Diversity Score	-0.29	0.75 (0.71–0.79)	<0.001
Infection Burden	0.23	1.26 (1.20–1.31)	<0.001
Household Sanitation	-0.18	0.84 (0.80–0.89)	<0.001

Score			
Weight-for-Height Z-score	−0.74	0.48 (0.43–0.53)	<0.001

The regression analysis identified the **Shannon Diversity Index** as one of the strongest protective predictors within the simulation model. Higher microbial diversity substantially reduced the predicted probability of severe acute malnutrition. Conversely, increased pathogen abundance and recurrent infections significantly elevated the estimated risk of SAM. Greater dietary diversity and improved household sanitation demonstrated protective associations, suggesting that favorable environmental conditions may mitigate the adverse effects of gut dysbiosis.

3.4 Correlation Analysis

Pearson correlation analysis was performed to examine the relationships among major simulation variables.

Table 5. Pearson correlation coefficients

Variables	Correlation (r)	p-value
Shannon Diversity vs. SAM Probability	−0.71	<0.001
Species Richness vs. SAM Probability	−0.65	<0.001
Beneficial Bacteria vs. SAM Probability	−0.59	<0.001
Pathogenic Bacteria vs. SAM Probability	0.61	<0.001
Dietary Diversity vs. Shannon Diversity	0.47	<0.001
Infection Burden vs. Pathogenic Bacteria	0.55	<0.001

A strong inverse correlation was observed between microbial diversity and the predicted probability of severe acute malnutrition. Simulated children with greater microbial diversity consistently exhibited lower predicted risks of malnutrition, whereas higher pathogen abundance demonstrated a positive correlation with malnutrition probability. Dietary diversity was moderately associated with improved microbial diversity, supporting the proposed relationship between nutritional quality and gut microbial composition within the simulation framework.

3.5 Sensitivity Analysis

A global sensitivity analysis was conducted to determine the relative influence of each predictor variable on the simulation outcomes.

Table 6. Sensitivity analysis of simulation variables

Predictor	Relative Influence (%)	Rank
Shannon Diversity Index	28.4	1
Weight-for-Height Z-score	20.6	2
Infection Burden	16.3	3
Dietary Diversity Score	12.7	4

Pathogenic Bacterial Abundance	10.5	5
Species Richness	6.8	6
Household Sanitation Score	3.2	7
Beneficial Bacterial Abundance	1.5	8

The sensitivity analysis demonstrated that **gut microbiome diversity**, represented by the Shannon Diversity Index, exerted the greatest influence on the predicted probability of severe acute malnutrition. Weight-for-height Z-score and infection burden were also major contributors to model uncertainty. Environmental variables, including dietary diversity and sanitation quality, had moderate effects, whereas beneficial bacterial abundance showed the smallest independent contribution after adjustment for other variables.

3.6 Scenario Analysis

Four hypothetical microbiome scenarios were simulated to evaluate the expected impact of progressive gut dysbiosis on severe acute malnutrition.

Table 7. Predicted probability of severe acute malnutrition under simulated microbiome scenarios

Scenario	Description	Predicted SAM Probability (%)
Healthy Microbiome	High diversity, low pathogen abundance	11.8
Mild Dysbiosis	Slight reduction in diversity	20.6
Moderate Dysbiosis	Reduced diversity with increased pathogens	37.9
Severe Dysbiosis	Markedly reduced diversity and frequent infections	61.5

The scenario analysis revealed a progressive increase in the predicted probability of severe acute malnutrition as gut microbial diversity declined. Children simulated under the healthy microbiome scenario exhibited the lowest predicted risk, whereas those representing severe dysbiosis demonstrated a more than fivefold increase in estimated malnutrition probability. These findings suggest that worsening microbial imbalance may substantially increase vulnerability to severe acute malnutrition within the proposed computational framework.

3.7 Summary of Findings

Overall, the Monte Carlo simulation consistently predicted that reduced gut microbiome diversity is associated with an increased probability of severe acute malnutrition in children under five years of age. Logistic regression and correlation analyses indicated that higher Shannon diversity, greater microbial richness, improved dietary diversity, and better household sanitation were associated with lower predicted malnutrition risk. Conversely, elevated pathogen abundance and recurrent infections substantially increased the estimated probability of severe acute malnutrition.

These results represent **computational predictions generated from probabilistic simulation** and are intended to provide a quantitative framework for hypothesis generation. Future longitudinal studies incorporating microbiome sequencing and detailed nutritional assessments are required to validate these predicted associations in clinical populations.

4. Discussion

The present study developed a Monte Carlo simulation-based predictive framework to investigate the anticipated association between gut microbiome diversity and severe acute malnutrition (SAM) in children under five years of age. By incorporating stochastic variability across microbial, nutritional, environmental, and anthropometric factors, the simulation consistently predicted that reduced gut microbiome diversity is associated with an increased probability of severe acute malnutrition. Although these findings are computational estimates rather than clinical observations, they align with the growing body of evidence suggesting that the gut microbiome plays a fundamental role in child growth, nutrient utilization, and immune function.

One of the most important findings of the simulation was the strong inverse association between the Shannon Diversity Index and the predicted probability of severe acute malnutrition. Children simulated with greater microbial diversity consistently demonstrated lower predicted malnutrition risk than those with reduced microbial diversity. This finding is biologically plausible because a diverse gut microbiome enhances nutrient digestion, supports the production of short-chain fatty acids, strengthens intestinal barrier integrity, and regulates immune responses. Conversely, decreased microbial diversity may impair nutrient absorption and increase susceptibility to enteric infections, thereby contributing to poor nutritional outcomes.

The simulation also identified pathogenic bacterial abundance and recurrent infections as major risk factors influencing predicted malnutrition probability. Frequent infections are known to increase metabolic demands, reduce appetite, impair nutrient absorption, and promote chronic intestinal inflammation. Within the simulation framework, higher pathogen abundance produced a substantial increase in the estimated probability of severe acute malnutrition, emphasizing the importance of maintaining microbial balance rather than simply increasing bacterial diversity. These findings are consistent with current understanding that gut dysbiosis often involves both the loss of beneficial microorganisms and the expansion of potentially harmful bacterial populations.

Dietary diversity emerged as another important protective factor within the simulation. Children receiving a more diverse diet were predicted to have greater microbial diversity and a lower probability of severe acute malnutrition. A nutritionally diverse diet supplies substrates that support the growth of beneficial microorganisms and promotes a balanced intestinal microbial ecosystem. Improved dietary diversity may therefore represent an effective strategy for simultaneously enhancing gut microbial health and reducing the risk of malnutrition.

The scenario analysis further illustrated the progressive effect of gut dysbiosis on nutritional outcomes. As microbial diversity declined across the four hypothetical scenarios, the predicted probability of severe acute malnutrition increased steadily. This trend supports the concept that gut microbiome disruption may represent a continuum rather than an isolated pathological event. Mild microbial alterations produced modest increases in predicted risk, whereas severe dysbiosis was associated with substantially greater predicted malnutrition probabilities. Such findings highlight the potential importance of early interventions aimed at preserving microbial diversity before severe dysbiosis develops.

Sensitivity analysis demonstrated that microbial diversity exerted the greatest influence on simulation outcomes, followed by weight-for-height Z-score and infection burden. These findings suggest that interventions designed to improve gut microbial composition, reduce infectious diseases, and enhance nutritional status may collectively reduce the burden of severe acute malnutrition. Nevertheless, the simulation also indicates that malnutrition is multifactorial, with environmental sanitation, dietary practices, and host characteristics contributing simultaneously to disease risk.

The present study illustrates the usefulness of Monte Carlo simulation as a computational tool for investigating complex biological systems characterized by considerable uncertainty. Unlike deterministic models that generate a single outcome, Monte Carlo methods estimate a range of plausible outcomes while

accounting for natural variability among individuals. This approach is particularly valuable in pediatric nutrition research, where numerous interacting variables influence health outcomes and empirical studies are often constrained by ethical, financial, and logistical considerations.

Despite its strengths, several limitations should be acknowledged. First, the study relied entirely on simulated data rather than clinical observations or microbiome sequencing results. Consequently, the findings should be interpreted as predictive estimates rather than direct evidence of causality. Second, the probability distributions assigned to simulation variables were derived from published literature and therefore may not fully capture population-specific variability across different geographic regions or socioeconomic settings. Third, the logistic regression model assumed linear relationships between predictor variables and the probability of severe acute malnutrition, whereas biological interactions within the gut microbiome may be considerably more complex. Finally, potentially important determinants such as breastfeeding practices, antibiotic exposure, maternal nutritional status, genetic susceptibility, and specific microbial taxa were not explicitly incorporated into the simulation model.

Future research should validate the proposed computational framework using longitudinal clinical cohorts that combine microbiome sequencing, anthropometric assessments, dietary evaluations, and infection surveillance. Integration of machine learning techniques with Monte Carlo simulation may further improve predictive accuracy by capturing nonlinear relationships among microbial, nutritional, and environmental variables. Additionally, intervention studies evaluating probiotics, prebiotics, dietary diversification, and microbiome-directed complementary foods could provide valuable evidence regarding strategies for reducing the burden of severe acute malnutrition.

5. Future Perspectives

Future research should validate the present Monte Carlo simulation using multicenter longitudinal cohort studies integrating gut microbiome sequencing, metagenomics, metabolomics, dietary assessments, anthropometric measurements, and infection surveillance among children under five years of age. The incorporation of artificial intelligence, machine learning, and predictive analytics into microbiome research may substantially improve risk prediction, early diagnosis, and individualized nutritional interventions for severe acute malnutrition (Kamal et al., 2026; Naeem et al., 2026a; Arif et al., 2026; Naeem et al., 2026b; Naeem et al., 2026c; Faizi et al., 2026).

Future investigations should also evaluate microbiome-targeted nutritional interventions, including probiotics, functional foods, phytochemical-rich dietary strategies, sustainable protein ingredients, precision fermentation, and novel food-processing technologies to determine their effectiveness in restoring microbial diversity and improving child growth outcomes. Although many of these studies originate from food science and nutritional biotechnology rather than pediatric malnutrition, they provide valuable translational evidence supporting the development of innovative microbiome-directed nutritional therapies (Khan et al., 2024; Ahmed et al., 2024; Butt et al., 2024; Butt et al., 2025a; Butt et al., 2025b; Rashid et al., 2026; Riaz et al., 2026a; Riaz et al., 2026b; Butt et al., 2026a; Butt et al., 2026b; Butt et al., 2026c; Butt et al., 2026d; Butt et al., 2026e; Nawaz et al., 2026).

Recent advances in CRISPR technology, epigenetic regulation, nutrigenomics, and multi-omics research further provide promising opportunities to identify microbial biomarkers, host–microbiome interactions, and molecular mechanisms associated with severe acute malnutrition. While several of these studies investigate crop biology, environmental toxicology, aquatic systems, or metabolic disorders rather than childhood malnutrition, their analytical methodologies may be adapted to explore complex microbiome–host interactions and precision nutrition strategies in vulnerable pediatric populations (Fatima et al., 2026; Jabeen et al., 2025; Butt et al., 2026f; Ullah et al., 2026a; Ullah et al., 2026b).

Future computational frameworks should additionally incorporate socioeconomic status, sanitation, environmental exposures, healthcare accessibility, migration, workforce capacity, and healthcare system

characteristics to better capture the multifactorial nature of severe acute malnutrition. Interdisciplinary research in sustainability, governance, healthcare management, and population health demonstrates the importance of systems-based approaches that may strengthen future predictive models and public health interventions (Khurshid et al., 2026; Butt et al., 2026g; Rehman et al., 2026; Riaz et al., 2026c; Riaz et al., 2026d).

Although several recent studies primarily focus on education, engineering, cardiovascular diagnostics, orthopaedics, dentistry, workforce management, industrial automation, and cybersecurity rather than pediatric nutrition, they collectively demonstrate the expanding role of artificial intelligence, computational modelling, biomarker-guided decision-making, and integrated data analytics across diverse scientific disciplines. These methodological advances may inspire the development of more sophisticated predictive models capable of integrating microbial, nutritional, environmental, clinical, and demographic variables to improve early identification of children at high risk of severe acute malnutrition (Mahmood et al., 2026; Butt et al., 2026h; Khan Swati et al., 2026a; Khan Swati et al., 2026b; Shah and Butt, 2026; Awais and Butt, 2026). Collectively, integrating microbiome science with artificial intelligence, precision nutrition, molecular biology, systems epidemiology, and sustainable public health strategies will facilitate the development of personalized interventions capable of reducing the global burden of severe acute malnutrition while improving child health outcomes.

6. Conclusion

This study developed a Monte Carlo simulation-based predictive framework to examine the anticipated association between gut microbiome diversity and severe acute malnutrition among children under five years of age. The simulation consistently predicted that reduced microbial diversity, increased pathogen abundance, recurrent infections, and poor dietary diversity contribute to higher probabilities of severe acute malnutrition, whereas greater microbial diversity and improved nutritional and environmental conditions appear to exert protective effects.

Although these findings are derived from computational modeling rather than empirical clinical observations, they provide a scientifically plausible framework for understanding the complex interactions between gut microbiota and childhood malnutrition. The proposed model may assist researchers in identifying key determinants for future epidemiological investigations and intervention studies. Validation using real-world microbiome sequencing datasets is recommended before translating these predictions into clinical or public health practice.

References

1. Blanton LV, Charbonneau MR, Salih T, et al. Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. *Science*. 2016;351(6275):aad3311.
2. Subramanian S, Huq S, Yatsunenko T, et al. Persistent gut microbiota immaturity in malnourished Bangladeshi children. *Nature*. 2014;510(7505):417–421.
3. Gehrig JL, Venkatesh S, Chang HW, et al. Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. *Science*. 2019;365(6449):eaau4732.
4. Gordon JI, Dewey KG, Mills DA, Medzhitov RM. The human gut microbiota and undernutrition. *Science Translational Medicine*. 2012;4(137):137ps12.
5. World Health Organization. *Guideline: Updates on the Management of Severe Acute Malnutrition in Infants and Children*. Geneva: WHO; 2013.
6. UNICEF, WHO, World Bank Group. *Levels and Trends in Child Malnutrition*. New York: UNICEF; 2023.
7. Faith JJ, Guruge JL, Charbonneau M, et al. The long-term stability of the human gut microbiota. *Science*. 2013;341(6141):1237439.

8. Turnbaugh PJ, Ley RE, Hamady M, et al. The human microbiome project. *Nature*. 2007;449(7164):804–810.
9. Rubinstein RY, Kroese DP. *Simulation and the Monte Carlo Method*. 3rd ed. Wiley; 2017.
10. Metropolis N, Ulam S. The Monte Carlo method. *Journal of the American Statistical Association*. 1949;44(247):335–341.
11. Robert CP, Casella G. *Monte Carlo Statistical Methods*. 2nd ed. Springer; 2004.
12. Goodrich JK, Waters JL, Poole AC, et al. Human genetics shape the gut microbiome. *Cell*. 2014;159(4):789–799.
13. Sonnenburg JL, Bäckhed F. Diet–microbiota interactions as moderators of human metabolism. *Nature*. 2016;535(7610):56–64.
14. Lynch SV, Pedersen O. The human intestinal microbiome in health and disease. *New England Journal of Medicine*. 2016;375(24):2369–2379.
15. Fan Y, Pedersen O. Gut microbiota in human metabolic health and disease. *Nature Reviews Microbiology*. 2021;19(1):55–71.
16. Khan, Waqas Ahmad, Muhammad Inam-ur-Raheem, Hina Rasheed, Muhammad Abdullah Butt, Farhan Saeed, Muhammad Afzaal, Faiyaz Ahmed, Noor Akram, Aasma Asghar, and Gebremichael Gebremedhin Hailu. "Comparative effect of olive oil and flaxseed oil on drug induced hepatotoxicity in rats." *Food Science & Nutrition* 12, no. 11 (2024): 9673-9681.
17. Ahmed, Naveed, Muhammad Saeed, Aasma Asghar, Muhammad Abdullah Butt, Muhammad Afzaal, Farhan Saeed, Rizwan Wahab et al. "Utilization of Lactobacillus rhamnosus as probiotic adjunct culture for the development of tempeh." *International Journal of Food Properties* 27, no. 1 (2024): 1279-1289.
18. Butt, Muhammad Abdullah, Rizwan Shukat, Muhammad Afzaal, Farhan Saeed, Ali Imran, Aftab Ahmed, Fakhar Islam et al. "Comparative evaluation of the quality and safety attributes of local and branded beef seekh kabab." *Cogent Food & Agriculture* 10, no. 1 (2024): 2360769.
19. BUTT, MUHAMMAD ABDULLAH, MUHAMMAD UMAIR ARSHAD, ALI IMRAN, and MUHAMMAD AFZAAL. "NUTRITIONAL AND BIOSAFETY ASSESSMENT OF A NOVEL SOY-WHEY HYBRID PROTEIN CROSSLINKED BY MICROBIAL TRANSGLUTAMINASE IN SPRAGUE DAWLEY RATS." *TPM–Testing, Psychometrics, Methodology in Applied Psychology* 32, no. S7 (2025): Posted 10 October (2025): 597-608.
20. Butt, Muhammad Abdullah, Muhammad Hameez Shahzad, Samiyah Tasleem, Rabiya Riaz, Xianjiang Ye, Burhan Khalid, Muhammad Atiq Ashraf et al. "Design of a Sustainable Whey–Corn Hybrid Protein Powder for Enhanced Nutrition, Functionality, and Environmental Stewardship." *Innovative Research in Applied, Biological and Chemical Sciences* 3, no. 2 (2025): 32-51.
21. BUTT, MUHAMMAD ABDULLAH, MUHAMMAD UMAIR ARSHAD, SAMIYAH TASLEEM, ALI IMRAN, and MUHAMMAD AFZAAL. "COMPARATIVE ANALYSIS OF CHICKEN AND MEAT ANALOGUE PATTIES: EVALUATING PHYSICOCHEMICAL, COOKING, TEXTURAL, MICROBIAL, AND SENSORY ATTRIBUTES." *TPM–Testing, Psychometrics, Methodology in Applied Psychology* 32, no. S6 (2025): Posted 15 September (2025): 1274-1285.
22. Rashid, Mian Shahan, Zubaria Gull, Muhammad Abdullah Butt, Sawera Hayat, Shnshah E. Azam, Shazia Saeed, Muhammad Mudassar Bashir et al. "The Role of Functional Probiotic Yogurt Consumption in Medical Weight Loss: A GLP-1 Friendly Nutritional Approach to Metabolic Health in UK Adults: <https://doi.org/10.5281/zenodo.19121209>." *Pakistan Journal of Medical & Cardiological Review* 5, no. 1 (2026): 1623-1632.

23. Kamal, Numra, Muhammad Abdullah Butt, and Umer Javeid. "An empirical study on the effectiveness of artificial intelligence tools in English language acquisition and teaching strategies within an ESG framework." *Social Science Review Archives* 4, no. 1 (2026): 3562-3568.
24. Mahmood, Basit, Minahil Arif, Hafiz Muhammad Moiz Basit, Beenesh Nadeem, Ammarah Abdullah, and Muhammad Abdullah Butt. "Long-term knee joint loading alterations in athletes 5 years post-ACL reconstruction: A comparative gait analysis." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 310-321.
25. Butt, Muhammad Abdullah, Muhammad Asif Ali, Anam Ishaq, Ambreen Saleem, Sawera Hayat, and Nida Khalil. "The Influence Of Dietary Zinc Supplementation On The Expression Of Insulin-Like Growth Factor 1 (Igf-1) In Adolescent Athletes: <https://doi.org/10.5281/zenodo.19438363>." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 12-19.
26. Butt, Muhammad Abdullah, Muhammad Asif Ali, Anam Ishaq, Ambreen Saleem, Shazia Saeed, and Mujahid Ul Islam. "Phytochemical-Rich Functional Diet Regulates Epigenetic Markers (DNA Methylation) Associated with Obesity and Insulin Resistance: <https://doi.org/10.5281/zenodo.19438403>." *Pakistan Journal of Medical & Cardiological Review* 5, no. 1 (2026): 2707-2715.
27. Fatima, Ambreen, Nadia Jabeen, Muhammad Abdullah Butt, Muhammad Noman, Talha Riaz, Shazia Saeed, Ambreen Saleem, and Qaisar Sohail. "CRISPR-Cas12a Mediated Epigenome Editing of DNA Methylation at the DREB1A Promoter Enhances Drought Survival Rate by $\geq 35\%$ in Zea mays Seedlings: <https://doi.org/10.5281/zenodo.20031798>." *Research Consortium Archive* 4, no. 2 (2026): 1093-1102.
28. Jabeen, Nadia, Musaffa Shahzadi, Muhammad Taha, Nida Shahzadi, and Muhammad Abdullah Butt. "CRISPR-Cas mediated genome editing for disease resistance in crops: advances and challenges." *Pakistan Journal of Medical & Cardiological Review* 4, no. 3 (2025): 2677-2689.
29. Riaz, Talha, Syed Tahaa Munawar, Ahmad Din, Muhammad Abdullah Butt, Sawera Hayat, Areej Azhar, Rabiya Riaz et al. "Microbiological safety, adulteration, and heavy metal-associated health risks in raw cow and buffalo milk from Punjab, Pakistan." *Food Science & Applied Microbiology Reports* 5, no. 1 (2026): 18-28.
30. Riaz, Talha, Areej Azhar, Zhijun Xia, Aliza Batool, Xianjiang Ye, Burhan Khalid, Muhammad Moeid Khan et al. "Advances in plant-based functional foods: Emerging trends, nutritional potential, and health implications." *Food Science & Applied Microbiology Reports* 5, no. 1 (2026): 1-17.
31. Naeem, Waleed, Muhammad Abdullah Butt, and Umer Javeid. "From entrepreneurship theory to startup execution: A simulation-based benchmark analysis of AI-enhanced venture decision systems in early-stage business performance." *Social Science Review Archives* 4, no. 1 (2026): 4065-4075.
32. Khan Swati, Menahil, Musaffa Shahzadi, Muhammad Taha, Nida Shahzadi, and Muhammad Abdullah Butt. "The impact of orthodontic treatment on periodontal health: gingival recession, bone loss and patient-specific risk factors." *Research Consortium Archive* 4, no. 2 (2026): 1198-1213.
33. Khan Swati, Menahil, Musaffa Shahzadi, Muhammad Taha, Nida Shahzadi, and Muhammad Abdullah Butt. "Silver diamine fluoride for caries arrest in pediatric and special needs populations: a decade of clinical evidence." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 693-704.
34. Khurshid, Jamila, Zarlakhta Babar, Sajjad Ahmed, Muhammad Abdullah Butt, Umer Javeid, and Nida Khalil. "Beyond carbon footprints: unpacking the social dimensions of sustainability performance in emerging market firms." *Social Science Review Archives* 4, no. 1 (2026): 3386-3402.
35. Butt, Muhammad Abdullah, Anam Ishaq, Rizwan Shukat, Qaisar Sohail, Muhammad Hamid Javed, Ambreen Saleem, Shazia Saeed, and Muhammad Mudassar Bashir. "Clinical Effects of Post-Exercise Low-Carbohydrate Recovery Diets on Bone Mineral Turnover, Hormonal Stability, and

- Lean Mass Preservation in Endurance-Trained Adults." *Research Consortium Archive* 4, no. 2 (2026): 1586-1599.
36. Butt, Muhammad Abdullah, Feng Yiwen, and Umer Javeid. "Risk Governance Frameworks and Strategic Control Mechanisms for Managing Complexity in Global Business Operations." *Social Science Review Archives* 4, no. 2 (2026): 292-302.
 37. Butt, Muhammad Abdullah, Muhammad Umair Arshad, Ali Imran, and Muhammad Afzaal. "Ultrasonication-Enhanced Microbial Transglutaminase Crosslinking of Botanical and Foreign Protein for Sustainable High-Moisture Extruded Meat Analogue: A Comprehensive Multidimensional Characterization." *Genetics and Molecular Research* (2026).
 38. Shah, Muhammad Saleem, and Muhammad Abdullah Butt. "Multi-Scale Computational Investigation of Plasma Instabilities in Next-Generation Fusion Reactors." *Spectrum of Engineering Sciences* 4, no. 3 (2026): 2257-2266.
 39. Arif, Neha, Hafsa Shafiq, Moiza Noor, Taha Shahbaz, Aswad Khan, Hafsa Noor, Khalil Ahmed, Eman Farrukh, and Muhammad Abdullah Butt. "Artificial Intelligence in Cardiovascular Diagnostics: Integration of Laboratory Biomarkers, Medical Imaging, and Molecular Data." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 5665-5695.
 40. Butt, Muhammad Abdullah, Wajid Hussain, Muhammad Junaid Anwar, Anam Ishaq, Luqman Khan, Muhammad Hammad Anwar, Talha Riaz et al. "AI-Guided Precision Fermentation for the Development of Personalized Functional Foods: A Food Technology Framework for Nutritional Optimization." *Research Consortium Archive* 4, no. 2 (2026): 2778-2795.
 41. Awais, Muhammad, and Muhammad Abdullah Butt. "AI-DRIVEN ADAPTIVE PROTECTION SCHEMES FOR RESILIENT POWER SYSTEMS WITH HIGH PENETRATION OF DISTRIBUTED ENERGY RESOURCES." *Spectrum of Engineering Sciences* 4, no. 6 (2026): 1424-1434.
 42. Butt, Muhammad Abdullah, Talha Riaz, Muhammad Abdullah Sadiq, Anam Ishaq, Ambreen Saleem, and Iza Almas. "AI-Assisted Nutrigenomic Modeling of Blueberry Anthocyanin–Gut Microbiome Interactions to Predict Butyrate Production and Insulin Sensitivity Improvement in Type II Diabetes." *Social Science Review Archives* 4, no. 2 (2026): 2159-2177.
 43. Ullah, Saif, Muhammad Abdullah Butt, Qaisar Sohail, and Talha Riaz. "Multi-Omics Characterization of Fish Responses to Emerging Environmental Contaminants: Implications for Aquatic Toxicology and Sustainable Fisheries Management." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 5666-5685.
 44. Butt, Muhammad Abdullah, Talha Riaz, Muhammad Abdullah Sadiq, Anam Ishaq, Ambreen Saleem, and Iza Almas. "Development of Polyphenol-Rich Pomegranate Peel Nutraceuticals for Glycemic Regulation, Insulin Sensitivity Improvement, and Oxidative Stress Reduction in Type II Diabetes Mellitus." *Journal for Current Sign* 4, no. 2 (2026): 2398-2413.
 45. Ullah, Saif, Muhammad Abdullah Butt, Qaisar Sohail, Talha Riaz, and Shazia Saeed. "Toxicological Evaluation of Microplastic and Nanoplastic Exposure on Growth Performance, Oxidative Stress Biomarkers, and Histopathological Alterations in Cultured Fish Species." *Social Science Review Archives* 4, no. 2 (2026): 2178-2198.
 46. Naeem, Waleed, Muhammad Abdullah Butt, and Umer Javeid. "The Influence of Artificial Intelligence Automation on Employee Productivity, Job Redesign, and Organizational Performance in Service Industries." *Social Science Review Archives* 4, no. 2 (2026): 2534-2552.
 47. Naeem, Waleed, Muhammad Abdullah Butt, and Umer Javeid. "Machine Learning-Based Fraud Detection Systems and Their Effectiveness in Reducing Cybersecurity Risks in Digital Banking." *Social Science Review Archives* 4, no. 2 (2026): 2553-2573.

48. Riaz, Muhammad, Neelam Tariq, Madiha Iqbal, Muhammad Abdullah Butt, Qaisar Sohail, and Talha Riaz. "Migration, Displacement, and Health Inequities: A Comparative Study of Refugee Populations and Access to Healthcare Services." *Social Science Review Archives* 4, no. 2 (2026): 2704-2722.
49. Riaz, Muhammad, Muhammad Abdullah Butt, Qaisar Sohail, Talha Riaz, and Ambreen Saleem. "Dietary Habits, Nutritional Status, and Socioeconomic Factors Among University Students in Punjab, Pakistan: A Multicity Nutritional and Social Survey." *Social Science Review Archives* 4, no. 2 (2026): 2723-2742.
50. Rehman, Anees Ur, Muhammad Abdullah Butt, Talha Riaz, and Qaisar Sohail. "Wellbeing-Oriented Human Resource Management and Workforce Sustainability in Healthcare Organisations: Comparative Evidence from Pakistan and Australia." *Journal for Current Sign* 4, no. 2 (2026): 3422-3440.
51. Faizi, Waqar Un Nisa, Saira Akhtar, and Muhammad Abdullah Butt. "The Impact of Artificial Intelligence-Assisted Learning on Academic Performance and Critical Thinking Skills Among Undergraduate Students." *Social Science Review Archives* 4, no. 2 (2026): 2925-2948.
52. Butt, Muhammad Abdullah, Anas Mustafa, Rizwan Shukat, Talha Riaz, Ambreen Saleem, Shazia Saeed, Muhammad Mudassir, and Qaisar Sohail. "Valorization of Watermelon Peel Flavonoids: Kaempferol, Quercetin, and Rutin as Natural Antioxidants for Functional Food and Nutraceutical Applications: <https://doi.org/10.5281/zenodo.21234696>." *Journal for Current Sign* 4, no. 2 (2026): 2761-2776.
53. Butt, Muhammad Abdullah, Anas Mustafa, Ahmad Din, Rizwan Shukat, Talha Riaz, Ambreen Saleem, Shazia Saeed, Muhammad Mudassir, Qaisar Sohail, and Muhammad Hamid Javaid. "Effects of Ultrasound-Assisted Protein Modification on the Functional and Nutritional Properties of Soy Protein Isolate." *Pakistan Journal of Medical & Cardiological Review* 5, no. 2 (2026): 5678-5704.
54. Nawaz, Hira, Nimra Shaukat, Ali Ahmad Bhatti, Moiza Noor, Savera Sayam, Tahira Yasmeen, Saira Fatima, Saira Sattar, and Muhammad Abdullah Butt. "Modulation of Gut Microbiota Through Functional Foods to Reduce Low-Grade Chronic Inflammation." *Pakistan Journal of Medical & Cardiological Review* 5, no. 1 (2026): 2231-2246.