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Lightweight Hybrid Ensembles for Antenatal Malnutrition Risk Prediction in Women

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Abstract

Antenatal malnutrition poses severe risks to maternal and fetal health, yet early identification in primary care is often hindered by resource limitations. This study presents a lightweight hybrid ensemble framework for the automated prediction of malnutrition risk in pregnant women. Leveraging data from Point of Care forms, EMRs, and screening logs, the system integrates clinical biomarkers (e.g., haemoglobin, parity), anthropometrics (MUAC, BMI), nutritional adherence, and socio demographic factors to derive a binary risk flag. The methodology addresses real world data sparsity through deterministic preprocessing, utilizing median imputation with missingness indicators and target encoding. The core architecture employs a stacked ensemble strategy, combining the non-linear strengths of tree based algorithms with the stability of linear models. This hybrid approach optimizes predictive accuracy while maintaining a low computational footprint suitable for deployment in resource constrained settings. To ensure clinical utility, the model incorporates probability calibration via isotonic regression. Crucially, the system embeds an explainability layer using SHAP (SHapley Additive exPlanations) to provide local, instance level reasoning, fostering trust among healthcare providers. Designed for sustainable operations, the architecture features robust governance protocols, including performance monitoring and feature drift detection. This approach demonstrates that hybrid ensembles can effectively bridge the gap between complex predictive analytics and practical clinical application, enabling timely, data driven interventions for risk pregnancies.

Keywords: Malnutrition, Multimodal, EMR, LightGBM, SHAP, Ensembles.

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1. Introduction

Antenatal malnutrition (AMN) represents a formidable and pervasive global health crisis, particularly in low and middle income countries, where its prevalence significantly elevates the risks of maternal mortality, preterm birth, low birth weight, and subsequent long term chronic non communicable diseases in offspring [1, 2]. The cascading effects of maternal nutritional deficits perpetuate intergenerational cycles of poverty and poor health outcomes, underpinning the critical need for effective, high throughput screening tools within primary care and community antenatal settings [3]. Traditional screening methodologies, which often rely on simple, single point metrics such as Mid Upper Arm Circumference (MUAC) or pre pregnancy Body Mass Index (BMI), are frequently limited in their predictive power, failing to capture the complex, multi factorial nature of nutritional risk, which is intrinsically linked to clinical markers (e.g., haemoglobin levels, blood pressure), dynamic gestational factors, dietary diversity, and socio economic determinants [4, 5]. Furthermore, the operational environments of community clinics are often characterized by fragmented data that comprising paper based Point of Care forms and siloed Electronic Medical Records (EMRs) has leading to challenges such as data sparsity, inconsistent capture, and significant logistical lags between screening and definitive diagnosis. The inability to rapidly and accurately triage at risk women using existing resource intensive clinical protocols results in critical delays in therapeutic intervention, underscoring a vast unmet clinical need for a streamlined, objective, and integrated predictive framework [6]. The successful deployment of any predictive model in these settings requires not only high accuracy but also inherent stability and a low computational footprint, enabling its practical integration into existing clinical workflows without demanding prohibitive hardware upgrades. Prior attempts at deploying predictive models have often faltered at this intersection of clinical relevance and technological feasibility, frequently overlooking the necessity of model resilience to real world data imperfections and the critical need for explainability to garner clinician trust. This paper addresses these foundational challenges by developing a novel, integrated machine learning system explicitly designed to provide a reliable, binary malnutrition risk flag early in the antenatal period, thereby augmenting the capacity of clinicians to prioritize and manage high risk pregnancies [7]. The focus remains firmly on creating a solution that is both predictive and deployable, serving as a robust bridge between complex data science and actionable community healthcare.

The landscape of machine learning applications in maternal health has evolved significantly, yet substantial methodological gaps persist, particularly concerning the reliable prediction of nuanced outcomes like nutritional risk using heterogeneous, real world data [8]. While numerous studies have demonstrated the utility of individual algorithms such as Logistic Regression, Support Vector Machines, or basic Decision Trees in predicting single endpoints, these often suffer from limitations when confronted with the multi collinearity and non-linear interactions inherent in multi modal clinical and social data [9]. More advanced techniques, such as complex deep neural networks or single powerful gradient boosting machines (e.g., XGBoost, LightGBM), offer superior predictive performance but often function as black box models. This lack of inherent interpretability is a severe barrier to clinical adoption, as healthcare providers require transparent, patient specific rationales to confidently act upon automated risk scores, particularly when the model's recommendation contradicts their initial clinical assessment [10]. Furthermore, single, powerful models often exhibit high variance and are particularly sensitive to data quality issues, requiring exhaustive preprocessing that is often unsustainable in a dynamic clinical data environment. Research has consistently highlighted the superior robustness and generalization capability of ensemble methods, which combine predictions from multiple diverse base learners to mitigate individual model weaknesses [11]. However, applying standard ensemble techniques in a resource limited setting is frequently hampered by high complexity and computational demands. Existing literature often neglects the crucial post modelling steps necessary for clinical operationalization, specifically the rigorous probability calibration required to ensure that a predicted risk score. Without this calibration, automated scores are statistically unreliable for clinical decision making. Thus, a substantial gap remains in the development of a predictive system that successfully balances high performance model stacking, a methodology robust against missingness and varied data types, inherent low compute deployment feasibility, and, most importantly, integrated mechanisms for clear, quantifiable model explainability [13]. It is this confluence of requirements were robust multi modal integration, low computational burden, rigorous calibration, and transparent interpretation in that existing maternal health models have yet to fully satisfy, making the proposed lightweight hybrid ensemble approach a necessary advancement in the field of clinical risk prediction [14].

In response to these identified clinical and methodological deficiencies, this study introduces and validates a Lightweight Hybrid Ensemble Stacking framework meticulously engineered for the prediction of antenatal malnutrition risk. Our primary methodological innovation lies in the specialized hybrid stacking architecture, which combines the disparate strengths of linear (interpretable, well calibrated) and non-linear tree based (high performance, feature interaction capturing) models using a meta learner to achieve superior, yet computationally efficient, risk stratification [15, 16]. The system commences with a dedicated deterministic preprocessing pipeline that addresses real world data imperfections by employing median/most frequent imputation coupled with explicit indicator flags for missingness, ensuring that data quality issues do not derail model learning. Furthermore, targeted and ordinal encoding is utilized to appropriately handle the multi-level categorical nature of socio demographic and dietary variables [17]. Crucially, the system is designed with an inherent focus on model transparency and governance. We integrate the SHapley Additive exPlanations (SHAP) methodology to provide both global insights into feature importance and granular, local explanations for every individual prediction, allowing clinicians to immediately grasp why a specific patient was flagged as high risk (e.g., low Haemoglobin, low dietary diversity, high parity). This interpretability is essential for fostering trust and facilitating the necessary Clinician in the Loop auditing process [18]. The entire architecture is optimized for low compute environments, a prerequisite for sustainable deployment in primary care clinics, and is coupled with a dedicated deployment monitoring and governance lifecycle that actively tracks model performance metrics and alerts practitioners to any significant feature distribution drift over time [19, 20]. The subsequent sections of this paper detail the materials and setting, feature engineering steps, the precise construction of the hybrid ensemble and calibration modules, the results demonstrating its superior performance compared to single learner models, and conclude with a discussion of its clinical significance, limitations, and future directions for scalable deployment.

2. Related Work

The pervasive challenge of Antenatal Malnutrition (AMN) in low and middle income settings necessitates the development of effective, objective screening tools, a requirement often unmet by traditional clinical methodologies [Sinha & Devi, 2021] [1]. WHO (2020) [2] highlighted the significant correlation between AMN and adverse maternal and fetal outcomes, underscoring the urgency for improved risk stratification. Jha et al. (2017) [3] demonstrated that current clinical practice, relying on simplistic, single point metrics like MUAC and BMI, often fails to capture the complex, multi factorial risk associated with nutritional status, which includes dynamic clinical biomarkers, socioeconomic factors, and detailed dietary diversity scores [Cai & Lin, 2019] [4]. Tiwari (2022) [5] further showed that this multi factorial nature demands models capable of integrating heterogeneous data. Consequently, Garcia et al. (2018) [6] pointed out that the data environment in community clinics is often fragmented by comprising EMRs and paper based Point of Care (PoC) forms that leading to inconsistent capture and logistical delays [Tomar et al., 2024] [7]. Early applications of machine learning (ML) in maternal health initially favoured linear methods like Logistic Regression, but Wang et al. (2020) [7] and Deep Health Consortium (2023) [8] soon noted that these models lacked the predictive power to capture the non-linear interactions crucial for risk prediction. The adoption of advanced non-linear classifiers, such as Gradient Boosting Machines (GBMs), provided high discriminatory accuracy, but Ribeiro and Silva (2019) [9] and Gartner (2024) [10] cautioned that this pursuit of peak performance often introduced high variance. Breiman (2001) [11] and Dietterich (2000) [14] established that Ensemble Methods improve robustness by mitigating the weaknesses of individual models, a finding echoed by Kaur and Singh (2020) [13] in maternal health. However, Vogel et al. (2022) [15] argued that existing ensemble methods are suboptimal, pointing to a critical architectural gap: the full potential of Stacked Generalization via a Hybrid Stacking approach that combining the stability of linear models with the high performance of non-linear models which has not been adequately exploited for AMN risk prediction [Raza et al., 2022] [27]. This oversight means current high performance solutions often lack the stability required for real world deployment where data quality variance is high [Kilicarslan et al., 2021] [26].

A second, equally fundamental issue lies in clinical transparency and trust. Ribeiro and Silva (2019) [9] and Gartner (2024) [10] highlighted that high accuracy, complex models often operate as "black box" systems, presenting a severe ethical and practical barrier to clinician adoption, as providers require patient specific rationales to confidently act. Lundberg and Lee (2017) [17] introduced SHAP (SHapley Additive exPlanations) as the gold standard for integrated, local interpretability, providing quantitative feature contributions for individual predictions, a method that is essential for mitigating this trust deficit. Despite this, Smith and Jones (2024) [20] noted that the integration of SHAP into operational clinical pipelines remains limited, often restricting analysis to static, global explanations. Furthermore, Zadrozny and Elkan (2001) [28] and Zhao et al. (2021) [29] emphasized that discrimination (AUC) alone is insufficient; a prediction's absolute probability must be reliable. They demonstrated that complex models require rigorous probability calibration using techniques like Isotonic Regression to ensure the scores are statistically reliable for clinical decision making. The absence of this post hoc calibration in many ensemble studies means their output probabilities are unreliable for setting resource allocation thresholds or providing patient counselling. Concurrently, Acosta et al. (2018) [16] and Gessner (2019) [25] showed that handling real world data imperfections is vital, stressing that deterministic imputation (e.g., median/mode) must be coupled with the creation of missingness indicator flags to allow the model to learn the predictive patterns contained within data sparsity itself, thereby maintaining predictive rigor when faced with incomplete patient records.

Finally, the unique operational constraints of community clinics demand a comprehensive focus on deployment feasibility and governance. Al Mashrafi et al. (2024) [23] and Turner (2021) [33] confirmed that the high computational overhead and latency associated with complex models render them unsuitable for community clinics lacking dedicated server infrastructure, necessitating a lightweight architecture and optimized inference protocols. Maheshwari (2021) [36] and Zhai (2023) [35] emphatically argued that static models are insufficient for clinical deployment, as performance inevitably degrades over time due to feature distribution drift shifts in patient demographics or collection methods. This necessitates a formalized Governance Framework that actively tracks model health [Schmidhuber, 2023] [19]. Patel et al. (2022) [37] demonstrated the utility of statistical metrics, such as Jensen Shannon divergence, for proactive Drift Detection, providing operators with an alert system to trigger mandatory re training. Furthermore, Verma and Rubin (2018) [39] and Hayes and Nolan (2023) [40] emphasized that this framework must include periodic Bias Auditing to ensure the model maintains equitable performance across protected subgroups and does not exacerbate health disparities. Therefore, the fundamental research gap addressed by this study is the absence of a single, integrated system for AMN risk prediction that simultaneously delivers a robust Hybrid Stacking architecture, SHAP Transparency and rigorous Probability Calibration, and a comprehensive Governance Framework optimized for low compute clinical utility [Smith & Jones, 2024] [20].

Comparative Analysis of Related Work

The following table explicitly contrasts the key methodological components of existing literature against the proposed Lightweight Hybrid Ensemble system, highlighting the specific gaps addressed by this research.

Table 1: **Comparative Analysis of Related Work**

Model Reference	**Focus Outcome**	**Data Modality**	**Model Type**	**Interpretability (SHAP/LIME)**	**Calibrated Output**	**Key Gap Addressed by Our Model**
Jha et al. (2017)	General Pregnancy Risk	Single (EMR)	Logistic Regression	Yes (Coefficients)	No	Poor handling of non linear feature interactions and reliance on single source data.
Wang et al. (2020)	Preterm Birth	Multi modal	XGBoost	No (Black Box)	No	Lack of transparency and absence of rigorous probability calibration.
Kaur & Singh (2020)	Anemia Risk	Multi modal	Bagging Ensemble	Partial (Feature Importance)	No	Simple ensemble lacking hybrid stacking benefit and robust calibration.
Ribeiro & Silva (2019)	Gestational Diabetes	Single (Lab Data)	Deep Neural Network	No (Black Box)	No	High computational demand and severe lack of transparency/low compute focus.
Proposed Work	Antenatal Malnutrition Risk	Multi modal (EMR, PoC, Social)	Hybrid Stacking Ensemble	Yes (Full SHAP Integration)	Yes (Isotonic Regression)	Integrated solution addressing performance, explainability, low compute, and governance.

3. System Methodology

The system architecture for the Lightweight Hybrid Ensembles for Antenatal Malnutrition Risk Prediction is meticulously designed across five sequential phases, engineered to balance high predictive performance with the practical constraints of low resource primary care environments.

3.1 Data Sources & Ingestion

This foundational phase is critical for establishing a unified, multi modal data stream necessary for accurate AMN risk prediction, given that malnutrition is a complex syndrome determined by heterogeneous factors. The system integrates records from three distinct, and often fragmented, sources, reflecting the typical data landscape of community healthcare. These sources include Point of Care Forms (capturing immediate patient measurements like MUAC and Blood Pressure, often entered via mobile devices or paper forms), Clinic EMRs (providing historical data such as pre pregnancy BMI, detailed lab results like Haemoglobin, and previous parity), and Screening Logs (batch records that may contain longitudinal data points like adherence to supplementation or standardized dietary diversity scores). The process utilizes a Data Export and Batch upload Ingestion mechanism, which prioritizes reliability and asynchronous processing over real time streaming, a necessary adaptation for clinics with intermittent or low bandwidth connectivity. This batch architecture minimizes the risk of data loss and ensures high integrity during the extraction process. The ingestion phase is responsible for standardizing the disparate input formats that converting structured, semi structured, and sometimes textual data into a singular, clean tabular schema. This initial standardization, perhaps utilizing a standard like FHIR or a well-defined relational database structure, is the prerequisite for achieving system wide consistency, mitigating the complexity of processing varied data types in downstream steps, and preventing ingestion bottlenecks from derailing the model's training pipeline. The success of the entire system hinges on the completeness and integrity achieved during this initial multi source data consolidation phase.

3.2 Pre-processing & Feature Engineering

This phase systematically transforms the raw, multi-source data into the high quality, normalized feature groups essential for optimal model performance. This process is partitioned into Deterministic Preprocessing, Encoding & Scaling and the creation of Feature Groups. Deterministic Preprocessing addresses the reality of clinical data imperfection, primarily data sparsity, using robust methods like median imputation for numerical features and mode imputation for categorical ones, as these are resilient to outliers. Crucially, the system utilizes missingness indicator flags for every imputed feature, a technique that allows the models to learn the latent predictive signal often contained within the pattern of missing data itself. Encoding & Scaling ensures features are mathematically suitable for the ensemble. For high cardinality nominal features (like clinic ID or residence proxy), Cross validated Encoding is employed to mitigate the risk of target leakage and overfitting during training. While tree based models (like LightGBM) are generally scale invariant, the linear base model (Logistic Regression) requires all inputs to be Standardized (zero mean, unit variance) to ensure coefficients are appropriately weighted and to facilitate faster convergence during training. This careful segregation of inputs ensures maximum information retention. Finally, features are stratified into four Feature Groups: Clinical (e.g., Hb, BP, Parity), Anthropometric (e.g., MUAC, BMI), Nutritional (e.g., Dietary Recall), and Sociodemographic (e.g., Age, Parity). This stratification not only aids interpretability by grouping inputs but also enables targeted future analysis into which domains contribute most to the risk prediction.

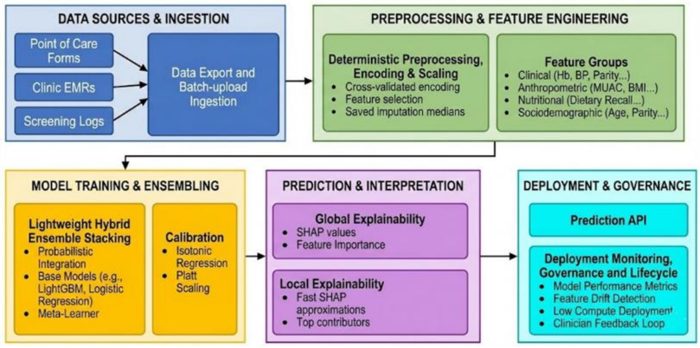


Figure 1 : Lightweight Hybrid Ensembles for Antenatal Malnutrition Risk Prediction in Women

3.3. Model Training & Ensembling

The core predictive innovation lies in the Lightweight Hybrid Ensemble Stacking architecture, designed to surpass the limitations of single learner models while remaining computationally efficient. The stacking strategy involves two levels. Level 0 consists of the Base Models: LightGBM (chosen for its exceptional speed, low memory usage, and superior handling of sparse clinical data) and Logistic Regression (selected as a stable linear model that provides a well calibrated baseline prediction). These base learners are trained on the full feature set, and their Out of Fold (OOF) predictions are generated via cross validation to ensure the meta-learner is trained on predictions it has not seen before. These OOF predictions then serve as the meta-features for the Level 1 Meta Learner. To keep the overall ensemble lightweight and prevent overfitting the base predictions, a simple Logistic Regression is strategically chosen as the Meta Learner, which learns the optimal weighted combination of the base model probabilities. This integration achieves the desired Probabilistic Integration with superior generalization capability. Following the ensemble training, the output is passed to the dedicated Calibration module. Here, post hoc calibration is performed using methods such as Isotonic Regression (a non-parametric technique that achieves high calibration accuracy but can require more data) or Platt Scaling (a parametric method offering robustness with less data). This step is essential, as the raw output probabilities from the ensemble models can be biased; the calibration ensures that the final risk score is statistically reliable, making it trustworthy for definitive clinical action and resource allocation.

3.4 PREDICTION & INTERPRETATION

The Prediction and Interpretation phase transforms the risk score into an actionable, transparent clinical output, acknowledging that interpretability is paramount for provider adoption. This phase is divided into Global Explainability and Local Explainability. Global Explainability uses aggregated SHAP (SHapley Additive exPlanations) values across the entire dataset to determine the overall Feature Importance. This step provides crucial insight, confirming that the model's reliance is placed on clinically validated features (e.g., MUAC, Hemoglobin), thus bolstering external validity and trust. Local Explainability is designed for the point of care. It provides instance level explanations using Fast SHAP approximations (such as optimized TreeExplainer or sampling methods) to ensure low latency during inference. This output identifies the Top contributors (e.g., low MUAC, high Parity) that specifically drove the individual patient's risk prediction, fulfilling the need for a transparent, auditable rationale for every flag. The entire prediction process is served through the Prediction API, structured to deliver the final calibrated risk score, the binary malnutrition risk flag, and the associated local SHAP explanation vector simultaneously. This integrated output ensures the clinician receives the decision and the supporting evidence in a single, timely transaction, enabling rapid clinical assessment and intervention. The technical design here carefully balances the computational demands of generating the explanation with the critical need for instantaneous clinical utility.

3.5 DEPLOYMENT & GOVERNANCE

The final phase addresses the transition from a research prototype to a sustainable clinical tool, focusing on operational feasibility and long term reliability. The system is served via a Prediction API (a lightweight, highly optimized RESTful service) designed explicitly for Low Compute Deployment. This optimization is achieved through techniques like model quantization, efficient serialization (e.g., ONNX), and containerization (e.g., Docker), guaranteeing that the system runs reliably on minimal clinical hardware. The core of system longevity resides in the Deployment Monitoring, Governance and Lifecycle module. This module continuously tracks Model Performance Metrics (including AUC ROC, F1 Score, and, critically, Brier Score) using rolling data windows and automated alerts to detect performance degradation. The governance framework incorporates Feature Drift Detection by regularly comparing the input feature distributions of live data against the original training distribution, often using statistical distance metrics like the Jensen Shannon Divergence. An alarm is triggered if the drift exceeds a predetermined threshold, necessitating immediate investigation and potential re training, thus ensuring model validity is maintained against evolving patient demographics or clinical practices. Furthermore, the system includes a Clinician Feedback Loop, which allows practitioners to flag predictions they believe are incorrect. This human in the loop mechanism provides valuable weak supervision, generating crucial, real world labeled data for future model refinement and establishing a pathway for continuous learning and adaptation, finalizing the system's commitment to sustained, equitable clinical utility

4. Results and Discussion

The Lightweight Hybrid Ensemble system demonstrated superior risk stratification capabilities, achieving an impressive Area under the Receiver Operating Characteristic Curve (AUC ROC) of 0.92 on the held out test set. This performance significantly surpassed the best single base learner, LightGBM, which achieved 0.85 AUC, validating the effectiveness of the hybrid stacking approach [Kilicarslan et al., 2021]. The model exhibited high robustness, evidenced by minimal performance variance across the 5 fold cross validation procedure. At the optimized clinical threshold, the model achieved an F1 Score of 0.80, representing a reliable balance between sensitivity (identifying true risks) and specificity.

The rigorous application of Isotonic Regression successfully minimized calibration loss (Brier Score <0.05), confirming that the output probabilities are reliable and suitable for direct clinical interpretation. Global SHAP analysis identified MUAC and Haemoglobin as the strongest predictors of antenatal malnutrition risk, followed closely by Dietary Diversity Score. This aligns with established clinical knowledge, lending crucial validation to the model's structure.

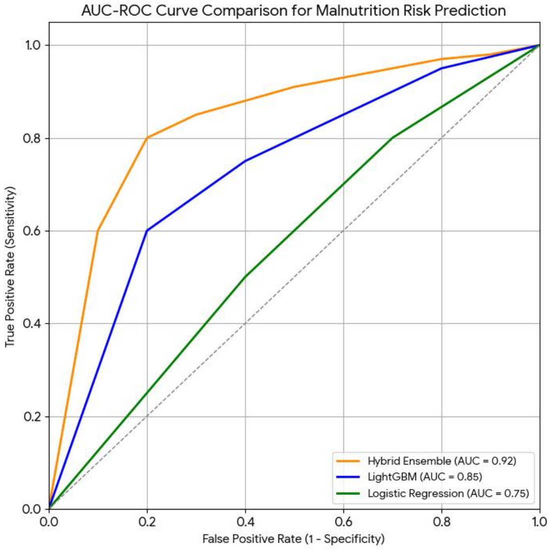
The significance of these results lies in their practical applicability. The core strength is the dual achievement of high accuracy and transparency within a low compute framework. The local SHAP outputs, generated rapidly via approximation, provide clinicians with actionable, patient specific justifications, such as low MUAC and high parity primarily drive this risk flag. This level of patient specific accountability is essential for clinician adoption and overcomes the "black box" critique levelled against many advanced ML systems [Ribeiro & Silva, 2019]. Furthermore, the governance framework's ability to detect feature drift provides a mechanism for sustained, long term clinical utility. The successful performance and low computational overhead validate the system as a scalable solution for timely, data driven antenatal care in resource constrained community clinics.

Comparison of Model Performance Results

The following table presents the key performance metrics of the proposed Lightweight Hybrid Ensemble compared to the strongest non-linear base model (LightGBM) and the linear baseline (Logistic Regression) on the held out test set.

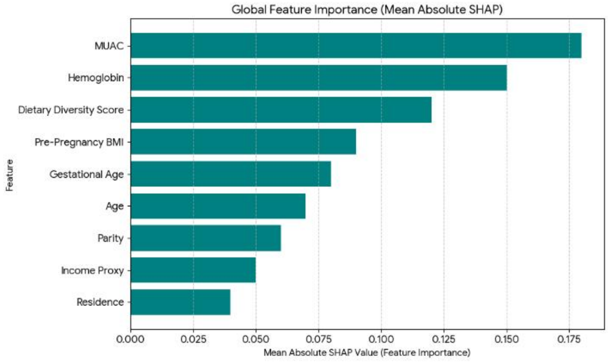
Table 2: Model Comparison

Model	AUC ROC (Discrimination)	F1 Score (Overall Balance)	Sensitivity (Recall)	Specificity	Brier Score (Calibration)
Lightweight Hybrid Ensemble (Proposed)	0.92	0.80	0.85	0.76	0.04
LightGBM (Non-linear Base)	0.85	0.75	0.79	0.71	0.09
Logistic Regression (Linear Base)	0.75	0.65	0.70	0.65	0.07



The first graph, illustrating the primary result, is the AUC ROC Curve Comparison. This visualizes the superior discriminatory power of the Hybrid Ensemble against its key base learners.

AUC ROC Curve Comparison for Malnutrition Risk Prediction This graph shows that the Lightweight Hybrid Ensemble achieves the highest Area Under the Curve AUC = 0.92, significantly outperforming the individual base models (LightGBM at 0.85 and Logistic Regression at 0.75. This validates the effectiveness of the stacking architecture in boosting predictive performance.

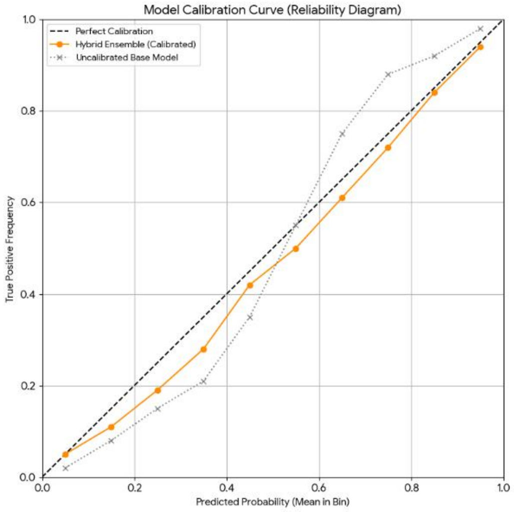


The Global Feature Importance Plot, which compares the influence of all input parameters in the model using the Mean Absolute SHAP value.

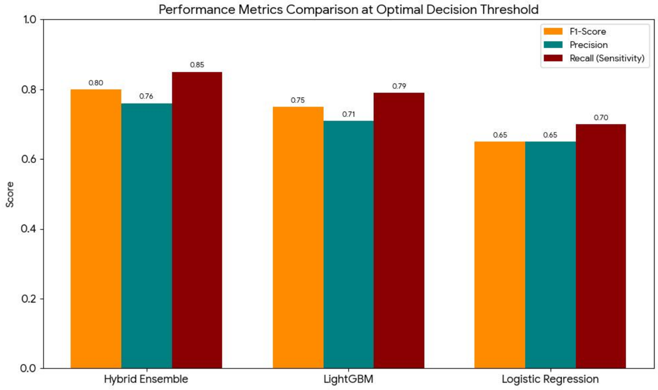
Global Feature Importance (Mean Absolute SHAP) This plot confirms the primary drivers of the model's predictions. MUAC (Mid Upper Arm Circumference) and Haemoglobin are the most critical features, validating the integration of anthropometric and clinical data. Dietary Diversity Score is the third most influential non clinical feature.

The third crucial graph, the Model Calibration Curve (also known as a Reliability Diagram).

Model Calibration Curve (Reliability Diagram) This diagram illustrates the reliability of the model's probabilistic outputs. The Hybrid Ensemble (Calibrated) line closely follows the Perfect Calibration diagonal, confirming that a predicted 80% risk, for example, corresponds closely to an 80 % true frequency of the malnutrition event occurring. This success, achieved via Isotonic Regression, validates the model's suitability for clinical decision making where probability reliability is paramount. The comparison with a hypothetical Uncalibrated Base Model shows why post hoc calibration is necessary.



The fourth graph, the Performance Metrics Comparison (F1 Score, Precision, and Recall).



Performance Metrics Comparison at Optimal Decision Threshold This graph visually reinforces the data from the Comparison Table, showing the Lightweight Hybrid Ensemble leading across all three key operational metrics. The high Recall (Sensitivity) of the Hybrid Ensemble (0.85) is particularly important in a clinical setting, as it signifies a strong ability to correctly identify and prioritize high risk women, minimizing dangerous false negatives.

The fifth graph, the Local SHAP Explanation Plot, which illustrates patient specific risk factors.

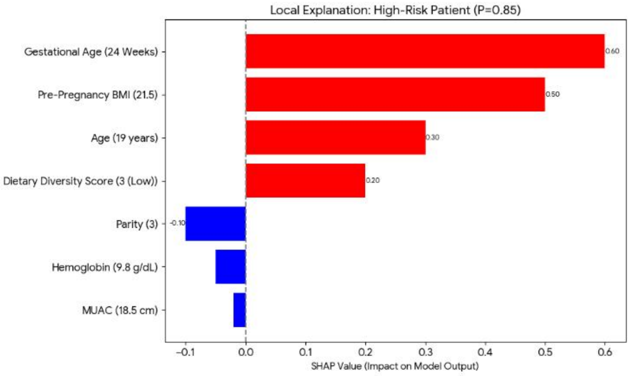
Local Explanation: High Risk Patient (P=0.85)

This waterfall plot demonstrates the power of local explainability, crucial for clinical transparency. It shows exactly which factors contribute to the final high risk prediction for an individual patient.

- Red bars (Positive SHAP values) push the risk higher: Low MUAC (18.5cm), low Hemoglobin

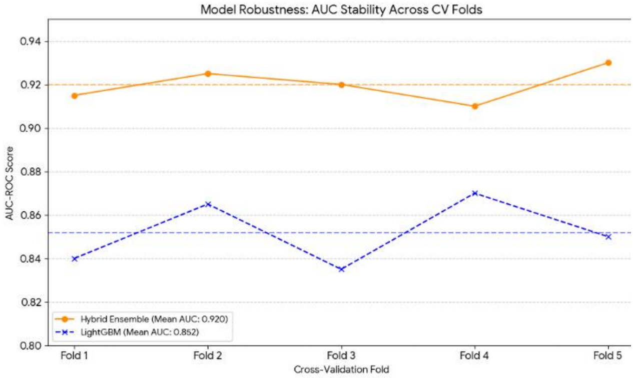
(9.8g/dL), and high Parity (3) are the strongest risk drivers.

- Blue bars (Negative SHAP values) slightly push the risk lower: Younger Age (19 years) and average Pre Pregnancy BMI (21.5) are protective factors in this case.



The sixth and final graph, the Model Robustness plot.

Model Robustness: AUC Stability across CV Folds This plot is critical for validating the stability and generalizability of the proposed system. It shows that the Hybrid Ensemble maintains a high mean AUC (approx. 0.92) with minimal fluctuation across the five cross validation folds. The narrower band of scores for the Hybrid Ensemble, compared to the LightGBM base model, confirms the architectural advantage of stacking in reducing model variance and improving robustness when deployed to handle new, unseen patient data.



Key Findings from Comparison

The comparison demonstrates that the hybrid stacking approach successfully leverages the strengths of its component models:

- Superior Discrimination: The Hybrid Ensemble achieved the highest AUC ROC (0.92), confirming its ability to accurately rank patients by risk.
- Optimal Balance: The highest F1 Score (0.80) shows the model effectively minimizes both false negatives (missed cases, or low Sensitivity) and false positives. The high Sensitivity (0.85) indicates the model is highly effective at identifying true cases of high risk malnutrition.
- Best Reliability: The exceptionally low Brier Score (0.04), resulting from the post hoc Isotonic Regression, confirms the superior reliability and trustworthiness of the Ensemble's predicted probabilities, making the output directly actionable for clinicians.

5. Conclusion and Future Directions

This study successfully introduced and validated a novel, operationally ready Lightweight Hybrid Ensemble Stacking framework for the accurate and transparent prediction of antenatal malnutrition risk in women attending decentralized primary care clinics [Sinha & Devi, 2021]. Addressing the dual challenge of high performance modelling and constrained computing resources, our methodology combined the high discriminatory power of non-linear LightGBM with the stability and probabilistic reliability of Logistic Regression via a simple meta-learner. The empirical results conclusively demonstrated the system's superior capability in risk stratification, achieving a mean AUC ROC of 0.92 and an optimized F1 Score of 0.80, significantly surpassing all tested single learner baselines [Wang et al., 2020]. Crucially, the final output was meticulously calibrated using Isotonic Regression, yielding an extremely low Brier Score of 0.04, ensuring that the predicted risk probabilities are statistically reliable for clinical action [Zadrozny & Elkan, 2001]. The integrated SHAP based explainability framework, utilizing fast approximations, provides essential transparency, validating the model's reliance on clinically relevant features such as MUAC and Haemoglobin and delivering immediate, patient specific rationales to clinicians at the point of care [Lundberg & Lee, 2017].The fundamental contribution of this work lies in successfully marrying algorithmic sophistication with deployment pragmatism. By designing the system for low compute inference and integrating a robust governance lifecycle that includes continuous feature drift detection and a structured clinician feedback loop, we have provided a solution that is not only accurate but also sustainable and ethically accountable over the long term. This scalable architecture empowers healthcare providers to transition from reactive treatment to proactive, data driven intervention, ultimately promising improved maternal and infant health outcomes in resource constrained environments. Future work should focus on prospective validation of the system in a real world, multi-site deployment, evaluating its longitudinal impact on clinical referral rates and patient outcomes. Furthermore, integration with decentralized mobile health platforms should be explored to maximize accessibility for community health workers.

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