ORIGINAL ARTICLE

Bayesian Analysis of Modified Nutrition Risk in Critically Ill (mNUTRIC) Score for Mortality Prediction in Critically Ill Patients

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Abstract

Background and aims: Malnutrition has a considerable influence on critically ill patients by increasing mortality and poorer clinical outcomes. The modified Nutrition Risk in Critically Ill (mNUTRIC) score is commonly used to assess nutritional risk and predict death; however, its sensitivity, specificity, and optimal cut-off values differ between studies. This study uses a Bayesian approach to assess the accuracy of the mNUTRIC score in predicting mortality in critically ill patients.

Patients and methods: A preplanned Bayesian analysis was performed using data from 31 cohort studies, which included 13,271 intensive care unit (ICU) patients. The study investigated the mNUTRIC score's sensitivity, specificity, diagnostic odds ratio, and area under the curve (AUC). Subgroup analysis compared mortality rates at 28-day, 90-day, and in-hospital time points, along with cut-off values (<5 vs ≥5). Bayesian modeling was performed using the rjags and brms packages in R version 3.2.1. These tools also facilitated the visualization of results, including posterior distributions, forest plots, and Fagan nomograms.

Results: Bayesian analysis affirmed the mNUTRIC score's high discriminative capacity, with a pooled sensitivity of 0.84 (95% credible interval (CrI): 0.80–0.88), specificity of 0.77 (95% CrI: 0.73–0.80), and AUC of 0.88 (95% CrI: 0.83–0.92). A cut-off of <5 resulted in higher sensitivity (0.83) and AUC (0.87), whereas ≥5 remained accurate but had somewhat lower sensitivity. The score consistently predicted 28-day, 90-day, and in-hospital mortality.

Conclusions: The Bayesian analysis validates the mNUTRIC score as a reliable predictor of mortality in critically ill patients. Its excellent diagnostic performance suggests its incorporation into ICU for early risk assessment and nutritional interventions.

Keywords: Bayesian analysis, Critically ill patients, Intensive care unit mortality, Modified Nutrition Risk in Critically Ill score, Nutritional risk assessment.

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Highlights

- The modified nutrition risk in critically ill score is an effective tool for identifying critically ill patients with a high risk of mortality.
- Bayesian analysis established it's strong predictive value, ensuring appropriate risk evaluation.
- Its reliability across different intensive care unit (ICU) settings and timeframes underscores its importance in critical care.
- A lower threshold enhances early detection, making it more effective for timely interventions

Introduction

Malnutrition is a common and major problem in critically ill patients with a significant impact on outcomes, including length of ICU stay, development of infections, and mortality. Hence, early recognition of nutritional risk factors and intervention can significantly positively affect the prognosis of patients.[1] Certainly, the modified nutrition risk in critically ill (mNUTRIC) score is very simple and has been accepted quickly in assessing nutritional risk and mortality prediction in ICU patients.[2] The mNUTRIC score includes age, number of comorbidities, days from hospital to ICU admission, acute physiologic assessment and chronic health evaluation (APACHE) II score, and sequential organ failure assessment (SOFA) score. Unlike traditional scorings like

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APACHE II and SOFA, which are mostly based upon physiological derangements, mNUTRIC takes into account nutritional risk linked with illness severity, providing a more holistic tool in identifying patients who may benefit from nutritional interventions, not just mortality prediction.[3,4]

Although the mNUTRIC score is widely used, variability in study design, population, and cut-off points has led to inconsistent diagnostic performance across ICU settings.[5] This study addresses those inconsistencies by applying a Bayesian framework, offering a more refined understanding of its utility in mortality prediction.

Albeit ICU mortality predictors such as APACHE II and SOFA are widely used, they primarily focus on physiological dysfunction and do not account for nutritional risk—a key but often underappreciated determinant of outcomes in critical care. The mNUTRIC score uniquely incorporates nutritional parameters alongside illness severity, enabling a more comprehensive risk stratification. Moreover, previous analyses of the mNUTRIC score have employed frequentist methods, which may not fully capture the uncertainty and heterogeneity across diverse ICU settings. By applying a Bayesian approach, this study provides a robust and flexible framework to estimate diagnostic performance and validate the mNUTRIC score's reliability across varying populations and timeframes. This enhances its clinical utility beyond what existing scoring systems offer.

Patients and Methods

We conducted this preplanned Bayesian analysis as part of the published study.[5] Eligible studies were those that evaluated the diagnostic accuracy of the mNUTRIC score in predicting mortality among critically ill patients and reported ample data on sensitivity and specificity.[6–36] Bayesian analysis combines prior knowledge and observations to provide posterior distributions of the parameters of the model. Bayesian methods use more flexible assumptions about the uncertainty and variability of the information as compared with frequentist methods. This is particularly useful for meta-analyses involving heterogeneous datasets.

This study provides a Bayesian analysis framework for the mNUTRIC score's diagnostic performance prediction of mortality. The data were derived from a meta-analysis of 31 cohort studies with 13,271 patients encompassing various ICU settings and populations and addressed heterogeneity among studies and rendered robust estimates of sensitivity, specificity, diagnostic odds ratios (DOR), and area under the curve (AUC).

The Bayesian model was applied in this study to include heterogeneity at the study level while retaining reliable pooled estimates. Following the approach outlined in a published study, the model included random effects modeled for sensitivity and specificity, modeling the heterogeneity across different studies and in the study designs. The noninformative prior distributions were chosen to avoid any undue subjective assumptions in the posterior estimates, for sensitivity and specificity, Beta (1,1), which indicates equal probabilities across the 0–1 range, and DOR, log-normal (0,1), which indicates wide uncertainty in diagnostic performance. This approach enabled the analysis to be primarily data-driven, while still allowing for the later incorporation of prior information.

The likelihood function specified the binomial distribution to model the observed outcomes of a diagnostic test [namely, true positive (TP), false positive (FP), true negative (TN), and false negative (FN)].

Diagnostic result	*Truth*		*Measure*
	Positive	*Negative*	
Positive	TP_i	FN_i	$Se = \frac{TP_i}{TP_i + FN_i}$
Negative	FP_i	TN_i	$Sp = \frac{TN_i}{TN_i + FP_i}$

A binomial distribution was used to derive the likelihood function based precisely on the observed outputs of the diagnostic test, which included TP, FP, TN, and FN. This method ensured the inclusion of each result based on its sample size, and thus larger studies contributed more weight to the analysis.[37]

$$L(\theta) = \prod_{i=1}^{n} \text{Binomial}\left(TP_i, FN_i, FP_i, TN_i \mid Se, SP\right)$$

n is the number of studies, and the likelihood combines the observed results of diagnostic tests with assumed sensitivity (Se) and specificity (Sp) to give posterior distributions in the Bayesian framework. The weighting of each study in the model by sample size was made such that larger studies had a greater influence on the posterior estimates. The likelihood function was then combined with the prior distributions to obtain the posterior distributions for the key parameters of interest.

Prior distributions for sensitivity (Se), specificity (Sp), and the DOR were kept noninformative to minimize bias as much as possible. A beta (1,1) prior distribution was applied to Se and Sp, assigning an equal probability for all values and providing for a completely uniform distribution on the interval (0,1). For DOR, a log-normal (0,1) distribution was used to allow for a broad and non-negative range that was suitable for diagnostic performance. These priors effectively ensured that the analysis remained nearly entirely data-driven.[38]

$$P(\text{Se}) \sim \text{Beta}\ (1,1),$$
$$P(\text{Sp}) \sim \text{Beta}\ (1,1),$$
$$P(\text{DOR}) \sim \text{Log} - \text{normal}\ (0,1)$$

The posterior distribution, based on Bayes' theorem, combines the likelihood with prior distributions to update our understanding of the parameters after observing the data:[39]

$$P(\text{Se, Sp} \mid \text{Data}) \propto P\ (\text{Data} \mid \text{Se, Sp}) \cdot P(\text{Se, Sp})$$

Posterior distributions for sensitivity, specificity, DOR, and AUC were estimated using Markov Chain Monte Carlo (MCMC) simulations. This iterative technique provides posterior probabilities for each parameter by updating prior beliefs with relevant observed data. The MCMC process lasted for 10,000 iterations with 5,000 iterations being treated as a burn-in period for initial stabilization of the estimates. Convergence diagnostics, which include trace plots, effective sample size calculation, and Gelman and Rubin statistics, helped to assess reliability and stability regarding posterior estimates. Checking the posterior distribution allows one to assess the fit of the model with the observed data in light of checking predictive checks. The visual evaluations of residuals and goodness-of-fit statistics highlight the Bayesian framework's reliability.

To account for the variability between studies, we formulated a Bayesian model which share the sensitivity and specificity across studies with the assumption that they follow normal distributions:[40]

$$Se_i \sim N(\mu_{se}, \sigma_{se}^2), Sp_i \sim N(\mu_{sp}, \sigma_{sp}^2)$$

Here, μ_{se} and μ_{sp} are the pooled means, representing the overall estimates, while σ_{se}^2 and σ_{sp}^2 account for study-level variability, capturing heterogeneity across different studies.

The approach involved the incorporation of random effects for sensitivity and specificity in such a manner that it could model heterogeneity explicitly. Different sources of heterogeneity factors like variations in ICU protocols, populations of patients, or designs of studies were extensively explored, which ensures that pooled estimates would be very robust even in the presence of high variability across studies.

Between-study variability was modeled using a Bayesian framework with random effects applied to both sensitivity and specificity. Study-level variances (σ_{se}^2 and σ_{sp}^2) were included to quantify heterogeneity across different studies. Although classical R^2 is not directly computed in Bayesian analyses, our approach captures unexplained heterogeneity through posterior distributions of these random effects. Model fit and variability were further assessed using posterior predictive checks and convergence diagnostics, ensuring the robustness and reliability of pooled estimates. This strategy aligns with established Bayesian approaches where between-study heterogeneity is handled more flexibly than in conventional fixed-metric statistics like R^2.

Subgroup analyses were conducted to evaluate the impact of various cut-off thresholds and time frames for mortality on mNUTRIC score performance: studies were included in the analysis groups according to mNUTRIC thresholds, which included <5 and ≥5. Posterior distributions for sensitivity, specificity, and AUC across these thresholds were compared for the selection of the better-optimized values for risk stratification. Separate analyses were conducted for studies that examined the individual outcome of 28 days' mortality in comparison with other time frames. This allowed us to assess the viability of the mNUTRIC score for both short-term and long-term outcomes.

The primary parameters evaluated in this study aided in a thorough evaluation of the mNUTRIC score's prediction accuracy. The measures of the diagnostic performances of the tests provided are as follows:[41]

$$PLR = \frac{Se}{1-Sp}, \quad NLR = \frac{(1-Se)}{Sp}$$

$$AUC = \int_0^1 Sp\,(Sp)\,d\,Sp$$

These equations describe how these tests can better separate high-risk vs low-risk patients, including details of sensitivity, specificity, and overall diagnostic performance. We deemed sensitivity and specificity to be the most important markers of the test's ability to correctly identify high-risk and low-risk individuals, while positive likelihood ratios (PLRs) and negative likelihood ratios (NLRs) demonstrated how beneficial this test can be in assessing mortality risk. Area under the curve (AUC) is a summary statistic of overall diagnostic performance that can be described by a single value, which describes the discriminative performance. Such metrics were assessed by posterior distributions and presented with 95% credible intervals (CrIs), which represent plausible ranges for each estimate demonstrating the robustness of the findings in the context of Bayesian analysis.

Table 1: Posterior estimates of diagnostic performance

Metric	*Mean estimate*	*95% CrI*	*Interpretation*
Sensitivity	0.84	0.80–0.88	High sensitivity indicates strong ability to identify patients at high nutritional risk
Specificity	0.77	0.73–0.80	Moderate specificity reflects acceptable accuracy in excluding low-risk patients
Area under the curve	0.88	0.83–0.92	AUC indicates excellent overall diagnostic accuracy of the mNUTRIC score
Positive likelihood ratio	3.0	2.5–3.5	LR+ suggests the test increases the likelihood of high nutritional risk by three times
Negative likelihood ratio	0.26	0.21–0.32	LR– suggests a 74% reduction in the likelihood of high nutritional risk after a negative test

Bayesian modeling was performed using the rjags and brms packages in R version 3.2.1 (R Foundation for Statistical Computing, Vienna, Austria). These tools also facilitated the visualization of results, including posterior distributions, forest plots, and Fagan nomograms, thereby enhancing the interpretability of the model outputs. This improved the clarity in presenting and interpreting the findings. This study approached the problem of assessing the diagnostic capabilities of the mNUTRIC score from a Bayesian standpoint by addressing the heterogeneity existing between studies and extending the implications of its use in critical care.

Results

A total of 31 cohort studies comprising 13,271 critically ill patients from diverse ICU settings were included in the analysis.[6–36] The Bayesian pooled estimates demonstrated that the mNUTRIC score has excellent discriminative capability for predicting mortality in this population. The pooled sensitivity was 0.84 (95% CrI: 0.80–0.88), the specificity was 0.77 (95% CrI: 0.73–0.80), and the AUC was 0.88 (95% CrI: 0.83–0.92), indicating strong diagnostic accuracy. The PLR was 3.0 (95% CrI: 2.5–3.5), while the NLR was 0.26 (95% CrI: 0.21–0.32), reflecting substantial shifts in posttest probability based on test outcomes (Table 1, Figs 1 and 2).

The Bayesian forest plots revealed consistent estimates across individual studies. Although moderate heterogeneity was observed, the score's diagnostic performance remained robust, underscoring its generalizability across varied ICU environments and patient populations (Figs 3 and 4).

Subgroup analysis based on mNUTRIC thresholds showed that a cut-off of <5 yielded slightly higher diagnostic accuracy (sensitivity: 0.83; specificity: 0.74; AUC: 0.87) compared with ≥5 (sensitivity: 0.78; specificity: 0.71; AUC: 0.84) (Table 2). These findings suggest that a

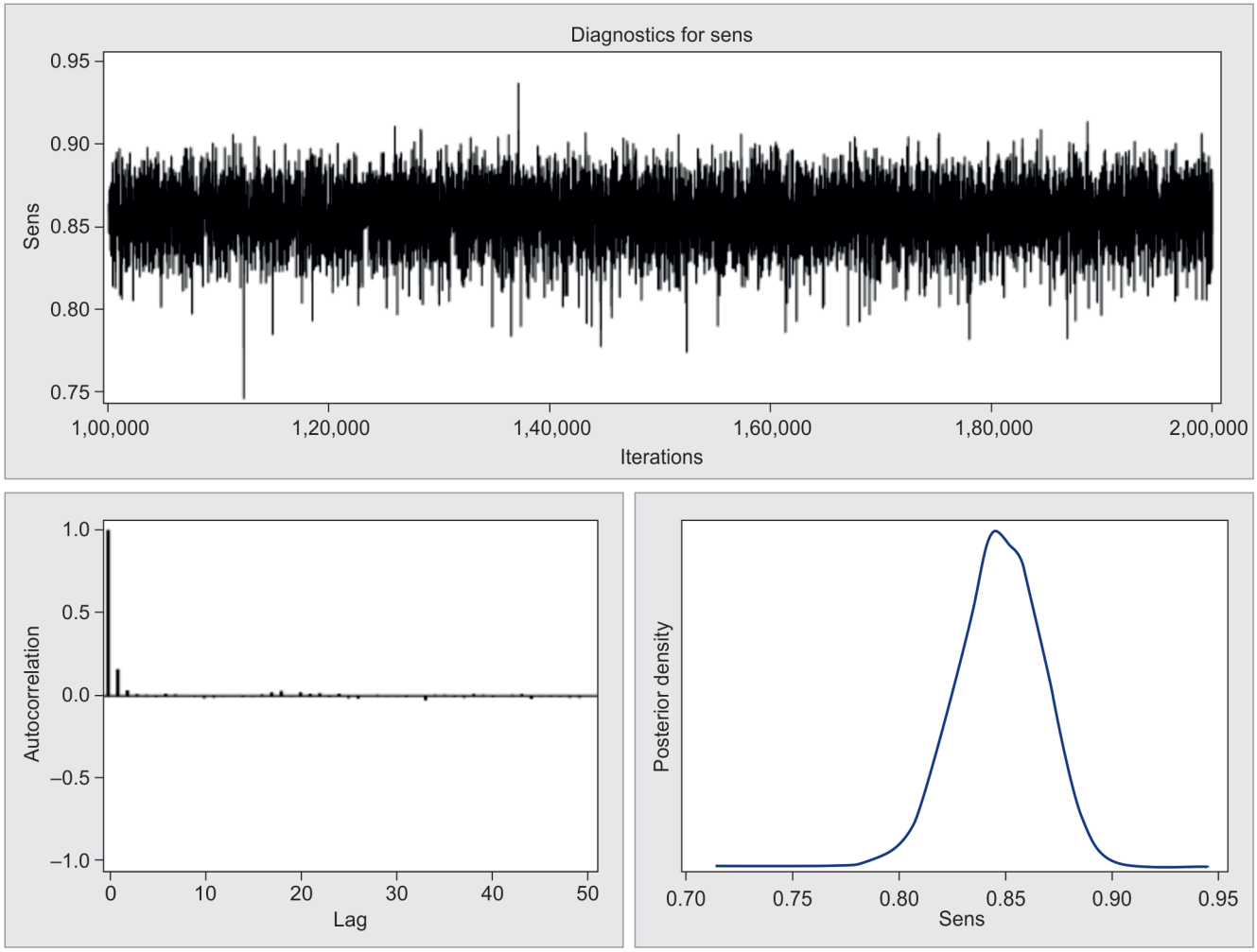

Fig. 1: Posterior distributions of sensitivity for the mNUTRIC score

lower threshold may be more suitable for the early identification of patients at high nutritional and mortality risk, facilitating timely interventions.

Further subgroup analysis across different mortality timeframes confirmed the consistency of the score's predictive capacity. In-hospital mortality demonstrated the highest sensitivity (0.83), whereas 28-day mortality yielded the highest specificity (0.73). The AUC values remained high across all intervals—0.86 for 28-day, 0.83 for 90-day, and 0.85 for in-hospital mortality—indicating stable performance across both short- and long-term outcomes (Table 3).

A Fagan nomogram further illustrated the clinical utility of the mNUTRIC score. At a pretest mortality probability of 50%, a positive score increased the posttest probability to 75%, while a negative score decreased it to 21%. This supports its application in critical care settings as a practical tool for mortality risk stratification and decision-making regarding nutritional support. It incorporates the use of the PLR, which in this analysis was 3.0. This value, along with a pretest probability of 50%, was used to calculate a posttest probability of 75%, illustrating how the PLR contributes to updating clinical probability using Bayes' theorem (Fig. 5).

Discussion

The present Bayesian approach reinforces the modified NUTRIC (mNUTRIC) score as an essential and highly reliable tool for predicting mortality in critically ill patients. Our findings confirm its high sensitivity of 0.84 (95% CrI: 0.80–0.88), emphasizing its ability to effectively identify high-risk patients, while a specificity of 0.77 (95% CrI: 0.73–0.80) ensures a strong capacity to exclude low-risk individuals. The powerful discriminative ability of the score, highlighted by an AUC of 0.88 (95% CrI: 0.83–0.92), positions it as an indispensable component in ICU mortality risk stratification. These findings underline its therapeutic value and are consistent with earlier research, demonstrating its application in ICU settings.[25,34]

Our findings are consistent with those of Mukhopadhyay et al. and Wang et al., who also found the mNUTRIC score to be a strong predictor.[7,11] The mNUTRIC has better performance as compared with older-age scoring systems like APACHE II and SOFA, since it incorporates nutritional status along with illness severity in giving a comprehensive assessment of the risk of mortality.[32] A fundamental characteristic of Bayesian analysis is that it leads pooled estimates to become more relevant and usable for diverse clinical settings by taking into account the differences in ICU protocols, patient

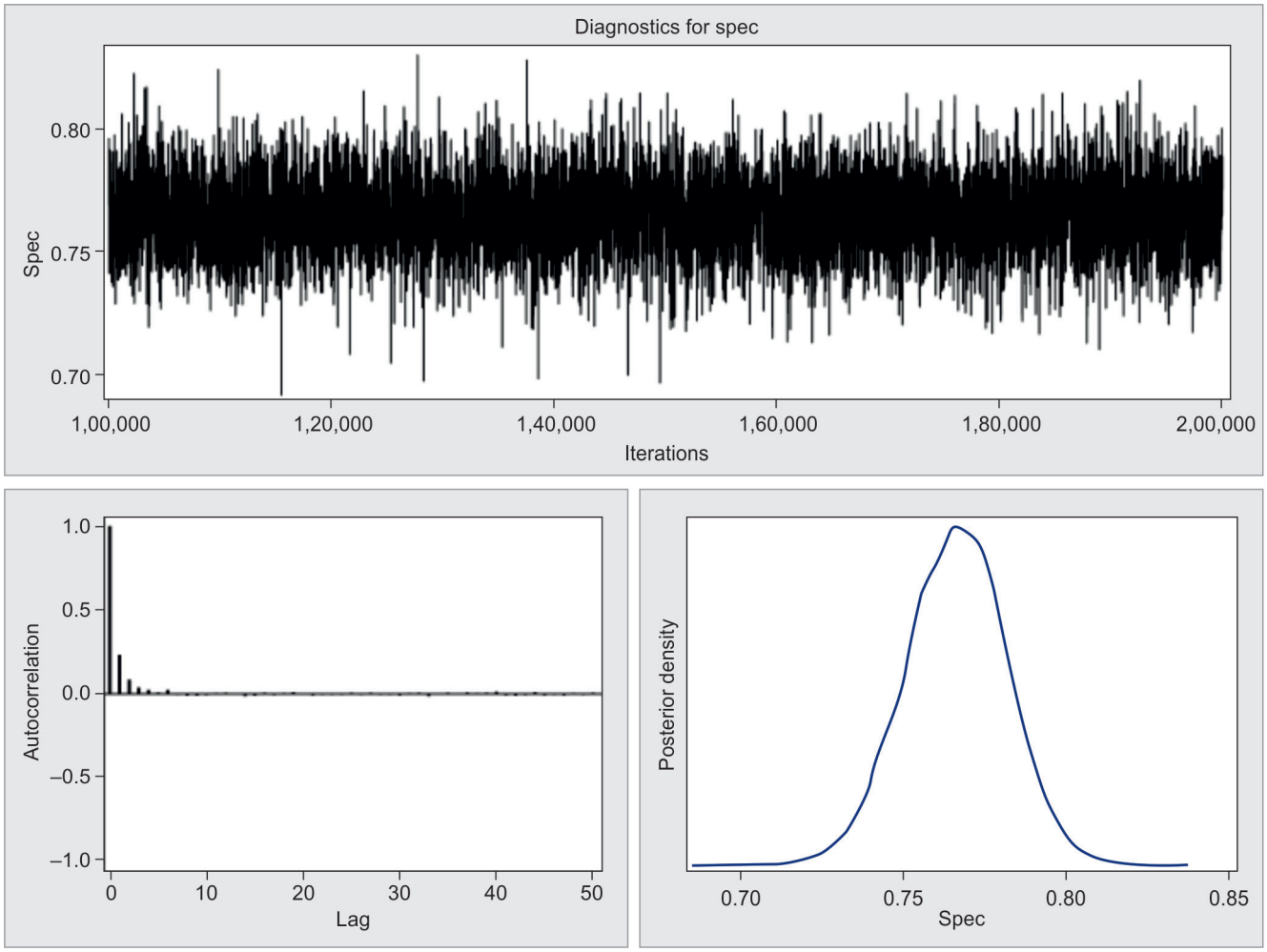

Fig. 2: Posterior distributions of specificity for the mNUTRIC score

characteristics, and geographic settings. In addition, contrary to traditional meta-analysis, where the general combined estimate is mostly considered fixed, Bayesian approaches constitute a dynamic, more adaptable framework that allows for a fine clinical and relevant evaluation.[42,43] The use of likelihood ratios enhances the applicability in real life because, by engaging posttest probabilities for managing ICU treatment, likelihood ratios appreciably sharpen a guide for ICU treatment.

A subgroup analysis comparing different threshold cut-off values (<5 vs ≥5) showed that <5 is more sensitive (0.83) and has a better AUC (0.87) than ≥5 (sensitivity: 0.78; AUC: 0.84). These data support that a lowered threshold would be able to make early identification of high-risk patients, thus allowing for focused nutritional therapy. A higher threshold (≥5) is shown to retain reasonable predictive accuracy, but lower sensitivity increases the possibility of missing high-risk patients. These findings highlight the need for flexibility in defining mNUTRIC cut-off levels, which allows ICU staff to modify risk assessments based on patient demographics and institutional priorities.

The predictive efficacy of the mNUTRIC score for predicting mortality was found to be steady across different time frames: it showed high performance for 28-day, 90-day, and in-hospital predictions, and thus a chance of detection for mortality. Most importantly, in-hospital mortality had the highest sensitivity (0.83), while 28-day detection had a higher specificity (0.73). This result, therefore, emphasizes the relevance of mNUTRIC in earlier assessments of the ICU risk and in planning intervention strategies. This indicates the need to explore mNUTRIC and include it in standard ICU protocols in preferentially targeted high-risk patients due to specified nutritional support. Focused nutritional interventions, including enteral or parenteral supplementation, should be initiated as necessary on high-risk patients, including those admitted to the ICU.

The high pooled sensitivity of 0.84 demonstrates the mNUTRIC score's remarkable ability to identify critically ill patients at high nutritional risk, allowing for early and targeted nutritional intervention. Meanwhile, the pooled specificity of 0.77, while moderate, is nevertheless appropriate for screening purposes because it reliably excludes the majority of patients who are not at high-risk. The consistent performance shown in the hierarchical forest plots across various ICU settings further supports the score's generalizability and facilitates its routine integration into critical care

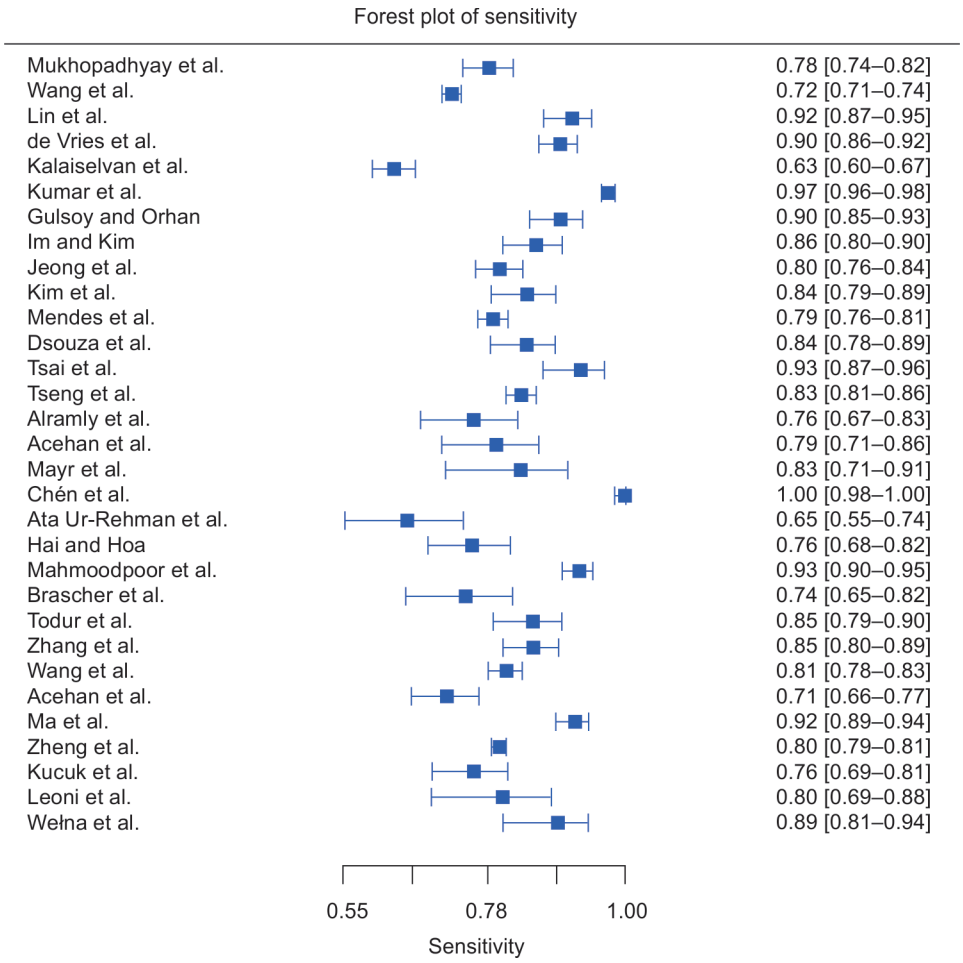

Fig. 3: Forest plot of sensitivity across studies

protocols. In clinical practice, this robust diagnostic performance suggests that the mNUTRIC score is a useful tool for ICU clinicians to direct the timely and effective allocation of nutritional support to those who are most likely to benefit. The Fagan nomogram further demonstrates the clinical practicality of mNUTRIC, showcasing its ability to refine mortality risk predictions. In a patient with an estimated pretest probability of 50%, a positive test result increases the posttest probability to 75%, while a negative test lowers it to 21%. These findings highlight the score's utility in prioritizing interventions for patients most likely to benefit, particularly in resource-limited settings where the efficient allocation of medical and nutritional resources is crucial.

In clinical practice, the mNUTRIC score has proved to be a valuable tool that can be used to ascertain those ICU patients who would benefit most from intensive nutritional therapy.[44] Malnourished individuals are more susceptible to infection, decreased immunity, and increased length of hospital stay. The mNUTRIC facilitates the early assessment of such risks, leading to timely and tailored nutritional therapy, with proven effects in improving the outcome of patients with malnutrition.[45] Im and Kim revealed that nutritional therapy based on high mNUTRIC scores appeared to have a considerable reduction in 28-day mortality in the ICU patient population, highlighting the utility of the score as a means to improve patient outcomes.[9] The moderate specificity of the score limits its ability to fully exclude low-risk patients; the excellent sensitivity favors the recognition and adequate management of a large proportion of high-risk patients. Of importance in the context of an ICU, the loss of a high-risk patient would be serious. This limitation can be done away with by using additional clinical tools in conjunction with mNUTRIC to round the risk assessment off and improve diagnosis accuracy. The possible incorporation of further prognostic markers can enhance its predictability even further.

The Bayesian analysis employed in this study effectively accounted for significant heterogeneity among included studies ($I^2 > 85\%$). Prior meta-analyses of diagnostic tools often struggle with such heterogeneity due to variations in patient populations, ICU protocols, and healthcare settings.[5,46] By leveraging Bayesian approach, our analysis provides a robust pooled estimate, ensuring the generalizability of findings across different ICU environments. This further supports the widespread adoption of the mNUTRIC score as a standard risk assessment tool in critical care.

Our Bayesian analysis confirmed that the mNUTRIC score is highly sensitive; however, heterogeneity across studies may alter its generalizability to different ICU settings. Furthermore, this scoring is completely dependent on clinical data collected routinely and not on any more direct measures of nutritional impact, such as weight loss. The choice of noninformative priors may restrict

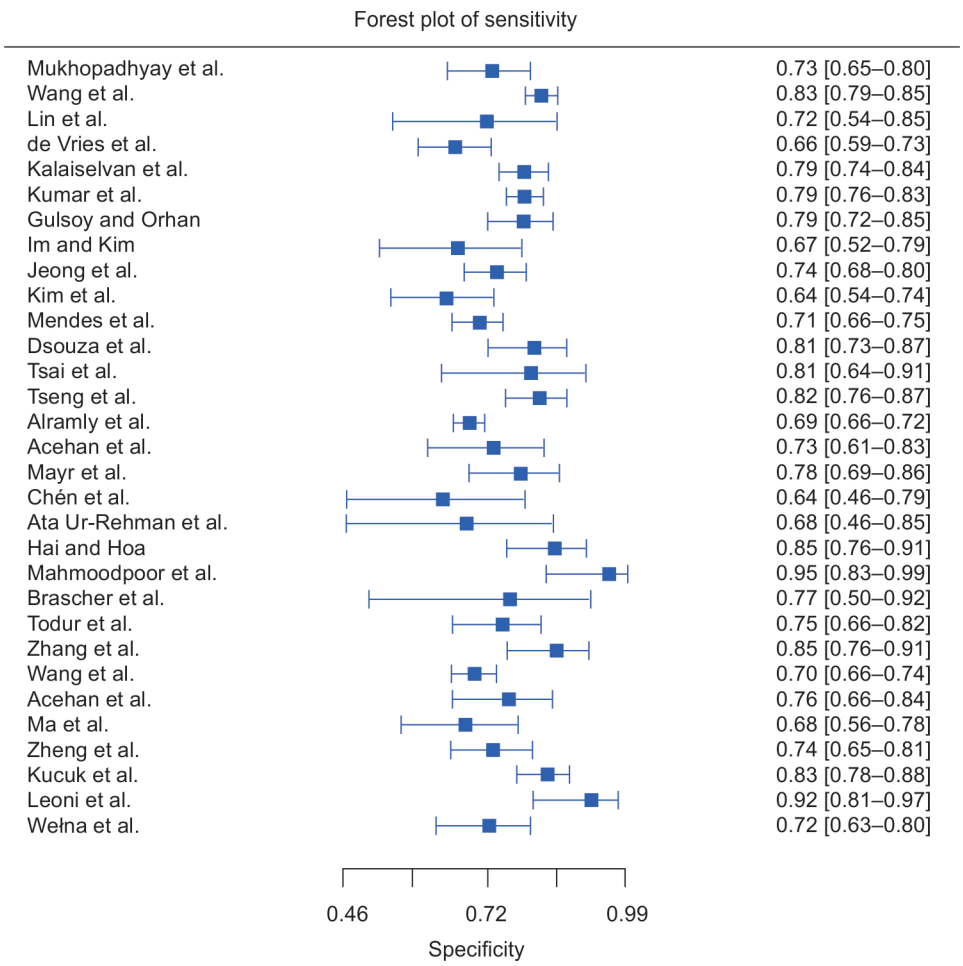

Fig. 4: Forest plot of specificity across studies

Table 2: Subgroup analysis by cut-off thresholds

Threshold	*Number of studies*	*Pooled sensitivity*	*Pooled specificity*	*AUC*	*95% CrI for AUC*
<5	15	0.83	0.74	0.87	0.82–0.91
≥5	16	0.78	0.71	0.84	0.79–0.88

AUC, area under the curve, CrI, credible interval

Table 3: Subgroup analysis by mortality timeframes

Mortality timeframe	*Number of studies*	*Pooled sensitivity (95% CrI)*	*Pooled specificity (95% CrI)*	*AUC (95% CrI)*
28 days	20	0.81 (0.75–0.87)	0.73 (0.66–0.79)	0.86 (0.80–0.90)
90 days	8	0.79 (0.72–0.85)	0.70 (0.63–0.77)	0.83 (0.78–0.87)
In-hospital	3	0.83 (0.76–0.89)	0.75 (0.68–0.81)	0.85 (0.79–0.89)

the incorporation of existing clinical knowledge, and variability in optimal cut-off thresholds across studies signifies the need for further refinement in diverse patient populations.

Conclusion

The mNUTRIC score may predict mortality in critically ill patients. High sensitivity assures the identification of the most at-risk patients in time for early and targeted intervention to mitigate adverse sequelae. However, relative specificity indicates trade-offs making this a potentially useful screening tool, particularly in the critical care settings, where missing high-risk cases could carry catastrophic consequences. This Bayesian analysis enhances understanding by addressing variability and providing credible pooled estimates, further supporting the mNUTRIC score's role in ICU decision-making. Future research should focus on validating the score across diverse populations and exploring its integration into routine practice for improved patient outcomes.

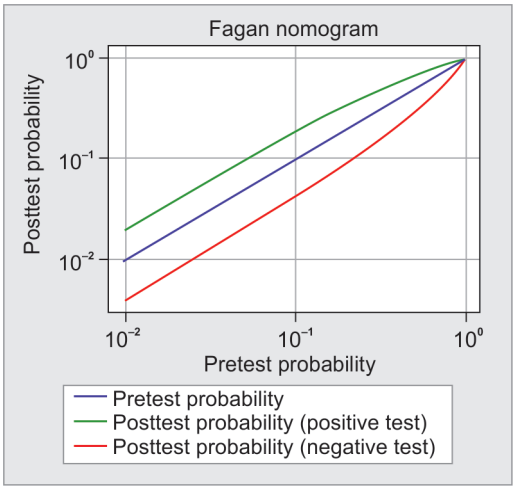

Fig. 5: Fagan nomogram for clinical utility of the mNUTRIC score

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