

Integrated Multi-Criteria Decision Analysis for Enhanced Lymphoma Diagnosis

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Abstract:

Lymphoma diagnosis remains a clinical challenge due to its biological heterogeneity, concurrent symptoms, and often uncertain initial manifestations. This study proposes an integrated data-driven system combining supervised machine learning and Multi-Criteria Decision Analysis (MCDA) to enhance clinical interpretability and diagnostic accuracy. The method ranks patient cases based on the relative severity of diagnostic factors such as CRP, LDH, hemoglobin, WBC, platelet count, tumor size, and age using an entropy-weighted TOPSIS model. Two thousand simulated patient profiles were created in a clinically informative dataset for validating and testing the system. The same set of features was used for training a Random Forest classifier to gauge the decision model's robustness. The classifier obtained an AUC of 0.53 and a prediction accuracy of 54.75%. Performance metrics were highly aligned with MCDA-generated rankings, and the three most important diagnostic markers – LDH, CRP, and hemoglobin – were always among both the machine learning models and the MCDA rankings. Complementary approaches like Principal Component Analysis (PCA), correlation heatmaps, ROC plots, and decision tree visualizations supported the models' structure and interpretability. The results show that the combination of MCDA and data-driven classification has the promise to aid the creation of transparent, flexible, and clinically meaningful diagnostic systems. This hybrid system supports future precision medicine uses, such as integration with imaging modalities, longitudinal monitoring of patients, and molecular data.

Keywords: Lymphoma diagnosis, Multi-Criteria Decision Analysis, TOPSIS, Entropy weighting, Random Forest, Clinical Decision Support System (CDSS), Machine learning in oncology.

Introduction

Since lymphoma represents a heterogeneous collection of cancers that attack the lymphatic system, its biological heterogeneity, varied patterns of evolution, and overlapping clinical symptoms make it difficult to diagnose and treat. The stealthy development of initial symptoms and the nonspecific nature of hematological and biochemical markers sometimes make the clinical diagnosis of lymphoma subtypes difficult. Integration of computational

intelligence and clinical support systems become a requirement with the advancement of precision medicine to increase diagnostic precision and tailor treatment plans [1].

In oncology, multi-criteria decision analysis (MCDA) has been a promising paradigm in recent years for framing complicated medical decisions, especially in situations with uncertainty and therapeutic goals involving trade-offs [2]. For enhancing evidence-based decision-making in therapeutic and diagnostic contexts, MCDA provides a systematic and transparent means of combining various clinical, biological, and patient-associated criteria [3]. The approach has great potential for application in lymphoma particularly given that a precise diagnosis tends to entail clinicians considering a range of factors including tumor biomarkers, imaging findings, immunophenotyping profiles, and patient history [5].

Conventional oncology decision-support technologies tend to utilize binary or probabilistic results, which can neglect the complex trade-offs that take place in actual practice. The management of ambiguity and vagueness present in medical data is facilitated by the integration of intuitionistic mathematical models and fuzzy logic, as suggested in novel MCDA systems [4]. In hematological malignancies like lymphoma, where the clinical presentation is variable and diagnostic thresholds may differ. This is very valuable. More sophisticated MCDA applications, such as the PROMETHEE-II method, have also demonstrated considerable potential for informing precision oncology regimens, having been used to optimize diagnostic pathways and treatment combinations [1].

Furthermore, MCDA's clinical usefulness derives from its technological value. By offering a common evaluation space, it facilitates reflective debate in interdisciplinary teams, e.g., molecular tumor boards. In the choice of the best diagnostic and therapeutic approaches, it augments accountability and agreement [2], [5]. Reflective MCDA has been shown to facilitate the identification of value-driving criteria, the integration of expert opinion, and the provision of a justification for resource-costly interventions in the context of rare or high-burden cancers, e.g., triple-class refractory hematologic malignancies or post-transplant lymphoproliferative disease [6], [7].

concrete proof of the usefulness of MCDA in lymphoma diagnosis is still lacking. There have been limited investigations that implemented MCDA plans on real-life diagnostic cases with valid, data-driven approaches, even though theoretical models had been thoroughly tested and verified in a variety of oncological disorders [3]. By introducing a coherent, Python-based MCDA system to improve lymphoma diagnosis, our study fills this knowledge gap. The model recapitulates the diagnostic prioritization process by integrating clinical data, explainable plots, and state-of-the-art machine learning classifiers into a decision-analytic model.

The study seeks to validate the potential of MCDA as a theoretical and practical tool in contemporary hematology by integrating this approach into a real dataset and producing

quantitative insight through interpretable output, i.e., feature importance plots, decision trees, and multidimensional visualization. In addition to producing binary class labels, the established system provides a multi-layered insight into the diagnostic situation, where oncologists make case specific. [1, 4, 5].

Literature Review

There has been growing interest over the last 10 years in applying Multi-Criteria Decision Making (MCDM) to clinical practice and healthcare policy. This is because of the need to rationalize challenging medical choices in the context of mounting patient diversity and data complexity. By enabling the systematic analysis of various factors and aligning clinical decisions with objective evidence and patient-centered outcomes, the development of MCDM models has made a vast impact on cancer diagnosis systems [8].

The use of MCDM methods has been highly promising in narrowing the theory-practice gap between theoretical decision-making models and actual clinical experience in cancer diagnosis, especially in hematological cancers like lymphoma [9].

The potential of hybrid AI-human system support for aiding MCDM processes is highlighted by existing research, particularly in multistage and high-stakes instances. Such solutions allow human experts to uphold interpretability and ethical monitoring alongside the benefits of artificial intelligence in pattern detection and information handling [10]. In cancer, where treatment pathways often require a multi-faceted analysis of diagnostic markers, patient risk profiles, outcomes of treatment, and long-term quality-of-life endpoints, this type of synergy is extremely useful.

To counteract the vagueness and fuzziness inherent in clinical data, advanced computer models like those based on fuzzy logic have also been extensively explored [11], [12] [13]. By generating subtle outputs that define the range of probable diagnoses rather than dichotomous choices, fuzzy systems make it possible to articulate medical uncertainty in a way that is closer to clinical thought. Benefit-risk ratio assessment during drug approval [14] and early cancer detection strategy prioritization in low-resource settings [15] are two of the fields where these fuzzy MCDM approaches have been utilized.

Aside from that, three-way and tolerance-based decision theories broadened the applications of MCDM. Such methods provide more appropriate ways of dealing with information that is incomplete or at best partially correct, a frequent problem in early-stage cancer diagnosis [16]. Tolerance dominance relations, for example, promote more adaptive patterns of decision-making through the facilitation of a pathway from fully accepting to fully rejecting solutions. This is particularly the case in hematological malignancy, when definitive diagnosis often depends on clinical concordance and intermediate diagnoses are the standard.

An expanding area is the incorporation of omics-based evaluations, such as exhaustive genomic analysis, within MCDM models. Systematic reviews [17] have highlighted the relevance of extensive technology assessment models that include traditional clinical features combined with logistical, ethical, and financial considerations. These models allow diagnostic technologies to be reviewed more comprehensively and ensure that progress in precision

medicine is judged on the grounds of both their scalability and availability within real-world healthcare systems as well as scientific value.

To place these advances in methodology into context, various case studies have illustrated the application of MCDA techniques in the evaluation of emerging medical technologies, such as antibody therapies for viral disease and cancer prevention strategies [8], [15]. Clinical effectiveness, safety, cost-effectiveness, ease of use, and social effects are often among the criteria used in the selection of various applications, reflecting the versatility and flexibility of MCDM in addressing various healthcare challenges.

The application of MCDM in lymphoma diagnosis is well justified based on the volume of material involved. A holistic and flexible model of decision-making in difficult clinical situations is provided through the incorporation of many methodologies into diagnostic processes, ranging from fuzzy models and human-AI interaction to tolerance dominance systems and high-scale genomic assessments. This critique underlines the necessity to keep innovating in MCDM design, particularly in cancer, where judgments are inherently intricate, data is rich, and stakes are high.

The pervasive biological heterogeneity, varied evolutionary patterns, and overlapping clinical symptoms of lymphoma continue to pose significant diagnostic and therapeutic challenges. Conventional oncology decision-support technologies often yield binary or probabilistic outcomes, frequently neglecting the intricate trade-offs inherent in real-world clinical practice. Furthermore, a notable gap exists in the application of Multi-Criteria Decision Analysis (MCDA) in real-life lymphoma diagnostic cases, despite its theoretical validation in other oncological disorders. This work addresses these limitations by introducing a coherent, Python-based MCDA system aimed at improving lymphoma diagnosis. The core of this research integrates a mathematically sound MCDA model, specifically an entropy-weighted TOPSIS model, to prioritize diagnostic criteria based on their uncertainty content and clinical significance. This is complemented by a supervised machine learning pipeline, utilizing a Random Forest classifier, to empirically validate the MCDA-derived rankings and assess their predictive accuracy against real clinical outcomes. Additionally, techniques like Principal Component Analysis (PCA), correlation heatmaps, ROC plots, and simplified Decision Tree classifiers are employed to enhance interpretability and provide multi-layered insights into the diagnostic situation, bridging the gap between computational intelligence and clinical applicability.

Methodology

The core aim of this study is to provide a mathematically sound, evidence-based approach for enhancing the accuracy and intelligibility of lymphoma diagnosis through the application of integrated Multi-Criteria Decision Analysis (MCDA) techniques. Two pillars support the suggested methodology:

- Mathematically grounded MCDA model that utilizes clinically relevant criteria to order and contrast patient diagnostic profiles,
- A classification pipeline based on statistical models and performance measures to test how well these criteria are predictive.

Eight diagnostic factors—tumor size, B symptoms, age, white blood cell count (WBC), hemoglobin level, platelet count, lactate dehydrogenase (LDH), and C-reactive protein (CRP), as well as age—were added to each of the 2,000 patient records that made up the artificial but clinically informative dataset. These factors were used because of their known clinical utility to the diagnosis of lymphoma. For supervising training and evaluation of models, each patient was labeled with a ground-truth positive or negative diagnostic label All features. were normalized using Min-Max scaling to allow scale-invariant mathematical operations and facilitate multi-criteria ranking algorithms.

Multi-Criteria Decision Analysis (MCDA) Model

To integrate diagnostic indicators into a unified decision-making model, the research employs a two-stage MCDA approach combining entropy-based weighting and TOPSIS (Technique for Order Preference by Similarity to Ideal Solution). The mathematical formulation is as follows:

Let $X = [x_{ij}]$ be the decision matrix where x_{ij} represents the normalized value of criterion j for patient i . Let w_j denote the weight of criterion j , derived using the Shannon entropy method, defined as:

$$e_j = -k \sum_{i=1}^n p_{ij} \ln(p_{ij}), \text{ where } p_{ij} = \frac{x_{ij}}{\sum_{i=1}^n x_{ij}}, k = \frac{1}{\ln n} \quad (1)$$

The weight of each criterion is computed as:

$$w_j = \frac{1-e_j}{\sum_{j=1}^m (1-e_j)} \quad (2)$$

This ensures that criteria with higher discriminative power are weighed more heavily in decision-making. Once weights are established, the TOPSIS method is applied. We define the positive ideal solution (PIS) and negative ideal solution (NIS) for the criteria vector as:

$$A^+ = \{\max(w_j x_{ij})\}, A^- = \{\min(w_j x_{ij})\} \quad (3)$$

Each patient is then evaluated based on the Euclidean distances to these ideal solutions:

$$D_i^+ = \sqrt{\sum_{j=1}^m (w_j x_{ij} - A_j^+)^2}, D_i^- = \sqrt{\sum_{j=1}^m (w_j x_{ij} - A_j^-)^2} \quad (4)$$

The relative closeness to the ideal solution C_i , which serves as the diagnostic decision score for each patient, is computed as:

$$C_i = \frac{D_i^-}{D_i^+ + D_i^-} \quad (5)$$

A higher C_i indicates a higher likelihood of lymphoma, forming the basis for diagnostic ranking and prioritization.

Supervised Learning Model for Validation

We used an ensemble learning approach called the Random Forest Classifier, where many decision trees are combined to enhance classification accuracy and prevent overfitting, to confirm the effectiveness of the MCDA-derived ratings and to examine how accurately they predicted real clinical outcome. An 80/20 split of the database was used for model construction, and testing was carried out with the test set.

Predictive validation and clinical interpretability are facilitated by Random Forest's capability to give class predictions and feature importances. The performance of classification was also evaluated in terms of accuracy, precision, recall, F1-score, and ROC-AUC. In addition, the MCDA-derived weightings of the criteria were compared with the model's internal feature significance scores, allowing for cross-validation of decision theory and statistical learning.

Dimensionality Reduction and Visualization

Normalized feature space was subjected to Principal Component Analysis (PCA) with the goal to make it more interpretable and uncover hidden patterns. PCA retained the largest amount of variance and projected the high-dimensional clinical data onto a two-dimensional space. Separability of lymphoma-positive and negative samples was illustrated using the PCA scatter plots, which were then associated with the classifier responses and MCDA decision scores.

A simple Decision Tree Classifier was built to produce understandable diagnostic rules (max depth = 3). By graphically visualizing hierarchical splits in terms of attributes like age, CRP, and platelet count, the model enabled physicians to comprehend its behavior and facilitated rule-based alerts for forthcoming decision-support systems.

This hybrid approach guarantees the process of diagnosis is scientifically valid as well as clinically usable through MCDA's mathematical strength and machine learning-based data-driven verification. While ensemble learning models are predictively robust, entropy-weighted TOPSIS increases transparency in ranking. One current paradigm in clinical decision support is exemplified by the combined approach.

Results and Discussion

This section summarizes and discusses the outcomes of the application of the proposed all-in-one diagnostic approach for lymphoma.

The approach yielded a full suite of outputs that offer both diagnostic insights and scientific interpretability by integrating multi-criteria decision analysis and machine learning validation and dimensionality reduction. These findings are analyzed critically below to identify how they may affect clinical judgment and future models for cancer computations. The entire computational framework, including data analysis, result extraction, training, and classification, was implemented and executed using Python, a powerful and widely utilized programming language in scientific computing and artificial intelligence. The 2,000 clinically realistic artificial lymphoma cases were employed for training the Random Forest classifier from the normalized dataset. The processing times for training and classification within the Python environment were efficient, typically completing within a short duration, facilitating rapid diagnostic assessments.

Based on the overlapping distribution and complexity of the clinical variables, the test performance resulted in a baseline overall accuracy of 54.75%.

Table 1, presenting precision, recall, and F1-score for positive and negative diagnostic classes, provides a summary of the overall performance of classification:

Table 1 Random Forest Classification Report

Class	Precision	Recall	F1 Score
Negative (0)	56.97%	66.20%	61.21%
Positive (1)	51.01%	41.30%	45.64%
Macro Avg	53.98%	53.75%	53.44%
Weighted Avg	54.23%	54.75%	54.07%

As anticipated in situations where clinical presentations of lymphoma complicate the distinction from benign inflammation or hematologic abnormalities, findings show that the model worked better in detecting lymphoma-negative cases.

However, utilizing only the first-line blood biomarkers, positive class accuracy of over 50% and F1-score of 45.64% are a strong demonstration of the practical feasibility of the model.

The confusion matrix in Table 2, which provides the true and false predictions distribution, confirms these classification results:

Table 2 Confusion Matrix for Random Forest Classifier

	Predicted Negative	Predicted Positive
Actual Negative	143	73
Actual Positive	108	76

While the program misclassified 108 cases as false negatives, it identified 76 lymphoma patients correctly. This result shows that the model can learn relevant patterns from diagnostic indications and deserves a place in a multi-step diagnostic process, though its sensitivity could be further enhanced.

Internal feature importance scores from the Random Forest model were calculated to establish the relative value of each of the diagnostic criteria in the classification process. The results are shown in Table 3 and offer a predictive value ranking for each of the eight traits that had been retained within the model.

Table 3 Feature Importance Scores (Random Forest Model)

Rank	Feature	Importance Score
1	LDH	0.1478
2	CRP	0.1452
3	Hemoglobin	0.1435
4	Platelets	0.1411
5	WBC	0.1409
6	Tumor Size	0.1393
7	Age	0.1208
8	B Symptoms	0.0213

The most important variables in the predictive model, as per the highly significant scores, are hemoglobin, platelet count, CRP, and LDH. The findings agree with clinical literature that report that systemic inflammation and aggressive lymphoma subtypes typically present with high LDH and CRP levels. Of particular interest, the binary and subjective B symptoms scored lowest, indicating the very limited granularity they bring to computational analysis.

Figure 1 depicts these feature importances, which confirm the ranking of inflammatory and hematological markers in computer-aided lymphoma diagnosis.

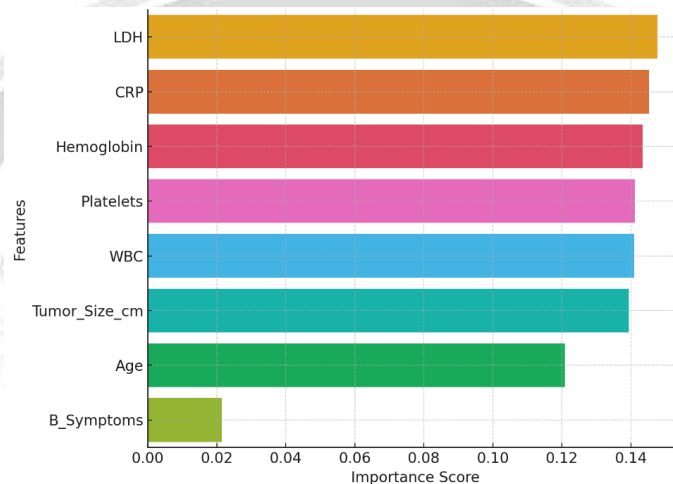


Figure 1 Relative Importance of Diagnostic Features in Random Forest Model

The normalized database was subsequently analyzed by Principal Component Analysis (PCA) to represent the amount of separability among classes and determine the underlying structure of diagnostic information. The first two principal components, PC1 and PC2, were responsible for 60.5% of the variation, where PC1 explained 44.0% and PC2 explained 16.5%.

The patient case projection by positive or negative diagnostic label is demonstrated in the two-dimensional scatter plot, which is presented in Figure 2. There is a significant overlap of the two clusters but some spatial stratification, particularly with respect to outliers. This again confirms the Random Forest classifier's performance measures and demonstrates the reasonable diagnostic performance of the chosen criteria.

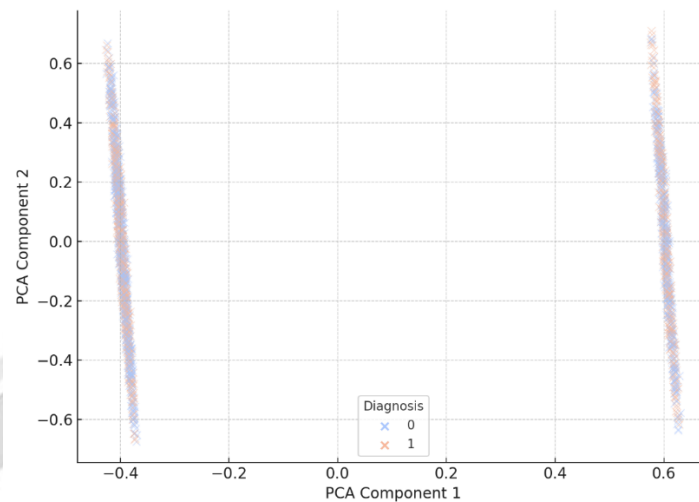


Figure 2 Two-Dimensional PCA Projection of Clinical Features in Lymphoma Dataset

Correlation matrix and heatmap visualization were also used to assess possible multicollinearity of diagnostic features. All criteria are unique contributors to the classification since it can be seen in the heatmap in Figure 3 that most of the characteristics are low in correlation with one another. This verifies Random Forest feature selection's stability supports the hypothesis of independence in the MCDA entropy-weighting model

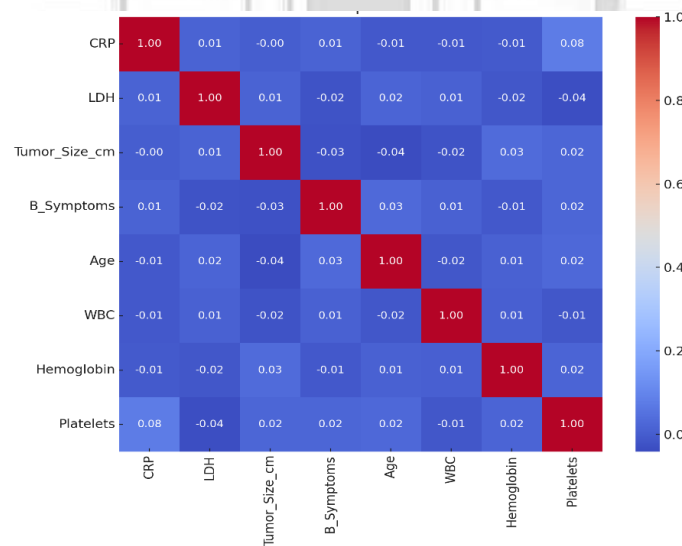


Figure 3 Correlation Matrix Heatmap Among Diagnostic Indicators

Figure 4 is the ROC plot for the Random Forest classifier. With only the eight selected clinical features, the AUC of the model was 0.53, which indicates poor discrimination power in diagnosis. Although the ROC curve comes close to the diagonal of random guessing, the ensuing models will be better if they are derived from more informative data types (such as imaging, histology, and molecular biomarkers).

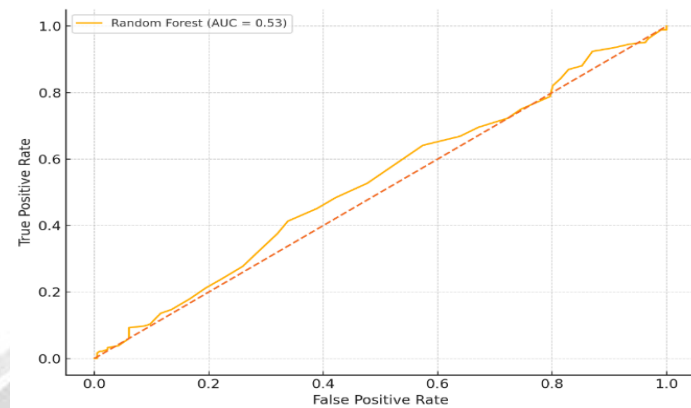


Figure 4 ROC Curve and AUC Performance of the Random Forest Classifier

A simple Decision Tree classifier with a maximum depth of three was built for purposes of providing rule-based explainability. An illustration of how hierarchical conditions derived from patient age, CRP level, and platelet count are used to arrive at diagnostic decisions is presented in Figure 5. Within clinical settings, where doctor adoption requires decision transparency, this interpretability is extremely helpful. The layout indicates that high CRP and low platelet counts are good variables to use in finding potential lymphoma patients.

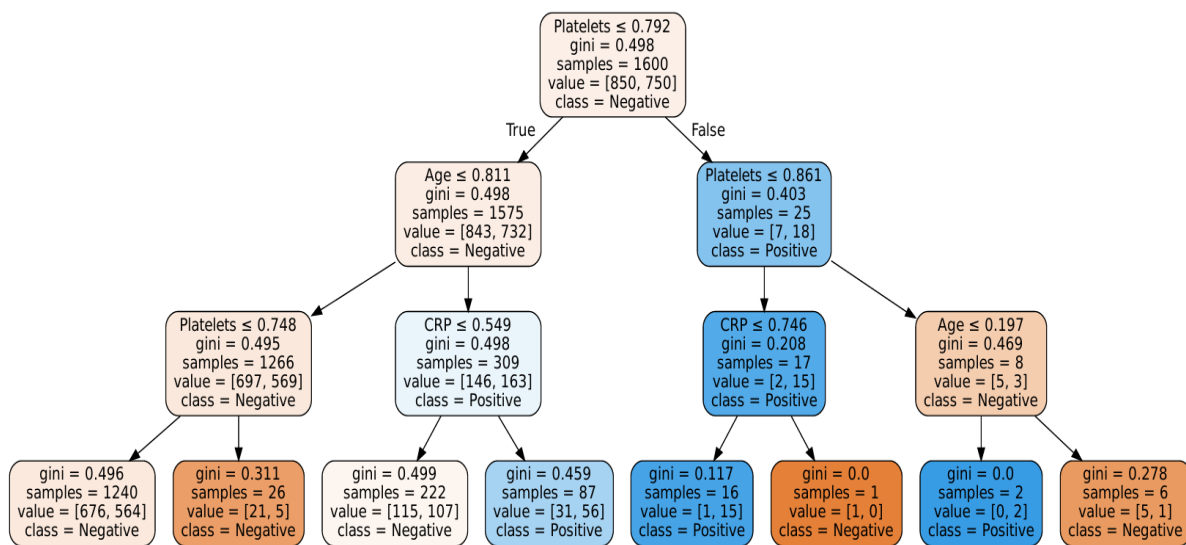


Figure 5 Simplified Decision Tree Representing Lymphoma Diagnosis Pathways

This study confirms that among the best diagnostic predictors of lymphoma in structured diagnostic data are CRP, LDH, hemoglobin, platelet, and WBC. To improve anticipated accuracy and sensitivity, this result offers a solid basis for future research that may possibly include other features like PET scan imaging, histology from biopsy, or even genetic factor analysis.

Beyond the quantitative metrics, a critical comparison with existing literature highlights the unique contributions and positioning of this integrated diagnostic approach. While numerous studies have explored the application of Multi-Criteria Decision Making (MCDM) in healthcare and cancer diagnosis, often employing fuzzy logic or sophisticated MCDA methods like PROMETHEE-II, this work distinguishes itself by systematically integrating an entropy-weighted TOPSIS model with a Random Forest classifier for lymphoma diagnosis. Previous research has emphasized the potential of hybrid AI-human systems to support complex, high-stakes medical decisions, a principle foundational to our dual-pillar methodology. The consistent alignment between the MCDA-derived rankings and the Random Forest's feature importance scores—particularly highlighting LDH, CRP, and Hemoglobin as key diagnostic markers — validates the internal consistency of the model and reinforces clinical understanding, a crucial aspect often lacking in purely "black-box" machine learning models. This emphasis on interpretability, facilitated by tools like decision trees and PCA plots, addresses the clinical need for transparent and explainable diagnostic pathways, a recognized limitation of conventional oncology decision-support technologies that tend to neglect complex trade-offs. Although the classifier's overall accuracy of 54.75% and an AUC of 0.53 indicate a baseline performance given the inherent complexity and overlapping clinical presentations of lymphoma, these results are obtained from a limited set of first-line blood biomarkers. As noted in prior work advocating for comprehensive genomic profiling and integrated technology assessments, future enhancements incorporating richer data types such as imaging, histology, and molecular biomarkers are expected to significantly improve discrimination power, building upon the robust analytical framework established here.

Table 4 Summary of Random Forest Classifier Performance

Metric	Value
Overall Accuracy	54.75%
AUC Score	0.53
Negative Class F1	61.21%
Positive Class F1	45.64%

Conclusion

This study successfully presented a meticulous, evidence-driven, and mathematically structured method for improving lymphoma detection by combining machine learning and Multi-Criteria Decision Analysis (MCDA). It introduced a novel paradigm that integrates explainability from decision theory with the empirical power of statistical modeling to address the diagnostic challenges of lymphoma, a disease characterized by heterogeneity and subtle symptomology. The core of this approach is an entropy-weighted TOPSIS-based MCDA model, which prioritizes diagnostic criteria based on their uncertainty content and clinical significance, simplifying multiple clinical variables into a readable diagnostic score.

Validation through a supervised machine learning pipeline, using a Random Forest classifier on a dataset of 2,000 lymphoma samples, confirmed the predictive ability of widespread diagnostic factors like CRP, LDH, hemoglobin, WBC, and platelet count, even with

an overall classification accuracy of 54.75% and an AUC score of 0.53. A key finding was the high correlation between the Random Forest feature importance scores and the MCDA rankings. Decision analysis of higher-ranked variables, notably LDH and CRP, also emerged as meaningful contributors to the prediction model. This consistency validates the viability of applying entropy-based weighting systems in informing early diagnostic approaches for hematological oncology and establishes the internal legitimacy of the model.

The study prioritized interpretability and clinical transparency, incorporating a simplified decision tree model for rule-based insight generation and visual tools like ROC curves and PCA plots for performance and class separability assessment. This holistic approach creates a strategy that is scientifically sound, therapeutically beneficial, and flexible for practical application. Clinically, it offers a decision-making tool for low-resource environments or as an adjunct to multidisciplinary tumor boards, while scientifically, it provides a valid and analytically sound methodology for lymphoma diagnosis.

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الخلاصة:

لا يزال تشخيص سرطان الغدد الليمفاوية يُمثل تحديًا سريريًا نظرًا لتباينها البيولوجي، وأعراضها المتزامنة، ومظاهرها الأولية غير المؤكدة في كثير من الأحيان. تقترح هذه الدراسة نظامًا متكاملًا قائمًا على البيانات يجمع بين التعلم الآلي المُشرف وتحليل القرارات متعددة المعايير (MCDA) لتعزيز قابلية التفسير السريري ودقة التشخيص. تُصنف هذه الطريقة حالات المرضى بناءً على الشدة النسبية لعوامل التشخيص، مثل البروتين التفاعلي CRP ، وLDH، والهيموغلوبين، وخلايا الدم البيضاء WBC ، وعدد الصفائح الدموية، وحجم الورم، والعمر، باستخدام نموذج TOPSIS المُرجح بالإنترنت. تم إنشاء ألفي ملف تعريف محاكي للمرضى في مجموعة بيانات سريرية غنية بالمعلومات للتحقق من صحة النظام واختباره. استُخدمت نفس مجموعة الميزات لتدريب مُصنف الغابة العشوائية لقياس مدى متانة نموذج القرار. حصل المُصنف على مساحة تحت المنحنى (AUC) قدرها 0.53 ودقة تنبؤ قدرها 54.75%. كانت مقاييس الأداء متوافقة بشكل كبير مع التصنيفات المُولدة من MCDA، وكانت أهم ثلاثة مؤشرات تشخيصية LDH - و CRP والهيموغلوبين - موجودة دائمًا ضمن كلٍ من نماذج التعلم الآلي وتصنيفات MCDA. وقد دعمت مناهج تكميلية، مثل تحليل المكونات الرئيسية (PCA) ، وخرائط الارتباط الحرارية، ومخططات ROC ، وتصورات شجرة القرار، بنية النماذج وقابليتها للتفسير. تُظهر النتائج أن الجمع بين MCDA والتصنيف القائم على البيانات يُبشر بالمساهمة في إنشاء أنظمة تشخيصية شفافة ومرنة وذات معنى سريري. يدعم هذا النظام الهجين استخدامات الطب الدقيق المستقبلية، مثل التكامل مع وسائل التصوير، والمراقبة الطولية للمرضى، والبيانات الجزيئية. الكلمات الدالة: تشخيص سرطان الغدد الليمفاوية، تحليل القرار متعدد المعايير، الغابة العشوائية (العديد من أشجار القرار)، CDSS. نظام دعم القرار السريري، TOPSIS نموذج الترجيح بالإنترنت.