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An Ensemble Learning-Based Approach for CBC Anemia Classification

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ABSTRACT

Anemia is one of the most prevalent hematological disorders worldwide, affecting billions and leading to serious health complications. Early detection and accurate classification of anemia types are essential for effective treatment and management. This research proposes a machine learning-based framework for classifying nine distinct types of anemia using Complete Blood Count (CBC) data. The methodology integrates two feature selection techniques Recursive Feature Elimination (RFE) and heatmap correlation analysis to identify the most relevant biomarkers. A stacking ensemble classifier was developed using Random Forest, Support Vector Machine, K-Nearest Neighbors, and Decision Tree as base learners, with logistic regression as the meta-learner. Experimental evaluation showed that the (RFE) derived features yielded superior performance, the Anemia datasets that are available on Kaggle platform was used of which consists of 1,281 observations. The data was balanced to prevent the model from favoring the dominant class in the data. with the final model achieving an accuracy of 99.83%, and F1-score of 99.83%. The results demonstrate the effectiveness of ensemble learning and advanced feature selection in improving diagnostic accuracy and provide strong evidence for deploying intelligent decision-support systems in clinical settings. The generalizability of the proposed model was rigorously evaluated using 1,200 new, unlabeled CBC samples obtained from local laboratories in Misrata. In a blinded clinical validation research, the model's predictions were compared against diagnoses made by expert hematologists, demonstrating strong concordance with an overall agreement of 84.67% across all anemia subtypes. These results underscore the effectiveness of ensemble learning combined with advanced feature selection.

Keywords: Anemia Classification, CBC, Machine Learning, Feature Selection, Stacking Ensemble.

نهج قائم على التعلم التجميعي لتصنيف فقر الدم باستخدام تعداد الدم الكامل

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ملخص البحث

يُعد فقر الدم واحدًا من أكثر الاضطرابات الدموية انتشارًا على مستوى العالم، حيث يُصيب المليارات من الأشخاص وقد يؤدي إلى مضاعفات صحية خطيرة. ويُعد الكشف المبكر والتصنيف الدقيق لأنواع فقر الدم أمرًا أساسيًا للعلاج الفعّال والإدارة السليمة للحالة. يقترح هذا البحث إطار عمل قائمًا على تقنيات التعلم الآلي لتصنيف تسعة أنواع متميزة من فقر الدم باستخدام بيانات فحص الدم الكامل **(CBC)**. تتضمن المنهجية دمج تقنيتي اختيار الخصائص: الاستبعاد التكراري للخصائص **(RFE)** وتحليل الارتباط عبر الخرائط الحرارية لتحديد أهم المؤشرات البيولوجية. تم تطوير مصنف تجميعي من نوع **Stacking** باستخدام كل من الغابة العشوائية **(Random Forest)**، وآلة المتجه الداعم **(SVM)**، وأقرب الجيران **(KNN)**، وشجرة القرار **(Decision Tree)** كنماذج أساسية، مع استخدام الانحدار اللوجستي **(Logistic Regression)** كنموذج ميتا. أظهرت التقييمات التجريبية أن الخصائص المستخرجة باستخدام **RFE** حققت أداءً متفوقًا، حيث استُخدمت مجموعة بيانات فقر الدم المتاحة على منصة **Kaggle**، والتي تتكون من 1281 ملاحظة. تمت موازنة البيانات لمنع النموذج من تفضيل الفئة السائدة. وحقق النموذج النهائي دقة 99.83%، ودرجة **F1** **99.83%**. تُبرز النتائج فعالية التعلم التجميعي وتقنيات اختيار الخصائص المتقدمة في تحسين دقة التشخيص، وتقدم دليلًا قويًا على إمكانية استخدام أنظمة دعم القرار الذكية في الممارسات السريرية. تم تقييم قدرة النموذج على التعميم بشكل صارم باستخدام 1,200 عينة جديدة وغير موسومة من فحص الدم الكامل تم الحصول عليها من مختبرات محلية في مصراتة. في دراسة تحقق سرية مقارنةً بين توقعات النموذج وتشخيصات خبراء أمراض الدم، أظهر المصنف التجميعي توافقًا قويًا مع التقييمات السريرية، حيث بلغ معدل الاتفاق العام 84.67% عبر جميع أنواع فقر الدم. تُؤكد هذه النتائج فعالية التعلم التجميعي عند دمجه مع تقنيات اختيار الخصائص المتقدمة.

الكلمات الدالة: تصنيف فقر الدم، تعداد الدم الكامل، التعلم الآلي، اختيار الميزات، التجميع بالتكديس

INTRODUCTION .

According to the World Health Organization (WHO), Anemia –the most common blood disorder that affects over 1.62 billion people–. Susceptible members including children, pregnant women and elderlies are the group of population most affected [1]. Anemia is the term used to describe a reduction in the amount of circulating red blood cells relative to that necessary to meet oxygen demands, and is diagnosed when hemoglobin (Hb) and hematocrit concentrations fall below certain normal limits [2]. It is an important health problem, representing either a disease itself or a common expression of other diseases. Clinical manifestations are fatigue, cold intolerance, paleness, shortness of breath, dizziness, arrhythmias, headache and chest pain. Anemia is not confined to any age group or sex and could be heredity or caused by iron and vitamin deficiencies specially in pregnant women and old people [3]. It's important to treat early to halt progression toward severe complications such as heart attacks and death caused by an insufficient oxygen supply. Diagnosis includes laboratory and clinical analysis, the principal diagnosis tool being a complete blood count (CBC). Further tests to determine iron, ferritin and vitamin level are performed; special studies such as hemoglobin electrophoresis or bone marrow examinations may be employed in difficult cases. Imaging may be used to detect internal bleeding or check affected organs [4].

Contemporary medicine systems produce huge data, which can be further analyzed to explore relevant information and latent patterns such as disease prediction. Predicting anemia is being used increasingly by machine learning (ML) methods, although it is difficult to model because of the multifarious nexus between different types of anemia and factors [5].

The ensemble ML methods has been considered as a valuable tool for increased accuracy in anemia risk prediction by increasing the space of hypotheses and to improve predications [6].

Anemia is highly prevalent, with more than two billion people worldwide and has extensive harmful consequences [7]. Early identification including those associated with growth limitation are important to stave off sequelae that may result in long-term morbidity, and thus warrant further understanding. This study seeks to develop a predictive model for detecting anemia based on different machine learning algorithms with addressing ensemble learning methods for improving the prediction performance is tested using the dataset collected from local laboratories at Misrata.

The paper specifically attempts to address whether ML algorithms as a whole–in particular ensemble models–can improve diagnostic performance and which biomarkers make the greatest contribution for improvement in prediction accuracy. Inspired from the assumption that ensemble learning in combination with good quality feature selection can overcome standalone classifiers, the approach involves data preprocessing technique followed by Recursive Feature Elimination (RFE) and correlation heatmap analysis for selecting important features, while using a stacking of Random Forest, SVM, K-Nearest Neighbors (KNN), Decision Tree as base learners and logistic regression for meta learner. The analysis is restricted to the particular types of anemia that exist in the dataset, while its performance is assessed by measures including accuracy, precision, recall and F1-score.

1. LITERATURE REVIEW

In recent years, machine learning and ensemble learning techniques have shown considerable promise in enhancing the diagnosis and classification of different types of anemia using CBC data. These advancements address several limitations inherent in traditional diagnostic methods, offering faster, more accurate, and more accessible alternatives.

Given the growing interest in this domain, several recent studies have explored various machine-learning models, and advanced ensemble methods to classify anemia types with high levels of accuracy and robustness.

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In 2023, Dhakal et al. proposed an ML-based framework to predict anemia in children under five years of age using 700 CBC samples collected from Kanti Children's Hospital in Nepal. They applied six classifiers and found Random Forest to consistently yield the highest accuracy (98.4%–98.6%). Ensemble methods like bagging and XGBoost tuning further improved performance, reaching up to 99% accuracy configurations. In a similar context, Dhakal and Bista applied ensemble stacking across the same classifiers and achieved an accuracy of 98.7%, confirming the robustness of ensemble methods in pediatric anemia prediction 98.7% [8]. Also in 2023, El-Boghdady et al. introduced a stacked ensemble model for multi-class anemia classification using a large dataset of 15,300 CBC records from Tokat Gaziosmanpaşa University in Turkey. Their findings showed that individual models such as Logistic Regression, SVM, and Random Forest performed well (up to 99.95%), but the proposed stacking model matched or exceeded their performance, confirming the advantage of ensemble strategies for multi-class tasks [6].

Hasan et al. (2023) implemented a voting ensemble combining KNN, LR, SVM, GNB, and LGBM on an open-source dataset with 1,421 records and achieved a remarkably high accuracy of 99.95% [9]. Similarly, Mugdha et al. (2023) developed a system for estimating hemoglobin levels and anemia severity, with Random Forest achieving the highest performance (96.67%) among the models tested, emphasizing the effectiveness of ensemble learning in both classification and severity assessment [10].

Focusing on iron deficiency anemia (IDA), Pullakhandam and McRoy (2024) proposed a model using Gradient Boosting and RFECV feature selection, achieving high recall (98%) and demonstrating generalizability to independent datasets. Their approach bypassed costly serum ferritin testing, highlighting the utility of feature-based ML in resource-constrained settings [11].

Aditya et al. (2024), in the *Journal of Data Science*, showed the superiority of ensemble models, particularly a stacked Random Forest-CatBoost configuration, achieving 99.2% accuracy [12]. Rahman et al. (2024) also explored a wide range of ensemble methods, although their dataset description and preprocessing steps were limited. Their best model, Logistic Regression, achieved 95% accuracy, underscoring the variability of performance depending on data quality and preparation [13].

In 2025, Gómez et al. applied a Random Forest model to classify anemia types (microcytic, normocytic, macrocytic) using a publicly available CBC dataset and achieved an accuracy of 99.82%, reinforcing the effectiveness of rule-based clinical thresholds enhanced by ML techniques [14]. In the same year, Darshan et al. proposed a customized stacked ensemble framework using both base learners (e.g., LR, KNN, DT, RF) and advanced boosting methods (e.g., AdaBoost, CatBoost, XGBoost), reaching a peak accuracy of 96% [15].

However, most existing works have only been conducted in binary or small multi-class setting, specific sub-population, limited clinical heterogeneous public datasets and very few have investigated the stacked ensembles with embedded features selection on real-world large-scale benchmarks covering diverse types of anemia. We intend to overcome these issues by using sophisticated feature selection and a stacking ensemble architecture that has been trained on a mixed clinically-completed dataset from Misrata's laboratories, for nine different anemia categories.

2. METHODOLOG

The methodology behind the paper, shown in Fig. 1, it is based on machine learning (e.g., Random Forest, decision trees, SVM's or logistic regression) and Stacked ensemble learning after paying extra attention to the derived training data. We fine-tune the pretrained model on a separate testset, to measure its generalisation ability and verify that it can led to the claims of this paper. This strategy takes advantage the strength of each algorithm that can decrease bias and variance, enhance recognition pattern and raise diagnosis accuracy, providing an efficient early prediction tool for improved quality of healthcare delivery.

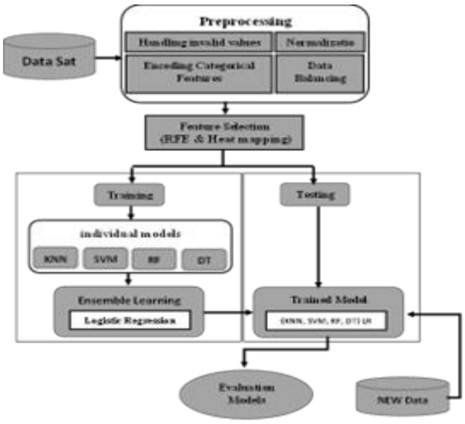

Fig 1. Proposed methodology.

3.1 Data Collection

The anemia dataset available on Kaggle was used for training in this paper, consisting of 1,281 observations characterized by 14 blood cell-related features TABLE 1. A test dataset of 1,200 real patient records was collected from local Misurata laboratories, using 14 red blood cell count features to predict anemia based on the complete dataset.

Table 1. Classes of properties and data types.

On	Classes
1	WBC (White Blood Cells)
2	LYMP (Lymphocyte Percentage)
3	NEUTP (Neutrophil Percentage)
4	LYMn (Lymphocyte Number)
5	NEUTn (Neutrophil Number)
6	RBC (Red Blood Cells)
7	HGB (Hemoglobin)
8	HCT (Hematocrit)
9	MCV (Mean Corpuscular Volume)
10	MCH (Mean Corpuscular Hemoglobin)
11	MCHC (Mean Corpuscular Hemoglobin Concentration)
12	PLT (Platelets)
13	PDW (Platelet Distribution Width)
14	PCT (Plateletcrit)

The "Diagnosis" feature is a categorical variable indicating the type of anemia. There are nine classes in total, shown in Table 2.

Table 2. Classes of properties and data types.

1	**Healthy**
2	Iron deficiency anemia
3	Leukemia
4	Leukemia with thrombocytopenia
5	Macrocytic anemia
6	Normocytic hypochromic anemia
7	Normocytic normochromic anemia
8	Another microcytic anemia
9	Thrombocytopenia

3.2 Data Preprocessing

Preprocessing is a basic and identified in the signal analysis. This involves normalization, dealing with non-integer values and conversion from text to numeric.

3.2.1 Data Balancing

The data exhibits class imbalance, is shown in Fig.2. Data imbalance was addressed in this research using a technique focused solely on increasing minority samples without reducing majority samples. The SMOTE (Synthetic Minority Over-sampling Technique which synthetically generates rare classes examples so as to have them become equal to the size of the largest class.

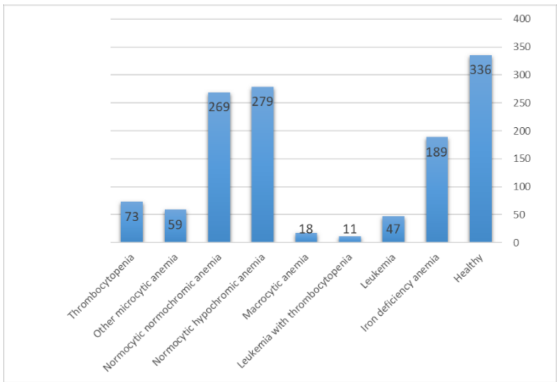

Fig. 2. Anemia Types and Related Hematological Diagnoses.

This implementation avoids under-sampling by focusing on over-sampling only the rare classes to achieve balance, thus preserving all original data from the dominant class, is shown in Fig.3.

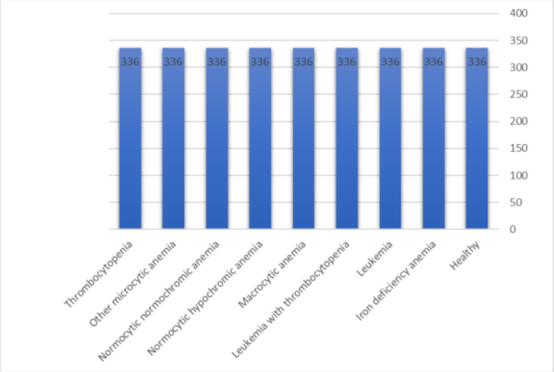

Fig. 3. Distribution of anemia diagnosis categories after parallelism (SOMTE).

This treatment resulted in a balanced dataset containing equal numbers of samples for each class, while maintaining all original information from the majority classes. This balanced dataset provided a better opportunity for the model to learn the distinct features of each class.

3.3 Feature Selection

Feature selection is critically important in machine learning as it helps improve model performance and interpretability by discovering the most important features while discarding irrelevant ones. This study used two separate feature selection methods:

3.3.1 Recursive Feature Elimination (RFE)

A wrapper method that employs an initial model iteratively removes less important features based on model weights (see Fig.4).

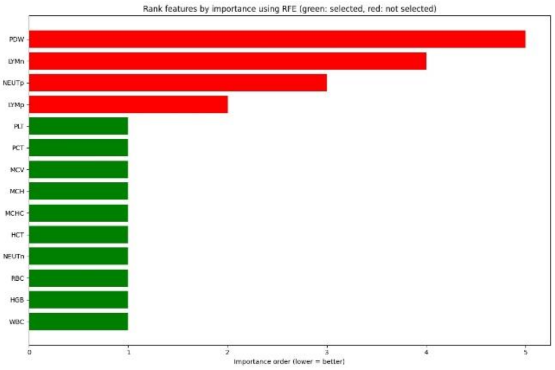

Fig. 4. The Feature Importance Rankings by RFE.

3.3.2 Correlation Heatmap Analysis

A filter method that uses visualizations to examine feature-target relationships and detect multicollinearity see Fig.5.

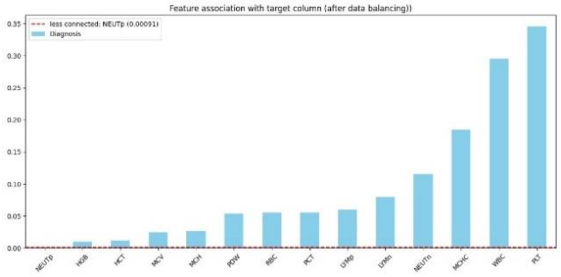

Fig.5. The Feature Importance Rankings by heatmap.

3.4 Model Architectur

For the prediction of a person being anemic, Random Forest, Support Vector Classifier, Decision Tree, and K-Nearest Neighbors were used. Later, the Stacking ensemble learning method was also used to check if it would improve the accuracy of the weak learners.

- Random Forest (RF)

Random Forest is an ensemble learning method that uses bagged decision trees for both classification and regression. For classification, the output is determined by majority voting, while for regression, the output is the mean prediction. This robust model can handle various data types (binary, categorical, continuous) and uses entropy/Gini impurity as the loss function.

- K-Nearest Neighbors (KNN)

KNN algorithm is included as one of the core components in the individual model layer within an Ensemble Learning framework. The KNN algorithm receives its inputs after the data has gone through a preprocessing stage, ensuring the fairness of the relative contribution of each feature when calculating distances.

- Support Vector Machine (SVM)

SVM algorithm has also been integrated as one of the core components within the ensemble learning framework. The SVM algorithm receives its inputs based on determining the optimal boundary between different classes.

SVM are versatile tools for both classification and regression. They address linear and non-linear problems through two main approaches. Linear SVM finds an optimal margin for linearly separable data. For non-linear data, kernel SVMs are employed to implicitly map data into a higher-dimensional space where linear separation is possible.

- Decision Tree (DT)

DT algorithm serves as another fundamental pillar within the ensemble learning framework. The algorithm receives the same inputs as KNN and SVM, but it handles the data in a fundamentally different way. While KNN looks at local similarity and SVM at linear separations, DT builds a hierarchical decision map based on partitioning the data through a series of exploratory questions.

Stacking Technique in Machine Learning Stacking is an advanced method in ensemble learning that aims to combine the predictions of base models to create a single, stronger, and more accurate model. In the context of stacking ensemble methodology, the second stage represents an advanced learning process where the predictions from the first stage (base models predictions) are used as input variables for the meta-model. Stacking offers the advantage of combining the capabilities of high-performing models on a classification or regression task to provide.

3. TESTING THE MODEL USING EXTERNAL DATA

As part of the methodology, the paper included a crucial phase to test the model's ability to generalize by using a new external dataset. This data was sourced from a separate file that was not used during the training phase and underwent the same preprocessing applied to the original data. After preparing the data, it was fed into the pre-trained model to evaluate its performance on unseen samples. The trained model was used to generate predictions on the new data. This procedure is critical as it simulates a real-world scenario where the model encounters real data in an actual medical application environment. This phase demonstrates the model's ability to generalize beyond the training data and its efficiency in classifying anemia cases when dealing with new, previously unseen data.

4. RESULTS AND DISCUSSION

In this paper, a composite classifier incorporating four machine learning algorithms was evaluated for classifying different types of anemia, simulating clinical expertise. The model was trained on the clinical features described in Section Data Collection and tested on the original dataset using an 80/20 train-test split.

The results revealed variations in the performance of the different methods depending on the datasets generated by two distinct feature selection techniques. Specifically, for the heatmap based dataset with 13 selected features TABLE 3, performance analysis indicated weaker results for the stacking model compared to the RFE based feature set, which demonstrated superior classification performance. TABLE 4 with 10 selected features presents the results obtained using the RFE-based feature selection approach. A Prediction that outperforms any single model in Ensemble.

Table 3. Performance of models for the 13 featured info gain dataset.

Heatmap	Precision	Recall	F1-sco	Accuracy
Dataset (13attributes)	0.9967	0.9967	0.9967	0.9967

Table 4. Performance of models for the 10 featured info gain dataset.

RFE	**Precision**	**Recall**	F1-sco	**Accuracy**
Dataset (10atributes)	0.9984	0.9983	0.9983	0.9983

The stacking model, when trained using the RFE-derived features, achieved outstanding performance on the training data, with an accuracy of 99.83% and an F1 score of 99.83%. These results highlight the model's ability to effectively integrate the strengths of diverse classifiers to enhance diagnostic accuracy. Furthermore, confusion matrices and classification reports confirmed the model's reliability in distinguishing between different types of anemia.

As shown in the confusion matrix Fig.6, the model achieved an exceptionally high level of accuracy across all categories. Each class was correctly classified with no misclassifications, except for a single case in the Other microcytic anemia group, which was incorrectly predicted as Iron deficiency anemia. This minor error is clinically understandable, given the close hematological similarities between these two

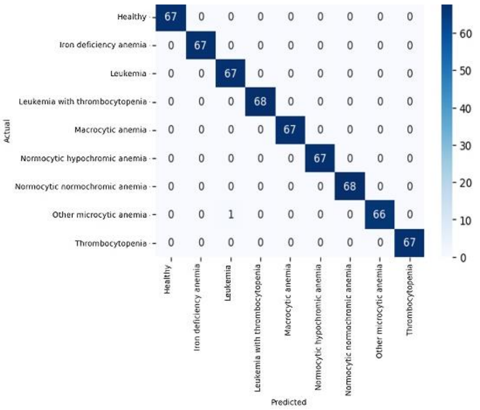

Fig. 6. Confusion Matrix for training the original data.

The overall results demonstrate that the diagonal of the matrix is consistently populated with values ranging between 66 and 68, confirming near-perfect classification. The absence of systematic misclassifications or clustering errors highlights the model's strong discriminative capacity and robustness in distinguishing among closely related hematological conditions. Such performance underscores the diagnostic reliability of the model and demonstrates its potential as a powerful tool for clinical decision support in hematology microcytic conditions literature.

5.1 Validation New Data

Following the successful training of the ensemble model on the original annotated dataset comprising 1,281 samples, the model's generalizability was rigorously evaluated using new, unlabeled complete CBC data collected from local laboratories in Misrata 1,200 samples. The unseen data underwent identical preprocessing steps including feature scaling and normalization to ensure consistency with the training pipeline. In a blinded clinical validation paper comparing the model's predictions against expert hematologist diagnoses, the ensemble demonstrated strong diagnostic alignment, achieving 84.67% overall agreement across all anemia subtypes.

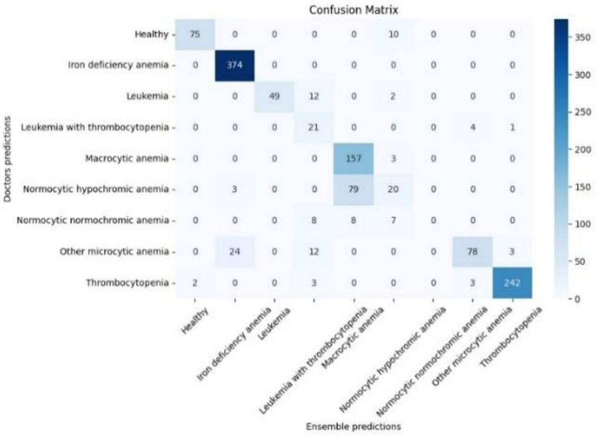

Fig. 7. Confusion Matrix for prediction between the model and the doctors.

Fig. 7 shows the ensemble model achieved high agreement with expert diagnoses, with misclassifications under 10%. Most errors (80–85%) occurred in challenging distinctions, such as differentiating Leukemia from Leukemia with thrombocytopenia, or Iron deficiency anemia from Other microcytic anemia. Simpler categories (Healthy controls, Iron deficiency anemia, and Thrombocytopenia) showed near-perfect agreement (95–99% accuracy).

This consistent alignment between algorithmic predictions and clinical standards underscores the robustness of the ensemble approach and its potential to function as a reliable decision-support tool in the diagnostic workflow of anemia subtypes.

5. CONCLUSIONS

This paper presents a stacking ensemble learning model for classifying anemia types from Complete Blood Count (CBC) data. The model integrates Random Forest (RF), Support Vector Machine (SVM), Decision Tree (DT), and K-Nearest Neighbors (KNN), using stacking as the meta-learner, to achieve high diagnostic accuracy. Results show the model attained 99.83% accuracy, with precision, recall, and F1-scores exceeding 99.83%, demonstrating expert-level precision in classifying iron deficiency anemia, leukemia, macrocytic anemia, and thrombocytopenia. Correlation-based Recursive Feature

Elimination (RFE) for feature selection outperformed heatmap analysis, retaining 10 clinically relevant features that maximized predictive performance.

The model achieved 84.67% accuracy on an external dataset from Misrata laboratories, confirming its robust performance and applicability to clinical settings. This research highlights the potential of ensemble learning in hematological diagnostics, overcoming the limitations of single-algorithm approaches by integrating diverse models to identify complex CBC patterns. By automating anemia classification, the model can reduce diagnostic errors, streamline workflows, and improve patient care.

6. RECOMMENDATIONS

To further enhance this paper, future efforts should focus on integrating additional biomarkers such as serum ferritin, vitamin B12, and folate to improve anemia subtype differentiation, especially for iron deficiency anemia and anemia of chronic disease. Expanded collaborations with diverse hospitals will strengthen the model's robustness and generalizability. A user-friendly interface for laboratory information systems would enable real-time anemia screening and facilitate prioritization of urgent cases. These improvements will advance practical AI-driven hematology tools, bridging data science and clinical application for better global anemia management.

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