Iranian Journal of Blood & Cancer

Iran J Blood Cancer, 2025, 17(3), 46-61
https://ijbc.ir

Review

The Role of Artificial Intelligence in Shaping the Future of Hematological Diagnosis and Treatment

Zahra Haghshenas[1#], Hassan Shokri Garjan[2#], Atefeh Moghassem[3#], Pooya Vahedi[4#], Yasmin Tabatabavakili[5#], Diana Hosseinzadeh[6#], Goli Asgari[7#], Elham Nazari[7*], Tahmine Aldaghi[8*]

[1] School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
[2] Department of Medical Informatics, School of Allied Medical Science, Urmia University of Medical Science, Urmia, Iran.
[3] Laboratory Hematology and Blood Bank Department, School of Allied Medical Science, Shahid Beheshti University of Medical Science, Tehran, Iran.
[4] School of Medicine, Shahid Beheshti University of Medical Science, Tehran, Iran.
[5] School of Nursing and Midwifery, Shahid Beheshti University of Medical Science, Tehran, Iran.
[6] Third faculty of medicine, Charles University, Prague, Czech Republic.
[7] Proteomics Research Center, Faculty of Paramedical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
[8] Institute of Biophysics and Informatics, First Faculty of Medicine, Charles University, Prague, Czech Republic

Scan and read the article online

Citation Haghshenas Z, Shokri Garjan H, Moghassem A, Vahedi P, Tabatabavakili Y, Hosseinzadeh D, Asgari G, Nazari E, Aldaghi T. The Role of Artificial Intelligence in Shaping the Future of Hematological Diagnosis and Treatment. Iran J Blood Cancer. 2025 Sep 30;17(3): 46-61.

doi 0

Article info:
Received: 10 Aug 2025
Accepted: 25 Sep 2025
Published: 30 Sep 2025

Keywords:
Artificial intelligence
Machine learning
Hematological disorders

Abstract

Hematological disorders continue to pose significant challenges in clinical practice due to their complexity and potential for severe outcomes. This review provides a comprehensive overview of the role of Artificial Intelligence (AI) in enhancing the diagnosis and treatment of these conditions. Drawing on 177 studies published between 2012 and 2025 from PubMed and Google Scholar, the review examines fundamental concepts of AI and machine learning, their applications in diagnostic and therapeutic processes, and the challenges and limitations associated with their clinical implementation. The findings highlight the potential of AI to improve diagnostic accuracy, optimize treatment strategies, and support decision-making in hematology. By synthesizing current knowledge, this study underscores the importance of integrating AI into research and clinical practice and offers insights into future directions for advancing patient care in hematological disorders.

1. Introduction

Hematological disorders are diseases that affect blood cells, bone marrow, and the lymphatic system. In this case, there is a problem with the stem cells in the bone marrow that are growing and changing in an unusual way due to genetic and other changes in the body's control systems (1). There are various types of these disorders with different symptoms, durations, complexity, and heterogeneity that make diagnosis and treatment challenging (2). These disorders include both non-cancerous conditions, such as anemias, blood disorders that affect hemoglobin, and diseases that

* Corresponding Author:
Elham Nazari
E-mail: Elham.Nazari@sbmu.ac.ir

Tahmine Aldaghi
E-mail: Tahmineh1989@gmail.com

#Equally contributed as the first author

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

make it hard for blood to clot, and cancerous conditions like myeloma, lymphoma, and leukemia. Some malignant blood disorders may not show symptoms at first and might be hard to find early on, but they can spread quickly and be life-threatening. Conversely, non-malignant ones may lead to chronic health problems, reduce quality of life, and increase the burden on the healthcare system (3). Among the non-malignant conditions, anemia is the most common, and it is estimated that approximately 1.92 billion people worldwide live with it (4). According to the Global Burden of Disease (GBD), the incidence of malignant tumors is estimated to be over 1.2 million new cases per year, and they account for nearly 700,000 deaths annually, making them the sixth leading cause of cancer-related death worldwide (1). This information highlights the increasing global health challenge posed by hematologic disorders and emphasizes the urgent need to improve strategies for early detection, precise diagnostics, and effective treatments.

The usual way to diagnose these diseases involves looking at blood cell shape, morphology (M), the type of markers on cells, immunophenotype (I), the genetic makeup of the cells, cytogenetics (C), and changes in DNA, molecular biology (M), collectively known as the MICM classification (4). Although these approaches are effective, they are time-consuming and resource intensive. Additionally, the interpretation of results from these methods can vary among specialists due to reliance on human expertise. Human errors during testing can also cause misdiagnoses (5, 6). As a result, the prognosis, treatment plan, and patient management will vary; the cost of therapy continues to increase, and many patients might not be able to afford these treatments. Additionally, disparities in the distribution of medical resources and unequal access to healthcare services further worsen these challenges. Therefore, early detection and intervention can prevent serious consequences and potentially save thousands of patients' lives.

New strategies have emerged to address these problems, especially with the rise of technology like Artificial Intelligence (AI). The early use of AI in healthcare dates to the 1970s, when researchers employed a rule-based system called "Expert System" to focus on detecting and treating bacterial infections, as well as diagnosing and managing glaucoma patients (7). Over the decades, the use of these automated approaches in clinical practice gradually grew and became well-known (**Figure 1**). AI is a computer-based program that simulates human intelligence and behaviors, utilizes complex algorithms, and processes high-dimensional data to make efficient decisions for improved

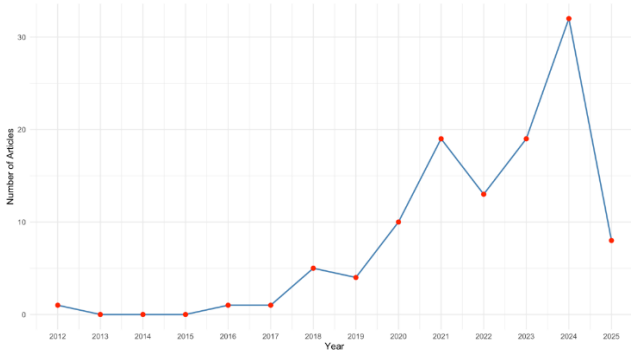

Figure 1. Number of articles per year.

clinical outcomes (7). These technologies have demonstrated effectiveness in various medical fields, including oncology, cardiology, ophthalmology, dermatology, radiology, psychiatry, and pathology (8, 9). AI in medicine is generally divided into two categories: virtual and physical. The virtual category includes a wide range of applications, from neural network-based systems to Electronic Health Record (EHR) systems. In contrast, the physical category involves robotic devices that assist with surgeries, advanced prosthetic devices for individuals with disabilities, and specialized care designed for elderly people (10).

AI and its subset, Machine Learning (ML), have expanded their roles well beyond initial expectations. Besides enabling accurate diagnoses, discovering biomarkers, predicting prognoses, monitoring patients, and optimizing treatments, they now impact many other areas of modern medicine. AI shows promise for improving the interpretation of MRI, CT, and PET scans across diverse fields such as dermatology, radiology, and pathology. In the pharmaceutical industry, AI algorithms can analyze biomedical data to design and develop drugs aimed at personalized medicine, potentially opening new pathways for treating previously incurable diseases. Examples of AI-based tools in healthcare include wearable devices that help manage chronic and neurological conditions, AI-guided robotic systems that improve the precision of minimally invasive surgeries, and AI-powered equipment that assists in diagnosing and managing mental health disorders (9, 11-13). Besides AI-powered technology supporting healthcare systems, it is also helpful for patients to perform certain tasks. For example, patients can receive assistance from AI virtual assistants to identify their issues, get advice, receive medication reminders, schedule doctor appointments, and conduct teleconsultations (14). Furthermore, Clinical Decision Support Systems (CDSS) use electronic health records (EHRs) to assist professionals in decision-making. Another key application of AI in medicine is predicting the occurrence of contagious diseases to help plan efforts to contain their spread (15). These strategies can alleviate the workload in healthcare, lower stress for both patients and professionals, reduce human errors, and make diagnosis, treatment, and patient management quicker and more affordable.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

This study aims to provide a comprehensive overview of how AI improves the accuracy and early detection of hematological disorders and its role in predicting treatment outcomes, ultimately seeking to enhance patient care. This paper not only emphasizes the benefits of AI in hematological disorders but also discusses current challenges and limitations of these technologies and explores their potential for future advances in precision hematology.

2. Artificial Intelligence and Machine Learning

When AI is discussed, it refers to systems, machines, or computer programs that aim to imitate human intelligence and vision. The main goals of these technologies are to perform tasks such as thinking, problem solving, forecasting, decision-making, and scheduling, often doing so without direct human intervention (16). In healthcare, AI has gained increasing attention for its ability to analyze complex datasets and assist clinicians in enhancing diagnostic accuracy, predicting patient outcomes, and guiding treatment plans. The key components of AI include learning, reasoning, problem-solving, perception, and natural language processing. Learning, as a fundamental part of AI, allows systems to improve their performance by utilizing prior knowledge, while reasoning employs algorithms to offer diagnostic and therapeutic recommendations. Additionally, AI can identify complex clinical challenges and find suitable solutions. Perception involves systems using sensors like cameras and microphones to gather and analyze external data to understand their environment. In medicine, this capability is applied to analyzing medical images, such as MRI, CT scans, and blood smear slides. AI also processes language to understand and communicate with humans, known as Natural Language Processing (NLP). This enables AI to recognize, generate, and respond to text or speech (17). Moreover, NLP can extract clinically relevant information from EHRs for better clinical decisions (18).

AI is a broad term that encompasses many fields of study used in medicine. Machine Learning (ML) is one of these subfields. It includes research areas like Deep Learning (DL), which have been highly effective at analyzing complex medical data. ML techniques enable computers to identify patterns from biomedical data, discover hidden connections, and make predictions without explicit programming; for example, forecasting how a patient might respond to a specific therapy. Since medical data are plentiful, diverse, and often challenging to interpret, ML can navigate these complexities to help clinicians achieve more accurate diagnoses and develop personalized treatment plans (19). The classical ML algorithms can be classified into supervised, unsupervised, semi-supervised, and reinforcement learning.

In supervised learning, predictive models are built using labeled datasets to perform tasks like classification and regression. Classification focuses on distinguishing between categories, such as separating healthy individuals from patients, while regression predicts continuous values, such as estimating hemoglobin levels in blood serum (20, 21). Commonly used supervised learning algorithms in medical research include K-Nearest Neighbor (KNN), Support Vector Machine (SVM), Decision Trees (DT), and Random Forest (RF). Here are some examples of applications of these algorithms: KNN has been used to predict chemotherapy response, SVM for patient classification, and DT for disease risk stratification. RF, as an ensemble of tree-based algorithms, can enhance disease prediction accuracy and reliability by combining multiple models (20). These examples demonstrate the wide-ranging clinical usefulness of traditional ML methods. Despite these benefits, supervised learning often demands large amounts of labeled data, which can raise annotation costs and increase computational requirements (24).

Unsupervised learning algorithms are designed to classify unlabeled data based on their features, primarily through methods like clustering, dimensionality reduction, and anomaly detection. The goal of clustering is to assign labels to data points. Common clustering algorithms in medicine include Hierarchical clustering, k-means clustering, DBSCAN, and Gaussian Mixture Models (GMM); for example, identifying subgroups of diabetic patients based on gene expression profiles to predict treatment response (20, 22, 23). Dimensionality reduction techniques, such as Principal Component Analysis (PCA), t-Distributed Stochastic Neighbor Embedding (t-SNE), Uniform Manifold Approximation and Projection (UMAP), and Autoencoders, convert thousands of features into a smaller set of variables while retaining the most important characteristics (24). This method is useful when the data contains thousands of features, such as in genomic research. It can simplify hundreds of gene expression levels into a small set of key variables, helping to visualize patterns that distinguish between healthy and unhealthy tissue samples (20). Additionally, anomaly detection is an important part of this type of learning. It involves identifying outlier data or unusual patterns that differ significantly from the norm. This approach can be applied in medical imaging to detect abnormalities (24). However, since unsupervised learning depends on unlabeled data, its results may be less dependable and harder to verify (25).

The rise of semi-supervised learning addresses the drawbacks of both supervised and unsupervised methods. Since labeling data is often expensive and requires trained human assistance (26). This strategy uses both a lot of unlabeled data and a limited amount of labeled data to achieve better results (20). In a study, researchers utilize this method to separate brain tissue from FLAIR MRI data, leading to improved segmentation and reduced the need for expert annotation, which helps to detect brain lesions in conditions like stroke, multiple sclerosis, and dementia with high performance (27).

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

In reinforcement learning, the agent interacts with its environment, takes actions, and makes decisions based on the rewards or penalties it receives. The goal is to learn the best strategy for maximizing long-term rewards (25). Popular algorithms include Q-learning, Monte Carlo learning, and Deep Q Network (28). Anzabi Zadeh et al. developed a deep reinforcement learning model to optimize warfarin dosing to balance clot prevention and bleeding risk (29).

Advances in data science and big data analytics have greatly influenced the medical industry's adoption of AI-based methods. In the early 2000s, DL models began to improve their performance and could overcome the limitations of older AI systems (30). This improvement marked the start of significant use of DL in medicine, especially in ophthalmology. Grzybowski and his team developed a DL model to detect exudates and hemorrhages in retinal images, which indicate diabetic retinopathy. The importance of this study lies in showing how deep learning can automate medical image exams, a task that used to be done by specialists (31).

The design of the human brain inspires deep learning. A biological neuron receives, processes, and sends messages to other neurons, which helps it make decisions. An artificial neural network (ANN) functions similarly; it uses artificial nodes that take input data, process it, and produce output results. These networks have an input layer, hidden layers, and an output layer. The number of hidden layers distinguishes a simple neural network from a deep one. Unlike traditional machine learning, deep learning can learn directly from raw data, process it quickly and accurately, extract features ranging from simple to complex, and represent them for precise prediction and classification without manual feature engineering (33, 34).

Convolutional Neural Networks (CNN), Recurrent Neural Networks (RNN), Restricted Boltzmann Machines (RBMs), Feed-Forward Neural Networks (FNN), and Autoencoders are deep learning architectures used in the healthcare system (32, 33). CNN have shown great potential in analyzing medical images such as MRI, X-rays, and CT scans for disease prediction, tissue and lesion segmentation, risk assessment, differential diagnosis, and large-scale image classification (32); for example, CNNs have been applied to predict Osteoarthritis risk using automated segmentation of knee cartilage MRI (34). RNNs are valuable for recognizing sequential patterns and data. They are especially effective in analyzing EHRs and physiological patterns, such as electrocardiograms (ECG), to create models for detecting heart failure (35, 36). Among these, CNNs and RNNs are the most used in medical applications. FNNs have been applied to structured data, such as laboratory test results and EHRs, to predict diseases, especially cardiovascular conditions (37, 38). Studies show that RBMs have been applied for predicting the suicide potential of mental health patients (39) and autoencoders for cancer classification using gene expression data (40). Moreover, DL algorithms enable the anticipation of tumor genetic alterations, the evaluation of therapy response, and the forecasting of survival outcomes. This allows for tailored treatment programs that enhance patient survival while lowering expenses (41). Overall, these technologies are recognized as powerful computational engines revolutionized the modern world.

3. Applications of artificial intelligence in the diagnosis of hematological disorders

The use of artificial intelligence in diagnosing various types of anemia has shown that this technology can be useful for non-invasive screening as well as differential diagnosis. At the laboratory level, models like artificial neural networks (ANN) and decision trees based on CBC data have demonstrated an accuracy of over 99% in distinguishing between iron deficiency anemia and beta-thalassemia minor (42). Furthermore, multiclass algorithms like Random Forest and MLP have shown an accuracy of over 95% in predicting the mild, moderate, and severe forms of anemia (43, 44). Conversely, non-invasive techniques have gained significant interest. CNN and hybrid models have been used to analyze images of patients' lips and palms, and it has been reported that anemia can be diagnosed with over 95% accuracy (45-47). In a different study, anemia was diagnosed with a respectable level of accuracy (about 89%) using conjunctival photos taken with smartphones (48). Additionally, some research has focused on categorizing different types of anemia. For example, ELM has classified anemia types (such as BTT, IDA, and HbE) with over 99% accuracy using CBC data (49). Using blood smear images and Multi-layer Perceptron and Random Forest algorithms, morphological, texture, and color analyses of red blood cells have produced accurate results in the field of thalassemia (50, 51). According to these studies, AI can offer low-cost, non-invasive methods for community-level anemia screening in addition to supporting laboratory diagnosis. One of the most researched topics in digital hematology is applying AI to diagnose leukemias, especially AML and ALL. CNN models trained on bone marrow smears have achieved over 95% accuracy in detecting blasts and even predicting important mutations like NPM1 in AML (52). Deep neural networks (DNN) are considerably more accurate than simpler models in diagnosing AML, achieving an accuracy of up to 96% based on gene expression data analysis (53).

Deep learning models have achieved 95% or higher accuracy in distinguishing between normal cells and blast cells in peripheral blood in ALL (54, 55). Additionally, over 96% accuracy in diagnosing ALL has been achieved by combining feature optimization techniques like Ant Colony Optimization (ACO) with simpler algorithms like Naïve Bayes (56). Quick diagnosis is essential in APL. Promyelocytes and particular characteristics like Auer rods in bone marrow smears can be recognized using CNN models in conjunction with Ensemble Neural Networks (ENN) (57). Additionally, using only

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

peripheral blood and bone marrow images, the MILLIE model (Multiple Instance Learning for Leukocyte Identification) with a weakly-supervised approach has demonstrated a very high accuracy (AUC ≈ 0.99) in diagnosing the disease. Additionally, APL can now be distinguished from other myeloid leukemias thanks to CNN models (58) and Multiple-Instance Learning (MIL) (59). Notable outcomes have also been documented in other types, including CLL and CML. Based on gene expression data, ANN and Random Forest models have demonstrated accuracy levels exceeding 98% in CLL (60). The diagnosis accuracy of CML has increased to 95% when CNN and transfer learning are applied to bone marrow smears (61). Overall, applying AI to leukemias has increased the speed and reliability of clinical settings while also improving diagnostic accuracy. AI has demonstrated impressive results in diagnosing lymphomas, especially in the DLBCL, Burkitt, and NKTCL subgroups. Whole Slide Imaging (WSI) images have been used with CNN models to identify lymphomas from benign lymph nodes with a high level of accuracy—up to 100% in some models (62, 63). Furthermore, models based on Bayesian Neural Networks have shown a 91% accuracy rate and an AUC close to 0.99 in differentiating follicular lymphoma from follicular hyperplasia. MRI and machine learning models have demonstrated performance that is comparable to or better than that of senior radiologists in diagnosing and predicting NKTCL at an advanced imaging level (64). Additionally, combining clinical data with algorithms like XGBoost has been shown to predict patient survival in high-grade B-cell lymphoma more accurately than traditional indices (65). In non-specialized centers, new techniques like ATR-FTIR spectroscopy combined with PLS-DA have also been used to accurately distinguish between lymphomatous and non-cancerous tissues (66). According to this data, AI could serve as a significant substitute for or supplement to traditional pathology in lymphomas. Early diagnosis and patient management in multiple myeloma have been greatly supported by machine learning algorithms based on laboratory data. Infections in new patients have been predicted with over 95% accuracy by the Random Forest and XGBoost models (67). Additionally, routine blood biochemistry analysis with GBDT enables early diagnosis of myeloma, achieving an AUC of nearly 0.98 (68). Disease staging has also been achieved with 93% accuracy using modern techniques such as LIBS spectroscopy combined with ANN and SVM (69). These achievements highlight the value of hybrid models (spectroscopy + AI) for the rapid treatment of myeloma patients. CNN analysis of bone marrow smears has shown an accuracy of over 92% in differentiating between AML, MDS, and aplastic anemia in bone marrow disorders (70). In clinical settings where access to molecular testing is limited, this capability is highly beneficial. CNN algorithms based on ultrasound images have demonstrated sensitivity and accuracy exceeding 90% in detecting joint bleeding (hemarthrosis) and synovial inflammation in coagulation disorders, especially Hemophilia A and B (71, 72). Even bleeding episodes not documented in the patient's medical history have been identified by these models. However, when FVIII gene mutations are analyzed using graph-based frameworks (GNN), the severity of hemophilia A can be predicted with over 70% accuracy (73). These findings show the potential of AI as a powerful tool for managing hemophilia patients at both genetic and imaging levels.

3-1. Artificial Intelligence-Based Analysis of Microscopic Blood Images

Images from peripheral blood and bone marrow microscopy serve as the main sources of information for developing AI-based diagnostic models. Convolutional neural networks (CNNs) were the first tools to identify immature cells and blasts with more than 95% accuracy (54).

Simple CNNs have been surpassed by more advanced models that use transfer learning, such as ResNet50 and DenseNet121, which can automatically extract features like chromatin density and nuclear shape (52, 74). Without the need for precise cellular labeling (AUC ≈ 0.99), diseases like APL can now be diagnosed using weakly-supervised methods such as MILLIE and architectures based on Multiple-Instance Learning (MIL) (58, 59). Additionally, the accuracy of distinguishing between benign and malignant cells has improved when morphological features extracted from cellular images are combined with classification models such as Random Forest (70, 75). AI significantly affects the prediction of laboratory results and patient outcomes, with its use in blood disorders going beyond just diagnosis. XGBoost and Random Forest models have been employed to forecast infection risk in multiple myeloma and have achieved over 95% accuracy in identifying high-risk patients (67, 68). Furthermore, machine learning algorithms combined with serum spectroscopy data analysis have helped predict disease stages (69). Using CBC data or demographic characteristics of pregnant women, AI has shown an accuracy of over 96% in predicting the severity of anemia (mild, moderate, and severe) (43, 44). Early disease management and preventative measures can benefit from this prediction. When it comes to lymphomas, machine learning models like Random Survival Forests have outperformed traditional clinical indices such as IPI in forecasting the prognosis of NKTCL patients based on MRI data (64). When it comes to coagulation disorders, graph-based frameworks (GNN) are used to predict the severity of hemophilia A based on mutations in the FVIII gene. These frameworks can also be helpful in selecting a treatment (73).

3-2. Forecasting Clinical Parameters and Laboratory Results

Artificial intelligence has significantly improved the analysis of laboratory results and clinical parameters in patients with hematology. Many predictive models rely on CBC data, which

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

is one of the most abundant sources. Machine learning algorithms can automatically classify anemia severity into three levels—mild, moderate, and severe—based on hematologic parameters. An accuracy of over 96% has been documented (43, 44). Furthermore, CBC data have shown an accuracy of nearly 99% in distinguishing between beta-thalassemia minor and iron deficiency anemia using ANN and decision tree models (42). Highly accurate results have been achieved in blood biochemistry by combining routine data with the XGBoost and Random Forest algorithms to predict infection risk or disease stage (67, 68). Microarray data and gene expression have also proven to be valuable tools for predicting disease progression. With over 95% accuracy, deep neural networks can identify genetic patterns and differentiate between patients with AML or CLL and healthy individuals (53, 60). These types of analyses can replace more costly molecular methods. With results showing up to 97% accuracy, spectroscopy techniques (like LIBS spectroscopy) combined with ANN and SVM algorithms have also helped predict disease stage and severity (69). Considering all factors, AI has become a powerful tool for predicting the clinical course, risk of complications, and disease severity in hematologic patients by analyzing laboratory data (CBC, biochemistry, genetics, spectroscopy).

3-3. Case Studies, Seminal Studies, and Important Discoveries

Artificial intelligence has the potential to significantly transform patient diagnosis and treatment, according to multiple studies in the field of hematologic diseases. One notable DLBCL study focused on developing a multi-center CNN platform that achieved nearly 100% diagnostic accuracy across three separate centers. This consistency demonstrated the model's strong generalizability across different institutions (63). Using only bone marrow and peripheral blood smears and no molecular data, a study employing a weakly-supervised approach (MILLIE) successfully diagnosed APL with an AUC of approximately 0.99 (58). In facilities lacking access to advanced testing, this achievement is particularly important. Non-invasive lip and conjunctival imaging have shown over 95% accuracy in anemia detection in independent studies. These studies proved that anemia screening can be done without blood samples by using CNN models and smartphones (45, 48). When LIBS spectroscopy was combined with ANN and SVM models for disease staging in myeloma, the results were highly accurate (93–97%). This study highlights the importance of integrating machine learning and spectroscopy techniques to develop fast and cost-effective diagnostic tools (69). In NKTCL, MRI combined with Random Survival Forest was more effective than traditional clinical indices at diagnosing and predicting prognosis (64). This study offered a model for the simultaneous integration of diagnosis and prognosis using AI.

These illustrations demonstrate that AI's most significant contributions to hematology involve enhancing accuracy and creating innovative and practical methods for early diagnosis, screening, and predicting disease progression.

3-4. Effective Models and Algorithms for Hematologic Disorders

Based on research analysis, some algorithms and AI models have been most significant in hematology's progress. The most used architecture for analyzing blood and bone marrow images is Convolutional Neural Networks (CNNs), which have achieved over 95% accuracy in detecting various leukemias, anemias, and lymphomas. Classifying leukemia subtypes and immature cells has been especially successful with advanced versions of these models, such as ResNet50 and DenseNet121 (52, 61, 74). In addition to these strategies, ensemble models like Ensemble Neural Networks (ENN) or stacking methods have shown remarkable results by delivering more accurate and stable performance than single models, especially in diseases like anemia and APL (48, 57). Tree-based algorithms like Random Forest and XGBoost have demonstrated the greatest success in the clinical data domain. To predict the severity of anemia and complications such as infections in patients with myeloma, these models have been effectively used to analyze CBC and biochemical parameters (43, 44, 67, 68). However, newer methods like Graph Neural Networks (GNNs), which have been introduced as a new generation of AI algorithms in hematology, have also shown promising results in genetic data, especially in predicting the severity of hemophilia A (73). As lighter and less computationally demanding alternatives to deep networks, more traditional models like Support Vector Machine (SVM) and k-Nearest Neighbor (kNN) are still in use and, when combined with ANN, have demonstrated adequate performance in analyzing spectroscopy data or non-invasive anemia images (47, 69). Furthermore, the use of Multiple-Instance Learning (MIL) and weakly-supervised models has become especially important in situations where precise cell labeling is difficult or costly. The MILLIE model, which was able to diagnose APL with nearly 99% accuracy using only cellular images and no molecular data, is a well-known example of this category (58, 59). Convolutional neural networks, or CNNs, are considered the most important and effective tools in artificial intelligence (AI) applications for blood disorders. They have also significantly influenced developments in digital pathology and microscopic image analysis. Besides CNNs, tree-based algorithms such as Random Forest and XGBoost have primarily been used as supplementary methods for analyzing laboratory and clinical data. Recently, emerging models like Multiple-Instance Learning (MIL) techniques and Graph Neural Networks (GNNs) have appeared, opening new possibilities for analyzing increasingly complex data, including genetic information and semi-labeled images. This trend suggests that the future of digital hematology will rely on integrating advanced algorithms

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

with established techniques like CNNs, enabling more accurate and personalized diagnosis and prognosis (**Figure 2** shows the accuracy of algorithms in hematological disorders).

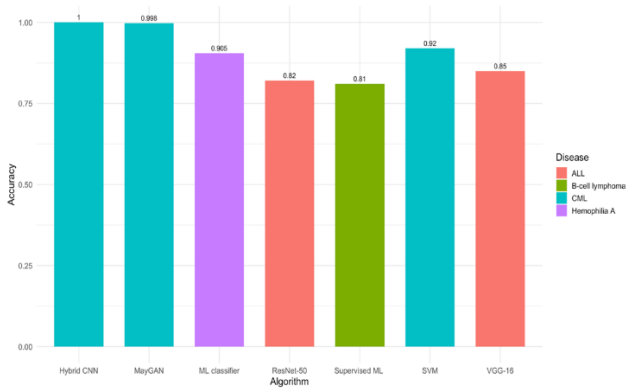

Figure 2. Accuracy of algorithms in hematological disorders.

4. Applications of artificial intelligence in the treatment of hematological disorders

Recent progress in artificial intelligence (AI) and machine learning (ML) has demonstrated strong potential in predicting treatment responses and adverse effects across various hematological diseases. In multiple myeloma (MM), ML models that combine molecular and clinical features with ex vivo drug-response data have successfully identified patients who are most likely to benefit from specific treatments (76) and improved prediction of disease progression and outcomes (77, 78). In acute myeloid leukemia (AML), knowledge-graph–driven ML improved the prediction of ex vivo drug sensitivity (79), while integrative multi-omics frameworks provided improved prognostic accuracy and therapeutic stratification (80) .

ML has also been used in preclinical leukemia models, where algorithms identified synergistic drug combinations with translational potential (81). Imaging-based approaches are equally effective: convolutional neural networks (CNNs) using MRI have precisely classified patients with NK/T-cell lymphoma (82) and interpretable histopathology-based models have predicted recurrence risk in diffuse large B-cell lymphoma (83). Chronic myeloid leukemia (CML) has received considerable attention, including predictive dashboards for therapy outcomes (84), blood count–based ML tools for early detection (85), and systematic reviews summarizing AI applications for personalized therapy (86). Beyond malignancies, AI has been used in bleeding disorders; for example, ML algorithms predicted bleeding risk in children with hemophilia A, enabling personalized prophylaxis strategies (87). Collectively, these studies demonstrate AI's capacity to optimize therapy selection, predict toxicity, and tailor treatment in hematology. However, broader validation, transparent reporting, and prospective clinical trials are still essential for clinical application (88, 89) (**Table 1** presents a selection of the references; the complete list is provided in Attachment).

Besides predicting treatment outcomes, AI plays a key role in customizing therapeutic strategies. In adoptive cell therapies, deep learning and multimodal ML approaches forecast which lymphoma patients will respond to CAR-T and also help guide CAR design and candidate selection to lower toxicity and boost effectiveness (78-80). CML has gained from AI that combines single-cell and bulk molecular data to identify likely non-responders to first-line tyrosine kinase inhibitors (TKIs) and to suggest alternative strategies (81, 86). Reinforcement-learning frameworks have even been proposed to suggest optimal sequencing of therapies to maximize progression-free survival in complex treatment pathways (84). Similarly, ML-driven systems have supported therapy management in anemia; for example, the AISACS model, trained using physician decisions, provided accurate ESA dosage recommendations for anemic patients on hemodialysis, reaching up to 98% clinically acceptable classification rates (90). AI has also proven highly effective in diagnosis, which is fundamental to tailoring treatment.

Deep learning models such as VGG-16 and ResNet-50, trained on microscopic cell images, demonstrated high validation accuracies of 84.62% and 81.63% for the prompt diagnosis of ALL (91), while a Random Forest model applied to blood test indices achieved an AUC of 0.950 for ALL and 0.909 for AML, enabling early childhood leukemia screening and better prognosis (92). In myelodysplastic syndromes (MDS), an ML model achieved a c-index of 0.74 for predicting overall survival, outperforming the conventional IPSS-R score (0.66) (93). AI has also been used to predict a diagnosis of CML years before symptom onset, demonstrating its potential for proactive intervention (85). In anemia, an artificial neural network model achieved 96.29% accuracy and an AUC of 0.982 in diagnosing iron deficiency anemia using only laboratory data (94) (**Table 2** presents a selection of the references; the complete list is provided in Attachment).

Collectively, these studies show that AI shifts hematology from general guidelines to personalized decision support. However, successful implementation will need prospective validation, explainability (XAI) to gain clinician trust, and thorough assessment of clinical usefulness and cost-efficiency.

Beyond personalization, AI now develops the development and design of new treatments. In adoptive cell and biologic therapies, ML methods assist in prioritizing antigen targets,

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

Table 1. Summary of studies on AI applications in the diagnosis of hematological disorders.

Authors	Years	Disease	AI algorithm	Type of data	Datasets	Sample size	Clinical application	Accuracy	Explain	Ref
David Reinecke	2024	Primary CNS lymphoma (PCNSL) and other CNS entities	Deep learning (RapidLymphoma, self-supervised learning)	Stimulated Raman histology (SRH) patch images (virtual H&E-like)	Four international tertiary medical centers + two independent test cohorts	Train: 54,000 SRH patch images; Test: 160 cases (cohort 1), 420 cases (cohort 2), 59 cases (cohort 3)	Intraoperative diagnosis and differentiation of PCNSL from other CNS lesions	Prospective test: Balanced accuracy 97.81% ±0.91; Additional tests: 95.44% ±0.74 and 95.57% ±2.47; PCNSL detection sensitivity 100% (vs frozen section 78.94%	RapidLymphoma provided fast (<3 min), high-accuracy intraoperative PCNSL detection with visual heatmap feedback, enabling rapid surgical decision-making	(117)
Fu-Ming Cheng	2024	Acute leukemia (AML and B-ALL)	Deep learning (ResNet-50, EverFlow)	Flow cytometry data (ALOT protocol, EuroFlow)		241 patients (retrospective study, 2017–2022)	Screening and classification of acute leukemia; differentiation of physiological vs pathological cells	AML: 94.6%, B-ALL: 98.2%, Physiological cells ≥ 80%	AI model showed high sensitivity in detecting AML and B-ALL and acceptable performance for physiological cells	(118)
Mohamed E Salama	2022	Chronic lymphocytic leukemia (CLL), minimal residual disease (MRD)	Deep neural networks (F-DNN, L-DNN, hybrid approach)	Flow cytometry (10-color CLL MRD panel)	Development cohort: 202 CLL patients post-therapy (Feb 2020–May 2021, peripheral blood & bone marrow), Independent clinical evaluation cohort: 34 "unknown" specimens	Training: 202 patients (F-DNN), 138 patients with low-event cases (L-DNN); Test: 34 unknown samples	Automated MRD detection in CLL to improve clinical lab workflow	97.1% (95% CI: 84.7–99.9%)	Hybrid DNN achieved high accuracy in MRD detection, reduced gating time from 15 min to 12 seconds per case, and showed excellent correlation with expert analysis	(119)
Turky Omar Asar	2024	Leukemia	Falcon Optimization Algorithm + Deep Convolutional Neural Network (FOADCNN-LDC), ShuffleNetv2, Convolutional Denoising Autoencoder (CDAE)	Medical images	Benchmark medical dataset		Automated leukemia detection and classification	99.62%	Proposed FOADCNN-LDC achieved high accuracy in leukemia detection and classification, outperforming existing techniques	(120)
Wei Yan	2021	Multiple myeloma	GBDT, SVM, DNN, RF	Routine blood and biochemical examination	4,187 records from Shengjing Hospital (1,741 MM, 2,446 non-MM)	4,187	Early assistant diagnosis of multiple myeloma	GBDT: Precision 92.9%, Recall 90.0%, F1 0.915, AUROC 0.975	AI model accurately diagnoses multiple myeloma from routine lab tests, improving early detection rate.	(68)
Liqiu Pan	2024	Thalassemia trait (TT) vs Iron	Stepwise discriminant analysis	Hematological lab data (RBC, Hb,	598 patients from	598 (320 TT, 278 IDA)	Differential diagnosis of TT and IDA	AUC = 0.936, Sensitivity =	A simple formula (TIDI) effectively distinguishes TT from IDA,	(121)

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

		deficiency anemia (IDA)	(TIDI formula)	MCHC, RET%)	Guangxi region, China			89.5%, Specificity = 89.2%	improving diagnostic accuracy in clinical practice.	
Jennifer Lyons	2018	Hemophilia A	Lasso logistic regression (predictive modeling with ML)	Medical and pharmacy claims data	US HealthCore Integrated Research Database (2006–2015)	2,252 identified patients; 400 medical records reviewed	Identify hemophilia A patients in administrative claims databases	PPV 94.7%, Sensitivity 94.4%	Algorithm accurately identifies hemophilia A cases from claims data, enabling reliable patient identification for research and clinical follow-up.	(122)

predicting CAR-T safety–efficacy tradeoffs, and even suggesting sequence or design modifications that decrease on-target/off-tumor toxicity while enhancing potency — a major advance for lymphoid malignancies and MM, where CAR and bispecific formats are rapidly expanding (95).

AI also powers CRISPR guide-RNA and vector design pipelines that enhance on-target efficiency and minimize off-target edits, which is essential as gene therapies for hemoglobinopathies and other inherited blood disorders advance toward wider clinical application (96-98). Drug-repositioning algorithms and explainable deep models have identified candidates for repurposing in leukemia and pediatric ALL, significantly shortening timelines to clinical testing (99). Moreover, the synthesis of patient-level synthetic cohorts is being used to design better trial endpoints and inform bispecific and CAR-T trials, thereby improving efficiency and patient selection (100, 101). Generative AI offers additional opportunities by producing synthetic data that enables researchers to test hypotheses and assess prognostic scores without relying solely on real patient cohorts, reducing research costs and accelerating discovery (102). Together, these innovations show how AI is transforming the development process, providing faster, safer, and more accurate treatment options in hematology.

5. Challenges and limitations of using artificial intelligence in the field of blood diseases

A major challenge in using artificial intelligence (AI) for blood disease detection is the inconsistent quality and limited availability of annotated datasets needed for effective model development (103). The lack of large, diverse, and well-curated datasets continues to be a major challenge, especially in hematology, where rare conditions make collecting reliable data particularly hard (104, 105). High-quality blood samples paired with expert manual annotation are both resource- and time-consuming, requiring significant effort from skilled hematologists and pathologists. This process, especially in whole-slide imaging (WSI), is laborious and expensive, making large-scale dataset creation impractical in many clinical settings (106, 107). Consequently, most existing datasets are small, narrowly focused by institutions, and do not adequately represent the global patient population. This issue is particularly evident in rare hematological conditions, where limited sample availability often results in imbalanced cohorts, sampling bias, and decreased model generalizability (105, 108). Moreover, datasets are often sourced from single institutions or homogeneous populations, creating demographic and geographic biases that restrict external validity and impede clinical translation (104, 108).

Adding further complexity, annotation quality itself is a major source of variability (109). Even among experienced clinicians, inter-observer agreement can be inconsistent, leading to labeling errors that undermine the reliability of supervised learning models (110). This "garbage in, garbage out" problem highlights how AI performance relies heavily on the quality and variety of the training data (109). These challenges emphasize the urgent need for collaboration across multiple institutions, standardized annotation protocols, and larger, more representative datasets to develop AI models in hematology that can be broadly applied (111, 112).

6. The Future of Artificial Intelligence in the Diagnosis and Treatment of Blood Diseases

The emergence of machine learning, deep learning, and convolutional neural networks (CNNs) has revolutionized this process by enabling automatic detection and classification of blood cell types, recognition of small morphological abnormalities, and analysis of genomic markers involved in hematological diseases, including leukemia and anemia (104). In hematopathology specifically, innovations in slide-level representation, such as compact vector embeddings derived from individual cell

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

Table 2. Summary of studies on AI applications in the treatment of hematological disorders.

Authors	Years	Disease	AI algorithm	Type of data	Clinical application	Accuracy	Explain	Ref
Lei et al.	2024	Acute Myeloid Leukemia (AML)	Deep survival model (DL)	EHR + labs	Mortality & treatment response prediction	C-index improved vs baseline		(123)
Didi et al.	2024	Acute Myeloid Leukemia (AML)	MLP neural network	Clinical + labs	Predict overall survival (treatment outcomes)	Accuracy ~overall survival (OS) of 68.5% and 62.1% in the IC and AZA cohorts		(124)
Ferle et al.	2025	Multiple myeloma (MM)	Hybrid NN	Labs	Predict progression to inform therapy changes	Outperformed baselines		(77)
Zhao et al.	2023	Diffuse large B-cell lymphoma (DLBCL)	Stacking ensemble	PET/CT radiomics	Outcome prediction to tailor therapy	Reported good prognostic accuracy		(125)
Jardim et al.	2024	Hemophilia A	ML classifier	Clinical + F8 genotype	Predict inhibitor development	90.5%		(126)
Kosvyra A. et al.	2024	AML	Integrative ML / network-based models	Multi-omics (expression, methylation) + clinical	Prognosis and drug sensitivity prediction	Improved prognostic stratification vs single-omic models; metrics reported.		(80)
Khosla et al.	2018	Chronic myeloid leukemia (CML)	CNN	LAB	Building a tool using TensorFlow to classify images and with the help of a CNN, so that it can be used to determine the phase and stage of chronic myeloid leukemia	NM	The CNN can correctly predicts the results with a confidence level of over 95% _ Help physicians make the correct diagnosis	(127)
Sasaki et al.	2021	Chronic myeloid leukemia (CML)	eXtreme Gradient Boosting (XGBoost)	LAB	Development of the Leukemia Artificial Intelligence Program (LEAP) to aid in treatment selection for patients with chronic myeloid leukemia	NM	A higher probability of survival for patients with chronic myeloid leukemia, who choose treatment based on personalized recommendations provided through the LEAP program _ Improve the treatment outcomes of patients with chronic myeloid leukemia	(128)
Naji H. et al.	2025	Diffuse large B-cell lymphoma (DLBCL)	Interpretable deep learning on histology (CNN + attention)	Whole-slide images (H&E) + clinical	a deep learning-based pipeline to predict recurrence of DLBCL based on histological images of a publicly available cohort	Reported high predictive performance (AUC / C-index reported).	Predict recurrence / risk after therapy	(83)
Mehrbakhsh et al.	2024	Acute lymphoblastic leukemia (ALL), pediatric	XGBoost / ensemble classifiers	Clinical and laboratory	Predict mortality and relapse risk		These results offer significant clinical insights into the prognostic factors for children with ALL, which can inform treatment decisions and improve patient outcomes	(129)
Saleem M. et al.	2023	Thalassemia	Feature selection + classification (ML)	CBC parameters, indices	Screen/diagnose thalassemia and predict transfusion needs		to investigate the influence of feature selection methods on the precision of thalassemia predictions.	(130)

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

features and multiple-instance learning, have appeared as promising tools for summarizing diagnostic information and aiding computational decision-making at the patient level (113).

At the same time, federated learning has become a practical method in hematology, allowing multiple institutions to collaboratively train AI models while ensuring sensitive patient data stays securely stored locally. Li and colleagues recently demonstrated its potential in transfusion medicine, where it enhanced predictive analytics and demand forecasting, providing a privacy-preserving alternative to centralized data collection (114). In rare hematological diseases, the GenoMed4all and SYNTHEMA initiatives have effectively used federated learning to combine genomic and clinical data, enabling personalized survival modeling in myelodysplastic syndromes without centralizing the data (115).

Multimodal AI models that integrate imaging, genomic, and clinical data show a promising improvement in diagnostic accuracy. Evidence from a recent scoping review suggests that these approaches outperform unimodal models, with significant gains in predictive performance, although issues like data heterogeneity and integration gaps still exist (116). Contributors from clinical hematology, data science, ethics, and health policy must collaborate to build validation frameworks, develop secure data-sharing infrastructures, and uphold ethical standards—foundational steps that have been emphasized in multisite federated implementations and AI pathology research.

7. Conclusion

The future of Artificial Intelligence (AI) in hematology depends on successfully addressing several key priorities. Ensuring high-quality, diverse, and representative datasets is crucial for reducing algorithmic bias and achieving fair outcomes across populations, including those with rare blood disorders. Improving explainability and transparency with tools like explainable AI (XAI) is vital for building clinician trust, supporting informed decisions, and meeting regulatory standards. Integrating multi-omics and longitudinal clinical data can advance personalized risk assessment and treatment plans, while real-world validation through prospective trials and pilot studies remains essential to prove AI's effectiveness outside research settings. Ethical and legal issues, such as patient privacy, data governance, and informed consent, must be carefully managed to ensure safe and sustainable use. Additionally, automation in laboratory and imaging workflows can boost efficiency, minimize human errors, and increase access, especially in resource-limited environments. Together, these advancements position AI as a transformative force in hematology — capable not only of improving diagnostic and treatment results but also of enhancing public health surveillance, preventive care, and evidence-based policies worldwide. In short, AI is a critical tool for advancing both clinical practice and research in hematology, with its full promise only realized through thoughtful, ethically sound integration into healthcare systems. A graphical abstract which summarizes the whole study has been provided in **Figure 3**.

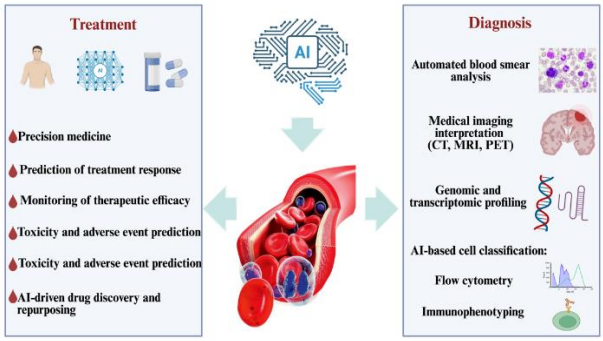

Figure 3. Graphical abstract.

Acknowledgment

The authors would like to thank all the people who contributed to the writing of this article.

Conflict of interest

The authors declared no conflict of interest.

Funding

No fund was received.

Ethical statement

This paper does not need any Ethical statement.

References

1. Pan T, Zhang J, Wang X, Song Y. Global burden and trends of hematologic malignancies based on Global Cancer Observatory 2022 and Global Burden of Disease 2021. Exp Hematol Oncol. 2025;14(1):98.

2. Sun D, Chen W, He J, He Y, Jiang H, Jiang H, et al. A novel method for screening malignant hematological diseases by constructing an optimal machine learning model based on blood cell parameters. BMC Medical Informatics and Decision Making. 2025;25(1).

3. Collaborators GBDA. Prevalence, years lived with disability, and trends in anaemia burden by severity and cause, 1990-2021: findings from the Global Burden of Disease Study 2021. Lancet Haematol. 2023;10(9):e713-e34.

4. Liao H, Zhang F, Chen F, Li Y, Sun Y, Sloboda DD, et al. Application of artificial intelligence in laboratory hematology: Advances, challenges, and prospects. Acta Pharmaceutica Sinica B. 2025.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

5. Isa A, Yusoff NM, Hamdani HY, Nazman HNM, Alhawamdeh M, Abeden Z, et al. Application of artificial intelligence in the diagnosis of haematological disorders. Biomedical Research and Therapy. 2024;11(12):6989-7002.

6. Wang S-X, Huang Z-F, Li J, Wu Y, Du J, Li T. Optimization of diagnosis and treatment of hematological diseases via artificial intelligence. Frontiers in Medicine. 2024;11.

7. El Alaoui Y, Elomri A, Qaraqe M, Padmanabhan R, Yasin Taha R, El Omri H, et al. A Review of Artificial Intelligence Applications in Hematology Management: Current Practices and Future Prospects. Journal of Medical Internet Research. 2022;24(7).

8. Ekpe N, Odii A, Adene G, Aguzu L. Applications of Artificial Intelligence and Machine Learning in Clinical Practice. 2025;3:1-15.

9. T S, B GJ. From algorithm to applications: Artificial intelligence – A future prospective in medicine. Sri Ramachandra Journal of Health Sciences. 2025;4:44-52.

10. Amisha, Malik P, Pathania M, Rathaur VK. Overview of artificial intelligence in medicine. J Family Med Prim Care. 2019;8(7):2328-31.

11. Srivastava R. Applications of Artificial Intelligence in Medicine. Exploratory Research and Hypothesis in Medicine. 2023;9(2):138-46.

12. Eskandar K. Artificial Intelligence in Healthcare: Explore the Applications of AI in Various Medical Domains, Such as Medical Imaging, Diagnosis, Drug Discovery, and Patient Care. 2023;1:37-53.

13. Walter W, Pohlkamp C, Meggendorfer M, Nadarajah N, Kern W, Haferlach C, et al. Artificial intelligence in hematological diagnostics: Game changer or gadget? Blood Reviews. 2023;58.

14. Alowais SA, Alghamdi SS, Alsuhebany N, Alqahtani T, Alshaya AI, Almohareb SN, et al. Revolutionizing healthcare: the role of artificial intelligence in clinical practice. BMC Medical Education. 2023;23(1).

15. Chimmula VKR, Zhang L. Time series forecasting of COVID-19 transmission in Canada using LSTM networks. Chaos Solitons Fractals. 2020;135:109864.

16. Xu Y, Liu X, Cao X, Huang C, Liu E, Qian S, et al. Artificial intelligence: A powerful paradigm for scientific research. Innovation (Camb). 2021;2(4):100179.

17. Akanksha M. A Comprehensive Review of Artificial Intelligence and Machine Learning : Concepts, Trends, and Applications. International Journal of Scientific Research in Science and Technology. 2024;11(5):126-42.

18. Rojas-Carabali W, Agrawal R, Gutierrez-Sinisterra L, Baxter SL, Cifuentes-González C, Wei YC, et al. Natural Language Processing in medicine and ophthalmology: A review for the 21st-century clinician. Asia Pac J Ophthalmol (Phila). 2024;13(4):100084.

19. Furizal F, Ma'arif A, Rifaldi D. Application of Machine Learning in Healthcare and Medicine: A Review. Journal of Robotics and Control (JRC). 2023;4(5):621-31.

20. Rashidi HH, Pantanowitz J, Hanna MG, Tafti AP, Sanghani P, Buchinsky A, et al. Introduction to Artificial Intelligence and Machine Learning in Pathology and Medicine: Generative and Nongenerative Artificial Intelligence Basics. Modern Pathology. 2025;38(4).

21. Taye MM. Understanding of Machine Learning with Deep Learning: Architectures, Workflow, Applications and Future Directions. Computers. 2023;12(5):91.

22. Kufel J, Bargieł-Łączek K, Kocot S, Koźlik M, Bartnikowska W, Janik M, et al. What Is Machine Learning, Artificial Neural Networks and Deep Learning?—Examples of Practical Applications in Medicine. Diagnostics. 2023;13(15).

23. Bali J, Bali O. Artificial Intelligence Applications in Medicine: A Rapid Overview of Current Paradigms. EMJ Innovations. 2020:73-81.

24. Trezza A, Visibelli A, Roncaglia B, Spiga O, Santucci A. Unsupervised Learning in Precision Medicine: Unlocking Personalized Healthcare through AI. Applied Sciences. 2024;14(20):9305.

25. Tettey-Engmann F, Parupelli SK, Bauer SR, Bhattarai N, Desai S. Advances in Artificial Intelligence-Based Medical Devices for Healthcare Applications. Biomedical Materials & Devices. 2025.

26. Woodman RJ, Mangoni AA. A comprehensive review of machine learning algorithms and their application in geriatric medicine: present and future. Aging Clinical and Experimental Research. 2023;35(11):2363-97.

27. Rieu Z, Kim J, Kim RE, Lee M, Lee MK, Oh SW, et al. Semi-Supervised Learning in Medical MRI Segmentation: Brain Tissue with White Matter Hyperintensity Segmentation Using FLAIR MRI. Brain Sciences. 2021;11(6):720.

28. Sarker IH. AI-Based Modeling: Techniques, Applications and Research Issues Towards Automation, Intelligent and Smart Systems. SN Comput Sci. 2022;3(2):158.

29. Anzabi Zadeh S, Street WN, Thomas BW. Optimizing warfarin dosing using deep reinforcement learning. J Biomed Inform. 2023;137:104267.

30. Kaul V, Enslin S, Gross SA. History of artificial intelligence in medicine. Gastrointestinal Endoscopy. 2020;92(4):807-12.

31. Grzybowski A, Brona P, Lim G, Ruamviboonsuk P, Tan GSW, Abramoff M, et al. Artificial intelligence for diabetic retinopathy screening: a review. Eye (Lond). 2020;34(3):451-60.

32. Miotto R, Wang F, Wang S, Jiang X, Dudley JT. Deep learning for healthcare: review, opportunities and challenges. Brief Bioinform. 2018;19(6):1236-46.

33. Chakraborty C, Bhattacharya M, Pal S, Lee S-S. From machine learning to deep learning: Advances of the recent data-driven paradigm shift in medicine and healthcare. Current Research in Biotechnology. 2024;7.

34. Prasoon A, Petersen K, Igel C, Lauze F, Dam E, Nielsen M. Deep feature learning for knee cartilage segmentation using a triplanar convolutional neural network. Med Image Comput Comput Assist Interv. 2013;16(Pt 2):246-53.

35. Chen R, Stewart WF, Sun J, Ng K, Yan X. Recurrent Neural Networks for Early Detection of Heart Failure From Longitudinal Electronic Health Record Data. Circulation: Cardiovascular Quality and Outcomes. 2019;12(10).

36. Choi E, Schuetz A, Stewart WF, Sun J. Using recurrent neural network models for early detection of heart failure onset. J Am Med Inform Assoc. 2017;24(2):361-70.

37. Si Y, Du J, Li Z, Jiang X, Miller T, Wang F, et al. Deep representation learning of patient data from Electronic Health Records (EHR): A systematic review. Journal of Biomedical Informatics. 2021;115:103671.

38. Joshi D, Singh B, Kalonia S, Kaushik AK, Goyal N, Maggu S, editors. Predictive Modeling of Cardiovascular Disease Using Feedforward Neural Networks. Proceedings of International Conference on Paradigms of Communication, Computing and Data Analytics; 2025 2025//; Singapore: Springer Nature Singapore.

39. Tran T, Nguyen TD, Phung D, Venkatesh S. Learning vector representation of medical objects via EMR-driven nonnegative restricted Boltzmann machines (eNRBM). J Biomed Inform. 2015;54:96-105.

40. Fakoor R, Ladhak F, Nazi A, Huber M. Using deep learning to enhance cancer diagnosis and classification2013.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

41. Reis TC. Deep learning in oncology: Transforming cancer diagnosis, prognosis, and treatment. Emerging Trends in Drugs, Addictions, and Health. 2025;5.

42. Ucucu S, Azik F. Artificial intelligence-driven diagnosis of beta-thalassemia minor & iron deficiency anemia using machine learning models. J Med Biochem. 2024;43(1):11-8.

43. Kitaw B, Asefa C, Legese F. Leveraging machine learning models for anemia severity detection among pregnant women following ANC: Ethiopian context. BMC Public Health. 2024;24(1):3500.

44. Vohra R, Hussain A, Dudyala AK, Pahareeya J, Khan W. Multi-class classification algorithms for the diagnosis of anemia in an outpatient clinical setting. PLoS One. 2022;17(7):e0269685.

45. Mansour M, Donmez TB, Kutlu M, Mahmud S. Non-invasive detection of anemia using lip mucosa images transfer learning convolutional neural networks. Front Big Data. 2023;6:1291329.

46. Ramzan M, Sheng J, Saeed MU, Wang B, Duraihem FZ. Revolutionizing anemia detection: integrative machine learning models and advanced attention mechanisms. Vis Comput Ind Biomed Art. 2024;7(1):18.

47. Appiahene P, Asare JW, Donkoh ET, Dimauro G, Maglietta R. Detection of iron deficiency anemia by medical images: a comparative study of machine learning algorithms. BioData Min. 2023;16(1):2.

48. Sehar N, Krishnamoorthi N, Vinoth Kumar C. Deep Learning Model-Based Detection of Anemia from Conjunctiva Images. Healthc Inform Res. 2025;31(1):57-65.

49. Saputra DCE, Sunat K, Ratnaningsih T. A New Artificial Intelligence Approach Using Extreme Learning Machine as the Potentially Effective Model to Predict and Analyze the Diagnosis of Anemia. Healthcare (Basel). 2023;11(5).

50. Tyas DA, Hartati S, Harjoko A, Ratnaningsih T. Morphological, Texture, and Color Feature Analysis for Erythrocyte Classification in Thalassemia Cases. IEEE Access. 2020;8:69849-60.

51. Aszhari FR, Rustam Z, Subroto F, Semendawai AS. Classification of thalassemia data using random forest algorithm. 2020;1490(1).

52. Eckardt JN, Middeke JM, Riechert S, Schmittmann T, Sulaiman AS, Kramer M, et al. Deep learning detects acute myeloid leukemia and predicts NPM1 mutation status from bone marrow smears. Leukemia. 2022;36(1):111-8.

53. Nazari E, Farzin AH, Aghemiri M, Avan A, Tara M, Tabesh H. Deep Learning for Acute Myeloid Leukemia Diagnosis. J Med Life. 2020;13(3):382-7.

54. Sampathila N, Chadaga K, Goswami N, Chadaga RP, Pandya M, Prabhu S, et al. Customized Deep Learning Classifier for Detection of Acute Lymphoblastic Leukemia Using Blood Smear Images. Healthcare (Basel). 2022;10(10).

55. Rezayi S, Mohammadzadeh N, Bouraghi H, Saeedi S, Mohammadpour A. Timely Diagnosis of Acute Lymphoblastic Leukemia Using Artificial Intelligence-Oriented Deep Learning Methods. Comput Intell Neurosci. 2021;2021:5478157.

56. El Houby EMF. Acute lymphoblastic leukemia diagnosis using machine learning techniques based on selected features. Sci Rep. 2025;15(1):28056.

57. Eckardt JN, Schmittmann T, Riechert S, Kramer M, Sulaiman AS, Sockel K, et al. Deep learning identifies Acute Promyelocytic Leukemia in bone marrow smears. BMC Cancer. 2022;22(1):201.

58. Manescu P, Narayanan P, Bendkowski C, Elmi M, Claveau R, Pawar V, et al. Detection of acute promyelocytic leukemia in peripheral blood and bone marrow with annotation-free deep learning. Sci Rep. 2023;13(1):2562.

59. Sidhom JW, Siddarthan IJ, Lai BS, Luo A, Hambley BC, Bynum J, et al. Deep learning for diagnosis of acute promyelocytic leukemia via recognition of genomically imprinted morphologic features. NPJ Precis Oncol. 2021;5(1):38.

60. Shaabanpour Aghamaleki F, Mollashahi B, Nosrati M, Moradi A, Sheikhpour M, Movafagh A. Application of an Artificial Neural Network in the Diagnosis of Chronic Lymphocytic Leukemia. Cureus. 2019;11(2):e4004.

61. Huang F, Guang P, Li F, Liu X, Zhang W, Huang W. AML, ALL, and CML classification and diagnosis based on bone marrow cell morphology combined with convolutional neural network: A STARD compliant diagnosis research. Medicine (Baltimore). 2020;99(45):e23154.

62. Achi HE, Belousova T, Chen L, Wahed A, Wang I, Hu Z, et al. Automated Diagnosis of Lymphoma with Digital Pathology Images

Using Deep Learning. 2018.

63. Li D, Bledsoe JR, Zeng Y, Liu W, Hu Y, Bi K, et al. A deep learning diagnostic platform for diffuse large B-cell lymphoma with high accuracy across multiple hospitals. Nat Commun. 2020;11(1):6004.

64. Zhang Y, Deng Y, Zou Q, Jing B, Cai P, Tian X, et al. Artificial intelligence for diagnosis and prognosis prediction of natural killer/T cell lymphoma using magnetic resonance imaging. Cell Rep Med. 2024;5(5):101551.

65. Kong H, Zhu H, Zheng X, Jiang M, Chen L, Lan L, et al. Machine Learning Models for the Diagnosis and Prognosis Prediction of High-Grade B-Cell Lymphoma. Front Immunol. 2022;13:919012.

66. Delrue C, Hofmans M, Van Dorpe J, Van der Linden M, Van Gaever Z, Kerre T, et al. Innovative label-free lymphoma diagnosis using infrared spectroscopy and machine learning on tissue sections. Commun Biol. 2024;7(1):1419.

67. Peng T, Liu L, Liu F, Ding L, Liu J, Zhou H, et al. Machine learning-based infection prediction model for newly diagnosed multiple myeloma patients. Front Neuroinform. 2022;16:1063610.

68. Yan W, Shi H, He T, Chen J, Wang C, Liao A, et al. Employment of Artificial Intelligence Based on Routine Laboratory Results for the Early Diagnosis of Multiple Myeloma. Front Oncol. 2021;11:608191.

69. Chen X, Zhang Y, Li X, Yang Z, Liu A, Yu X. Diagnosis and staging of multiple myeloma using serum-based laser-induced breakdown spectroscopy combined with machine learning methods. Biomed Opt Express. 2021;12(6):3584-96.

70. Wang M, Dong C, Gao Y, Li J, Han M, Wang L. A Deep Learning Model for the Automatic Recognition of Aplastic Anemia, Myelodysplastic Syndromes, and Acute Myeloid Leukemia Based on Bone Marrow Smear. Front Oncol. 2022;12:844978.

71. Nagao A, Inagaki Y, Nogami K, Yamasaki N, Iwasaki F, Liu Y, et al. Artificial intelligence-assisted ultrasound imaging in hemophilia: research, development, and evaluation of hemarthrosis and synovitis detection. Res Pract Thromb Haemost. 2024;8(4):102439.

72. Tyrrell PN, Alvarez-Roman MT, Bakeer N, Brand-Staufer B, Jimenez-Yuste V, Kras S, et al. Utilizing artificial intelligence for the detection of hemarthrosis in hemophilia using point-of-care ultrasonography. Res Pract Thromb Haemost. 2024;8(8):102602.

73. Ferreira MV, Nogueira T, Rios RA, Lopes TJS. A graph-based machine learning framework identifies critical properties of FVIII that lead to hemophilia A. Front Bioinform. 2023;3:1152039.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

74. Bibi N, Sikandar M, Ud Din I, Almogren A, Ali S. IoMT-Based Automated Detection and Classification of Leukemia Using Deep Learning. J Healthc Eng. 2020;2020:6648574.

75. Dasariraju S, Huo M, McCalla S. Detection and Classification of Immature Leukocytes for Diagnosis of Acute Myeloid Leukemia Using Random Forest Algorithm. Bioengineering (Basel). 2020;7(4).

76. Venezian Povoa L, Ribeiro CHC, Silva ITd. Machine learning predicts treatment sensitivity in multiple myeloma based on molecular and clinical information coupled with drug response. PLoS One. 2021;16(7):e0254596.

77. Ferle M, Grieb N, Kreuz M, Ader J, Goldschmidt H, Mai EK, et al. Predicting progression events in multiple myeloma from routine blood work. NPJ digital medicine. 2025;8(1):231.

78. Karathanasis N, Spyrou GM. Machine Learning Models for Predicting Multiple Myeloma Staging and MGUS Progression Using Gene Expression Data. bioRxiv. 2024:2024.11. 12.623149.

79. Qin Y. Machine learning-based biomarker screening for acute myeloid leukemia prognosis and therapy from diverse cell-death patterns. Scientific Reports. 2024;14:17874.

80. Kosvyra A, Karadimitris A, Papaioannou M, Chouvarda I. Machine learning and integrative multi-omics network analysis for survival prediction in acute myeloid leukemia. Computers in Biology and Medicine. 2024;178:108735.

81. Mitra A, Kumar A, Amdare NP, Pathak R. Current landscape of cancer immunotherapy: harnessing the immune arsenal to overcome immune evasion. Biology. 2024;13(5):307.

82. Zhang Y. Artificial intelligence for diagnosis and prognosis prediction of natural killer/T cell lymphoma using magnetic resonance imaging. Cell Reports Medicine. 2024;5:101551.

83. Naji H, Hahn P, Pisula JI, Ugliano S, Simon A, Büttner R, et al. Deep learning-based interpretable prediction of recurrence of diffuse large B-cell lymphoma. BJC Reports. 2025;3(1):34.

84. Ahmad W, Shahzad AR, Amin MA, Bangyal WH, Alahmadi TJ, Khan SH. Machine learning driven dashboard for chronic myeloid leukemia prediction using protein sequences. PLoS One. 2025;20(6):e0321761.

85. Hauser RG. A Machine Learning Model to Successfully Predict Future Diagnosis of Chronic Myelogenous Leukemia With Retrospective Electronic Health Records Data. Am J Clin Pathol. 2021;156:1142–8.

86. Ram M. Application of artificial intelligence in chronic myeloid leukemia (CML) disease prediction and management: a scoping review. BMC Cancer. 2024;24:1026.

87. Ai D, Cui C, Tang Y, Wang Y, Zhang N, Zhang C, et al. Machine learning model for predicting physical activity related bleeding risk in Chinese boys with haemophilia A. Thrombosis Research. 2023;232:43-53.

88. Allegra A, Tonacci A, Sciaccotta R, Genovese S, Musolino C, Pioggia G, et al. Machine learning and deep learning applications in multiple myeloma diagnosis, prognosis, and treatment selection. Cancers. 2022;14(3):606.

89. Abdel-Rehim A, Orhobor O, Griffiths G, Soldatova L, King RD. Establishing predictive machine learning models for drug responses in patient derived cell culture. npj Precision Oncology. 2025;9(1):180.

90. Azarkhish I. Artificial Intelligence Models for Predicting Iron Deficiency Anemia and Iron Serum Level Based on Accessible Laboratory Data. J Med Syst. 2012;36:2057–61.

91. Rezayi S. Timely Diagnosis of Acute Lymphoblastic Leukemia Using Artificial Intelligence-Oriented Deep Learning Methods. Computational Intelligence and Neuroscience. 2021;2021:5478157.

92. Cheng ZJ. Artificial intelligence reveals the predictions of hematological indexes in children with acute leukemia. BMC Cancer. 2024;24:993.

93. Alhajahjeh A, Nazha A. Unlocking the Potential of Artificial Intelligence in Acute Myeloid Leukemia and Myelodysplastic Syndromes. Current Hematologic Malignancy Reports. 2024;19:9–17.

94. Azarkhish I, Raoufy MR, Gharibzadeh S. Artificial intelligence models for predicting iron deficiency anemia and iron serum level based on accessible laboratory data. Journal of medical systems. 2012;36(3):2057-61.

95. Wang V, Gauthier M, Decot V, Reppel L, Bensoussan D. Systematic review on CAR-T cell clinical trials up to 2022: academic center input. Cancers. 2023;15(4):1003.

96. Qu Y, Huang K, Yin M, Zhan K, Liu D, Yin D, et al. CRISPR-GPT for agentic automation of gene-editing experiments. Nature Biomedical Engineering. 2025:1-14.

97. Abbaszadeh A, Shahlai A. Artificial Intelligence for CRISPR Guide RNA Design: Explainable Models and Off-Target Safety. arXiv preprint arXiv:250820130. 2025.

98. Cai S. Artificial intelligence for improving sickle cell retinopathy diagnosis and management. Eye. 2021;35:2675-84.

99. Boretti A. The transformative potential of AI-driven CRISPR-Cas9 genome editing to enhance CAR T-cell therapy. Computers in biology and medicine. 2024;182:109137.

100.Dermawan D, Alotaiq N. From Lab to Clinic: How Artificial Intelligence (AI) Is Reshaping Drug Discovery Timelines and Industry Outcomes. Pharmaceuticals. 2025;18(7):981.

101.Chihara D, Kane MJ, Flowers CR, Hobbs BP. Utilizing Synthetic Individual Patient Level Cohorts from Machine Learning on Clinical Trials to Define Endpoints for Bispecific Trials in Large B-Cell Lymphoma. Blood. 2024;144:4462.

102.D'Amico S. Synthetic Data Generation by Artificial Intelligence to Accelerate Research and Precision Medicine in Hematology. JCO Clinical Cancer Informatics. 2023;7:e2300021.

103.Li L, Peng M, Zou Y, Li Y, Qiao P. The promise and limitations of artificial intelligence in CTPA-based pulmonary embolism detection. Frontiers in Medicine. 2025;Volume 12 - 2025.

104.Obeagu EI. Revolutionizing hematological disorder diagnosis: unraveling the role of artificial intelligence. Annals of Medicine and Surgery. 2025;87(6):3445-57.

105.Karako K. Artificial intelligence applications in rare and intractable diseases: Advances, challenges, and future directions. Intractable Rare Dis Res. 2025;14(2):88-92.

106.Wang J. Deep Learning in Hematology: From Molecules to Patients. Clin Hematol Int. 2024;6(4):19-42.

107.Yang Y, Sun K, Gao Y, Wang K, Yu G. Preparing Data for Artificial Intelligence in Pathology with Clinical-Grade Performance. Diagnostics. 2023;13(19):3115.

108.Meng J, Wu M, Shi F, Xie Y, Wang H, Guo Y. Medical laboratory data-based models: opportunities, obstacles, and solutions. Journal of Translational Medicine. 2025;23(1):823.

109.Kang C, Lee C, Song H, Ma M, Pereira S, editors. Variability matters: Evaluating inter-rater variability in histopathology for robust cell detection. European Conference on Computer Vision; 2022: Springer.

110.Marrón-Esquivel JM, Duran-Lopez L, Linares-Barranco A, Dominguez-Morales JP. A comparative study of the inter-observer variability on Gleason grading against Deep Learning-based approaches for prostate cancer. Comput Biol Med. 2023;159:106856.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]

111.Cazzaniga G, Del Carro F, Eccher A, Becker JU, Gambaro G, Rossi M, et al. Improving the Annotation Process in Computational Pathology: A Pilot Study with Manual and Semi-automated Approaches on Consumer and Medical Grade Devices. J Imaging Inform Med. 2025;38(2):1112-9.

112.Wilm F, Bertram CA, Marzahl C, Bartel A, Donovan TA, Assenmacher C-A, et al., editors. Influence of inter-annotator variability on automatic mitotic figure assessment. Bildverarbeitung für die Medizin 2021: Proceedings, German Workshop on Medical Image Computing, Regensburg, March 7-9, 2021; 2021: Springer.

113.Dehkharghanian T, Mu Y, Tizhoosh HR, Campbell CJ. Applied machine learning in hematopathology. International Journal of Laboratory Hematology. 2023;45:87-94.

114.Li N, Lewin A, Ning S, Waito M, Zeller MP, Tinmouth A, et al. Privacy-preserving federated data access and federated learning: Improved data sharing and AI model development in transfusion medicine. Transfusion. 2025;65(1):22-8.

115.Asti G, D'Amico S, Carota L, Piscia D, Casadei F, Merleau NSC, et al. An Artificial Intelligence-Based Federated Learning Platform to Boost Precision Medicine in Rare Hematological Diseases: An Initiative By GenoMed4all and Synthema Consortia. Blood. 2024;144:4989.

116.Schouten D, Nicoletti G, Dille B, Chia C, Vendittelli P, Schuurmans M, et al. Navigating the landscape of multimodal AI in medicine: a scoping review on technical challenges and clinical applications. Medical Image Analysis. 2025:103621.

117.Reinecke D, Maroouf N, Smith A, Alber D, Markert J, Goff NK, et al. Fast intraoperative detection of primary CNS lymphoma and differentiation from common CNS tumors using stimulated Raman histology and deep learning. medRxiv. 2024.

118.Cheng FM, Lo SC, Lin CC, Lo WJ, Chien SY, Sun TH, et al. Deep learning assists in acute leukemia detection and cell classification via flow cytometry using the acute leukemia orientation tube. Sci Rep. 2024;14(1):8350.

119.Salama ME, Otteson GE, Camp JJ, Seheult JN, Jevremovic D, Holmes DR, 3rd, et al. Artificial Intelligence Enhances Diagnostic Flow Cytometry Workflow in the Detection of Minimal Residual Disease of Chronic Lymphocytic Leukemia. Cancers (Basel). 2022;14(10).

120.Asar TO, Ragab M. Leukemia detection and classification using computer-aided diagnosis system with falcon optimization algorithm and deep learning. Sci Rep. 2024;14(1):21755.

121.Pan L, Li L, Qiu Y, Ling X, Wang C, Wu Z, et al. A novel discriminant algorithm for differential diagnosis of mild to moderate thalassemia and iron deficiency anemia. Medicine (Baltimore). 2024;103(20):e38205.

122.Lyons J, Desai V, Xu Y, Ridgeway G, Finkle W, Solari P, et al. Development and Validation of an Algorithm for Identifying Patients with Hemophilia A in an Administrative Claims Database. Value Health. 2018;21(9):1098-103.

123.Lei Y, Wei H, Gao X. High temporal resolution prediction of mortality risk for single AML patient via deep learning. iScience. 2024;27(8):110458.

124.Didi I, Alliot JM, Dumas PY, Vergez F, Tavitian S, Largeaud L, et al. Artificial intelligence-based prediction models for acute myeloid leukemia using real-life data: A DATAML registry study. Leuk Res. 2024;136:107437.

125.Zhao S, Wang J, Jin C, Zhang X, Xue C, Zhou R, et al. Stacking Ensemble Learning–Based [¹⁸F]FDG PET Radiomics for Outcome Prediction in Diffuse Large B-Cell Lymphoma. Journal of Nuclear Medicine. 2023;64(10):1603-9.

126.Jardim LL, Schieber TA, Santana MP, Cerqueira MH, Lorenzato CS, Franco VKB, et al. Prediction of inhibitor development in previously untreated and minimally treated children with severe and moderately severe hemophilia A using a machine-learning network. J Thromb Haemost. 2024;22(9):2426-37.

127.Khosla E, Ramesh D. Phase classification of chronic myeloid leukemia using convolution neural networks2018. 1-6 p.

128.Sasaki K, Jabbour EJ, Ravandi F, Konopleva M, Borthakur G, Wierda WG, et al. The LEukemia Artificial Intelligence Program (LEAP) in chronic myeloid leukemia in chronic phase: A model to improve patient outcomes. Am J Hematol. 2021;96(2):241-50.

129.Mehrbakhsh Z, Hassanzadeh R, Behnampour N, Tapak L, Zarrin Z, Khazaei S, et al. Machine learning-based evaluation of prognostic factors for mortality and relapse in patients with acute lymphoblastic leukemia: a comparative simulation study. BMC Med Inform Decis Mak. 2024;24(1):261.

130.Saleem M, Aslam W, Lali MIU, Rauf HT, Nasr EA. Predicting thalassemia using feature selection techniques: A comparative analysis. Diagnostics. 2023;13(22):3441.

[Downloaded from ijbc.ir on 2026-10-14]

[DOI: 10.61882/ijbc.17.3.46]