IJRTSM

INTERNATIONAL JOURNAL OF RECENT TECHNOLOGY SCIENCE & MANAGEMENT

"THE ROLE OF AND DEEP LEARNING IN TRANSFORMING BLOOD CANCER DETECTION AND DIAGNOSIS"

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ABSTRACT

This review paper explores the transformative impact of Machine Learning (ML) and Artificial Intelligence (AI) in the realm of blood cancer detection. Blood cancers, comprising leukemia, lymphoma, and myeloma, represent a heterogeneous group of malignancies characterized by diverse genetic alterations and clinical manifestations. Leveraging ML and AI technologies, this review highlights how these tools have revolutionized early diagnosis, prognosis prediction, and personalized treatment strategies for blood cancer patients. From analyzing large-scale genomic data to enhancing medical imaging interpretation, these intelligent systems enable healthcare professionals to make more precise and timely decisions, ultimately contributing to improved patient outcomes and the advancement of blood cancer research and therapy.

Key Words: Artificial Intelligence, Machine Learning, Blood Cancer Detection.

I. INTRODUCTION

Red blood cells, platelets, and white blood cells are the three main types of cells that make up blood. It is necessary for red blood cells to carry oxygen from the heart to all of the body's organs and get rid of carbon dioxide1. About half of all the blood in the body is made up of these. White blood cells, or WBCs, are the main part of the immune system that the body uses to fight off harmful diseases and illnesses. Because of this, they are very important to the defense system. As a result, accurate classification of WBCs is needed and is becoming an area of greater attention and interest. White blood cells come in two different types, which can be told apart by how their cytoplasm looks. There are three main types of granulocytes, which are the first type of white blood cell: basophils, eosinophils, and neutrophils. The second group is made up of lymphocytes and monocytes, which are generally called agranulocytes. A type of cancer called leukemia is a growth that grows in cells. It has hurt millions and millions of people. Everything starts in the lymphatic system, which is where blood cells are made. Everything starts in the bone marrow and then spreads through the blood cells to the rest of the body. White blood cells (WBCs) typically form based on what the body needs, but when someone has leukemia, they form incorrectly and stop working. Even though they are often easy to spot because of their dark purple color, it is very hard to examine and process them further because their shape and texture are usually very different. It is because they are so diverse that cells in the leukocyte group can be very different from one another. They are hard to tell apart because they are surrounded by other blood cells like red blood cells and platelets. Their shape and size, on the other hand, make them easy to recognize. Lymphocytes have a pretty regular shape, as shown in Figure 1.1. The sides of their nuclei are also smooth and regular. Lymphocytes from people with acute lymphocytic leukemia (ALL), also called lymphoblasts, have a less normal envelope and have small holes in their cytoplasm called vacuoles as well as round particles called nucleoli. When the morphological abnormalities that have been mentioned

become more obvious, the disease is said to be more severe. At the moment, the best way to use medical images for things like detection and classification is through deep learning, which uses convolutional neural networks (CNN) 3, 4. 5, 6. CNNs work best with very large amounts of data, but they need a lot of data and computer resources to be trained. There are times when the dataset is small, and it's possible that it doesn't have enough data to teach a CNN from start. In this case, transfer learning could be a good choice because it lets you use the power of CNNs while also reducing the amount of computing that needs to be done. For this method to work, the CNN is first taught on a large and varied set of generic image data. Only then is it used for a specific task.Some neural networks that have already been trained and won international competitions are VGGNet10, Resnet11, Nasnet12, Mobilenet13, Inception14, and Xception15. It is possible to buy these networks. At the end of 2016, different CNN designs were tested. The results showed that transfer learning did the best on both thoraco-abdominal lymph node (LN) classification and interstitial lung disease (ILD) classification. The authors used average pooling classification to tell the difference between cancerous and non-cancerous cells in breast cancer images after extracting features from the images using pre-trained CNN models and feeding them into a fully connected classification layer. This helped them figure out which cells were dangerous and which ones were not. The results of the experiment showed that their model was better at finding breast tumors than any other CNN method when using cytological images to identify and classify them. This was shown by the fact that their model did better than all the other CNN methods. In a different study, different deep learning frameworks were combined into a single model to make transfer learning better for classifying images based on cells. It was possible to get around the problems with earlier models for finding breast cancer in cytology pictures by using transfer learning and standard benchmark datasets.

Cancer remains an issue all around the world despite the significant progress that has been made in diagnosing it. [14] The International Agency for Research on Cancer (IARC), which is a division of the World Health Organization (WHO), estimates that the worldwide cancer burden increased to 18.1 million new cases and 9.6 million deaths in 2018. This figure was determined by looking at cancer statistics from 2018. Because Asia is home to sixty percent of the world's population, it is the lone location where almost half of the newly diagnosed cases of cancer (48.4 percent) and more than fifty seven percent of all cancer deaths (57.3 percent) in 2018 have taken place. The total incidence is divided as follows: 23.4% occurs in Europe, 5.8% occurs in Africa, and 21% occurs in America. However, the percentage of fatalities caused by cancer in Europe,
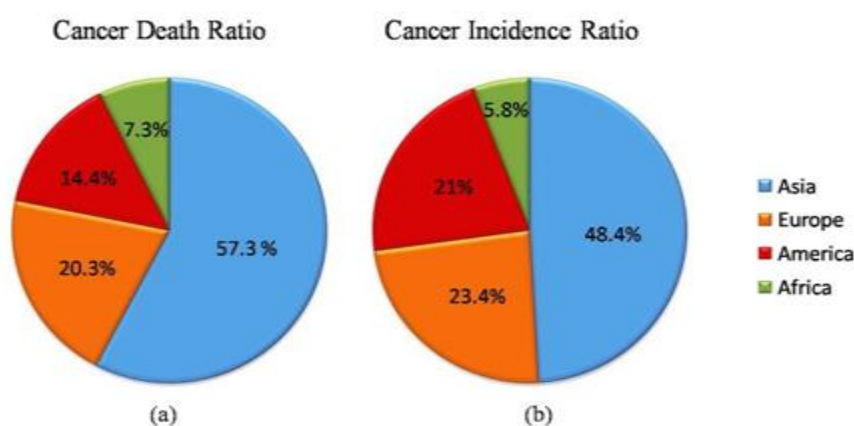

Figure 1.Global distributions of cancer death ratio and cancer incidence ratio

The percentages for countries in Africa and America are, respectively, 20.3%, 7.3%, and 14.4% (Figure 1). As a result of a poor prognosis, a delay in diagnosis, and treatment, the mortality rate is significantly higher in Asia and Africa in proportion to the number of new cases. One such factor that contributes to the high death rate is the inability of individuals living in poverty in developing nations to obtain access to new medical treatments and technologies. In order to effectively combat cancer, there is an immediate need for the development of methods that are both effective and cost-effective for early detection, diagnosis, and treatment.

In India also, cancer has become a national concern. Indian Council of Medical Research (ICMR) estimates 1157294 new cases and 784821 cancer-related deaths. About 2.25 million people are living with cancer. Among all type of cancer, oral cavity cancer is the most prevailing cancer in male (16% of all cancers) and breast cancer (BC) in female

(14% of all cancers). According to statistics provided, 1 in 22 women of an urban area is likely to develop BC in comparison of rural area where 1 in 60 women account BC in her lifetime.

Diagnosis of BC can be attained through non-invasive screening examination such as mammography, thermograph, magnetic resonance imaging (MRI), ultrasound, positron emission tomography (PET), and breast-specific gamma imaging. The biopsy is another method of screening which is an invasive method. All the imaging screening methods are evident that the images are playing an amazing role in the detection of BC. Despite the widespread use of imaging techniques in cancer detection and diagnosis, a final diagnosis of cancer is based on analysis of cells and tissues by a pathologist. The only method through which cells and tissue samples can be collected and fixed over a glass-slide. Further, staining has been performed in order to extract significant information about tissue compositions and the shape of the cells from histology slides. Histopathological modality of imaging is always acknowledged as a paragon of excellence in the diagnosis of almost all types of cancer. With due consideration of cancer impact on global health and an urgent need to provide tools in support of pathologists, efficient machine learning techniques are investigated to classify BC using digital histological images.

II. LITERATURE REVIEW

Asad Ulla et.al. (2022) Computer vision has a lot to give the field of biomedicine, and one of its most important topics is the automatic classification of cells. In the past few years, there have been a lot of studies that have tried to use label-free pictures of cells taken with an optical microscope to build an AI-based cell classification. A number of different countries have done these tests. Even though these studies showed positive results, these classifiers were not able to accurately reflect the biological complexity of the different types of cells. While on the other hand, everyone knows that the actin strands inside cancer cells are very different from how they should be. Researchers think this has a lot to do with how tumor cells grow and their tendency to break through and spread to other parts of the body. It is not only helpful, but it is also more helpful to use a computerized way to figure out the different types of cells based on the biological activities they carry out. This study shows that there is a difference between white blood cells that are healthy and those that have cancer. This can help us understand how cancer can spread and give us another way to diagnose it. We suggested using a convolutional neural network (CNN), which sorts white blood cells into groups based on whether they are normal or cancerous. The reason for this is that human eyes can't see the traits. The Inception-V3Cnn model was proven by testing it on different types of WBCs, including normal and cancerous cell pictures, as well as on normal and blood cancer cell lines that were aggressive at different levels. The study's results showed that CNN did better than a person expert at the cell classification method in terms of both accuracy and speed.

Ismail M. I. Alkafrawi et.al. (2022) The three main types of blood cells are red blood cells (also called erythrocytes), white blood cells (also called leukocytes) and platelets (also called thrombocytes). There are three different kinds of blood cells, and together they make up 45% of the blood tissue. The plasma, which is the liquid part of blood, makes up the last 55% of the amount. These three types are very important to the body because they boost defense and keep dangerous diseases away. When trying to figure out what's wrong with a patient, both the type of cells they have and the number of them are very helpful. It can also be used to help doctors figure out what's wrong with people who have infections, anemia, leukemia, cancer, and other illnesses. This will make it much easier for the hematologist to tell the difference between the different kinds of white blood cells, red blood cells, and platelets that are in the body and figure out why some disorders happen. At the moment, a lot of study is being done in this area. The deep learning method that will be used in this study is called Convolution Neural Networks. This method can sort pictures of different types of human blood cells into groups, such as neutrophils, eosinophils, basophils, lymphocytes, monocytes, immature granulocytes (promyelocytes, myelocytes, and metamyelocytes), red blood cells (erythroblasts), and platelets (thrombocytes). This article's discussion is based on a dataset that was collected in the Core Laboratory of the Hospital Clinic in Barcelona using convolutional neural networks.

Shantani K et.al. (2022) Cancer is marked by an overgrowth of abnormal cells that can divide quickly and spread and kill healthy tissue. This is the thing that makes cancer what it is. There are people of all ages who get this illness, which ends in death. On the other hand, mortality rates are going up for many types of cancer because of progress in finding cancer, treating it, and stopping it. Many people of any age can get lymphoma, and it spreads very quickly. There are a lot of people who get this type of cancer. The cells in our immune system that fight off infections are the first to be

affected. They are called lymphocytes. The lymph nodes, the spleen, the thymus, and the bone marrow are all places where these cells can be found. People who have cancer have cells that change and grow out of control. Follicular Lymphoma and Mantle Cell Lymphoma are more likely to happen to people over the age of 65. Every year, this sickness changes the lives of millions of people. One of the most important things that can be used to figure out what kind of cancer is present is the blood count. According to custom, counting by hand is used. This way does produce satisfactory results, but it takes a lot longer to process. One possible answer to these issues is deep learning methods, which can quickly and effectively pull out useful features from huge amounts of raw data sets. The use of deep learning techniques can help save lives because cancer needs to be found early. The project's goal is to use bone marrow microscopic images to find lymphoma in a patient and then divide the lymphoma into three groups: Follicular Lymphoma (FL), Mantle Cell Lymphoma (MCL), and normal tissues. The groups will be based on CNN architecture (Inception V3) and (ResNet-50), and the accuracy and efficiency will be predicted and compared to other models. Techniques from the field of image processing, like segmentation and filtering, have also been used to look for signs of cancer in the pictures.

Rida Arif et.al. (2022) Leukemia is a type of cancer that affects cells that make blood. It usually ends in death. The body makes an excessively large number of white blood cells (WBCs), which leads to it. This is likely to be suggested by the doctor as a way to find out if the person has leukemia or another type of leukemia. Acute leukemia and chronic leukemia are the two types of leukemia. So, finding leukemias early lets people take precautions to make sure there is no danger to life. There have also been a number of human and computer methods proposed, but they all have some problems and are not very good at accurately diagnosing leukemia. The study's results give us a system based on deep learning that can correctly and automatically spot leukemia by looking at pictures that are very small. The suggested framework has four steps: pre-processing, data enhancement, segmentation, and tumor classification. The pictures in the collection are also made better by pre-processing, which gets rid of the noise. After that, methods of data enrichment were used to add more pictures and fix the problems with class mismatch and overfitting at the same time. A changed form of the Convolutional Neural Network (CNN)-based model is used to separate the photos of leukemia. A well-known version of the AlexNet design that had already been trained was used for sorting. Another thing that was used to train and test the suggested model is the Acute Lymphoblastic Leukemia Image Database (ALL-IDB), which is a public collection that anyone can use. That model got an F1-score of 99.06%, an accuracy score of 98.05%, a precision score of 97.59%, and a recall score of 100%. The tests showed that this model works well and reliably to find leukemia using the ALL-IDB dataset. This means that it can be used in clinical settings and is suitable for usage in those settings.

Adnan Saeed et.al. (2022) Leukemia is a potentially deadly disease that can start in the bone marrow when there are an unusually high number of immature white blood cells. It is more likely that someone will fully heal from leukemia if it is found earlier. In most cases, trained medical staff must look at blood cells by hand to do structural analysis that helps find leukemia. This has many problems, such as not having enough medical staff, research taking too long, and predictions based on how well the medical staff can do their jobs. So, we suggested making an automatic system that can correctly diagnose leukemia and doesn't cost a lot of money. The suggested method depends on being able to spot acute lymphoblastic leukemia by looking at blood smear pictures under a microscope. We used three baseline architectures—VGG-16, Inception-V3, and ResNet50—that had already been trained on the ImageNet database to figure out what was written as "ALL." Data improvement and preprocessing methods have been used to cut down on the number of errors that the network makes. An approach called transfer learning is becoming more common in the area of health image processing. This is because, compared to other deep learning techniques, it can learn from a much smaller set of pictures. As a result of this study, we have come up with a new, transfer-based way for ALL to be automatically put into groups. Our suggested ResNet50 model was 100% accurate on the ALL_IDB dataset and 97% accurate on the C_NMC-2019 dataset.

G. Meena Devi et.al. (2022) Leukemia is a type of blood cancer that starts when white blood cells (WBCs) multiply too quickly in the bone marrow. These are the white blood cells (WBC) in question. At the moment, convolutional neural networks (CNN) are the best way to do medical picture analysis jobs like detection and classification (CNN). Full learning and transfer learning were used to test the structure of CNN using AlexNet, VGG16, GoogLeNet, and ResNet50. CNN is the base layer of the Convolution layer. Finally, the method could correctly identify WBC cells every single time, which was the end of the study. One type of CNN called VGG16 has shown to be the best at transfer

learning. It was 98.53% accurate to guess the type of lymphocyte cell, 97.41% accurate to guess the type of monocyte cell, 98.48% accurate to guess the type of basophil cell, 96.16 % accurate to guess the type of eosinophil cell, and 94.05 % accurate to guess the type of neutrophil cell. The results they got on all of these VGG16 datasets were some of the best, beating out a number of convolutional network models. With the methods that were used, image analysis showed that it was 97.16 percent successful at finding leukemia on average.

Ashik Iqbal et.al. (2021) Plasma cell cancer starts in the bone marrow and leads to the production of abnormal plasma cells. White blood cell cancer is a type of plasma cell cancer. Medical experts have to be very careful about what they look for when they try to find myeloma cells. Additionally, since the final decision is based on people's thoughts and choices, there is a chance that the result will be wrong. Finding and identifying myeloma cells in bone marrow scans will be easier with the help of software. This is important work. This is a big step forward in how myeloma is treated. MASK-Recurrent Convolutional Neural Network has been found to be the best tool for recognition, while Efficient Net B3 has been found to be the best tool for identification. If you look at the mean Average Precision (mAP), MASK-RCNN is 93% accurate, while Efficient Net B3 is 95% accurate. The study's findings show that the Mask-RCNN model can spot multiple myeloma, while the Efficient Net B3 model can tell the difference between myeloma cells and other types of cells.

Sai Mattapalli et.al. (2021) The use of machine learning architectures is required in order to make an accurate and timely differentiation between blood cells afflicted by Acute Lymphocytic Leukemia (ALL) and their healthy counterparts. This is because of the physical resemblance at the microscopic level between the two types of cells. However, three of the most frequent models, VGG (see Figure 3), ResNet (see Figure 4), and Inception (see Figure 5), each come with their own set of defects and there is potential for development, which necessitates the requirement for a more advanced model. ALLNet is a hybrid convolutional neural network architecture that was suggested. It is made up of a mixture of three different models: VGG, ResNet, and Inception. The photos of 10,691 white blood cells that are included in the ALL Challenge dataset of the ISBI 2019 may be found here. These images were used to train and test the models. There are 7,272 photos in the collection that depict cells that are affected by ALL, and there are 3,419 images that depict healthy cells. Sixty percent of the photographs were used to train the model, twenty percent of the images were used for the cross-validation set, and twenty percent of the images were used for the test set. ALLNet surpassed the VGG, ResNet, and the Inception models in every metric, obtaining an accuracy of 92.6567%, a sensitivity of 95.5304%, a specificity of 85.9155%, an AUC score of 0.966347, and an F1 score of 0.94803 in the cross-validation set. In addition, ALLNet had a specificity of 85.9155%, which was the highest of any model. In the test set, ALLNet obtained an accuracy of 92.0991%, a sensitivity of 96.5446%, a specificity of 82.8035%, an AUC score of 0.959972, and an F1 score of 0.942963. These numbers translate to an AUC score of 0.959972 and an F1 score of 0.942963. The application of ALLNet in the clinical setting enables for improved treatment of the thousands of people across the world who are afflicted with ALL; the majority of those affected are youngsters.

Sanju et.al. (2021) For the purpose of assisting in the diagnosis of multiple myeloma, a computerized diagnostic tool based on image processing has been created. The development of cancer in the white blood cells that reside in the bone marrow as a result of multiple myeloma can result in serious damage to both the bones and the kidneys, as well as in mortality. In the course of our research, we utilized a dataset (SegPC-2021 Challenge) of stained microscope pictures that had previously been made available to the public. This dataset included both normal and malignant cells. We obtained a good classification accuracy of 93.58% when we were tasked with determining whether or not images contained cancerous cells. This accuracy was further improved using Transfer Learning and Fine Tuning with various pre-trained Convolutional Neural Networks models, including VGG (Visual Geometry Group), VGG-16, VGG-19, MobileNetV1, and MobileNetV2, which gave an accuracy of 94.00%, 95.50%, 99.90%, and 97% respectively.

III. METHOD FOR BLOOD CANCER DETECTION

Methods for blood cancer detection encompass a wide range of diagnostic techniques that play a crucial role in identifying and characterizing various types of blood cancers, including leukemia, lymphoma, and myeloma. These methods are essential for early diagnosis and treatment planning.

Blood Tests: One of the most common methods for detecting blood cancer is through blood tests, including complete blood counts (CBCs) and peripheral blood smears. These tests assess the levels of different blood cell types and can reveal abnormalities in the white blood cells, red blood cells, or platelets, providing initial clues to the presence of blood cancer.

Bone Marrow Biopsy: To confirm a blood cancer diagnosis and determine its specific subtype, a bone marrow biopsy is often performed. During this procedure, a small sample of bone marrow is extracted from the hipbone or sternum and examined under a microscope. Abnormal cell morphology, proliferation, and genetic markers can be identified through this invasive yet vital diagnostic method.

Immunophenotyping: Immunophenotyping is a technique that utilizes flow cytometry to analyze the surface markers (CD markers) on white blood cells. This method helps classify blood cancers by their cellular characteristics, distinguishing between different subtypes and aiding in treatment decisions.

Cytogenetic Analysis: Cytogenetic analysis involves the study of the chromosomal abnormalities present in blood cancer cells. Techniques like karyotyping and fluorescent in situ hybridization (FISH) help identify genetic mutations, translocations, and deletions, which are critical for diagnosing and subtyping blood cancers.

Molecular Genetic Testing: Advances in molecular biology have led to the development of various genetic tests, such as polymerase chain reaction (PCR) and next-generation sequencing (NGS), which can detect specific genetic mutations and fusion genes associated with blood cancers. These tests not only aid in diagnosis but also guide targeted therapy decisions.

Imaging Techniques: Imaging methods, including computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), and ultrasound, are employed to assess the extent and location of blood cancers within the body They play a crucial role in staging the disease and monitoring treatment response.

Liquid Biopsies: Liquid biopsies have gained prominence in recent years as non-invasive methods for blood cancer detection. These tests analyze cell-free DNA, RNA, or other biomarkers circulating in the bloodstream, providing insights into disease progression and genetic changes.

Flow Cytometry: Flow cytometry is used to analyze the physical and chemical characteristics of individual cells. It is particularly valuable in identifying abnormal cell populations in blood samples and characterizing their features.

Protein Markers: Some blood cancers may exhibit specific protein markers or antigens. Enzyme-linked immunosorbent assays (ELISA) and immunohistochemistry (IHC) are methods commonly employed to detect these markers, aiding in diagnosis and prognosis.

Machine Learning (ML) and Artificial Intelligence (AI) have made significant strides in the field of blood cancer detection. These technologies offer the potential to enhance the accuracy and efficiency of diagnosis, prognosis, and treatment planning. Here's an overview of how ML and AI are applied in blood cancer detection.

IV. MACHINE LEARNING AND AI IN BLOOD CANCER DETECTION

Data Analysis and Pattern Recognition: ML algorithms can analyze large datasets of patient information, including clinical data, genetic profiles, and medical imaging. By identifying patterns and associations in this data, AI systems can help identify potential indicators of blood cancer or its subtypes.

Diagnostic Support: ML models can assist healthcare professionals in making accurate diagnoses by flagging subtle abnormalities in blood counts, genetic markers, or imaging results. These algorithms can provide real-time feedback, helping clinicians make informed decisions faster.

Predictive Modeling: AI can predict the likelihood of blood cancer development based on a patient's medical history, genetic predisposition, and lifestyle factors. This early risk assessment allows for proactive interventions and

monitoring.

Genomic Analysis: ML algorithms excel at analyzing complex genetic data. In blood cancer detection, AI can identify specific genetic mutations or fusion genes associated with different blood cancer subtypes. This information aids in subtype classification and guides treatment choices.

Imaging Analysis: AI-powered image recognition can enhance the interpretation of medical imaging, such as CT scans, MRIs, and PET scans. ML algorithms can identify subtle anomalies or track disease progression over time, supporting accurate staging and treatment planning.

Liquid Biopsy Analysis: ML algorithms are used to analyze liquid biopsy data, including circulating tumor DNA (ctDNA) and RNA. These non-invasive tests can provide real-time insights into disease status, allowing for early detection of minimal residual disease (MRD) and monitoring treatment response.

Personalized Medicine: ML-driven algorithms can recommend personalized treatment plans based on a patient's unique genetic profile and disease characteristics. This precision medicine approach minimizes unnecessary treatments and maximizes therapeutic effectiveness.

Drug Discovery: AI accelerates drug discovery by identifying potential therapeutic targets and predicting how specific drugs might interact with blood cancer cells. This can lead to the development of targeted therapies and novel treatment approaches.

Clinical Trial Matching: ML algorithms help match eligible patients with ongoing clinical trials, facilitating access to cutting-edge treatments and therapies tailored to their specific blood cancer subtype.

Data Integration: ML systems can integrate and analyze data from multiple sources, such as electronic health records, medical imaging, and genomics, to provide a comprehensive view of a patient's health status and treatment history.

Real-time Monitoring: AI-powered systems enable continuous monitoring of patients' health, including vital signs and biomarker levels. Any deviations from the expected patterns can trigger alerts for timely interventions.

Challenges in the application of ML and AI in blood cancer detection include the need for high-quality, annotated data, model interpretability, and regulatory considerations. Nonetheless, as technology continues to advance, the integration of ML and AI into clinical practice holds great promise for improving the accuracy of blood cancer detection and patient outcomes.

V. CONCLUSION

In conclusion, the integration of Machine Learning (ML) and Artificial Intelligence (AI) into blood cancer detection represents a promising avenue for enhancing diagnosis, treatment, and patient care. These technologies have demonstrated their ability to analyze vast datasets, recognize intricate patterns, and provide clinicians with invaluable decision support. ML and AI empower healthcare professionals to make more accurate and timely diagnoses, predict disease progression, and tailor treatment plans to individual patient profiles, ultimately improving the management and outcomes of blood cancer cases. As technology continues to evolve, it is imperative that collaboration between researchers, clinicians, and data scientists remains strong, ensuring that these innovations reach their full potential in transforming the landscape of blood cancer detection and treatment. Moreover, ongoing efforts should focus on addressing ethical considerations, data privacy concerns, and regulatory frameworks to facilitate the responsible and widespread adoption of ML and AI in clinical practice.

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