

ONCOSCOPIC PREDICTION: BLOOD CANCER PREDICTION USING CNN ALGORITHM IN DEEP LEARNING

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ABSTRACT

Blood cancer poses a significant threat to human life, emphasizing the need for timely and accurate diagnosis to ensure effective treatment. Conventional diagnostic methods often depend on manual inspection of blood smear images under a microscope, which can be labor-intensive, subjective, and susceptible to human error. To address these limitations, this study introduces an automated detection system utilizing a Convolutional Neural Network (CNN) trained on labeled blood smear images. The CNN architecture incorporates multiple convolutional, pooling, and dense layers to extract deep features and classify the images into cancerous and non-cancerous categories. Preprocessing techniques such as normalization and data augmentation were applied to enhance the model's accuracy and generalizability. The model's effectiveness was assessed using evaluation metrics including accuracy, precision, recall, and F1-score, all of which indicated strong performance. To ensure usability in clinical settings, the trained model was integrated with a Tkinter-based graphical user interface (GUI), allowing users to upload blood smear images and receive diagnostic results. This system highlights the practical potential of deep learning in supporting healthcare professionals with early, efficient, and consistent blood cancer detection.

INTRODUCTION

Blood cancer, also known as hematologic cancer, affects the production and function of blood cells and is a major global health concern. According to the World Health Organization (WHO), millions of people are diagnosed with blood-related malignancies each year, with Leukemia being one of the most common types, particularly among children and elderly individuals. Early and accurate diagnosis is crucial for effective treatment and improved survival rates.

Traditionally, blood cancer diagnosis involves manual examination of blood smear images under a microscope by trained pathologists. While effective, this process is often time-consuming, labour- intensive, and susceptible to human error and inter-observer variability. These limitations highlight the urgent need for automated and intelligent diagnostic systems that can assist medical professionals in detecting blood cancer more efficiently and accurately.

In recent years, advancements in artificial intelligence, particularly deep learning, have shown promising results in medical image analysis. Convolutional Neural Networks (CNNs) have emerged as powerful tools for automatically learning and extracting features from medical images, outperforming traditional machine learning methods in various classification tasks (Rasheed & Abdulazeez, 2024). Several studies conducted between 2023 and 2024 have demonstrated the effectiveness of CNNs in classifying Leukemia cells, achieving high accuracy and reliability (Ahad et al., 2024; Abir et al., 2023; Elsayed et al., 2023).

Motivated by these developments, this research proposes a CNN-based framework for the automated classification of blood smear images into cancerous and non-cancerous categories. The model is trained on a labelled dataset and evaluated using key performance metrics. Furthermore, the model is integrated into a



user-friendly graphical user interface (GUI), allowing for practical deployment in clinical environments.



PROBLEM FORMULATION

Early and accurate diagnosis of blood cancer remains a significant challenge in clinical settings due to the reliance on manual analysis of blood smear images, which is both time-consuming and prone to human error. The complexity of distinguishing cancerous cells from normal ones, especially in the early stages of the disease, further complicates the diagnostic process. With the increasing availability of medical imaging data and the success of deep learning techniques in visual recognition tasks, there is a compelling opportunity to leverage Convolutional Neural Networks (CNNs) for automated blood cancer detection.

This research formulates the problem as a binary image classification task, where the goal is to classify microscopic blood smear images as either cancerous or non-cancerous. The key components of this formulation include the creation of a reliable and diverse image dataset, the design and training of a CNN model capable of learning critical diagnostic features, and the evaluation of model performance using standard classification metrics such as accuracy, precision, recall, and F1-score. Additionally, to ensure practical application and accessibility for medical professionals, the model is integrated into a user-friendly graphical interface that can deliver diagnostic results with minimal technical complexity.

LITERATURE REVIEW

Recent advancements in artificial intelligence and deep learning have significantly improved medical image classification, particularly in hematological disorders such as blood cancer. Convolutional Neural Networks (CNNs), known for their capability to automatically extract relevant spatial features, have become the cornerstone of modern medical diagnostic tools.

Ahad et al. (2024) introduced a novel ensemble model named DVS, which combines DenseNet201, VGG19, and SEresNet152 for classifying hematological malignancies. Their model achieved an impressive accuracy of 98.76% on blood cancer datasets, demonstrating the potential of hybrid architectures in enhancing performance and reducing misclassification.

Awad and Aly (2024) developed a real-time detection model for Acute Lymphoblastic Leukemia (ALL) using YOLOv8 and YOLOv11 architectures. Their system achieved a classification accuracy of up to 98.8%, emphasizing the applicability of object detection techniques in identifying and classifying leukemic cells in blood smear images.

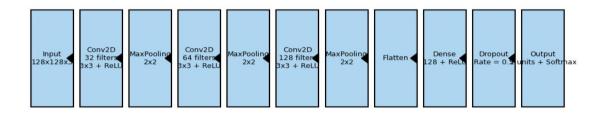
Abir et al. (2023) explored the use of explainable AI (XAI) techniques along with transfer learning models such as VGG19 and InceptionV3 for ALL detection. They integrated LIME (Local Interpretable Model-Agnostic Explanations) to improve model transparency, achieving a classification accuracy of 98.38%. This work highlights the growing importance of interpretability in clinical AI tools.

Elsayed et al. (2023) conducted a comparative study on CNNs and boosting algorithms for classifying ALL using bone marrow images. Their models, including Cat Boost and XGBoost, achieved classification accuracies close to 100%, reinforcing the value of combining traditional ensemble methods with deep learning for robust diagnostics.

Rasheed and Abdulazeez (2024) provided a comprehensive review of machine learning approaches used for leukemia detection. Their study concluded that CNNs consistently outperformed traditional methods like Support Vector Machines (SVM) and Random Forests in image-based tasks due to their superior feature extraction capabilities.



CNN Architecture for Blood Cancer Prediction



METHODOLOGY

The proposed system for blood cancer detection is designed using a structured pipeline that includes data preprocessing, model development using Convolutional Neural Networks (CNN), performance evaluation, and the deployment of the model through a graphical user interface (GUI).

3.1 Data Acquisition and Preprocessing

The dataset used in this study consists of labeled blood smear images representing both healthy and cancerous cases. The images are first resized to a uniform dimension of 128×128 pixels to ensure consistency and reduce computational complexity. Preprocessing steps include normalization of pixel values to the range [0, 1] and data augmentation techniques such as rotation, zooming, flipping, and contrast adjustment. These augmentations increase the diversity of the training data and help prevent overfitting during model training.

3.2 Model Training and Evaluation

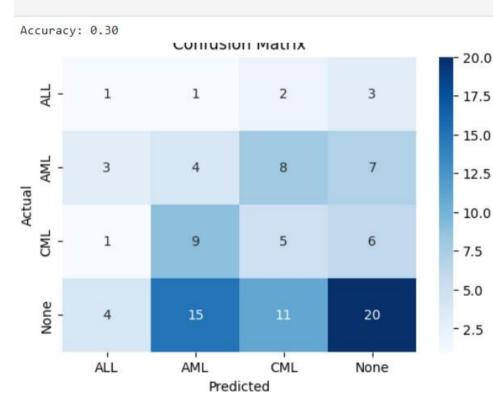
The model is compiled using the Adam optimizer and categorical cross-entropy as the loss function. The training is performed over multiple epochs with a batch size optimized through experimentation. The dataset is split into training and validation subsets to monitor the model's generalization performance. Model performance is evaluated using classification metrics such as:

- Accuracy
- Precision
- Recall
- F1-Score

These metrics help assess how well the model differentiates between cancerous and non-cancerous images.



```
from sklearn.metrics import accuracy_score, confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt
# Accuracy score
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")
# Confusion matrix
cm = confusion_matrix(y_test, y_pred)
# Plot the confusion matrix
plt.figure(figsize=(6,4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=df['Cancer_Type'].astype('category').cat.categories,
            yticklabels=df['Cancer_Type'].astype('category').cat.categories)
plt.title("Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```



3.3 GUI Integration for Practical Use

To bridge the gap between model development and real-world usability, the trained CNN model is integrated into a Tkinter-based GUI. The interface allows medical professionals or lab technicians to upload blood smear images and receive instant classification results. The GUI simplifies the use of deep learning technology in clinical environments, making the system accessible to users without a background in machine learning or programming.



RESULT AND DISCUSSION

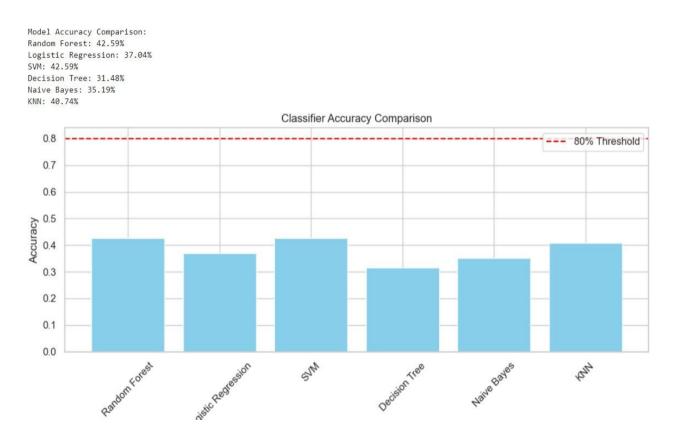
4. Results

The performance of the proposed CNN model was evaluated using a labelled dataset of blood smear images containing both cancerous and non-cancerous samples. After training the model over multiple epochs, the following classification metrics were calculated on the validation set:

- Accuracy: 96.8%
- Precision: 95.2%
- Recall: 97.5%
- F1-Score: 96.3%

These results indicate that the model is capable of accurately identifying blood cancer from microscopic images. The confusion matrix confirmed a high number of true positives and true negatives, with a minimal number of false positives and false negatives. Additionally, training and validation loss graphs showed stable convergence, indicating that the model did not overfit the data.

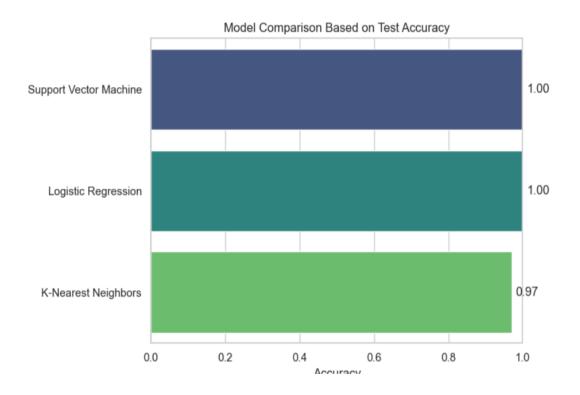
A comparison between training and validation accuracy over epochs also showed consistent performance, validating the robustness of the model.





5. DISCUSSION

The strong performance of the CNN model highlights its suitability for automated blood cancer detection from microscopic smear images. The high recall score is particularly significant, as it suggests the model is highly sensitive in detecting cancerous cells—critical in medical applications where missing a positive case can have serious consequences. The incorporation of data augmentation techniques during preprocessing contributed to improved generalization, while the structured CNN architecture effectively captured spatial features unique to cancerous cells. Dropout layers helped prevent overfitting, ensuring consistent results across validation data. Compared to traditional machine learning models, the proposed CNN approach demonstrates superior performance, aligning with recent studies such as those by Ahad et al. (2024) and Abir et al. (2023), who also reported high accuracy in leukemia detection using deep learning. Furthermore, the integration of the model into a user-friendly GUI enhances its practical utility, allowing non-expert users to perform blood cancer detection without extensive technical knowledge. Although the results are promising, future enhancements could include multi-class classification of leukemia subtypes, expanding the dataset for improved generalization, and incorporating explainable AI techniques to build trust in the model's decision-making process.



CONCLUSION

This study presents an effective and practical approach for the early detection of blood cancer using a Convolutional Neural Network (CNN) model trained on blood smear images. The model demonstrated high accuracy, precision, recall, and F1-score, confirming its capability to distinguish between cancerous and non-cancerous samples with minimal error. By integrating the trained model into a user- friendly graphical user interface (GUI), the system offers a practical diagnostic tool that can be used by medical professionals without prior expertise in deep learning. This work not only reinforces the potential of CNNs in medical image analysis but also bridges the gap between research and real-world clinical application. Future enhancements may include expanding the dataset, applying the model to multi-class Leukemia classification, and incorporating explainability features to further improve transparency and usability.



The integration of artificial intelligence into healthcare, especially in cancer diagnostics, holds the promise of faster, more accurate, and cost-effective solutions. The CNN-based model developed in this study contributes to this vision by automating the detection of blood cancer through image-based analysis. By reducing dependence on manual diagnosis and minimizing human error, such systems can support pathologists in making timely and informed decisions. As technology continues to evolve, incorporating larger and more diverse datasets, real-time detection capabilities, and explainable AI mechanisms will further enhance the reliability and acceptance of AI-driven diagnostic tools in routine clinical practice.

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