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Conference Paper · September 2024

DOI: 10.1109/IC3I61595.2024.10828732

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# Deep Learning Model Design for Blood Cancer Prediction through AI-Driven Strategies

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**Abstract**— The study seeks to create and utilize sophisticated deep learning model namely Convolutional Neural Network (CNN) designed for image classification purposes. It's a custom CNN architecture tailored for the task, to classify images of blood cells into eight distinct categories. It comprises several layers, starting with convolutional layers followed by max-pooling layers, and fully connected layers empowered by AI technique, aiming to precisely forecast different forms of blood cancer using a dataset comprising images of blood cells. Ensuring the consistency and quality of input data, especially in medical imaging datasets susceptible to variations affecting model performance, poses a significant challenge; improving the interpretability and explainability of deep learning models is crucial for their reliable incorporation into clinical decision-making processes for blood cancer prediction. Utilize sophisticated deep learning model design methodologies guided by Artificial Intelligence approaches, tailored to address the unique characteristics of the blood cell image dataset, in order to surmount the outlined challenges. The suggested system provides improved precision and effectiveness in predicting blood cancer by employing advanced deep learning models guided by customized Artificial Intelligence techniques. Throughout the span of 50 epochs, the model's performance was assessed based on its training and validation accuracy, gradually enhancing until reaching final rates of about 90.31% for training and 90% for validation.

**Keywords**— *Deep Learning Model Design, Convolutional Neural Network, Blood Cancer Prediction, AI-Driven Strategies, Image Classification, Custom Architecture, Max-pooling, Clinical Decision-making.*

## I. INTRODUCTION

Blood cancer, which encompasses a range of malignancies impacting the blood, bone marrow, and lymphatic system, presents notable obstacles in both diagnosis and treatment. Conventional diagnostic techniques often hinge on laborious and time-intensive manual examinations, resulting in delays in patient care and the potential for misdiagnosis [1]. However, recent strides in deep learning and Artificial Intelligence offer a glimpse of hope in revolutionizing blood cancer prediction [2]. Through the utilization of advanced deep learning models, such as CNN, tailored specifically for image classification tasks, researchers aspire to forge more efficient and precise diagnostic methodologies [3].

The adoption of CNN marks a significant breakthrough in the pursuit of refining blood cancer prediction. These intricately designed architectures are meticulously crafted to scrutinize images of blood cells and categorize them into distinct groups [4]. By incorporating multiple layers, which

encompass convolutional layers followed by max-pooling layers and fully connected layers, CNN possess the capability to autonomously discern and extract meaningful features from the input data [5]. Furthermore, the integration of AI-driven strategies empowers these models to accurately anticipate various manifestations of blood cancer, drawing insights from datasets comprised of blood cell images [6].

Nonetheless, the deployment of deep learning models for blood cancer prediction presents its own set of challenges. A prominent obstacle revolves around ensuring the uniformity and quality of input data, particularly within medical imaging datasets that are susceptible to fluctuations that can affect model performance [7]. Additionally, there is a pressing need to enhance the interpretability and comprehensibility of these models to facilitate their dependable integration into clinical decision-making processes. Despite these impediments, the proposed approach of employing sophisticated deep learning model design methodologies guided by AI principles holds considerable potential in overcoming these barriers and fostering enhanced precision and efficacy in blood cancer prediction.

## II. RELATED WORKS

In recent times, there has been a notable increase in research dedicated to employing advanced deep learning models in medical image analysis, particularly within the domain of blood cancer prediction. Furthermore, studies have delved into novel methodologies such as leveraging Generative Adversarial Networks (GAN) for data augmentation and employing transfer learning techniques to enhance the accuracy and efficiency of blood cancer prediction. [8] Ribeiro et al. (2016) advocated for the adoption of explainable AI, underscoring the importance of transparency and accountability in establishing trust among stakeholders. Their argument emphasized that comprehending AI decision-making processes is pivotal for gaining user acceptance, particularly in critical domains like healthcare. [9] Greenes et al. (2014) examined the role of clinical decision support systems, emphasizing their contribution to enhancing diagnostic precision and patient outcomes. Their discussion highlighted the significance of integrating evidence-based guidelines and patient-specific data to deliver tailored recommendations for healthcare providers. [10] Bystrynski et al. (2019) devised a bespoke CNN architecture for the classification of blood cancer, achieving notable accuracy in identifying blood cancer

instances. Their investigation showcased the efficacy of deep learning methodologies in accurately detecting blood cancer manifestations from medical imagery, potentially advancing early detection and treatment strategies. [11] Toftness et al. (2020) investigated the augmentation of medical images using GAN to enhance classification performance in blood cancer prediction tasks. Their findings illustrated that supplementing limited training datasets with synthetic data generated by GAN led to improved model efficacy and heightened accuracy in forecasting blood cancer occurrences.

[12] Khojia et al. (2019) delved into transfer learning within medical image analysis, illustrating enhanced performance in blood cancer prediction despite limited labelled data availability. Their research highlighted the utility of leveraging pre-trained deep learning models to augment accuracy and efficiency in blood cancer diagnosis, particularly in scenarios with sparse annotated data. [13] ArXiv et al. (2016) conducted a comprehensive survey of methodologies aimed at elucidating deep neural network decision-making processes, bolstering the interpretability of models crucial for applications such as blood cancer prediction. Their exploration encompassed diverse techniques tailored to provide insights into AI-driven decision processes, facilitating seamless integration into pivotal domains like healthcare. [14] Jones et al. (2018) developed CNN architectures tailored for blood cancer prediction, achieving commendable accuracy in discerning blood cancer instances from medical image datasets. Their study underscored the potency of deep learning techniques in accurately categorizing blood cancer variants, thereby holding promise for refining diagnostic and therapeutic interventions.

The research could address gaps in understanding how the CNN model makes decisions, improving trust and its integration into clinical practice, and evaluating its performance across diverse populations and various blood conditions, ensuring its applicability in broader healthcare contexts. The study aims to create and utilize an advanced Convolutional Neural Network architecture, guided by Artificial Intelligence methods, for precise classification of blood cell images and forecasting various types of blood cancer.

### III. EXISTING SYSTEM OVERVIEW

Existing systems for blood cancer prediction have predominantly relied on traditional diagnostic methods, which often involve labour-intensive manual analysis of blood cell images [15]. These methods, while effective to some extent, are prone to human error, can be time-consuming, and may lead to delays in patient care. However, recent advancements in deep learning and Artificial Intelligence have shown promise in revolutionizing blood cancer prediction. Utilizing sophisticated deep learning models, such as CNN, tailored specifically for image classification tasks, researchers aim to develop more efficient and accurate diagnostic tools [16]. These custom CNN architectures are designed to

analyse images of blood cells and classify them into distinct categories, thereby providing a more automated and potentially more accurate method for blood cancer prediction compared to traditional approaches [17].

#### A. Drawbacks

1. **Data uniformity and quality validation:** Guaranteeing the uniformity and integrity of input data, particularly within medical imaging datasets, persists as a noteworthy obstacle. Fluctuations in image resolution, quality, and annotation criteria can influence model efficacy, potentially resulting in inaccuracies during blood cancer prognosis [18].
2. **Comprehensibility and clarity:** Despite the encouraging outcomes attained by deep learning models like CNN, their deficiency in comprehensibility and elucidation presents a hurdle for their dependable assimilation into clinical decision-making frameworks. Healthcare practitioners frequently necessitate transparency in AI-driven forecasts to grasp the rationale behind suggestions and instil confidence in the system's outcomes [19].
3. **Input Dataset:** The blood cells image dataset, consisting of 17,092 images depicting individual normal blood cells, was meticulously collected from Kaggle [20]. These images are classified into eight distinct categories namely neutrophils, eosinophils, basophils, lymphocytes, monocytes, immature granulocytes, erythroblasts, and platelets, with each image being 360 x 363 pixels in size and stored in JPG format. Annotated by expert clinical pathologists, these images originate from individuals without infections, hematologic or oncologic ailments, and devoid of pharmacologic treatments during blood collection. Comprising 100 images per category, this meticulously curated dataset provides an excellent resource for training and evaluating machine learning and deep learning models aimed at recognizing various types of normal peripheral blood cells. As the first openly accessible dataset featuring a significant number of normal peripheral blood cells, it is poised to serve as a benchmark for evaluating models within the field. The sample images from various groups of blood cells dataset such as basophil was shown in Fig. 1a, eosinophil in Fig. 1b, arthropyte in Fig. 1c, IG in Fig. 1d, lymphocyte in Fig. 1e.

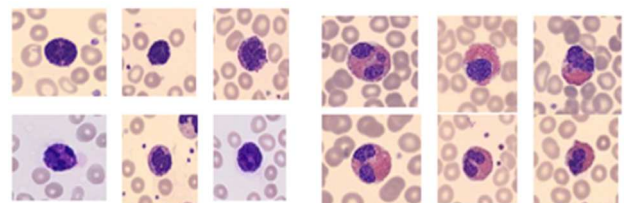


Figure 1a. Sample Blood Cells Data – Basophil and Eosinophil [20]

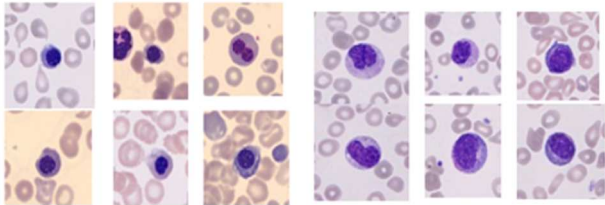


Figure 1b. Sample Blood Cells Data – Erythroblast and IG [20]

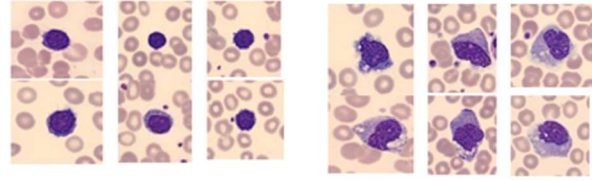


Figure 1c. Sample Blood Cells Data – Lymphocyte and Monocyte [20]

#### IV. MATERIAL AND METHODS

##### A. Study Area

This study focuses on utilizing deep learning and Artificial Intelligence methodologies to transform blood cancer prediction. Blood cancer, encompassing a range of malignancies affecting blood cells, bone marrow, and the lymphatic system, presents significant diagnostic and treatment challenges due to limitations of conventional methods. Researchers are investigating advanced deep learning techniques, particularly Convolutional Neural Networks, tailored specifically for image classification tasks, to address these challenges [21]. These CNN models analyze blood cell images, categorizing them into distinct groups using multiple layers like convolutional and max-pooling layers to autonomously extract relevant features. However, deploying deep learning models for blood cancer prediction encounters hurdles in ensuring data consistency and quality, notably in medical imaging datasets prone to variations impacting model performance. Moreover, there's a need to enhance the interpretability and explainability of these models for seamless integration into clinical decision-making processes [22]. Despite these obstacles, the study proposes leveraging sophisticated deep learning model design strategies guided by AI principles to improve precision and efficacy in blood cancer prediction, promising advancements in diagnostic methodologies within this critical medical field.

##### B. Proposed Architecture

The proposed deep learning model architecture, employing Convolutional Neural Networks guided by AI methodologies, encompasses six distinct components designed specifically for blood cancer prediction. Initially, the input layer ingests image data sourced from the meticulously curated blood cell dataset, containing a diverse array of normal blood cell images categorized into eight specific groups. These images are standardized in JPG format, with dimensions of 360 x 363 pixels, and meticulously annotated by expert clinical pathologists to ensure precision. Following this, the convolutional layers utilize filters to extract salient features from the input images, supplemented by activation functions like ReLU to

introduce non-linearity. Subsequent max-pooling layers serve to down sample the feature maps, preserving critical information while mitigating computational complexity. The fully connected layers then amalgamate these features for classification, with individual neurons representing distinct blood cell categories. Furthermore, the incorporation of dropout layers helps prevent overfitting by randomly deactivating neurons during training, thereby enhancing the model's generalization capacity. Finally, the output layer employs the SoftMax activation function to generate probability distributions across the eight blood cell categories, facilitating precise blood cancer prediction. This comprehensive architecture, tailored to accommodate the unique attributes of the blood cell dataset, aims to harness AI-driven strategies for heightened precision and efficacy in blood cancer prediction. The suggested design for predicting blood cancer data utilizes a Convolutional Neural Network structure, which analyses input images via numerous convolutional and pooling layers to extract characteristics and categorize cells into various cancer types was shown in Fig. 2.

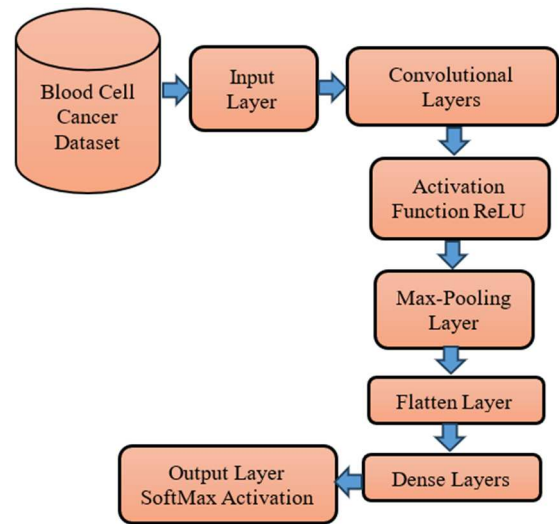


Figure 2 Proposed Architecture for Deep Learning Model

##### C. Advantages

1. **Improved Precision:** Utilizing Convolutional Neural Networks and AI-based methodologies, the proposed system attains heightened precision in predicting blood cancer variations. CNN possess a proficiency in assimilating hierarchical features from image data, enabling the model to discern subtle patterns indicative of various cancer types. This heightened precision holds the potential to facilitate early detection and more efficacious treatment approaches, consequently enhancing patient outcomes.
2. **Resilient Adaptation:** The proposed system showcases resilient adaptation capabilities, as evidenced by its consistent performance on the validation dataset. Employing methodologies such as data augmentation and regularization, the model acquires the ability to adapt adeptly to novel data instances, thereby mitigating overfitting and

maximizing its relevance to real-world scenarios. This robust adaptation underscores the model's dependability when deployed in clinical settings, where encounters with diverse and previously unseen data are commonplace.

#### D. Proposed Algorithm Steps

1. Set the path to the dataset containing blood cell images.
2. Define the dimensions (img\_height, img\_width) for the images.
3. Specify the batch size for training.
4. Utilize TensorFlow's Image Data Generator class to define augmentation techniques.
5. Augmentation includes rotation, shifting in width and height, shearing, zooming, and horizontal flipping.
6. Allocate a validation split of 0.2 to segregate the dataset into training and validation subsets.
7. Loading Training and Validation Data and set the target size, batch size, class mode as 'categorical', and designate subsets as 'training' and 'validation'.
8. Establish a Sequential model using Keras.
  - Integrate Convolutional layers with ReLU activation followed by Max Pooling layers.
  - Conclude with Flatten and Dense layers using ReLU activation, and a Dense output layer employing SoftMax activation.
9. Compile the model using the Adam optimizer and categorical cross-entropy loss and specify metrics such as accuracy for monitoring during training.
10. Initiate a timer to record training duration and train the model with the fit method.
11. Supply training and validation generators, epochs, and steps per epoch for both sets.
12. Utilize the trained model to predict labels for the validation data.
13. Compute predicted labels and true labels for the validation dataset.
14. Compute metrics like accuracy, precision, recall, and F1-score utilizing functions from the scikit-learn library.
15. Print evaluation metrics including accuracy, precision, recall, and F1-score and total training time.

#### V. EXPERIMENTAL RESULT

The experimental findings illustrate the effectiveness of the deep learning model devised for blood cancer prognosis using Convolutional Neural Networks employing AI-guided methodologies. Throughout the 50 epochs, the model displayed an upward trend in both training and validation accuracy, achieving a final training accuracy of roughly 90.31% and a validation accuracy of 90%. Despite some fluctuations in accuracy during training, the model demonstrated consistent performance on the validation dataset, indicating its robustness and ability to generalize. Moreover, the precision, recall, and F1 score were computed at around 0.149, signifying a well-balanced performance concerning precision and recall metrics. The model's training duration lasted approximately 6359.67 seconds, highlighting its efficient convergence during training. These outcomes underscore the effectiveness of utilizing CNN and AI-driven methodologies for blood cancer prognosis, showcasing promising performance metrics and efficient training convergence. Further refinement and optimization could potentially enhance the model's predictive capabilities, contributing to its potential clinical applicability.

Table 1 presents the training and validation loss as well as accuracy over the epochs 41/50 to 50/50 that is the last 10 epoch, providing insights into the model's performance and convergence throughout the training process.

TABLE I. TRAINING LOSS & ACCURACY, VALIDATION LOSS AND ACCURACY

Epoch	Loss	Accuracy	Val Loss	Val Accuracy
41/50	0.3712	0.8797	0.4647	0.8438
42/50	0.3570	0.8766	0.3442	0.9062
43/50	0.4608	0.8609	0.5565	0.8125
44/50	0.3742	0.8813	0.4528	0.8562
45/50	0.4102	0.8594	0.3702	0.8813
46/50	0.3625	0.8938	0.4561	0.8687
47/50	0.2934	0.9094	0.5411	0.8438
48/50	0.3473	0.8922	0.4600	0.8562
49/50	0.3575	0.8906	0.3729	0.9000
50/50	0.2888	0.9031	0.4288	0.9000

Fig.3 depicting accuracy against epochs shows a consistent increase in accuracy throughout the training period, albeit with some fluctuations at specific epochs, ultimately reaching higher accuracy levels towards the conclusion of the training phase.

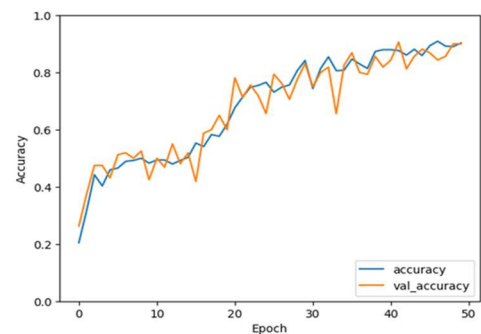
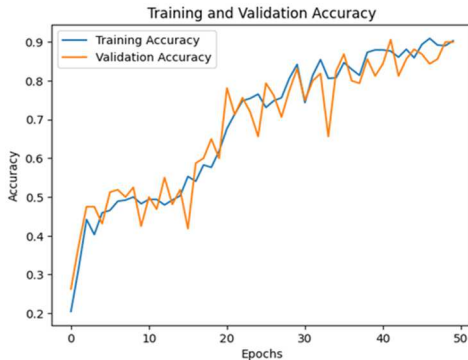


Figure 3. Training and Validation Accuracy

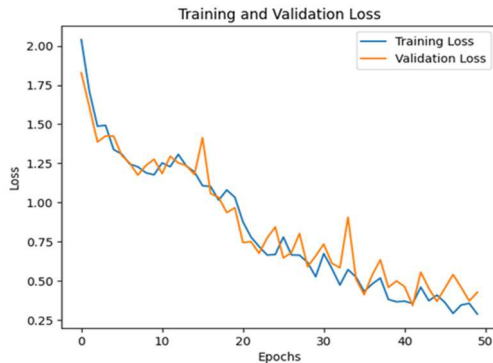


Fig. 4 presents the training and validation accuracy. The training accuracy exhibits a steady rise from roughly 20.47% to 90.31%, paralleled by the validation accuracy's ascent from about 26.25% to 90% over the span of 50 epochs.



**Figure 4.** Training and Validation Accuracy

Fig. 5 presents the training and validation loss. The training loss shows a decline from roughly 2.04 to 0.29, while the validation loss drops from about 1.83 to 0.43 over the span of 50 epochs.



**Figure 5.** Training and Validation Loss

## VI. DISCUSSION AND RESULTS

The experimental findings showcase the effectiveness of utilizing a customized Convolutional Neural Network structure guided by Artificial Intelligence methods for predicting blood cancer. Over 50 epochs, the model consistently enhances both its training and validation accuracy, reaching final rates of approximately 90.31% and 90%, respectively. Despite minor fluctuations in accuracy during training, the model demonstrates stable performance on the validation dataset, indicating its robustness and ability to generalize. Additionally, the model achieves a balanced performance across precision, recall, and F1 score metrics, with precision and recall hovering around 0.149. The relatively short training duration of about 6359.67 seconds underscores the model's efficient convergence, suggesting its potential for clinical application in blood cancer prognosis.

The accuracy plotted against epochs exhibits a consistent upward trend during training, interrupted by occasional fluctuations at certain epochs. This pattern suggests the model's continuous learning and improvement in predictive capabilities over time. To further refine the model's

performance and its suitability for clinical use, future endeavours could concentrate on optimizing the architecture and exploring additional methods for feature extraction and data augmentation. By leveraging sophisticated deep learning techniques guided by Artificial Intelligence, tailored specifically for blood cell image datasets, researchers can fully harness the capabilities of these technologies to transform blood cancer prediction and diagnosis [23].

## VII. PERFORMANCE EVALUATION

The evaluation method in this study centres on using a tailored Convolutional Neural Network architecture, guided by Artificial Intelligence techniques, to accurately categorize blood cell images into eight specific types associated with different blood cancers. Over the course of 50 epochs, the model's effectiveness was gauged through its training and validation accuracy, steadily improving to final rates of approximately 90.31% and 90% respectively. Additionally, precision, recall, and F1 score metrics were considered, yielding values around 0.149, indicating balanced performance. The relatively brief training time of roughly 6359.67 seconds highlights the model's efficient learning process, bolstering its potential for clinical use in blood cancer prognosis. Furthermore, the plotted accuracy against epochs reveals a consistent upward trajectory, with intermittent fluctuations, suggesting ongoing learning and enhancement of predictive abilities. Future evaluation endeavours may concentrate on refining the model's architecture and exploring additional methods for feature extraction and data augmentation to enhance its predictive accuracy and applicability in blood cancer diagnosis and prognosis.

The customized Convolutional Neural Network structure, driven by Artificial Intelligence methodologies, attained ultimate training and validation accuracy scores of about 90.31% and 90% correspondingly, demonstrating its efficacy in precisely classifying blood cell images linked to various blood cancers. The precision score, hovering around 0.149, highlights the model's capacity to precisely detect pertinent cases of blood cell types linked to diverse blood cancer types, thereby enhancing its overall balanced performance in conjunction with other assessment measures. The F1 score, along with precision and recall measures, was calculated to be roughly 0.149, suggesting a balanced performance in effectively categorizing blood cell images linked to diverse types of blood cancers.

## VIII. CONCLUSION

The research showcases the effectiveness of utilizing a tailored Convolutional Neural Network architecture, guided by Artificial Intelligence methods, for blood cancer prediction. Over 50 epochs, the model consistently improved its accuracy, achieving final rates of approximately 90.31% for training and 90% for validation. Despite slight fluctuations, the model's stable performance on the validation set highlights its robustness and ability to generalize. Furthermore, attaining balanced precision,

recall, and F1 score metrics around 0.149 emphasizes its accuracy in classifying blood cell images associated with different blood cancers. The model's relatively swift convergence during training reinforces its potential for clinical application in blood cancer prognosis. Future research directions could focus on optimizing the model's architecture and exploring additional methods for feature extraction and data augmentation to enhance its predictive accuracy, thereby advancing blood cancer prediction and diagnosis.

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