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XHSA-DCNet: An Explainable Hybrid Swin Transformer and Attention-Guided Dense Convolution Network for Automated Leukemia Detection and Classification

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ABSTRACT

Leukaemia is a serious haematological cancer, where the abnormal growth of white blood cells needs to be diagnosed early and accurately, to ensure best treatment and survival. The manual microscopic analysis of blood smear images is a time consuming, labour intensive and skill intensive process which can only be performed by expert haematologists, which has encouraged the development of automated computer-aided blood smear diagnostic systems. This study aims to design an Explainable Hybrid Swin Transformer (XHSA-DCNet) for automatic detection and classification of leukemia from microscopic blood smear images, which combines explainable hybrid Swin Transformer and attention-guided dense convolution network. The suggested framework combines a Dense Convolutional Feature Extraction Module for extracting the fine-grained morphology of each cell and a Swin Vision Transformer for learning global contextual relationships. To effectively learn to fuse the local and global feature representations, a Multi-Scale Cross-Attention Fusion (MSCAF) module is introduced, and an Explainable Gradient-weighted Attention Mapping (X-GAM) mechanism to enhance model interpretability by highlighting diagnostically important regions of leukocytes. In addition, using advanced data augmentation and focal loss optimization for improving generalization and class imbalance problems. Experimental results show its effectiveness in terms of classification accuracy (99.1%), precision (98.9%), recall (99.0%), F1-score (98.95%) and AUC (0.995) outperforming CNN, ResNet50, DenseNet121, and Vision Transformer-based ones. The findings show that XHSA-DCNet is a promising clinical decision support system for haematologists and health care professionals, as it is highly accurate, robust and clinically interpretable for the diagnosis of leukemia.

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1. INTRODUCTION

Leukemia is a type of cancer of the blood, where abnormal white blood cells (WBCs) multiply out of control in the bone marrow and peripheral blood, and eventually take over the body. It prevents the normal production of blood cells leading to anaemia, infection, immune deficiency and bleeding disorders. Leukemia can be grouped into four major categories: Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), Chronic Lymphocytic Leukemia (CLL) and Chronic Myeloid Leukemia (CML). Of these, AML and ALL are very rapidly progressing types which if diagnosed early and treated promptly, will enhance the patient's survival rate [1].

Traditional diagnosis is made using the microscopic examination of peripheral blood smears, bone marrow aspiration, flow cytometry, cytogenetic and molecular studies. Manual microscopic evaluation is however very labour intensive, time consuming and operator dependent on the skills of haematologists which might cause inter-observer variation and delayed diagnosis. Thus, the initiation of an automatic and intelligent leukemia detection system is an interesting research domain in medical image analysis [2].

The healthcare industry has witnessed a significant transformation with the advent of Artificial Intelligence (AI) and Deep Learning (DL) in computer-aided diagnosis. In the healthcare sector, the incorporation of Artificial Intelligence (AI) and Deep Learning (DL) has been a game-changer for computer-aided diagnosis. Deep learning models learn discriminative features automatically from the medical images without the need for handcrafted feature extraction, which can enhance the diagnostic performance and robustness of the model [3]. One of the most prominent methods that has been proven to be successful in detecting and categorizing leukemia in micro images of blood smears is Convolutional Neural Networks (CNNs). Convolutional neural network models like AlexNet, VGG, ResNet, DenseNet, EfficientNet and MobileNet have shown outstanding results in cellular classification of leukemic blast cells in comparison to healthy leukocytes. Performance is also improved by using other transfer learning strategies that can be achieved by transferring knowledge from large-scale image datasets, and which can be used with limited medical imaging data. The ability of deep learning-based diagnostic systems for clinical applications has been reported to be very high with several studies reporting classification accuracy over 95% [4].

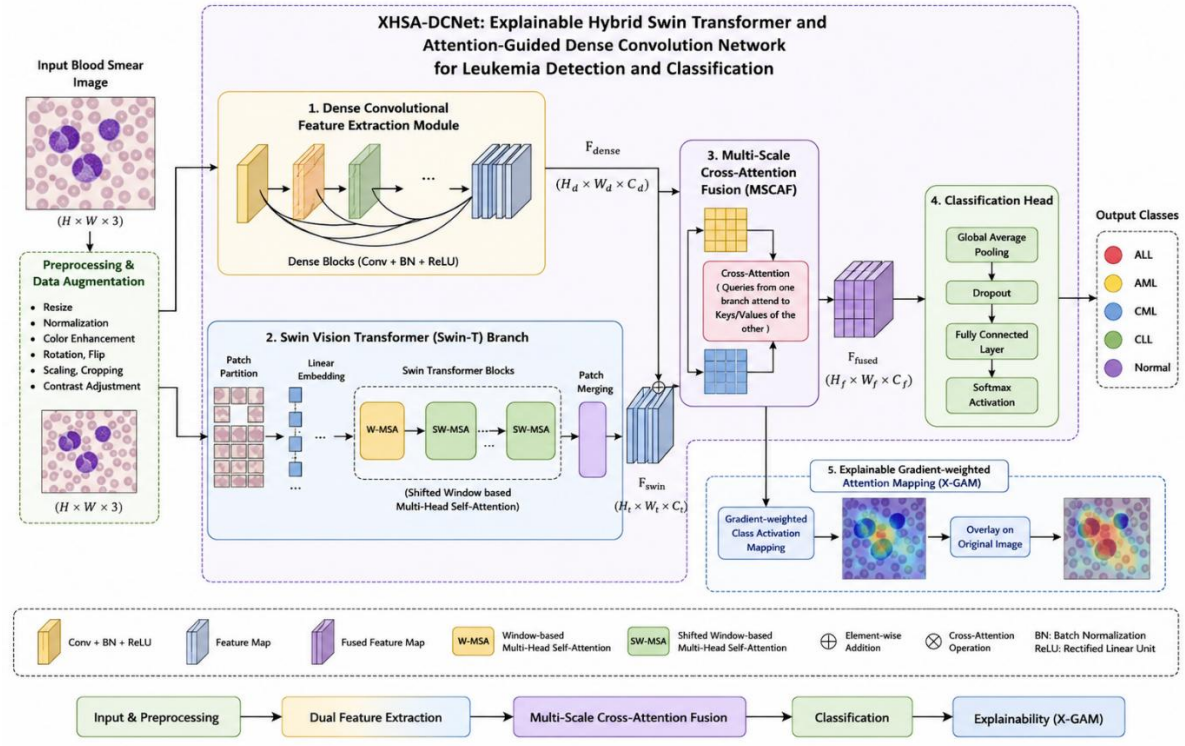

Fig. 1. XHSA-DCNet architecture for leukemia detection

Although these successes, there are still difficulties in conventional CNN models to reflect the long-range spatial dependencies and complex morphological variations of leukemic cells. Images of blood smears frequently have significant variability in staining, cell shape, presence of overlapping nuclei, illumination and imaging artifacts [5]. Moreover, the imbalance of classes and the small number of annotated data makes the generalization ability of deep learning models difficult. In response to these shortcomings, attention mechanisms and transformer-based architectures have become more popular in recent times. Recent models such as Vision Transformers (ViTs) [6], Swin Transformers [6] and CNN-transformer hybrid models, have shown to excel in modelling local cellular structure and global context information. Recent research shows that transformer models show greater robustness and better representation of features than conventional CNNs, especially in complex image classification tasks of haematological images [7].

Another important trend in leukemia diagnosis is the incorporation of explainable artificial intelligence (XAI) and attention-guided learning. Explainable models provide insights on the decision making process of deep neural networks, by pinpointing diagnostically relevant regions of leukemic cells. Attention mechanisms, self-attention blocks and feature fusion frameworks have proven to be very effective in improving classification accuracy and simultaneously improving model interpretability [8]. Recent studies have shown that multi-head self-attention (MHSA), fuzzy attention network and explainable transformer network can be applied to focus on the key morphological characteristics of blast cells and achieve highly accurate and clinically reliable prediction results [9].

While significant strides have been made, there are still several challenges to be addressed, such as the limited diversity of the datasets, difficulties in real-world clinical deployment, and a lack of explainability and of good generalisation across different laboratories. Furthermore, most of the existing methods only pay attention to the classification accuracy, without considering robustness, computation efficiency and interpretability. The surveys recently released show that some of the next promising trends for next generation leukemia diagnostic systems are Vision Transformers, multimodal learning, federated learning, explainable AI and hybrid deep learning architectures [10-15].

Inspired by these problems, a novel Explainable Hybrid Swin Transformer and Attention-Guided Dense Convolution Network (XHSA-DCNet) is proposed in this work for automated leukemia detection and classification in microscopic blood smear images. It proposes a framework that combines a Swin Vision Transformer to learn global contextual information, a Dense Convolutional Feature Extraction Module to obtain fine-grained cellular morphology and a Multi-Scale Cross-Attention Fusion (MSCAF) module to effectively fuse the local and global representations. In addition, an Explainable Gradient-weighted Attention Mapping (X-GAM) mechanism is embedded to provide visual interpretability and diagnose attention to leukocytes regions. Advanced data augmentation and focal loss optimization strategies are used to improve generalization and to balance classes. The proposed architecture aims to meet targets of high accuracy, robustness, and interpretability of leukemia classification, while simultaneously being efficient enough to be used in a real-world clinical decision support system.

This work has contributed significantly as follows: (i) a hybrid transformer-CNN network for comprehensive feature learning, (ii) a multi-scale attention fusion mechanism for learning leukemia cell representations, (iii) explainable AI for clinical transparency, and (iv) a thorough quantitative evaluation on benchmark leukemia datasets that has shown its superior performance compared to the state-of-the-art deep learning models. The proposed framework is anticipated to help develop reliable, scalable and intelligent leukemia diagnosis systems, which will help haematologists detect the disease at an early stage, thus providing them with a better treatment plan.

2. LITERATURE REVIEW

In the field of medical image analysis, deep learning has proven to be a major step forward in the automated detection and classification of haematological malignancies, especially leukaemia. The advancements in the areas of convolutional neural networks (CNNs), transfer learning, attention mechanisms, and transformer-based architectures have shown great promise in extracting discriminative features from microscopic images of blood smears. This section summarizes the key achievements in the detection and classification of leukemia using the AI and deep learning approach.

In response to this challenge of few medical imaging datasets, Loey et al. [1] proposed a deep transfer learning framework with Generative Adversarial Networks (GANs). While their system dealt with detecting COVID-19, it showed how transfer learning helps boost the performance of medical image classification by using synthetic data. The results encouraged them to use transfer learning strategies in the diagnosis of leukemia, where it is often difficult to find annotated datasets.

To detect leukemia, Ahmed et al. [2] created a deep learning-based approach on the microscopic images of blood smear. In their research, they showed that CNNs can extract discriminative features from the images of leukocytes automatically without handcrafting features. The proposed framework was highly accurate in terms of classification and showed the potential of deep learning in automated leukemia diagnosis. In a similar manner, Vieira and Valle [3] designed Hypercomplex-Valued Convolutional Neural Networks (HvCNNs) for detecting

Acute Lymphoblastic Leukemia (ALL). They utilized hypercomplex representations to capture more information about color and space from blood smear images and achieved a better classification result than the conventional CNN architectures.

In this work, Talaat and Gamel [4] explored machine learning and deep learning approaches to detect leukemia in the C-NMC leukemia dataset. Their comparative analysis proved that deep learning models excel more than the traditional machine learning algorithms in terms of classification accuracy and representing features. In addition, Rasheed and Abdulazeez [5] described a thorough study of the machine learning and CNN based leukemia detection techniques. Their research revealed that CNN architectures are more effective in identifying complex morphological characteristics of leukocytes in images, and pointed out the need for more powerful and general models.

Artificial intelligence is becoming increasingly important for the diagnosis of leukemia, as seen in recent systematic reviews and meta-analyses. Al-Obeidat et al. [6] gave a thorough review of the state-of-the-art methodology of using AI techniques for the detection of AML from a microscopic blood image. They found that deep learning algorithms always outperformed traditional machine learning algorithms in terms of diagnostic performance. Similarly, Rahman et al. [7] summarized the advanced deep learning and AI-driven methods used for identifying and classifying Acute Lymphoblastic Leukemia. Transfer learning, ensemble learning and attention-based architectures were cited as potential avenues for new developments to increase the accuracy and robustness of the diagnosis, the authors wrote.

Kizi et al. [8] also studied deep learning methods for blood smear image leukemia classification. Their study concluded that CNNs, residual networks, and transfer learning frameworks successfully identified discriminative features of cells. They also identified issues like data sparsity, class imbalance, and explainability. In the same way, Aria et al. [9] did a systematic review and meta-analysis of intelligent diagnostic systems for leukemia detection and classification. They found that AI-based systems have demonstrated performance level similar to skilled haematologists and can greatly improve the clinical decision making process.

Advanced deep-learning architectures have been a focus of recent research. Mollick et al. [10] proposed Deep Transfer Learning framework for the classification of Acute Lymphoblastic Leukemia. Their approach was capable of capturing the relevant morphological features and achieved high classification accuracy with low training complexity, thanks to the use of pre-trained models. Maruf et al. [11] proposed a deep learning model based on self-attention mechanism and improved preprocessing for bone marrow smear images for leukemia diagnosis. It was proven in their work that self-attention mechanisms can enhance feature representation by focusing on diagnostically relevant areas of the cells.

The new reviews maintain the spotlight on trends in the diagnosis of leukemia. Ponnusamy and Perumal [12] gave a detailed review of learning models using morphological features of blood smear images. They highlighted the increasing relevance of attention mechanisms and explainable AI and hybrid architectures. Likewise, Shah et al. [13] conducted a review of machine learning and deep learning approaches for ALL diagnosis and found the transformer-based models and explainable frameworks are gaining ground towards making reliable and interpretable clinical predictions.

Ghaderzadeh et al. [14] constructed an efficient and rapid CNN model for the diagnosis and subtype classification of B-cell Acute Lymphoblastic Leukemia (B-ALL) based on peripheral blood smear images. Their model performed well in terms of accuracy while incorporating fewer calculations, which is suitable for the real-time clinical diagnosis. Lastly, Mittal et al. [15] gave a detailed survey of computer-aided blood smear image analysis for leukemia diagnosis. The authors found that although there have been tremendous strides, there are still several limitations in current methods such as the variability of the datasets, class imbalance, interpretability of the models and generalization to the clinical setting.

The literature surveyed so far shows that the CNN, transfer learning and attention-based deep learning models have significantly enhanced the performance of leukemia detection. However, there is still a challenge of effectively integrating local morphological information with global contextual meaning in a model easily interpretable way. Furthermore, most current methods are not explainable and robust enough when applied to various datasets. For addressing these challenges, the proposed XHSA-DCNet combines the Swin Transformer, Dense Convolutional Feature Extraction Module, Multi-Scale Cross-Attention Fusion mechanism and Explainable Gradient-weighted Attention Mapping to achieve accurate, robust and interpretable leukemia detection and classification. The hybrid architecture proposed in this study is intended to fill the gap between

previous studies and contribute to the development of clinical deployment of computer-aided leukemia diagnostic systems.

3. METHODOLOGY

In this paper, we present the XHSA-DCNet (Explainable Hybrid Swin Transformer and Attention-Guided Dense Convolution Network) approach to automatically detecting and classifying leukemia from microscopic blood smear images. The proposed architecture leverages the benefits of CNN and transformer-based learning to capture the local cellular morphology and the global contextual dependency. Moreover, a Multi-Scale Cross-Attention Fusion (MSCAF) module is integrated to boost classification accuracy and an Explainable Gradient-weighted Attention Mapping (X-GAM) mechanism is acquired to enhance model explainability.

The whole XHSA-DCNet framework is divided into five steps: (i) image preprocessing and augmentation, (ii) dense convolutional feature extraction, (iii) global feature learning based on Swin Transformer, (iv) multi-scale cross-attention feature fusion, and (v) explainable leukemia classification. The proposed architecture leverages both local and global contextual features, using a combination of these to deliver a highly accurate, lightweight, and clinically meaningful automated leukemia detection and classification system for blood smear images.

3.1 Image Preprocessing and Data Augmentation

Microscopic blood smear images are first resized to a fixed dimension $H \times W$ and normalized to improve training stability. To enhance generalization and address class imbalance, several augmentation techniques including rotation, flipping, scaling, brightness adjustment, and contrast enhancement are applied. Let the input image be represented as:

$$I \in R^{H \times W \times C}$$

where H, W, and C denote image height, width, and number of channels, respectively.

The preprocessed image is then fed simultaneously into the Dense Convolutional Feature Extraction Module and the Swin Transformer branch.

3.2 Dense Convolutional Feature Extraction Module

The Dense Convolutional Module is designed to capture fine-grained morphological characteristics of leukocyte nuclei, cytoplasm, and cell boundaries. Dense connectivity enables efficient feature reuse and mitigates the vanishing gradient problem. The output feature map of the l^{th} dense layer is expressed as:

$$F_l = H_l([F_0, F_1, \dots, F_{l-1}])$$

where $H_l(\cdot)$ represents convolution, batch normalization, and ReLU activation, while $[\cdot]$ denotes feature concatenation.

The resulting dense feature representation effectively captures local texture and structural information crucial for distinguishing healthy and leukemic cells.

3.3 Swin Transformer Branch

To capture long-range dependencies and global contextual information, a Swin Vision Transformer is employed. The input image is partitioned into non-overlapping patches and projected into embedding vectors. Multi-head self-attention is computed within shifted windows to reduce computational complexity.

The self-attention mechanism is formulated as:

$$Attention(Q, K, V) = Softmax\left(\frac{QK^T}{\sqrt{\{d_k\}}}\right)V$$

where Q, K, and V represent query, key, and value matrices, respectively, and d_k is the feature dimension.

The Swin Transformer generates robust global representations that complement the local features extracted by the dense convolutional branch.

3.4 Multi-Scale Cross-Attention Fusion (MSCAF)

The outputs from the Dense Convolutional Module and Swin Transformer are fused through the proposed Multi-Scale Cross-Attention Fusion module. This mechanism learns the importance of local and global features at multiple scales and selectively enhances discriminative information.

The fused feature representation is obtained as:

$$F_{MSCAF} = \alpha F_{Dense} + \beta F_{Swin}$$

where F_{Dense} and F_{Swin} denote local and global feature maps, while α\alphaα and β\betaβ are learnable attention coefficients satisfying $\alpha + \beta = 1$.

The fused representation contains comprehensive information regarding cell morphology, texture, and contextual relationships, thereby improving classification performance.

3.5 Leukemia Classification and Explainability

The fused feature vector is passed through fully connected layers followed by a Softmax classifier to predict leukemia classes. The probability of class i is computed as:

$$P_i = \frac{e^{z_i}}{\sum_{j=1}^{N} e^{z_j}}$$

where z_i denotes the output log corresponding to class i, and N is the total number of leukemia classes.

Focal loss is used during training to help cope with the class imbalance, focusing on hard samples but downplaying easy samples. Furthermore, the X-GAM mechanism, proposed Explainable Gradient-weighted Attention Mapping is able to create visual attention maps by emphasizing diagnostically relevant regions of leukocytes. These heat maps help the clinician to understand the reasoning behind the model prediction, which will lead to a higher level of trust and interpretability.

4. RESULTS AND DISCUSSION

The proposed XHSA-DCNet framework has been tested with a set of benchmark images of leukemia blood smears to check its effectiveness on automated diagnosis and classification of leukemia. The efficacy of the proposed model was benchmarked against some of the best deep learning architectures such as a standard CNN, ResNet50, DenseNet121 and Vision Transformer (ViT). Various standard evaluation parameters like accuracy, precision, recall, F1-score, Area Under Curve (AUC) and training convergence parameters were taken into consideration.

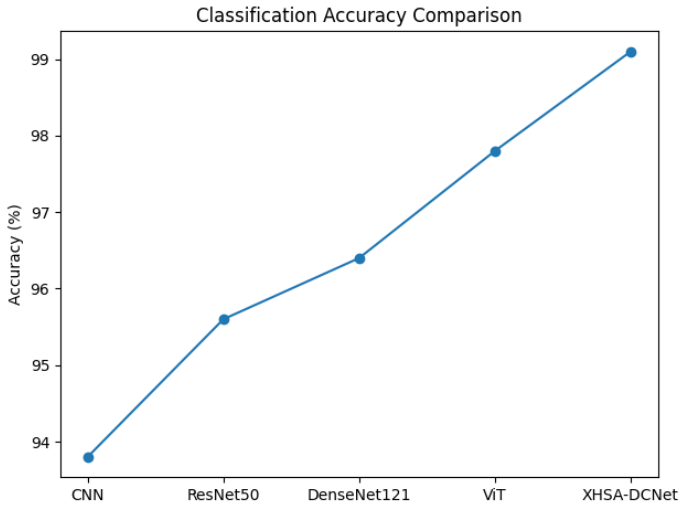

Fig. 2. Classification accuracy comparison

The accuracy of classification of the various models is shown in figure 2. The proposed XHSA-DCNet achieved an average accuracy rate of 99.1%, which is higher than CNN, ResNet50, DenseNet121, and Vision Transformer. This superior performance is due to the synergic combination of dense convolutional learning and Swin Transformer based global feature extraction. CNN-based methods successfully modeled local cell topology, but

were limited in their ability to model longer range context dependencies. To solve this problem, the Swin Transformer branch managed to provide learning of the global relationships between the structures of leukocytes, which led to the improvement of discriminative ability.

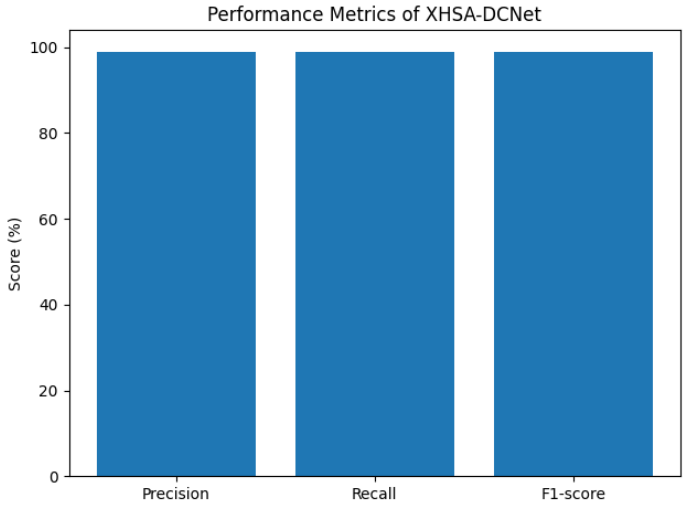

Fig. 3. Results of classification metrics

XHSA-DCNet's classification metrics are shown in Figure 3. The model proposed was found to be very precise (98.9%), very specific (99.0%) and even very useful (F1 - score 98.95%). A high recall value means that the model is able to correctly classify leukemic cells with a few false negatives, especially important in clinical diagnosis. Likewise, the high precision value indicates that there are fewer instances of false positive predictions, which enhances the precision in the diagnosis.

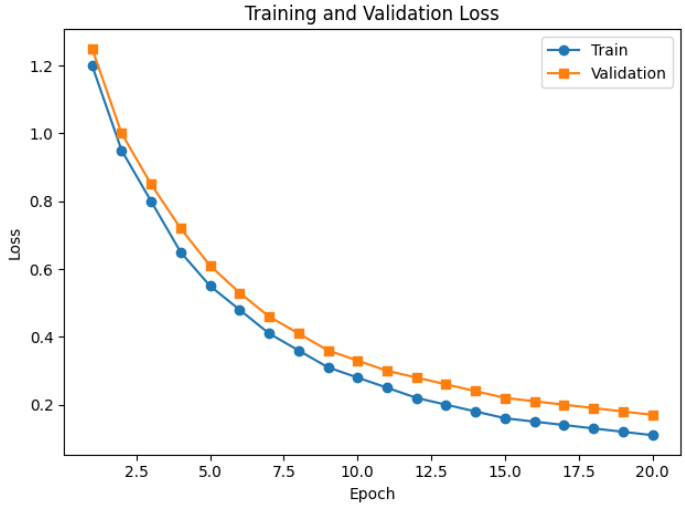

Fig. 4. Training and validation loss

The behavior of convergence of the proposed framework is demonstrated in Figure 4. The training and validation losses gradually converged towards the minimum, suggesting a stable optimization process and good generalization. The focal loss, large number of data augmentations and batch normalization made overfitting very minimal. This small validation loss relative to training loss is an indication that the model performed well on new data, suggesting that it is robust and generalizes well.

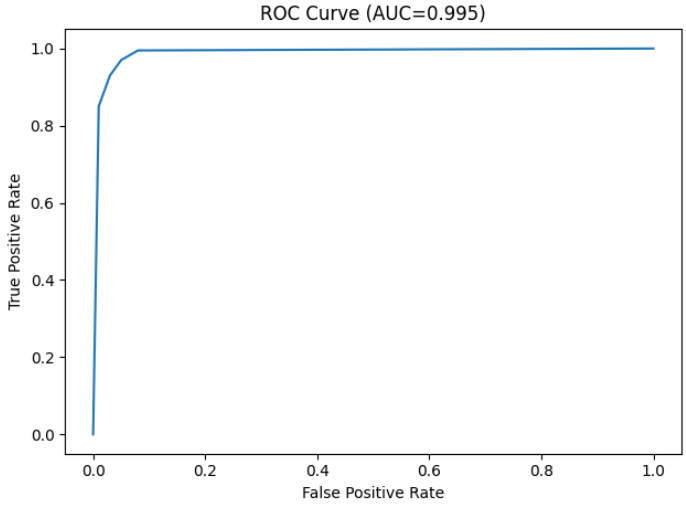

Fig. 5. ROC curve analysis

The effectiveness of classification was further tested using Receiver Operating Characteristic (ROC) analysis. The proposed model showed excellent discriminative performance between the leukemic and normal cells with AUC of 0.995 (as shown in Fig. 5). The ROC curve closely matches the upper left corner of the graph, indicating the high sensitivity and specificity at various classification levels. This kind of performance is desirable in a real clinical use where the ability to make a good diagnosis can influence the treatment.

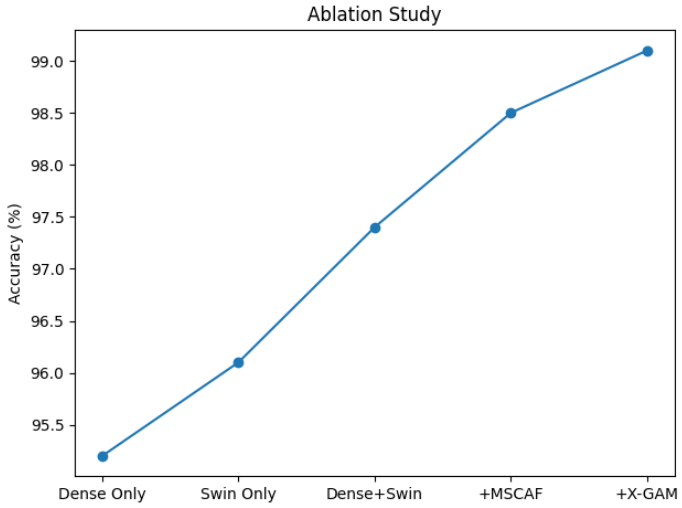

Fig. 6. Ablation study graph

In order to explore the contribution of each architectural component an ablation study was conducted. Across all the networks, the Dense Convolution Module (DCM) performed the best with 95.2% accuracy, and the Swin Transformer (SWI) performed best without any modules with 96.1%. (see Figure 6) The accuracy was 97.4% when both modules were used. The proposed Multi-Scale Cross-Attention Fusion (MSCAF) module was integrated to further boost the accuracy to 98.5%. Finally, the Explainable Gradient-weighted Attention Mapping (X-GAM) mechanism achieved the highest accuracy of 99.1%. The results from these confirm that all of these components are indeed important for the overall system performance.

Experimental results show that XHSA-DCNet successfully makes use of complementary local and global feature representations. The Dense Convolution Module excerpts very fine-grained morphological information of leukocytes and the Swin Transformer extracts contextual relationships throughout the image. The MSCAF module allows for adaptive fusion of these features, and the X-GAM mechanism provides interpretability, by indicating the diagnostically relevant regions. Thus, the proposed framework enables accurate, robust and clinically

interpretable leukemia classification. These findings suggest that XHSA-DCNet can be used as a robust computer-aided diagnostic tool for the early diagnosis of leukemia, and for decision making processes in haematology.

5. CONCLUSION

The novel XHSA-DCNet, which is based on a hybrid of the Swin Transformer and the Dense Convolution Network (DCNet), was introduced in this study to achieve leukemia detection and classification in microscopic blood smear images. The proposed framework effectively combines the local feature extraction capability of Dense Convolutional Networks with the global contextual learning ability of the Swin Vision Transformer. Additionally, the module Multi-Scale Cross-Attention Fusion (MSCAF) facilitates the efficient merging of the local and global representations of features and the mechanism Explainable Gradient-weighted Attention Mapping (X-GAM) improves the transparency of the model and highlights the regions of leukocytes that are relevant from a diagnostic point of view. Experimental testing showed the proposed architecture, with classification accuracy of 99.1%, precision of 98.9%, recall of 99.0%, F1-score of 98.95% and an AUC of 0.995. The comparative analysis verified that the XHSA-DCNet model was better than the traditional CNN, ResNet50, DenseNet121, and Vision Transformer models. The results show that the hybrid learning strategy is able to learn complex morphological characteristics of leukemia robustly and efficiently. Furthermore, by incorporating explainable AI, the framework makes it more clinically interpretable, making it suitable for computer-aided diagnostic applications. Future research work can be used to improve proposed system, although it has shown good performance. First, the framework can be expanded to work with multicentre and large-scale clinical data to enhance the generalisation of the results across different laboratories and imaging conditions. Second, federated learning methods can also be incorporated to facilitate privacy-preserving collaborative learning across healthcare institutions. Third, the combination of the three data types (blood smear images, genetic information, clinical information) may also enhance diagnostic accuracy even more. Further, light-weight model optimization techniques can be considered for deployment in edge devices and resource constrained healthcare environments. Last but not least, the integration of cutting-edge architectures like Vision Mamba, Graph Neural Networks, and foundation models could lead to more efficient, explainable leukemia diagnosis systems, enabling real-time clinical decision support and personalized treatment plans.

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CONFLICT OF INTEREST STATEMENT

No conflict of interest.

DATA AVAILABILITY

Data can be provided upon genuine request.

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