Integrating Multi-scale Feature Extraction into EfficientNet for Acute Lymphoblastic Leukemia Classification

Fallah H. Najjar[1, 2, *], Salman Abd Kadum[1], and Nawar Banwan Hassan[3]

[1] Department of Computer System Techniques, Technical Institute of Najaf, Al-Furat Al-Awsat Technical University, 54001 Najaf, Iraq
[2] Department of Emerging Computing, Faculty of Computing, Universiti Teknologi Malaysia, Johor Bahru, Malaysia
[3] Department of Computer Engineering Techniques, Imam Alkadhim University College, Baghdad, Iraq
Email: fallahnajjar@atu.edu.iq (F.H.N.); salman.kadhum@atu.edu.iq (S.A.K.); nawarbanwan@alkadhum-col.edu.iq (N.B.H.)
*Corresponding author

***Abstract*—Acute lymphoblastic leukemia is a cancer of the white blood cell. It originates in the bone marrow, the spongy tissue inside bones responsible for the production of blood. Despite being the most common cancer in children, Acute Lymphoblastic Leukemia (ALL) has remained an enormous health concern. The results of traditional diagnosis, including morphological examination, immunophenotyping, and genetic marker analysis, are relatively slow, subjective, and depend considerably on the ability of a hematopathologist, hence restricting the classification result's consistency. These disadvantages underline the pressing need for automatic diagnostic systems that are fair and satisfactory. This work presents the Multi-Scale Enhanced EfficientNet, which, through several innovative architectures, can increase sensitivity and specificity in accurately identifying subtle ALL variations. We assess the MSEENet's performance using a dataset of numerous ALL phenotypes. We achieve excellent performance in multiple metrics, like an overall accuracy of 98.77%, an accuracy of 98.99%, a recall of 98.49%, a Matthews Correlation Coefficient of 98.34%, and an F1-Score of 98.72%. This research shows the potential for MSEENet as a feasible, precise, and dependable ALL diagnostic tool, further strengthening patient-specific cancer treatment advancements.**

***Keywords*—Leukemia, blood cancer, Acute Lymphoblastic Leukemia (ALL) dataset, MSEENet, medical imaging**

I. Introduction

Acute Lymphoblastic Leukemia (ALL) has emerged as a neoplasm originating in white blood cells. The bone marrow represents a central site for the genesis of blood cells, which is nestled within the spongy structure of bones [1]. However, while this type of cancer is prevalent among children, the most common cancer affecting children, according to the American Cancer Society, is not that adults are affected by this condition [2]. The characteristic marked against ALL is the inundation of the bone marrow with lymphoblasts, an immature variant of white blood cells, outnumbering healthy blood cells [3, 4]. The stratification of ALL remains the centerpiece of the individualization of the treatment modalities and the prognostication of the journey that the patient will be going through. ALL categorization in history has depended on morphological scrutiny, genetic markers, and immunophenotyping [5]. These methods, although contributing critically to the diagnosis and stratification of ALL, yet are imprisoned by being time-consuming and subjective, just like their dependence on the discernment of specialized hematopathologists [6, 7]. This initiates a subjective morphologic interpretation, which puts the discrepancies in the classification outcomes [8].

Nevertheless, this has changed with the arrival of deep learning into the field of medical imaging analysis [9, 10], which introduces radically new methodologies for the classification of diseases like ALL. With artificial intelligence, this subfield, by its very name, copies architecture and how the human brain operates; it is better poised to sense the patterns of intricate features straight from raw data, hence assisting automated and classified endeavors very precisely. One such sub-domain of deep learning, which is currently leading medical imaging innovations, as in the case of ALL classification referred to in this study, is Convolutional Neural Networks (CNNs). CNNs perform autodidactic learning of feature representations that span over many layers of abstraction and, hence, are well suited for the analysis of images. CNNs are able to distinguish between various types and subtypes of leukemia with uncanny accuracy and robustness. The main hurdle in the use of deep learning for ALL classification is these annotated datasets development. Despite a growing number of medical image datasets, the work of annotating them remains laborious and lengthy. The scarcity of specific ALL subtypes and the heterogeneity in morphological features further

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complicate dataset assembly. To surmount these obstacles, researchers have deployed strategies like data augmentation, transfer learning, and semi-supervised learning. Data augmentation expands training datasets through image manipulation techniques such as rotation and flipping, enhancing dataset volume and variability. Transfer learning extracts insights from one domain to bolster task performance in a correlated domain, allowing for the efficient fine-tuning of pre-trained Convolutional Neural Networks (CNNs) on smaller, specialized datasets, thereby economizing computational resources. Beyond image-centric classification, the integration of multi-modal data, including gene expression patterns and clinical records, holds the promise of refining ALL diagnostic models. This holistic approach captures the disease's multifaceted nature, augmenting model predictiveness. Multi-modal data integration paves the way for comprehensive diagnostic and prognostic frameworks that encompass both genetic and phenotypic ALL facets. However, in this paper, we aim to overcome these challenges by:

- Introduce the integration of the Multi-Scale feature extraction within the Enhanced EfficientNetV2B0 (MSEENet), specifically designed for the classification of ALL.
- MSEENet works on the idea of multi-scale feature extraction, which improves classification accuracy.
- Experiments on the ALL subtype classification task showed that MSEENet can achieve an accuracy of 98.77%.

II. Literature Review

In this view, there have been a number of studies that have highly contributed to further detection and classification of the Acute Lymphoblastic Leukemia (ALL) dataset [11] using deep learning and machine learning. While marking outstanding signs of progress, each of the studies faces some specific limitations that are inherent in the methodologies themselves and on account of the complexity of medical diagnostics. Furthermore, these works will be presented further, and their limitations will be reviewed. For example, the deep neural network has been used to differentiate ALL subtypes accurately by researchers such as Atteia *et al.* [12], who hybridized the feature-learning-based method with Particle Swarm Optimization (PSO) and Principal Component Analysis (PCA) to sustain high relevancy in the classification of blood cancers, leading to the following accuracy: 97.4%. However, the tuning of hyperparameters with regard to PSO and PCA is intricate in a way that may make it hard to handle very carefully to avoid any case of overfitting or underfitting. Gokulkrishnan *et al.* [13] used pre-trained CNNs and reported an accuracy of 96.77%. Transfer learning would make the possibility of having the model trained on the dataset feasible, but pre-trained CNNs might not thoroughly learn the specific image characteristics of medical images. They, therefore, may fail in such cases to give the model transfer performance over diverse or novel datasets of medical images. Hagar *et al.* [14] suggested a novel model that could classify blood cancer using deep learning with a range of 98.1% to 98.2% accuracies. The underlying architectures of such deep-learning models are essentially required to rely on a massive volume of labeled training data to show their best performance, which might not be practical even in some sparse subtypes of blood cancers. Rejula *et al.* [15] proposed an enhanced Adaptive Neuro-Fuzzy Inference System (ANFIS) model with 97.14% as a promising classification accuracy for acute lymphoblastic leukemia. However, though this is definitely an innovative approach to combining fuzzy logic with neural networks, it again puts another layer of complexity in model interpretation. Further, expertise in two areas is required to fine-tune the model and interpret its decisions accurately. As noted earlier,

Kadhim *et al.* [16] had earlier deployed the use of a CNN and achieved an accuracy of 98.15% in the classification of leukemia from Acute Myeloid Leukemia (AML) images. The model's performance depends on the quality and diversity of AML images. Such a model is likely to perform well across various stages of leukemia, whereas it may perform very poorly when discriminating it from various imaging techniques if there are not enough of them in the training images. Tusar *et al.* [17] designed and optimized multi-deep learning models, Deep Neural Network (DNN), Convolutional Neural Network (ConvNet), MobileNetV2, and Residual Neural Networks 50 (ResNet50) to classify the ALL dataset into its corresponding classes. The best accuracy scored by the MobileNetV2 was 97.00. Mustafa *et al.* [18] introduced the success of the You Look Only Once (YOLOv5) in classifying the ALL disease utilizing Peripheral Blood Smear (PBS) images. Their proposed method achieved 96.7%, 96%, and 97.8% for recall, precision, and accuracy, respectively. Together, these studies represent, move further, and set the limits of the applicability of computational models in the area of medical diagnostics, more particularly in the case of leukemia, detection, and classification. On the other hand, highlighted limitations point toward reducing the computational demand, increasing the generalizability of models, making complex models interpretable, and ensuring robust performance on diverse medical imaging datasets in the future.

III. Materials and Methods

This paper introduces MSEENet, an integrating multi-scale feature extraction into the EfficientNetV2B0 deep learning model specifically developed to effectively and precisely classify ALL images dataset using the Inception module to capture features at different scales. Since EfficientNetV2B0 adopts a more balanced design in terms of accuracy/efficiency, the model was chosen for study as well. So, this makes it an excellent choice for the task of classifying large-scale images. A fundamental use case can be used to classify ALL. Nevertheless, to further encompass the intricate morphology that is native in ALL, we included the Inception Module in our model. We speculate that listening to contiguous fragments is actually increasing the receptive field for features of an appropriate size and spatial extent, enabling the network to

successfully capture multi-scale cues important for discerning fine-grained differences among ALL subtypes. At the same time, customized data-tailoring and analogous image preprocessing techniques coupled with attention to the hyper-parameters were employed here in training the network for ALL dataset. However, Fig. 1 displays the proposed MSEENet architecture. Moreover, the architecture consists of three primary sections: Block 1, Blocks 2 to 7, and the Inception Module, each playing a crucial role in feature extraction and classification. Block 1: The first layer is the Conv2D, followed by Batch Normalization, both together doing initial feature extraction from input images. This layer captures lower features like edges and textures, which sets them up for more advanced feature learning in the upcoming layers.

Blocks 2–7: These blocks use Depthwise separable convolutions, which are meant to reduce the number of parameters and computational costs without losing expressive power. Every block has a Depthwise Conv2D followed by Batch Normalization and then a normal Conv2D. This setup subsequently enables us to obtain more abstract features from the images.

Inception Module: Among MSEENet, the Inception module is one of the most significant breakthroughs. It uses multiple parallel convolution operations (1×1, 3×3, and 5×5) along with max pooling to capture features at different scales. These are paddings, convolutions, and max-pooling operations. Then, their outputs can concatenate together, which enables the model to extract features at different scales, which is essential in correctly classifying stages of ALL. See in Fig. 2.

The research work, therefore, aims to prepare the dataset, model architecture, training strategy, and evaluation protocol. The all-inclusive dataset includes microscopic images of blood samples and their annotations from the class standard to the different stages of ALL. This process is done in such a manner that the data is divided into sets of training (80%), validation (10%), and testing (10%) to establish a robust framework of evaluation.

Further, each image goes through a set of preprocessing steps that includes resizing to the size of 224×224 pixels to meet the input layer requirement, normalization of pixel values at runtime to the range [0, 1], and there are no augmentation techniques that would strengthen model generalizability. MSEENet enhances the EfficientNetV2B0 model with the Inception module to capture features at different scales. The EfficientNetV2B0 base model is absolutely an underlying feature extractor. The weight of the base model is kept frozen in the first training phases so as not to destabilize its feature extraction abilities.

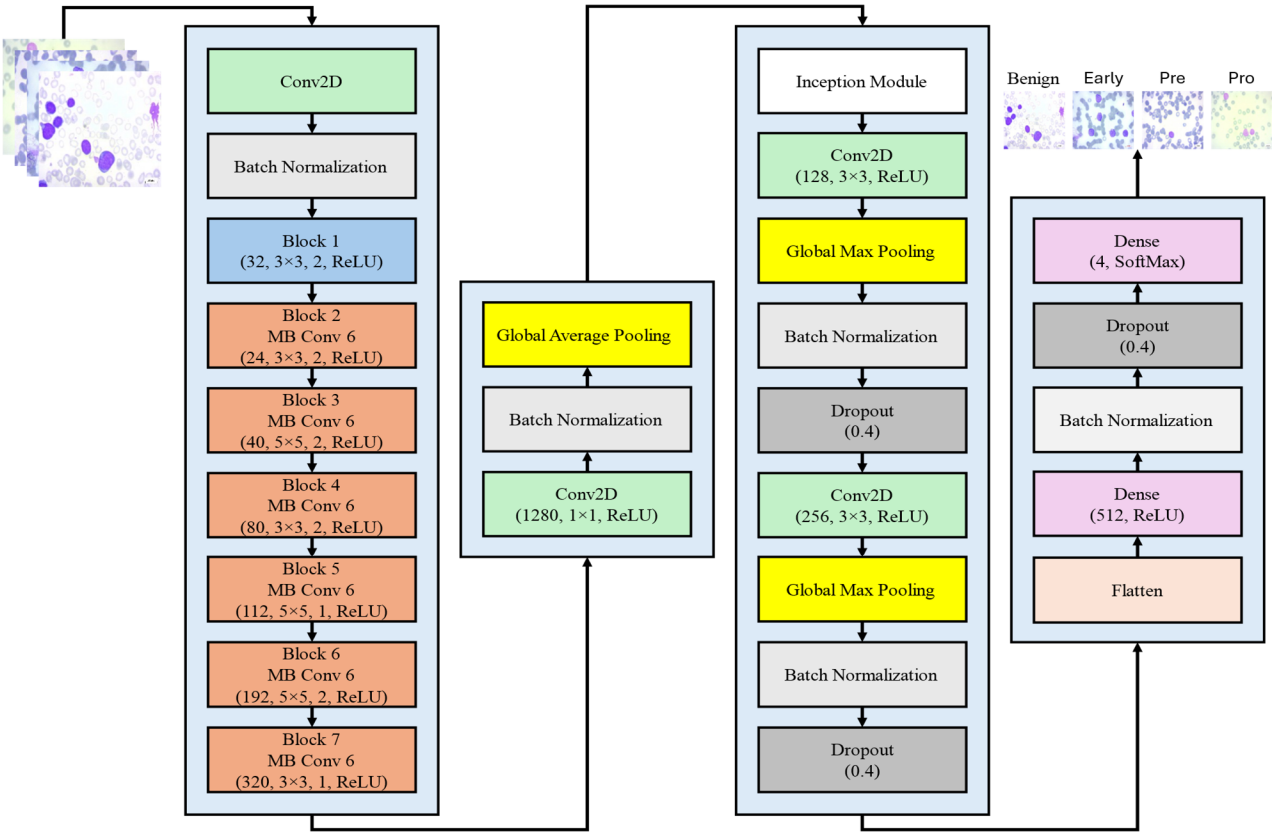

Fig. 1. MSEENet architecture.

The MSEENet was trained using the training dataset and validated its performance on the validation dataset. Implement techniques such as early stopping and learning rate reduction on the plateau to optimize the training process. In the evaluation of our MSEENet model, we utilize several key metrics to gauge its performance, defined in the context where True Positives (TP) and False Positives (FP) denote correctly identified positive

instances and mistakenly identified negative instances as positive, respectively. Similarly, True Negatives (TN) and False Negatives (FN) represent correctly identified negative instances and mistakenly identified positive instances as negative, respectively. Here is a detailed explanation of how these definitions apply to each metric.

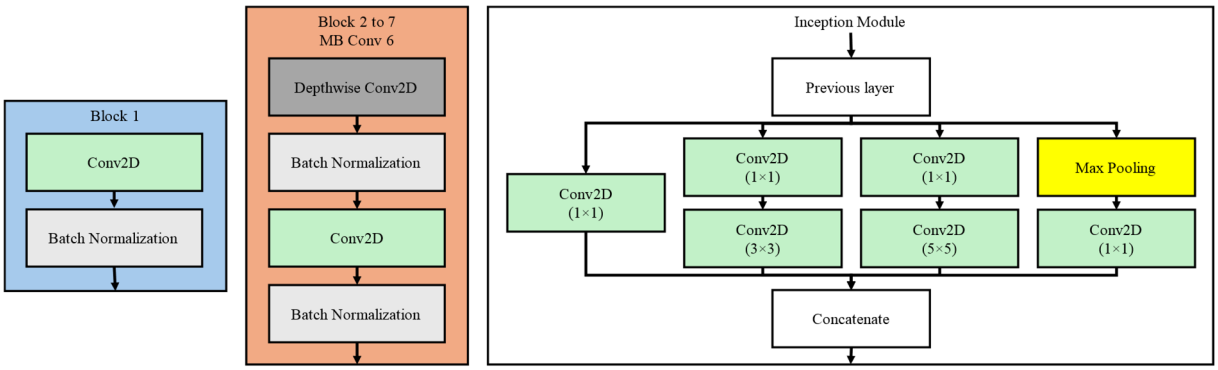

Fig. 2. Structure of left (Block 1), middle (Blocks 2 to 7), and right (Inception module).

Accuracy measures the proportion of true results (both TP and TN) among the total number of cases examined. It provides a general sense of the model's overall correctness.

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \quad (1)$$

Precision (Positive Predictive Value) quantifies the number of true positive outcomes divided by the number of all positive outcomes (including both TP and TN).

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

Recall (sensitivity or true positive rate) is true positive results divided by the sum with false negatives, representing the capability of the model to indicate all cases that would be relevant.

$$Sensitivity = \frac{TP}{TP+FN} \quad (3)$$

F1-Score seeks, by its harmonic mean, a balance between precision and recall, considering false positives and false negatives.

$$F1-Score = 2 \times \frac{Precision+ Sensitivity}{Precision+ Sensitivity} \quad (4)$$

Matthews correlation coefficient (MCC), a summary measure of model quality that accounts for true and false positives and negatives, is a measure of balance even if the two classes are of very different sizes.

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)\times(TP+FN)\times(TN+FP)\times(TN+FN)}} \quad (5)$$

IV. Result and Discussion

In this study, we used the Acute Lymphoblastic Leukemia (ALL) image dataset [11, 19]. It consists of a total of 3256 Peripheral Blood Smear (PBS) images, all collected from 89 subjects suspected of the disease. The dataset includes the images marked as Benign (Hematogones) and Malignant (ALL) and classifies them into three subtypes of ALL: Early Pre-B, Pre-B, and Pro-B ALL, see Fig. 3. The obtained images were captured with 100× magnifications, taken from the obtained images of a Zeiss camera, and stored in a JPG format. The obtained images through the flow cytometry definitively classified it. The database further consists of divided images processed through color thresholding in the HSV color space to aid early cancer screening and reduction in diagnostic errors related to non-specific symptoms of ALL.

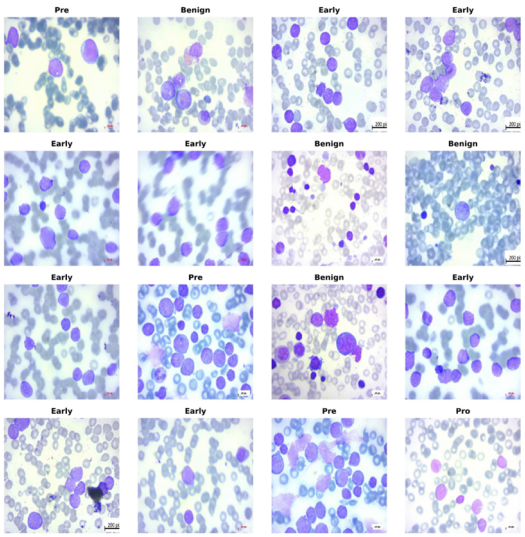

Fig. 3. Sample image from the ALL image dataset [11, 19].

The ALL image dataset is used to train, validate, and test the model. The image dataset contains four classes, benign, early, pro, and pre, which represent various stages of the disease. The training process was closely monitored to ensure that the model learned well from the dataset that had been shown through performance to generalize well on unseen data. The dataset was divided into a training set of 80%, a validation set of 10%, and a testing set of 10%, as shown in Fig. 4.

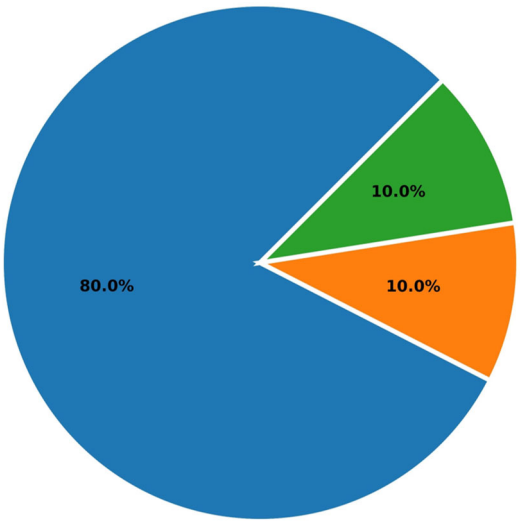

Fig. 4. Dataset splitting ratio: blue (training), green (validation), and orange (testing).

MSEENet is an advanced form of EfficientNetV2B0 architecture integrated with the inception module that is designed to cater to the complexity of the classification task of ALL. By having specific dedicated convolutional layers and fine-tuning the training regimen, the model aims to ensure that the specific minute differences across the subtypes of ALL are better captured.

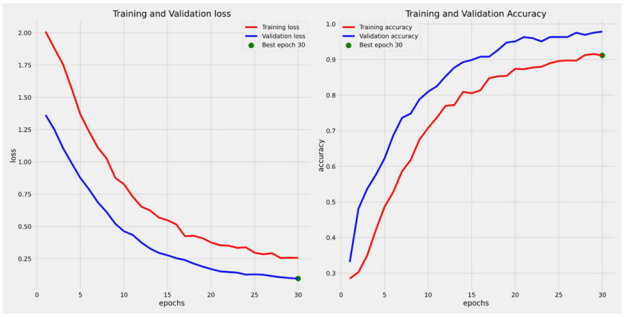

Fig. 5. Training and validation performance over epochs.

The model showcased intense learning and generalization behavior in the course of training epochs. The introduced architectural advancements for MSEENet allowed the model to demonstrate excellent performance increase according to all considered metrics. It is particularly noteworthy in a challenging multi-class classification task such as ALL stage detection. The promising results from this study of MSEENet suggest that this model could be a giant stride in applying deep learning to medical diagnostics, especially in the detection and classification of ALL, see Fig. 5. The evolutionary improvements in this architecture may potentially give clinicians a potent tool for timely diagnosis and intervention and, hence, perhaps grant patients suffering from ALL more individualized and efficacious treatment strategies. However, further exploration of improvements in the balance between classification accuracy and computational efficiency is needed. Also, the confusion matrix of the test set is displayed in Fig. 6.

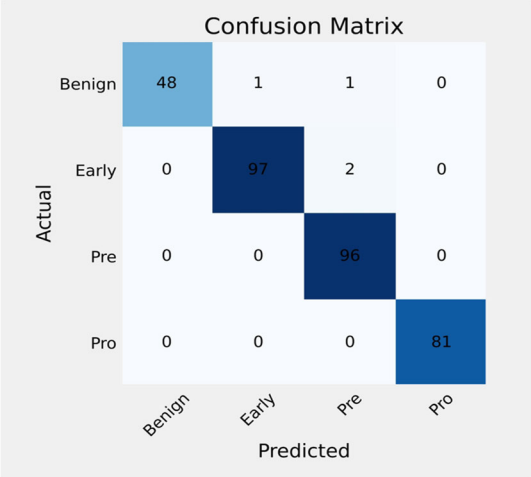

Fig. 6. Confusion matrix.

Our MSEENet model does have a powerful discriminative ability with very few misclassifications, as presented by the confusion matrix. Results do point out that the model has learned distinguishing features of each category, which are pretty effective in their ability with very high precision, especially noticeable in the early and pro classes. The few errors that do occur do not cross over between distant categories (e.g., benign misclassified as pro or vice versa).

TABLE I. ANALYZING THE PERFORMANCE OF THE MSEENET AGAINST THE CURRENT BENCHMARKS

Authors (Year)	Method	Dataset	Accuracy	Precision	Sensitivity	F1	MCC
Atteia *et al.* [12]	Feature-learning, PSO and PCA	ALL dataset [11, 19]	97.40	-	96.60	-	-
Gokulkrishnan *et al.* (2023) [13]	Pre-trained CNNs	ALL dataset [11, 19]	96.77	-	-	-	-
Kadhim *et al.* (2023) [16]	Their own CNN	ALL dataset [11, 19]	98.15	-	94.73	-	-
Hagar *et al.* (2023) [14]	Their own model	ALL dataset [11, 19]	98.20	-	-	-	-
Rejula *et al.* (2023) [15]	ANFIS	ALL dataset [11, 19]	95.67	-	-	-	-
Tusar *et al.* (2024) [17]	DNN, ConvNet, MobileNetV2, and ResNet50	ALL dataset [11, 19]	97.00	97.00	96.00	96.00	-
Mustafa *et al.* (2024) [18]	YOLOv5	ALL dataset [11, 19]	97.80	96.00	96.70	-	-
MSEENet (2024)	MSEENet	ALL dataset [11, 19]	**98.77**	**98.99**	**98.49**	**98.72**	**98.34**

Table I shows a competitive edge of our proposed method across different performance metrics compared to other contemporary research. With the accuracy almost hitting 98.77%, it paves the way for proper detection and classification in methodological rigor. This is the highest precision ever recorded for its use, hence low rates of false

positives, which are always crucial in reliable classifications. Also, the highest sensitivity indicates better performance in the identification of true positives. The F1-Score, while being a balanced score for precision and sensitivity, is coherent with other metrics for the performance of the model. Further, MCC stands at 98.34%, showing it as one of the reliable statistical measures in varied dataset sizes; this subsequently underscores the robustness of the model.

On the other hand, other studies exhibit accuracies with very high values, all above 95%, with Kadhim *et al.* [16] and Hagar *et al.* [14] reaching above 98%. However, they lag in some areas with reference to the proposed method, yet they could not point out their prowess across the spectrum of metrics in which the proposed method is excelling. Based on the performance metrics, these studies do not show the complete set of performance metrics for this study. However, the present study definitely has the set benchmark on accuracy by going even beyond by demonstrating exceptional performance in nuanced classification abilities reflected in the presented comprehensive metrics.

V. Conclusion

This paper presented MSEENet as a highly improved deep learning model that affects enhancement explicitly for the purpose of classifying ALL. The need for such an innovation arises out of the complexity that the malaise entails and a very pressing need for accurate diagnostic tools to vividly segregate various stages of the ailment. The accuracy and reliability in the ALL classification have gone way higher by MSEENet; they really blew up the roof. This enhancement was done by integrating multi-scale feature extraction into the EfficientNetV2B0 deep learning model. The dataset was an image of ALL, including four main classes of progression: benign, early, pre, and pro. It was a kind of comprehensive dataset—so comprehensive, in fact, that this represented a complete dataset base for our evaluation. The performance of the ALL dataset on accuracy, precision, sensitivity, F1, and MCC with respect to MSEENet shows clear evidence that the proposed adaptations have the best and soundest performances. With an accuracy of 98.77%, precision of 98.99%, sensitivity of 98.49%, F1 of 98.72%, and MCC of 98.34%, this model gives a new benchmark in the classification of ALL, besides carrying potential abilities towards the possibility of a significant impact on the clinical outcome through enabling early and accurate diagnosis. Thus, the hope for MSEENet is to turn into a gigantic and very accurate, super-efficient tool for healthcare professionals who diagnose ALL. Therefore, it is likely that subsequent studies and more data sources in this model will open new opportunities for improving the presented model and could make its use even more widespread, helping not only in breast cancer but also in other cancer types, possibly even more for the whole area of medical imaging tasks. The successful classification with such high accuracy and precision of MSEENet in ALL stages represents an auspicious step toward the actual potential of deep learning in medical diagnostics and developing even more personalized and effective strategies in cancer treatment. Future studies could focus on integrating further modalities, such as genetics information or proteomics, which could help improve the power of prediction and increase confidence in model scores. In addition, it has been suggested that a multi-modal approach could lead to insights into the disease at its early stage and may result in better classification.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Lect. Eng. Fallah H. Najjar conducted the initial research, designed the study framework, and contributed to the data collection process. Assist. Prof. Dr. Salman Abd Kadum analyzed the collected data, performed the statistical analysis, interpreted the results, and contributed significantly to the discussion and conclusion sections of the manuscript. Lect. Eng. Nawar Banwan Hassan drafted the initial manuscript, coordinated the writing process, and ensured the coherence and clarity of the final version. All authors had approved the final version.

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