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Genetic Algorithm-Based Hyperparameter Optimization of Convolutional Neural Network Models For White Blood Cells Classification

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***Abstract*—** Detecting white blood cells (WBC) in microscopic images is essential in medical diagnosis. Manual analysis of these images is time-consuming and has a high error rate. Using object detection for WBCs detection with deep convolutional neural networks (CNN) can be considered a practical and effective solution. In this study, a CNN model is proposed to classify these images. In order to achieve optimal training performance, CNNs have many hyperparameters, such as dropout rate, number of hidden units in each hidden layer, activation function, loss function and optimizer, which need to be optimized. Therefore, a hyperparameter optimization approach based on a genetic algorithm is suggested, which can then be used to select the best combination parameters to improve accuracy and efficiency in detecting white blood cells in microscopic images. This new approach is significant and flexible for medical technicians to use in clinical practice for examining blood cell microscopy. In this research, the images were classified into five classes and the mean accuracy of the model for the five classes was 87%, which is considered a good accuracy for classification into five classes.

Keywords— Image Processing, Deep Learning, Metaheuristic Algorithm, Convolutional Neural Network, Histopathology image processing

Introduction (*Heading 1*)

Accurate and timely detection of abnormalities in peripheral white blood cells (WBC) plays an important role in evaluating people's health and diagnosing and prognosing hematological diseases. For example, some blood disorders and diseases related to the immune system are diagnosed by the differential count of white blood cells, which is one of the common laboratory tests. In the field of biomedicine, the identification and analysis of WBC is very important in the diagnosis and treatment of diseases [1].

A differential blood count (DBC), which is a component of a complete blood count (CBC), helps in identifying conditions such as inflammation, infections, leukemia, and specific immune system disorders. Traditionally, medical professionals perform cell counting manually by observing samples under a microscope [2]. This process is often time-intensive, and its accuracy depends on the specialist's expertise and potential fatigue, which can impact reliability. While DBC can also be conducted using laser-based, electrical, or photodetector systems, these methods are costly and typically demand specialized training [3]. Consequently, rapidly identifying WBCs in microscopic images is crucial

Currently, deep learning technology is extensively utilized for object recognition in various research studies [4]. In a number of recent studies, Such networks have been employed for diagnosing lesions [5].

However, in microscopic analysis, factors such as detection accuracy, processing speed, and user-friendliness are particularly important. Nevertheless, certain challenges and issues remain, such as, it necessitates hyperparameters tuning. There are two types of parameters within machine learning models. Model parameters that reflect the data characteristics are one of them. Hyperparameters, which affect learning quality and algorithm performance but do not change during training, are the other two. On the other hand, the model parameters of an artificial neural network (ANN) are weights; parameters such as the number of hidden layers, the number of neurons in the layers, activation functions, optimizers, and learning rate are known as hyperparameters. The performance of a learning algorithm is affected by the appropriate configuration of hyperparameters. Thus, the AI engineer configures hyperparameters with various techniques which require careful study[6].

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In recent years, Convolutional Neural Networks (CNNs) have demonstrated remarkable advancements in the domain of image classification, attaining notable achievements. However, the efficacy of CNNs is intricately tied to the design of their underlying architectures. The prevailing trend among state-of-the-art CNN architectures involves the labor-intensive process of manual construction, undertaken by domain experts possessing extensive proficiency in both CNNs and the specific problem domains under investigation. Consequently, individuals lacking substantial expertise in CNNs encounter challenges when endeavoring to devise highly efficient architectures tailored to their unique image classification tasks.

This study introduces a new method for tackling image classification tasks by utilizing a genetic algorithm-based automatic design process for Convolutional Neural Networks (CNNs). A key benefit of this approach is its effortless implementation, making it accessible to users without extensive familiarity with CNNs. Despite this, users can still achieve an optimized CNN architecture that is well-suited for their specific images. To the best of our knowledge, there is no study on hyperparameter optimization in WBC classification.

background

Utilizing a microscope device, WBC detection can be achieved by implementing a lightweight and efficient object detection algorithm on computers or smartphones. Nevertheless, due to the diversity of WBCs, the task of diagnosis is more challenging. Several Researchers have explored various methods for this detection task. Modern blood testing devices typically identify WBCs through conventional image processing techniques, including preprocessing, image segmentation, feature extraction, feature selection, and classification.

Abdullah [7] and Mohammad [8] were among the first to segment WBCs from blood microscopic images, extracting features using various classification methods to differentiate between normal and abnormal cells. This work led to the proposal of an efficient computer-aided diagnosis (CAD) system. The authors reported accuracy rates of 98.7% and 97.0%, respectively. In more recent research, the edge box technique has been employed, incorporating knowledge-based constraints to rapidly and efficiently generate cell proposals for WBC detection. With the rise of deep learning methods, some researchers have integrated deep learning with machine learning approaches for WBC detection.

Kumar et al. [9] introduced a hybrid model combining feature engineering and deep learning for leukemia diagnosis. The K-Best selection algorithm was developed to identify and extract relevant features, while a convolutional neural network was employed for classification [10]. In their study, They applied the Gram-Schmidt algorithm for segmentation and utilized a deep convolutional neural network (CNN) in combination with scale-invariant feature transform (SIFT) to classify WBC categories, achieving an accuracy rate of 97.14%. However, these methods require manual feature extraction design, including shape, texture, statistical, geometric, and discrete cosine transform (DCT) features, which can be cumbersome.

Kotlow et al. [11] utilized ResNet50 as the backbone and regional convolutional neural networks (R-CNN) for training and testing by combining the BCCD and LISC datasets. Furthermore, the authors introduced an automated computer-aided system for blood image analysis [12]. They proposed a framework for WBC segmentation and detection, which achieved a higher F1 score by merging a private dataset with the LISC dataset.

One limitation observed in previous research is the scarcity of data, with most models categorized into healthy and diseased classes. However, thanks to Iranian researchers, a large amount of data spanning five different classes has been collected and made freely available to the public.

Table I presents a thorough look into the most prominent deep learning techniques discovered through extensive research. These approaches boast remarkable efficiency, effectively extracting vital information from data to produce precise predictions. With impressive success rates surpassing 90%, these models are an indispensable asset for WBC classification. However, their complex architecture and dependence on large amounts of data can result in significant computational expenses, serving as a notable drawback. To tackle this obstacle, it is crucial to devise simpler models that maintain exceptional performance while requiring fewer trainable parameters. However, implementing these methods does pose a challenge.

Table I Comparison of WBC classification results (NI indicates no information)

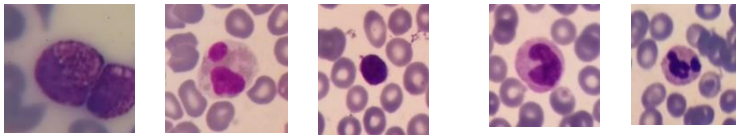
Authors	Model Description	Parameters	Layers	Accuracy (%)	Recall (%)	F Score (%)
Abou et al.[13]	CNN model with a custom-designed structure	NI	5	96.8	-	-
Baghel et al.[14]	CNN model	519860	7	98.9	97.7	97.6
Banik et al. [15]	CNN that combines features from both the first and last convolutional layers	10^5	10	97.9	98.6	97
Basnet et al.[16]	DCNN model incorporating image preprocessing and a modified loss function	-	4	98.9	97.8	97.7
Baydilli et al.[17]	WBC classification using a limited dataset with capsule networks	8238608	6	96.9	92.5	92.3
Çınar et al.[18]	Hybrid model combining AlexNet, GoogleNet networks, and a support vector machine	60 × 10^6(AlexNet) 7 × 10^6(GoogleNet)	8 22	99.7	99	99
Hegde et al.[19]	AlexNet and a CNN model with a custom architecture	60 × 10^6(AlexNet)	8	98.7	99	99
Huang et al.[20]	MFCNN, a CNN model integrated with hyperspectral imaging and modulated Gabor wavelets	-	4	97.7	-	-
Jiang et al.[21]	Residual convolutional architecture.	-	33	83	-	-
Khan et al.[22]	AlexNet model combined with a feature selection strategy and extreme learning machine (ELM)	60 × 10^6(AlexNet) 40 × 10^6(ELM)	8 3	99.1	99	99
Liang et al.[23]	Combining Xception-LSTM	23 × 10^6 (Xception)	71	95.4	96.9	94
Özyurt [24]	Ensemble of CNN models (AlexNet, VGG16, GoogleNet, ResNet) for feature extraction, combined with the MRMR feature selection algorithm and an ELM classifier	60 × 10^6 (AlexNet) 7 × 10^6 (GoogleNet) 138 × 10^6 (VGG16) 26 × 10^6 (Resnet)	8 22 16 50	96.03	-	-
Patil et al.[25]	Combining canonical correlation analysis (CCANet) with convolutional neural networks (Inception V3, VGG16, ResNet50, Xception) and a recursive neural network (LSTM)	23 × 10^6 (Xception)	71	95.9	95.8	95.8
Razzak [26]	CNN combined with extreme learning machine (ELM).	-	3	98.8	95.9	96.4
Togacar et al.[27]	AlexNet with QDA	60 × 10^6 (AlexNet)	8	97.8	95.7	95.6
Wang et al.[28]	Three-dimensional attention networks for hyperspectral image analysis	30 × 10^6	18	97.7	-	-
Yao et al.[29]	Two-module weighted optimized deformable convolutional neural network	60 × 10^6	55	95.7	95.7	95.7
Yu et al.[30]	Ensemble of CNN models (Inception V3, Xception, VGG19, VGG16, ResNet50)	23 × 10^6(InceptionV3) 23 × 10^6(Xception) 138 × 10^6(VGG19) 26 × 10^6(Resnet50)	48 71 19 50	90.5	92.4	86.6
Cheuque et al.[31]	Multi-level convolutional neural network approach using multi-source datasets, combining Faster R-CNN for cell detection and MobileNet for type classification	1 × 10^6(MobileNet)	28	98.4	98.4	98.4

Research methods and materials

To conduct this research, four stages of the cross-industry standard process for data mining (CRISP) have been utilized, which include: A) data acquisition, B) data preparation and preprocessing, C) modeling, and D) evaluation.

Introduction to the dataset

The dataset used in this research is taken from Robin's open access database. This database is Iranian and contains 40,000 images of WBC and colored spots that include five classes of basophils, neutrophils, eosinophils, monocytes and lymphocytes. A significant number of cells were labeled by two experts to ensure the validity of the data. Robin, as a general database in the field of health, can be used for model development, testing in various machine learning tasks, including classification, diagnosis, segmentation, and localization [32]. The **Figure I** show the picture of each classUnits



Basophil **Eosinophil** **Lymphocyte** **Monocyte** **Neutrophil**

Figure I dataset classes

Preprocessing

When starting a new model, it is essential to do data preprocessing according to the model's specific requirements. For this particular dataset, the images come in vibrant colors and have a resolution of 575x575 pixels. There are a total of 14514 images in the training set. As a first step, we convert the images from color to black and white. Then, before inputting the data into the model, we use one-hot encoding to transform it into five columns. In each row, only one column can have a value of 1, while the others are set to 0, ensuring efficient data feeding into the model.
In the last step, we separate our data into two sets of training and testing, in such a way that we consider 0.2 of the total data as testing and the rest as training, then from the training set, we consider 0.1 of the data as validation set.

Table II Diversity of each class

Sets	**Lymph**	**Mono**	**Neut**	**Eos**	**Bas**
Total	**3461**	**795**	**8891**	**1066**	**301**

Modeling

The following sections first provide an explanation of the GA method, followed by a description of the proposed CNN optimized through GA.

1.1.1.1 Genetic Algorithm

GA is a well-known metaheuristic algorithm, inspired by biological processes [33].The GA method was used to tune the CNN hyperparameters for classifying the images. The GA iteratively evolved a population of potential hyperparameter sets over multiple generations, guided by the principles of selection, crossover, and mutation [6].

Table III GA hyperparameters

Hyperparameter	Value or range	Data type
Epoch	From 7 to 10	Integer
Batch Size	128	Constant
Filter size	[32, 64, 128]	integer
Kernel size	[3, 5]	Integer
Dropout rate	uniform (0.1, 0.5)	Continuous
Activation function	ReLU, Selu, Elu, Tanh	Categorical
Optimizer	Adam, Adadelta, Adagrad, Adamax	Categorical

1.1.1.2 Convolutional neural network model

The architecture of the best model was proposed by GA, which can be seen in **Figure II**. This architecture includes 4 deep convolutional layers, each convolutional layer includes Dropout with probability 0.2 for randomly disabling neurons and Maxpooling with size (2,2). ReLU activity function is used in all layers except the last layer and Softmax activity function is used in the last layer. More details about the layers of the CNN architecture can be seen in Figure 2.

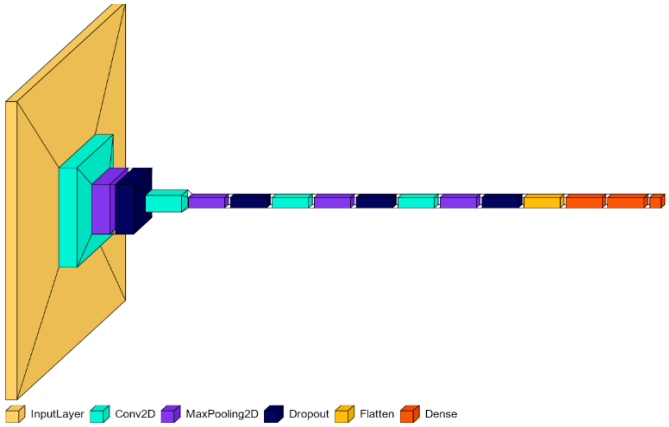


Figure II Architecture of the proposed model

1.1.1.3 Evaluation

Images were classified into five classes. **Figure III** and **Figure IV** respectively demonstrate that the proposed model is well-trained, exhibiting a high accuracy in image classification. As seen in Figures 3 and 4, the model demonstrates good performance with evident convergence. **Table IV** provides a detailed report for each class, indicating an overall model accuracy of 0.87. Notably, the highest accuracy is observed in the class of lymphocyte images.

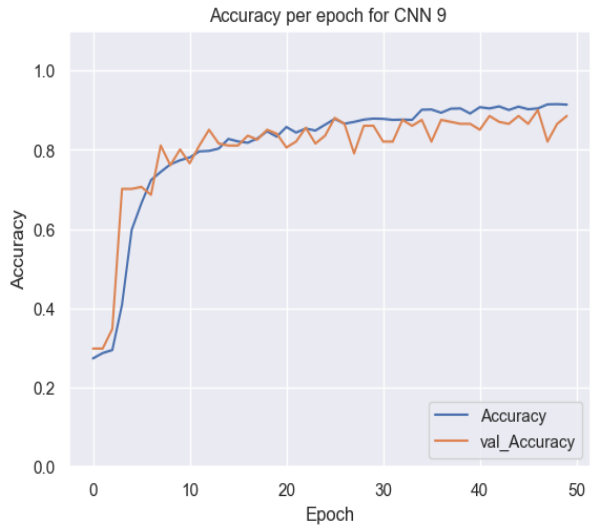


Figure III accuracy per epoch

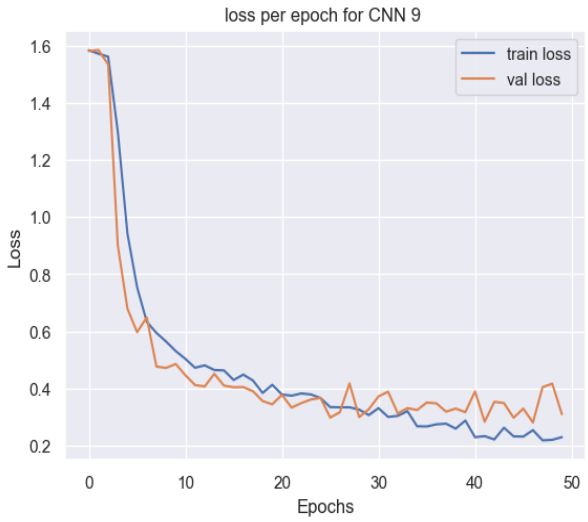


Figure IV loss per epoch

Table IV classification report

	precision	recall	f1-score	support
Basophil	0.94	1.00	0.97	89
Eosinophil	0.86	0.94	0.90	64
Lymphocyte	0.98	0.98	0.98	129
Monocyte	0.85	0.62	0.71	99
Neutrophil	0.68	0.79	0.73	87
accuracy			0.87	468
macro avg	0.86	0.87	0.86	468
weighted avg	0.87	0.87	0.86	468

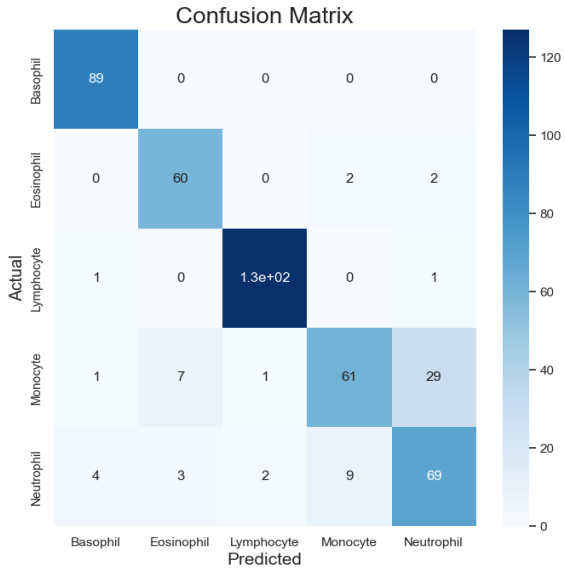


Figure V confusion matrix

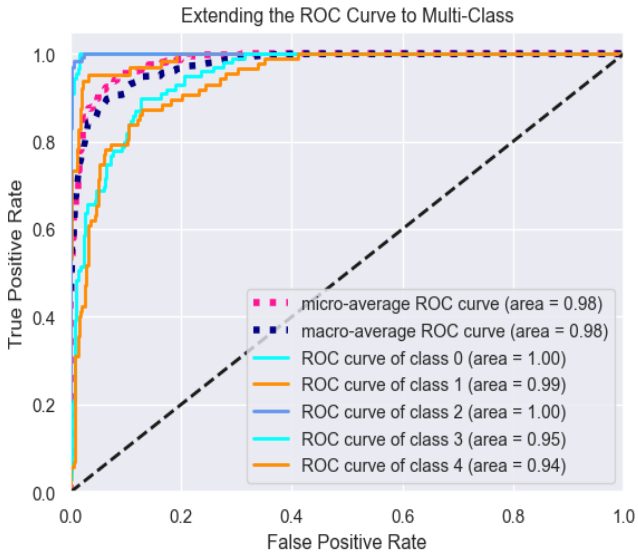


Figure VI ROC curve

Conclusion

The purpose of this research was to prove the ability of classification models and to recognize objects in WBC, which was demonstrated using CNN. One of the achievements of this research was the achievement of high accuracy, despite the fact that the models used for prediction were not of high complexity and at the same time had high power in classification. For future research, one ofs the things that can be done to improve the accuracy of the model is the simultaneous use of images along with clinical data of patients. This study can be a prelude to the development of smartphone software, which can be used to easily classify WBC with a personal smartphone with high accuracy.

1.1.1.3.1 References

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