Turkish Journal of Electrical Engineering & Computer Sciences

http://journals.tubitak.gov.tr/elektrik/

Research Article

Turk J Elec Eng & Comp Sci
(2021) 29: 2742 – 2757

doi:10.3906/elk-2104-183

# Leukocyte classification based on feature selection using extra trees classifier: a transfer learning approach

**Diana BABY**[1], **Sujitha Juliet DEVARAJ**[1], **Jude HEMANTH**[2,*], **Anishin Raj M M**[3]
[1]Department of Computer Science and Engineering, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India
[2]Department of ECE, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India
[3]Department of CSE, Viswajyothi College of Engineering and Technology, Kerala, India

**Received:** 26.04.2021 • **Accepted/Published Online:** 09.08.2021 • **Final Version:** 04.10.2021

**Abstract:** The criticality of investigating the white blood cell (WBC) count cannot be underestimated, as white blood cells are an important component of the body's defence system. From helping to diagnose hidden infections to insinuating the presence of comorbidities like immunodeficiency, an accurate white blood cell count can contribute significantly to shape a physician's assessment. The manual process performed by the pathologists for the classification of WBCs is a time consuming and tedious task, which is further disadvantaged by a lack of accuracy. This study concentrates on the automatic detection and classification of WBC without data augmentation into four subtypes such as eosinophil, monocyte, lymphocyte and neutrophil based on images from three different datasets. The methodology adopted in this paper is transfer learning approach in which the features are extracted using ResNet50, DenseNet121, MobileNetv2, Inceptionv3 and Xception deep learning models.The extra trees classifier is used as an intermediate stage for selecting most predominant features, which reduce the execution time. When evaluating the performance on the basis of recall, precision, F-measure and accuracy parameters, the classification of ResNet50 features selected by extra trees classifier using multi-class support vector machine (SVM) provides the highest accuracy of 90.76% .

**Key words:** Extra trees classifier, deep learning, multi-class support vector machine, transfer learning

## 1. Introduction

Analysis of the differential count of blood plays a vital part in diagnosing a multitude of conditions. Blood is suspended in plasma; the transportation system carries oxygen and other nutrients to the various cells in the human body. Blood is primarily composed of three types of cells such as erythrocytes, white blood cells and platelets [1]. The total volume of human blood is about 5 L depending on body size of which RBCs compose approximately 40%. Compared to Red blood cells (RBCs), leukocytes, which fight infections, are lesser in number. The decrease of WBCs beyond a certain level, however, can result in leukopenia, a condition that renders the patient more vulnerable to infections. On the other hand, an unusually large presence of WBCs in the bloodstream is an indicator of serious infections, inflammations or leukaemia. Basu et al.[2] discusses about the blood and the functionalities of each component of blood in detail. Our work focuses on the automatic classification of leukocytes. Leukocytes are generated by stem cells present in the bone marrow and are categorized into three main types: lymphocytes, granulocytes and monocytes. Granulocytes are further classified into eosinophils, basophils, and neutrophils [3]. The WBC count is analyzed for allergy test,

*Correspondence: judehemanth@karunya.edu

detecting infections, identifying leukaemia and for monitoring the effectiveness of different types of treatments like radiation, chemotherapy, bone marrow transplantation etc.

The medical professionals identify and categorize the different types of WBCs by analyzing the granules present in the cytoplasm and the shape of the nucleus. The lymphocyte cells possess a spherical shaped nucleus with cytoplasm granules of a very clear pale blue color. Lymphocytes represent 20%–40% of differential WBC count, which may be large or small in size. The varying count of lymphocytes is the sign of chronic infections or AIDS. The monocytes are large cells with kidney bean shaped nucleus and light blue cytoplasm granules, normally comprising around 2%–10% of WBC count. An irregular monocyte count may be a red flag for disease conditions such as inflammation, immunity disorders, various blood disorders, malaria, typhoid etc. The eosinophils contain bi-lobed nucleus connected by a thin nuclear band and large pink or red colored cytoplasm granules, which represents 1%—6% of WBC count. The irregular count of eosinophils is caused by bronchial asthma, hay fever, parasite diseases etc. The neutrophil consists of a multi-lobed nucleus where the different lobes are connected with nuclear material consisting of thin strands and also comprises very tiny cytoplasm granules with less visibility; this subtype covers approximately 50%–70% of the entire WBC. If the count of neutrophils is irregular, it indicates infections such as appendicitis, smallpox, rheumatic fever, influenza, hepatitis, rubella etc. [4].

Various techniques like deep learning, machine learning and image processing play significant roles in leukocyte classification. The information about the leukocytes helps the medical professionals to identify various disease conditions at an earlier stage and make the diagnosis faster and reliable. In conventional models, various image processing techniques are used to pre-process, segment and extract clinically useful features from leukocyte images. Nowadays, different problems based on image classification are addressed by various deep learning techniques, which do not need any pre-processing or feature extraction[5]. Many researches are carried out for the automatic segmentation; classification and counting of leukocytes from peripheral blood smear images with the help of computer aided methodologies. Mirčić et al.[6] proposed a method for the automatic leukocyte classification based on artificial neural networks (ANN) with an accuracy of 86%. In their work, the input image required pre-processing, segmentation and manual feature extraction based on digital image processing techniques before the classification process, which causes high execution time. Cinar et al.[7] performed a comparative classification of leukocytes into lymphocytes, monocytes, eosinophils, and neutrophils, utilizing Alexnet-Googlenet-SVM model. In their work, the dimension of feature vector is very high since it combines the feature vectors from two different pre-trained models. Tiwari et al. [8] proposed a CNN-based method for leukocyte subtype classification; this method provides 94% accuracy for the classification into two classes such as polynuclear and mononuclear. But the accuracy of classification into four classes such as eosinophil, lymphocyte, neutrophil and monocyte is only 78%. AL-Dulaimi et al. [9] presented a detailed study on the various techniques and challenges faced for the classification of WBC types from microscopic blood smear images. The analysis work performed by them concluded that the major challenge in leukocyte classification lies in the accurate detection of diverse images.

Sarrafzadeh et al. conducted a research on the classification of eosinophil, neutrophil, basophil, lymphocyte and monocyte cells from blood smear images using SVM, provides an accuracy of 93%. Their work is based on the extraction of distinguishable features separately from the segmented nucleus and cytoplasm of the WBCs, as a pre-processing stage, which takes long execution time compared to deep learning methods [10]. The work conducted by Reena et al. is based on a single LISC dataset of 257 similar images where the WBC classification entails three steps, including semantic segmentation of input images, modification of the database,

and transfer learning based on AlexNet, which takes more execution time [11]. An experiment was conducted by Umpon et al. on the nucleus segmentation and classification using morphological features. In their work, classification was based on Bayesian classifier and artificial neural networks (ANNs). Their study provides only a classification accuracy of 77% using the features extracted from the nucleus of the leukocyte [12].

Huang et al. proposed a WBC classification method based on segmentation followed by fine tuned ResNet50 based classification, which provides test accuracy over 90%. In their work, the leukocytes are classified only into three basic classes like granulocytes, lymphocytes and monocytes [13]. Maier et al. presented a detailed study on the application of various deep learning techniques for medical image processing [14].The method proposed by Mohamed et al. comprises of segmentation based on the thresholding followed by MobileNet224 based feature extraction and classification by Logistic regression. Although it provides greater classification accuracy, their studies are conducted on an augmented dataset [15]. Su et al. developed a neural network based WBC classification system. In their work, the shape, color, and texture features are extracted separately after segmentation, takes a long execution time compared to the automatic feature extraction by pre-trained models [16]. Alam et al. employed a technique for the automatic counting and detection of three main types of blood cells such as RBCs, WBCs and platelets from blood smear based on You-Only-Look-Once (YOLO) algorithm. The subtypes of WBCs are not identified in their study [17]. In a study by Wang et al., an improved You-Only-Look-Once (YOLO) algorithm is used for leukocyte detection, in which the leukocyte detection is performed as object detection, with an accuracy of 90.09% [18].

The transfer learning approach is used for leukocyte classification in our work. This allows us to incorporate the knowledge acquired by performing one task into other similar tasks. The image classification using transfer learning approach can be employed by using any deep learning models such as VGG model, ResNet, MobileNet, Inception, Xception, DenseNet etc. as the feature extraction models [19]. Many researchers have implemented various automations based on transfer learning approach. Zhuang et al. conducted a detailed study on transfer learning in which forty representative homogeneous transfer learning approaches and its applications are explained. Their work is concentrated on two main areas such as text characterization and object detection using transfer learning [20]. Weiss et al. performed a detailed investigation on various aspects and applications of transfer learning techniques in which the previous works and applications of transfer learning are addressed [21]. Yildirim et al. discussed the image classification using the models like Alexnet, ResNet50, DenseNet201 and GoogleNet [22]. Almezhghwi et al. investigated the WBC classification using DenseNet169 network. But their work is based on augmented dataset created using the existing data by performing image transformation operations and generative adversarial networks (GAN) [23]. Hüseyin et al. proposed a transfer learning approach for WBC detection and classification based on ResNet50 along with SVM classifier, which involves augmentation of data to improve accuracy [24]. Vatathanavaro et al. performed a WBC subtype classification and comparison based on VGG16 and ResNet50 models in which the ResNet50 model provided the highest accuracy of 88.29% [25].

Our work proposes a leukocyte classification method, which is based on feature selection using extra trees classifier, which enhances the accuracy and reduces the execution time of the classification process. This methodology uses the ResNet50 deep learning model to extract features for transfer learning. In our work, no pre-processing or segmentation methods are needed before feature extraction, which is usually a time consuming process in existing methods. Leukocyte types are further classified and evaluated using a multi-class SVM. This study uses a heterogeneous dataset, without any data argumentation, constructed from three different datasets

having diverse colors and patterns. Many state-of-the-art techniques involve increasing the quantity of data through data augmentation, which has the disadvantage of limiting data diversity. As this classifier model is constructed based on the features of multiple images rather than using the same type of image from a single database, this model is more effective at detecting diverse images of leukocytes. Furthermore, the paper analyzes the performance of the system with different accuracy metrics. This performance score is then juxtaposed with that of other feature extraction models such as DenseNet121, MobileNetv2, Inceptionv3 and Xception model. Our results have shown that ResNet50 delivers superior features when analyzing leukocyte images.

The remaining part of the paper is organized as follows: proposed methodology in Section 2, details about the dataset in Section 3, experimental results, performance evaluation and discussion are presented in Section 4 and the concluding remarks in Section 5.

## 2. Proposed methodology

The desired outcome of this method, as depicted in Figure 1 is to design an efficient and accurate classification pipeline using transfer learning approach [20] that has the ability to distinguish the input leukocyte images into four different types such as eosinophil, monocyte, lymphocyte and neutrophil. The features from the leukocyte images are extracted using a convolutional neural network (CNN) based pre-trained feature extraction model [26]; the most prominent features are then filtered out based on their importance using extra trees classifier. These refined features are forwarded to the multiclass SVM for the actual classification step. In this methodology, the features extracted using ResNet50, DenseNet121, MobileNetv2, Inceptionv3 and Xception model are fed separately to the extra-trees and SVM pipeline.

Some main contributions of this work are as follows:

- This method reduces the execution time to 1.28 s from 23.5 s for the same number of data items by selecting the most predominant features using extra trees classifier.
- With the use of a pre-trained ResNet50 model, extra trees classifier, and multi-class SVM without data augmentation, an accuracy of 90.76% is achieved.
- Since the classifier model is constructed and evaluated using diverse images from three different datasets, this leukocyte classification system is able to detect different types of leukocyte images with respect to size, color, and pattern.

### 2.1. Feature extraction based on CNN models

In this work, the features are extracted from the leukocyte images using the following convolutional neural network (CNN) models:

**ResNet50 Model**: A deep residual pre-trained model introduced by Microsoft in 2015, this learning framework consists of a few stacked layers that fit a residual mapping, which can be obtained by feed forward neural network with Shortcut or Skip connections [27, 28]. The identity mapping performed in each block is combined with the output of stacked layers, which aids in reducing the training error and allows uncomplicated optimization. In ResNet50 model, a pre-processing function is used to scale the input leukocyte images according to the model size specification of $224 \times 224$. The pre-processed image goes through a zero padding operation, followed by five stages of computation. In the first stage, a convolution operation is performed using 64 kernels of size $7 \times 7$ with a stride of size 2 tailed by a batch normalization block, a ReLU (rectified linear unit activation function), and a max pool layer with a stride of size 2. The stage 2, which is iterated 3 times, comprises of a

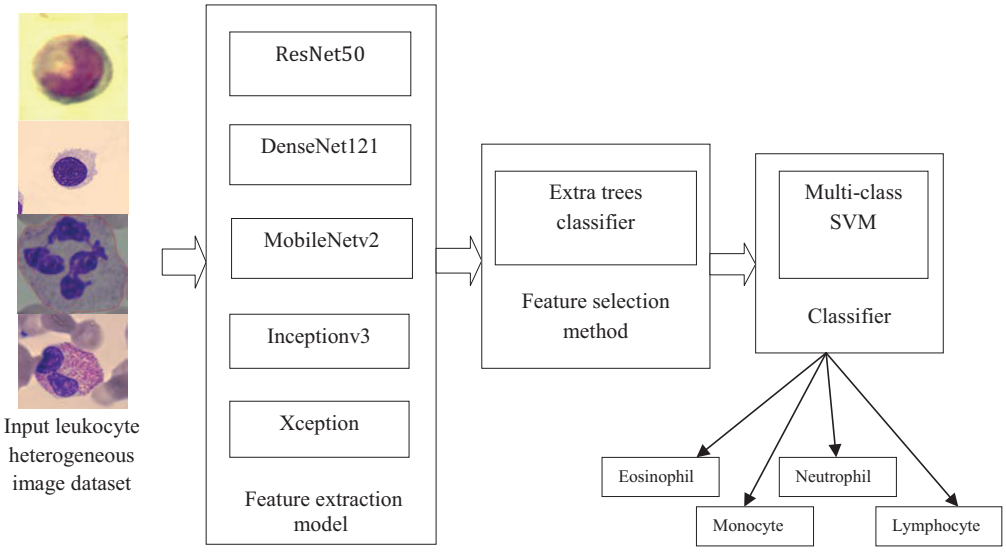


**Figure 1**. Leukocyte classification process.

convolution block with $1 \times 1$ sized 64 kernels, followed by $3 \times 3$ sized 64 kernels, and at last a $1 \times 1$ sized 256 kernels followed by an identity block. The next Next stage, which is executed 4 times, is composed of 128 kernels of size $1 \times 1$, followed by 128 kernels of size $3 \times 3$, and finally 512 kernels of size $1 \times 1$. The succeeding stage consists of 256 kernels of size $1 \times 1$, 256 kernels with size $3 \times 3$ followed by 1024 kernels of size $1 \times 1$; this step is repeated 6 times. The last stage of the architecture comprises of a repeated computation for 3 times, which consists of 512 kernels of sizes $1 \times 1$ and $3 \times 3$, and 2048 kernels of size $1 \times 1$. After undergoing the 49 layers worth of operations, the output of the last stage goes through an average pooling and flattening operation, which produces the feature map corresponding to each image. The final fully connected layer is excluded, as it is usually designated for classification and prediction, and, in this methodology, the SVM is already tasked with this role. The layered architecture of ResNet50 feature extractor model[29] is shown in Figure 2 .

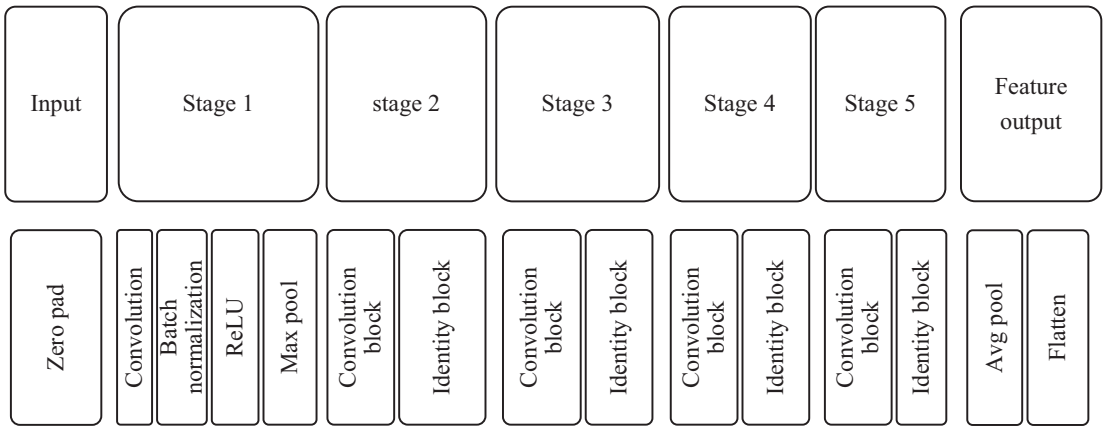


**Figure 2**. Layers of ResNet50 feature extractor [27].

**DenseNet121**: DenseNet121 (dense convolutional network) comprises of a feed forward connectivity from each layer to every other layer, which are called dense connections [19]. DenseNet is similar to ResNet,

which is mainly used for object recognition. The DenseNet concatenates the result of the preceding layer to the result of the future layer to enhance the accuracy for avoiding the vanishing gradient caused by the lengthy path between the input and the output layer. The outcome of the preceding layer serves as an input to the subsequent layer by using an operation called "composite function", which comprises of pooling layer, convolution layer, batch normalization and non-linear activation layer. The different stages of DenseNet121 are shown in Figure 3 . For the feature extraction, the classification part is excluded; this component includes the Average Pool layer and Softmax layer as shown in the architecture diagram. If there are 'n' layers, then there will be $(n(n+1))/2$ direct connections. This has added advantages like strengthening feature propagation, increasing feature reuse and avoiding gradient problems. This network consists of a convolution layer followed by a max pool layer in the initial stage. The further stages are four consecutive dense blocks with dense connections. A transition layer, which is a combination of convolution and max pool layer, is present between two dense layers. In the case of dense connection, let 'n' be a layer, which receives the feature maps from all preceding input layers $x_0, x_1 x_{(n-1)}$ then the feature map of $n^{th}$ layer can be represented as follows [19] :

$$x_n = H_n(x_0, x_1 x_{(n-1)}) \tag{1}$$

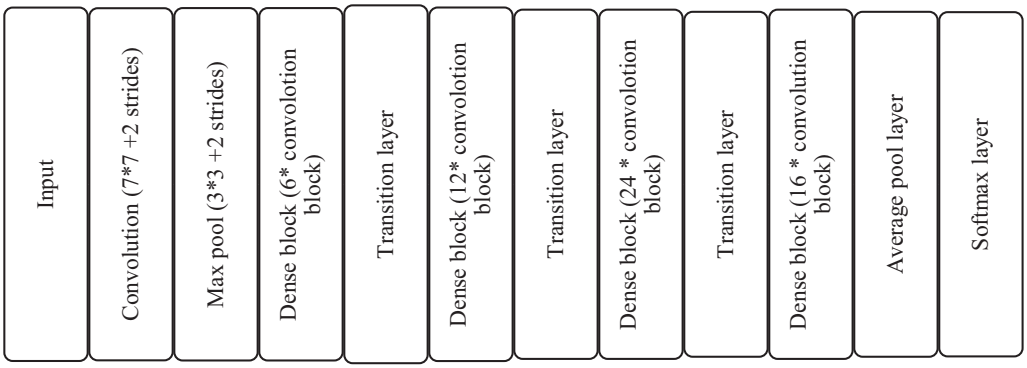


**Figure 3**. Architecture of DenseNet121[19].

**MobileNetv2**: The model Mobilenetv2, introduced by Google, is the expansion of Mobilenetv1. In this network, there is a depth-wise separable convolution, which will lessen the complexity and is also suitable to mobile devices, which have low computational power consumption. In the earlier version, MobileNetv1, the number of channels was the same or twice as much when performing point-wise convolution. In MobileNetv2, the $1 \times 1$ convolution operation produces smaller number of channels, which is called "projection layer" or "bottleneck layer" whose function is to reduce the amount of information passes through it. There are two types of blocks in MobileNetv2: one is bottleneck residual block with stride 1 and the other type of block, with two numbers of strides, is intended for trimming. Each of these blocks consists of 3 convolution layers each. The first layer comprises of $1 \times 1$ convolutions along with ReLU6, the next layer is the depth wise convolution layer, and the third layer is the linear convolution layer. The first layer is an expansion layer, which expands the number of channels that pass through it based on a default expansion factor of 6. ReLU6 is used as an activation function, which can be represented as $min(max(x, 0), 6)$. In this model, every layer other than the project layer has a batch normalization layer and activation function (ReLU6). The model size varies from 1.7M to 6.9M parameters. A kernel size of $3 \times 3$ is used for spatial convolution in the MobileNetv2 [30].

**Inceptionv3**: The Inceptionv1 (GoogLeNet) was the architecture presented at ILSRVRC in the year 2014 [31]. In the first version, Inceptionv1 used the $5 \times 5$ convolutions that resulted in the reduction of input dimensions; this affected the accuracy. In the revised version, Inceptionv2, the $5 \times 5$ convolutions are replaced by two $3 \times 3$ convolutions, which increased the accuracy and reduced the computational time. Inceptionv3 model introduced by Google manages to require less computational power by introducing RMSProp optimizer, label smoothing by using regularization, factorized $7 \times 7$ convolutions, batch norm in the Auxiliary classifiers, dimensionality reduction and parallel computations. A module of Inceptionv3 is shown in Figure 4. Factorized convolutions will reduce the number of parameters, which will in turn increase the network efficiency. In this network the bigger convolutions are replaced by smaller and asymmetric convolutions. An auxiliary classifier is used as a regularizer between layers during training. The grid size reduction is performed in Inceptionv3 by pooling operations to reduce the computational cost [31, 32].

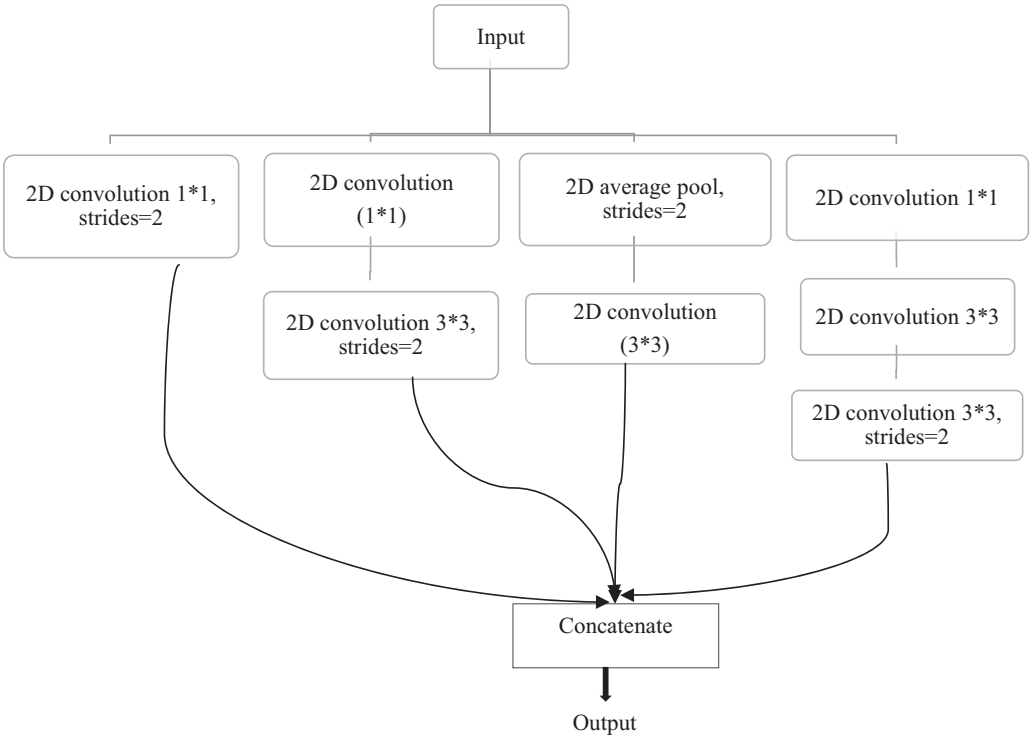


**Figure 4**. A module of Inceptionv3 [31].

**Xception model**: Xception (Extreme Inception), introduced by Google, is a depth wise separable convolution network, which is better than Inceptionv3 for image classification [33]. In this model, the depth wise separable convolution is modified by performing depth wise convolution, a spatial convolution designated separately for each channel as shown in Figure 5 . This is followed by a point wise $1 \times 1$ convolution across different channels with residual connections in each convolution block [33]. The Xception architecture consists of 36 convolutional layers forming the feature extraction part of the model. These layers are divided into 14 different modules with linear residual connections except for the starting and ending modules.

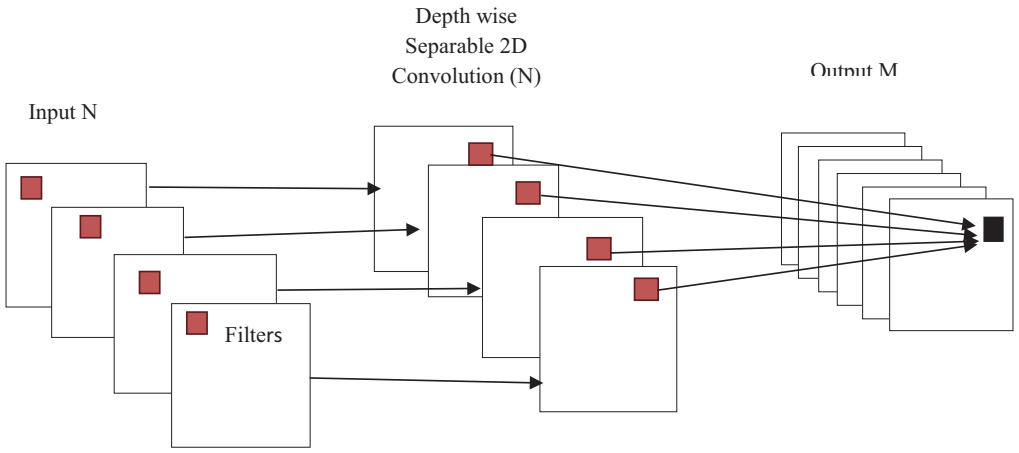


**Figure 5**. Depth wise separable convolution in Xception model[33].

### 2.2. Feature selection using extra trees classifier

In the proposed methodology, an embedded method known as extra trees classifier is incorporated for the purpose of feature selection. It is performed as a midway between feature extraction and classification. The feature selection is the process of automatic identification of the important features, which will contribute the maximum information to the prediction variable. The processing of irrelevant features will decrease the model accuracy and will also increase the computational time. In this work, the feature selection using extra trees classifier has substantially reduced the execution time for the classification.

In this ensemble learning method, the output of the multiple de-correlated trees, which are created from the training dataset are aggregated in a forest is considered for the classification [34].Each tree is provided with a random sample of $'n'$ leukocyte features, which are extracted using a deep learning model. From this, the most relevant feature based on Gini index is used by the corresponding decision tree to split the data. The feature selection is performed by ordering the random features in descending order based on the Gini importance of each feature and the number of top features can be selected according to the requirement. Gini index, which measures the probability of a specific feature being incorrectly classified when it is chosen randomly, is represented as follows:

$$Gini = 1 - \sum_{i}^{n} (\mu_i)^2 \tag{2}$$

where 'n' is the number of data items and $\mu_i$ is the probability of a feature being classified as a particular class.

### 2.3. Classification based on multi-class SVM

The support vector classifier(SVC) is one of the most powerful and supervised machine learning tools for classification, due to its advantage of avoiding the over fitting problem [35]. It also provides better accuracy for majority of the classifications. The 'one-versus-one' approach is used for multi-class classification since normal SVM is a binary classifier. If there are $'n'$ classes then SVC constructs $(n(n--1))/2$ classifiers, wherein each classifier deals with data from two different classes. The SVC constructs a decision surface based on the input

feature vector extracted from leukocyte images. The classification accuracy is proportional to the distance between the data points and the decision surface; it is important to ensure that this distance is maximized [36, 37].

In this work, the non-linear multi-class SVM (SVC) with radial basis function as a kernel is used to classify the leukocyte image into various classes.The radial basis function is represented as follows:

$$K(x, y) = e^{(-(1/(n\sigma^2))\times\|x-y\|^2)} \tag{3}$$

where $'n'$ is the number of features and $\|x - y\|^2$ is the squared euclidean distance between the feature vectors x and y.

## 3. Dataset

The input dataset considered in this work consists of 431 images sourced from three different publicly available datasets; the images are diverse in terms of the color of the cell, shape of the nucleus, background color etc. The dataset consists of 77 eosinophil samples, 123 lymphocyte samples, 83 monocyte samples and 148 neutrophil samples. The MISP dataset utilized in this work is provided by Medical Image and Signal Processing Research Center (MISP) and department of pathology at Isfahan University of Medical Sciences, presented by Sarrafzadeh et al.[10]. This dataset contains blood smear microscopic images captured by ECLIPSE 50i microscope with a magnification rate of 100. The other two datasets are collected from Jiangxi Tecom Science Corporation, China and CellaVision blog, presented by Xin Zheng et al.[38]. The Jiangxi dataset consists of WBC images of size 120*120 with color depth of 24 bits, acquired by a Motic Moticam Pro 252A optical microscope camera with a N800-D motorized auto-focus microscope where a newly developed haematology reagent is applied for staining. The dataset available from CellaVision blog comprises of color images of size $300 \times 300$ in which the white blood cells are surrounded by many red blood cells.

## 4. Experimental results and discussion

The overall experiment is conducted in Google Colaboratory (GoogleColab), a powerful data analytics tool developed by Google.

### 4.1. Results of feature extraction, feature selection and classification

In this work, the feature extraction is performed using multiple pre-trained deep learning models like ResNet50, DenseNet121, MobileNetv2, Inceptionv3 and Xception. Every model extracts a minimum of 50,000 features from each leukocyte image. ResNet50 model extracts more than 0ne hundred thousand features, which provides a better accuracy when compared with other models. The most relevant features are selected based on their Gini importance using extra tree classifier to improve the accuracy and to reduce the dimensionality. The 100,352 features initially extracted using the ResNet50 model is reduced to 4734 features, which augments the accuracy from 88.46% to 90.76%. The reduced features are further used for classification into four distinct classes with the aid of multi class SVM. The number of features extracted using the various pre-trained feature extraction models such as ResNet50, DenseNet121, MobileNetv2, Inceptionv3 and Xception, along with the count of prominent features selected using extra trees classifier and confusion matrix of classification, is depicted in Table 1. The feature map extracted, which consists of 431 vectors corresponding to each input leukocyte image, is bifurcated for classification. In this work, 70% of the dataset is intended for training and the remaining 30% is for testing.

**Table 1**. Feature extraction, feature selection and confusion matrices of leukocyte classification models.

| Leukocyte classification model | No: of features extracted from leukocyte image | No: of features selected using extra trees classifier | Confusion matrix | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Feature selection with extra trees classifier | | | | | Without feature selection | | | | |
| ResNet50 +SVM | 100352 | 4734 | | E | L | M | N | | E | L | M | N |
| | | | E | 25 | 5 | 2 | 1 | E | 22 | 7 | 3 | 1 |
| | | | L | 0 | 31 | 0 | 0 | L | 0 | 31 | 0 | 0 |
| | | | M | 0 | 0 | 21 | 3 | M | 0 | 1 | 21 | 2 |
| | | | N | 0 | 0 | 1 | 41 | N | 0 | 0 | 1 | 41 |
| DenseNet121+SVM | 100352 | 5085 | | E | L | M | N | | E | L | M | N |
| | | | E | 6 | 8 | 16 | 3 | E | 5 | 8 | 16 | 4 |
| | | | L | 0 | 30 | 0 | 1 | L | 0 | 30 | 0 | 1 |
| | | | M | 0 | 5 | 17 | 2 | M | 1 | 4 | 17 | 2 |
| | | | N | 0 | 0 | 1 | 41 | N | 0 | 0 | 1 | 41 |
| MobileNetv2+SVM | 62720 | 4839 | | E | L | M | N | | E | L | M | N |
| | | | E | 23 | 7 | 1 | 2 | E | 20 | 8 | 1 | 4 |
| | | | L | 0 | 30 | 1 | 0 | L | 0 | 30 | 0 | 1 |
| | | | M | 0 | 2 | 20 | 2 | M | 0 | 3 | 19 | 2 |
| | | | N | 0 | 0 | 1 | 41 | N | 0 | 0 | 1 | 41 |
| Inceptionv3+SVM | 51200 | 4742 | | E | L | M | N | | E | L | M | N |
| | | | E | 18 | 6 | 6 | 3 | E | 9 | 7 | 13 | 4 |
| | | | L | 1 | 28 | 2 | 0 | L | 0 | 27 | 3 | 1 |
| | | | M | 1 | 4 | 13 | 6 | M | 0 | 3 | 14 | 7 |
| | | | N | 0 | 1 | 0 | 41 | N | 0 | 1 | 1 | 40 |
| Xception+SVM | 50176 | 4360 | | E | L | M | N | | E | L | M | N |
| | | | E | 14 | 4 | 6 | 9 | E | 7 | 4 | 7 | 15 |
| | | | L | 2 | 25 | 2 | 2 | L | 1 | 24 | 2 | 4 |
| | | | M | 0 | 1 | 16 | 7 | M | 0 | 1 | 16 | 7 |
| | | | N | 2 | 3 | 0 | 37 | N | 0 | 3 | 0 | 39 |

### 4.2. Performance evaluation

The performance evaluation of the leukocyte classification technique, which is represented in a confusion matrix using metrics like accuracy, precision, recall and F1-score, is calculated as follows [39]:

$$Accuracy = (TP + TN)/(TP + TN + FP + FN) \tag{4}$$

$$Precision(P) = TP/(TP + FP) \tag{5}$$

$$Recall(R) = TP/(TP + FN) \tag{6}$$

$$F - measure(F1 - score) = 2 \times (R \times P)/(R + P) \tag{7}$$

The values of true positives(TP), true negatives (TN), false positives (FP) and false negatives (FN), as computed from the confusion matrix for the corresponding method, are shown in Table 2. The performance evaluation of different methods in terms of accuracy, recall, precision and F1-score adopted for leukocyte classification based on transfer learning with and without feature selection are shown in Table 3. It clearly conveys that the classification based on the features reduced using extra trees classifier provides a better result. The values of Recall, Precision and F1-Score normally span a range of 0–1 where the values proximal to 1 show a better performance of the model. The proposed method (ResNet50+ Extra Trees + Multi-class SVM) provides the highest accuracy of 90.76% and performance parameters close to 1 for all the classes, which surpasses the performance of other features extractors considered in this work.

**Table 2**. TP, TN, FP and FN values computed from confusion matrix shown in Table 1.

| Leukocyte classification model | Class | Performance evaluation | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Feature selection using extra trees classifier | | | | Without feature selection | | | |
| | | TP | TN | FN | FP | TP | TN | FN | FP |
| ResNet50+SVM | E | 25 | 97 | 8 | 0 | 22 | 97 | 11 | 0 |
| | L | 31 | 94 | 0 | 5 | 31 | 91 | 0 | 8 |
| | M | 21 | 103 | 3 | 3 | 21 | 102 | 3 | 4 |
| | N | 41 | 84 | 1 | 4 | 41 | 85 | 1 | 3 |
| DenseNet121+SVM | E | 6 | 97 | 27 | 0 | 5 | 96 | 28 | 1 |
| | L | 30 | 86 | 1 | 13 | 30 | 87 | 1 | 12 |
| | M | 17 | 89 | 7 | 17 | 17 | 89 | 7 | 17 |
| | N | 41 | 82 | 1 | 6 | 41 | 81 | 1 | 7 |
| MobileNetv2+SVM | E | 23 | 97 | 10 | 0 | 20 | 97 | 13 | 0 |
| | L | 30 | 90 | 1 | 9 | 30 | 88 | 1 | 11 |
| | M | 20 | 103 | 4 | 3 | 19 | 104 | 5 | 2 |
| | N | 41 | 84 | 1 | 4 | 41 | 81 | 1 | 7 |
| Inceptionv3+SVM | E | 18 | 95 | 15 | 2 | 9 | 97 | 24 | 0 |
| | L | 28 | 88 | 3 | 11 | 27 | 88 | 4 | 11 |
| | M | 13 | 98 | 11 | 8 | 14 | 89 | 10 | 17 |
| | N | 41 | 79 | 1 | 9 | 40 | 76 | 2 | 12 |
| Xception+SVM | E | 14 | 93 | 19 | 4 | 7 | 96 | 26 | 1 |
| | L | 25 | 91 | 6 | 8 | 24 | 91 | 7 | 8 |
| | M | 16 | 98 | 8 | 8 | 16 | 97 | 8 | 9 |
| | N | 37 | 70 | 5 | 18 | 39 | 62 | 3 | 26 |

### 4.3. Discussion

For the purpose of comparing execution time of classification, the entire dataset is partitioned into four sets, each containing 100, 208, 316 and 431 diverse leukocyte images from three different datasets. The processing time required for the classification with and without extra trees classifier is examined with varying numbers of data items. The comparison between the execution time with and without feature selection using extra trees

**Table 3**. Performance evaluation of different methods for leukocyte classification.

| Leukocyte classification model | Class | Performance evaluation | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Feature selection using extra trees classifier | | | | Without feature selection | | | |
| | | Acc. | Precision | Recall | F1-Score | Acc. | Precision | Recall | F1-Score |
| ResNet50+SVM | E | **90.76** | 1 | 0.76 | 0.86 | 88.46 | 1 | 0.67 | 0.80 |
| | L | | 0.86 | 1 | 0.93 | | 0.79 | 1 | 0.89 |
| | M | | 0.88 | 0.88 | 0.88 | | 0.84 | 0.88 | 0.86 |
| | N | | 0.91 | 0.98 | 0.94 | | 0.93 | 0.98 | 0.95 |
| DenseNet121+SVM | E | 72.3 | 1 | 0.18 | 0.31 | 71.53 | 0.83 | 0.15 | 0.26 |
| | L | | 0.7 | 0.97 | 0.81 | | 0.71 | 0.97 | 0.82 |
| | M | | 0.5 | 0.71 | 0.59 | | 0.5 | 0.71 | 0.59 |
| | N | | 0.87 | 0.98 | 0.92 | | 0.85 | 0.98 | 0.91 |
| MobileNetv2+SVM | E | 87.69 | 1 | 0.7 | 0.82 | 84.61 | 1 | 0.61 | 0.75 |
| | L | | 0.77 | 1 | 0.86 | | 0.73 | 0.97 | 0.83 |
| | M | | 0.87 | 0.83 | 0.85 | | 0.90 | 0.79 | 0.84 |
| | N | | 0.91 | 0.98 | 0.94 | | 0.85 | 0.98 | 0.91 |
| Inceptionv3+SVM | E | 76.92 | 0.9 | 0.55 | 0.68 | 69.23 | 1 | 0.27 | 0.43 |
| | L | | 0.72 | 0.9 | 0.8 | | 0.71 | 0.87 | 0.78 |
| | M | | 0.62 | 0.54 | 0.58 | | 0.45 | 0.58 | 0.57 |
| | N | | 0.82 | 0.98 | 0.89 | | 0.77 | 0.95 | 0.85 |
| Xception+SVM | E | 70.26 | 0.78 | 0.42 | 0.55 | 66.15 | 0.88 | 0.21 | 0.34 |
| | L | | 0.76 | 0.81 | 0.78 | | 0.75 | 0.77 | 0.76 |
| | M | | 0.67 | 0.67 | 0.67 | | 0.64 | 0.67 | 0.65 |
| | N | | 0.67 | 0.88 | 0.76 | | 0.6 | 0.93 | 0.73 |

classifier is shown in Figure 6. Based on Figure 6, it can be observed that, with an increase in the number of data items, the execution time increases up to 23.5 s for 431 images, while performing the classification without extra trees based feature selection. When the extra tree classifier for feature selection is incorporated, the execution time for classification process is reduced drastically to 1.28 s for 431 images. The average execution time for the feature selection using extra trees classifier is 3 s. The experimental results indicate that selecting the most prominent features makes the system more efficient and faster.

The classification method proposed in this paper is based on three different datasets, which comprise of 431 diverse images in terms of color and background without performing data augmentation technique. The use of the feature selection model in this work has increased the accuracy of classification from 88.46% (without using extra trees classifier) to 90.76% (feature selection using extra trees classifier), and also the execution time of the classification process is reduced from 23.5 s (without using extra trees classifier) to 1.28 s (feature selection using extra trees classifier). The reduction in execution time will make the system more convenient, especially when the dataset is expanded for future works. Even though this proposed method has acquired overall classification accuracy of 90.76%, the classification accuracy for eosinophil is only 75.5%, whereas the classification accuracy for lymphocyte is 100%, for neutrophil is 97.61% and for monocyte is 87.5%, which

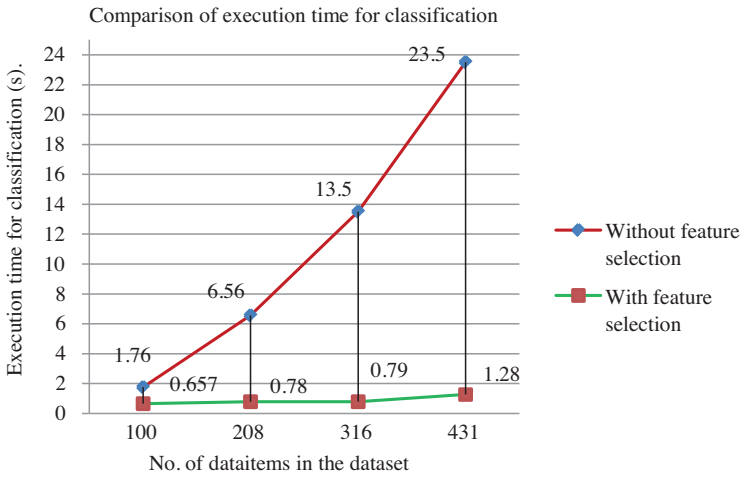


**Figure 6**. Comparison of execution time for classification with and without extra trees classifier for same dataset.

is much higher when compared to eosinophil.Therefore, the methods to improve the positive classification of eosinophil images will be focused in the future work. The mixed dataset used in this work consist of only 431 images, which can be expanded by incorporating WBC images from any another dataset in the future works.The accuracy comparison with other existing methods for leukocyte classification is shown in Table 4.

**Table 4**. Comparison of test accuracy of our method with existing methods.

| **Work** | **Methodology** | **Accuracy** |
|---|---|---|
| Proposed methodology | ResNet50 + Extra trees + Multi-class SVM | 90.76% |
| (2021)[13] | Segmentation + fine-tuned ResNet50 | over 90% |
| (2019)[18] | Single Shot Multibox Detector + You Only Look Once(YOLO) | 90.09% |
| (2019)[40] | LeNet-5 | 87% |
| (2018)[25] | ResNet50 | 88.29% |
| (2019)[22] | ResNet50, AlexNet, DenseNet and GoogleNet + Filters | 75.21-83.44% |
| (2018)[41] | WBCNet | 83% |
| (2007)[12] | Manual segmentation + mathematical morphology + ANN | 77% |

## 5. Conclusion

The leukocyte subtype classification and counting is a major task in haematology analysis, which helps the medical professionals in the identification of serious diseases at the earlier stage itself. This work provides an automated system for the classification of leukocytes into four different classes such as eosinophil, monocyte, lymphocyte and neutrophil based on transfer learning approach. The features are extracted based on ResNet50 deep learning model, and then further selected using extra trees classifier, post, which the final classification

is accomplished using the multi-class SVM model. This proposed model delivers 90.76% prediction accuracy, which is higher when compared to other deep learning models like DenseNet121, MobileNetv2, Inceptionv3 and Xception model. The time saving and convenient method adopted here performed quite well on limited and diverse leukocyte data and did not necessitate any data augmentation. The results indicate that by incorporating the proposed method in automated haematology analysis at health care systems, it has the potential to increase the speed of computation and, in turn, reduce the error rate of the classification.

## References

[1] Adewoyin AS, Nwogoh B. Peripheral blood film - a review. Annals of Ibadan postgraduate medicine 2014; 12 (2): 71-79. doi: 10.4314/AIPM.V12I2

[2] Basu D, Kulkarni R. Overview of blood components and their preparation. Indian Journal of Anaesthesia 2014; 58 (5): 529-537. doi: 10.4103/0019-5049.144647

[3] Young IT. The classification of white blood cells. IEEE Transactions on Biomedical Engineering 1972; 19 (4): 291-298. doi: 10.1109/TBME.1972.324072

[4] Prinyakupt J, Pluempitiwiriyawej C. Segmentation of white blood cells and comparison of cell morphology by linear and naive Bayes classifiers. Biomedical engineering online 2015; 14 (63): 1-19. doi: 10.1186/s12938-015-0037-1

[5] Patel S, Patel A. Deep Leaning Architectures and its Applications A Survey. International Journal of Computer Sciences and Engineering 2018; 6 (6): 1177-1183. doi: 10.26438/ijcse/v6i6.11771183

[6] Mirčić S, Jorgovanovic N. Automatic classification of leukocytes. Journal of Automatic Control 2006; 16 (1): 29-32. doi: 10.2298/JAC0601029M

[7] Çınar A, Tuncer SA. Classification of lymphocytes, monocytes, eosinophils, and neutrophils on white blood cells using hybrid Alexnet-GoogleNet-SVM. SN Applied Sciences 2021; 3 (4): 1-11. doi: 10.1007/s42452-021-04485-9

[8] Tiwari P, Qian J, Li Q, Wang B, Gupta D et al. Detection of Subtype Blood Cells using Deep Learning. Cognitive Systems Research 2018; 52: 1036-1044. doi: 10.1016/j.cogsys.2018.08.022

[9] AL-Dulaimi K,Banks J,Chandran V,Tomeo-Reyes I, Nguyen K. Classification of White Blood Cell Types from Microscope Images: Techniques and Challenges. In: Mendez-Vilas A, Torres-Hergueta E (editors). Microscopy science: Last approaches on educational programs and applied research. Microscopy Book Series, 8, Spain: Formatex Research Center, 2018, pp. 17-25.

[10] Sarrafzadeh O, Rabbani H, Talebi H, Banaem HU. Selection of the best features for leukocytes classification in blood smear microscopic images. In: SPIE Medical Imaging 2014: Digital Pathology conference; San Diego, California, United States; 2014. pp. 1-9.

[11] Reena MR, Ameer PM. Localization and recognition of leukocytes in peripheral blood: A deep learning approach. Computers in Biology and Medicine 2020; 126: 1-12. doi: 10.1016/j.compbiomed.2020.104034

[12] Umpon NT, Dhompongsa S. Morphological granulometric features of nucleus in automatic bone marrow white blood cell classification. IEEE Transactions on Information Technology in Biomedicine 2007; 11 (3): 353–359. doi: 10.1109/titb.2007.892694

[13] Huang X, Liu J, Yao J, Wei M, Han W et al. Deep-Learning Based Label-Free Classification of Activated and Inactivated Neutrophils for Rapid Immune State Monitoring. Sensors 2021; 21 (2): 1-14. doi: 10.3390/s21020512

[14] Maier A, Syben C, Lasser T, Riess C. A gentle introduction to deep learning in medical image processing. Zeitschrift für Medizinische Physik 2019; 29 (2): 86-101. doi: 29. 10.1016/j.zemedi.2018.12.003

[15] Mohamed EH, El-Behaidy WH, Khoriba G, Li J. Improved White Blood Cells Classification based on Pre-trained Deep Learning Models. Journal of Communications Software and Systems 2020; 16 (1): 1-9. doi: 10.24138/jcomss.v16i1.818

[16] Su M, Cheng C, Wang P. A Neural-Network-Based Approach to White Blood Cell Classification. The Scientific World Journal 2014, 2014: 1-9. doi: 10.1155/2014/796371

[17] Alam MM, Islam MT. Machine learning approach of automatic identification and counting of blood cells. Healthcare technology letters 2019; 6 (4): 103-108. doi: 10.1049/htl.2018.5098

[18] Wang Q, Bi S, Sun M, Wang Y, Wang D et al. Deep learning approach to peripheral leukocyte recognition. PLoS ONE 2019; 14 (6): 1-9. doi: 10.1371/journal.pone.0218808

[19] Huang G, Liu Z, Maaten LVD, Weinberger KQ. Densely Connected Convolutional Networks. In: IEEE 2017 Computer Vision and Pattern Recognition Conference; Honolulu, HI, USA; 2017. pp. 2261-2269.

[20] Zhuang F, Qi Z, Duan K, Xi D, Zhu Y et al.A Comprehensive Survey on Transfer Learning. Proceedings of the IEEE 2020; 109 (1): 43-76. doi: 10.1109/JPROC.2020.3004555

[21] Weiss K, Khoshgoftaar TM, Wang D. A survey of transfer learning. Journal of Big Data 2016; 3 (9): 1-40. doi: 10.1186/s40537-016-0043-6

[22] Yildirim M, Çinar A. Classification of white blood cells by deep learning methods for diagnosing disease. Revue d'Intelligence Artificielle 2019; 33 (5): 335-340. doi: 10.18280/ria.330502

[23] Almezhghwi K, Serte S. Improved Classification of White Blood Cells with the Generative Adversarial Network and Deep Convolutional Neural Network.Computational Intelligence and Neuroscience 2020; 2020: 1-12. doi: 10.1155/2020/6490479

[24] Kutlu H, Avci E, Özyurt F. White Blood Cells Detection and Classification Based on Regional Convolutional Neural Networks. Medical Hypotheses 2019; 135 (10): 1-17. doi: 10.1016/j.mehy.2019.109472

[25] Vatathanavaro S, Tungjitnob S, Pasupa K. White Blood Cell Classification: A Comparison between VGG-16 and ResNet-50 Models. In: IEEE 2018 6th Joint Symposium on Computational Intelligence Conference; Bangkok, Thailand; 2018. pp. 1-2.

[26] Rajaraman S, Antani SK,Poostchi M,Silamut K, Hossain MA. Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images. PeerJ 2018; 6 (1): 1-17. doi: 10.7717/peerj.4568

[27] He K, Zhang X, Ren S, Sun J. Deep Residual Learning for Image Recognition. In: IEEE 2016 Computer Vision and Pattern Recognition Conference; Las Vegas, NV, USA; 2016. pp. 770-778.

[28] Khan RU, Zhang X, Kumar R, Aboagye EO. Evaluating the Performance of ResNet Model Based on Image Recognition. In: 2018 Computing and Artificial Intelligence International Conference; Chengdu, China; 2018. pp. 86-90.

[29] Peng J, Kang S, Ning Z,Deng H, Shen J et al. Residual convolutional neural network for predicting response of transarterial chemoembolization in hepatocellular carcinoma from CT imaging. European Radiology 2019; 30 (1): 413-424. doi: 10.1007/s00330-019-06318-1

[30] Sandler M, Howard A, Zhu M, Zhmoginov A, Chen L. MobileNetV2: Inverted Residuals and Linear Bottlenecks. In: IEEE/CVF 2018 Computer Vision and Pattern Recognition Conference; Salt Lake City, UT, USA; 2018. pp. 4510-4520.

[31] Szegedy C, Vanhoucke V, Ioffe S, Shlens J, Wojna Z. Rethinking the Inception Architecture for Computer Vision. In : IEEE 2016 Computer Vision and Pattern Recognition Conference; Las Vegas, NV, USA ; 2016. pp. 2818-2826.

[32] Wang C, Chen D, Hao L, Liu X, Zeng Y et al. Pulmonary Image Classification Based on Inception-v3 Transfer Learning Model. IEEE Access 2019; 7: 146533-146541. doi: 10.1109/ACCESS.2019.2946000

[33] Chollet F. Xception: Deep Learning with Depthwise Separable Convolutions. IEEE 2017 on Computer Vision and Pattern Recognition Conference; Honolulu, HI, USA; 2017. pp. 1800-1807.

[34] Sharaff A, Gupta H. Extra-Tree Classifier with Metaheuristics Approach for Email Classification. In: Bhatia S, Tiwari S, Mishra K, Trivedi M (editors). Advances in Computer Communication and Computational Sciences: Advances in Intelligent Systems and Computing, Singapore: Springer, 2019, pp. 189-197.

[35] Osowski S, Siroic R, Markiewicz T, Siwek K. Application of support vector machine and genetic algorithm for improved blood cell recognition. IEEE Transactions on Instrumentation and Measurement 2009; 58 (7): 2159–2168. doi: 10.1109/TIM.2008.2006726

[36] Chen H, Haoyu C. Face Recognition Algorithm Based on VGG Network Model and SVM. In: 2019 3rd Machine Vision and Information Technology International Conference; Guangzhou, China; 2019. pp.1-8.

[37] Thai LH, Hai TS, Thuy NT. Image Classification using Support Vector Machine and Artificial Neural Network. International Journal of Information Technology and Computer Science 2012; 5: 32-38. doi: 10.5815/ijitcs.2012.05.05

[38] Zheng X, Wang Y,Wang G, Liu J. Fast and robust segmentation of white blood cell images by self-supervised learning. Micron 2018; 107: 55-71. doi: 10.1016/j.micron.2018.01.010

[39] Powers DMW. Evaluation: From precision, recall and F-measure to ROC, informedness, markedness & correlation. Journal of Machine Learning Technologies 2011; 2 (1): 37-63. doi: 10.9735/2229-3981

[40] Sharma M, Bhave A, Janghel RR. White Blood Cell Classification Using Convolutional Neural Network. In: Wang J, Reddy G, Prasad V, Reddy V (editors). Soft Computing and Signal Processing: Advances in Intelligent Systems and Computing, Singapore: Springer, 2019, pp. 135-143.

[41] Jiang M, Cheng L, Qin F, Du L, Zhang M. White Blood Cells Classification with Deep Convolutional Neural Networks. International Journal of Pattern Recognition and Artificial Intelligence 2018; 32 (9): 1-11. doi: 10.1142/S0218001418570069