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A Robust Deep Learning Model for WBC Classification using Capsule Net and Stacked Sparse Auto Encoder coupled with Mayfly Optimization

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Abstract: White Blood Cells build the base of the human immunity and hence hold a critical place in haematological disease diagnosis. Since there exist 12 distinct types in white blood cells which vary by only a small margin, propose a hybrid classification model which combines deep learning techniques along with optimization algorithms for achieving higher performance. The proposed model utilizes high-performance, state-of-the-art technologies. A total of 1460 images are obtained from the standard Kaggle database. The input images are preprocessed using bilateral filter and contrast limited adaptive histogram equalization algorithm is applied for contrast enhancement. The preprocessed imaged are then segmented using UNet architecture of convolutional neural networks. Features are then extracted using Capsule Net machine learning approach. Finally, WBC images are classified into five types namely Eosinophils, Neutrophils, Basophils, Lymphocytes and Monocytes using stacked sparse auto encoder and optimized with Mayfly optimization algorithm. The proposed model is compared with existing algorithms like Support Vector Machine, DenseNet, Inceptionv3, ResNet, Convolutional Neural Network and is found to have superior performance. It achieves an accuracy of 97.79%, precision score of 97.40%, Recall of 97.40%, specificity of 97.17%, F1-Score of 97.4% and ROC value of 0.998.

Keywords*: *WBC, Bilateral filter, CLAHE, Capsule Net, Auto encoder, Mayfly optimization

1. Introduction

World Health Organization has stated that infections due to virus forms the 4th significant reason for mass death of human population and in all of these infections, blood is the first point of attack [1]. Hence, blood cell classification is a very essential process in various disease screening activities. Blood Cell research has become one of the most popular field of medical research after the onset of novel coronavirus disease. Post COVID-19, there is a sudden surge in non-communicable diseases, many of which are related to blood. Also, many people have started to monitor their health in order to avoid any future health concerns. Hence the number of people screening their blood for abnormalities has risen exponentially.

Extracting WBC separately from the blood smear and counting them manually is very time consuming and also needs to be done under medical expertise [2]. In the blood of those who are affected by cancer, WBC becomes very small in size and the nucleus disappears. The count of WBC's also increases rapidly. In such extreme cases, classifying WBCs would really be laborious. Also, certain treatments like chemotherapy and radiation therapy alter the blood cell counts and texture to a very great extent. Therefore, medical practitioners have expressed the dire need for an inevitable blood cell classification system.

Leukocytes also known as white blood cells constitute the base of human disease immunity [3]. The normal range of WBC in a healthy adult is around 4,000 to 11, 000 in 1µL of blood. WBCs can be divided into two types based on the type of cell lineage and granules. On the basis of granules, they are divided into two types called granulocytes and agranulocytes. Three types of granulocytes are eosinophils, basophils and neutrophils. Agranulocytes can be divided into lymphocytes and monocytes. This type of classification was the first kind of WBC division, and it is more likely to be of use in today's medical field. Classification of WBC as shown in Figure 1.

Lymphocytes form the most important type of WBC that produces antibodies and kills foreign agents that enter the human body. They constitute about 20 to 45% of total WBCs [4]. Neutrophils are the first ones to react to any attack and they form about 40 to 70% of WBC. It is not surprising if half of a person's WBC are neutrophils. Monocytes form 2% to 10% of WBCs and the duty of monocytes is to clear the dead cells. Eosinophils are very less in number, accounting for only 1 to 6%. They play an especially important role in fighting against parasitical attacks. Basophils are responsible for building immune response and are found to be less than 1%.

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White Blood cells form the basic unit of immunity and is often the first part of human body to be affected and also the first one to react to the attack. There are several diseases related to the WBCs. Less number of WBCs is a condition called Leukopenia, whereas higher number of WBC results in Leukocytosis. We know that many infectious diseases like Typhoid, Malaria, Sepsis, Dengue, HIV, Hepatitis can affect white blood cells to a greater extent. Apart from these general diseases, any alteration either increase or decrease of WBC types leads to different complications. For example, increase in lymphocytes leads to Brucella, Hepatitis, Bordetella pertussis etc. [5]. Increase in number of monocytes causes many viral and bacterial infections and diseases such as Malaria and Listeriosis. Any imbalance in basophils leads to Hyperthyroidism and Myeloproliferative diseases. The disease list related to white blood cells can be alarming and each of these diseases modifies the underlying blood cell to a significant extent. This explains the sincere need for an automated WBC detection system.

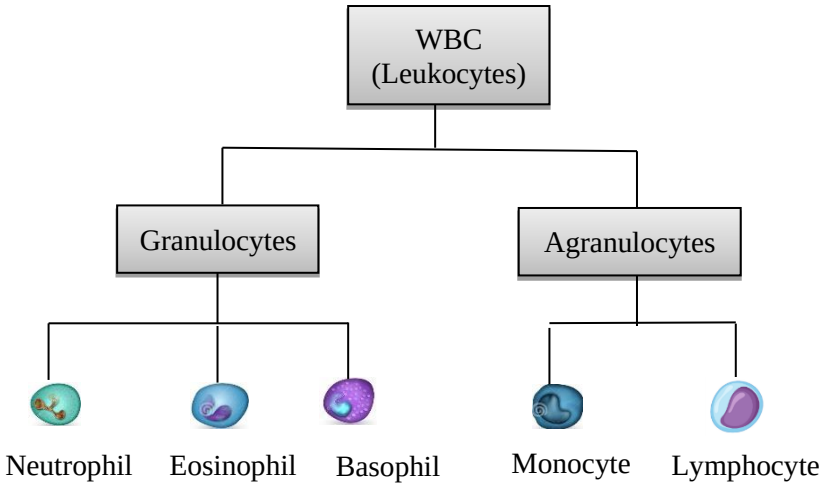

Fig 1: Classification of WBC

2. Related Works

Recent studies that have been carried out regarding WBC classification are discussed here. With the development of medical science, it is highly necessary that we classify white blood cells more precisely with higher rate of accuracy for exact identification of disease and appropriate treatment needed further.

For example, according to Kassani et al., [6] blood cancer commonly called as Leukemia can be divided into four types namely Acute Myelogenous Leukemia (AML), Acute Lymphoblastic Leukemia (ALL), Chronic Myeloid Leukemia (CML), Chronic Lymphocytic Leukemia (CLL). Each of them requires different treatment and protocol to be followed for quick recovery and avoid any loss of life. ALL accounts for 25% of pediatric cancer which when untreated can lead to death of affected children within weeks. Therefore, it becomes absolutely necessary for the hematologist to examine the blood cells and classify them precisely amidst the variations that could be caused by the underlying disease.

Alharbi et al., [7] segments and classifies WBCs using UNET architecture of Convolutional Neural Network (CNN). Data was extracted from ISBI CNMC 2019 data set and utilized in the ratio 80:10:10 for the purpose of training, validation and testing. NVIDIA Lenovo Think Station was employed for execution. Segmentation accuracy of 96% was attained using classifiers of Deep Lab V3 and Resnet 50.Bairaboina and BattulaRao propose an effective WBC classification system using Mobile NetV3 and ShuffleNetV2 with the help of BCCD and Raabin WBC datasets containing 14,514 images. The images were of size 575*575. The Contrast Limited Adaptive Histogram Equalization (CLAHE) algorithm was used for preprocessing to enhance the contrast. The proposed approach achieves an accuracy of 99.19%.

Alagu et al., [8] use UNet classifier to identify ALL with the help of fused deep features. ALL IDB2 database containing 198 images was used for the study. Features are extracted using recursive feature elimination method and statistical analysis is carried out using ANOVA technique which finally arrives at an accuracy of 98.2%

Neenavath et al. use Mayfly optimization algorithm along with Generative Adversarial Network (GAN) to classify leukemia from blood smears using Olympus CX51 microscope. 1200 images in JPEG format of size 1600*1200 were split in the ratio 70:30 for training and testing which finally achieves an accuracy of 99.8%.

Meenakshi and Uma have proposed an automatic classification system of WBC that makes use of CNN and deep learning together. 12,500 images were used for this

purpose. CNN is used for feature extraction and Recurrent Neural Network (RNN) based Long Short-Term Memory (LSTM) classifier was utilized for executing the proposed idea. The May fly algorithm is also used for optimization. The classification accuracy obtained finally is 97%.

Kadey et al. conducts a study of various CNN algorithms for segmenting leukocytes. LLC database was used for experimentation. Results have shown that VGG UNet is better than all other segmentation algorithms such as Segnet, UNet etc. The accuracy obtained by unit VGG UNet was 97.7316%. Yentrapragada [9] detects WBC from blood smears using a hybrid system that combines CNN and Deep learning. 12,500 images were obtained from Kaggle dataset. The hybrid optimization algorithm is used as feature extractor and CNN plus LSTM is used as a classifier with 97% accuracy.

AsimShahzad et al. categorizes WBC by employing AdditionNet4B along with ant colony optimization. CLAHE algorithm is used for preprocessing. Resnet50 and EfficientNetB0 was used for feature extraction. Support Vector Machine (SVM), Linear Discriminant Analysis (LDA) and K Nearest Neighbor (KNN) algorithms were used for classification. 12,500 images from BCCD database was used for classification purpose. Classification accuracy obtained for each of the WBC cell type is given separately. For monocytes, the classification accuracy is 99.80% and for Eosinophils, the accuracy achieved is 97.92%. Neutrophils and Lymphocytes achieve an accuracy of 96.08% and 99.84% respectively.

Munir et al., [10] makes use of auto encoder to classify breast cancer images. 569 samples were taken, out of which 357 were benign and 212 were malignant in nature from Wisconsin Diagnostic data set and used MATLAB R2017 platform to execute the proposed work. The proposed auto encoder achieved a false positive rate of 0%. Jiang et al., [11] proposes an automatic classification system of RBCs using quantitative phase imaging combined with deep learning. He obtained samples from 18- to 30-year-old healthy individuals using inverted fluorescence microscope of size 1920*1200 pixels. The proposed method yields an accuracy of 97.3% by employing Stacked Sparse Auto Encoder (SSAE) and convolutional neural networks.

3. Proposed System

The proposed system uses many robust deep learning techniques for classifying WBCs. 1460blood smear images are obtained from the Kaggle dataset website mentioned here, https://www.kaggle.com/datasets/brikwerk/bccd-white-blood-cell. The first step of the proposed system is to preprocess the given image using bilateral filter and enhance contrast of the image using CLAHE algorithm. Preprocessed images are fed as input to the Unet segmentation algorithm.

This algorithm segments the needed areas from the blood smear image. Relevant features needed for WBC classification are extracted from the segmented image using CapsuleNet and classified using stacked sparse autoencoder (SSAE) machine learning algorithm. Mayfly optimization algorithm is applied in order to achieve better performance. The workflow of the proposed system is illustrated in Figure 2 below.

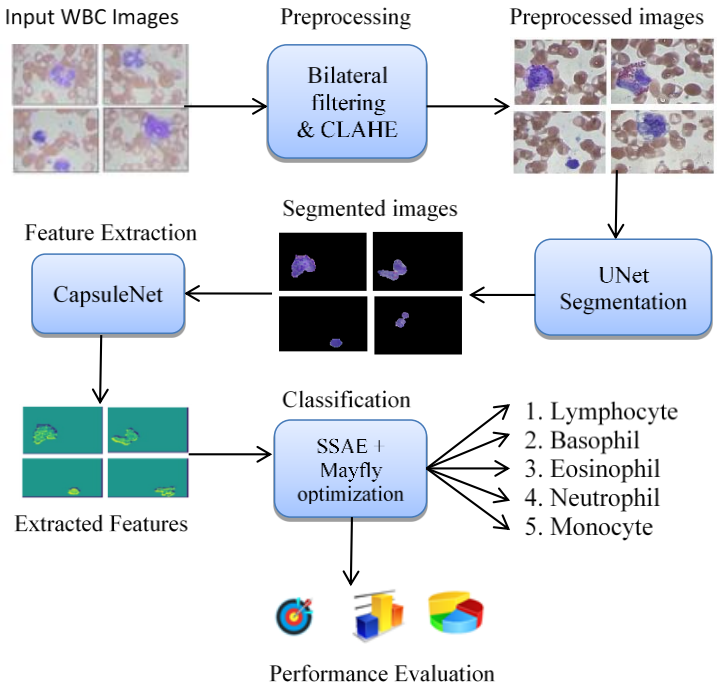

Fig 2: Proposed system workflow depiction

3.1 Image Acquisition

1460 images are utilized to carry out this experiment from the standard Kaggle database. Data is split in the order of 70:30 for conducting classifier training and testing. 1022 inputs are employed to train the chosen classifier and the remaining 438 images are utilized to test the classifier. A sample of each of the WBC type is presented in Figure 3.

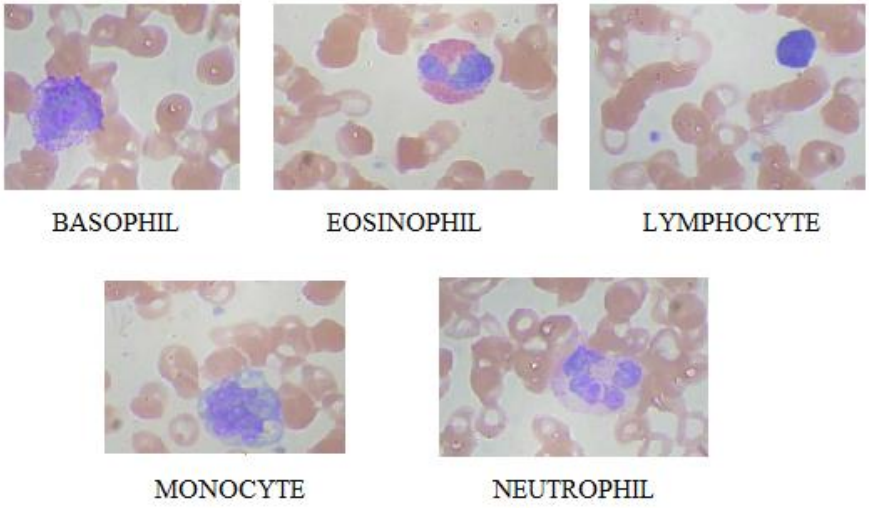

Fig 3: Input WBC Images

3.2 Preprocessing

This step becomes very essential in medical imaging as every detail present in the image is very vital for further processing. Different laboratories and medical practitioners may use different lighting conditions and equipment and follow different protocols to obtain the blood smear images [12]. Hence it is essential to preprocess the images. But it is also important to ensure that edges and data bearing surfaces are not lost. While there are many techniques available for preprocessing, the proposed system chooses two techniques namely filtering and contrast enhancement.

It uses bilateral filter, which is a nonlinear type of filter that produces a smoothened effect by using spatial information. It also inherently reduces noise and preserves edges, thus making it very suitable for medical imaging [13]. It uses pixel values from the neighborhood and averages each pixel value based on the Gaussian distribution. The only disadvantage with bilateral filter is that, sometimes it gives rise to Staircase effect and introduces false edges. It also possesses high computational cost. The formula for bilateral filter is given in Equation 1.

$$BF[I] = \frac{1}{W_P}\sum_{q\epsilon S} G_{\sigma_s}(||p-q||)G_{\sigma_r}(|I_P - I_q|)\, I_q \qquad (1)$$

where Wp stands for factor of normalization, p and q represent the pixel coordinates, G_{σ_s} is the space kernel and G_{σ_r} is the range kernel.

In order to produce a better visual quality of images for satisfactory purpose contrast enhancement is used here. CLAHE algorithm is applied to enhance the contrast of the input images [14]. It is nothing but an advanced form of Adaptive Histogram Equalization (AHE). The main purpose of CLAHE is to improve the contrast of the image and prevent contrast amplifications. AHE is also similar to CLAHE, but it amplifies noise when improving the contrast. In order to overcome this issue of AHE, CLAHE algorithm was introduced which limits contrast enhancement. It has two important parameters called clip limit and tile grid size. Clip limit shows the threshold value that has been set for contrast. If not set explicitly, the default value of clip limit is 40. The next parameter, tile grid size indicates the number of tiles into which the image has to be divided. The default tile grid size is 8*8.

The working idea of CLAHE is to compute many histograms and distribute contrast values according to them. Edges are automatically enhanced in this process. The input image is divided into tiles and histograms are calculated for each tile. The computed histograms are equalized using clip limit parameter. The values of histogram which are higher than clip limit are given to others. The cumulative distribution function is then calculated and finally the divided tiles are merged together. Figure 4 presents the process of CLAHE. The algorithmic steps for CLAHE is mentioned below.

Algorithm for CLAHE

Step 1: Get values of clip limit and tile grid size.

Step 2: Split input image into number of tiles based on tile grid size.

Step 3: Assess histogram of each tile.

Step 4: Calculate the excess bin values of each histogram using clip limit.

Step 5: Distribute excess values to other tiles.

Step 6: Calculate Cumulative Distribution Function (CDF)

Step 7: Perform scaling and mapping operations.

Step 8: Merge tiles using bilinear interpolation.

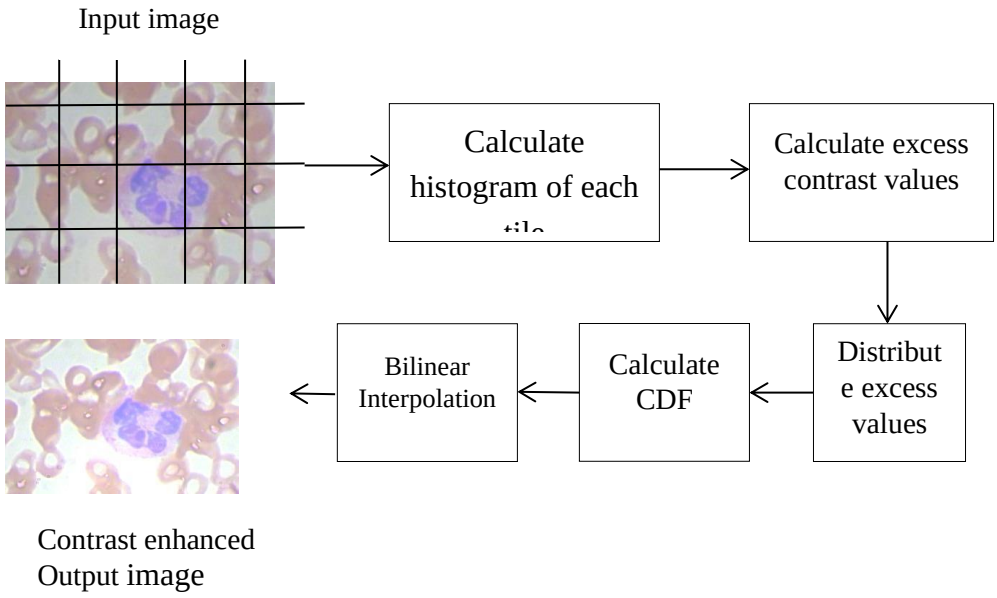

Fig 4: CLAHE Working Process

3.3 Image Segmentation

The required WBCs needs to be extracted from the background of the blood smear. This is achieved through segmentation. After preprocessing, the images are next segmented using UNet algorithm. It is a variant of CNN that was introduced particularly for processing medical images [15]. It is very suitable for image segmentation and is also capable of locating the abnormal regions in the image. Its architecture has a U shape consisting of two parts(contraction and expansion) and hence has been named so. Both parts are symmetric in nature. The contracting path has two convolutional operations followed by Max pooling layer. This process is repeated twice in the path. The expanding path contains transposed convolutional operations and concatenations. It brings back the image to its original size. It acts like a feed forward network where input from previous layers are used by consecutive layers. It is being extensively applied because of its speed and simple architectural design. Figure 5 shows the architecture of UNet.

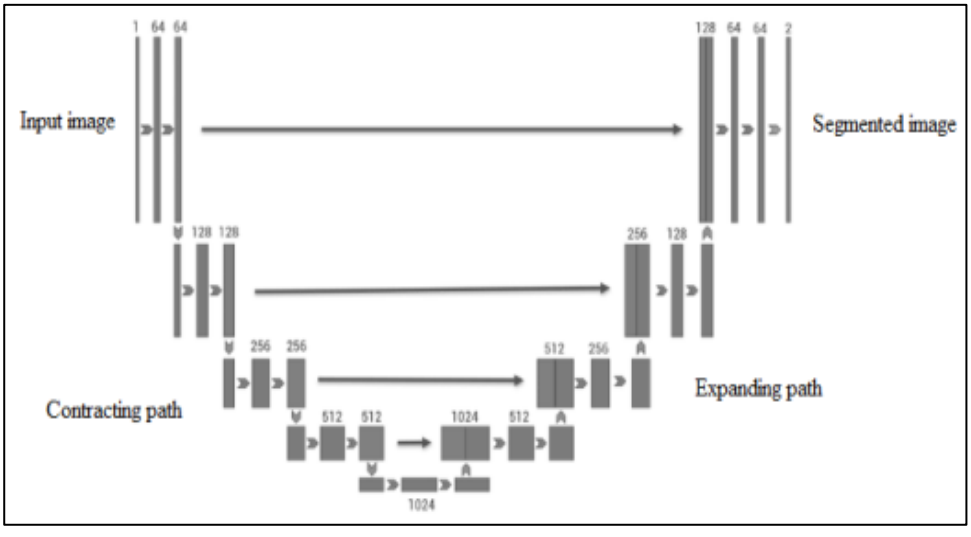

Fig 5: UNet Architecture

3.4 Feature extraction

Once the image has been segmented, relevant features are extracted using CapsuleNet. It preserves hierarchical features very well and hence finds a good place in digital medical image field. It performs better than CNN as CNN fails to record the positional properties such as orientation and relations among features. But CapsuleNet overcomes this problem and captures all the above said information. Hence it is believed to be very promising as a feature extractor as medical classification requires the highest possible accuracy. Our proposed system chooses to use CapsuleNet as the feature extractor which captures convolutional features. It contains a bunch of capsules, where capsules are nothing but a collection of neurons [16].

The output from CapsuleNet is also a vector. It does not make use of soft Max pooling, instead it uses routing by agreement protocol where the output of one capsule routes to another capsule based on the decision of the capsule. Capsules are independent in nature and since they agree with each other with the decision, the accuracy achieved could be really high. Capsules are interconnected where the output from lower capsules are used by higher order capsules. Due to pooling avoidance, it greatly escapes from any loss of features. It also saves time. It has good generalization power and addresses the Picasso problem effectively. It is already portraying superior results and hence can be expected to revolutionize the medical field in future. Figure 6 best describes the working model of Capsule Net.

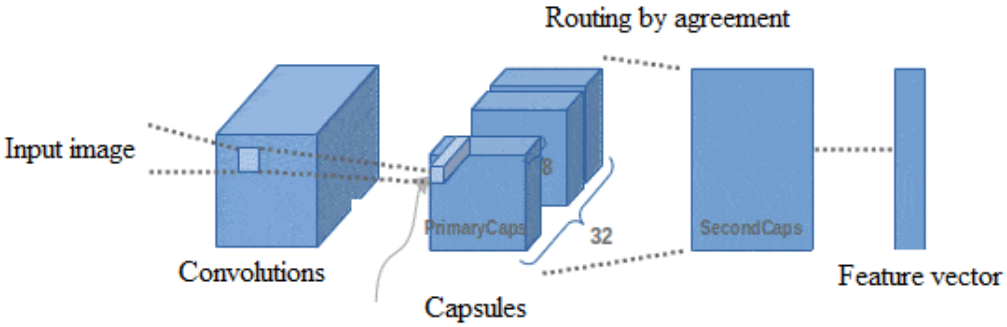

Fig 6: Capsule Net architecture

3.5 Classification

The proposed system uses a state-of-the-art classifier known as the Stacked Sparse Autoencoder (SSAE) along with Mayfly optimization algorithm. Auto encoders are unsupervised deep learners that uses back propagation technique [17]. The ultimate aim of an auto encoder is to compress the size of the data by transforming the input from one form to another better form. Auto encoder organization is depicted in Figure 7 below. The process for the coding and decoding are shown up in equations (2) and (3) below.

$$h = \sigma(W_x + b) \quad (2)$$

$$x^{\wedge} = \sigma(W' \ \ h' + b') (3)$$

where x represents the input, h stands for the data from hidden layer and x^ is the recreated input. W stands for weighted matrix and b is the bias value.

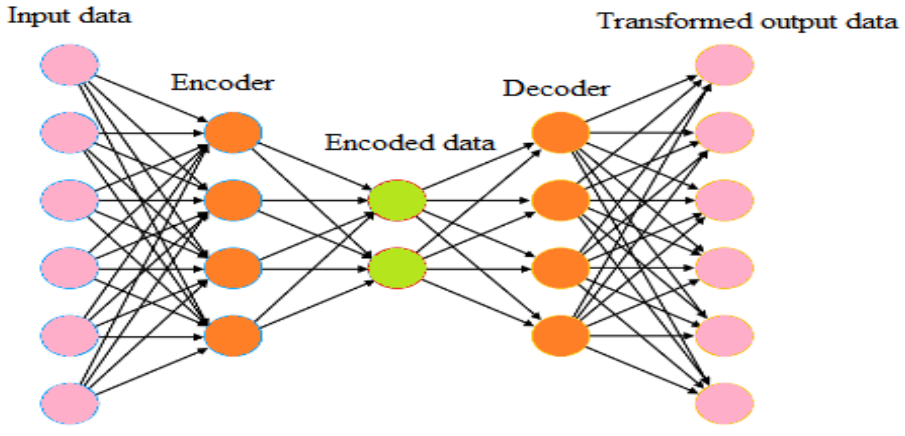

Fig 7: Auto encoder architecture

There are many varieties of auto encoders available such as convolutional autoencoders, sparse auto encoders, zero biased auto encoders, denoising and contractor auto encoders [18]. Among these sparse auto encoders are the most efficient ones. It adds asperity constraint to the auto encoder and restricts the number of codes for reproduction. Sparsity is nothing but a limitation being imposed on the underlying system. It is a fully connected network model that uses a bottom-up approach and is suitable for high level classification of medical images. It is similar to auto encoders in workstyle that compresses data and contains a coder and decoder part. The correlation among the input features are also learned during the encoding process which is immensely helpful in augmenting the accuracy obtained. Finally, it can also be used for active learning of features. It can also extract data from hidden layers.

Because of high structural similarity between the WBC cell types, we are in need of a high result yielding classifier. Auto encoders are best suited for representative learning also. Stacked Sparse auto encoder is a pile up of sparse auto encoders that are placed one after the other and a SoftMax classifier is used at the end of the stack [19]. Figure 8 shows the setup of SSAE working model.

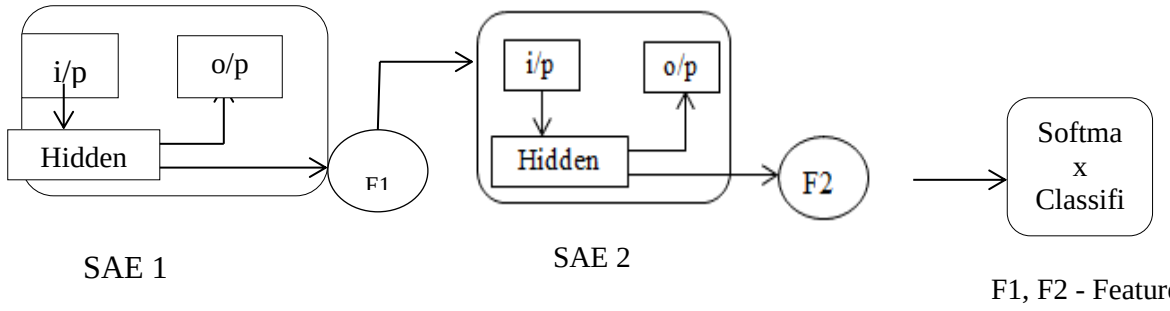

Fig 8: SSAE Assembly

SSAE yields better accuracy when compared to others because it handpicks the most relevant features rather than dealing with the entire feature vector set. The three main steps involved in stacked sparse auto encoders are to train the first sparse auto encoder and get learned data. Use the learned data from Auto Encoder 1 and pass it as input to the next one. SoftMax classifier is used for classification at the end.

3.5.1 Mayfly optimization Algorithm

In order to optimize the solutions provided by Stacked Sparse Auto encoder classifier, the proposed system employs an optimization algorithm called the Mayfly optimization algorithm. Optimization algorithms are generally used to improve performance and reduce losses using hyperparameters and a loss function. They fine tune the results obtained by the classifier to attain peak accuracy. Optimization algorithms can be divided into two types, one that gives a single solution and the other gives a set of solutions [20]. Both of these are meta heuristic and non-numeric in nature.

Optimization algorithms yielding many solutions are called as population-based algorithms since it gives a set of solutions which are updated iteratively in order to find the best optimal solution. They can be further divided into swarm intelligence and evolutionary algorithms. Evolutionary algorithm examples are Genetic Algorithm and Differential Evolution algorithm, both of which are based on the Darwinian theory of evolution. Each of these optimization algorithms have their own merits and demerits, but combining the advantage of both these algorithms is the specialty of Mayfly optimization algorithm.

Mayfly optimization algorithm is believed to have been named after Mayflies (A kind of fly that appears in the month of May in United Kingdom). It is a combination of Swarm optimization technique and evolutionary algorithm [21]. Mayflies are insects that belong to Paleoptera that are known popularly for their mating and flighting behavior. They use techniques like crossover mutation, random walk and nuptial dance to attract their mates. The aim of a mayfly is to reproduce healthier and long-lasting young ones. The Figure 9 below shows the classification of optimization algorithms.

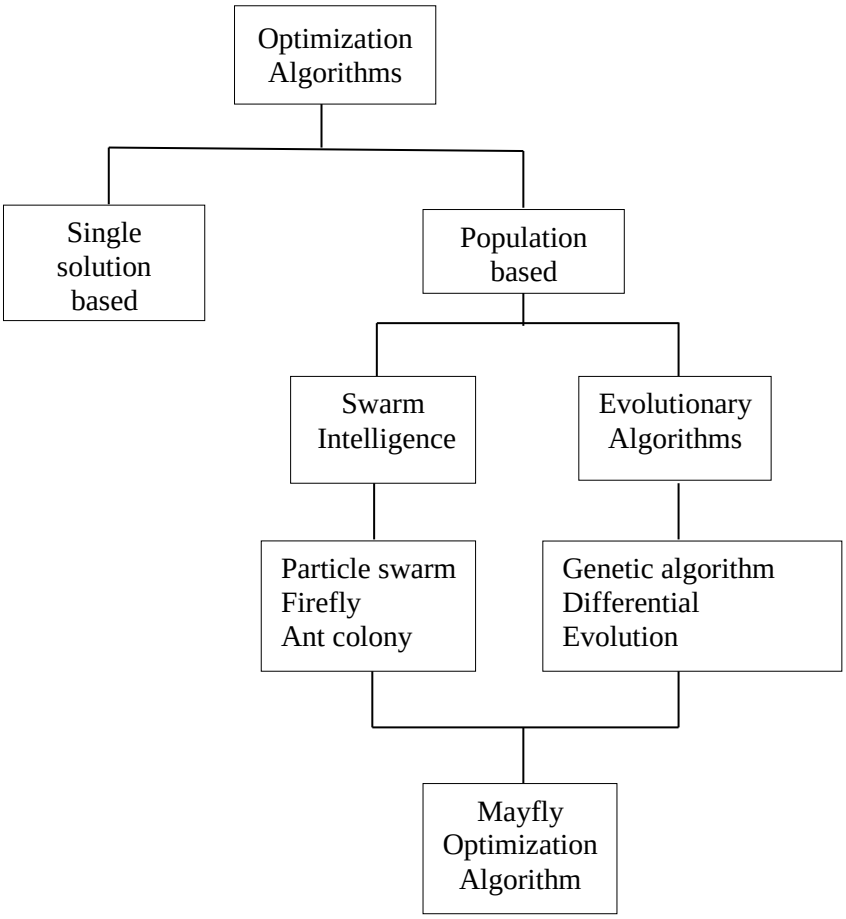

Fig 9: Optimization algorithm classification

It is believed that this aim of Mayflies could have been the inspiration for the development of Mayfly optimization algorithm. Though it was recently proposed, it has carved a prominent place for itself in many fields of science and technology. It has gained limelight as it is quite simple to use and does not involve any complex mathematical operations. The biggest advantage of mayfly optimization algorithm is that it does not get caught in local optimums. It performs way better than Particle Swarm Optimization, Differential Evolution and Genetic Algorithms. The only disadvantage possessed by Mayfly optimization algorithm is the problem of parameter tuning. The algorithm of Mayfly optimization is given in detail below.

Mayfly Optimization Algorithm

Step 1: *Initialize values of male and female populations and velocity values.*

Step 2: *Findviable solutions.*

Step 3: *Evaluate the best solution.*

Step 4: *Do while*

Update velocities of male and female.

Calculate the solution rank mayflies.

Mate mayflies.

Find the offspring

Separate the offspring

Replace the solution with optimum solution.

Update the solution.

4. Results and Discussion

The outcomes of proposed system execution and the statistical analysis of performance are discussed here. The proposed model utilized benchmark BCCD White Blood Cell (WBC) dataset which is available in Kaggle repository. The dataset includes 1460 images consisting of five WBC types as discussed earlier. Figure 10 shows output from preprocessing stage that was done using bilateral filter and CLAHE algorithm.

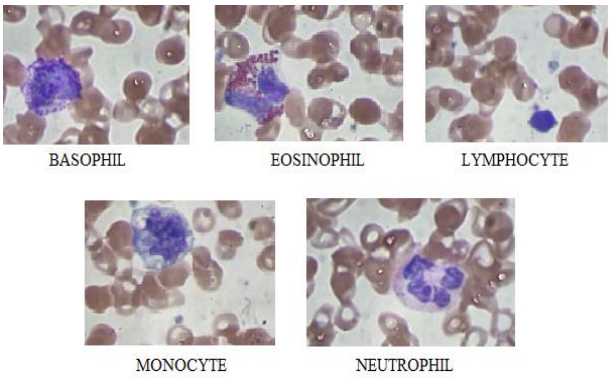

Fig 10: Preprocessed images

The output of segmented WBC images using UNET architecture is depicted in Figure 11.

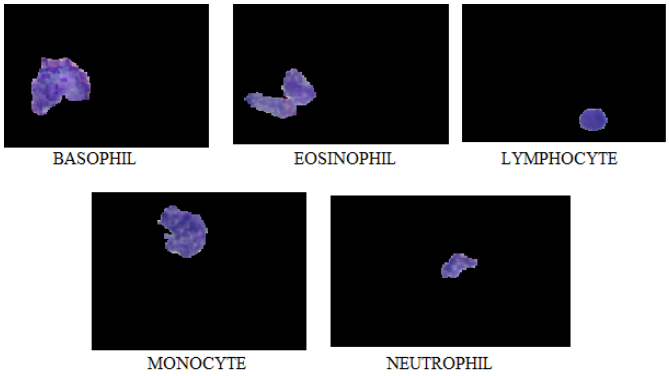

Fig 11: Segmented WBC images

Figure 12 displays the features that have been extracted using CapsNet

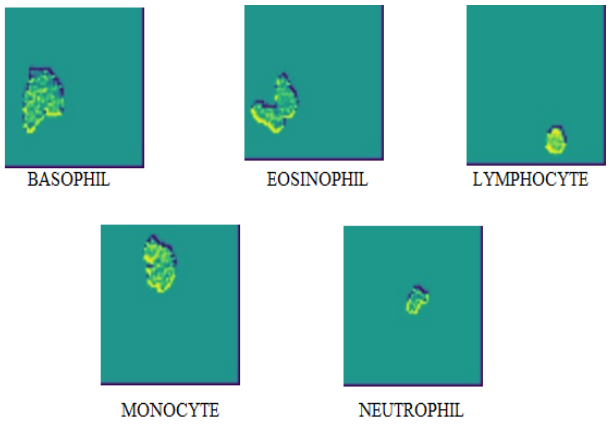

Fig 12: Extracted WBC features

4.1 Confusion Matrix

A confusion matrix gives a clear indication of classification performance [22]. It contains True Positive

(TP), True Negative (TN), False Positive (FP) and False Negative (FN) scores of classifications. The resulting confusion matrices of both training and testing phases are depicted in Figure 13 below.

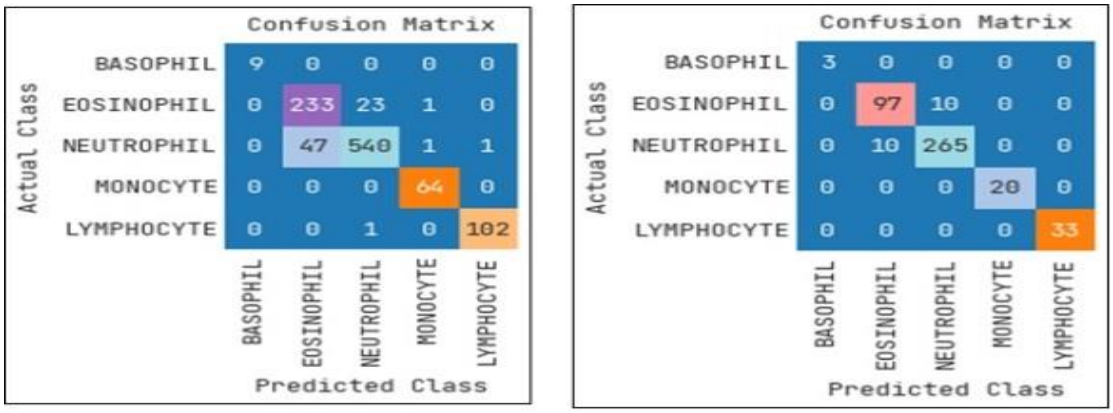

Fig 13: Confusion Matrix of WBC Classification

4.2 Performance Indices

From the values obtained in confusion matrix, we can easily arrive at various indices of performance such as accuracy, precision, Recall, specificity, F1 Score and ROC using the below equations (3), (4), (5) and (6) [23].

$$\text{Accuracy} = \frac{TP+TN}{TP+FP+TN+FN} \quad (3)$$

$$\text{Precision} = \frac{TP}{TP+FP} \quad (4)$$

$$\text{Recall} = \frac{TP}{TP+FN} \quad (5)$$

$$F_1\ score = \frac{2*Precision*Recall}{Precision+Recall} \quad (6)$$

Table 1 shows the result of training classification performance of the proposed system.

Table 1: Training performance metrics

S.NO.	Metrics	Values
1.	Accuracy	0.9694
2.	Precision	0.9499
3.	Recall	0.9627
4.	Specificity	0.976
5.	F1	0.9559
6.	ROC	0.9908

Figure 14 shows the graphical representation of training performance achieved by the stacked sparse auto encoder classifier along with mayfly optimization algorithm.

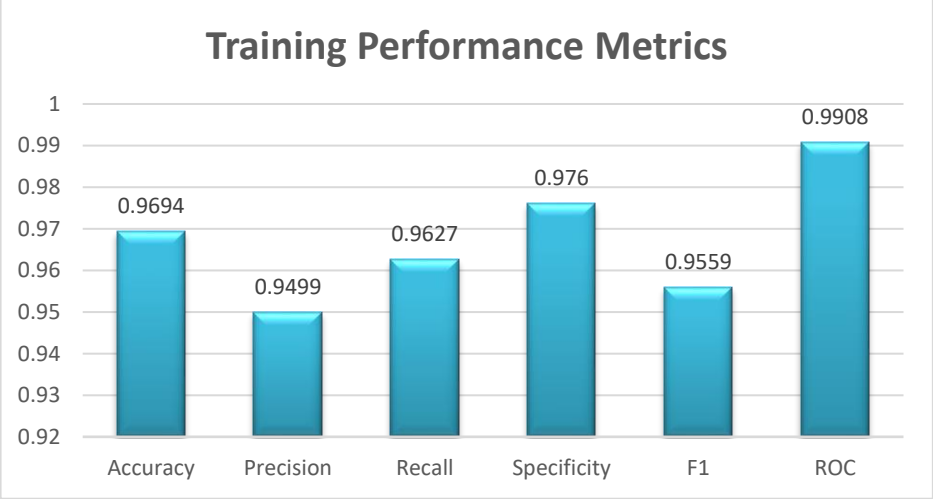

Fig 14: Training performance illustration

Table 2 shows the result of testing classification metrics.

Table 2: Testing performance metrics

S.NO.	Metrics	Values
1.	Accuracy	0.9779
2.	Precision	0.9764
3.	Recall	0.9757
4.	Specificity	0.9817
5.	F1	0.974
6.	ROC	0.992

Figure 15 shows the graphical representation of testing performance achieved by the proposed classifier.

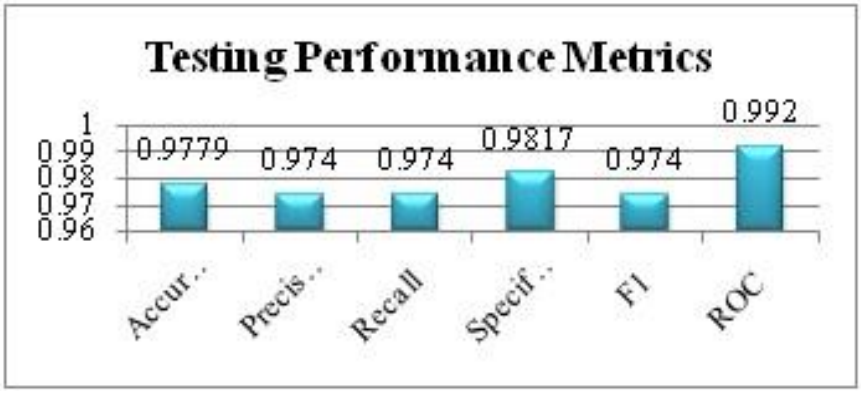

Figure 15: Testing performance illustration

4.3 Analysis of performance curves

Receiver Operating Characteristics (ROC) curve generated by the proposed classifier is presented in Figure 16. For each type of WBC, Area Under the Curve (AUC) score has been calculated. It is said that if the score is higher than 0.9, then the performance of the classifier is considered to be excellent [24]. From Figure 16, we can observe that all the five types of WBC have attained values above 0.99 which indicates the excellent performance of the proposed model.

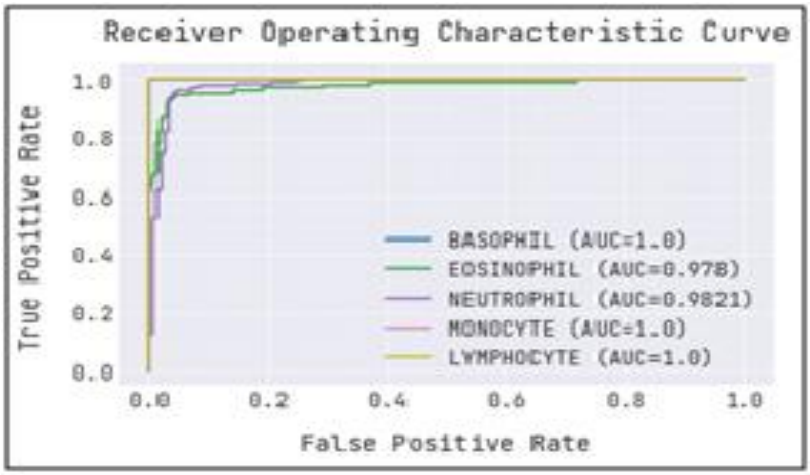

Fig 16: ROC Curve

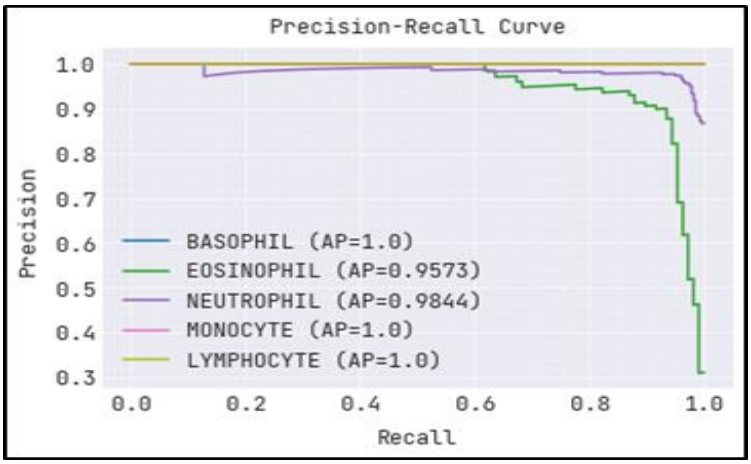

Fig 17: Precision - Recall Curve

Similarly Figure 17 shows the precision recall curve. The average precision (AP) value calculated for all the types of WBC is above 0.95. This indicates how precisely the proposed classifier works.

4.4 Comparative Performance Analysis

Table 3 displays the comparative analysis between the proposed model and SVM, DenseNet, Res-DenseNet, Inceptionv3, ResNet and CNN models. [25].

Table 3: Comparative Performance Analysis

S.No	Algorithms	Metrics			
		Accuracy	Precision	Recall	F1-Score
1	Inception v3	62.8	67.71	62.79	63.52
2	ResNet	84.71	87.06	84.73	85.15
3	CNN	86.77	89.28	86.79	87.1
4	DenseNet	87.14	89.36	87.16	87.48
5	Res-DenseNet	88.44	90.84	88.45	88.73
6	SVM	94.7	98.07	91.91	94.67
7.	Proposed model	97.79	97.64	97.57	97.4

Figure 18 depicts the precision and Recall comparative analysis of the proposed system with existing algorithms. The proposed model is seen to possess better precision and Recall scores than all other existing algorithms which proves it to be the best.

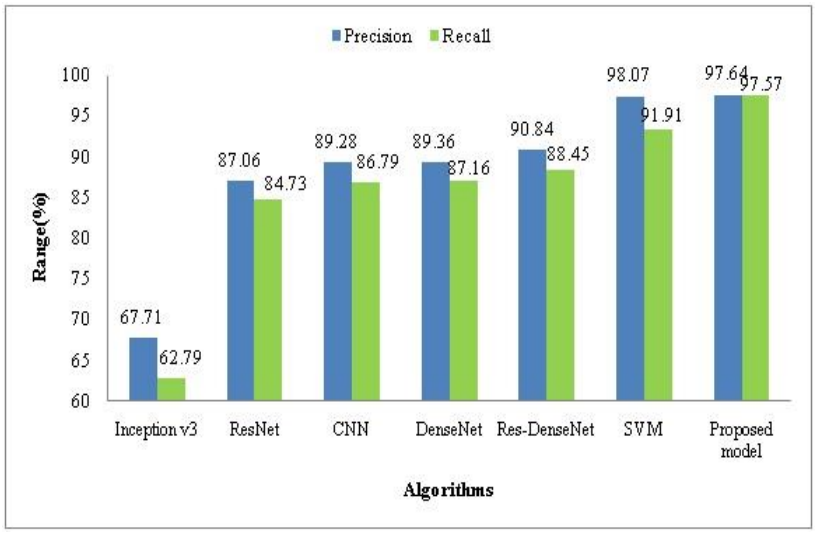

Fig 18: Precision-Recall Comparative Analysis

Figure 19 illustrates the comparative analysis of Accuracy of the proposed system with existing algorithms. It is very clear from the figure that the proposed model performs superiorly than all other existing algorithms and there is a hike in accuracy of 3% than the SVM classifier.

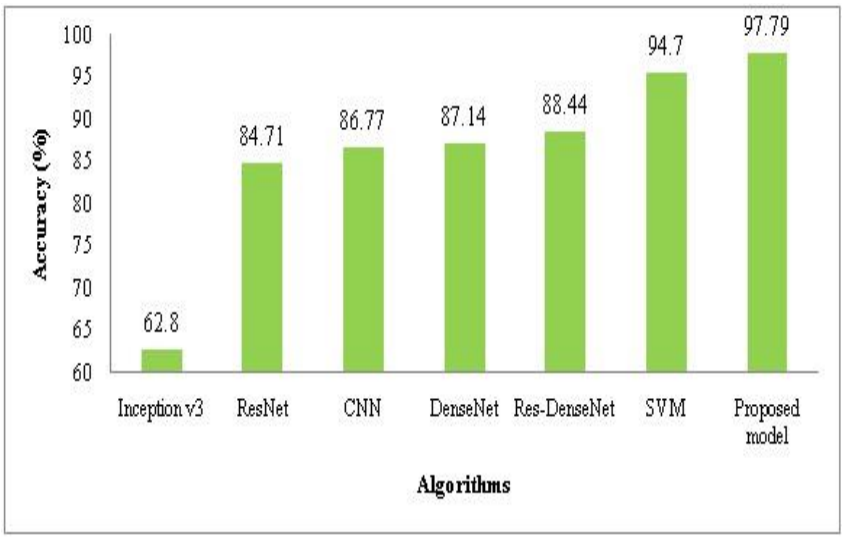

Fig 19: Comparative Analysis of Accuracy

Figure 20 shows the comparative analysis of F1 Score of the proposed system with existing algorithms. F1-Score of the proposed model is better and higher than all other existing algorithms. The attained F1-Score of proposed model is approximately 2% higher than SVM, 9% better than the Res-DenseNet model, 10% greater than the DenseNet and CNN models, 12% higher than the ResNet model and 34% better than Inception v3 model.

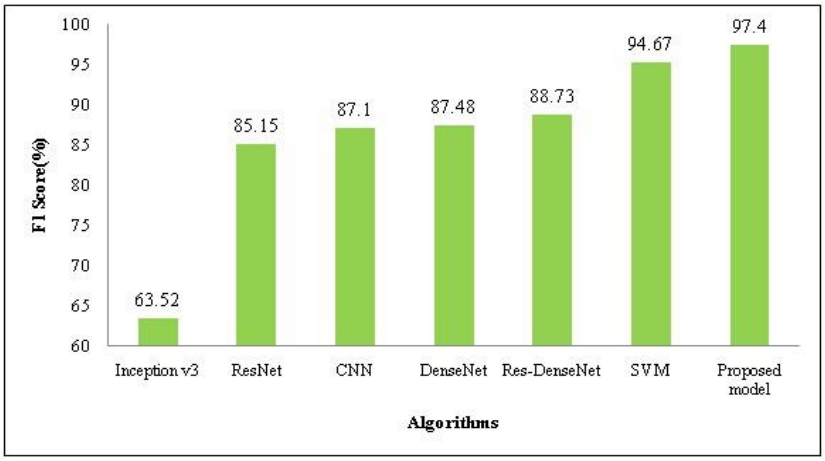

Fig 20: F1-Score Comparative Analysis

5. Conclusion

Artificial intelligence supported medical diagnosis is gaining popularity in recent times. This is especially helpful for medical practitioners in times of health emergency, pandemic crisis and when global disease threats are encountered. An automated deep learning-based WBC classification system is proposed here which makes best use of emerging techniques such as Bilateral Filter, Contrast Limited Adaptive Histogram Equalization CapsuleNet, Unet, Stacked Sparse Auto Encoder and Mayfly Optimization algorithm and achieves an excellent accuracy of 98.35%. From the results we come to know that our proposed deep learning-based system performs way better than very many existing techniques such asSVM, DenseNet, Inceptionv3, ResNet, CNN etc. Futuristic extension of the proposed work could possibly classify more intense subtypes of WBC based on the type of cell lineage.

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