

WHITE BLOOD CELL CLASSIFICATION USING SERIAL DEEP FEATURE FUSION AND GENETIC ALGORITHM FEATURE SELECTION

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Abstract

This study reports a white blood cell (WBC) classification framework that combines deep feature extraction, serial feature fusion, genetic algorithm (GA)-based feature selection, and support vector machine (SVM) classification. A public blood-cell dataset comprising 12,500 enhanced JPEG images with CSV cell-type labels for Eosinophil, Lymphocyte, Monocyte, and Neutrophil was used. AlexNet, ResNet-101, and DarkNet-53 extracted 4096, 1024, and 1024 features, respectively. Serial concatenation produced a 6144-feature representation, which was reduced using a GA with Roulette Wheel Selection and a crossover rate of 0.5. Six SVM variants were evaluated using the reported five-fold validation procedure. Three selected-feature configurations were examined: 500, 2500, and 3130 features. The strongest detailed result was reported for Cubic SVM with 3130 features: 98.9% accuracy, 0.99 precision, 0.9925 recall, and 0.99 F1-score. Under the reported configuration, the 3130-feature setting produced the highest performance among the reported experiment rows.

1. INTRODUCTION

White blood cells (WBCs) are a major component of peripheral-blood analysis. This study considers four WBC classes in the reported

dataset: Eosinophil, Lymphocyte, Monocyte, and Neutrophil. Reliable image-level classification of these classes remains relevant to the automated analysis of blood-smear imagery.

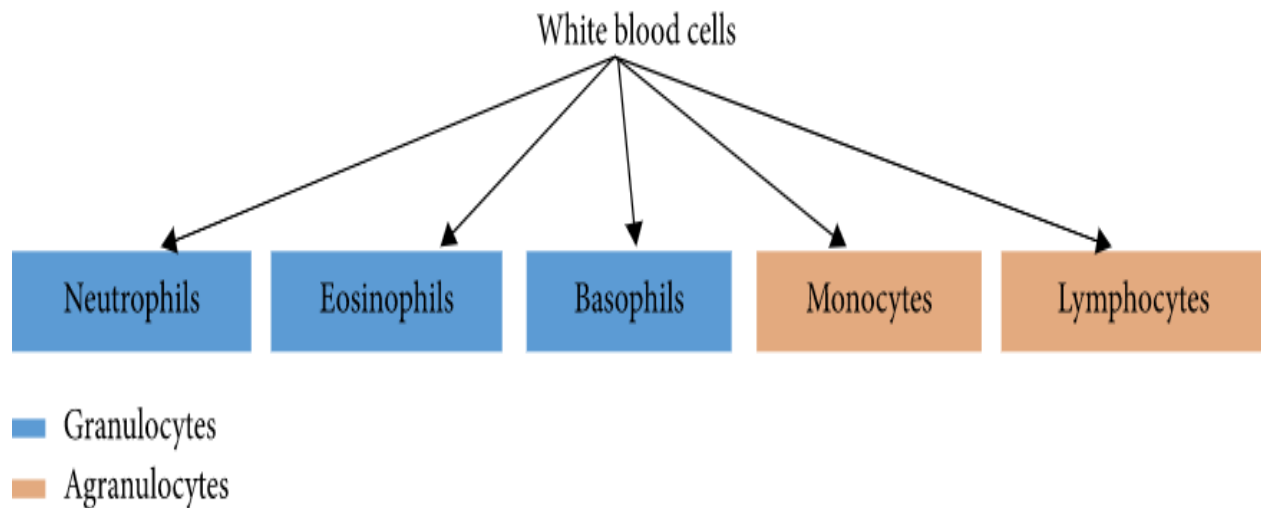


Figure 1. Taxonomy of white blood cells.

Image-level WBC classification is complicated by visual similarity between cell types, as well as staining variation, illumination differences, blur, and cell overlap. These sources of variation affect the representation of cells in microscopy images and motivate the use of feature representations that can accommodate heterogeneous visual patterns.

Earlier WBC studies commonly combined preprocessing and segmentation with handcrafted descriptors and conventional classifiers. CNN and transfer-learning methods learn image representations directly from data, but their reported performance still depends on the dataset, class definition, preprocessing, and validation design [1–5].

Recent WBC studies have also examined multi-CNN feature fusion, evolutionary feature selection, attention-enhanced CNNs, and transformer-oriented comparisons [6–11]. Their reported values require separate interpretation because the datasets and experimental protocols differ.

Combining outputs from multiple feature extractors can produce a high-dimensional representation. Studies of feature fusion and evolutionary selection support evaluating feature reduction after fusion, but they do not establish a universally best pipeline [6–8,10].

The framework uses AlexNet, ResNet-101, and DarkNet-53 to generate three feature vectors. Serial feature fusion combines the vectors, GA-assisted selection reduces the fused representation, and six SVM variants perform classification. The contributions are (i) deep feature extraction with the three CNNs, (ii) serial fusion of their feature vectors, (iii) GA-assisted feature selection or reduction, (iv) evaluation of six SVM variants, and (v) analysis across 500, 2500, and 3130 selected features. The contribution is the integrated configuration; the individual methods are established.

Objective

This study evaluates an integrated WBC classification framework that combines features extracted from AlexNet, ResNet-101, and DarkNet-53 through serial feature fusion, applies GA-assisted feature selection, and compares SVM classification across three selected-feature configurations.

Novelty Statement

The study integrates AlexNet, ResNet-101, and DarkNet-53 feature representations through serial fusion, then applies GA-assisted feature selection and compares six SVM variants across three selected-feature configurations. The contribution is this specific experimental configuration.

2. Related Work

2.1 Conventional and Handcrafted Approaches

Conventional WBC analysis typically combined image preprocessing and segmentation with handcrafted color, shape, texture, or morphological descriptors and a conventional classifier. These approaches established the importance of cell appearance and image preparation, but their performance depended on manually designed representations and task-specific processing choices.

Detection and segmentation remain relevant when an analysis requires cell localization or boundary delineation [4,12]. The tasks are methodologically different from the isolated four-class classification experiment that is the subject of this examination. These give context to the analysis of blood cells in images, but not a direct benchmark.

2.2 CNN and Transfer-Learning Approaches

CNN and transfer-learning methods have emerged as common techniques in the research of WBC classification. Tamang et al. performed comparison of pretrained CNNs on BCCD [1] and Saidani et al. on four classes of blood cells [2] employed preprocessing, CNN and transfer-learning. Other studies examined train-independent evaluation, attention-enhanced CNNs, and transformer-oriented comparisons [3,5]. Each result is valid for a certain experimental set-up, as the data and the validation method are different.

2.3 Deep Feature Extraction and Classical Classifiers

Another set of research works employs CNNs to extract features and then feeds this extracted feature set to a traditional classifier that is used to classify the vectors generated by the CNN. This design classifies the classification step explicitly, and can also incorporate feature selection. Ahmad et al. integrated deep features with quantum inspired evolutionary selection for the

classification of leukocytes [8]. This hybrid framework is discussed in this section, along with a report of all the six variants of SVM including the results below the best row.

2.4 Feature Fusion and Multi-Model Approaches

Feature fusion is the merging of representations from more than one model/class. Parayil and Aravindh adopted Transfer learning feature fusion [6] and Dong combined Hand-crafted and Deep Representations [7] and Ullah et al., reported Multi-CNN fusion with Fuzzy logic [10]. These studies are examples of an established line of multi-model fusion research. The framework examined here uses a configuration-specific combination of AlexNet, ResNet-101, and DarkNet-53.

2.5 Feature Selection and Optimization Approaches

Fusion can expand the dimensionality of a representation, creating a role for feature selection. Evolutionary and related optimization methods have been applied to deep features in leukocyte research [8]. In this framework, the reported GA procedure follows serial fusion. Table 1 compares earlier and recent studies; the values reflect their respective study settings and do not form a direct ranking.

2.6 Current Positioning of the Present Study

The referenced research in the field of WBC includes multi-model feature fusion [8], evolutionary feature selection [9], attention-enhanced CNNs [10] and transformer-oriented approaches [11]. In this method three popular CNN based feature extractors are integrated, serial feature fusion and GA based reduction are used and SVM is used for classification. This result was reported for this dataset and protocol, and may not correspond to the results of studies that utilize different image collections, class counts, augmentation procedures, metrics or despite variations in validation procedures.

Table 1. Comparison with recent and earlier white blood cell classification studies.

Ref	Year	Dataset	Method	Classes	Reported result	Notes on comparability
Recent studies						

[11]	2026	PBC, LDWBC, Raabin-WBC	ConvNeXt-Mamba attention fusion	Dataset-specific	99.32%, 98.18%, 99.03%	NO: different modern architecture and datasets
[10]	2025	Kaggle Blood Cell Images	DenseNet121/MobileNetV2/ResNet101 fusion + fuzzy EDAS	4	99.79% precision	PARTIALLY: multi-CNN fusion; metric/protocol differ
[3]	2024	Combined four datasets	CNN classification and segmentation	5	98.03% balanced accuracy; 97.27% independent test	NO: combined datasets and separate evaluation
[2]	2024	Four-class blood-cell dataset	Preprocessing + CNN/transfer learning	4	99.86%	PARTIALLY: four classes; protocol differs
[8]	2023	Public 5000-image WBC dataset	Deep features + quantum-inspired evolutionary selection	5	~99%	PARTIALLY: feature selection but different task and optimizer
[6]	2022	WBC image dataset (reported by authors)	DenseNet201/VGG16 transfer-learning feature fusion	WBC task	89.75%	NO: different dataset and end-to-end CNN classifier
Earlier studies						
[22]	2021	Not reported	GA-enhanced deep CNN	Not reported	93%	Historical context
[21]	2020	Not reported	Swarm-optimized deep features	Not reported	96.11%	Historical context
[20]	2019	Not reported	Machine-learning algorithms	Not reported	92.2%	Historical context
[19]	2018	Not reported	CNN optimized through GA	Not reported	91%	Historical context

3. Materials and Methods

3.1 Dataset

The study employed a publicly accessible dataset from Paul Moore consisting of 125×10^3 enhanced blood-cell JPEG images labeled with the cell-type in CSV format [13]. There are

between 3000 and 4000 images per class, each in the Eosinophil, Lymphocyte, Monocyte and Neutrophil classes. In addition, another set of 410 original images of subtype labels with bounding box information is described in the dataset but not used in the 4-class experiment.

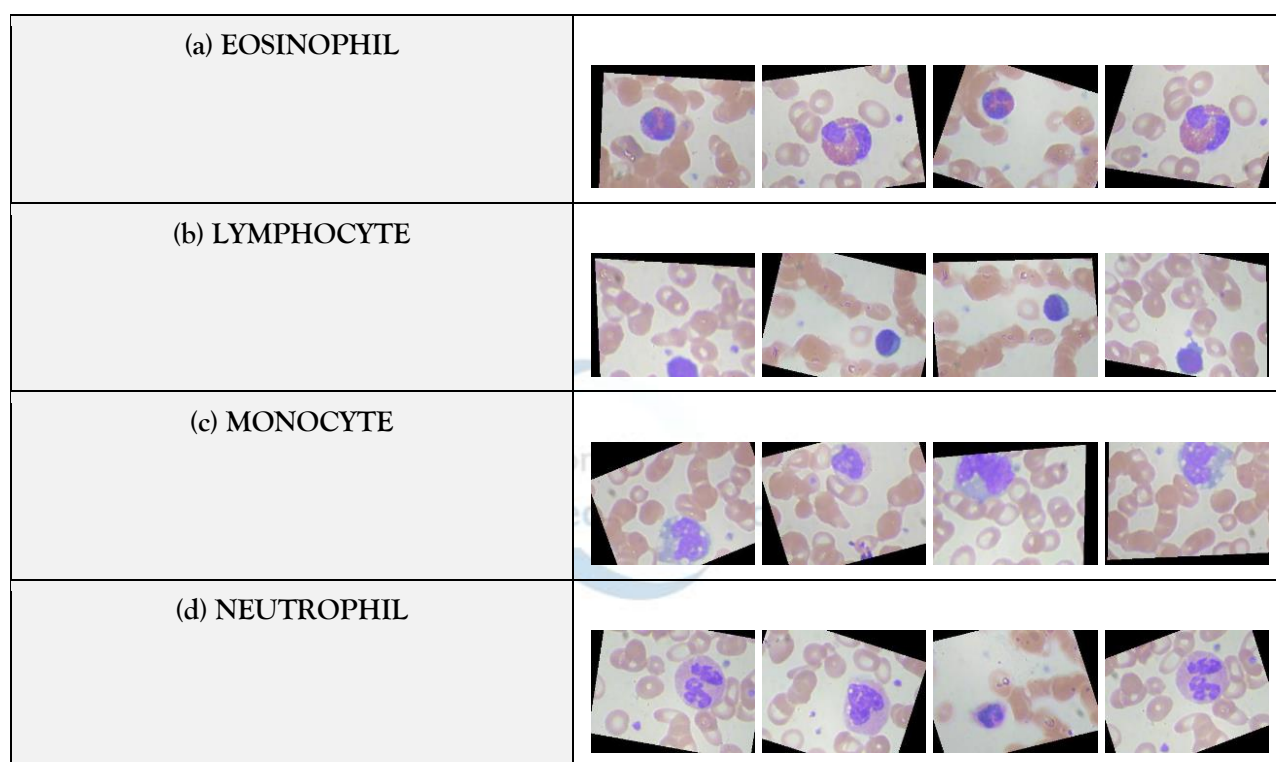


Figure 2. Representative images of the four WBC classes in the dataset.

Representative images of the four WBC classes used in the study.

3.2 Proposed Framework

The proposed framework consists of three CNN feature extractors, namely, AlexNet, ResNet-101, and DarkNet-53, that process the dataset. They are fused serially followed by feature selection

and dimensionality reduction with GA and finally classified with different variants of SVM. This fixed processing sequence is summarised in figure 3.

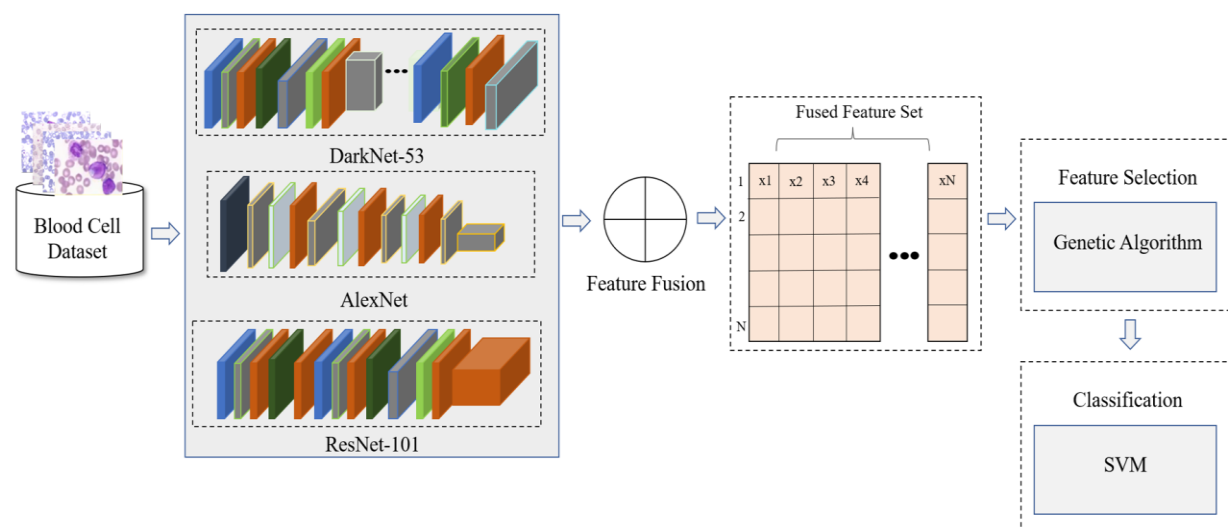


Figure 3. Overview of the proposed serial deep-feature fusion framework.

3.3 Deep Feature Extraction

3.3.1 AlexNet

AlexNet was used to extract deep features from the dataset [14]. Input images of size (240, 320, 3) were converted to (227, 227, 3). Ninety-six 11 x

11 filters produced a 55 x 55 x 96 representation, and max pooling produced 27 x 27 x 96. A 4096-dimensional feature vector was obtained from fc7.

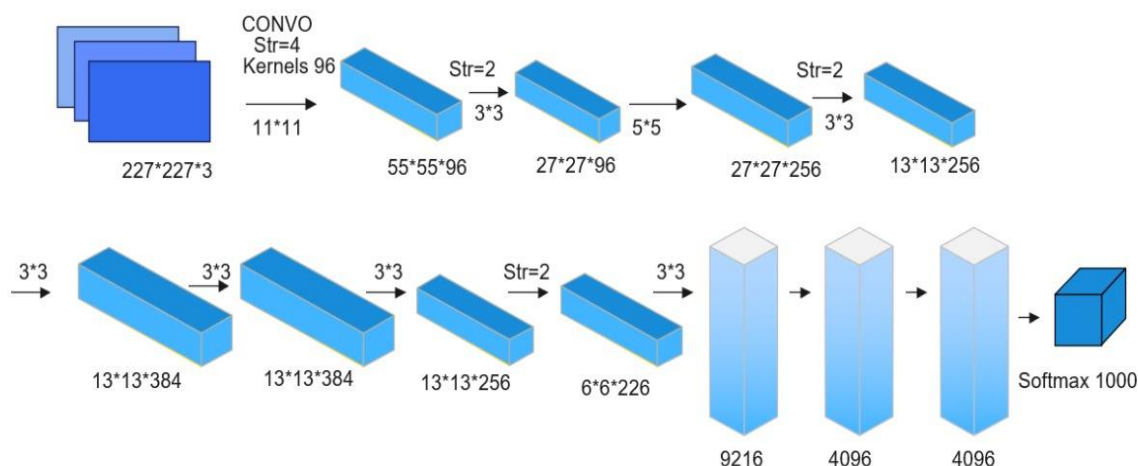


Figure 4. AlexNet architecture used for deep feature extraction.

3.3.2 ResNet-101

ResNet-101 was used as a feature extractor [15] and yielded a 1024-dimensional feature representation. Its residual-learning formulation

is expressed as $y_1 = h(x_1) + F(x_1, W_1)$, where $h(x_1)$ denotes the mapping and $F(x_1, W_1)$ denotes the stacked nonlinear component.

$$y1=h(x1)+F(x1,W1) \quad (3.9)$$

$$x1 + 1 = f(y1) \quad (3.10)$$

Here, F denotes a ReLU activation function and a stacked nonlinear layer. When $f(y1)$ and $h(x1)$ represent identical mappings, the formulation

describes direct signal propagation between units. Applying ResNet-101 to the dataset yielded a 1024-dimensional feature representation. Figure 5 presents the ResNet-101 structural design.

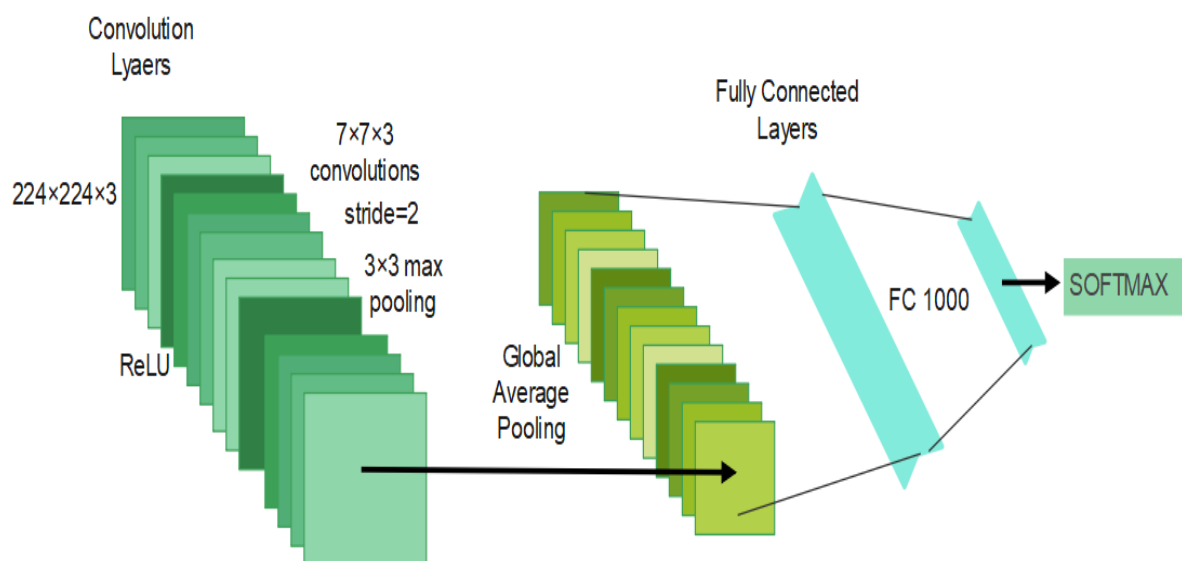


Figure 5. ResNet-101 architecture used for deep feature extraction.

3.3.3 DarkNet-53

DarkNet-53 was used with an input size of 256 x 256 x 3. The network has 53 layers and yields 1024 features from the global-average-pooling layer named avg1. It includes convolutional, residual, average-pooling, fully connected, and softmax stages [16].

$$FV = "V1"&"V2"&"V3 \quad (3.11)$$

3.4 Serial Feature Fusion

Serial feature fusion concatenates the feature vectors obtained from AlexNet (4096), ResNet-101 (1024), and DarkNet-53 (1024), resulting in a 6144-dimensional fused representation. The serial feature-fusion equation is shown below.

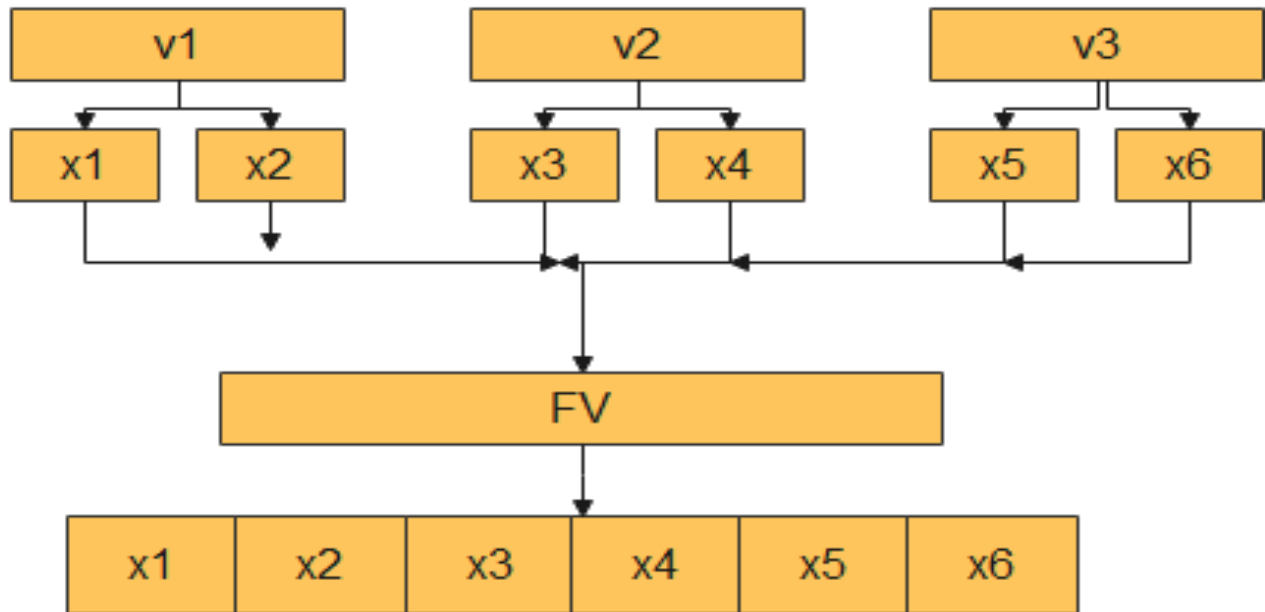


Figure 6. Serial concatenation of the three deep feature vectors.

3.5 Genetic Algorithm Based Feature Selection

A genetic algorithm selects and reduces features from the fused representation [17]. The GA workflow includes initialization, selection, crossover, and mutation, with candidate features chosen according to the stated criteria.

Roulette Wheel Selection determines the parents using the probabilities defined by the equations below. Crossover exchanges genes or bits between two selected parents to generate a new individual, and the reported crossover rate is 0.5. The procedure stops when the predetermined iteration condition is reached or when the fitness function approaches values lower than the optimum solution. Selection is linked to accuracy, and the optimized feature-vector dimension is reported as 681 x 261. Population

size, mutation rate, the exact iteration limit, and the initialization method were not documented.

$$X \frac{x_i}{\sum x_i} \quad (3.12)$$

$$x_i = \exp(-y_1 X \frac{p_a}{q_b}) \quad (3.13)$$

3.6 SVM Classification

The classifier stage evaluates Linear SVM, Quadratic SVM, Cubic SVM, Fine Gaussian SVM, Medium Gaussian SVM, and Coarse Gaussian SVM [18].

3.7 Performance Evaluation Metrics

The evaluation measures are Accuracy, Precision, Recall/Sensitivity, Specificity, F1-score, the confusion matrix, Obs/sec, and Time (s). The metric equations used in the study are reported in Table 2.

Table 2. Performance evaluation metrics used in the study.

Performance Measures	Evaluation
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$
Precision	$\frac{TP}{TP + FP}$
Sensitivity/Recall	$\frac{TP}{TP + FN}$

Specificity	$\frac{TN}{TN + FP}$
F1-score	$\frac{2 \times \text{precision} \times \text{sensitivity}}{\text{precision} + \text{sensitivity}}$

3.8 Experimental Setup

The experiments were conducted in MATLAB R2020b. The study reports five-fold cross-validation together with a 70/30 training-testing split. The confusion matrices contain 2400 samples per class, which is consistent with an 80% subset of approximately 3000 images per class. However, because the original implementation records are no longer available, the exact relationship between the five-fold validation and the reported 70/30 split cannot be reconstructed with certainty. The selected-feature configurations were 500, 2500, and 3130

features. Deep features were obtained using pretrained deep models.

4. Results

4.1 Experiment 1: 500 Features

Experiment 1 uses 500 deep CNN features selected from the serially fused representation. Under the reported validation procedure, accuracy ranges from 31.3% for Cubic SVM to 36.3% for Medium Gaussian SVM in Table 3. Obs/sec and Time (s) also vary across the six classifiers. Figure 7 shows the Medium Gaussian SVM confusion matrix, and Figure 8 gives the training-time values.

Table 3. Results for Experiment 1 (500 fused features).

Classifier	Accuracy	Precision	Recall	F1-score	Obs/sec	Time (s)
Linear SVM	34.8	0.3485	0.34	0.34	8600	249.87
Quadratic SVM	34.1	0.34	0.34	0.3425	340	971.43
Cubic SVM	31.3	0.3125	0.315	0.3125	540	6611.9
Fine Gaussian SVM	33.4	0.3075	0.3325	0.33	310	283.06
Medium Gaussian SVM	36.3	0.3625	0.36	0.36	400	213.54
Coarse Gaussian SVM	33.8	0.3375	0.3475	0.31	380	223.01

Medium Gaussian SVM

True Class	E	739	458	602	601
	L	512	658	655	575
	M	405	474	976	545
	N	454	287	547	1112
		E	L	M	N
		Predicted Class			

Figure 7. Confusion matrix for Experiment 1 (500 features). E, L, M, and N denote Eosinophil, Lymphocyte, Monocyte, and Neutrophil, respectively.

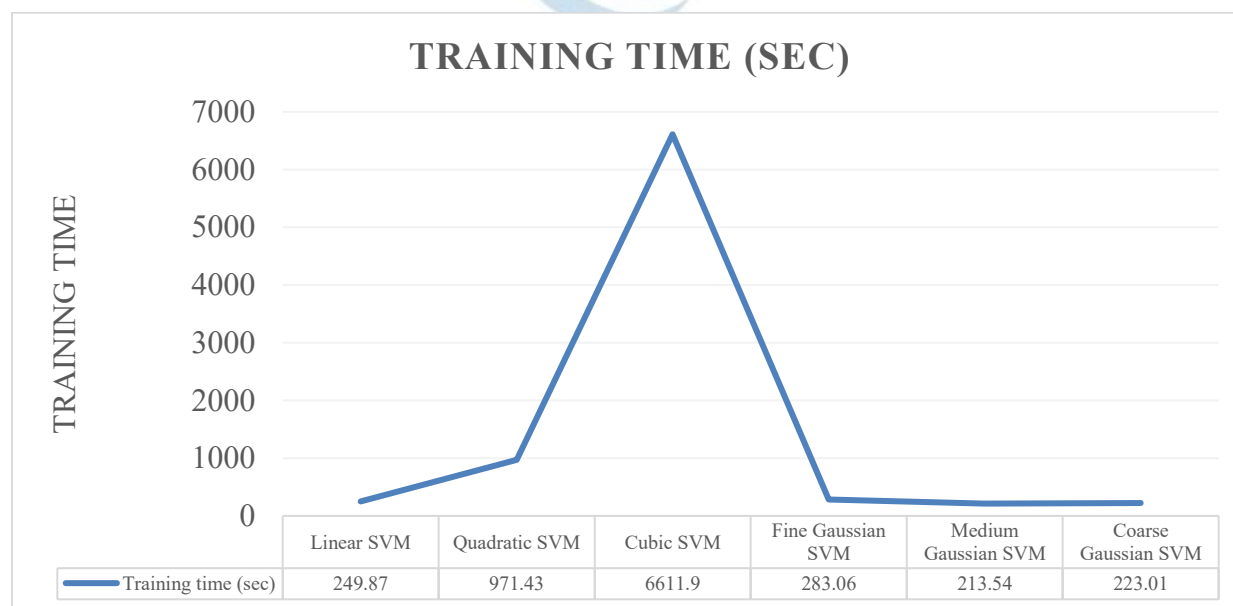


Figure 8. Training time for Experiment 1 (500 features).

4.2 Experiment 2: 2500 Features

Experiment 2 uses 2500 selected features under the reported validation procedure. Table 4 lists the highest accuracy for Medium Gaussian SVM (38.3%), followed by Quadratic SVM (38.0%);

Cubic SVM has the lowest accuracy (34.3%). Figure 9 shows the Medium Gaussian SVM confusion matrix, and Figure 10 gives the training-time values for all six SVM variants.

Table 4. Results for Experiment 2 (2500 fused features).

Classifier	Accuracy	Precision	Recall	F1-score	Obs/sec	Time (s)
Linear SVM	35.2	0.3525	0.35	0.35	2700	976.6
Quadratic SVM	38.0	0.38	0.38	0.3775	34	3627.7
Cubic SVM	34.3	0.3425	0.3425	0.3425	56	4547.3
Fine Gaussian SVM	37.7	0.355	0.375	0.3775	43	1615.7
Medium Gaussian SVM	38.3	0.3825	0.3825	0.38	48	1484.4
Coarse Gaussian SVM	35.1	0.35	0.3575	0.35	44	1576

Medium Gaussian SVM

True Class	E	646	594	545	615
	L	444	986	446	524
	M	387	471	946	596
	N	378	411	509	1102
		E	L	M	N
		Predicted Class			

Figure 9. Confusion matrix for Experiment 2 (2500 features). E, L, M, and N denote Eosinophil, Lymphocyte, Monocyte, and Neutrophil, respectively.

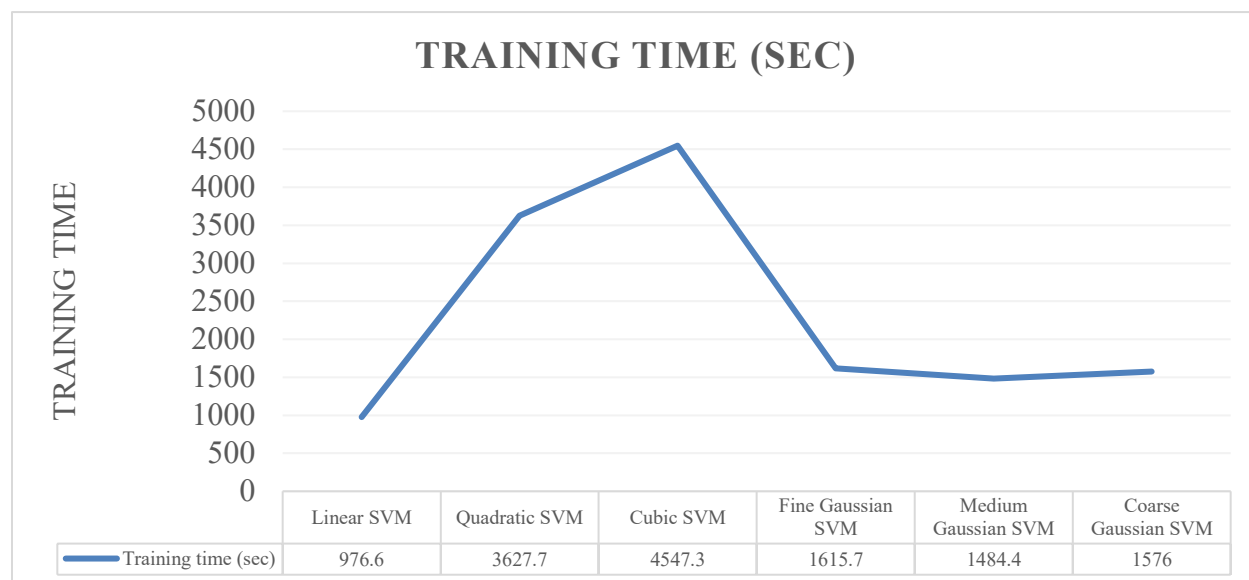


Figure 10. Training time for Experiment 2 (2500 features).

4.3 Experiment 3: 3130 Features

Experiment 3 uses 3130 selected features under the reported validation procedure. In Table 5, Cubic SVM has the strongest detailed result: 98.9% accuracy, 0.99 precision, 0.9925 recall,

and 0.99 F1-score. Quadratic SVM has 98.6% accuracy, while Fine Gaussian SVM has the lowest accuracy (46.2%). Figures 11 and 12 show the Cubic SVM confusion matrix and training-time values, respectively.

Table 5. Results for Experiment 3 (3130 fused features).

Classifier	Accuracy	Precision	Recall	F1-score	Obs/sec	Time (s)
Linear SVM	92.7	0.95	0.952	0.955	1000	580.71
Quadratic SVM	98.6	0.9875	0.9875	0.985	100	787.66
Cubic SVM	98.9	0.99	0.9925	0.99	100	785.46
Fine Gaussian SVM	46.2	0.462	0.83	0.45	26	2492.1
Medium Gaussian SVM	97.9	0.98	0.9775	0.98	65	1043.5
Coarse Gaussian SVM	83.4	0.8275	0.825	0.825	33	2097.3

Cubic SVM				
True Class	E	L	M	N
	2370	5	1	24
	4	2391	1	4
	1		2395	4
	55	2	3	2340
Predicted Class				
	E	L	M	N

Figure 11. Confusion matrix for Experiment 3 (3130 features). E, L, M, and N denote Eosinophil, Lymphocyte, Monocyte, and Neutrophil, respectively.

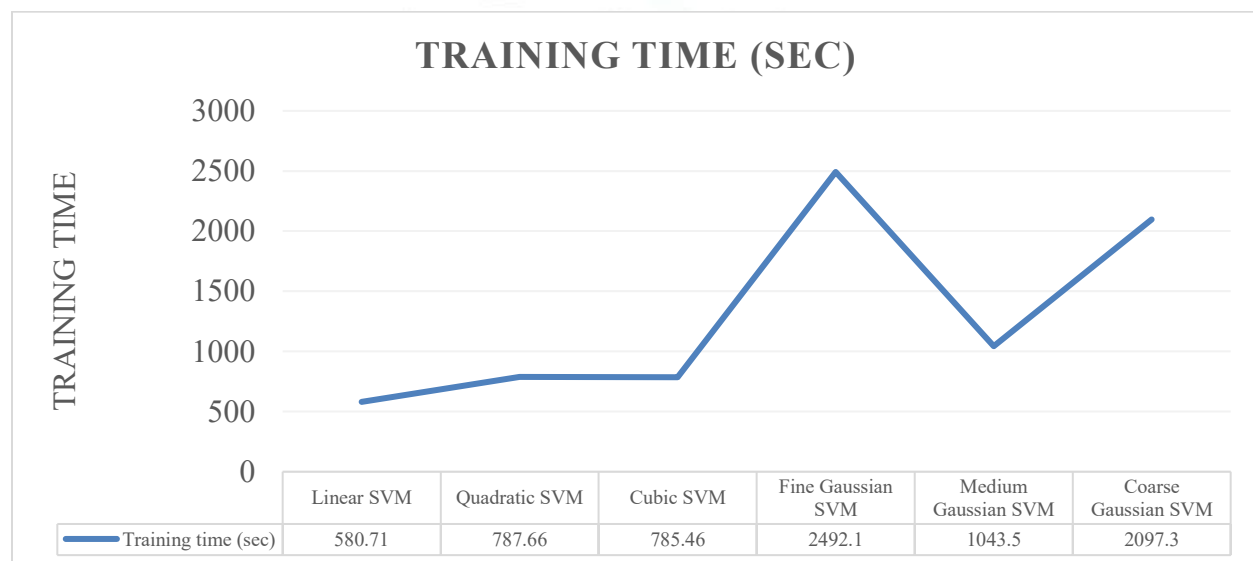


Figure 12. Training time for Experiment 3 (3130 features).

4.4 Individual CNN Results

Standalone classification accuracies of 97%, 92%, and 98% were reported for AlexNet, ResNet, and DarkNet, respectively. Detailed experimental settings for these standalone results were not documented.

4.5 Comparison with Existing Techniques

The highest detailed accuracy is 98.9% for 3130 features, Cubic SVM. Comparing this result with previous and recent studies, the result is

presented in Table 1. These contextual values cannot be used to make clear-cut comparisons of performance because they vary due to dataset, class definition, metrics, augmentation procedures, and validation protocols.

5. Discussion

There is a significant variation in accuracy among the three feature configurations that can be reported. Experiments 1 and 2: All six variants of

SVM are below 40%. The large numbers of features (3130) give a higher value for the linear, quadratic, cubic, medium gaussian, and coarse gaussian SVMs, whereas the fine gaussian SVM stays at 46.2% in the Experiment 3. These observations are qualitative and do not offer any logic to explain the differences in performance between the configurations.

The ranking of classifiers is dependent on the feature configuration. For Experiment 1 and 2, medium Gaussian SVM has the highest accuracy and for experiment 3, Cubic SVM has the highest detailed result. Among the best rows (3130 features), Quadratic SVM is also included. For all six variants, it can be seen that the top-classifier is different in each configuration.

This evaluated pipeline comprises of three well known CNN feature extractor, serial feature fusion, GA assisted reduction and SVM classification. It is part of the previously known body of hybrid deep features system. The results do not report on the causal complementarity of feature sources.

Recent works on transfer learning [8, 9], attention-enhanced CNNs [10, 11] and multi-CNN fusion, evolutionary feature selection, and transformer-oriented approaches are explored in some of the recent studies [8-11] conducted by WBC. Result of 98.9% is for the reported data set and protocol. Unfortunately, direct comparison between these studies is still restricted due to the different image sets, classes, preprocessing, augmentation, metrics and test-set designs used in the cited studies.

The following columns describe the reported configurations in an additional manner: Configurations are reported in terms of the number of Observations (Obs/sec) and the time that elapsed (Time (s)) between each report. Training-time values differ across SVM variants and experiments, including the higher reported times for some Gaussian-kernel rows. The reported experiments do not provide sufficient evidence to make a general efficiency claim.

Some implementation details were not documented. These include the experimental conditions for the standalone CNN accuracies

and the GA population size, mutation rate, exact iteration limit, and initialization method. The experiment also predates current transformer and lightweight architectures, which are relevant to present-day positioning but were not evaluated in this study. The exact relationship between the reported five-fold validation procedure and the 70/30 training-testing description could not be reconstructed from the surviving implementation records.

6. Conclusion

The WBC classification framework uses AlexNet, ResNet-101, and DarkNet-53 for deep feature extraction, producing 4096, 1024, and 1024 features, respectively. It then applies serial feature fusion, GA-assisted feature selection, and six SVM variants. Cubic SVM with 3130 features has the strongest detailed result: 98.9% accuracy, 0.99 precision, 0.9925 recall, and 0.99 F1-score. Within the reported dataset and experimental configuration, the 3130-feature setting has the highest performance among the experiment rows. This result provides contextual evidence and is not a direct comparison with studies using different datasets and protocols.

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