

Synergetic Fusion Of CNN-SVM And CNN-RF For Enhanced Leukemia Detection In Biomedical Applications

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Abstract- In medical diagnostics, leukemia identification is a crucial where precise and effective approaches are essential for prompt treatment and prognosis. In this article, we present a novel method, i.e., Convolutional Neural Networks (CNN) in conjunction with Support Vector Machines (SVM) and Random Forest (RF) classifiers for leukemia identification. Our technique extracts discriminating features from medical imaging data by utilizing CNNs' potent feature learning capabilities. Furthermore, the collected characteristics are then applied to RF and SVM classifiers to be classified. The hybrid CNN-SVM and CNN-RF models leverage the complimentary advantages of conventional machine learning methods and deep learning to enhance both interpret-ability and excellent classification accuracy. We also test the suggested approach using a public dataset of ALL IDB1 and ALL IDB2. Performance metrics including accuracy, precision, recall, F1-score, the results demonstrate the efficacy of the CNN-SVM and CNN-RF models for Leukemia detection, showcasing their potential as reliable tools for aiding clinicians in diagnosing this life-threatening disease. The CNN-RF outperforms with accuracy of 95% compared to CNN-SVM.

Keywords—Leukemia, Convolutional Neural Networks (CNN), Support Vector Machines (SVM), Random Forest (RF), Medical imaging, feature extraction, hybrid models, classification, deep learning, machine learning.

I. INTRODUCTION

Affected white blood cells (WBCs) are the main sites of leukemia, a commonly recognized malignant disease that can spread to other blood types and bone marrow. The classification of leukemia depends on whether it is chronic (progressively developing) or acute. In the present's scenario, we observed that from hospitals the Leukemia disease growing quickly. Moreover, in similar blood vessels, it begins with lymphatic cells or myeroids. In current conditions, according to the GLOBOCAN study, 9,500 people suffer from leukemia [1]. The main signs of leukemia [2-3] include easy access, weight loss, recurring infections, and fatigue. Swelling and bleeding are signs of a rapidly progressing type of cancer. Depending on the malignant form and immature cell growth, leukemia is classified as acute or chronic. Acute lymphocytic leukemia (ALL) is type -1. Furthermore, in ALL children are generally more affected than adults [4]. Acute myeroid leukemia (AML), the second type, often affects people under the age of 20. The following categories affect both (children as well as adults) such as CLL, or chronic lymphocytic leukemia, and the elderly and myerogenic (CML).

Early detection and diagnosis can help patients live longer, reduce treatment costs, and improve forecasts. The most typical massage tests are a method to identify leukemia [5]. Blood samples are taken and passed a series of tests to predict leukemia. In addition, the manual diagnosis is essentially flawed as it takes time to complete and is sensitive to differences between observers, within 13 to 15 days.

The creation of autonomous, low-cost devices that can differentiate between normal and aberrant blood cells without any involvement by humans. Numerous traditional computer-aided technologies use machine learning (ML) to process images approaches

to ML and deep learning (DL) [6–10], which frequently consist of multiple stages, such as per-processing, categorization, feature extraction, and segmentation. Both DL and ML methods take too much time to handle this problem [11–13], the suggested transfer learning is used in the model [14–17]. Consequently, rather than starting from scratch when creating deep neural networks, use the transfer learning principle [18], whereby the neural networks that are effective in solving problem is optimized to fix other problems. The transfer learning is used that combines with two deep neural networks namely VGG-19, and ResNet-50 is used for feature extraction. The relevant features are selected by LASSO (Least absolute shrinkage and selection operator) and then the features are fused. SVM (support vector machine) is used to classify the four types of leukemia with high accuracy rate and low cost of computation [19–22].

RELATED WORK

Many DL techniques have been recently proposed by researchers, mostly to improve the accuracy of blood cell picture classification. Shaheen M. et. al. in [23], established the Acute Myeloid Leukemia forecast. This algorithm for DL such as AlexNet and Lenet- 5 models, comparing the two respective performances. Moreover, Acevedo and colleagues provided the datasets. Small samples of peripheral blood that are accessible to the public. Comparing the two performances Low score for Lenet-5 model exactness. However, AlexNet achieves great accuracy and can recognize AML only. Das and colleagues et. al. in [24], created a gray level co-occurrence matrix (GLCM) and gray level run length matrix (GLRLM) in 2020. These methods are used to derive the features of cells and identify ALL. The data sets were captured by ALL image database. Moreover, SVM is employed to categorize the WBCs; contrast-limited adaptive histogram, or CLAHE equalization is used to improve the quality of the sample. However, large dataset training takes longer with SVM.

A dense convolutional neural network (DCNN) framework was presented by Kumar D. et al. in [25], to distinguish between the two forms of leukemia: ALL (acute multiple myeloma (MM) and lymphoblastic leukemia. The research on SMS spam produced datasets that were gathered. In this case, two processes were introduced by data augmentation; the first is rotating the pictures in accordance with specific degrees and the second involves just updating the perimeters or edges of the original picture. Selection of univariate features had been presented and uses univariate analysis to choose the traits statistical analyses, and it processes data quickly. Authors in [26], incorporated, a transfer learning technique for repurposing previously learned model knowledge for a new task. This work presented, Regression analysis, classification, and Transfer learning can be useful for any clustering problems. VGG-16 was trained using pretrained InceptionV1, InceptionV2, and ImageNet, which offers a large selection of image classes. The outcome shows how the newly introduced model achieves a high level of accuracy in comparison to the other models. Cao, G., et al., in [27] proposed a method to enhance the dimmed images by using the gamma correction controlled by shorter CDF, whereas the distinct utilizing negative sample methodology, the CE of the intelligent ones. The algorithm complexity of the suggested approach is evaluated. Extensive testing, both quantitative and qualitative shows that the recommended course of action offers superior or similar improving advantages over previous tactics. Furthermore, Adaptive Gamma Correction) (AGC) was presented by Rahman, S., et al., in [28], which was means of appropriately enhancing the image quality. The characteristics of AGC include changed dynamic data according on the input pictures. A thorough experimentation, in addition to qualitative and quantitative evaluations, show that the AGC concert is higher than other strategies now in use. AGC provides the most fulfilling contrast rises in a variety of illumination conditions when in contrast to other

enhancement techniques currently in use. A method called Adaptive Gamma Correction with Weighted Histogram Distribution (AGCWHHD) was introduced by Veluchamy, M., and Subramani, B. [29] in 2019 to improve contrast while maintaining the deeper color and natural hue details of the input pictures. To evaluate the work of the recommended methodology, studies are conducted and based on 500 benchmark images from TID 2008. When in contrast to current practices, experimental results demonstrated that the recommended approach produced incredibly good pictures. An approach for diagnosing leukemia using transfer learning was proposed by Loey, M., et al. reported in [30]. It consists of two automatic classification algorithms based on the images of the blood microscopic inspection, rather than employing outdated tactics that have serious drawbacks. The fundamental technique denoising involves tiny photographs and after that, deep CNN is used to extract attributes. The Findings indicate that the suggested model can identify leukemia. More effectively than with other models. Ahmed N. et al. in [31] illustrated that the CNN be used to categorize leukemia subgroups such as ALL, AML, CLL, and CML. The two publicly are gathering up the datasets. All image databases and leukemia datasets are currently available. ASH picture collection. There are several ways to modify images. These methods are used the stage of feature extraction is completed in the pooling and convolution layers. Adam and SGD Optimizer are utilized. However, Random Gradient Descent (GCD) continuously updates with significant changes, resulting in a large difference in the objective function. Shafique, S. and Tehsin, S. in [32], presented an AlexNet to classify its subtypes automatically and apply to ALL. The photos were captured using publicly accessible datasets and four datasets with various color selections had been made. In picture rotation, mirroring, and data augmentation had been supplied to expand the training set. In total datasets, the accuracy of ALL detection was good; nevertheless, the sub type categorization accuracy was not as good as the RGB picture datasets. This study shows that a variety of ML and DL techniques are comfortable for achieving high accuracy. The suggested approach incorporates VGG-based transfer learning-19 and ResNet-50 in order to extract the characteristics and the Leukemia categorization is carried out using support vector machine (SVM) to obtain increased precision and with minimal rate of calculation. Author's et.al. in [33], discussed the contributions of multi class blood cancer classification with maximum accuracy of 99.84% achieved through the combination of LR classifiers, SVC feature selector, and ResNet50. The authors proposed CNN architecture to use CNN models that have already been trained to extract information from individual photos of four key stages in both malignant and healthy tissues. They had applied feature selection algorithms in conjunction with optimized deep features to follow the performance and examine the deep aspects.

More than 20,000 cases of pediatric blood cancer are detected annually in India, with approximately 15,000 cases of leukemia only reported in [34]. Authors et. al. in [35], provided a clever way to automatically identify lymphoblasts, or blast cells, in the single-celled image for the purpose of diagnosing leukemia. When implementing the strategy, a CNN is utilized to Differentiate between healthy and cancerous blood cells. The C NMC 2019 data set was employed to assess and train the exclusive ALLNET model. The dataset has 10,661 images in it. The maximum precision attained by 95.54 was the custom ALL-NET classifier based on deep learning. Again, Authors in [36], illustrated the classified ALL as a model that autonomously adjusts its own learning rate using the EfficientNet-B3 CNN framework. The C-NMC Leukemia dataset was used to test the proposed model includes 27,558 images of RBCs. Classifiers that have recently been developed were utilized to evaluate the suggested model. Overall, the suggested model had with 98.31% accuracy and a Disc similarity coefficient (DSC) of 98.05%. The suggested process was also applied to distinguish between healthy and produced

parasitized microscopic images with a mean precision of 97.68%, demonstrating its value beyond ALL detection.

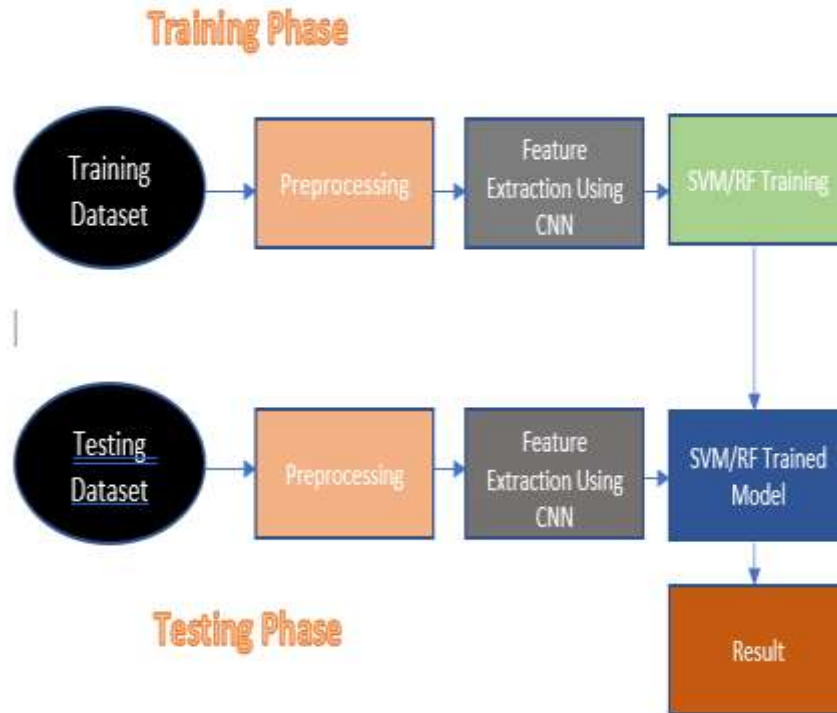
To mitigate above problems, in this article we proposed the Convolutional Neural Networks (CNN) in conjunction with Support Vector Machines (SVM) and Random Forest (RF) classifiers for leukemia identification. The advantage of this CNN-SVM and CNN-RF model is developed without augmentation techniques with accuracy 92% and 95% respectively.

The remaining work has been divided into following upcoming five Sections. In Section II, we illustrate the proposed methodology of the proposed work. While, in Section III presented the results on performance outcomes and associated analysis. And finally in Section IV contains the conclusion remarks of the proposed work.

II PROPOSED METHOD

Process of Proposed Work

Figure 1: Model Architecture for Leukemia Detection



A. Dataset Description

In this study the blood sample images are taken from the commonly available two dataset library namely ALL-IDB-1 and ALL-IDB2. The dataset contains 368 images collectively from ALL-IDB-1 and ALL IDB-2 datasets. ALL-IDB1 contains 108 images of 1712×1368 resolution and ALL-IDB-2 contains 260 images of resolution 257×257 . The annotation of ALL-IDB2 is as follows. The ALL-IDB2 image files are named with the

notation ImXXX_Y.jpg where XXX is a progressive 3-digit integer and Y is a boolean digit equal to 0 if the cell placed in the center of the image is not a blast cell, and equal to 1 if the cell placed in the center of the image is a blast cell. Please note that all images labeled with Y=0 are from healthy individuals, and all images labeled with Y=1 are from ALL patients. The dataset is divided into Training and Testing sub datasets for our research purpose.

B. Image pre-processing

The 368 images from ALL-IDB-1 and ALL-IDB-2 datasets are converted into numpy arrays using Open CV library in python. The target image size or the numpy array size is kept 128×128 . Moreover, the image size of this dimension is helpful to bring uniformity in different image sizes of the 2 datasets.

C. Proposed CNN Architecture for Feature Extraction

In this step, the four Convolutional layers from Keras library in python are taken and followed by Max Pooling layers. The Dropout layers are inserted between each pair of Convolutional and Max Pooling Layers to avoid over fitting problem. This CNN Feature extraction model is trained on the given dataset.

D. Training SVM/RF

In the training phase, the feature extractor CNN model is utilized for feature extraction of training dataset. These extracted features are further provided to SVM Classifier model. The SVM model uses RBF kernel for classification purpose. The well-trained Feature extracted model and SVM models are saved for testing purpose. Similar procedure is carried out for Random Forest Classifier.

E. Testing Phase

In this phase the test dataset is fed to the feature extractor CNN model and SVM/RF models. The accuracy along with precision, recall, F1-score are noted.

CNN: A CNN or Convolutional Neural Network, is a type of deep literacy algorithm generally used in image recognition and classification task. There are some basics and functional features of CNNs.

Convolutional Layers: The core structure blocks of CNNs. Convolutional layers apply complication operations to the input image using pollutants or kernels. These pollutants help in rooting features like edges, textures, or shapes from the input images.

Pooling Layers: These layers down sample the point maps generated by convolutional layers, reducing their dimensionality while retaining the most important information. Max pooling and average pooling are common pooling operations used in CNNs.

Activation Functions: Activation functions introduce non-linearities into the network, allowing it to learn complex patterns. Common activation functions used in CNNs include ReLU (remedied Linear Unit), sigmoid, and tanh.

Completely Connected Layers: Also known as thick layers, these layers connect every neuron from one sub caste to every neuron in the coming sub caste, forming the final bracket or retrogression affair. Completely connected layers are generally set up towards the end of the CNN armature.

Training CNNs: These are trained using large datasets through a process called back propagation. During training, the network learns to acclimate its weights and impulses to minimize the difference between its prognostications and the factual markers.

Loss Function: The loss function measures the difference between the prognosticated affair of the network and the factual marker. Common loss functions used in bracket

tasks include categorical cross-entropy and double cross-entropy.

Optimization Algorithm: Optimization algorithms like Stochastic Gradient Descent (SGD), Adam, or RMSprop are used to modernize the weights of the network during training in order to minimize the loss function.

Regularization ways: The ways like powerhouse and weight decay are employed to help over-fitting, where the model learns to study the training data rather than generalize to unseen data.

Data Augmentation: To ameliorate conception and robustness, data addition ways similar as gyration, flipping, cropping, and scaling are applied to instinctively increase the diversity of the training data.

Transfer Learning: Transfer literacy involves using a pre-trained CNN model on a large dataset and fine-tuning it on a lower dataset specific to the task at hand. This can significantly reduce training time and ameliorate performance, especially when the target dataset is limited.

These are some of the introductory features and functional aspects of CNNs. They've revolutionized colorful fields similar as computer vision, natural language processing, and indeed audio analysis, owing to their capability to automatically learn hierarchical representations of data [16].

Support Vector Machines (SVM): Supervised learning models called SVM are applied to regression and classification problems. They work very well in high-dimensional spaces for classification. SVMs function by locating the feature space hyperplane that optimally divides classes. The margin between the closest data points from various classes referred to as support vectors is maximized by this hyperplane. By mapping the input data into higher-dimensional spaces using kernel functions, SVMs are able to handle both linear and non-linear classification tasks. The trade-off between maximizing the margin and avoiding misclassifications is managed by the regularization parameter (C). SVMs function effectively with small to medium-sized datasets and are resistant to over-fitting. They are used in many different fields, including bioinformatics, image recognition, and text classification reported in [26].

Random Forest (RF): RF is a decision tree-based ensemble learning method [37]. It uses random samples of data and attributes to form several decision trees, then combines their predictions for tasks involving regression or classification. Strong, capable of managing big datasets, Random Forest offers feature relevance metrics.

Random Sampling: To generate additional training datasets, randomly select N samples from the original dataset using replacement (bootstrap). At each decision tree node, choose a subset of features (m) at random. This process is known as random feature selection. This brings variation among the trees.

Build Decision Trees: Using the features that were chosen in step 2 and the training datasets that were produced in step 1, build decision trees. Divide nodes according to feature values that reduce variance for regression or optimize information gain for classification.

Voting or Averaging: Each decision tree forecasts the class label of the incoming data point for classification tasks. Among all decision trees, the majority vote determines the final prediction. To get the final result for regression tasks, the predictions from each tree are summed.

Feature Importance: Determine the relative value of each feature by calculating its contribution to the overall reduction of error or impurity in all decision trees.

Ensemble Model: To increase accuracy and generalization performance, Random Forest aggregates the forecasts of several decision trees.

For every new data point that needs to be categorized or predicted, this procedure is repeated. Random Forest is renowned for its durability, simplicity, and capacity to handle large amounts of data.

II. EXPERIMENTAL ANALYSIS AND RESULT

This section provides experimental data analysis of proposed system. Firstly, the section represents the performance analysis with the Feature extractor CNN and SVM classifier and afterwards Feature extractor CNN model and Random Forest Classifier. To evaluate the efficacy of the proposed model, the set of performance evaluation matrices have been enumerated such as, Accuracy (A), Precision (P), Recall (R), and F1-score (F1).

A. Performance Measure

Accuracy: Accuracy the proportion of correctly classified instances over the total instances in the dataset.

Precision: Precision measures the proportion of true leukemia cases among all instances classified as leukemia.

Recall: Recall (Also known as Sensitivity or true positive rate) measures the proportion of true leukemia cases that are correctly identified.

F1-Score: F1-Score is the harmonic mean of precision and recall. It provides a balance between precision and recall.

Here,

TP = True Positives (Correctly classified leukemia cases)

TN = True Negatives (Correctly classified non-leukemia cases)

FP = False Positives (non-leukemia cases classified as leukemia)

FN = False Negatives (leukemia cases classified as non-leukemia)

Table-1 represents performance evaluation metrics with mathematical annotations. However, the experimentation outcome using CNN, SVM and RF on the database provides the performance metric values as shown in the Table 2.

Table1: Performance Metrics and mathematical equations

Index	Metric	Formula
1	Accuracy	$(TP+TN)/(TP+TN+FP+FN)$
2	Precision	$TP/(TP+FP)$
3	Recall	$TP/(TP+FN)$
4	F1-score	$2*(Precision*Recall)/(Precision+Recall)$

Table2: Comparison of Performance Metrics Deceived

Model	Accuracy	Precision	Recall	F1-score
CNN SVM Classifier	92%	91%	92%	91%
CNN RF Classifier	95%	94%	94%	94%

B. Confusion Matrix

Figure 2: Confusion Matrix for CNN SVM Classifier

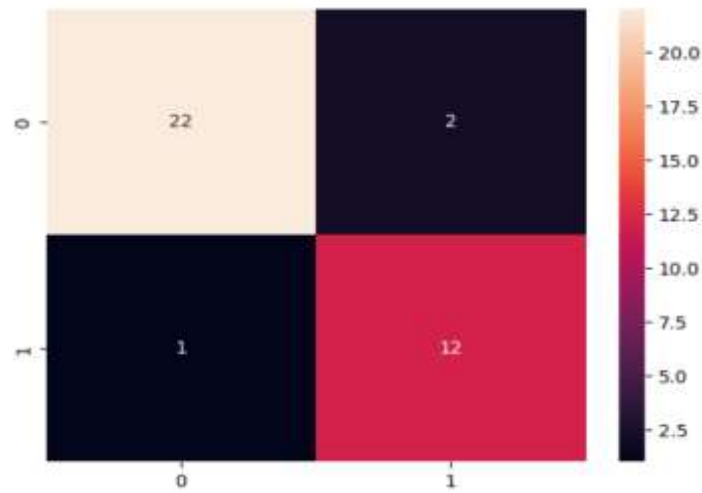
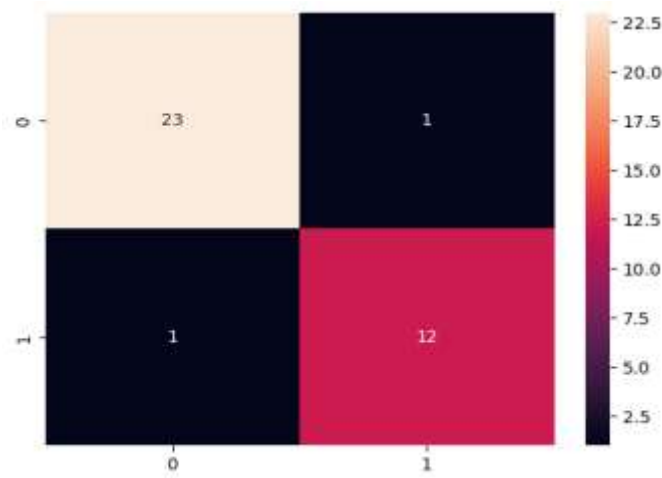


Figure 3: Confusion Matrix for CNN RF Classifier



C. Classification Report

i) Classification Report CNN-SVM Classifier

	precision	recall	f1-score	support
0	0.96	0.92	0.94	24
1	0.86	0.92	0.89	13
accuracy			0.92	37
macro avg	0.91	0.92	0.91	37
weighted avg	0.92	0.92	0.92	37

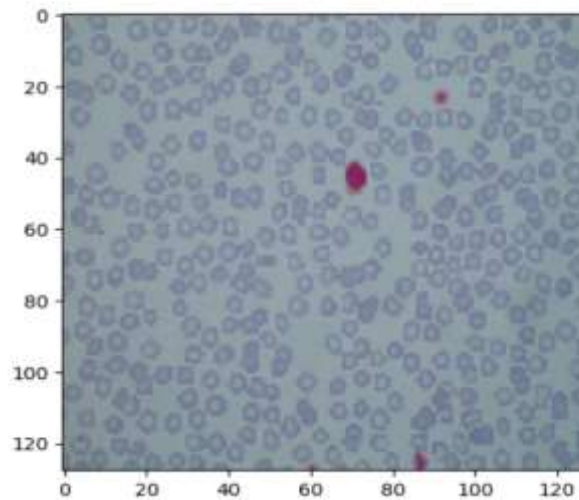
ii) Classification Report CNN-RF Classifier

	precision	recall	f1-score	support
0	0.96	0.96	0.96	24
1	0.92	0.92	0.92	13
accuracy			0.95	37
macro avg	0.94	0.94	0.94	37
weighted avg	0.95	0.95	0.95	37

D. Evaluation on test dataset images

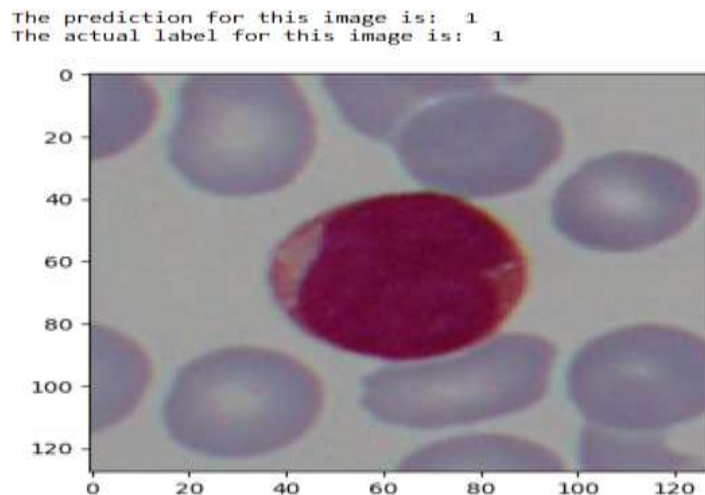
Figure 4: Evaluation of test Dataset image using CNN-SVM

The prediction for this image is: 0
The actual label for this image is: 0



Classifier

Figure 5: Evaluation of Test image using CNN-RF Classifier



In the context of CNNs, abstract features refer to higher-level representations of input images that capture complex and semantic information. As the network progresses through its layers, the features become increasingly abstract. Here are some examples of abstract features that CNNs may learn to extract:

Textures and Patterns: In early layers, CNNs may learn to detect simple patterns and textures such as edges, corners, and gradients. These features provide basic information about the structure of objects in the image.

Shapes and Structures: As the network goes deeper, it can learn to detect more complex shapes and structures, such as curves, contours, and parts of objects. These features help in understanding the spatial layout of objects within the image.

Object Parts and Hierarchies: CNNs can learn to detect specific parts of objects and their spatial relationships. The accuracy obtained on CNN-RF model is 95% and the accuracy obtained on CNN-SVM model is 92%. Certainly, the CNN-RF model has outperformed the CNN- SVM model in terms of accuracy. Even precision recall and f1-score are higher in CNN-RF model as compare to CNN-SVM Model. This experiment is carried out on Intel Core i7 processor helped by 6GB GPU unit of Nvidia Geforce RTX. The python libraries used are Tensorflow, Keras, Scikit Learn and Matplotlib.

III. CONCLUSION

In the proposed work, we present a novel method, i.e., Convolutional Neural Networks (CNN) in conjunction with Support Vector Machines (SVM) and Random Forest (RF) classifiers for leukemia identification. Furthermore, the CNN feature extractor captures the abstract features such as edges, structures, outlines. The manual part of these feature extraction is done automatically in CNN model. Since the complexity of CNN model is suitable for any CPU-GPU combination, it can be implemented easily. The small dataset like ALL-IDB-1 and IDB-2 is used for research without over-fitting problem. The advantage of this CNN-SVM and CNN-RF model is developed without augmentation techniques with accuracy 92% and 95% respectively. The precision score for class 0 is higher than class 1. It indicates that the True positive recognition rate is higher in both the models. The future scope for this research work is to use transfer learning CNN model along with RF and SVM Classifier on larger datasets.

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