AUTOMATED DETECTION OF ACUTE LEUKEMIA USING K-MEANS CLUSTERING ALGORITHM

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Minakshi Arya

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By

Minakshi Arya

The Supervisory Committee certifies that this disquisition complies with North Dakota State University’s regulations and meets the accepted standards for the degree of

MASTER OF SCIENCE

SUPERVISORY COMMITTEE:

Dr. Simone Ludwig
Chair

Dr. Saeed Salem

Dr. Maria Alfonseca-Cubero

Approved:

May 8, 2019
Date

Dr. Kendall Nygard
Department Chair
ABSTRACT

Detection of ALL can be done through the analysis of white blood cells (WBCs) called leukocytes. Usually, the analysis of blood cells is performed manually by skilled operators, have numerous drawbacks, such as slow analysis, a non-standard accuracy and skill of the operator. Hence many automated systems are using in order to analyze and classify the blood cells. This paper focuses on an automatic system based on image processing algorithms for the classification of blood cells for detection of Acute Lymphocytic Leukemia (ALL).

Experiments were ran using 20 models with PCA and seven models namely Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted trees and Ensemble Bagged trees had 99.9% accuracy. These models are evaluated based on the prediction speed, training time, confusion matrix and ROC. Of all models, the weighted KNN classifier is best when using PCA.
ACKNOWLEDGEMENTS

First of all, I would like to express my sincere gratitude to my research advisor, Dr. Simone Ludwig at North Dakota State University for trusting me and giving me the opportunity of research in this new area on Image Processing and Machine Learning. I have learned a lot in this whole process. Her indispensable guidance and encouragement during the research and execution of experiments made this paper possible.

Lastly, I wish to thank my spouse and my children for their continuous support, faith, and encouragement throughout my master studies.
DEDICATION

I would like to dedicate this paper to the beginners who are interested in massively growing Image Processing and Machine Learning field.
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LIST OF ABBREVIATIONS

RBC....................................................Red Blood Cells
WBC ..................................................White Blood Cells
GLCM ................................................Gray-Level Co-occurrence Matrix
ALL....................................................Acute lymphocytic leukemia
DNA ...................................................Deoxyribonucleic acid
KNN....................................................Nearest Neighbor
EU ......................................................Euler Number
PCA....................................................Principal Component Analysis
ROC ...................................................Receiver Operating Characteristic
NCI....................................................National Cancer Institute
1. INTRODUCTION

There are many types of cancer. Cells in any part of the body can become cancerous when cells in the body begin to grow uncontrolled. Leukemia is cancer that starts in blood cells. Leukemia is divided based on whether the leukemia is acute (fast-growing) or chronic (slower growing), and whether it starts with myeloid cells or lymphoid cells.

Acute lymphocytic leukemia (ALL) is a cancer of the blood and bone marrow. Acute lymphocytic leukemia (ALL) is also called acute lymphoblastic leukemia. “Acute” means that leukemia can progress quickly and creates immature blood cells, rather than mature ones and if not treated, would probably be fatal within a few months. "Lymphocytic" means it develops from early (immature) forms of lymphocytes, a type of white blood cell (WBC). Acute lymphocytic leukemia is a common form of cancer in children, and treatments result in a good chance for a cure, whereas in adults, treatment is greatly reduced. However, if left untreated, acute lymphocytic leukemia is eventually fatal; it will spread to the lymph nodes, spleen, liver, central nervous system, and other organs.

Acute lymphocytic leukemia occurs when a bone marrow cell develops errors in its deoxyribonucleic acid (DNA). The errors tell the cell to continue growing and dividing, while a healthy cell would stop growing and dividing and eventually die. When this happens, blood cell production becomes abnormal. The bone marrow produces immature cells that develop into leukemic white blood cells called lymphoblasts. These abnormal cells are unable to function properly, and they can build up and crowd out healthy cells. It is not clear what causes the DNA mutations that can lead to acute lymphocytic leukemia.
The symptoms of leukemia include fatigue, unexplained fever, abnormal bruising, headaches, excessive bleeding (such as frequent nosebleeds), unintentional weight loss, and frequent infections, to name a few.

There are around 60,000 new cases of leukemia each year in the U.S. and over 24,000 deaths due to leukemia. Leukemia makes up about 3.7% of all new cancer cases. Acute lymphocytic leukemia is the most common type of leukemia in children, but it can also affect adults. In this type of leukemia, immature lymphoid cells grow rapidly in the blood. It affects almost 6,000 people per year in the U.S. [34].

In addition, the cost of leukemia treatment can be overwhelming. The average total cost of inpatient ALL treatment (induction phase) is $31,694 for both adults and children. The cost of consolidation therapy is $29,244 and $12,753 in adults and children, respectively. The maintenance therapy cost is $7,288 and $3,452 in adults and children, respectively. The high-risk therapy following relapse is $17,100 and $12,000 in adults and children, respectively. The total treatment cost for ALL is estimated at $85,326 for adults and $59,899 for children. [33]. In general, about 40 percent of adults with ALL are considered cured at some point during their treatment, estimates the American Cancer Society.

According to the National Cancer Institute (NCI), the five-year survival rate for American children with ALL is around 85 percent. This means that 85 percent of Americans with childhood ALL live at least five years after they receive a cancer diagnosis. The NCI states that among American children with ALL, an estimated 98 percent achieved remission. Remission means a child does not have any signs or symptoms of the condition and blood cell counts are within normal limits. A number of factors can affect a person’s survival rate following an ALL diagnosis, such as a person’s age or WBC count at the time of diagnosis [35].
The early and fast identification of the leukemia aids in providing the appropriate treatment. Therefore, image processing techniques can decrease the cost of treatment by fast and parallel diagnosis in the early stages of the disease. Image processing techniques can assist pathologists to have a more accurate diagnosis by improving the clarity of concerned features in WBC images.

The classification of blood cells is important for the evaluation and diagnosis of many diseases in medical diagnosis systems. WBC reveals diagnostic information about different diseases like Leukemia, Malaria, Multiple Myeloma, dengue fever, etc. Blood is the circulating fluid in the body composed of Leucocytes or White Blood cells (WBC), Erythrocytes or Red Blood Cells (RBC) and Platelets. The Erythrocytes and Leukocytes are differentiated from the fact that WBC’s has a nucleus in the middle while RBC’s have no nucleus. Detection of ALL can be done through the analysis of white blood cells (WBCs). Microscopic pictures are reviewed visually by hematologists and the procedure depends on the skill of the operator, is tedious, time taking and have numerous drawbacks, such as slow analysis and a non-standard accuracy, which causes late detection.

Recently, computerized methods for cancer detection have been explored towards minimizing human intervention and providing accurate clinical information. This paper focuses on a computer-based system for automated detection of Acute Lymphocytic Leukemia based on image processing algorithms for the classification of blood cells as an assistive diagnostic tool for pathologists. The proposed strategy is effectively connected to many numbers of the picture, demonstrating accurate results for distinctive picture handling calculations, for example, Clustering, Mathematical process, and Labeling are executed utilizing MATLAB.
2. RELATED WORK

Several algorithms of identification and detection of Leukemia have been implemented. Sanal & Balakrishnan (2015) [24] proposed image preprocessing, WBC extraction, separation of adjacent WBCs, feature extraction and classification. Image preprocessing is done by converting RGB images into Lab color space images to enhance the visual appearance of the image and to reduce the memory requirements. Then, the WBC are identified by using the fuzzy C means clustering algorithm. Separation of adjacent leukocytes is done by using Marker-based watershed segmentation. For feature extraction, the features of WBC such as area, energy, entropy, etc. are considered. To detect whether a patient has leukemia or not, a classifier based on a neuro-fuzzy system is used.

Ruberto, Loddo, & Putzu (2015) [21] realized reliable automated multiple classifier systems based on Nearest Neighbor and Support Vector Machine in order to manage all the regions of immediate interests inside a blood smear: white blood cells nucleus and cytoplasm, erythrocytes and background. The experimental results demonstrate that the proposed method is very accurate and robust being able to reach an accuracy in the segmentation of 99%, indicating the possibility to tune this approach to each microscope and camera.

Rejintal & Aswini (2016) [20] utilized image enhancement strategies, segmentation is done to concentrate on the nucleus, followed by feature extraction to detect cancer cells. Features such as Angular Second Moment (energy), contrast, autocorrelation, Entropy, variance, dissimilarity, homogeneity, cluster prominence and the Inverse Difference Moment, etc. are considered for accurate precision of identification. The results show that the k-means method is applied to the best segmentation performance.
Kumar, Mishra, Asthana & Pragya (2017) [10] implemented the use of a basic enhancement, morphology, filtering and segmenting technique to extract a region of interest using the k-means clustering algorithm. The proposed algorithm achieved an accuracy of 92.8% and is tested with Nearest Neighbor (KNN) and Naïve Bayes Classifier on a dataset of 60 samples.

Ruberto, Loddo & Putzu (2017) [22] focused on measuring the accuracy of moments (Hu, Legendre, Zernike), Local Binary Patterns and co-occurrence matrices in classifying histological images. The experimentation has been conducted on well-known public datasets: HistologyDS, Pap-smear, Lymphoma, Liver Aging Female, Liver Aging Male, Liver Gender AL, and Liver Gender CR. The comparison results show that when combined with co-occurrence matrices and extracted from the RGB images, the orthogonal moments improve the classification performance considerably, showing themselves as very powerful descriptors for histological image analysis.

Candradewi & Bagasjvara (2018) [2] performed segmentation of white blood cells using the moving k-means algorithm. This research produced a system performance with results in a sensitivity of 85.6%, precision 82.3%, F-score of 83.9% and accuracy of 72.3%. Based on the results of the research on the classification of white blood cells and lymphoblast cells it can be concluded that the system successfully segmented white blood cells with an accuracy of 72.3%, sensitivity 85.6%, and precision 82.3%. The separation of white blood cells was successfully carried out with an accuracy of 75.5%.

Hegde, Prasad, Hebbar & Singh (2018) [7] presented a robust image processing algorithm for the detection of nuclei and classification of white blood cells based on features of the nuclei. The authors used a novel image enhancement method to manage illumination.
variations and Tissue Quant method to manage color variations for the detection of nuclei. Dice similarity coefficient of 0.95 was obtained for nucleus detection. Classification of white blood cells by Cell-by-cell approach offered a 1.4% higher sensitivity in comparison with the 5-class approach. The authors obtained an accuracy of 100% for lymphocyte and basophil detection. Hence, they concluded that lymphocytes and basophils can be accurately detected even when the analysis is limited to the features of nuclei whereas, accurate detection of other types of WBCs will require analysis of the cytoplasm too.


All the studies that have been done so far aimed at automation of diagnostic tasks, thus providing an alternative to manual evaluation by pathologists. However, it can be observed that no study has addressed the need for a unified approach to match human evaluation. Therefore, there is a need for an automated system which identifies each object in a blood smear image and classifies it into one. This can be done if the images are segmented on the basis of the nucleus. With nucleus segmentation, RBC, WBC, and Platelets are differentiated as only WBC have a nucleus and we need only leukocytes (WBC) to identify Leukemia. This method analyzes blood smear images and confirms if it represents a healthy or disease patient, hence, it would play an important role in lowering the burden on pathologists by eliminating the cases requiring manual evaluation. Microscopic images suffer from non-uniform illumination and color shade variations. These variations occur due to inconsistent staining procedure, the illumination source, and imaging variations. This issue can be minimized by acquiring images under a controlled environment but it is not always practically feasible to follow such protocols. Hence, it is desirable for studies on automation of peripheral blood smear analysis to focus on the development of a robust method to handle these variations.
3. EXPERIMENT ARCHITECTURE

In this section, the ALL-IDB data set used for the experiments, the evaluation measures and lastly the results are discussed in detail.

3.1. Data Set

For the experiments a new public and free dataset of microscopic images of blood samples by Labati, Piuri, Scotti [31] "ALL-IDB: the acute lymphoblastic leukemia image database for image processing", specifically designed for the evaluation and the comparison of the algorithms for segmentation and image classification is used.

The images of the dataset have been captured with an optical laboratory microscope coupled with a Canon PowerShot G5 camera. All images are in JPG format with 24bit color depth, resolution 2592 x 1944.

3.1.1. Dataset ALL_IDB1

The ALL_IDB1 version 1.0 can be used both for testing the segmentation capability of the algorithms as well as the classification system and image preprocessing methods. This dataset is composed of 108 images collected during September 2005. It contains about 39,000 blood elements, where the lymphocytes have been labeled by expert oncologists. The images are taken with different magnifications of the microscope ranging from 300 to 500.

The annotation of ALL-IDB1 is as follows. The ALL-IDB1 image files are named with the notation ImXXX_Y.jpg where XXX is a 3-digit integer counter and Y is a boolean digit equal to 0 is no blast cells are present, and equal to 1 if at least one blast cell is present in the image. Please note that all images labeled with Y=0 are from for healthy individuals, and all images labeled with Y=1 are from ALL patients. Each image file ImXXX_Y.jpg is associated with a text file ImXXX_Y.xyc reporting the coordinates of the centroids of the blast cells, if any.
3.1.2. Dataset ALL_IDB2

This image set has been designed for testing the performances of classification systems. There are 260 images. The ALL-IDB2 version 1.0 is a collection of cropped area of interest of normal and blast cells that belong to the ALL-IDB1 dataset. ALL-IDB2 images have similar gray level properties compared to the images of the ALL-IDB1, except the image dimensions.

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 for healthy individuals, and all images labeled with Y=1 are from ALL patient.
4. EXPERIMENTS AND RESULTS

This paper focuses on the segmentation by K-Means of WBC microscopic images. There are two datasets ALL_IDB1 and ALL_IDB2. First, the images are divided into healthy and disease subfolders depending upon whether the images are from healthy or disease patients, then the folder, where the files live, are specified. Then, check to make sure that the folder actually exists. Warn user if it does not exist. Then, load the data as an Image Datastore object. The dataset is divided into training and testing data sets by using 80% of the images for training, and 20% for testing. Then, the images from the training dataset are read.

First, the dataset ALL_IDB2 was used as it has 260 images with one nucleus. The images are converted into a gray image and binary image. The properties of regions in the image and return the data in a table as stats using region props were calculated. Then, the Euler Number (EU) for binary Image, the mean, the entropy of grayscale image and the mean hue, mean saturation and mean value, the standard deviation was calculated.

With the grayscale image in the workspace, calculate the standard deviation of the pixel intensity values. Calculate the gray-level co-occurrence matrix (GLCM) for the grayscale image. By default, gray comatrix calculates the GLCM based on horizontal proximity of the pixels: [0 1]. That is the pixel next to the pixel of interest on the same row. This example specifies a different offset: two rows apart on the same column. Statistics on contrast, homogeneity and correlation of the image from the GLCMs are calculated.

Table 1 shows the EU, Mean Hue(M Hue), Mean Sat(M Sat), Mean (hsv)(Mhsv), Mean I, Std (gray), Contrast, Correlation(Corr), Homogeneity(H).
Table 1: Image Characteristics

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4.1. The Results of the Different Classifiers and Classification Models

The Ensemble Subspace Discriminant shows that the accuracy is 4.2%, the prediction speed 300 observations/seconds and the training time as 4.9518 seconds. This was the best result for the classification using Image Characteristics as a variable. Figure 1 shows the result of the ensemble subspace discriminant classifier.

Figure 1: Mean Ensemble Subspace Discriminant

Then, the stats variable was classified for various models. Figure 2 shows the scatter plot for the stats variable without classification.
Figure 2: Scatter Plot Stats

The result of the classification model of the Fine tree classifier was 69.0% accuracy, the prediction speed 6100 observations/sec and the training time as 82.901sec. This was the best result for the classification using stats as a variable. Figure 3 shows the result of the Fine tree classifier.

Figure 3: Scatter Plot Stats Fine Tree Model

Since the results of stats and image characteristics were not as expected it was decided to investigate the k-means segmentation as given in the following sections.
4.2. Evaluation Measures

The $L_{\text{blue}}$ variable having 2591/2591 features from the segmentation is used for the classification task. The experiments are run using 20 models and the accuracy in %, prediction speed in observations/sec, and the training time in sec was used as evaluation measures.

4.3. Results

At first, the identification and segmentation of WBCs were done by means of image clustering. Color features are extracted from the nucleus in the whole images, each of which contains multiple nuclei [36]. The dataset ALL IDB1 was used. The images generated by digital microscopes are usually in RGB color space, which is difficult to segment. In practice, various reasons such as camera settings, varying illumination, and aging stain may cause the blood cells and image background to vary greatly with respect to color and intensity. For making the cell segmentation robust with respect to these variations, reducing the memory requirement and improving the computational time, an adaptive procedure is used:

Figure 4 shows the original image (RGB), and Figure 5 shows the gray image.

Figure 4: Original Image
The RGB input image is converted into the CIELAB format or more correctly, the CIEL*a*b* color space. This color space consists of a luminosity layer L*, which represents the lightness of the color, chromaticity layers, a* represents its position between red/magenta and green, and b* represents its position between yellow and blue. Since all the color information is in the a* and b* layers, we use these two components for nucleus segmentation. Moreover, the perceptual difference between the colors is proportional to the Cartesian distance in the CIELAB color space. Therefore, the color differences between two samples can be calculated using the Euclidean distance. L*a*b produces a proportional change visually for a change of the same amount in color value due to its perceptual uniformity. Therefore, every minute difference in the color value is noticed visually. The image is converted to the L*a*b* color space using rgb2lab and classify the colors in the 'a*b*' space using K-Means Clustering. Clustering is a way to separate groups of objects. K-means clustering treats each object as having a location in space. It finds partitions such that objects within each cluster are as close to each other as possible, and as far as possible from the objects in other clusters. K-means clustering requires to specify the
number of clusters to be partitioned and a distance metric to quantify how close two objects are to each other.

Since the color information exists in the 'a*b*' color space, our objects are pixels with 'a*' and 'b*' values. The data is converted into data type single for use with imsegkmeans to cluster the objects into three clusters. The clustering is repeated 3 times to avoid local minima.

For every object as input, imsegkmeans returns an index, or a label, corresponding to a cluster. Label every pixel in the image with its pixel label. Images are created that segment the image by color. Using pixel labels, the objects are separated in I by color, which will result in three images - Cluster1, Cluster2, Cluster3. Figure 6 shows Cluster1, Figure 7 shows Cluster 2, and Figure 8 shows Cluster 3, respectively.

Figure 6: Cluster1
Figure 7: Cluster 2

Figure 8: Cluster 3
To segment the nuclei, Cluster 3 contains the blue objects. There are dark and light blue objects. Dark blue is separated from light blue using the 'L*' layer in the L*a*b* color space. The cell nuclei are dark blue.

The 'L*' layer contains the brightness values of each color. The brightness values of the pixels in this cluster are extracted and thresholded with a global threshold using im binarize. The mask is light blue and gives the indices of light blue pixels.

The mask of blue objects, mask3 are copied, then the light blue pixels from the mask are removed. Afterward, the new mask is applied to the original image and the result is displayed. Only dark blue cell nuclei are visible.

During the segmentation, all the images of the training datasets were saved as respective figure a, b, c, d, e, f. Figure 9 shows the Blue nuclei. In this system, the color-based clustering segmentation is performed for extracting the nuclei of the leukocytes.

4.3.1. Results of Segmentation

Figure 9: Blue Nuclei

The segmented output of the image obtained after applying the K-means clustering algorithm is shown in Figure 9.
4.4. Characteristics of Classifier Types

For choosing the best classifier type for the problem. Table 2 is showing the typical characteristics of different supervised learning algorithms. The table was used as a guide for our final choice of algorithms. The decision is a tradeoff between speed, memory usage, flexibility, and interpretability. The best classifier type depends on our data [39].

Table 2: Characteristics of Classifier Types

<table>
<thead>
<tr>
<th>Classifier</th>
<th>Prediction Speed</th>
<th>Memory Usage</th>
<th>Interpretability</th>
<th>All predictors numeric</th>
<th>All predictors categorical</th>
<th>Some categorical, some numeric</th>
</tr>
</thead>
<tbody>
<tr>
<td>Decision Trees</td>
<td>Fast 0.01 second</td>
<td>Small 1MB</td>
<td>Easy</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Discriminant Analysis</td>
<td>Fast 0.01 second</td>
<td>Small for linear, large for quadratic</td>
<td>Easy</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Logistic Regression</td>
<td>Fast 0.01 second</td>
<td>Medium 4MB</td>
<td>Easy</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Support Vector Machines</td>
<td>Medium 1 second  for linear. Slow for others</td>
<td>Large 100MB for binary.</td>
<td>Easy for Linear SVM. Hard for all other kernel types.</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Nearest Neighbor</td>
<td>Slow 100 seconds for cubic. Medium for others</td>
<td>Medium 4MB</td>
<td>Hard</td>
<td>Euclidean distance only</td>
<td>Hamming distance only</td>
<td>No</td>
</tr>
<tr>
<td>Ensembles</td>
<td>Fast to medium depending on the choice of algorithm</td>
<td>Low to high depending on the choice of algorithm</td>
<td>Hard</td>
<td>Yes</td>
<td>Yes, except Subspace Discriminant</td>
<td>Yes, except any Subspace</td>
</tr>
<tr>
<td>Naive Bayes</td>
<td>Medium for simple distributions. Slow for kernel distributions or high-dimensional data</td>
<td>Small for simple distributions. Medium for kernel distributions or high-dimensional data</td>
<td>Easy</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>
4.4.1. Decision Trees

Decision trees are easy to interpret, fast for fitting and prediction, and low on memory usage, but they can have low predictive accuracy. The idea is to grow simpler trees to prevent overfitting. Control the depth with the Maximum number of splits set [38]. Table 3 shows different types of decision trees classifiers.

Table 3: Different Types of Decision Trees Classifiers

<table>
<thead>
<tr>
<th>Classifier Type</th>
<th>Prediction Speed</th>
<th>Memory Usage</th>
<th>Interpretability</th>
<th>Model Flexibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coarse Tree</td>
<td>Fast</td>
<td>Small</td>
<td>Easy</td>
<td>Low</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Few leaves to make coarse distinctions between classes (maximum number of splits is 4).</td>
</tr>
<tr>
<td>Medium Tree</td>
<td>Fast</td>
<td>Small</td>
<td>Easy</td>
<td>Medium</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Medium number of leaves for finer distinctions between classes (maximum number of splits is 20).</td>
</tr>
<tr>
<td>Fine Tree</td>
<td>Fast</td>
<td>Small</td>
<td>Easy</td>
<td>High</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Many leaves to make many fine distinctions between classes (maximum number of splits is 100).</td>
</tr>
</tbody>
</table>
### 4.4.2. Support Vector Machines

In Classification Learner, you can train SVMs when your data has two or more classes.

Table 4 shows the different types of Support Vector Machines Classifiers.

<table>
<thead>
<tr>
<th>Classifier Type</th>
<th>Prediction Speed</th>
<th>Memory Usage</th>
<th>Interpretability</th>
<th>Model Flexibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linear SVM</td>
<td>Binary: Fast</td>
<td>Medium</td>
<td>Easy</td>
<td>Low  Makes a simple linear separation between classes.</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Medium</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Quadratic SVM</td>
<td>Binary: Fast</td>
<td>Binary: Medium</td>
<td>Hard</td>
<td>Medium</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Slow</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cubic SVM</td>
<td>Binary: Fast</td>
<td>Binary: Medium</td>
<td>Hard</td>
<td>Medium</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Slow</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fine Gaussian SVM</td>
<td>Binary: Fast</td>
<td>Binary: Medium</td>
<td>Hard</td>
<td>High  decreases with kernel scale setting. Makes finely detailed distinctions between classes, with kernel scale set to sqrt(P)/4.</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Slow</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Medium Gaussian SVM</td>
<td>Binary: Fast</td>
<td>Binary: Medium</td>
<td>Hard</td>
<td>Medium  Medium distinctions, with kernel scale set to sqrt(P).</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Slow</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coarse Gaussian SVM</td>
<td>Binary: Fast</td>
<td>Binary: Medium</td>
<td>Hard</td>
<td>Low  Makes coarse distinctions between classes, with kernel scale set to sqrt(P)*4, where P is the number of predictors.</td>
</tr>
<tr>
<td></td>
<td>Multiclass:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Slow</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
An SVM classifies data by finding the best hyperplane that separates data points of one class from those of the other class. The best hyperplane for an SVM means the one with the largest margin between the two classes. Margin means the maximal width of the slab parallel to the hyperplane that has no interior data points.

The *support vectors* are the data points that are closest to the separating hyperplane; these points are on the boundary of the slab. The following figure illustrates these definitions, with + indicating data points of type 1, and – indicating data points of type –1.

Figure 10 shows Support Vectors

![Support Vectors](image)

SVMs can also use a soft margin, meaning a hyperplane that separates many, but not all data points.
4.4.3. Nearest Neighbor Classifiers

Nearest neighbor classifiers typically have good predictive accuracy in low dimensions, but might not in high dimensions. They have high memory usage and are not easy to interpret. Table 5 shows different types of nearest neighbor classifiers.

Table 5: Different Types of Nearest Neighbor Classifiers

<table>
<thead>
<tr>
<th>Classifier Type</th>
<th>Prediction Speed</th>
<th>Memory Usage</th>
<th>Interpretability</th>
<th>Model Flexibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fine KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Finely detailed distinctions between classes. The number of neighbors is set to 1.</td>
</tr>
<tr>
<td>Medium KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Medium distinctions between classes. The number of neighbors is set to 10.</td>
</tr>
<tr>
<td>Coarse KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Coarse distinctions between classes. The number of neighbors is set to 100.</td>
</tr>
<tr>
<td>Cosine KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Medium distinctions between classes, using a Cosine distance metric. The number of neighbors is set to 10.</td>
</tr>
<tr>
<td>Cubic KNN</td>
<td>Slow</td>
<td>Medium</td>
<td>Hard</td>
<td>Medium distinctions between classes, using a cubic distance metric. The number of neighbors is set to 10.</td>
</tr>
<tr>
<td>Weighted KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Medium distinctions between classes, using a distance weight. The number of neighbors is set to 10.</td>
</tr>
</tbody>
</table>

\(k\)-Nearest Neighbor classification is categorizing query points based on their distance to points (or neighbors) in a training dataset can be a simple yet effective way of classifying new points. You can use various metrics to determine the distance. Given a set \(X\) of \(n\) points and a distance function, \(k\)-nearest neighbor (\(k\)NN) search lets you find the \(k\) closest points in \(X\) to a query point or set of points. \(k\)NN-based algorithms are widely used as benchmark machine learning rules.
4.4.4. Ensemble Classifiers

Ensemble classifiers meld results from many weak learners into one high-quality ensemble model. Qualities depend on the choice of algorithm. Table 6 shows different types of Ensemble Classifiers.

Table 6: Different Types of Ensemble Classifiers

<table>
<thead>
<tr>
<th>Classifier Type</th>
<th>Prediction Speed</th>
<th>Memory Usage</th>
<th>Interpretability</th>
<th>Ensemble Method</th>
<th>Model Flexibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>Boosted Trees</td>
<td>Fast</td>
<td>Low</td>
<td>Hard</td>
<td>AdaBoost, with Decision Tree learners</td>
<td>Medium to high — increases with Number of learners or a Maximum number of a split set.</td>
</tr>
<tr>
<td>Bagged Trees</td>
<td>Medium</td>
<td>High</td>
<td>Hard</td>
<td>Random forest Bag, with Decision Tree learners</td>
<td>High — increases with Number of learners setting.</td>
</tr>
<tr>
<td>Subspace Discriminant</td>
<td>Medium</td>
<td>Low</td>
<td>Hard</td>
<td>Subspace, with Discriminant learners</td>
<td>Medium — increases with Number of learners setting. Good for many predictors</td>
</tr>
<tr>
<td>Subspace KNN</td>
<td>Medium</td>
<td>Medium</td>
<td>Hard</td>
<td>Subspace, with Nearest Neighbor learners</td>
<td>Medium — increases with Number of learners setting. Good for many predictors</td>
</tr>
<tr>
<td>RUS Boost Trees</td>
<td>Fast</td>
<td>Low</td>
<td>Hard</td>
<td>RUS Boost, with Decision Tree learners</td>
<td>Medium — increases with Number of learners or a Maximum number of a split set. Good for skewed data (with many more observations of 1 class)</td>
</tr>
</tbody>
</table>
4.5. Results of Classification

Following the classification, cross-validation is used for evaluating and comparing the different learning algorithms. Cross-validation is a technique for judging how the results of the statistical analysis will generalize to an independent data set.

Experiments were ran using 20 models namely Fine Tree, Medium Tree, Coarse Tree, Linear SVM, Quadratic SVM, Cubic SVM, Fine Gaussian SVM, Medium Gaussian SVM, Coarse Gaussian SVM, Fine KNN, Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted Trees, Ensemble Bagged Trees, Ensemble Subspace Discriminant, Ensemble Subspace KNN, Ensemble RUS Boosted Trees as also given in the list below.

List of Models Used for Classification

Model
1. Fine Tree
2. Coarse Tree
3. Quadratic Discriminant
4. Fine Gaussian SVM
5. Coarse Gaussian SVM
6. Medium KNN
7. Cosine KNN
8. Weighted KNN
9. Ensemble Bagged Trees
10. Ensemble Subspace KNN
11. Medium Tree
12. Linear Discriminant
13. Cubic SVM
14. Medium Gaussian SVM
15. Fine KNN
16. Coarse KNN
17. Cubic KNN
18. Ensemble Boosted Trees
19. Ensemble Subspace Discriminant
20. Ensemble RUS Boosted Trees

First, the experiment was run using 20 models with the data set stats with observations 17,717, Predictors 18, Response Perimeter, Response Classes 2,372, and the result of the training for the Fine Tree classifier accuracy was 69% with prediction speed ~6,100 observations/sec and training time was 82.901 sec.

The result of the classification model of the Fine Tree classifier with the L_Blue dataset was 99.7% accuracy, the prediction speed 1,100 observations/sec and the training time as 8.6611 sec. This was the best result for the classification using stats as the variable.

Figure 11 shows the result of the Fine Tree Classifier.
Then, the experiment was run using 20 models with data sets L_blue. Of the 20 models, only 10 models had an accuracy of 99.9%. These 10 models namely Linear SVM, Medium Gaussian SVM, Coarse Gaussian SVM, Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted Trees, Ensemble Bagged Trees. Among these the prediction speed and training time is different and these models are evaluated based on the prediction speed and training time. Table 7 shows the results of the different classifier models showing accuracy, prediction speed, and training time.
Table 7: Model, Accuracy and Training Time

<table>
<thead>
<tr>
<th>Model</th>
<th>Accuracy (%)</th>
<th>Prediction speed (observations/sec)</th>
<th>Training time (sec)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fine Tree</td>
<td>99.7</td>
<td>~1200</td>
<td>6.1802</td>
</tr>
<tr>
<td>Medium Tree</td>
<td>99.7</td>
<td>~1200</td>
<td>5.8724</td>
</tr>
<tr>
<td>Coarse Tree</td>
<td>99.7</td>
<td>~1200</td>
<td>5.8936</td>
</tr>
<tr>
<td>Linear SVM</td>
<td>99.9</td>
<td>~1100</td>
<td>20.499</td>
</tr>
<tr>
<td>Quadratic SVM</td>
<td>99.7</td>
<td>~710</td>
<td>24.218</td>
</tr>
<tr>
<td>Cubic SVM</td>
<td>99.3</td>
<td>~710</td>
<td>24.094</td>
</tr>
<tr>
<td>Fine Gaussian SVM</td>
<td>95.1</td>
<td>~540</td>
<td>36.778</td>
</tr>
<tr>
<td>Medium Gaussian SVM</td>
<td>99.9</td>
<td>~760</td>
<td>24.621</td>
</tr>
<tr>
<td>Coarse Gaussian SVM</td>
<td>99.9</td>
<td>~750</td>
<td>24.188</td>
</tr>
<tr>
<td>Fine KNN</td>
<td>99.7</td>
<td>~490</td>
<td>15.87</td>
</tr>
<tr>
<td>Medium KNN</td>
<td>99.9</td>
<td>~500</td>
<td>15.159</td>
</tr>
<tr>
<td>Coarse KNN</td>
<td>99.9</td>
<td>~500</td>
<td>15.327</td>
</tr>
<tr>
<td>Cosine KNN</td>
<td>99.9</td>
<td>~470</td>
<td>15.299</td>
</tr>
<tr>
<td>Cubic KNN</td>
<td>99.9</td>
<td>~86</td>
<td>78.014</td>
</tr>
<tr>
<td>Weighted KNN</td>
<td>99.9</td>
<td>~520</td>
<td>14.889</td>
</tr>
<tr>
<td>Ensemble Boosted Trees</td>
<td>99.9</td>
<td>~1200</td>
<td>6.8817</td>
</tr>
<tr>
<td>Ensemble Bagged Trees</td>
<td>99.9</td>
<td>~720</td>
<td>18.466</td>
</tr>
<tr>
<td>Ensemble Subspace</td>
<td>99.8</td>
<td>~160</td>
<td>227.47</td>
</tr>
<tr>
<td>Ensemble Subspace KNN</td>
<td>99.8</td>
<td>~47</td>
<td>136.58</td>
</tr>
<tr>
<td>Ensemble RUS Boosted Trees</td>
<td>98</td>
<td>~720</td>
<td>11.367</td>
</tr>
</tbody>
</table>
The result of the classification model of the Coarse KNN classifier with the L_Blue dataset was 99.0% accuracy, the prediction speed 480 observations/sec and the training time as 15.395 sec. Figure 12 shows the result of the Coarse KNN classifier with the confusion matrix, and Figure 13 shows the result of the Coarse KNN classifier showing the ROC curve.
The result of the classification model of the Cosine KNN classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 470 observation/sec and the training time as 15.299 sec. Figure 14 shows the result of the Cosine KNN classifier with the confusion matrix, and Figure 15 shows the result of the Cosine KNN classifier and the resulting ROC curve.
The result of the classification model of the Cubic KNN classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 86 observations/sec and the training time as 78.014 sec. Figure 16 shows the result of the Cubic KNN classifier with the resulting confusion matrix, and Figure 17 shows the result of the Cubic KNN classifier and the ROC curve.

Figure 16: Cubic KNN

Figure 17: Cubic KNN ROC
The result of the classification model of the Ensemble Bagged Trees Confusion Matrix classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 720 observations/sec and the training time as 18.466 sec. Figure 18 shows the result of the Ensemble Bagged Trees Confusion Matrix classifier with a confusion matrix, and Figure 19 shows the result of the Ensemble Bagged Trees Confusion Matrix classifier with a ROC curve.

Figure 18: Ensemble Bagged Trees Confusion Matrix

Figure 19: Ensemble Bagged Trees ROC
The result of the classification model of the Ensemble Boosted Trees classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 1,200 observations/sec and the training time as 6.8817 sec. Figure 20 shows the result of the Ensemble Boosted Trees classifier with the confusion matrix.

Figure 20: Ensemble Boosted Trees

The result of the classification model of the KNN Medium classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 500 observations/sec and the training time as 15.150 sec. Figure 21 shows the result of the KNN Medium classifier with a confusion matrix, and Figure 22 shows the result of the KNN Medium classifier with the ROC curve.

Figure 21: KNN Medium Confusion Matrix
The result of the classification model of the Linear SVM classifier with the L_Blue dataset was 99.9% accuracy, the prediction speed 1100 observations/sec and the training time as 20.499 sec. Figure 23 shows the result of the Linear SVM classifier with a confusion matrix, and Figure 24 shows the result of the Linear SVM classifier with the ROC curve.
Figure 24: Linear SVM ROC

The result of the classification model of the SVM Medium Gaussian classifier with the L.Blue dataset was 99.9% accuracy, the prediction speed 760 observations/sec and the training time as 24.621 sec. Figure 25 shows the result of the SVM Medium Gaussian classifier with a confusion matrix, and Figure 26 shows the result of the SVM Medium Gaussian classifier with a ROC curve.
The result of the classification model of the SVM Coarse Gaussian classifier with the L Blue dataset was 99.9% accuracy, the prediction speed 750 observations/sec and the training time as 24.188 sec. Figure 27 shows the result of the SVM Coarse Gaussian classifier.
The result of the classification model of the Weighted KNN classifier with the L\_Blue dataset was 99.9 % accuracy, the prediction speed 520 observations/sec, and the training time as 14.889 sec. Figure 28 shows the result of the Weighted KNN classifier with a confusion matrix, and Figure 29 shows the result of the Weighted KNN classifier with the ROC curve.

Figure 28: Weighted KNN

Figure 29: Weighted KNN ROC
Figure 30 shows the bar chart for the training time. From the bar chart, the maximum training time is used by Ensemble Subspace Discriminant and the least is used by the Fine Tree, Medium Tree, Coarse Tree models.

![Bar Chart Model - Training Time](image)

Figure 30: Bar Chart Model - Training Time

Figure 31 shows the bar chart of the accuracy showing an accuracy of 99.9% for most of the models. Fine Gaussian SVM and Ensemble RUS Boosted Trees have lesser accuracy values compared to other models.

![Bar Chart Model Type and Accuracy](image)

Figure 31: Bar Chart Model Type and Accuracy
Figure 32 shows the stacked plot of accuracy vs training time. In the plot, the accuracy decreases and the training time increases for some models but it is not a general pattern. Fine Gaussian SVM (7) has an increased training time and the least accuracy. Cubic KNN (14) and Ensemble Subspace Discriminant (18) had an increased training time but the accuracy was not affected.

![Accuracy vs Training Time](image1)

Figure 32: Stacked Plot Accuracy vs Training Time

Figure 33 shows the stacked plot of model and training time.

![Model and Training Time](image2)

Figure 33: Stacked Plot Model and Training Time
Figure 34 shows the stacked plot of model and accuracy.

![Stacked Plot Model and Accuracy](image)

Figure 34: Stacked Plot Model and Accuracy

Figure 35 shows the area plot of accuracy and training time.

![Area Plot Accuracy and Training Time](image)

Figure 35: Area Plot Accuracy and Training Time

Figure 36 shows the X bar control chart of accuracy and prediction speed. There is a drastic decrease in the accuracy at two points, but the pattern is not followed by all models.
Figure 36: The X Bar Control Chart Accuracy and Prediction Speed

Figure 37 shows the scatter plot of accuracy and training time. Most models achieved an accuracy of around 99.5% to 100%, and the training time is less than 50 sec. In a few models, the accuracy is decreased but the training time is less than 50 sec. But in some other models, the accuracy is above 99.5% but the training time needed is longer than 50 secs.

Figure 37: Scatter Plot between Accuracy and Training Time
Figure 38 shows the histogram of the test data.

Figure 38: Histogram Test Data

Figure 39 shows the histogram of the train data.

Figure 39: Histogram Train Data
Figure 40 shows the histogram of the L_blue.

![Figure 40: Histogram L_blue](image1)

Figure 41 shows the contour pixel_label.

![Figure 41: Contour pixel_label](image2)
Of all the models, the Ensemble Boosted Trees model has the least training time and the best prediction speed. If the prediction speed is taken into consideration then Linear SVM comes second and if training time is given priority then KNN (Medium, Coarse, Cosine and Weighted) are the second. If the worst performance based on the training time and prediction speed is taken into consideration then Cubic KNN, Coarse Gaussian SVM, and Medium Gaussian SVM are last, second last and third last, respectively.

Since there were 10 models with 99.9 % accuracy without PCA, it was difficult to find a model which would be best to choose from. The dataset L_blue was again classified using Principal Component Analysis (PCA) as the preprocessing method for all the 20 models. PCA reduces the dimensionality of data by replacing several correlated variables with a new set of variables that are linear combinations of the original variables. With 95% variance, there were 11 models with 99.9% accuracy, so the variance was increased to 99.9%.

The models were run on 271 features and 1943 observations using 99.9% variance, there were seven models namely Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted trees and Ensemble Bagged trees which had 99.9% accuracy.

Cubic KNN has the maximum training time and the least prediction speed while all the others had approximately the same prediction speed and training time. The Confusion Matrix and Receiver operating characteristic (ROC) curve were taken into consideration to select the best model.

Table 8 shows the results of the different classifier models showing accuracy, prediction speed, and training time using PCA with 99.9 variances.
Table 8: Model, Accuracy and Training Time using PCA

<table>
<thead>
<tr>
<th>Model</th>
<th>Accuracy (%)</th>
<th>Prediction speed (observations/sec)</th>
<th>Training time (sec)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medium KNN</td>
<td>99.9</td>
<td>~1600</td>
<td>19.083</td>
</tr>
<tr>
<td>Coarse KNN</td>
<td>99.9</td>
<td>~1500</td>
<td>19.89</td>
</tr>
<tr>
<td>Cosine KNN</td>
<td>99.9</td>
<td>~1600</td>
<td>19.738</td>
</tr>
<tr>
<td>Cubic KNN</td>
<td>99.9</td>
<td>~220</td>
<td>41.914</td>
</tr>
<tr>
<td>Weighted KNN</td>
<td>99.9</td>
<td>~1600</td>
<td>19.37</td>
</tr>
<tr>
<td>Ensemble Boosted Trees</td>
<td>99.9</td>
<td>~1900</td>
<td>18.89</td>
</tr>
<tr>
<td>Ensemble Bagged Trees</td>
<td>99.9</td>
<td>~1700</td>
<td>21.436</td>
</tr>
</tbody>
</table>

4.6. Result of Classification using PCA

The result of the classification model of the KNN Medium classifier using PCA with the L_Blue dataset was 99.9% accuracy, the prediction speed was 1600 observations/sec, and the training time was 19.083 sec. Figure 42 shows the result of the KNN Medium classifier using PCA with ROC, and Figure 43 shows the result of the KNN Medium classifier using PCA with the confusion matrix.

Figure 42: Medium KNN using PCA with ROC
The result of the classification model of the Weighted KNN classifier using PCA with the L_Blue dataset was 99.9% accuracy, the prediction speed was 1600 observations/sec, and the training time was 19.37 sec. Figure 44 shows the result of the Weighted KNN classifier using PCA with a ROC curve. Figure 45 shows the result of the Weighted KNN classifier using PCA with the confusion matrix.
The result of the classification model of the Ensembled Bagged classifier using PCA with the L_Blue dataset was 99.9% accuracy, the prediction speed 1700 observations/sec, and the training time was 121.436 sec. Figure 46 shows the result of the Ensembled Bagged classifier using PCA with a ROC curve. Figure 47 shows the result of the Ensembled Bagged classifier using PCA with the confusion matrix.
Figure 47: Ensembled Bagged using PCA with Confusion Matrix

Of all the remaining models Weighted KNN was the only model with 100% Positive Predictive value in the Confusion matrix and the ROC curve was showing maximum true positive value with zero positive rates. All other models were also good as they were showing more than 99% Positive Predictive value and less than 1% False discovery rate. So weighted KNN was chosen as the best model. The test data was segmented through k-means clustering and the L_blue3 dataset was used to test the data. The L_blue3 has the last column as a response which was not used to test the data. As the data used should have the same number of columns as the train data. Y fit is the expected result, which is equal to the response column of the L_blue3 of the test data. Hence the result was 100 %. But if we use the new dataset then the result can be different.
5. CONCLUSION

Many of the previously proposed methods were able to recognize ALL up to a certain extent. Moreover, some of these methods which were applied to ALL and had good results, have used a proprietary dataset, so the reproducibility of the experiment and comparisons with other methods was not possible. In fact, many authors tested their system with their own data sets, which were not publicly available. Thus, we could not directly compare our findings with the results obtained by various proposed systems. As a result, to have a comparison, we had to apply their methods on our dataset.

A color segmentation and classification task with 20 models were taken into consideration. Experiments were ran using 20 models using PCA namely Fine Tree, Medium Tree, Coarse Tree, Linear SVM, Quadratic SVM, Cubic SVM, Fine Gaussian SVM, Medium Gaussian SVM, Coarse Gaussian SVM, Fine KNN, Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted Trees, Ensemble Bagged Trees, Ensemble Subspace Discriminant, Ensemble Subspace KNN, and Ensemble RUS Boosted Trees. Along with the accuracy in %, prediction speed in observations/sec, and training time in a sec, Confusion Matrix and ROC curve were used as evaluation measures. Of the 20 models, only 7 models had an accuracy of 99.9%. These 7 models were Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN, Weighted KNN, Ensemble Boosted Trees, and Ensemble Bagged Trees. Among these the prediction speed and training time was different and these models were evaluated based on the prediction speed and training time.

Of all the remaining models Weighted KNN was the best model with 100% Positive Predictive value in the Confusion matrix and the ROC curve was showing maximum true
positive value with zero positive rates. All other models were also good as they were showing more than 99% Positive Predictive value and less than 1% False discovery rate.
REFERENCES


