Research Article

Image Segmentation and classification Hepatitis viral infection in human blood smear with a hybrid algorithm combining Naive Bayes Classifier

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Abstract: The field of medical informatics incorporates two types of medical data: biological records and imaging data. Pixels that correspond to a part of a physical entity and are created by imaging modalities make up medical image records. Exploration of medical image data techniques is difficult in terms of determining their importance in terms of insight, analysis, and diagnosis of a particular illness. Image processing is a significant problem in image processing activities and plays a vital part in computer-aided diagnosis. This task was about using tools and techniques to manipulate image processing results, pattern recognition results, and classification methods, and then validating the image classification results against medical expert expertise. The primary goal of medical image segmentation and classification is not only to achieve high precision, but also to classify which form of virus infects the patient. Here we are going to perform segmentation of blood cells then classify different categories of Hepatitis virus that affect human blood using the efficient algorithm taken from above comparative analysis performed in previous work.

I.   INTRODUCTION

The most common illness in the world is caused by a virus [1]. Based on their specialty and effects, viral hepatitis is classified into five groups. Hepatitis A and E are considered normal and transmitted by water and food contamination, Hepatitis B is spread through sexual contact and even from mother to child during births, people who have Hepatitis B have a higher risk of contracting Hepatitis D, and treatment of these viral diseases can be accomplished through immunizations and various drugs. Another kind of hepatitis disease is Hypergammaglobulinemia and reactivity autoantibodies, especially anti-smooth muscle, anti-nuclear, and anti-liver kidney microsome autoantibodies, characterise autoimmune hepatitis (AIH). AIH affects more women than men, and it usually responds to immunosuppressive treatment with clinical, biochemical, and histological remission. [2].Chronic hepatitis is a clinical and neurological condition that has several origins and is characterised by differing degrees of hepatocellular necrosis and inflammation [3][4]. HBV infection is also a major public health concern around the world. About 257 million people have been contaminated with HBV, and more than 350 million people have CHB. [5].

A probabilistic statistical classifier, A probabilistic predictive classifier is a Naive Bayesian classifier. The fact that such features are present in a data set does not suggest that others are present is referred to as "naive." The "naive" assumption simplifies the equation to a simple probability multiplication [6]. The Nave Bayes classification is a probabilistic classification based on the Bayes theory that measures the maximum posterior probability from the preceding chance and the observed probability of preaching the sample class. Despite this daring assertion, the Nave Bayes classifier normally produces good results in a wide range of realistic implementation circumstances [7].

The Random Forest is a popular group learning method for creating an efficient classifier by integrating the forecasts of various decision makers (individual decision tree can be regarded as a weak classifier). Specific decision-tree classifiers are prone to overfitting, which the RF classifier usually mitigates. As a result, Random Forest is unaffected by the presence of distinct values in the function vectors.

In image and pattern recognition technology, the fuzzy c-means (FCM) algorithm and its variants are commonly used. For noiseless recordings, the FCM is ideal. The standard FCM algorithm, on the other hand, has the downside of ignoring any spatial information during segmentation, rendering it vulnerable to noise.[8].

In this article, we will segment the input images. The segmented images are then analysed with feature extraction and filtering, as well as various algorithms such as Random forest, FCM clustering, and Nave Bayes classifier.

II.   LITERATURE SURVEY

T.Karthikeyan et al. [9] mainly dealt with Bayes' theorem. Bayes, Bayes, Bayes, Bayes, Bayes, Bayes, Bayes The classification algorithms BayesNet, Bayes.NaiveBayesUpdatable, J48, Randomforest, and UC Irvine machine learning library. Precision and time are the outputs of the classification model. Finally, it is concluded that for hepatitis patients, the Naive Bayes classification approach outperforms other classification approaches.

Adriana ALBU et al. [10] the objective of this thesis is to provide evidence for the choice of the most suitable mechanism for artificial intelligence for basic medical predictions. In order to predict hepatitis B-virus patients' growth, the researchers used the classification of Naive Bayes and the artificial neural networks. A thorough examination of their characteristics and success is given. Both approaches provide accurate outcomes and can be used to aid in patient decision-making.

Sara Omer Hussien et al. [11] provides a summary of the most up-to-date Cutting-edge hepatitis detection data processing tools, as well as a measure of their accuracy and training time. In contexts where precise diagnosis is critical, this form of research helps to design, implement and evaluate efficient support programmes for clinical decision-making. Data mining methods for the analysis of biomedical data are often used in bioinformatics. These methods have shown their accuracy in estimating and assessing disease incidence, as well as in detecting illnesses. Hepatitis is a liver infection that affects people of all ages.Hepatitis is believed to concern millions of people worldwide. Many patients will be saved if hepatitis is diagnosed correctly and early. Owing to the limited scientific detection of hepatitis disease in its early stages, hepatitis remains a significant problem for public health care providers.

Visali Lakshmi P R et al. [12] provide a comparison of the different methods used in the field of sorting and analysing vast amounts of data the data mining method is used for this. The method of collecting useful knowledge from a vast collection of datasets is known as data mining. The latter approach yields more accurate findings with less variation from the hepatitis profile guide. This approach provides a first-hand view of the findings obtained by medical research. As a result, the SVM technique can be used practically in the medical field.

Huina Wang et al. [13]built random forest and Bayesian classification prediction models with to determine the risk factors of HBV reactivation after accurate radiation therapy for patients with PLC. We'll include a doctor's guide based on the identified risk factors in order to reduce the disease's prevalence. First, we proposed the random forest approach for selecting key elements, and then we used the key subset to construct classification prediction models. Many of the features are ranked in order of priority. We choose the five most important features, which are then combined to form a completely new function subset, for which HBV DNA stage, TNM tumour staging, V10, V20, and radiotherapy outer margin, according to our results, are all risk factors for HBV reactivation. Random forest classification accuracy is 85.15 percent when using 5 fold cross validation under 200 decision trees, while Bayesian classifier classification accuracy is 84.57 percent when using 10 fold cross validation. The random forest can be used to define main characteristics and quantify the value of variables, according to the results of the experiment. Furthermore, it is a more efficient strategy for resolving the classification prediction issue of HBV reactivation.

Tahira Islam Trishna et al. [14] presents a variety of data mining approaches for hepatitis detection, as well as the effect of different approaches on training time and precision. To calculate the consequence, we used the WEKA programme and the K-nearest neighbour, Random Forest classifiersand naive bayes. The Nave Bayes algorithm is used to solve text classification problems. The Knearest neighbour is a simple, supervised learning algorithm for both regression and grading problems. Random Forest is a popular algorithm due to its simplicity and ability to be used for both regression and classification. The precision of our result in naive bayes is 93.20 percent. The Random Forest classification achieves 98.60 percent precision by using ten fold cross-validation, while the K-classification achieves an accuracy of95.80 percent.

III.   METHODOLOGY

Pattern recognition results and classification processes, followed by validation of image classification results into medical professional information The primary goal of medical image segmentation and classification is not only to achieve high precision, but also to determine which form of virus causes the infection. Here we are going to perform segmentation of blood cells then classify different categories of Hepatitis virus that affect human blood using the efficient algorithm taken from above comparative analysis performed in previous work. In this paper we are going to segment the input images. The segmented images are then analysed with feature extraction and filtering, as well as various algorithms such as Random forest, FCM clustering, and Nave Bayes classifier. The suggested method's block diagram as shown below..
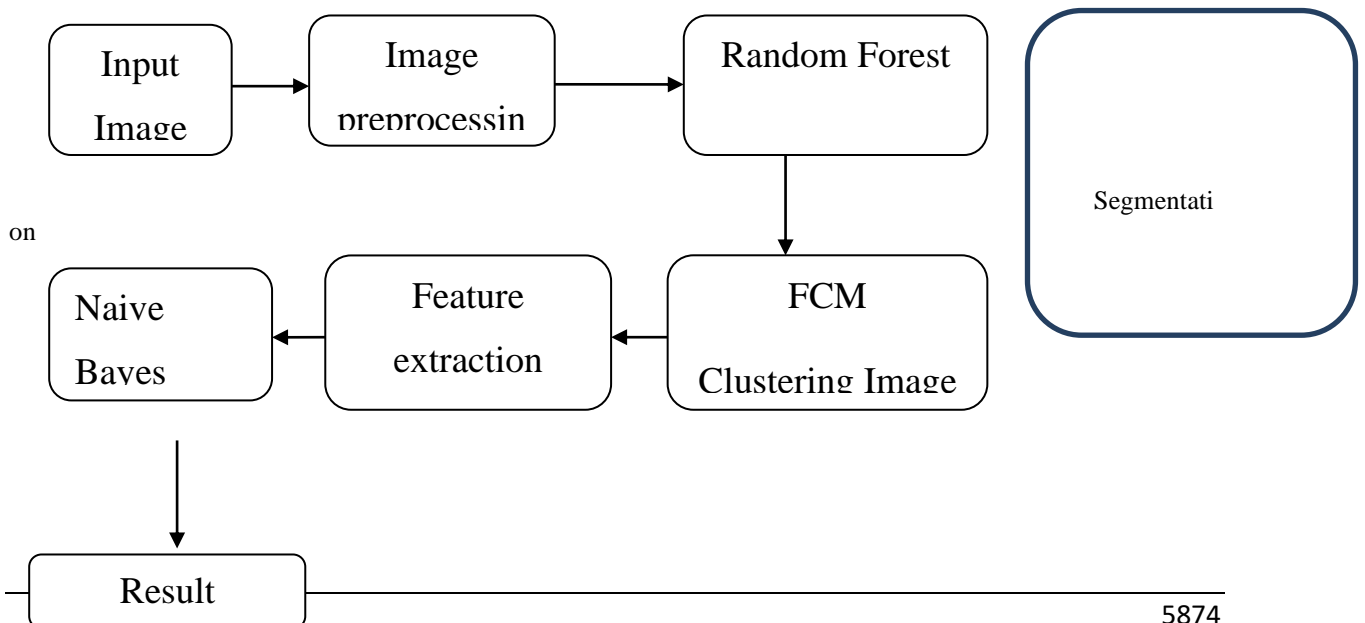
Figure1. Overall Block Diagram of the proposed system

i.   Image Input And Pre-Processing
a) Input images

Input images are obtained from online dataset source for medical image analysis. Images of blood smear affected by hepatitis viral infection with different types of virus like A,B,C,D and E. Microscopic images of blood smear are collected and processed.

b) Pre-processing

In pre-processing stage various operations are performed like gray scale conversion, filtering and image enhancement

Alpha-trimmed Mean Filter:

Let x(i),x(i-1),....x(i-n+1) display a n sample value set in a browser, Wi, where n=2N+1 is seen. If such values are in ascending order of amplitude, the order statistics would result.

$$x1(i) \leq x2(i) \leq \cdots \leq xn(i) \qquad (2)$$

where x1(i) is the lowest signal value, xn(i) is the highest signal value, and x(N+1)(i) is the middle signal value. [18].

$$yn(i,\beta) = \frac{1}{n-2[\beta n]}\sum_{j=[\beta n]+1}^{n-[\beta n]} xj(i) \qquad (3)$$

Where $0\leq \beta<0.5$ denotes the greatest integer part and above denotes the greatest integer part. As βcan be seen from (3), denotes the percentage of samples that have been trimmed. As a result, when close β to 0.5, the alpha-trimmed average filter is functions the same as a median filter, and β is near 0, it behaves like a moving average filter. If the time index I is removed and the trimmed-mean filter is denoted by m(β), the moving average filter is m. (0). While βnever equals 0.5, we can describe median filter as m(0.5) for the sake of convenience since βis very similar to 0.5 for this filter.

ii.   Segmentation

Image segmentation is a critical and difficult challenge, as well as a crucial first step in image processing and robot vision, object recognition, and medical imaging are examples of high-level visual detection and understanding. Picture segmentation divides an image into disjointed regions of uniform and homogeneous attributes including strength, colour, sound, texture, and so on. Several different segmentation techniques have been established, and detailed surveys can be found in the references. The image segmentation technology can be classified into four groups, according to other references: thresholding, clustering, border detection and field extraction. In this article we will examine a clustering image segmentation process.

Clustering is the practise of combining artefacts or shapes into groups such that samples from the same group are more identical than samples from different groups. Many clustering schemes, such as the fuzzy clustering scheme (FCM), have been used, each with its own set of characteristics. The downside of the traditional hard clustering approach is that each point in the data set is limited to only one cluster. As a result, we use FCM clustering in this article. The segmentation effects from this process are often very crisp, indicating that each pixel in the image belongs to exactly one class. Challenges such as poor space resolution, low contrast, overlapping intensity, noise and inhomogeneity of control, however, make it difficult to (crisp) segment in many real situations.[15].

A) Random Forest technique

A supervised machine learning classifier for data collection, sorting, and regression is a Breiman's Random Forest system. It is a classification machine that excelles with several variables in classification problems. Random forests have been created to prevent high variance problems and to improve the robustness of decision-making treaties (error spreading and small data changes lead to many decision trees).

Random forest is a kind of ensemble classifier that improves accuracy by combining many decision trees. The contribution of the classifier is the number of predictions of all trees (votes aggregation). It blends options, compilation and storage with random use (bootstrap aggregation).

The random forest algorithm can handle high-dimensional data without excluding attributes, calculate classification-related characteristics and actively estimate missing data. If a significant volume of data is lost, random forest has the same precision.

Random Forest is a randomised research approach that recognises the target class a priori. To model potential responses, a pattern (classification or regression) is created. The aim of many of the 100 decision trees is to train bootstrap samples. However, in the tree form, m from the p predictors can be selected at random for each iteration, and the distribution can be performed only on one of those m variables. The aim is to use a method that has proved to be very effective to improve the quality of the solutions derived from materials.

$$Propbability = (p - m)/p \qquad (4)$$

Theoretically the most powerful predictor, It saves the work of hitting a tree. By blocking the dominants, other predictors would have a chance to emerge, increasing the tree's diversity.

Algorithm1. Random Forest Algorithm

1. Input: Many decision trees for training Similarity threshold d Level of accuracy 5-0077
2. Input: Modern Algorithm of Random Forest RF:
3. In order to classify and forecast the set of research samples, every decision tree is used;
4. For each treeCM decision, the classification findings of each tree are counted and the uncertainty matrix is generated.
5. Creating a metric matrix of similarities for random forestsMF: for (a, b = 1 to T) & (a < b))) Measuring the difference Matrix between decision tree I and decision tree DCMa(ab) Measuring the difference Matrix is derived from DCMa(ab) Calculates DCMa(ab) at that point as the element value of MF.
6. The criterion for comparisons is d and the threshold for grouping capacity is 5-007.
7. At present, Minab=MF is the smallest non-zero factor.
8. (<E minab)
9. The row and column components in Decision Tree and in MF are all set to 0 if (Decision Tree I with less grouping capabilities) (Delete Decision Tree a)
10. Minab = The smallest non-zero element next
11. Otherwise, the element row's tree integration and the non-zero column will join the existing RF End random forest.

B) FCM

Let X=x1, y, and a data collection is represented by xn, And c represents a positive integer larger than one.Sets X1, y, Xc to X1,..., Xc=X or to the corresponding attribute of the predictor 1,..., c to μi(x)=1 if x to Xi is to Xi and mi(x)=0 if the x does not to Xi is to all i=1,,..c represent a division of X through c clusters. μ1,..., μc is X1, … , Xc Clustering X into c clusters is what this is called. With a fuzzy expansion, mi(x) will take values in the range [0, 1], resulting in $\sum_{i=1}^{c} \mu i(x)$ for all x in X. X is defined as μ 1,...,μc it is a fuzzy c-partition of in this case. As a result, JFCM [19] is known as the FCM objective function.

$$J_{(FCM)}(\mu, v) = \sum_{i=1}^{c} \sum_{j=1}^{c} \mu_{ji}^{m} d^{2}(xj, yi) \qquad (5)$$

where μij=μi(xj), μ={μ1, … , μc} Weighted m exponent is a number of c cluster centres that is larger than one and indicates the v={v1, y, vc}. With the following update equations, the FCM algorithm iterates over the required conditions for minimising JFCM.

$$vi = \frac{\sum_{i=1}^{c} \mu_{ji}^{m} x_j}{\sum_{j=1}^{c} \mu_{ji}^{m}} \ (i = 1, ..., c) \qquad (6)$$

QUOTE μ and v are revised at the end of each iteration (5). JFCM(μ, v) is iteratively optimised by the FCM algorithm until| μ(l+1)- μ^1 |≤e is the number of iterations.

iii) STICA

STICA – Spatio-Temporal Independent Component Analysis [16] [17]

Provided the eigendecompositionX˜ 5 U˜ V˜ t, stICA encapsulates that each U-image is a linear mixture of spatially independent k-pictures S and each V-string is a linear mixture of k T-strings temporarily independent.

$$X˜ = S\Delta Tt \qquad (1)$$

T is a n x k matrix consisting sequences of each other, Δ a scaling matrix diagonal. S is a matrix of k images that are mutually independent, T is a matrix of n x k sequences that are mutually exclusive. Ensures Δthat S and T have amplitudes that are sufficient for their respective cdfs αS and αT.

iv)   Naïve Bayes Classifier:

A probabilistic statistical classifier, A probabilistic predictive classifier is a Naive Bayesian classifier. 'Naive' refers to the assumption that there is little influence on the nature of certain characteristics in a data set. The "naive" assumption reduces computational complexity to a straightforward probability multiplication. The Naive Bayesian classifier has the greatest advantage in terms of time since it is the simplest algorithm among classification algorithms. This algorithm's simplicity aided in the easy handling of datasets with highdimensional feature room.

The naive Bayesian classifier develops accurate parameter estimates for small training data sets since it calculates pair and attribute frequencies from the training datasets. The algorithm measures the posterior probability of P(c | x) in the following parameters: x, y (p(x), p(c) and p(x|c).

$$p(c|x) = \frac{p(c|x)p(c)}{p(x)} \qquad (7)$$

The following is how the Naive Bayesian classifier works:

1. Make a frequency table out of the data collection.
2. To compile a Likeness Table divide the frequency by the total number of data samples.
3. Using the posterior likelihood formula, calculate the posterior probability (2).
4. As a result, choose the lass with the highest chance of success..

Despite abuses of the attribute independence assumption, the naive Bayesian classifier achieves high classification accuracy. In the field of medical evidence, the Naive Bayesian method is commonly used.

v)   Performance Measures

In a classification problem, the accuracy rate is used as the model's assessment exponent, and it reflects the classifier's capacity to judge all of the results. In simple terms, the consistency rate is the number of correctly labelled datasets divided by the total number of datasets. In general, the greater the classifier, the higher the precision. However, when dealing with unbalanced numbers, Precision isn't necessary in either case because correct identification of the minority is still more important than overall precision. [20].

Creation of a new model required for classification problems, or the use of existing models and achieving success on that model are calculated by means of the number of accurate estimates. This is effective on the accuracy of the classification rather than the estimation of whether the model is good or not. This is why the complexity matrix is used to explain the predictive evaluations of classification. The matrix that provides information about the real classes with the estimated classes performed via a classification model on the Test data is the complexity matrix.

The complexity Matrix has four parameters these are;

- tp: true positive
- fp: false positive
- fn: false negative
- tn: true negative

For two-class classification performance measurements, success criteria such as Accuracy, Specificity Sensitivity, Precision, Specificity, False Positive Rate, False Discovery Rate, F1- Score, Negative Predictive Value, False Negative Rate are calculated using Table 1. Calculation formulas are given

$$Accuracy\ ACC = \frac{tp+tn}{tp+fp+tn+fn} * 100 \qquad (8)$$

$$Sensitivity\ TPR = \frac{tp}{tp+tn} * 100 \qquad (9)$$

In true negative cases, the right proportion is TNR, and in true positive cases TPR is the right proportion. The better classifier is to accurately name all samples, so FP=0, FN=0. As a result, TPR=1, TNR=1 for the optimal classifier.

$$specificity\ SPC = \frac{tn}{tn+tp} * 100 \qquad (10)$$

$$Precision\ PPV = \frac{tp}{tp+fp} * 100 \qquad (11)$$

$$F1 - Score\ F1 = \frac{2tp}{2tp+fp+fn} * 100 \qquad (12)$$

$$Negative\ Predicitive\ value\ NPV = \frac{tn}{tn+fn} * 100 \qquad (13)$$

$$False\ Positive\ Rate\ FPR = \frac{fp}{tn+fp} * 100 \qquad (14)$$

$$False\ Discovery\ Rate\ FDR = \frac{fp}{tp+fp} * 100 \qquad (15)$$

$$False\ Negative\ Rate\ FNR = \frac{fn}{tp+fn} * 100 \qquad (16)$$
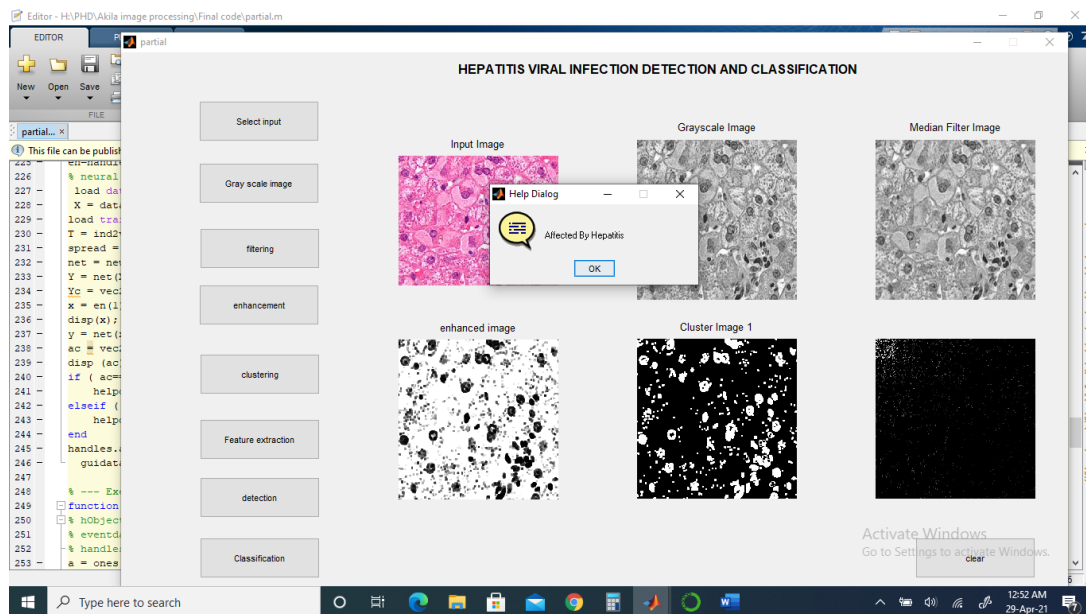
IV.   RESULT ANALYSIS

Figure2. Detection of Hepatitis viral infection and SITCA feature extraction

In above fig.2. Input image has been selected and subjected to preprocessing steps like gray scale conversion, Filtering and image enhancement, then subjected to segmentation based on combined clustering technique with random forest and fuzzy c-means methodology. Then the segmented image has been applied with SITCA method for image features extraction detection of infection has been performed with clustering and feature ectraction.
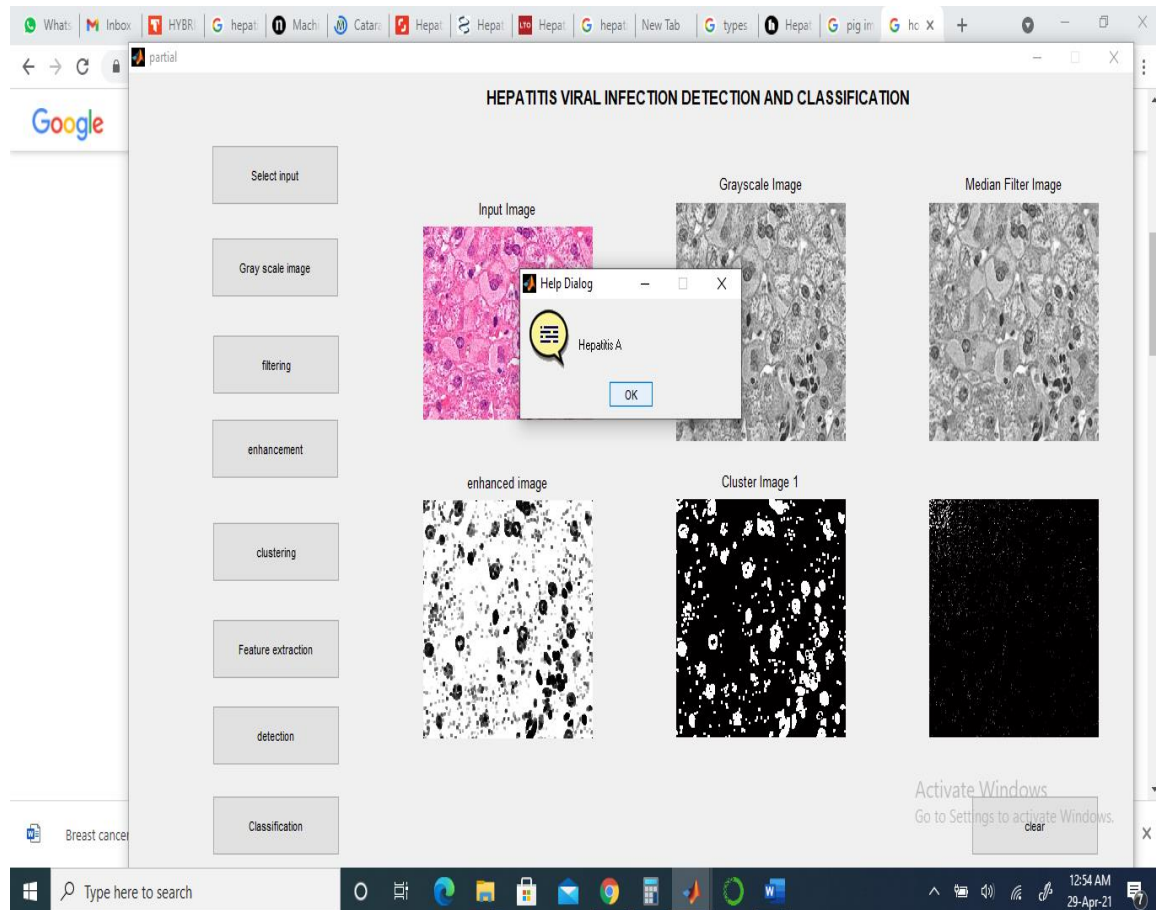
Figure3. Classification of Hepatitis viral type A

In above figure along with previous detection process those features extracted with SITCA are taken for classification of type of virus affected. There are 5 major catogeries of Hepatitis virus like A,B.C D and E. Classification has been performed with naïve bayes methodology.

Table I. comparative analysis accuracy of classification on types of viral infection

	A	B	C	D	E	Normal
Random forest segmentation and naïve bayes classification	79.8	81.4	83.2	84.4	80.2	86.7
FCM segmentation and naïve bayes classification	76.3	79.9	87.4	87.3	81.4	81.1
Hybrid (Random forest + FCM) segmentation and naïve bayes classification	87.1	84.3	89.7	88.3	86.7	89.4

Classification accuracy
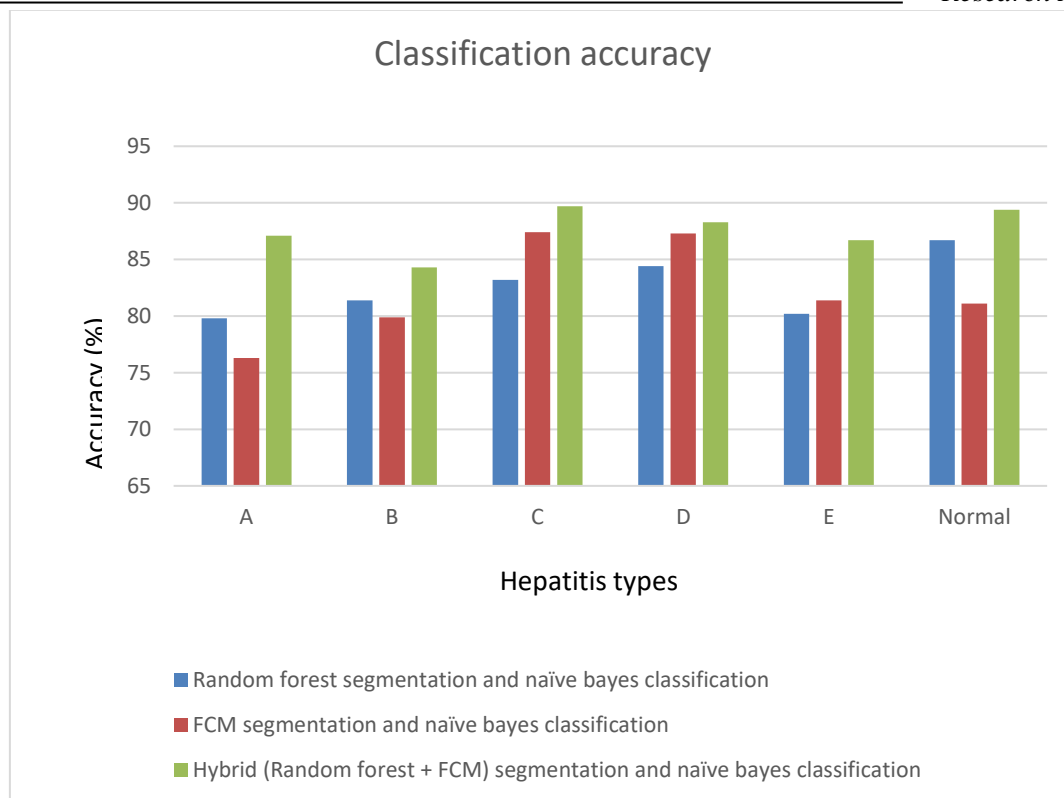
V.   CONCLUSION:

Here we have performed segmentation of hepatitis blood smear with Fuzzy C-means and random forest segmentation algorithm. Segmented images are subjected to feature extraction with SITCA (Spatio- Temporal Independent Component Analysis) that extracts every necessary feature for disease detection and classification. Extracted features are processed for disease detection and classification with Naïve bayes classifier. The detection gives 89% of accuracy in detection and classification.

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