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Graphics & Vision

Color Image Segmentation

Malaria Infected Erythrocyte

Highlights

Review of Microscopic Image

Technique of Motion Estimation

Discovering Thoughts, Inventing Future

Dr. Anis Bey

Dept. of Comput. Sci.,

Badji Mokhtar-Annaba Univ.,

Annaba, Algeria

Er. Pritesh Rajvaidya

Computer Science Department

California State University

BE (Computer Science), FICCT

Technical Dean, US

Email: pritesh@computerresearch.org,

deanusa@globaljournals.org

Er. Suyog Dixit

(M.Tech), BE (HONS. in CSE), FICCT

SAP Certified Consultant

CEO at IOSRD, Ph.DGAOR OSS

Technical Dean, Global Journals Inc.(US)

Website: www.suyogdixit.com

Email: suyog@suyogdixit.com,

deanind@globaljournals.org

Dr. Chutisant Kerdvibulvech

Dept. of Inf.& Commun. Technol.,

Rangsit University

Pathum Thani, Thailand

Chulalongkorn University Ph.D. Thailand

Keio University, Tokyo, Japan

Dr. Abdurrahman Arslanyilmaz

Computer Science & Information Systems Department

Youngstown State University

Ph.D., Texas A&M University

University of Missouri, Columbia

Gazi University, Turkey

Web: cis.ysu.edu/~aarslanyilmaz/professional_web

Dr. Sotiris Kotsiantis

Ph.D. in Computer Science, University of Patras, Greece

Department of Mathematics, University of Patras, Greece

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A Novel Search Technique of Motion Estimation for Video Compression

By Pranob K Charles, Dr. Habibulla Khan & Dr. K.S. Rao

JNTUH

Abstract- Video Compression is highly demanded now a days as due to the fact that in the field of entertainment, medicine and communication there is high demand for digital video technology. For the effective removal of temporal redundancy between the frames for better video compression Motion estimation techniques plays a major role. Block based motion estimation has been widely used for video coding. One such method is the Hierarchical Search Technique for BMA. By amalgamating the three different search algorithms like New three step search, New Full search and New Cross diamond search a novel hierarchical search methodology is proposed. Subsampling the original image into additional two levels is done and thereby the New Diamond search algorithm and a new three-step search algorithm are used in the bottom two levels and the Full Search is performed on the highest level where the complexity is relatively low. In terms of PSNR with reduced complexity this new proposed algorithm showed better performance.

Keywords: hierarchical search, motion estimation, PSNR, new cross diamond search, new three step search, BMA.

GJCST-F Classification: I.4.2, H.3.3

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A Novel Search Technique of Motion Estimation for Video Compression

Pranob K Charles [α] Dr. Habibulla Khan [σ] & Dr. K.S. Rao [ρ]

Abstract- Video Compression is highly demanded now a days as due to the fact that in the field of entertainment, medicine and communication there is high demand for digital video technology. For the effective removal of temporal redundancy between the frames for better video compression Motion estimation techniques plays a major role. Block based motion estimation has been widely used for video coding. One such method is the Hierarchical Search Technique for BMA. By amalgamating the three different search algorithms like New three step search, New Full search and New Cross diamond search a novel hierarchical search methodology is proposed. Subsampling the original image into additional two levels is done and thereby the New Diamond search algorithm and a new three-step search algorithm are used in the bottom two levels and the Full Search is performed on the highest level where the complexity is relatively low. In terms of PSNR with reduced complexity this new proposed algorithm showed better performance.

Keywords: hierarchical search, motion estimation, PSNR, new cross diamond search, new three step search, BMA.

I. Introduction

Video compression is the process of representing the video data using fewer bits than the original representation. Motion estimation plays a major role in Video Compression. As video requires much more space to store than still image, video compression is very much useful in reducing the storage space and which will eventually lead to lesser cost. It is carried out mainly by using BMA. In BMA both the reference frame and current frame are divided into blocks and for each block in the current frame the algorithm searches for a best match block in the reference frame. The search in the reference frame is conducted within a search window defined by parameter p. The displacement of the macro block in the reference frame with respect to macro block in the current frame is represented by a vector known as motion vector. The most suitable matching criteria that are used are mean square error (MSE), sum of absolute difference (SAD) etc.

Several BMA's have been developed over the years. The most basic is the FSA [1], where all the blocks are searched for a best match (255 comparisons). It is the best algorithm in terms of efficiency but the most computationally expensive and it is very time consuming. The TSS in comparison to FSA requires only 25 comparisons. Since it follows a fixed pattern, it works inefficiently on slow motion video sequences. The NTSS [2] enhances the TSS by using a half way stop technique. NTSS is more complex than TSS. The FSS [3] uses a centre biased checking point pattern with a half way stop technique being more complex. The CDS [4] uses a cross and diamond shape pattern. They are very complex. In Neighborhood Elimination approach [5] we use a spatial correlation property and a half way stop technique. This approach however has low PSNR for medium and fast motion sequences. The ABC Algorithm [6] has a low PSNR compared to FSA. The Modified PSO [7] offers reduced number of computations and high PSNR for large motion, but not for slow and medium motion sequences. The Octagon Square BMA [8] uses an octagon and square shape pattern and can identify both large and small motion. It has the disadvantage of being a fixed pattern algorithm. The BBGDS [9] Algorithm works better in small motion but it has very large motion vector for large motion video sequences.

Most of these BMA perform well in terms of estimating slow, medium and fast motion video sequences. The performance of the proposed hierarchical search technique unlike the other algorithms is close to the Full Search with reduction in complexity.

II. Motion Estimation Algorithms for Hierarchichal Search

a) Full Search Algorithm (FS)

FS Algorithm searches all the search points within the search window for a best match. Therefore it is very simple to implement and is highly efficient but it has very high computational time.

b) New Cross Diamond Search Algorithm (NCDS)

The NCDS [10] Algorithm follows a pattern. The first step stop involves a search of only 5 search points while the second step stop required 8 search points. An unrestricted large diamond search (DS) pattern was employed in the subsequent steps followed by a final small diamond search.

Author α: External Research Scholar, JNTUH Faculty, Department of ECE, ALIET Vijayawada, A.P, India. e-mail: pranob2005@gmail.com
Author σ: Professor & Dean, Department of ECE, K L University, Vijayawada, A.P, India. e-mail: habibulla@rediffmail.com
Author ρ: Professor & Director, Anurag Group of Institutions, Hyderabad, Telangana State. e-mail: ksrao_prn@rediffmail.com

c)   New Three Step Search Algorithm (NTSS)

The NTSS Algorithm is an improvement on the TSS Algorithm so as to find small motions. It has a half way stop for first and second steps.

III.   PROPOSED METHOD

In the proposed hierarchical search technique, an input and reference frame are subsampled into three levels. Level 1 is subsampled both horizontally and vertically by a factor of 2 to get Level 2. This level in turn is subsampled both horizontally and vertically by a factor of 2 to get Level 3 as shown in Fig 1.The three different algorithms such as Full Search Algorithm, New Cross Diamond Search Algorithm and New Three Step Search Algorithm are applied to the various Levels .The best match motion vector obtained from Level 3 is passed on to Level 2 and the best match motion vector obtained from Level 2 is passed on to Level 1.The motion vector so obtained from Level 1 is considered the final motion vector of the motion estimation process.
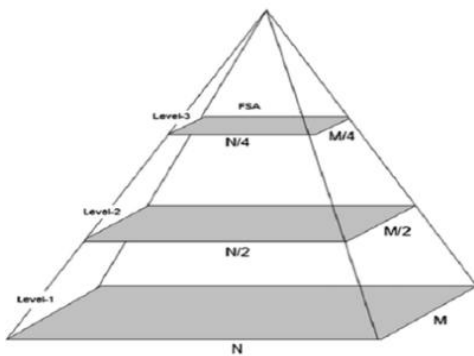
Fig.1: Different Levels in a HS algorithm

IV.   PROPOSED HSBMA ALGORITHM

Step 1: Level-1 is the lowest level and consists of the original frame at its full resolution. This level is subsampled by a factor of 2 in vertical and horizontal directions to produce Level-2.

Step 2: This step involves sub -sampling Level-2 in the same way to produce Level-3 (highest level).The sub-sampling process ends, by getting Level-1, Level-2 and Level-3.

Step 3: In this step, the search starts from the highest level (Level-3) using 4 X 4 block sizes, where a FS algorithm will be performed to get the initial coarse motion vector and the best match position will be passed to the lower level (Level-2).

Step 4: This step involves searching Level-2 by using the new proposed cross-diamond search pattern (using 8 X 8 block sizes) to get a new motion vector, and the

best match position will be passed to Level-1 (Lowest level).

Step 5: In this step, the New Three-Step-Search algorithm is used on Level-1 utilizing 16 X 16 block sizes. Hence the final motion vector is obtained and that will be added to the previous image to get the next predicted image frame.

V.   IMPLEMENTATION AND RESULTS

The section presents the results of applying the various algorithms included in the proposed Hierarchical Search Motion Estimation technique. Simulations have been performed over the standard Video Sequence "Sample Video.avi" has moderately complex motion getting medium content regarding its motion content. By using the matlab the The video is extracted into frames. Here the video is initially run in MATLAB using the "VideoReader" command. It is then extracted into frames as shown in Fig 2.
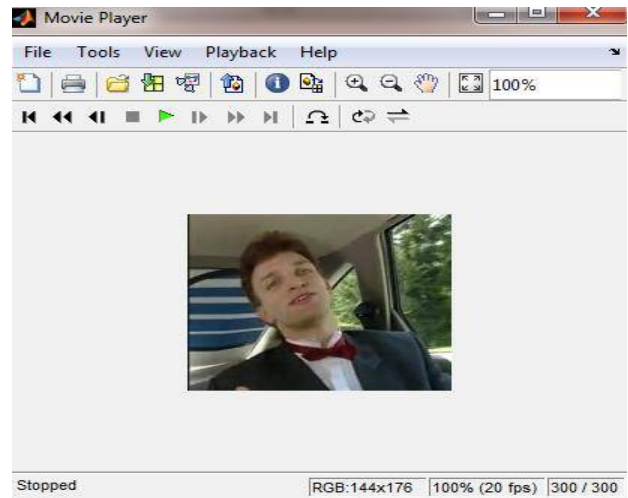
Fig. 2: Video Played in MATLAB

Fig 3 shows the lowest level (Level-1) consists of the original frame at its full resolution. The next Level-2 consists of Level-1 image sub-sampled by a factor of 2 in vertical and horizontal directions as in Fig (b).And again sub-sampling Level-2 in the same way produces Level-3 image (highest level) as in Fig (c).

Fig. 3: Input image subsampled into three Levels of different resolutions

The Input frame and Reference frame are as shown in Fig 5,6,7. Motion estimation is performed using the three above mentioned algorithms on the three levels. The Compensated Image at the end of HSBA is shown in Fig 8.

(a)

(b)
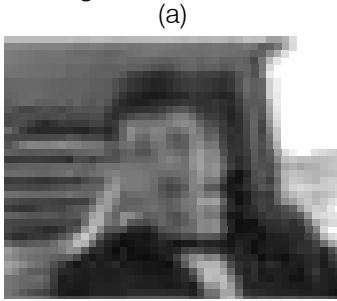
Fig. 4: Input (a) and Reference Frame (b) for Full Search Algorithm

(a)

(b)

Fig. 5: Input (a) and Reference Frame (b) for New Cross Diamond Search Algorithm

(a)

Fig. 6: Input (a) and Reference Frame (b) for New Three Step Search Algorithm

Fig. 7: Compensated Image of Input and Reference for Carphone using HS Algorithm

VI. Performance

The PSNR plot and the plot for No of Search Points per MacroBlock vs Frame Number for the Carphone sequence with the FS different algorithms are as shown below:
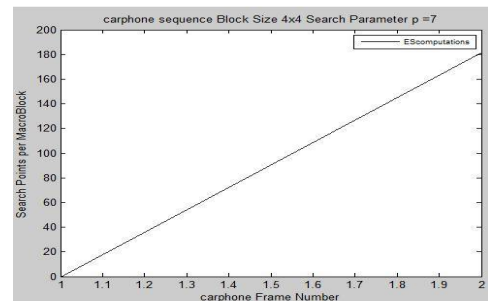
Fig. 8: Search Points per MacroBlock vs Frame Number in FS Algorithm
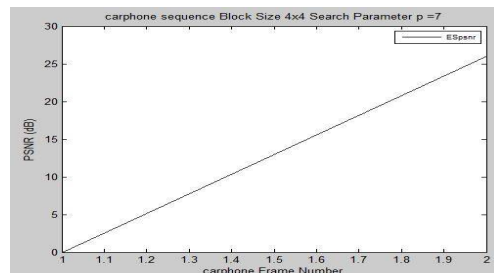
Fig. 9: PSNR of the motion compensated image w.r.t. original image vs Frame Number in FS Algorithm
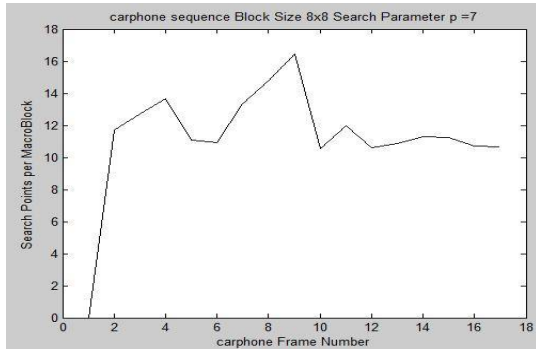
Fig.10: Search Points per Macro Block vs Frame Number in NCDS Algorithm
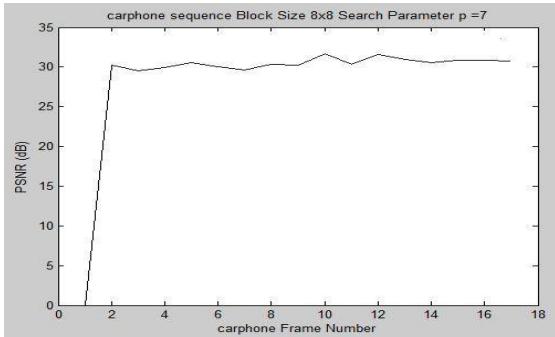
Fig. 11: PSNR of the motion compensated image w.r.t. original image vs Frame Number in NCDS Algorithm
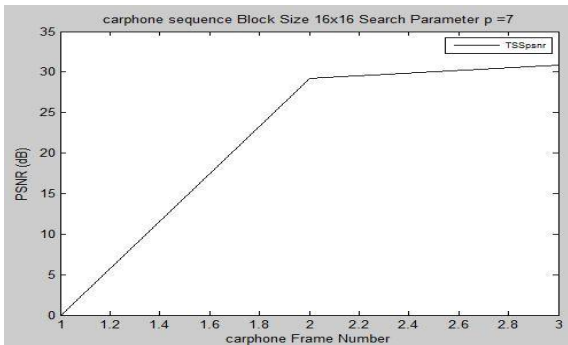
Fig.12: PSNR of the motion compensated image w.r.t. original image vs Frame Number in TSS Algorithm

The value of No of computations for the Full Search Algorithm is shown as below:

Table I: No of Computations

Algorithm	No of Computations
FULL SEARCH	213.38

The value of the No of computations for the HS Technique which is the sum of all the computations by the three algorithms in the three levels of the frame is lesser than that of the Full Search algorithm.

Table II: No of Computations

HIERARCHICHAL SEARCH	
Algorithm	No of Computations
FULL SEARCH	181.444
NEW CROSS DIAMOND	5.1708
NEW THREE STEP SEARCH	22.3485

Also the value of PSNR for the HS Technique is approaching that of the most efficient FS Algorithm.

Table III: PSNR and MSE of the FS and HS Technique

ALGORITHM	PSNR	MSE
FULL SEARCH	32.3436	37.9074
HIERARCHICHAL SEARCH TECHNIQUE	29.2417	22.3485

VII. CONCLUSION

Motion estimation algorithms intend to construct the current frame as accurately as possible while keeping the computational complexity acceptable. Full Search Algorithm is the most efficient for Motion Estimation. But its highly expensive. Hierarchical Fast Search motion estimation is in order to reduce the Full Search complexity. Therefore, a new Hierarchal Search technique is developed that achieves a performance much better than the existing hierarchical techniques with reduction in complexity.

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Review of Microscopic Image Processing Techniques to wards Malaria Infected Erythrocyte Detection from Thin Blood Smears

By Md. Jaffar Sadiq & Dr. V.V.S.S.S. Balaram

Sreenidhi Institute of Science & Technology

Abstract- In order to diagnose malaria, the test that has traditionally been conducted is the gold standard test. The process mainly entails the preparation of a blood smear on glass slide, staining the blood and examining the blood through the use of a microscope so as to observe parasite genus plasmodium. Although these are several other kinds of diagnostic test solutions that are available and which can be adopted, there are numerous shortcomings which are always observed when microscopic analysis is carried out. Presently, the treatments are hugely conducted based on symptoms and upon the occurrence of false negatives, it might be fatal and may result into the creation of different kinds of implications. There have been a number of deaths which have been associated with malaria and as a result, there is the dire need to ensure that there is early detection of malarial infection among the people.

Keywords: texture features, soft computing, morphological features, microscopic image processing, malaria parasite, malaria detection, machine learning, heuristic scale, feature selection, erythrocyte, disease diagnosis, classifiers, case based reasoning, blood samples.

GJCST-F Classification: J.3

REVIEWOFMICROSCOPICIMAGEPROCESSINGTECHNIQUESTOWARDSMALARIAINFECTEDERYTHROCYTEDETECTIONFROMTHINBLOODSMEARS

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Keywords: texture features, soft computing, morphological features, microscopic image processing, malaria parasite, malaria detection, machine learning, heuristic scale, feature selection, erythrocyte, disease diagnosis, classifiers, case based reasoning, blood samples.

I. Introduction

It is worth pointing out that Malaria is one of the epidemic health disease which is having huge implications on peoples' health. In a number of nations globally, individuals faces the risk of malaria and based on the World Health Organization reports, annually, millions of individuals die as a result of malaria. The reports also indicate that about 250 million infections takes place every year as a result of the parasites of genus plasmodium, with over 98 percent of deaths being brought about by plasmodium falciparum. The different kinds of techniques which are currently being used in order to diagnose infections from Falciparum include various manual process.

This takes place even in the developing nations. Despite the fact that there are a number of highly advanced techniques which can be adopted, the process of manual microscopy of blood films over the slides is still considered as the golden standard solution. The manual microscopy has more advantages in comparison to the other kinds of techniques due to sensitivity, as well as because of specifics. Among the disadvantages associated with the use of manual microscopy techniques, the need for human intervention in the process is very high, and at the same time, there is the possibility that it may result into late diagnosis and at the same time, there may also be erroneous diagnosis.

The use of the microscope requires extensive training to gain sufficient expertise in diagnosis. In addition, the huge volume of samples which are supposed to be analyzed may result into various kinds of inconsistencies in the reports which are generated. In addition, the other impacting factors include blood smear, the quality of the stain, as well as the quality of microscope which is used during the process of analysis. The expertise of pathology professionals is also one of the leading factors which have to be taken into consideration.

The use of microscope requires quality training to ensure that expertise is gained in the process of diagnosis. Considering the quantum of samples which have to be analyzed, this microscopic method may be inconsistent. In addition, factors such as stain quality, blood smear, microscopic quality, as well as the domain expertise of the professionals play a huge role in ensuring that the diagnosis is done effectively. When computer aided diagnostic techniques such as image-based diagnosis technique are employed, the different kinds of limitations which are associated with the manual process can be adequately looked into.

The main aim of this report is to study the semi-automatic diagnosis technique based on image processing, as well as the ones which offer highly effective and highly reliable solution. In the past, a number of studies have been carried out which have proposed different kinds of computer vision or image based algorithms. However, a number of the algorithms are supervised and complex solutions, which needs manual intervention, as well as calibration. Taking into

Author α: Associate Professor, Dept., of IT, Sreenidhi Institute of Science & Technology, Ghatkeser, Hyderabad, Telangana State, India. e-mail: jaffer_610@yahoo.com
Author σ: Professor& HOD, Dept., of IT, Sreenidhi Institute of Science & Technology, Ghatkeser, Hyderabad, Telangana State, India.

consideration the rate at which the given disease is impacting, as well as the volume of the samples which are supposed to be analyzed, there is the integral need for a highly effective and a robust solution that requires minimal human intervention.

In conditions like that, computer aided solutions are capable of ensuring that there is a highly accurate and a highly consistent diagnosis of the true causes of malaria. It can also make sure that highly appropriate diagnosis of the symptoms of malaria in the case samples are carried out. Process of Manual microscopy is aimed at investigating under the microscope, the thin blood films on the slides for assessing the ratio of the infected red blood cells (iRBCs) which are referred to as Parasitemia over about 100 microscopic fields. At the same time, the pathologists should also study parasite morphology by different life cycle stages for specification advocated by World Health Organization practical microscopy guide.

In most cases, Giemsa staining technique is always used in order to highlight the parasites. There are a number of disadvantages which are brought as a result of the use of Giemsa method. These include the fact that it always stains the other blood film features such as the WBC, platelets, as well as the slide artifacts. The other stained objects may result into various kinds of implications during the process of analysis of the results through the use of the manual microscope.

In the whole world, with the ever increasing population, even the risk of individuals who are prone to malaria is also increasing at an alarming rate and every year, there is an increase indeaths which are linked to malaria.

Malaria Parasitemia is always used as the parameter to affirm the quantum of parasites in the blood of the patients and besides, it is also considered to be one of the main indicators of the levels of infection of malariain the body of the human beings. Manual process of assessing thin blood smears through the use of the microscope is highly tedious and at the same time, it generally consumes a lot of time. Besides, it is associated with so many errors. Although the automated assessments are capable of effectively addressing some of these limitations, the in ability in terms of assessing cases which are different from the standard model have turned out to be a huge challenge.

Althougha microscope malaria parasite is always detected in the blood slides, detection, as well as the recognition of plasmodium is always possible by the staining method (Giemsa), and this is a chemical process. It highlights the life treating plasmodium parasites, WBC, and the RBCs.

a) *Microscopic Image Processing*

Microscopic images are always employed in molecular biology, as well as in medical domain. Because the image modalities are diverse, several

issues always arise after the first data acquisition stage. In this report, numerous algorithms have been reviewed so as to observe the existing solutions besides proposing highly essential pipeline of microscopic image storage or compression and the ones which may be assessed in a manner that is highly efficient.

II. Nomenclature of the Erythrocyte Features

Erythrocyte refers to the cell which is always observed in the blood, which is having a life of approximately 120 days. Analysis of the microscopic image of the blood cells are carried out in order to diagnose different diseases such as cancer and malaria among others [1]. Using the size, texture, as well as the color, the various differences between the abnormal and the normal erythrocyte can easily be noted. During the normal conditions, the mature erythrocytes are always round, biconcave disc-shaped and at the same time, the diameter of the nuclear cell is about 7-8 microns. In addition, it is worth pointing out that the erythrocytes which are normal are always termed as normocytic while the ones which comprises malarial infection have changes in their features as indicated in Fig.1

(a) The normal Erythrocyte

(b) The infected Erythrocyte
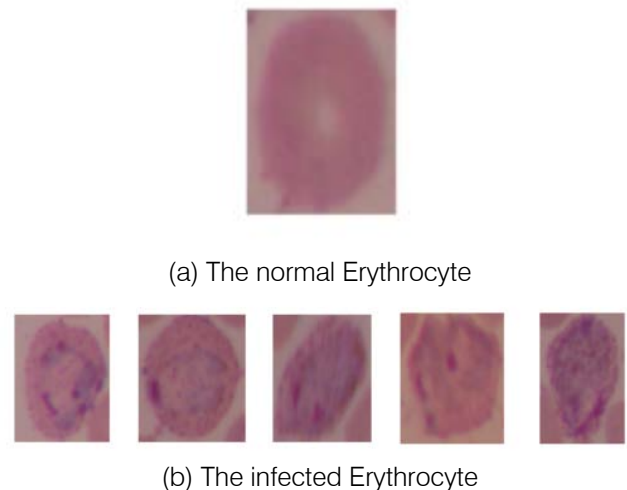
Figure 1: Infected and Normal Erythrocytes

a) *Feature extraction from Microscopic Blood Smear Images*

Feature extraction refers to the approach that entails the evaluation of the different kinds of images for the identification of objects or the regions of interest and analyzing tissues in pathology slides for structure as well as for other kinds of features. In order to make sure that the right features are used in the process of analysis, highly appropriate selection of subgroup is vital for improving the levels of accuracy of classification as well as for the minimization of any type of complexities. In order to distinguish the non-infected and the infected erythrocytes, different features can be adopted from a

wide array, and computation of fresh variables can be conducted.

Feature sets as indicated above are comprising factors that are aimed at distinguishing variance for class and in class of feature vector space, i.e. differentiating the classes by various features. Texture features, morphological features, as well as intensity features are some example of the set of features that are highly resourceful in distinguishing between the non-infected and the infected erythrocytes.

The morphological features are signifying the shape and the size of erythrocyte without considering the density, and strongly in the case of P.Ovaleand P.Vivaxinfections, the erythrocytes are enlarged. However, erythrocyte generally remains the same in the case of the P.falciparum. several factors such as the perimeter, area, compactness ratio, eccentricity, minor axis of best fit ellipse, major axis of best fit ellipse, bending energy, as well as roundness ratio [2] some of the features which are highly significant with the Morphological features. It is also worth pointing out that spatial distribution of intensity within a given range is offered by texture features exploration. Gray level co-occurrence matrix (GLCM) is an integral element of intensity, as well as texture features, saturation histogram, local binary pattern, laplacian and the gradient textures [3] [4] [5].

It is also worth pointing out that researchers have laid much emphasis on several features for the classification of the non-infected and the infected erythrocyte. F.BorayTek et.al has employed the feature set which comprises are agranuometry, color histogram, relative shape measurements, and auto-correlogram for the diagnosis of malaria parasite infection in the erythrocyte [4]. As [5] indicates, in order to detect erythrocyte observation, the technique of automated image processing have been proposed.

[6] Proposessemi-automated technique for the quantification, as well as for the classification of the malaria infected erythrocytes. Some of the main features which have been used in the model include gray scale histogram, sobel histogram, saturation level histogram, as well as the gray scale histogram.

Spirngl et.al proposes the mode of automatic malaria diagnosis through the use of microscopic imaging process. The main key features which have been chosen in the model include Hu set of invariant moment, flat texture, intensity histogram, gradient features, run-length matrix, and co-occurrence matrix for the classification of theerythrocytes [7].

In [8] Perimeter area, as well as the form factor are employed in digital analysis of the changes by the plasmodium vivax. They are followed by [9] content based retrieval technique which depends on features such as Hu moment and intensity histogram as the major features have been proposed.

Color and the statistical features are comprising the perimeter, the area, the grey scale histogram, metric and saturation histogram are majorly employed in [10] for the detection of malaria. In [11] the researchers employed various feature sets such as the nuclear density and Nucleon cytoplasmic ratio in detecting the stages of malaria parasite in a manner that is automated. In [12], the quantum of pixels which comprises of chromatin dot stain and standard deviation linked to value channel of the HSV representation for every ROI, are chosen as the main features during the classification of the erythrocytes which are infected by malaria. In [13], researchers have laid much emphasis on the development of web based frame work for classification on the basis of texture, as well as automated storage of the malaria parasite images through the use of some features such as run length matrix, fractal dimension, local binary pattern, as well as gray level co-occurrence matrix.

Features such as color auto-correlogram, color histogram, Hu moment, and relative shape measurement which depends on Mobile support for the Diagnosis of Communicable Diseases within the Remote Locations have been proposed by [14]. [15] Proposesimage analysis system which is dependent on feature sets such as color attributes, gray level texture, as well as geometric features to ensure the automatic detection and automatic classification.

[16] Proposes multi-scale laplacian of Gaussian and Gabor filter based technique. At the same time, the process of quantitative characterization for plasmodium vivax in infected erythrocytes has generally been proposed in [17].

[18] Proposes automatic screening of the malaria parasite based on machine learning which comprises 96 features which generally includes gray level run length matrix, fractal dimension, entropy, heraldic texture, histogram based features, and several other such features sets.

Malaria Parasite Detection in the Giemsa-Stained Blood Cell images which rely on features have been proposed by [19]. [20] proposes morphological features based diagnosis of malaria infections while in [21], the researchers proposed a highly effective technique for ensuring automatic classification of vivid blood diseases through the use of the digital image processing methods. In it, histogram based features for different color channels such as the intensity, hue, as well as saturation are employed in the identification of the erythrocytes, which are normal and the ones which have been infected. [22] Proposes that automatic detection of the malaria parasite can be carried out through the usage of histogram of color channel, as well as fractal dimension. Symptom analysis of malaria disease can be done through the use of histogram, as well as through the use of image processing features as [23] proposes. [24] Proposed morphological feature, as

well as textural features based solution for ensuring rapid diagnosis of malaria.

At the same time, it is worth pointing out that diagnosis of malaria over the thin blood smears was proposed where features such as energy, standard deviation, phase of image, skewness, and energy among others are employed. [25].

[26] Also proposed the technique of computer vision screening of the plasmodium falciparum candidate areas in blood smears. Feature sets such as scale invariant feature transformation and local binary pattern rotation invariant local contrast are employed during the process of analysis. Automatic characterization based analysis of the microscopic images of the thin blood smears have also been proposed which comprises about 16 morphological features, as well as 80 texture feature sets.

III. Review of Learning Based Malaria Detection Strategies

Makkapati and Rao [27] supports segmentation of HSV color space in which Red Blood Cells, WBCs, as well as Parasites are color space segmented besides the estimation of the optimal saturation thresholds. The process is associated with 83 percent sensitivity, and at the same time, it always operates in HSV space. However, it has a challenge which generally includes the fact that it is only capable of detecting the optimal threshold but is not capable of determining any type of global or local threshold. At the same time, it is worth pointing out that the solution generally reflects on color image processing methods.

Ravi raja and et.al [28] proposed the techniques of blood image processing for the detection of malarial parasites which comprises infected erythrocytes after the use of statistical based approach for classification. A wide array of information such as the color of the infected blood, shape and size are always used in the process of the analysis. When the images are compared to infected images, the process of image transformation is conducted through the use of shaping and scaling, for the reconstruction of the image.

Ruberto et.al [29] introduced the Morphological approach technique where segmentation of the cell images are highly accurate in comparison to the traditional watershed based algorithm. The non-flat disk-shape structuring components are adapted so as to enhance the level of accuracy of the normal watershed oriented algorithm and this has made the performance to be highly effective. The use of such kind of methods has brought about better understanding of the structure of the RBC structure, in the existing watershed based algorithm.

Sadeghian et.al [30] has generally illustrated a framework, where digital image processing is employed in the segmentation of the white blood cells. The gray level image processing is employed in order to classify it into two parts: one as morphological analysis based nucleus segmentation while the other one as cytoplasm segmentation depending on thresholding of pixel intensity. [27] Offers a discussion of the various kinds of processes which depends on RGB color space which segments the RBC's, as well as malarial parasites. In this solution's experiments, images are taken from Leishman-stained blood smears. 83 percent of sensitivity has also been observed in this model.

[28] Proposes automated image analysis based solution. This process is founded on detection of parasite boundaries, as well as edge detection for representing cell. Stages such as pre-processing, edge linking, edge detection, as well as clump split are employed in order to ensure effective processing of the proposed solution.

[31]Proposes the use of solution of digital images through the use of microscopic slides. For training sets, feed forward back propagation neural network has been employed. 64 X 64 pixel images are employed in order to train the data set, as well as segmentation into digital image.

Chen Pan et.al [32] proposed Image retrieval based solution. Its classifying cell of image is comprising high image databases. Two kinds of histogram are employed during the process. Kernel Principal Component Analysis (KPCA) is employed in order to extract highly effective features from feature vector.

In [33], the researcher proposes techniques of automatic detection, as well as classification of the MCCs. The technique of block region growing, as well as that of k-means clustering is used for the extraction of the region. Accordingly, the blanket technique is employed during the identification of the MMCs clusters. The solution has gained 95 percent high classification and about 93 percent detection rate.

Amit and P U [34] introduced the segmentation of the infected cells in blood smear images which comprises adoptive threshold that is carried out through the application of Otsu algorithm, and it is capable of generating better result in comparison to the averaging technique.

Rapid Diagnostic Tests (RDTs)as [35] points out are employed in immune chromatographic techniques for the detection of the antigens which are derived from malaria in the lyses blood. Tests like that are presently used in detecting Histidinerich protein II, as well as Parasite lactate dehydrogenizes (pLDH). [36] Points out that Histidinerich protein II is always produced by the trophozoites, as well as by the young gametocytes of P.

Quantitative Buffy Coat (QBC) speed was proposed by [35] for the detection of malarial parasites and it is having definitive advantage in laboratories. It is comprising several samples. It is often noted that there

is barely any loss of the parasites as a result of the usage of the procedure. [36] Lays much focus on the advantage of the QBC model. Technicians are capable of carrying out QBC test besides detecting malaria parasite in a less than one day. On the contrary, the constraints include the comparatively higher costs of carrying out the given model, as well as the scope of leak or the breakage of the blood filled QBC tubes. In addition, the lack of scope for the management of the permanent record of the test is the other major disadvantage which is associated with the given model [37].

In addition, it is worth pointing out that QBC techniques generally reflect very high levels of sensitivity and specificity during the tests which are being carried out in the laboratory in comparison to the field level tests when compared to the blood smears technique. Otsu algorithm approach is highly effective in comparison to the other kinds of models, and the main advantage of this algorithm is the fact that despite the numerous evaluations, less time is always consumed when it is employed. Among every data science strategy which is considered for carrying out the feature sets, computer vision of the microscopic images provides better quality outcome. This reviews points out that there is huge scope for enhancing the feature optimization strategies for the diagnosis of the disease through the application of data science strategies on computer vision of the microscopic images.

IV. Conclusion

This report has mainly reviewed various data science strategies such as mining, machine learning, heuristic, as well as statistical approaches which are used over microscopic image features such as the local binary patterns, texture, as well as morphological features, for the achievement of disease prediction during the early stages. Focus has been more on comprehending the scope, as well as the implications envisaged in the computer vision of the microscopic image analysis which ought to be capable of observing the Parasitemia counts within sub-standard smears. The review has provided some of the main limitations such as the lack of optimal feature set optimization techniques. The report also notes that accuracy of the search strategies are often observed in the existing techniques which are provided by the contemporary literature. The report has also reviewed some of the highly suitable description features which constitutes discriminative properties for the classification of blood smears as erythrocytes, as well as parasite infected erythrocytes. According to the report, highly efficient features have to be used for the analysis aimed at improving the process outcome. The key areas such as the feature extracting techniques, image research, as well as classification strategies are highly significant and should be taken into consideration when carrying out future research.

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Towards Arabic Alphabet and Numbers Sign Language Recognition

By Ahmad Hasasneh & Sameh Taqatqa

Palestine Ahliya University

Abstract- This paper proposes to develop a new Arabic sign language recognition using Restricted Boltzmann Machines and a direct use of tiny images. Restricted Boltzmann Machines are able to code images as a superposition of a limited number of features taken from a larger alphabet. Repeating this process in deep architecture (Deep Belief Networks) leads to an efficient sparse representation of the initial data in the feature space. A complex problem of classification in the input space is thus transformed into an easier one in the feature space. After appropriate coding, a softmax regression in the feature space must be sufficient to recognize a hand sign according to the input image. To our knowledge, this is the first attempt that tiny images feature extraction using deep architecture is a simpler alternative approach for Arabic sign language recognition that deserves to be considered and investigated.

Keywords: component; arabic sign language recognition, restricted boltzmann machines, deep belief networks, softmax regression, classification, sparse representation.

GJCST-F Classification: I.5, I.7.5

TOWARDSARABICALPHABETANDNUMBERSSIGNLANGUAGERECOGNITION

Strictly as per the compliance and regulations of:

Towards Arabic Alphabet and Numbers Sign Language Recognition

Ahmad Hasasneh [α] & Sameh Taqatqa [σ]

Abstract- This paper proposes to develop a new Arabic sign language recognition using Restricted Boltzmann Machines and a direct use of tiny images. Restricted Boltzmann Machines are able to code images as a superposition of a limited number of features taken from a larger alphabet. Repeating this process in deep architecture (Deep Belief Networks) leads to an efficient sparse representation of the initial data in the feature space. A complex problem of classification in the input space is thus transformed into an easier one in the feature space. After appropriate coding, a softmax regression in the feature space must be sufficient to recognize a hand sign according to the input image. To our knowledge, this is the first attempt that tiny images feature extraction using deep architecture is a simpler alternative approach for Arabic sign language recognition that deserves to be considered and investigated.

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I. Introduction

Sign language continues to be the best method to communicate between the deaf and hearing impaired. Hand gestures enable communication between deaf people during their daily lives rather than speaking. In our society, Arabic Sign Language (ArSL) is only known for deaf people and specialists, thus the community of deaf people is narrow. To help people with normal hearing communicate effectively with the deaf and the hearing-impaired, numerous systems have been developed for translating diverse sign languages from around the world. Several review papers have been published that discuss such systems and they can be found in [1]–[7].

Generally, the process of ArSL recognition (ArSLR) can be achieved through two main phases: detection and classification. In stage one, each given image is pre-processed, improved, and then the regions of interest (ROI) is segmented using a segmentation algorithm. The output of the segmentation process can thus be used to perform the sign recognition process. Indeed, accuracy and speed of detection play an important role in obtaining accurate and fast recognition process. In the recognition stage, a set of features (patterns) for each segmented hand sign is first extracted and then used to recognize the sign. These features can be used as a reference to understand the differences among the classes.

Recognizing and documenting of ArSL have only been paid attention recently, where few attempts have investigated and addressed this problem, see for example [8]–[11]. The question of ArSL recognition is therefore a major requirement for the future of ArSL. It facilitates the communication between the deaf and normal people by recognizing the alphabet and numbers signs of Arabic sign language to text or speech. To achieve that goal, this paper proposes a new Arabic sign recognition system based on new machine learning methods and a direct use of tiny images.

The rest of the paper is organized as follows. Section2 presents the current approaches to Arabic alphabet sign language recognition (ArASLR). Section 3 describes the proposed model for ArASLR. Conclusions and future works are presented in section 4.

II. Current Approaches

Studies in Arabic sign language recognition, although not as advanced as those devoted to other scripts (e.g. Latin), have recently shown interest [8]–[11]. We have also seen that current research in ArSLR has only been satisfactory for alphabet recognition with accuracy exceeding 98%. Isolate Arabic word recognition has only been successful with medium-size vocabularies (less than 300 signs). On the other hand, continuous ArSLR is still in its early stages, with very restrictive conditions.

Current approaches on sign language recognition usually falls into two major approaches. The first one is sensors based approaches, which employs sensors attached to the glove. Look-up table software is usually provided with the glove to be used for hand gesture recognition. Recent sensors based approaches can be found, for instance, in [11]–[14]. The second approaches, vision-based analysis, are based on the use of video cameras to capture the movement of the hand that is sometimes aided by making the signer wear a glove that has painted areas indicating the positions of the fingers and the wrist then use those measurements in the recognition process. Image-based techniques exhibit a number of challenges. These include: lighting conditions, image background, face and hands segmentation, and different types of noise.

Author α σ: Information Technology Department Palestine Ahliya University Bethlehem, West Bank, Palestine.
e-mails: ahasasneh@paluniv.edu.ps, sameh@paluniv.edu.ps

Among of image-based approaches, some authors [15] introduced a method for automatic recognition of Arabic sign language alphabet. For feature extraction, Hus moments were used followed by support vector machines (SVMs) to perform the classification process. A correct recognition rate of 87% was achieved. Other authors in [16] developed a neuro-fuzzy system. The proposed system includes five main steps: image acquisition, filtering, segmentation, and hand outline detection, followed by feature extraction. Bare hands were considered in the experiments, achieving a recognition accuracy of 93.6%. In [17], the authors proposed an adaptive neuro-fuzzy inference system for alphabet sign recognition. A colored glove was used to simplify the segmentation process, and geometric features were extracted from the hand region. The recognition rate was improved to 95.5%. In [18], the authors developed an image-based ArSL system that does not use visual markings. The images of bare hands are processed to extract a set of features that are translation, rotation, and scaling invariant. A recognition accuracy of 97.5% was achieved on a database of 30 Arabic alphabet signs. In [19], the authors used recurrent neural networks for alphabet recognition. A database of 900 samples, covering 30 gestures performed by two signers, was used in their experiments. The Elman network achieved an accuracy rate of 89.7%, while a fully recurrent network improved the accuracy to 95.1%. The authors extended their work by considering the effect of different artificial neural network structures on the recognition accuracy. In particular, they extracted 30 features from colored gloves and achieved an overall recognition rate of 95% [20].

A recent paper reviews the different systems and methods for the automatic recognition of Arabic sign language can be found in [7]. It highlights the main challenges characterizing Arabic sign language as well as potential future research directions. Recent works on image-based recognition of Arabic sign language alphabet can be found in [9], [10], [21]–[25]. In particular, Naoum et al. [9] proposes an ArSLR using KNN. To achieve good recognition performance, they proposed to combine this algorithm with a glove based analysis technique. The system starts by finding histograms of the images. Profiles extracted from such histograms are then used as input to a KNN classifier. Mohandes [10] proposes a more sophisticated recognition algorithm to achieve high performance of ArSLR. The first attempt to recognize two-handed signs from the Unified Arabic Sign Language Dictionary using the CyberGlove and SVMs to perform the recognition process. PCA is used for feature extraction. The authors in [21] proposed an Arabic sign language alphabet recognition system that converts signs into voice. The technique is much closer to a real-life setup; however, recognition is not performed in real time. The system

focuses on static and simple moving gestures. The inputs are color images of the gestures. To extract the skin blobs, the YCbCr space is used. The Prewitt edge detector is used to extract the hand shape. To convert the image area into feature vectors, principal component analysis (PCA) is used with a K-Nearest Neighbor Algorithm (KNN) in the classification stage. Furthermore, the authors in [22] and [23] proposed a pulse-coupled neural network (PCNN) ArSLR system able to compensate for lighting nonhomogeneity and background brightness. The proposed system showed invariance under geometrical transforms, bright background, and lighting conditions, achieving a recognition accuracy of 90%. Moreover, the authors in [24] introduced an Arabic Alphabet and Numbers Sign Language Recognition (ArANSLR). The phases of the proposed algorithm consists of skin detection, background exclusion, face and hands extraction, feature extraction, and also classification using Hidden Markov Model (HMM). The proposed algorithm divides the rectangle surrounding by the hand shape into zones. The best number of zones is 16 zones. The observation of HMM is created by sorting zone numbers in ascending order depending on the number of white pixels in each zone. Experimental results showed that the proposed algorithm achieves 100% recognition rate.

On the other hand, new systems for facilitating human machine interaction have been introduced recently. In particular, the Microsoft Kinect and the leap motion controller (LMC) have attracted special attention. The Kinect system uses an infrared emitter and depth sensors, in addition to a high resolution video camera. The LMC uses two infrared cameras and three LEDs to capture information within its interaction range. However, the LMC does not provide images of detected objects. The LMC has recently been used for Arabic alphabet sign recognition with promising results [25].

After presenting the different existing image-based approaches that have been used to achieve ArASLR, we have noted that these approaches generally include two main phases of coding and classification. We have also seen that most of the coding methods are based on hand-crafted feature extractors, which are empirical detectors. By contrast, a set of recent methods based on deep architectures of neural networks give the ability to build it from theoretical considerations.

ArSLR therefore requires projecting images onto an appropriate feature space that allows an accurate and rapid classification. Contrarily to these empirical methods mentioned above, new machine learning methods have recently emerged which strongly related to the way natural systems code images [26]. These methods are based on the consideration that natural image statistics are not Gaussian as it would be if they have had a completely random structure [27]. The auto-similar structure of natural images allowed the evolution

to build optimal codes. These codes are made of statistically independent features and many different methods have been proposed to construct them from image datasets. Imposing locality and sparsity constraints in these features is very important. This is probably due to the fact that any simple algorithms based on such constraints can achieve linear signatures similar to the notion of receptive field in natural systems. Recent years have seen an interesting interest in computer vision algorithms that rely on local sparse image representations, especially for the problems of image classification and object recognition [28]–[32]. Moreover, from a generative point of view, the effectiveness of local sparse coding, for instance for image reconstruction [33], is justified by the fact that an natural image can be reconstructed by a smallest possible number of features. It has been shown that Independent Component Analysis (ICA) produces localized features. Besides it is efficient for distributions with high kurtosis well representative of natural image statistics dominated by rare events like contours; however the method is linear and not recursive. These two limitations are released by DBNs [34] that introduce nonlinearities in the coding scheme and exhibit multiple layers. Each layer is made of a RBM, a simplified version of a Boltzmann machine proposed by Smolensky [35] and Hinton [36]. Each RBM is able to build a generative statistical model of its inputs using a relatively fast learning algorithm, Contrastive Divergence (CD), first introduced by Hinton [36]. Another important characteristic of the codes used in natural systems, the sparsity of the representation [26], is also achieved in DBNs. Moreover, it has been shown that these approaches remain robustness to extract local sparse efficient features from tiny images [37]. This model has been successfully used in [32] to achieve semantic place recognition. The hope is to demonstrate that DBNs coupled with tiny images can also be successfully used in the context of ArASLR.

III. Proposed Model

The methodology of this research mainly includes four stages (see figure 1) which can be summarized as follows: 1) data collection and image acquisition, 2) image pre-processing, 3) feature extraction and finally 4) gesture recognition.

a) Description of the Database

The alphabet used for Arabic sign language is displayed in Figure 2, left [38], will be used to investigate the performance of the proposed model. In this database, the signer performs each letter separately. Mostly, letters are represented by a static posture, and the vocabulary size is limited. In this section, several methods for image-based Arabic sign language alphabet recognition are discussed. Even though the Arabic alphabet only consists of 28 letters, Arabic sign language uses 39 signs. The 11 additional signs represent basic signs combining two letters. For example, the two letters "ال" are quite common in Arabic (similar to the article "the" in English). Therefore, most literature on ArASLR uses these basic 39 signs.

b) Image Pre-processing

The typical input dimension for a DBN is approximately 1000 units (e.g. 30x30 pixels). Dealing with smaller patches could make the model unable to extract interesting features. Using larger patches can be extremely time-consuming during feature learning. Additionally the multiplication of the connexion weights acts negatively on the convergence of the CD algorithm. The question is therefore how could we scale the size of realistic images (e.g. 300x300 pixels) to make them appropriate for DBNs?
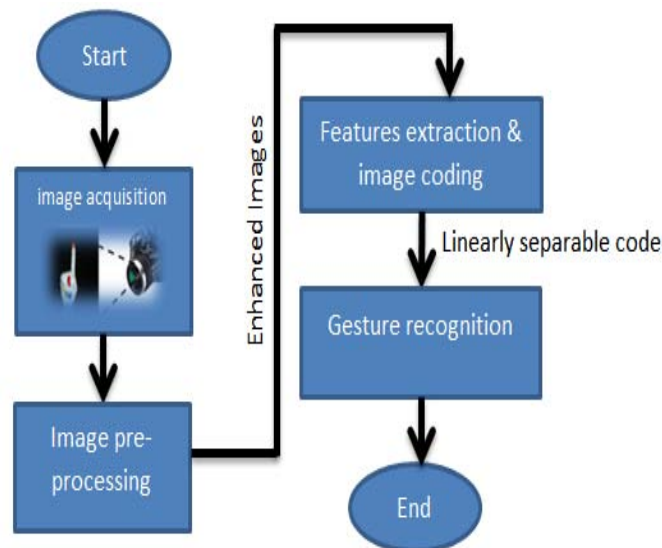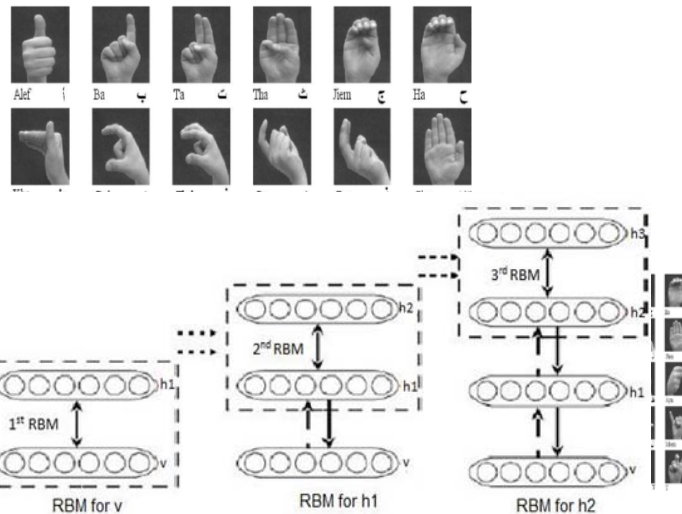

Figure 1: Proposed model

Figure 2: Left: Original Arabic sign language alphabet. Right: The corresponding tiny images of Arabic sign language alphabet. One can see that, despite the size reduction, these small images remain fully recognizable

Three solutions can be envisioned. The first one is to select random patches from each image as done in [39], the second is the use of convolutional architectures, as proposed in [40], and the last one is to reduce the size of each image to a tiny image as proposed in [37]. The first solution extracts local features and the characterization of an image using these features can only be made using BoWs approaches we wanted to avoid. The second solution shows the same limitations as the first one and additionally gives raise to extensive computations that are only tractable on Graphics Processing Unit architectures. Features extraction using random patches is irrespective of the spatial structures of each image [41]. In the case of structured scenes like the ones used in semantic place recognition these structures bear an interesting information.

Besides, tiny images have been successfully used in [37] for classifying and retrieving images from the 80-million images database developed at MIT. Torralba in [37] showed that the use of tiny images combined with a DBN approach led to code each image by a small binary vector defining the elements of a feature alphabet that can be used to optimally define the considered image. The binary vector acts as a bar-code while the alphabet of features is computed only once from a representative set of images. The power of this approach is well illustrated by the fact that a relatively small binary vector largely exceeds the number of images that have to be coded even in a huge database ($2^{256} \approx 10^{75}$). So, for all the se reasons we have chosen image reduction.

On the other hand, natural images are highly structured and contain significant statistical redundancies, e.g. their pixels have strong correlations [42], [43]. Removing these correlations is known as whitening. It has been shown that whitening is a mandatory step for the use of clustering methods in object recognition [44]. Whitening being a linear process and it does not remove the higher order statistics present in the data.

As a consequence, as proposed by [37] and [32], after color conversion and image cropping, the image size is reduced to 42x24 as shown in figure 1. The final set of tiny images is centered and whitened in order to eliminate order 2 statistics. Consequently the variance in equation 6 will be set to 1. Contrarily to [37], the 42x24 = 1008 pixels of the whitened images will be used directly as the input vector of the network for features extraction purpose.

c) *Features Extraction*
Next the feature extraction stage comes. This stage is the most significant stage which is based on using a new unsupervised machine learning model DBNs. DBNs are probabilistic generative models composed of multiple RBMs layers of latent stochastic variables. The latent variables typically have binary values. They correspond to hidden units or feature detectors. The input variables are zero-mean Gaussian activation units and are often used to reconstruct the visible units. As shown in figure 3, the top two layers have undirected, symmetric connections between them and they form the weights or the features. These features are extracted using the principle of energy function minimization according to the quality of the image reconstruction. It has been shown that features extracted by DBNs are more promising for image classification than hand-engineered features [32], [45], [46]. So, we hope that, due to the statistical independence of the features and their sparse nature, learning in the feature space will become linearly independent, greatly simplifying the way we will learn to classify the signs.
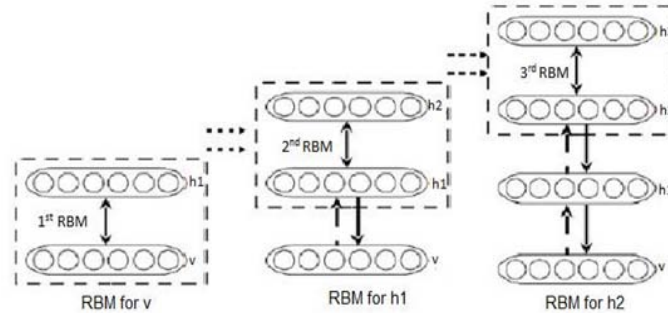
Figure 3: Stacking Restricted Boltzmann Machines (RBM) to achieve Deep Belief Network. This figure also illustrates the layer-wise training of a DBN

1) Gaussian-Bernoulli Restricted Boltzmann Machines

Unlike a classical Boltzmann Machine, a RBM is a bipartite undirected graphical model, $\theta = \{w_{ij}, b_i, c_j\}$ linking, through a set of weights w_{ij} between visible and hidden units and biases $\{b_i, c_j\}$ a set of visible units v to a set of hidden units h [27]. For a standard RBM, a joint configuration of the binary visible units and the binary hidden units has an energy function, given by:

$$E(v, h; \theta) = -\sum_{i,j} v_i h_j w_{ij} - \sum_i b_i v_i - \sum_j c_j h_j \quad (1)$$

Probabilities of the state for a unit in one layer conditional to the state of the other layer can therefore be easily computed. According to Gibbs distribution:

$$P(v, h; \theta) = -\frac{1}{Z(\theta)} exp^{-E(v,h,\theta)} \quad (2)$$

where $Z(\theta)$ is a normalizing constant.

Thus after marginalization:

$$P(h, \theta) = \sum_v P(v, h; \theta) \quad (3)$$

it can be derived [47] that the conditional probabilities of a standard RBM are given as follows:

$$P(h_j = 1|v; \theta) = \sigma\left(c_j + \sum_i w_{ij} v_i\right) \quad (4)$$

$$P(v_i = 1|h; \theta) = \sigma\left(b_i + \sum_j w_{ij} h_j\right) \quad (5)$$

where $\sigma(x) = 1/(1 + e^{-x})$ is the logistic function.

Since binary units are not appropriate for multi-valued inputs like pixel levels, as suggested by Hinton [48], in the present work visible units have a zero-means Gaussian activation scheme:

$$P(v_i = 1|h; \theta) = N\left(b_i + \sum_j w_{ij} h_j, \sigma^2\right) \quad (6)$$

In this case, the energy function of Gaussian-Bernoulli RBM is given by:

$$E(v, h; \theta) = -\sum_i \frac{(v_i - b_i)^2}{2\sigma_i^2} - \sum_j c_j h_j - \sum_{i,j} \frac{v_i}{\sigma_i} h_j w_{ij} \quad (7)$$

2) Learning RBM Parameters

One way to learn RBM parameters is through the maximization of the model log likelihood in a gradient ascent procedure. The partial derivative of the log-likelihood for an energy-based model can be expressed as follows:

$$\frac{\partial}{\partial\theta} L(\theta) = -\left\langle\frac{\partial E(v, \theta)}{\partial\theta}\right\rangle_{data} + \left\langle\frac{\partial E(v, \theta)}{\partial\theta}\right\rangle_{model} \quad (8)$$

where $\langle\ \rangle_{model}$ is an average with respect to the model distribution and $\langle\ \rangle_{data}$ an average over the sample data. The energy function of a RBM is given by:

$$E(v, \theta) = log \sum_h e^{-E(v,h,\theta)} \quad (9)$$

and

$$\partial E(v, \theta)/\partial\theta = \sum_h p(h|v; \theta) \partial E(v, h; \theta)/\partial\theta \quad (10)$$

Unfortunately, computing the likelihood needs to compute the partition function, , that is usually intractable. However, Hinton [28] proposed an alternative learning technique called Contrastive Divergence (CD). This learning algorithm is based on the consideration that minimizing the energy of the network is equivalent to minimize the distance between the data and a statistical generative model of it. A comparison is made between the statistics of the data and the statistics of its representation generated by Gibbs sampling. Hinton [36] showed that usually only a few steps of Gibbs sampling (most of the time reduced to one) are sufficient to ensure convergence. For a RBM,

the weights of the network can be updated using the following equation:

$$w_{ij} \leftarrow w_{ij} + \eta\left(\langle v_i^0 h_j^0\rangle - \langle v_i^n h_j^n\rangle\right) \qquad (11)$$

where η is the learning rate, v^0 corresponds to the initial data distribution, h^0 is computed using equation 4, v^n is sampled using the Gaussian distribution in equation 6 and with n full steps of Gibbs sampling, and h^n is again computed from equation 4.

3) Layerwise Training for Deep Belief Networks

A DBN is a stack of RBMs trained in a greedy layer-wise and bottom-up fashion introduced by [34]. The first model parameters are learned by training the first RBM layer using the contrastive divergence. Then, the model parameters are frozen and the conditional probabilities of the first hidden unit values are used to generate the data to train the higher RBM layers. The process is repeated across the layers to obtain a sparse representation of the initial data that will be used as the final output.

d) Gesture Recognition

Assuming that the non-linear transform operated by DBN improves the linear separability of the data, a simple regression method will be used to perform the classification process. To express the final result as a probability that a given sign means one thing, we normalize the output with a softmax regression method. According to maximum likelihood principles, the largest probability value gives the decision of the system. The classification process will also be investigated using a more sophisticated classifier, a SVM classification method instead of softmax regression. In case of comparable results; this will underline that the DBN computes a linear separable signature of the initial data.

IV. EXPERIMENTAL RESULTS

For this task, we have conducted an experiment using the pre-processed dataset (the tiny-normalized dataset) which are randomly sampled from the Arabic Alphabet dataset which contains 28 letters. A complete structure (1024-1024) of the first RBM layer was used for this case. Figure shows features extracted using the locally normalized data. These features remain sparse but cover a broader spectrum of spatial frequencies. An interesting observation is that they look closer to the ones obtained with convolutional networks [40] for which no whitening is applied to the initial dataset.

The features shown in figure 4 have been extracted by training the first RBM layer on 6000 normalized image patches (32x32 pixels) sampled from the Arabic Alphabet database. One can see that the extracted features represent most of the 28 signs of the letters. Some others are localized and correspond to small parts of the initial views, like edges and corners that can be identified as hand elements (i.e. they are not specific of a given sign). These features can thus be used to code the initial data to achieve the linear separability, which will greatly simplifies the recognition process.
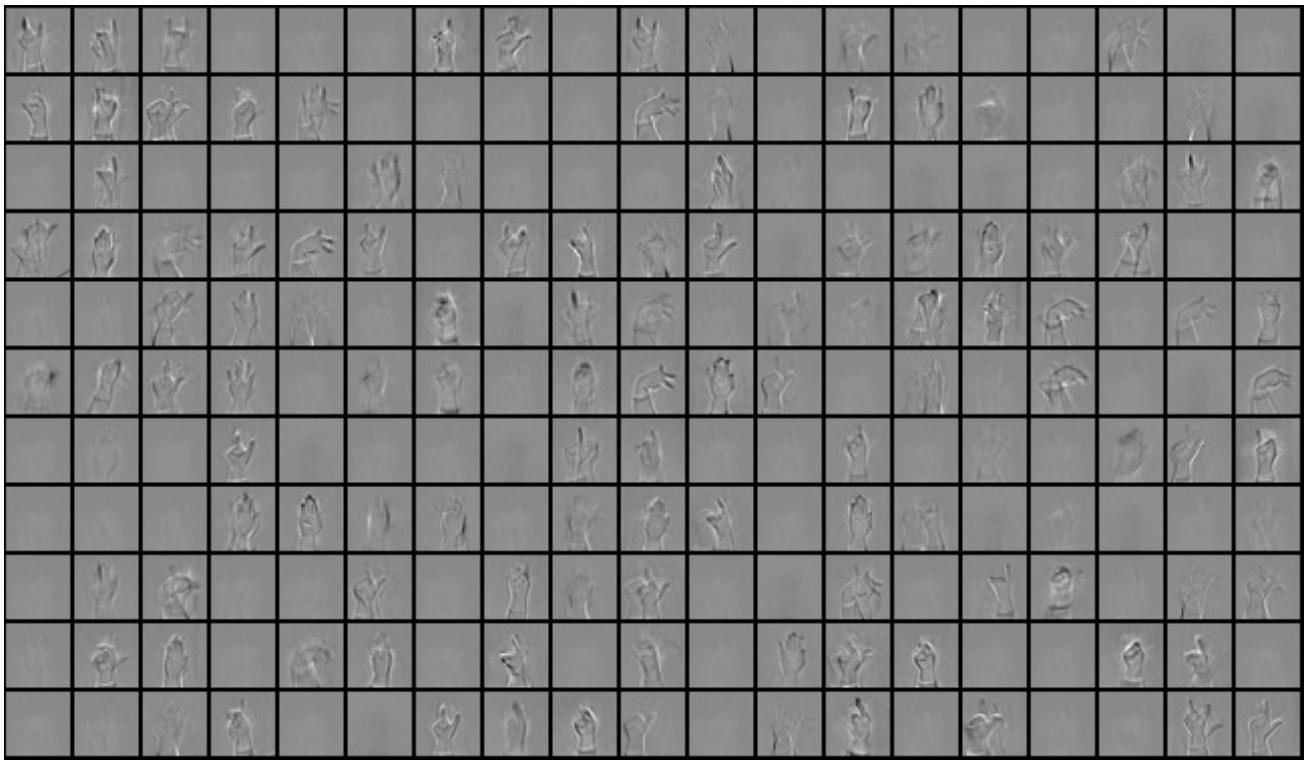
Figure 4: Learned over-complete natural image bases. Sample of the 1024 features learned by training the first RBM layer on normalized image patches (32x32) sampled randomly from gesture dataset. For this experiment, the training protocol is similar to the one proposed in [40] (300 epochs, a mini-batch size of 200, a learning rate of 0:02, an initial momentum of 0:5, a final momentum of 0:9, a weight decay of 0:0002, a sparsity target of 0:02, and a sparsity cost of 0:02).

V. Conclusions and Future Works

The aim of this paper is therefore to propose to use DBNs coupled with tiny images in a challenging image recognition task, view-based ArASLR. The expected results should demonstrate that an approach based on tiny images followed by a projection onto an appropriate feature space can achieve interesting classification results in an ArASLR task. Our hope is to get comparable results or even to outperform the results obtained in [10], [24] based on more complex techniques. In case of comparable results, this paper is thus offer a simpler alternative to the method recently proposed in [10], [24] based on cue integration and the computation of a confidence criterion in a HMM or a SVM classification approach.

Our future work is to empirically investigate the proposed model to achieve Arabic sign language alphabet recognition. The first step is to code the initial dataset using the extracted features. Assuming that the non-linear transform operated by DBN improves the linear separability of the data, a simple regression method will be used to perform the classification process. The classification process will also be examined using a sophisticated classification techniques like SVM in order to investigate whether the linear separability is gained by DBN or not.

After investigating the classification results of the system, this research can be extended to investigate the recognition of further deaf sign groups, such as Arabic numbers, basic Arabic words. Also, this system could be developed to be provided as a web service used in the field of conferences and meetings attended by deaf people. Finally, it can be used in intelligent classrooms and intelligent environments for real time translation for sign language.

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Color Image Segmentation using Automated K-Means Clustering with RGB and HSV Color Spaces

By Md. Rakib Hassan, Romana Rahman Ema & Tajul Islam

North Western University

Abstract- Segmentation implies the division of an image into different objects or connected regions that do not overlap. Though, extensive research has been done in creating many different approaches and algorithms for image segmentation, however, it is still not very clear to assess whether one algorithm produces more accurate segmentations than another, whether it be for a particular image or set of images, or more generally, for a whole class of images [7]. A reliable and accurate segmentation of an image is, in general, very difficult to achieve by purely automatic means. Present researches on image segmentation using clustering algorithms reveals that K-means clustering algorithm so far produces best results but some improvements can be made to improve the results. The biggest disadvantage of our heavy usage of k-means clustering, is that it means we would have to think of a k each time, which really doesn't make too much sense because we would like to algorithm to solve this on his own. Therefore we tried to find the K automatically and so create segmentation without any human giving "hints" to the algorithm.

Keywords: automated k-means, clustering, RGB, HSV, segmentation, color space, cluster, image processing, color image, K-means clustering.

GJCST-F Classification: I.2.10, I.3.3

COLORIMAGESEGMENTATIONUSINGAUTOMATEDKMEANSCLUSTERINGWITHRGBANDHSVCOLORSPACES

Strictly as per the compliance and regulations of:

Color Image Segmentation using Automated K-Means Clustering with RGB and HSV Color Spaces

Md. Rakib Hassan [α], Romana Rahman Ema [σ] & Tajul Islam [ρ]

Abstract- Segmentation implies the division of an image into different objects or connected regions that do not overlap. Though, extensive research has been done in creating many different approaches and algorithms for image segmentation, however, it is still not very clear to assess whether one algorithm produces more accurate segmentations than another, whether it be for a particular image or set of images, or more generally, for a whole class of images [7]. A reliable and accurate segmentation of an image is, in general, very difficult to achieve by purely automatic means. Present researches on image segmentation using clustering algorithms reveals that K-means clustering algorithm so far produces best results but some improvements can be made to improve the results. The biggest disadvantage of our heavy usage of k-means clustering, is that it means we would have to think of a k each time, which really doesn't make too much sense because we would like to algorithm to solve this on his own. Therefore we tried to find the K automatically and so create segmentation without any human giving "hints" to the algorithm. So we tried to make the process automatic. In this paper, the combined segmentation of RGB and HSV color spaces give more accurate segmentation result compared to segmentation of single color space. For keeping the k parameter as small as possible, we had to keep different intensity levels of the same color on the same segment to estimate the right k automatically for the algorithm.

Keywords: automated k-means, clustering, RGB, HSV, segmentation, color space, cluster, image processing, color image, K-means clustering.

I. Introduction

With the impetuous improvement in the digital technology, digital image play very significant role in modern era with its rapidly uses at medical sector and the visualization sector. Digital image can be described as a large number array of discrete dots where each dot has a brightness level associated with it.

These dots are simply represents as pixels or picture elements. Image segmentation is defined as; "the search for homogeneous regions in an image and later the classification of these images". Segmentation signifies the partition of an image into different objects or connected regions that do not overlap. Highly use of Real world image segmentation issues have multiple objectives like reduce overall deviation, maximize property, reduce the options or reduce the error rate of the classifier. In image processing, it is still not very clear to measure whether one algorithm express more accurate segmentation than another, whether it be for related image, particular image or set of images, or more usually, for a whole class of each images [4].
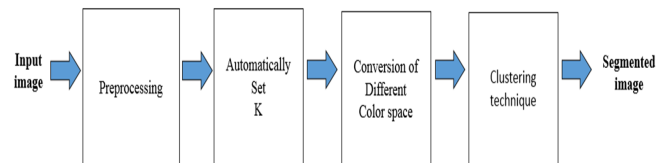
Figure 1: Segmentation Technique with automated "K"

The modern researches on digital image segmentation generally use K-means clustering algorithm which doesn't express best results but after some elevation of K-means algorithm, it could express the results better. In this paper, the combined segmentation of RGB and HSV color spaces give more accurate segmentation result compared to segmentation of single color space our main objectives while segmenting images of different kind like using the RGB color space where we wanted to get rid of different intensity level of the same color shade which is not satisfied. Hence, we thought of another representation to color images the HSV color space which will ease our solution to segmentation

II. Related Work

Gudrun J. Klinker, Steven A. Shafer and Takeo Kanade observed Physical Approach to Color Image understanding with additional example through opposed to k means and Anil Z Chitade evaluated the Color based image segmentation using kmeans clustering. R. C. Gonzalez and R. E. Woods described Digital Image Processing where YZang presented a review on image segmentation techniques with remote sensing perspective.

Pena M, Barbakh W, Fyfe C discussed the Principal Manifolds for Data Visualization and Dimension Reduction. McAndrew A analyzing Digital Image Processing with Matlab Notes for SCM2511 Image Processing. Marques, Blanca NP, Pina P works with

Author α σ ρ: Dept. of Computer Science and Engineering (CSE), North Western University, Khulna, Bangladesh. e-mails: sonet94@gmail.com, romanacsejstu@gmail.com, tajulkuet09@gmail.com

Pattern Recognition and Image Analysis MacQueen J proposed some methods for classification and analysis of multivariate observations.

Y. Li and Y. Shen done a great job about Robust image segmentation algorithm using fuzzy clustering based on kernel-induced distance measure whereas D. E. Ilea and P. F. Whelan gave a complete overview about Color image segmentation using a spatial k-means clustering algorithm.

N. R. Pal and S. K. Pal gave A review on image segmentation techniques and Pattern Recognition in their paper and H. C. Chen and S. J. Wang works with Visible color difference-based quantitative evaluation of color segmentation,

III. Description of Image Segmentation Features

a) Clustering

Clustering (also called unsupervised learning) is the method of partitioning a data-set into various groups. Sometimes the members of every group are as similar (close) as probable to one another, and sometimes different groups are as dissimilar (far) as possible from one another [9]. Clustering can discover previously unperceived relationships in a data set. There are various applications for cluster analysis. Cluster ana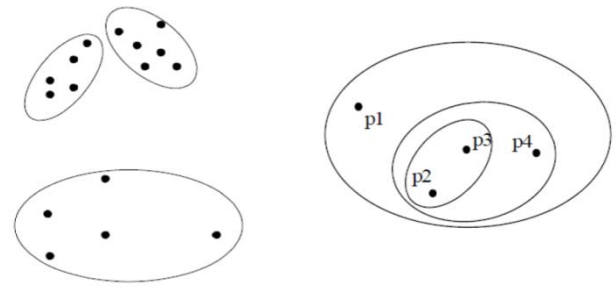lysis can be used to discover and distinguish customer segments for marketing purposes. In Biology, it uses at alignment of plants and animals given their features. Not only that it can also be used in pattern recognition spatial data analysis, image processing etc. [20] In other words, clustering means collection of data or distribution a large data set into smaller data sets of some similarity [5]. An important appearance in clustering is how to designate the similarity between individual objects, Clusters can be made from objects with the possibility of high similarity within clusters and low similarity between clusters [7]. Commonly, to measure similarity or dissimilarity between objects there are many popular methods, such as Euclidean, Manhattan and Minkowski are used. A distance function executes a lower value for similar objects that are more similar to one another. Requirements of good cluster:

- The ability to discover some or all of the hidden clusters also handle high dimensionality.
- Within-cluster similarity and between-cluster dissimilarity and Scalable, Interpretable and usable
- Ability to deal with various types of attributes, can deal with noise and outliers.

Hierarchical Clustering is a set of nested clusters organized as a hierarchical tree and on the other hand Partitioning Clustering is a division data objects into non-overlapping subsets (clusters) such that each data object is in exactly one subset [4].

Figure 2: Partioning and Hierarchical Clustering

b) K-Means Clustering

The k-means algorithm works like to cluster "n" number of objects based on characteristic into k partitions, where k < n. Simply speaking it is an algorithm to group or to classify objects based on their corresponding features into K number of group. Here K is always positive integer number [16]. In general, the group is created based on minimizing the sum of distances between the corresponding clusters centroid and data [5] [11].
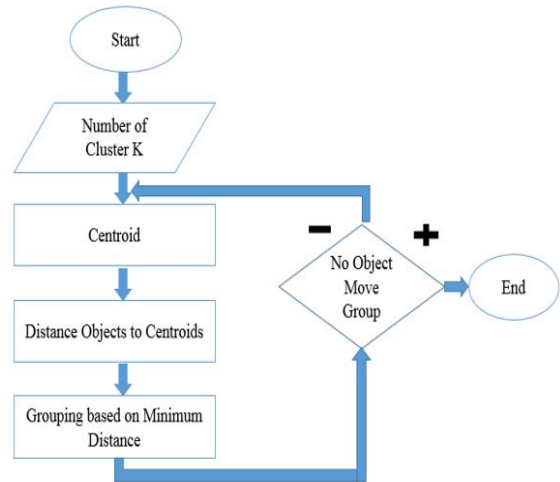
Figure 3: Procedures of K-Means Clustering Algorithm

c) Basic Steps of K-Means Clustering Algorithm

Given n objects, choose k number of clusters to be determined. Choose k objects randomly as the initial cluster. Assign each object to their closest cluster center. Update the center of each cluster (Calculate mean points) until no changes on cluster centers (i.e. Centroids do not change location any more). A number of other strategies stands for verifying K, including cross-verify, information criteria, the information the silhouette procedure, theoretic jump procedure and also the G-means algorithm. In addition, monitoring the classification of data points across various groups provides acumen into how the algorithm is partitioning the data for each K.

d) Choosing "K" of K -Means Clustering Algorithm

The algorithm described over discovers the clusters and data set labels for an individual pre-chosen K. To discover the number of clusters in the data, the user needs to operate the K-means clustering algorithm for a range of K values and compare the outcomes. In general, there is no procedure for recognizing exact value of K [18].
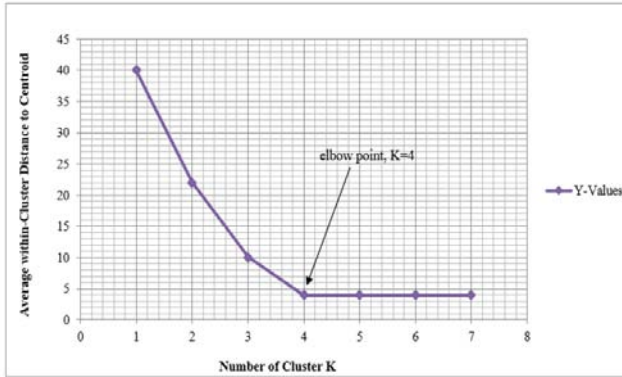
Figure 4: Elbow Point Example

One of the metrics that is generally used to compare outcomes across several values of K is the mean distance between data points and their cluster centroid. Since increasing the number of clusters will always maximize this metric and minimize the distance to data points to the ultimate of reaching zero when K is the same as the number of data points. Thus, this metrics cannot be used as the absolute target.

e) HSV Color Space

HSV color space will be more compatible for conduct with segmentation of rough color images. We can describe HSV color space with the help of a hex cone with three extensions where the middle vertical axis describes the intensity [level 18]. Here H represents Hue. Basically Hue is an angle, which range is $[0, 2\pi]$ comparative to angle 0 at red axis, $2\pi/3$ at green axis, $4\pi/3$ at blue axis and red again at 2π. S represents Saturation, which represents how authentic the hue is with respect to a white section. This can be concern of as the depth or integrity of color and is measured as a long range distance from the middle axis with properties between 0 at the center to 1 at the outer surface [13]. While, for a given intensity and hue, if the saturation is qualified from 0 to 1, the comprehend color switch from a shade of gray to the most authentic form of the color represented by its hue. Diagrammatic view is given below [5]:
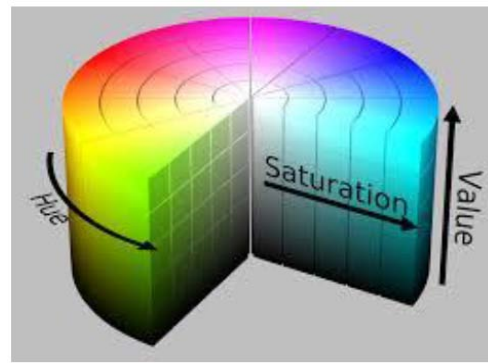
Figure 5: HSV Color Space

V represents Value which percentage is between 0 to 100. This percentage range can be concern as the amount of light expressing a color. For example, the value is high and when the hue is red, the color seems bright. On the other hand, it looks dark when the value is low. Following figures show the HSV converted image of the original image [5]:
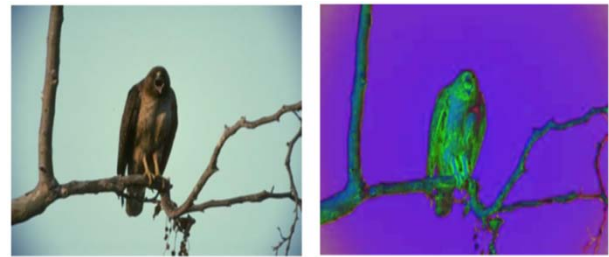
Figure 6: Sample to HSV Converted Result

f) RGB Color Space

A color image f$\in$RN×3 is made of three independent images, one for each channel red, green and blue which is called RGB color space [11]. Here Size N= n×n of the image; where n = 256; N = n*n. RGB is the most widely used color space, that each color image is combination of three different images, those are Red image, Blue image and black image [12].
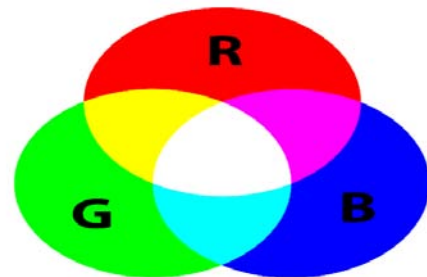
Figure 7: RGB Color Space

RGB color space is also called additive color space, which can be described well based on the RGB color model [10]. Three chromaticity's is represented by a particular RGB color space which includes the red, green, and blue additive primaries, and also generate any chromaticity with a triangle which represented by

those fundamental colors. A gamma correction curve and a white point chromaticity also requires for the total specification of an RGB color space [12].
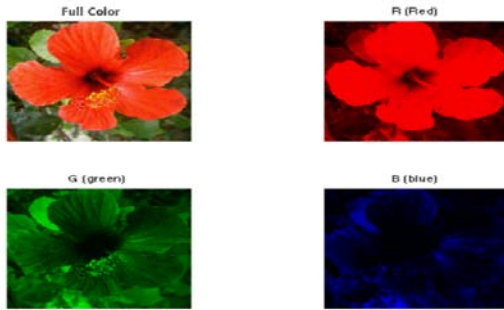
Figure 8: Sample to RGB Converted Result

Three colored lights for red, green, and blue are produced and described from An RGB color space, for example, shining three lights together onto a white wall in a dark room: one red light, one green light, and one blue light, each with dimmers. If only the red light is on, the wall will be red. If only the green light is on, the wall will look green. If the red and green lights are on together, the wall will look yellow. Dim the red light and the wall will become more of a yellow-green. Dim the green light instead, and the wall will become more orange. Typical RGB input devices are color TV and video cameras, image scanners, video games, and digital cameras.

IV. Methodology

To generate the best practical segmentation, we intend to use images with known characteristics, where most popular use about the segmentation is color. Our aim is to find out an amusing way to segment the image by the colors with the k means clustering algorithm, which includes mapping the image pixels to the RGB color space and HSV color space (i.e. if pixel 4, 5 holds the values red: 50, green: 30, blue: 20, we map it to the point (50, 30, 20) on a 3d space representing the RGB and HSV values). Our proposed function works like to adjust the input to the format of k means procedure for expects to get and ran a few tests. Our motivation was to keep the k parameter as small as possible to estimate the right k automatically for the algorithm. For that, we had to keep different intensity levels of the same color on the same segment; for example trying to keep light green and dark green in the same segment. Our basic supposition for this part of the work, was that whether given a data set of n clusters, when we operate K means algorithm with parameter k=m (Where m>n). The centers which is created by the algorithm would be closer to each other than if we ran the algorithm with the parameter k=n (the actual number of clusters). So the minimum distance between the cluster centers would decrease.
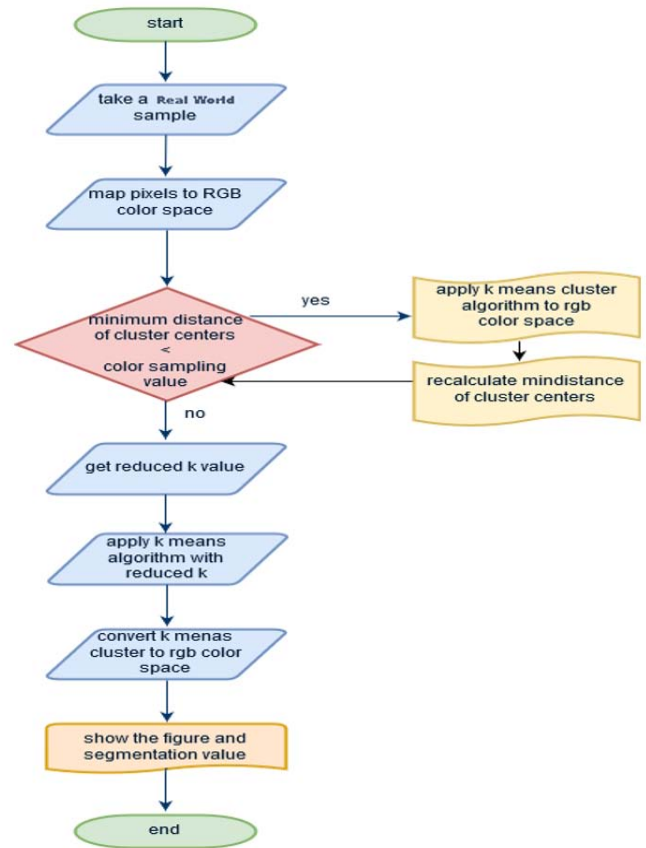

Figure 9: Proposed Technique of RGB Color Segmentation

To reduce the K parameter, we start with a high value of K, and iteration ally reducing it, until we go an indicated condition, which normally has to do with the minimum distance between the centers of the segmentation resulted by the k-means algorithm. For calculate the sample values of RGB and HSV we used Matlab. Of the colors we wanted to separate, we tried to take the algorithm to a point where it wouldn't accumulate those colors under the corresponding segment. If we consider the minimum distance between the colors then we can use a condition that will force the k to be small enough that the various segments generated will be at least as far from one another, as the various colors of the game play world, we won't get a segment with colors "close to one another". We confined heavily on our basic supposition, associated with hope that various intensity of the same color may be closer to one another, after decreasing K value and increases the minimum distance our proposed algorithm is ends. Basically various "shades" of the same color are multiplication by a constant of a basic vector in the RGB space. If in the data set there are several clusters, each one representing several intensity level of the color.
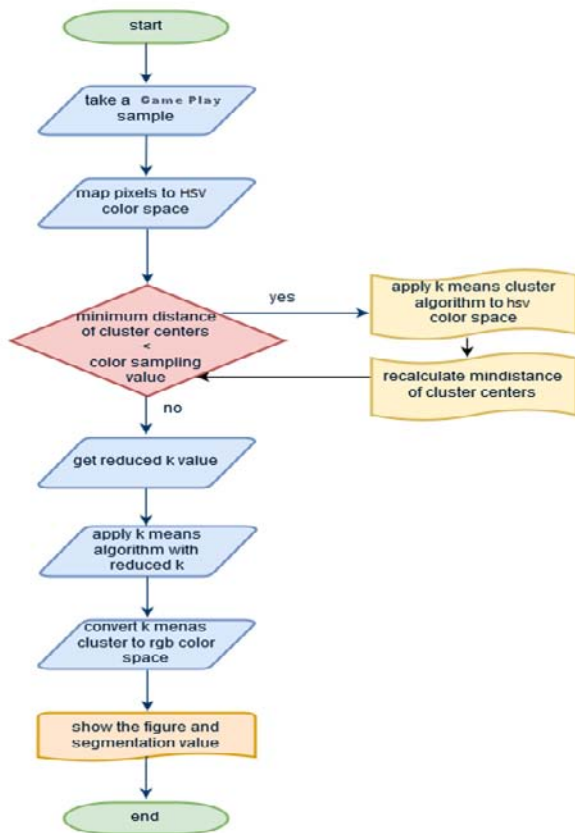
Our main goal is to get rid of various intensity level of the same color hue. Hence, the illustration to color images the HSV color space which will comfort our solution to segmentation [8]. The HSV color space has several parameters for the HUE, SATURATION and VALUE (intensity) of the pixel, and so we get instinctive access to the actual hue of the pixel, without any concerns about several intensity level.

V. Performance Results

a) Performance Matrices

We discovered that even though the K-Means algorithm does a great job, but when we tried to make the process automatic with the right automatic K, even though we were in a restricted world of images, the process wasn't easy, and obviously our results are not perfect, but not too far away. On images of unknown source, the problem becomes much harder. So we proposed an algorithm to minimize the K parameter by itself, at the beginning of time it starts with high value of K, and then iteration ally reducing it, until we meet a certain condition, which generally has to do with the minimum distance between the centers of the segmentation. Now, the problem is to choose a condition which will make the algorithm stop and calculate the "right" k. We can easily fix this certain

condition based on our knowledge of the game play images, like the colors existing in the world.

Figure 11: Sample Image from Fruit-Ninja Game

On fruit ninja game play image we sampled the different colors from all the individual fruits in the game, and using the minimum distance between the fruits as a starting point for a terminating condition. We noticed with this result, the perceive areas to be segment and assigned to in the result. The background got divided to two segments. Here someone can argue that if we segment the image based only on colors, but we wanted it to be a good pre-processing for a later by object recognition algorithm. But as we started implementing this method, we realized that there is much simpler solution.

Figure 12: HSV Result with Automated K after Color Segmentation

Hence, we thought of another representation to color images the HSV color space which will ease our solution to segmentation. The HSV color space has different parameters for the HUE, the SATURATION and the VALUE (intensity) of the pixel. Again, the fully automatic algorithm isn't perfect, the usage of the minimum distance condition isn't enough to accurately estimate the K parameter but we do ideas on how to improve it. In the restricted world of game play images, HSV based segmentation did much better than the RGB version. The fact that we can ignore the pixels intensity level opened up a way to clearly segment the picture based on hue only, which, in this scenario specifically is very good.
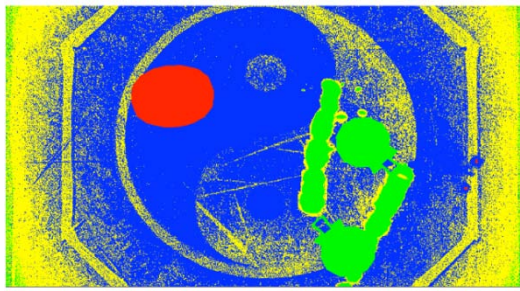
Figure 13: RGB Result with Automated K after Color Segmentation

No representation is better than the other though we wanted to emphasize this fact, so we provide examples from real world images; there HSV color space to eliminate different intensities of the same hue isn't performing too well, as opposed to RGB.

b) *Working Results when HSV is better than RGB*

The major step we did was the HSV color space to get a clearer segmentation view to us, for better out come in the future we like to add the K recognition feature which still requires work to be fully functional. Here is several samples of the results we achieved, with some annotations:
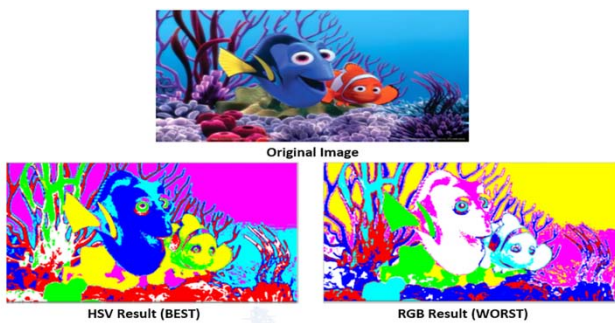
Figure 14: HSV Result on Fish image after Color Segmentation

We know about the importance of having different representations of the same object, and how each one opens up a world of tools to use on it, lets you get a part of the information easily, while hiding some of the redundant information.

Figure 15: HSV Result on Bird image after Color Segmentation

From the figure number 12 and 13 we get a clear view that our proposed K-means clustering algorithm give better output on Game play images and also can segment properly without giving any human hints of find out the number of "K."

c) *Working Results when RGB is better than HSV*

Segmentation by colors generally show a very perfect sense of the picture, and can be a decent preprocessing for stages like object visualization. The role of segmentation is authentic in most tasks requiring image analysis. The success or failure of the process is often a direct result of the success or failure of segmentation. However, an authentic and exact segmentation of an image is, in general, very difficult to acquire by purely automatic means. Considering the pros and cons of the main algorithm used (K-Means Clustering) and the fact that segmentation can be understand differently by different people, we set our minds to several goals. When we worked with Real world Images our RGB results were so much better than HSV Color Space method. We got proper segmentations. Here some results are given below:

Figure 16: RGB Result on Flower image after Color Segmentation

For the segmentation we have proposed the idea of k means clustering algorithm which involves mapping the image pixel to the RGB color space and HSV color space. We proposed some function to set the input to the format the k-means iteration expects, and ran few tests where the outputs were quite impressive [8]. For keeping the k parameter as small as possible, to estimate the right k automatically for the algorithm, we had to keep various intensity levels of the color on the same segment.
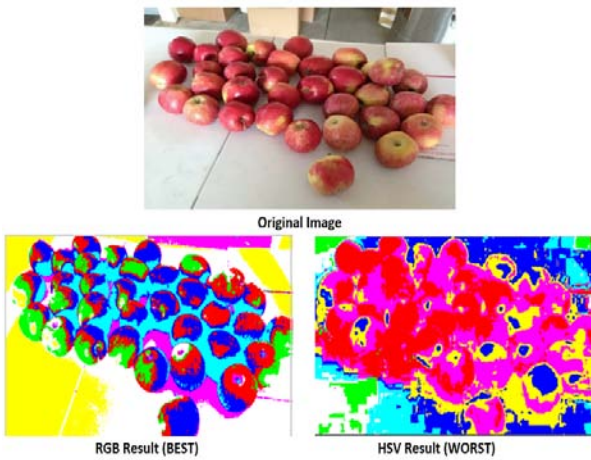
Figure 17: RGB Result on Fruit image after Color Segmentation

We know that different "shades" of the same color (different intensities) are basically multiplication by a constant of a basic vector in the RGB space. The most disadvantage of our excessive usage of k-means clustering is that it means we would have to think of a k every time, which really not the perfect way because we would like to proposed the algorithm to solve this by own. Therefore we attempted to get the K automatically and so express segmentation without any user giving "hints" to the algorithm. As we explained before, for these scenarios (Game play images), RGB isn`t Performing exceptionally well.

d) Comparison between optimal K-Means and Automated K-Means Algorithom

For the scenario (Game play images), RGB isn`t Performing well. If the color set is known then for the same color hue we don't need to give different Segments to different intensity levels, K-Means algorithm on the HSV color space does more impressive job. From below example we can easily compare the K value between Optimal K-Means and our Automated K-Means at RGB and HSV Color space.
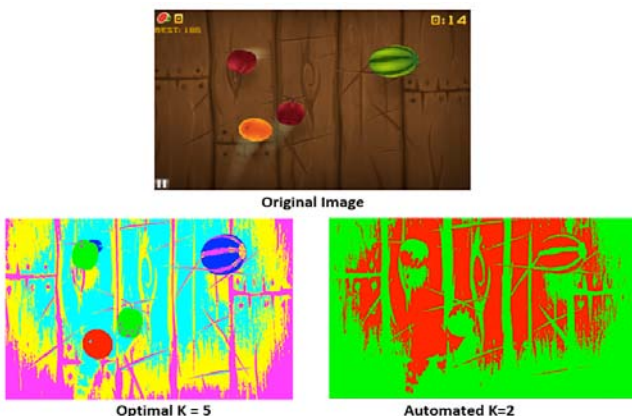
Figure 18: Optimal and Automated K value on RGB

On RGB color space, the optimal K value and the Automated K value was not so close. So on game play images, our proposed automated K-Means algorithm could not provide impressive result; On the other hand when we worked with automated K-Means on HSV Color space, we got the K value so much closer with optimal K-Means value. So most of the times it gave us impressive result and also achieved our goal. But it is difficult to say HSV result is all time better than RGB result with our proposed automated K-Means algorithm. Although K-means algorithm does comparatively better task but the process commits little bit ambiguous while we have try to choose the actual k. We efficient about various ways to select the right "K" for the algorithm, like G-Means clustering, which uses statistics and hypotheses about the data to calculate the K, and X-means algorithm which didn't supposed to give a result that would glut [2]. So we tried to make the method instinctive, even though we were in a strict world of images, the work is not easy and accurate but not impossible by any means. When worked with RGB color space, our proposed technique is not gave us suitable result. The optimal K value and the automated K value is quite difference.
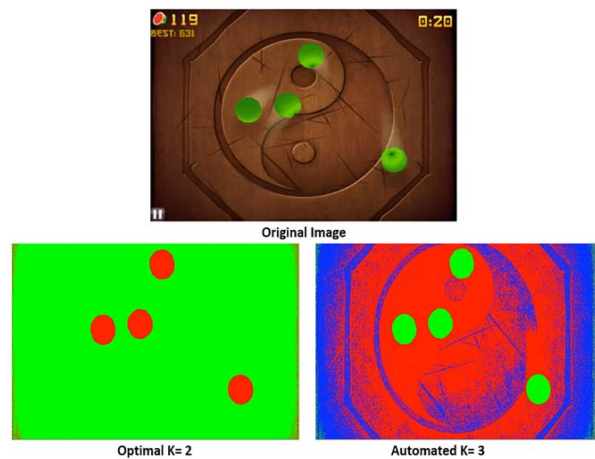
Figure 19: Optimal and Automated K value on HSV

Work with normal K-means algorithm has quite few problems regarding the color segmentation of images that it we would have to think of "K" each time for segmentation result, which is one of the biggest disadvantage of k-means clustering algorithm. Basically it doesn't make too much intuition because we would like to do algorithm to execute this by own. When we worked with HSV Color space, the optimal K vale and the automated K value is quite same which assure us that our automated K-means algorithm performed better at HSV color space.

VI. Conclusion and Future Work

We discovered that even though the K-Means algorithm does a great job, the fact that we have to

choose a k makes using it a bit problematic. When we tried to make the process automatic but the job wasn't easy, and obviously our results are not perfect, but not too far away. The characteristics which we use for our working procedure is color: As most of us know, the different figures in the game are fruits, which usually have very different colors, and so segmentation by colors usually gives a very correct feel of objects, and can be a good preprocessing for stages like object recognition. We found the numbers we used to terminate the reduction of K based on samplings from game play images and manipulations on the results, general pictures are not supposed to work this way. However we wanted to emphasize the fact that no representation is better than the other. In the restricted world of Game play images, HSV based segmentation did much better than the RGB version. The fact that we can ignore the pixels intensity level opened up a way to clearly segment the picture based on hue only, which, in this scenario specifically is very good. HSV representation is not better generally all the time, because for real world images, the RGB representation gave us better outcomes which show us about the importance of having different representations of the same object. Those methods we implemented that did not get the best performance. We tried to get the right K but it was so much difficult for us to detect it. We only worked with RGB color pace and HSV color space. We tried to get best result with RGB and HSV color space with our automated K-Means algorithm but all time we did not get best result from our proposed algorithm. Not only that, it was so much difficult to get the right K from our proposed algorithm. In future we will try to modify our proposed automated K-Means algorithm to get the accurate K all time at all color space. Now we only worked with two color space but in future we will like to work with more color space like CMYK, L*a*b, YCBCR, HSL etc. after work with these color spaces we can easily compare which will be best for image segmentation.

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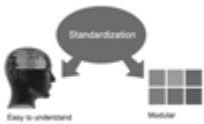
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1. General,

2. Ethical Guidelines,

3. Submission of Manuscripts,

4. Manuscript's Category,

5. Structure and Format of Manuscript,

6. After Acceptance.

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· Shun use of extra pictures - include only those figures essential to presenting results

Title Page:

Choose a revealing title. It should be short. It should not have non-standard acronyms or abbreviations. It should not exceed two printed lines. It should include the name(s) and address (es) of all authors.

Abstract:

The summary should be two hundred words or less. It should briefly and clearly explain the key findings reported in the manuscript-- must have precise statistics. It should not have abnormal acronyms or abbreviations. It should be logical in itself. Shun citing references at this point.

An abstract is a brief distinct paragraph summary of finished work or work in development. In a minute or less a reviewer can be taught the foundation behind the study, common approach to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Yet, use comprehensive sentences and do not let go readability for briefness. You can maintain it succinct by phrasing sentences so that they provide more than lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study, with the subsequent elements in any summary. Try to maintain the initial two items to no more than one ruling each.

- Reason of the study - theory, overall issue, purpose
- Fundamental goal
- To the point depiction of the research
- Consequences, including <u>definite statistics</u> - if the consequences are quantitative in nature, account quantitative data; results of any numerical analysis should be reported
- Significant conclusions or questions that track from the research(es)

Approach:

- Single section, and succinct
- As a outline of job done, it is always written in past tense
- A conceptual should situate on its own, and not submit to any other part of the paper such as a form or table
- Center on shortening results - bound background information to a verdict or two, if completely necessary
- What you account in an conceptual must be regular with what you reported in the manuscript
- Exact spelling, clearness of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else

Introduction:

The **Introduction** should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable to comprehend and calculate the purpose of your study without having to submit to other works. The basis for the study should be offered. Give most important references but shun difficult to make a comprehensive appraisal of the topic. In the introduction, describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will have no attention in your result. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here. Following approach can create a valuable beginning:

- Explain the value (significance) of the study
- Shield the model - why did you employ this particular system or method? What is its compensation? You strength remark on its appropriateness from a abstract point of vision as well as point out sensible reasons for using it.
- Present a justification. Status your particular theory (es) or aim(s), and describe the logic that led you to choose them.
- Very for a short time explain the tentative propose and how it skilled the declared objectives.

Approach:

- Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done.
- Sort out your thoughts; manufacture one key point with every section. If you make the four points listed above, you will need a least of four paragraphs.

- Present surroundings information only as desirable in order hold up a situation. The reviewer does not desire to read the whole thing you know about a topic.
- Shape the theory/purpose specifically - do not take a broad view.
- As always, give awareness to spelling, simplicity and correctness of sentences and phrases.

Procedures (Methods and Materials):

This part is supposed to be the easiest to carve if you have good skills. A sound written Procedures segment allows a capable scientist to replacement your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt for the least amount of information that would permit another capable scientist to spare your outcome but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section. When a technique is used that has been well described in another object, mention the specific item describing a way but draw the basic principle while stating the situation. The purpose is to text all particular resources and broad procedures, so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step by step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

- Explain materials individually only if the study is so complex that it saves liberty this way.
- Embrace particular materials, and any tools or provisions that are not frequently found in laboratories.
- Do not take in frequently found.
- If use of a definite type of tools.
- Materials may be reported in a part section or else they may be recognized along with your measures.

Methods:

- Report the method (not particulars of each process that engaged the same methodology)
- Describe the method entirely
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures
- Simplify - details how procedures were completed not how they were exclusively performed on a particular day.
- If well known procedures were used, account the procedure by name, possibly with reference, and that's all.

Approach:

- It is embarrassed or not possible to use vigorous voice when documenting methods with no using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result when script up the methods most authors use third person passive voice.
- Use standard style in this and in every other part of the paper - avoid familiar lists, and use full sentences.

What to keep away from

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings - save it for the argument.
- Leave out information that is immaterial to a third party.

Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part a entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Carry on to be to the point, by means of statistics and tables, if suitable, to present consequences most efficiently.You must obviously differentiate material that would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matter should not be submitted at all except requested by the instructor.

Content

- Sum up your conclusion in text and demonstrate them, if suitable, with figures and tables.
- In manuscript, explain each of your consequences, point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation an exacting study.
- Explain results of control experiments and comprise remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or in manuscript form.

What to stay away from

- Do not discuss or infer your outcome, report surroundings information, or try to explain anything.
- Not at all, take in raw data or intermediate calculations in a research manuscript.

- Do not present the similar data more than once.
- Manuscript should complement any figures or tables, not duplicate the identical information.
- Never confuse figures with tables - there is a difference.

Approach

- As forever, use past tense when you submit to your results, and put the whole thing in a reasonable order.
- Put figures and tables, appropriately numbered, in order at the end of the report
- If you desire, you may place your figures and tables properly within the text of your results part.

Figures and tables

- If you put figures and tables at the end of the details, make certain that they are visibly distinguished from any attach appendix materials, such as raw facts
- Despite of position, each figure must be numbered one after the other and complete with subtitle
- In spite of position, each table must be titled, numbered one after the other and complete with heading
- All figure and table must be adequately complete that it could situate on its own, divide from text

Discussion:

The Discussion is expected the trickiest segment to write and describe. A lot of papers submitted for journal are discarded based on problems with the Discussion. There is no head of state for how long a argument should be. Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implication of the study. The purpose here is to offer an understanding of your results and hold up for all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of result should be visibly described. Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved with prospect, and let it drop at that.

- Make a decision if each premise is supported, discarded, or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."
- Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work
- You may propose future guidelines, such as how the experiment might be personalized to accomplish a new idea.
- Give details all of your remarks as much as possible, focus on mechanisms.
- Make a decision if the tentative design sufficiently addressed the theory, and whether or not it was correctly restricted.
- Try to present substitute explanations if sensible alternatives be present.
- One research will not counter an overall question, so maintain the large picture in mind, where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

Approach:

- When you refer to information, differentiate data generated by your own studies from available information
- Submit to work done by specific persons (including you) in past tense.
- Submit to generally acknowledged facts and main beliefs in present tense.

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Introduction	Containing all background details with clear goal and appropriate details, flow specification, no grammar and spelling mistake, well organized sentence and paragraph, reference cited	Unclear and confusing data, appropriate format, grammar and spelling errors with unorganized matter	Out of place depth and content, hazy format
Methods and Procedures	Clear and to the point with well arranged paragraph, precision and accuracy of facts and figures, well organized subheads	Difficult to comprehend with embarrassed text, too much explanation but completed	Incorrect and unorganized structure with hazy meaning
Result	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
Discussion	Well organized, meaningful specification, sound conclusion, logical and concise explanation, highly structured paragraph reference cited	Wordy, unclear conclusion, spurious	Conclusion is not cited, unorganized, difficult to comprehend
References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring

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