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Analysis of Malignant Nucleus and Cytoplasm Segmentation using ASIC algorithms (Accurately Segmenting the Individual Cell)

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ABSTRACT

In this paper we describe an algorithm for accurately segmenting the individual cell and ability to distinguish sub cellular components, likes cytoplasm and nucleus from a clump of cervical cells. Proposed method for the segmentation of digital two-dimensional color tissue images acquired by an optical microscope from histological segments of the cells. The main aim of this paper is to segmentation to the two dominant elements. They are nucleus and cytoplasm. The segmentation process using a proposed segmentationwork that consists of an integration of AS1C plus many digital image processing algorithms.

This work is one of the parts of a medical research project on studying the process of an important and dangerous disease. Current methods cannot undertake because of complete segmentation due to the challenges involved in delineating cells with severe poor contrast. The proposed method is based on a fusion of various results of application uses size and color characteristics. For the evaluation and for testing the reliability of the proposed segmentation algorithm, we use a set of real 2D color images of cell.

Keywords: Nucleus, cytoplasm, segmentationframework, 2D color images.

1. INTRODUCTION

Automated image analysis of cells and tissues has been an active research field in medical informatics that decades but the recently attracted increased attention due to the developments in computer, microscopy hardware, the awareness that scientific and diagnostic pathology require novel approaches they are perform objective quantitative analyses of cellular and tissue specimens.Segmentation in biology refers to the division of some animal and plantbody plans in a series of repetitive segments.Cell segmentation has various applications in cytometry, and the nucleus is often very distinct andeasy to identify, the cytoplasm provides a lot more challenge.

A new combination of image analysis algorithms that is ASIC for segmentationof cells imaged by fluorescence microscopy is presented. The algorithm consists of an image pre-processing step, general segmentation and Segmentation and object detectionfollowed by the segmentation quality measurement.Objects that have features that differ to that of correctly segmented single cell. The quality measurement consists of a statistical a number of shape descriptive features.

Cytoplasm has performed various functions in the cell. Cytoplasm is present in to the cell membrane of all the cell types and contains organelles and cell parts.Most of the important activities of the cellsare, occur in the cytoplasm. Cytoplasm contains molecules suchas enzymes which are representing for breaking down not used and also aid in metabolic behave.

Cytoplasm representing for giving a cell its size. It helps to full up the cell and take original in the place. Don not using cytoplasm, the cell would be different and materswould not be able to move freefrom one original to another original.

Instead, cytosol is containing by the end line of a matrix which fills the part of the cell that does not contain originals.Cytosol is one of the main areas of the cytoplasm that does not contain originals.

Segmentation is one of most intensely problems and process in image analysis and still no robust general purpose methods exist. There are many various application adapted methods which take advantages of the a priori knowledge about the images are needed.We have developed a sequence of processing steps that are lead to the cytoplasm segmentation of fluorescence microscopy cell images.Traditionally the task of automatic cell analysis is methods for extraction of cells location and shapes that are to approach through the use of image segmentation.

Image segmentation, although fundamental, is neither robust to image quality changes nor an easy in computer vision. This makes image segmentation for cell detection semi-automation requiring frequent tuning with parameters.Using k-means clustering ASIC algorithm for segmenting cellsK-means clustering aims to partition observations into clusters in which each observation belongs to the cluster with the nears, serving as a prototype of the cluster.

2. LITERATURE REVIEW

2.1 A Framework process for White Blood Cell Segmentation in Microscopic Blood Images Using DIP (digital image processing).

Evaluation of blood smear is commonly clinical test these days. For the hematologists areinterested in white blood cells (WBCs) only [2]. For example, acute leukemia is type of disease is detected depend ting up on the amount and conditionof the cell structure. Digital image processing techniques is using to analysis and diagnosis. This segmentation is conducted using in proposedsegmentationsystem [2].

The main abbreviate aim of this system is to segment the white blood particular cells to its two parts of dominant elements. 20 microscopicblood images were tested, and the exitfor framework managed to obtain 78% for cytoplasm segmentation and 92% accuracy for nucleussegmentation

[2][1]. Nucleus and cytoplasmwork that consists of a margining of several digital imagesto processing algorithms.
Indication of the exited framework results is ability to trace the both nucleus and cytoplasm region in imagesample.WBC other leukocytes play a similar role in all other dialyses of different diseases, and that, tacking informationis valuable for hematologist's algorithm.
In the past, DIP techniques have to maintenance the cellsthat they are lead to moreaccurate and automaticdetection diagnosistechnology. More over, there are complications in recovery thedata from White blood cells due to wide variation of cells in position,shape, size,andedge. Moreover, since illumination is imbalanced, the background variesdepend up on that condition during the capturing process andthe imagecontrast between cell boundaries.
This study system is focusing on WBC segmentation using level 2 microscopicimages. Our main aim is segment the cytoplasmusing a work that has been developed using DIPimage processing [2][3][1]. The use of the DIP techniques havedeveloped changing in the most few years, to the point where hematologists technologycan use white blood nucleus cell blood images removing process bloodslides for the begin screening in detecting fault.

2.2 Segmentation of Sub cellular Compartments Combining Super pixelRepresentation with Voronoi Diagrams.

They proposed a computer vision algorithm fordetecting an individual cell,such as nucleus and cytoplasm. Approach consists of three main steps,including the ability to distinguishsub cellular compartments: cellular massEstimation and nuclei detection through super pixel Representation and,graph-based region growing andVoronoidiagrams [5].

2.3 Unsupervised Segmentation on of Overlapping Cervical Cell Cytoplasm.

They test and implementation on both realand simulated individual cell images, containing assortmentof cells and cell configurations that often present occlusionand then contrast. Results show both qualitative and quantitative assign of datasets, using completelyautomated program. The qualitative performancepresents available Coefficient greater than 86 percentages for bothtesting sets andtraining.
Automated cell analysis to the digitized Pap smear slidesrequires segmentation of subcellular compartments, like that asnucleus and cytoplasm. such assuperpixel representation with Voronoi diagrams to identified the individualcells, and split cellular inside mass into individual nuclei andcytoplasm.
According to segmentation, Threshold-based, mathematical morphology-based andothers based on front propagation are 3 important main approaches to cervical cell segmentation. Algorithm also includes other supportprocessing functions, noiseminimization, like as image enhancement, segmentation of cellular inside mass, flow bynuclei and other cytoplasm detection analysis on a database withboth real time process and simulated cervical cell images[5][1].
In Pap test, the cervical cells are examined under a microscope. The Pap smear or Pap test is a procedure to detect cervical cancer. For automatic analysis of Pap smear, the cervical cells need to detected and segmented accurately. However, the presence of blood, mucus,inflammatory cells and other debris makes the detection process unreliable. Thecytoplasm of cervical cells has poor contrast and irregular shape [4][2][1]. Segmenting the overlapping cervical cells is also major issue. An unsupervised method of cell segmentation is proposed foracurate and automatic segmentation of overlapping cervical cells.
The dataset provided in "The Second Overlapping Cervical Cytology Image Segmentation Challenge"containsof multilayer cytology volumeconsisting multifocal images acquired from same specimen [2]. A stack of 20 images, eachof size1024x1024pixels, at different focal planesare provided for each specimenimage and they contain solitaryor different degree of overlappingcervical cells Thecontrastandthe texture of cells are also not consistent.

2.4 Image analysis without segmentation: A new methodto measure cytoplasm to nucleus translocation.

A common approach to measuring many cellular processes by image analysis to start with segmenting the image into compartments interest.Vitra Bioscience has developed a method of analysis of cytoplasm to nucleus translocation (CNT) that doesnot require subcellularsegmentation. Itcan be performed individually on a cell-by-cell basis or globally on whole image [6][1][2]. The method based on modeling and analysis of 2D distribute on of stains: signal (i.e. protein stain) and nuclear counter stain.
The method does not have any userparameters andis very tolerant to variation in the image acquisition. We analyzed performance of this new method with respect to cell type, magnification, number of analyzed cells, depth of field,accuracy of focusing,,and plate flatness. Using statistical methods to measure quality of data produced by this new algorithm, we confirmed that it performsbetter than our implementation of algorithms based on segmentation [6][2]. The performance assessmentmethodology will be discussed in context of Vitra'sapplication of this algorithm to measure translocation events at varying magnifications on Cell Card System andinthe future on Cell Plax assays.
Furthermore,the presented performance assessment methodology cans bemused in the future to design best screening strategy and to compare different cell analysis algorithms.1. Direct minimization of filter interpolation error on real training images various in window sizes and filter types (separable, non-separable, and symmetric). 2 large optimization problems.3 Limited Memory Quasi-Newton methods.4 Generate training data by sub sampling large images at sub pixel shifts. 5 exploit scale-invariance & edge-dominated high-freq. spectra of natural images. 6 to mimic real zooms;[6][1] subsample using a realistic Pixel Response Function (PRF).
The theory does not ensure that the deletion of an h-component of an image will effectively change image Proposition [6][4]. The corollary of this observation is that deleted h-components of an image may reappear in result. As the h-component is just a representation of the decomposition of image according to a particular h-connection, its properties are thus inherited from the chosen h-connection, and they cannot be specified until such an h-connection has been

chosen. These theoretical developments are illustrated by application on a fuzzy h-connection recently. Existing approach allows us to represent different fuzzy h-connected components of an image in a single tree structure. This provides a convenient representation to design fuzzy h-connected operators and to reuse all existing algorithms imagined for connected component tree in this new context.

2.5 Quality Measures for Imaging-based Cellular Assays.

Z-factor and related measures are useful in estimating assay variability in HTS whichcaused by assay biology and by instrumentation. Imaging-based cellular assays introduce several new sources of variability: imaging resolution and other image acquisition parameters, size of imaged area, image analysis algorithm and its parameters [8][3][4]. The algorithms that derive assay measures from images may complex and may saturate the values from the positive and negative states of the assay, thus artificially reducing variability.

We proposev-factor, a new quality measure, which generalizes z-factor for a dose-dependent sequence of assay states. It gives a more realistic measure of the overall assay performance by accounting for intermediate points in the dose curve, which have higher variability due to effects of computation and dispensing errors. The use of v-factor as a quality measure allows comparing algorithms and rationally determining imaging resolution and size requirement cellular imaging assays, measure (or measures) used to characterize the assay is far removed from the signal registered by camera. Different algorithms will produce different assay measures on same image.

This is especially acute for redistribution assays where total intensity may not change and the assay result may depend more on the algorithm than on raw image. In high through drug screening it is common to evaluate the quality of assays by a statistical parameter that depends on the dynamic range and variability of assay. Several such parameters have been introduced with z-factor being most popular [5][6]. For cell-based assays, z-factor above 0.5 is considered good. This type of measures proved to be very useful to capture and compare variability caused by assay biology and by instrumentation (e.g., pipe ting). Cell assays based on imaging introduce several new variables: imaging resolution, size ofimaged areaand data extraction algorithm

3.PROPOSED DESIGN.

Proposedsegmentation is induced for single-cell cervical cell images. A Radiating Gradient Vectoraiming at accurate extraction both the cytoplasmand nucleus from a single-cell curved image is proposed. Involves a new edge map computation method and refinement based on stack, and is thus robust contamination robustcan effectively locate the obscure boundaries.After preprocessing, the areas in the image are clustered roughly to nucleus, cytoplasm and the background by a spatial *K*-means clustering algorithm. The boundaries can also be nearly correctly traced even if cytoplasm is near to interference.

3.1 Cell segmentation strategies.

When extracting features of individual cells in an image, the first task is to find and define the individual cells that are cell segmentation. The method for cytoplasm segmentation of labeled cells presented in this paper consists of a number of processing steps like as over and under segmentation produced by the initial processing steps can be corrected after the automatic quality control step and feedback step.

3.2cell Segmentation ASIC algorithm

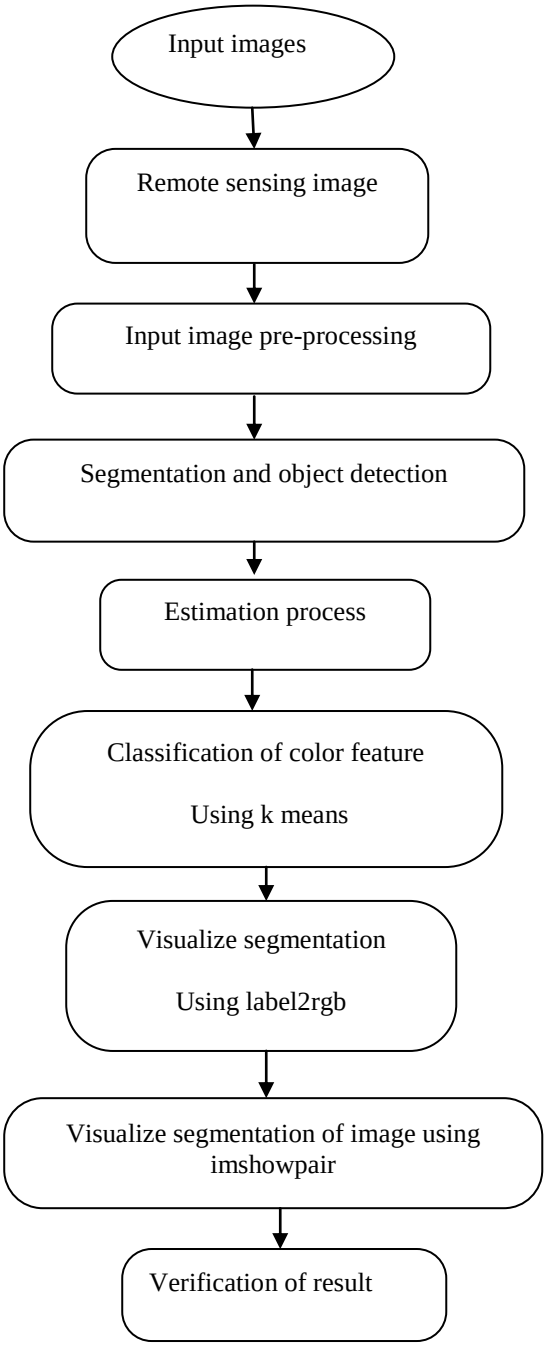

Fig.1 Procedure for ASIC algorithm.

Our main goal of segmenting a particular cell region containing a single cell or multiple cells is to geta relevant

segment for allnucleuses that capturethe original structure of that nucleus. First to automatic sensing the nucleus image and preprocessing the image.Segmentation of thecytoplasm of the cell region into many parts is nota critical task because they obtained segments is later to beclassified as nucleus and cytoplasm. We present a non-parametric segmentation ASIC algorithm where a tree is built fromthe candidate parts separated by multi-scale watershedparts. We select a meaningful region in theimage by optimizing a measure and classification of color feature using k means algorithm.

3.3Region selection

Our next aimis to select the most reasons and accurate segmentsamong those appearing and different levels of theVisualize segmentation. Nucleus regions are considered as the more meaningfulsegments where they can be differentiated through color segmentation according to theirspectral single and size.The puritymeasure for a node is acted to bethe property of two factors.

3.4 Nucleus and Cytoplasm Classification

We introduce a single measurement as the first factor. Single nucleus region is obtained at some levels of the hierarchy theystay the similar for few count of levels and then the face alarge change in terms ofsingle due to merging withtheir surrounding cytoplasm segments. The segments we areinterested in correspond to the single regions rightbefore this change.

3.5 Classify color features

The feature based classification and segmentation of remotely sensed imageis used to assign corresponding levels with respect to groups with singlecharacteristics, with the aim of discriminating multiple objects from each other within the cell image. Every level of an image is called class. This will be executed on the basis of spectraldefined features such as density, texture and many other things in the feature space.This paper focuses remote sensing image classification of color feature based using ASIC k-means clustering method.
As the result of this loop may notice that the cells change their location step by step process until no more changes are done. Here we introduce several widely used algorithms that consolidate data by clustering or grouping and then present a suitable method is remote sense application basedASIC k-means cluster algorithm. It is possible to reduce the computational cost and gives a high discriminative power of regions present in the image.

4. General Procedure for Classification

Remote sensing image classification refers to the task of extracting information classes from a Multiband raster image. The resulting raster from image classificationcan be used to create color segmentation. Depending on the interaction between the analyst and the computer during classification, there are two types of classification: supervised and unsupervised. The objective of image classification is to identify and portray, as a unique gray level (or color), the features occurring in an image in terms of the object or type of land cover these features actually represent on the ground.A broadgroup of
Digital image processing techniques of remote sensing application explains the image classification techniques are most generally applied to the spectral data of a single date image or to the varying spectral data of a series of multidimensional images.
Clustering involves a set of point into nonoverlapping groups or points; where points in a cluster are more similar to one another than points in other clusters or cells. The term more similar, when applied to clustered points, usually means closer by some measure of proximity. When a dataset is clustered, every point is assigned to some cluster and every cluster can be characterized by a single reference point, usually take an average of the points in the cluster. Any particular division of all points in a dataset into clusters is called a partitioning.

4.1. Clustering Method

Clustering is a grouping of data with similar Characteristics. This similarity in a given set may vary according to data, because clustering is used in various fields such as numerical taxonomy, morph metric, systematic, etc. Thus, a ASIC algorithm that fits the numerical measure of optimization in a data may not optimize another set of data. There are many algorithms to solve a clustering problem but we using ASIC algorithm.
The algorithms used in our applet concentrate on joining, splitting, and switchingsearch methods this also called bottom up, top down, and interchange, respectively. The clustering method uses a threedimensional model for demonstration purposes.However the algorithms can calculate clusters in infinite dimensions. We are planning to an algorithm based on principal component analysis, projecting the infinitedimensional data onto athree dimensional space. There are many methods of clustering developed for wide variety of purposes. Clustering ASIC algorithms used for supervised classification of remote sensing data vary according to the efficiency with which clustering takes place. Clustering is divided into hierarchical clustering and non-hierarchical clustering as mentioned as follows. The distances to evaluate the similarity are selected from the following methods.
In this paper, we present a fully automated method for annotating segmentation images in highly complex conditions. The proposed method relies on a multi-layered segmentation and clustering process, which begins with an adaptive segmentation step using anASIC Method. The second layer is comprised of two probabilistic classifiers, responsible for determining how many components may be containing each segmented region.

5. ALGORITHM

A = imread(' ') //convert image to double //
Displays binary image in handle graphics
NumRows = size();
NumCols = size (); //capture number of rows and no. of columns reshapes image using the dimension
Use bsxfun to subtract the column mean from the corresponding column elements of a matrix.Use bsxfun to Right array divide for matrix X //

L = kmeans( ); //determine clusters using kmeans inbuilt function to get three clusters.centroid of cluster is determined with the given measurereshapes image with the given rows and columns//

Figure
Imshow(label2rgb ()); //create a figure //

Aseg1 = zeros(size(),'like', A);
Aseg2 = zeros(size(),'like', A); // converts label matrix to rgb color image and show it Create an array of zeros that is the same size as an existing array.
Repeat matrix//

// check for automatic segmentation equals to binary converted grey scale imagea visualization of the differences between images Aseg1 and Aseg2 //

6. RESULT

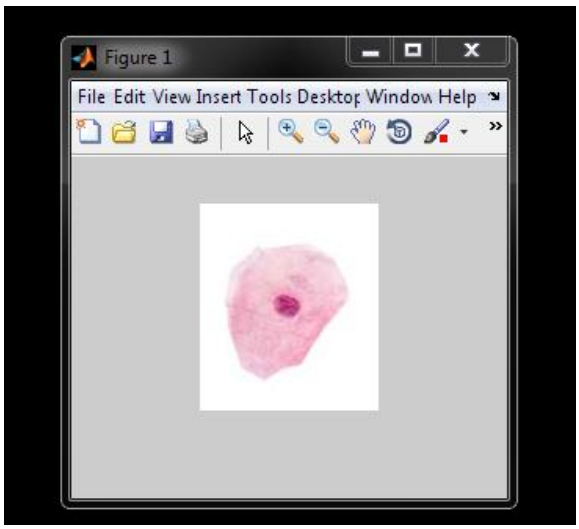

Fig. 2 input segmenting image.

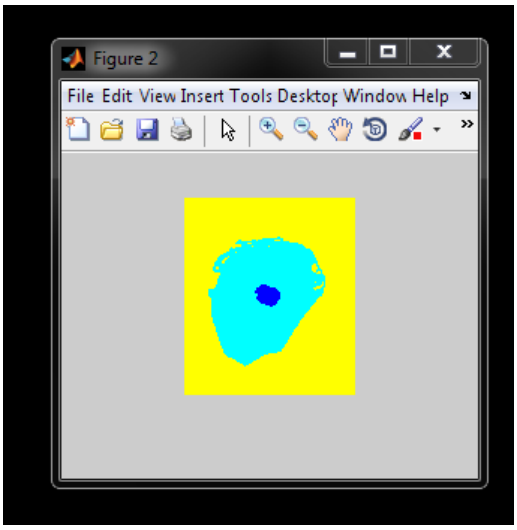

Fig. 3 Visualize segmentation image.

CONCLUSION

In general clustering algorithm is a wellknownalgorithm for classifying the Land sat images. But k-means clustering algorithm is also a wellknown clustering algorithm to classify the remote sensing images. This algorithm splits the given image into different clusters of pixels in the feature space, each of them defined by its center. Initially each pixel in the image is allocated to the nearest cluster. Then the new centers are computed with the new clusters. These steps are repeated until convergence. We could assume random objects as the initial centroids or the first k objects in sequence could also serve as the initial centroids.Thesealgorithms are robust and very effective in producingdesired classifications especially in the field of patternrecognition as per the region of interest as demonstrated by the experimentalresults.
This work presents a novel image segmentation based on color features from the images. In this we did not used any training data and the work is divided into two stages. First enhancing color separation of satellite image using decor relation stretching is carried out and then the regions are grouped into a set of five classes using K-means clustering algorithm. Using this two-step process, it is possible to reduce the computational cost avoiding feature calculation for every pixel in the image.In future different neural network algorithms and fuzzy set algorithms can be used to classify the satellite images instead of above clustering algorithm and the classification results of those will be compared with the existing algorithms

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