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Research Paper

A novel approach for cDNA image segmentation using SLIC based SOM methodology

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Abstract

In the segmentation of computer vision images, Super pixels are act as key role from last decade. There are multiple algorithms and techniques to analyze the Super pixels but amount all of them the best super pixel analyzing method is Simple Linear Iterative Clustering (SLIC) have come to pivot increasingly in recent years. The studying of micro array gene expression from MRI imaging is more useful to detect tumors or any other cancer diseases, so that the complementary DNA (cDNA) microarray is a well established tool for studying the same. The segmentation of microarray images is the main step in a microarray analysis. In this paper, we proposed an algorithm to segmenting the cDNA micro array image using Simple Linear Iterative Clustering (SLIC) based Self Organizing Maps (SOM) methodology. However, the proposed algorithm is taken up a challenging task to study the poor quality of images also. There are two steps to analyze the image, first, a pre-processing the applied image to reduce noise levels and second, to segment the image using SLIC based SOM methodology.

Keywords: *Simple Linear Iterative Clustering; Segmentation; Gridding.*

1. Introduction

A super pixel is a stack of structural proximal and homogeneous pixels. The homogeneous would be defined as in terms of size, depth of color, depth of texture and etc. The Super pixels [3][15] are known to conserve the local image attributes such as object boundaries, shape and area, and decrease the cost of calculation of many computer vision segmentation problems. Due to this, super pixel over segmentation capably reduces the no. of units to be handling with an image. The SOM methodology is best ever to study the image pixels and here we are introducing a new methodology of microarray image segmentation using SLIC over SOM. The major advantages for using this technology are; to compute features with more meaningful regions and to reduce the input objects for the sub-sequent algorithms.

GENE articulation microarray (GEM) tests [2] gather basic natural data gathering organic information from tests like tissues, cell lines recorded GEM information hold quality data over all specimens in the perception. As of late a huge number of qualities is measured and recorded all the while. In numerous points of view these specimens can be diverse under perception. To locate the significant qualities for a specific target is an essential region of research. These qualities are called enlightening qualities. The revelation of enlightening qualities is critical to the doctor for judge a patients and for the organization that are making drugs over the most recent couple of years, a great deal of exertion has been placed in the improvement of answer for the educational qualities disclosure. Till now the undertaking is extremely testing and some transformative methodologies are concocted to beat the ordinary Approaches. The microarray image analysis is shown in figure 1.

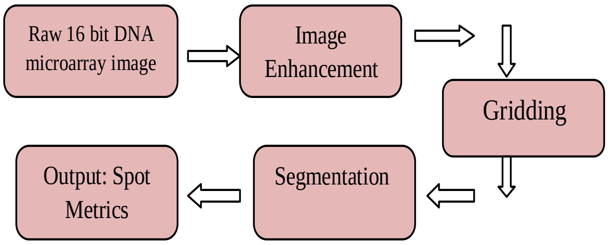

Fig. 1: Analysis of Microarray Image.

Feature determination when utilized for microarray quality articulation information is called quality choice. Apart from revile of dimensionality there are numerous different issues looked in quality determination like mislabeled information, repetitive information, superfluous and boisterous information, and issue of cross-stage examinations, wrong and predisposition issue and trouble in natural data recovery. Different quality choice techniques and calculations are proposed in writing which can diminish the dimensionality by expelling unessential, repetitive and loud qualities. The quality articulation information which is attracted the frame network additionally contains some missing esteems which are caused by factors like lacking determination, picture debasement or due to scratches on slide. Different strategies have been utilized to fill those missing esteems. Normally utilized Naive strategies are attributing the missing esteems with zeros or column midpoints or evacuating the quality articulation profile containing missing worth. These strategies don't give finish estimation of missing quality and looses helpful data. So some different strategies have been produced to attribute the qualities like KNN ascribe strategy, Bayesian key parts investigation credit technique, Support Vector Regression strategy (SVR).

In this paper, we are going to propose a novel approach for cDNA microarray gene image segmentation process using Simple Linear Iterative Clustering (SLIC) based Self Organizing Maps (SOM) methodology of adaptive elements. Segmentation is a collection of methods or functions to allowing interpreting areas of the image as elements or objects. The object is everything what is of interest in the image and the rest of the image is background. And extensively in my research represents comparison of spatial filters approaches i.e. filtering approach using linear and Non-linear filters accounting Peak Signal to Noise Ratio, Root Mean Square Error, and Universal Quality Index, Structural Similarity Index and Run Time as performance parameters.

2. Related work

Simple linear iterative clustering (SLIC)[12] is an espousal of k-means for Super pixels generation with two major distinctions like the no. of distance computations in the optimization is dramatically decreased by the complexity to be linear in the number of pixels N and independent of the no. of Super pixels k and the other one is a weighted distance quantify incorporate the color and spatial nearness while concurrently providing control over the size of pixel and solidness of the Super pixels.

"The segment of shading picture has been ended up being troublesome in light of the fact that it includes an immense measure of information processing. Albeit incredible endeavors have been given to it, a few issues are as yet not completely tended to. Dong and Xie [9] ace represented a mixture framework which includes unsupervised segmentation and directed division. The unsupervised division is accomplished by a two-level approach, i.e., lesser shading and shading grouping. The regulated segmentation includes shading learning and pixel grouping. Simulated strengthening (SA) has been utilized for finding the ideal bunches shape SOM models".

The algorithm of SLIC Super pixels generation is given below.

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1) Initialize p initial cluster centers in
$C = [k, x, y, r, s]^T$
By sampling pixels at regular grid steps S.
2) For generation of equal sized super pixels the grid interval S is given by $S=\sqrt{\frac{N}{P}}$
3) Set label k (j) =-1 for each pixel j.
4) Set distance d (j) = ∞ for each pixel j.
5) For each cluster center C do
6) For each pixel j in a 2S X 2S region around C do
7) Compute the distance D between C and j.
8) The distance D depends on pixel's color (color proximity) and pixel position (spatial proximity), whose values is known. The value of D is given by

$$d_s = \sqrt{(r_j - r_i)^2 + (s_j - s_i)^2}$$

$$d_c = \sqrt{(l_j - l_i)^2 + (x_j - x_i)^2 + (y_j - y_i)^2}$$

$$D = \sqrt{\left(\frac{d_c}{N_c}\right)^2 + \left(\frac{d_s}{N_s}\right)^2}. \tag{7}$$

The maximum spatial distance expected within a given cluster should correspond to the sampling interval, $N_S = S$. Determining the maximum color distance Nc is not so straightforward, as color distances can vary significantly from cluster to cluster and image to image. The value of Nc in the range from [1, 40].
1) if D < d(i) then set d(i)=D and k(i)=p go to 6.
2) Go to 5, the same process for each cluster
3) Compute new cluster centers.

The clustering and updating processes are repeated until a predefined number of iteration is achieved. The SLIC algorithm can generate compact and nearly uniform Super pixels with a low computational overhead.

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3. Proposed work

The SLIC algorithm generates Super pixels which are used in our clustering algorithm. The Super pixels are generated based on the colour similarity and proximity in the image plane. The algorithm depends on two values N_S and Nc, the higher value of N_S corresponds to more regular and grid-like Super pixels structure and lower value of Nc captures more image details.

The primary goal was to distinguish the central stressors influencing biotic uprightness in each of the three states assessed in the present report. The stressor and organic files information were accessible in various databases that are clarified later in the present report. SOM were the device used to distinguish bunches or homogenous gatherings of stressors and they are clarified in detail in the present report. Essentially, SOM are a device to compose profoundly dimensional information in homogeneous gatherings or bunches in which the information having a place with these gatherings are as comparable as could be expected under the circumstances.

The SLIC Super pixel based SOM clustering algorithm is given below:

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1) Collect necessary information of Super pixels by generate the Super pixels representation of original image.
2) Initialize cluster centroids v_i, i=1, ... , C.
3) The objective function F is given by

$$F = \sum_{i=1}^{C}\sum_{j=1}^{Q}\gamma_j u_{ij}^m \|\xi_j - v_i\|^2 + \frac{\alpha}{N_R}\sum_{i=1}^{C}\sum_{j=1}^{Q} u_{ij}^m \Big(\sum_{s_r \in N_j}\gamma_r \|\xi_r - v_i\|^2\Big) + \sum_{j=1}^{Q}\lambda_j\Big(1 - \sum_{i=1}^{C} u_{ij}\Big) \tag{10}$$

4) The membership values uij is updated given by

$$u_{ij} = \left(\sum_{k=1}^{C}\left(\frac{\gamma_j\|\xi_j - v_i\|^2 + \frac{\alpha}{N_R}\sum_{s_r \in N_j}\gamma_r\|\xi_r - v_i\|^2}{\gamma_j\|\xi_j - v_k\|^2 + \frac{\alpha}{N_R}\sum_{s_r \in N_j}\gamma_r\|\xi_r - v_k\|^2}\right)^{1/(m-1)}\right)^{-1} \tag{11}$$

Where γ_j is the number of pixels in super pixel s_j,
u_{ij} denotes the membership of super pixel s_j to the ith cluster.
Q is the number of Superpixels in images and
ξ_j is the average colour value of super pixel s_j,
N_j stands for the set of neighbouring Superpixels that are adjacent to sj and
NR is the cardinality of N_j.
||·|| is a norm metric, denoting Euclidean distance between pixels and clustering centroids.
The parameter m is a weighting exponent on each SOM membership and determines the amount of self mapping of the resulting classification.

5) The cluster centroids vi is updated given by

$$v_i = \left(\sum_{j=1}^{Q} u_{ij}^m\left(\gamma_j\xi_j + \frac{\alpha}{N_R}\sum_{s_r \in N_j}\gamma_r\xi_r\right)\right)\left(\sum_{j=1}^{Q} u_{ij}^m\left(\gamma_j + \frac{\alpha}{N_R}\sum_{s_r \in N_j}\gamma_r\right)\right)^{-1} \tag{12}$$

6) Repeats Steps 3 to 4, until ||Vnew-Vold||< ε.

4. Experimental results

This experiment was implemented in MATLAB 7.8 and used the Intel-based workstation with Windows OS. The experimental microarray images were split into two different data sets and every block was kept in TIFF files with l6-bit grey level. The first data set contains of a set of images from microarray gene expression and the other one contains fourteen images drawn from the Stanford Microarray Database (SMD). For the much of spot pixels, there is a separation between the background calculations from the foreground exactly. The experiment calculation was happened in the process of, first we identified and reduced the noisy of image [2], analyzing the microarray gene expression and finally segmented the image. The final result of the segmentation is near to the real pixel. The original image and its corresponding segmentation result are shown in Fig 6.

The proposed SLIC algorithm is performed on two microarray gene expression images of brain tumor category [18]. The figure 3 shows that the original two types of brain tumor images. The image 3.1 in figure 3 consists a total of 200, 500 Super pixels and image 3.2 in figure 3 consists 200, 500 Super pixels. The figure 2 shows that gridded images for original image for figure 1. Thereafter the process of gridding, the image is considered in to compartments, such that each compartment is having one spot and one background. The experiment was done for K-means [16], Fuzzy C-means [12] and SLIC based SOM methodologies. The SLIC was generated Super pixels for these two compartments and segmented using SLIC based SOM algorithm.

The Mean Square Error (MSE) [17] is significant metric to validate the quality of image. It measures the square error between pixels of the original and the resultant images.

The MSE is [18] mathematically defined as

$$\mathrm{MSE} = \frac{1}{N}\sum_{j=1}^{k}\sum_{i\in c_j} \|vi-cj\|2 \tag{13}$$

Where N is the total number of pixels in an image and xi is the pixel which belongs to the jth cluster. The lower difference between the resultant and the original image reflects that all the data in the region are located near to its centre. Table 1 shows the quantitative evaluations of clustering algorithms. The results confirm that SLIC based SOM algorithm produces the lowest MSE value for segmenting the microarray image.

Table 1: MSE Values

Method	Compartment No 1 in image 2.1	Compartment No 1 in image 2.2
K-means	96.4	93.6
Fuzzy c-means	93.1	89.4
SLIC SOM	82.8	77.4

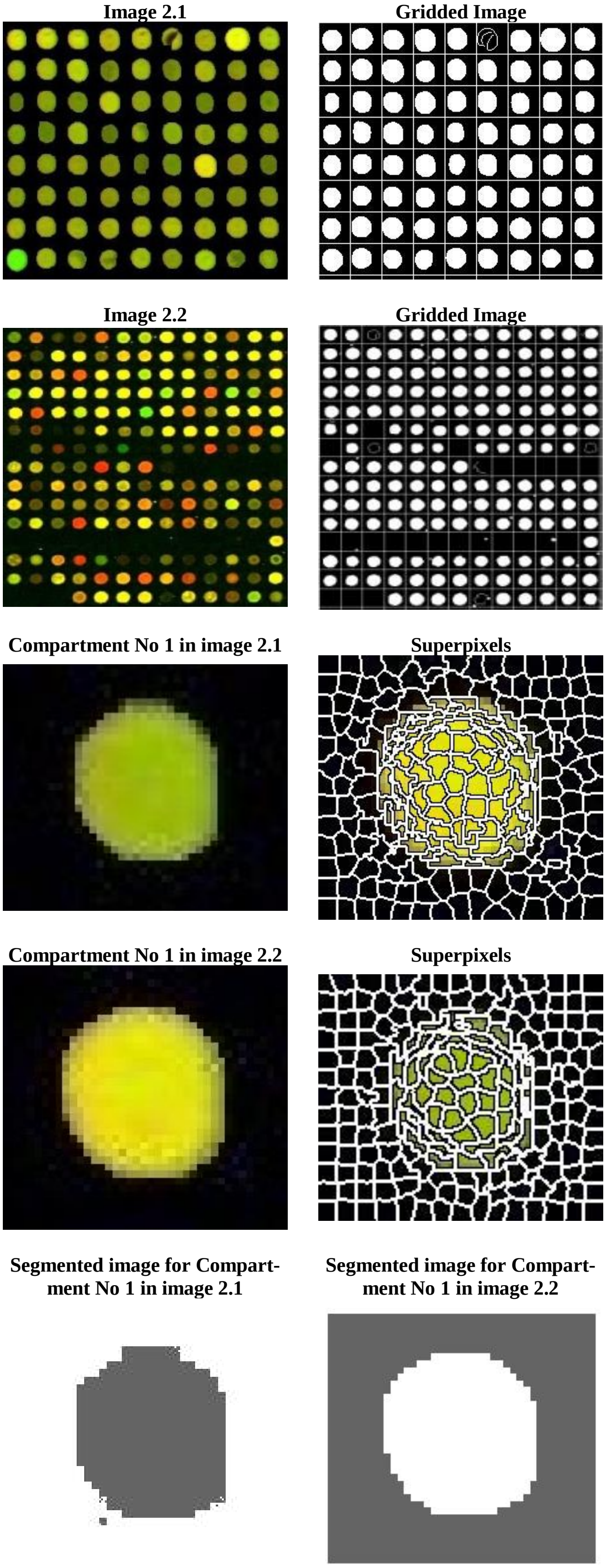


Image 2.1 **Gridded Image**

Image 2.2 **Gridded Image**

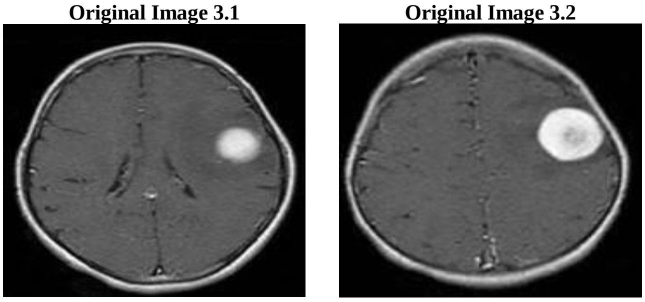
Compartment No 1 in image 2.1 **Superpixels**

Compartment No 1 in image 2.2 **Superpixels**

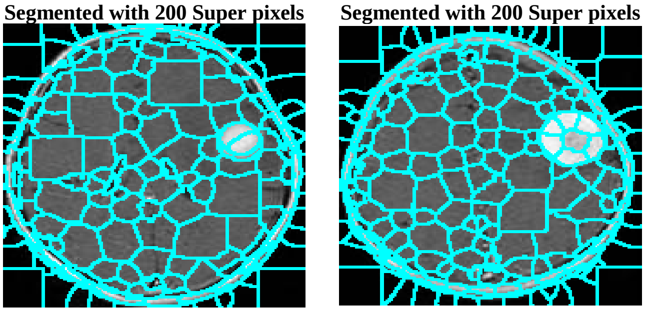
Segmented image for Compartment No 1 in image 2.1 **Segmented image for Compartment No 1 in image 2.2**

Fig. 2: Super Pixel Based SOM Segmentation.

Original Image 3.1 **Original Image 3.2**



Segmented with 200 Super pixels **Segmented with 200 Super pixels**



Segmented with 500 Super pixels **Segmented with 500 Super pixels**

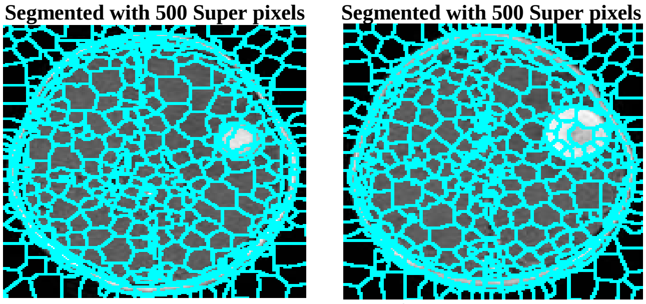


Fig. 3: Super Pixels Segmentation for Brain Images.

5. Conclusion

The process of analysis of segmentation of microarray gene expression is performed with gridding, reducing the noise, study the microarray gene expression and finally segmentation. The process of gridding and de-nosing [1] is done using our previous work, nest analysis the micro array gene expression [2] and then in current paper, we proposed the microarray image segmentation using SLIC based SOM methodology. The proposed analysis was verified with mean square error values and got accurate than others previous algorithms. The replication of a very large quantity between two genes under this experiment is the expression ratio for every gene pixel objects. The spot pixel information contains the compute of expression ratio for every gene spot pixel in the microarray image. The expression ratio replicates a very large quantity between the two sample gene pixels. This proposed process gives the better performance to compute the microarray tumor tissue problem and produces best ever segmentation results. Also this is having many desired qualities like, efficient calculation, less complexity, efficient representation.

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