Spot Edge Detection in cDNA Microarray Images using Window based Bi-Dimensional Empirical Mode Decomposition

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Abstract— Ongoing Microarray is an increasingly playing a crucial role applied in the field of medical and biological operations. The initiator of Microarray technology is M. Schena et al. \cite{1} and from past few years microarrays have begun to be used in many fields such as biomedicine, mostly on cancer and Diabetic, and medical diagnoses. A Deoxyribonucleic Acid (DNA) microarray is a collection of microscopic DNA spots attached to a solid surface, such as glass, plastic or silicon chip forming an array. Processing of DNA microarray image analysis includes three tasks: gridding, segmentation and intensity extraction and at the stage of processing, the irregularities of shape and spot position which leads to generate significant errors. This article presents a new spot edge detection method using Window based Bi-dimensional Empirical Mode Decomposition. On separating spots form the background area and to decreases the probability of errors and gives more accurate information about the states of spots we are proposing a spot edge detection via WBEMD. By using this method we can identify the spots with low density, which leads to increasing the performance of cDNA microarray images.

Index Terms— cDNA Microarray Image; Edge Detection; WBEMD; Image Processing

I. INTRODUCTION

Spot Edge Detection plays a fundamental role in processing of cDNA Microarray Images. While processing microarray the edge includes very most important information, such that edges which are used for labeling the points with a significant variation in gray level, and it can provide the position of object. Until now, we have been applied some edge detections algorithms based on multi-resolution and gradient operators.\textsuperscript{7} Mean while several gradient operators have Sobel\textsuperscript{1}, Prewitt\textsuperscript{2}, Marr\textsuperscript{3} and Canny\textsuperscript{4} are used. Multi-resolution (multi-scaled) algorithms include wavelet based edge detection \cite{5, 6} and multi-scaled mode based edge detection \cite{7, 8} have been used. Edge detection basically refers to identifying points of an image at which the image brightness changes discontinuously (sharply) The goal of Edge Detection is to finding sharp changes in image brightness to capture the important changes in the properties of the events and to detect a desired object, extract features of the image for further analysis. An edge is the boundary between two different regions in an image. Edge detection is widely recognized as the next revolution in image processing and computer vision. Edge detection can be broadly categorized into

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two major approaches: search-based and zero-crossing based [1-2]. In search-based methods first compute the strength of edge by using first-order derivative. While coming to the zero-crossing methods usually find the edges by using second-order derivative of the image.

Microarray is an innovative tool in biomedical research which enables researchers to analyze genes, proteins and other biological molecules. A microarray is a collection of spots containing DNA deposited on the solid surface of glass slide. Each of the spot contains multiple copies of single DNA sequence [2]. Microarray expression technology helps in testing and extracting the expression of large number of genes in parallel and its applications can vary from cancer diagnosis to human identification. While preprocessing microarray image is mainly to improve its defects including noise and poorly expressed spots. The processing of cDNA Microarray Images constitutes of following steps: Gridding, Segmentation and Intensity Extraction. In order to identify where exactly the spots are located, gridding is critical step in microarray image processing and it is a process in which segments the microarray image into compartments Segmentation is the process of dividing each compartment into spots and image background. In Intensity extraction, this calculates the foreground and background intensity pairs. This Article is organized as follows: Section II presents Window based Bi-Dimensional Empirical Mode Decomposition, Section III presents, Spot Edge Detection of cDNA Microarray image, Section IV presents Experimental results, and finally Section V reports conclusion.

II. WINDOW BASED BI-DIMENSIONAL EMPIRICAL MODE DECOMPOSITION

In the upcoming part, the theory of WBEMD will be described; Firstly, the Bi-dimensional empirical mode decomposition algorithm will be overviewed.

A. Bi-Dimensional Empirical Mode Decomposition overview

Bi-dimensional empirical mode decomposition is a 2D extension of the concept of empirical mode decomposition, originally developed to analyze nonlinear and nonstationary 1D signals. Besides BEMD, the 2D version of the EMD process is also known as 2DEMD, IEMD and so on. Processing of non-stationary and nonlinear signal functions Huang et al. [5] proposed Empirical Mode Decomposition. The Empirical Mode Decomposition differs from the traditional signal decomposition method which does not need to choose the primary function in advance. Basically the empirical approach that can be applied to a data set, rather than a theoretical tool. In this method any complicated data set can be decomposed into a finite and often a small number of intrinsic mode functions and the decomposition are based on the local characteristic, it is applicable to non-stationary processes. The Empirical approach has been successfully applied in image processing, medicine, fault diagnosis and so on. BEMD is applied to do the multi-scale decomposition to the data. BEMD is a new, unsupervised, adaptive, proved reliable mono dimensional signals and sifting process that decomposes a signal into its BIMFs and a bi-dimensional residue (BR) on the local frequency (or oscillation information). Here instead of decomposition data or signal we are decomposing image, BEMD decomposes an image into several bi-dimensional intrinsic mode functions (BIMFs) and a bi-dimensional residue (BR). In Empirical Mode Decomposition has better time-frequency properties and it can be applied in several fields like the mechanical fault detection, the electromagnetic wave and the acoustic signal analysis. Now a day’s Empirical Mode Decomposition which grabs the attention of image analysts. The main contribution of our approach is to apply the EMD to Spot Edge Detection in cDNA Microarray Images which are widely recognized as a difficult and challenging problem in computer vision. IMFs satisfying the following two conditions:

1. The number of extrema and zero-crossings must either equal or differ by at most one.
2. At any case, the mean value of the envelope defined by the local maxima and the local minima is zero.

Bi-Dimensional Empirical Mode[10] Decomposition algorithm extracts Bi-dimensional Intrinsic Mode Functions (BIMF) that is intrinsic to the original image through a sifting procedure. The decomposition method in Empirical Mode Decomposition is called Shifting Process. The shifting process of the two dimensional signals such as image can be adapted from the one-dimensional signal as follows.

1. Fix $I_{\text{original}}$ as a Microarray image to be decomposed. Let $j=1$ is the starting index of Intrinsic Mode Function

\[ I= I_{\text{original}} \]

2. We have to spot the local maxima and local minima points in I.
3. Create the upper envelope $E_{\text{up}}$ of local maxima and the lower envelope $E_{\text{lo}}$ of local minima by using interpolation approach.
4. Work out the mean of the upper envelope and lower envelope.
\[ \text{E}_{\text{mean}} = \frac{\text{E}_{\text{up}} + \text{E}_{\text{lw}}}{2} \]
5. Work out the Image Intrinsic Mode functions
\[ \text{IMF}_i = \text{I} - \text{E}_{\text{mean}} \]
6. Repeat steps 2-5 until \( \text{IMF}_i \) can be considered as an IMF
7. Recomputed Image Intrinsic values until \( \text{IMF}_j \)
\[ \text{IMF}(j) = \text{IMF}_j = \text{I} - \text{IMF}_j \]
8. Repeat steps 2-7 until all the standard deviation of two consecutive IMFs is less than a predefined threshold.

**B. Window based Bi-dimensional Empirical Mode Decomposition.**

Empirical Mode Decomposition[9] analyzes the data not in the local area but in a whole area, which leads to have gray spots, so that the high-frequency components having low-frequency components cannot be separated. Here, the high-frequency component represents detail information and the low-frequency component represents the trend information making a big splash in multi-scale signal analysis.

\[ \text{I} = \sum_{i=1}^{n} \text{IMF}_i + \text{Res} \tag{1} \]

Where \( n \) is the required number of Intrinsic Mode Functions and Res Residue function. We can use square-adaptive sliding window or Windowed Fourier transform (WFT) in which the number of regional maxima is equal to regional minima, is applied in WEMD to get the regional mean value then we have to work out the intensity of the corresponding pixel in the transformed image and later on we have to calculate the first IMF that is to be subtracted from original image. This algorithm is listed as follows:

1. Fix \( \text{I}_{\text{original}} \) as an Microarray image to be decomposed. Let \( j=1 \) is the starting index of Intrinsic Mode Function, \( \text{I} = \text{I}_{\text{original}} \)
2. We have to spot the local maxima and local minima points in \( \text{I} \).
3. Perform the following according to the value of IMF.
   3.1) Set the max length of the quadrangle window side \( N \), where \( N \) must be odd and no less than 3, so that the max area of the window is \( N^2 \);  
   3.2) Center the window at the first pixel \((1,1)\) of \( \text{I} \); 
   3.3) Let \( K=3 \), where \( K \) denotes the actual length of the quadrangle window side; 
   3.4) Adjust the area of the window to \( K^2 \) while keep the window centered at the current pixel \((m,n)\), and turn to \( \text{c}(m,n) \) if \( K < N \) and the number of max in the window is not equal to that of min, or else turn to \( \text{c}(m,n) \); 
   3.5) Let \( K=K+2 \), then turn to \( \text{c}(m,n) \).
   3.6) Figure out \( c(m,n) \), which denotes the mean value of intensities of pixels in the window centered at the pixel \((m,n)\) of \( r \), and then turn to the next pixel and go back to (3.3) until all the mean values is worked out;
4. Let \( \text{C} \) denote the matrix constructed by \( c(m,n) \), and let \( \text{IMF}_i=\text{I}-\text{C} \), \( \text{I} = \text{C} \), and \( i\equiv i+1 \);
5. Let \( \text{Res} = \text{I} - \text{IMF}_i \) and break if \( i \) reaches the required value, or else turn back to step (2).

WBEMD algorithm seems to be complex, but her actually need first Intrinsic Mode Function which contains most quality Edge Information and counter equation can be calculated using following equation:
\[ f(x,y) = \begin{cases} \text{if} f(x,y) < 0 \text{ and} \\ \text{o} \text{, if} f(x,y) \geq 0 \end{cases} \tag{2} \]

**III. cDNA Microarray Spot Edge Detection**

A new spot edge detection of cDNA microarray image will be presented using Bi-dimensional Intrinsic Mode Functions (BIMF). The IMF that has been generated by applying empirical approach which contains sufficient edge information and coming to next IMFs gradually reduced. Suppose if the contrast of the edge description of the original microarray image is low, then the quality of the edges extracted by the first IMF will be poor. If we want to improve the quality of the spot edges can be applied by using Bi Histogram Equalization (BHE) [6] to the original Microarray image prior to the computation of WBEMD. Consider a Microarray image with gray levels in the range \([0, L-1]\) To [10]obtain the quality image following operations should be meat. Work out the probability density function (PDF)
Fig 1: IMF of Microarray Image

\[ p(r_k) = \frac{n_k}{N} \quad k = 0, 1, 2, \ldots, L - 1 \quad (3) \]

Calculate the cumulative distribution function (CDF)

\[ C(r_k) = \sum_{k=0}^{k} p(r_k) \quad k = 0, 1, 2, \ldots, L - 1 \quad \text{and} \quad 0 \leq C(r_k) \leq 1 \quad (4) \]

Where \( n_k \) is the no of pixels in the image having gray level \( r_k \) and \( r_k \) is the \( k^{th} \) gray level in the image. To improve the contrast enhancement of microarray image we going for Bi Histogram Equalization to be considered. It will find out the average gray level pixels in histogram of the microarray image[11] and then sub divides the histogram in to two segments based on the pixels. Later on Bi histogram equalization operation is applied to each segment.

The average of gray levels of the histogram is computed as

\[ L_1 = \sum_{k=0}^{k-1} p(r_k) * (r_k) \quad (5) \]

Later on apply Window based Bi-Dimensional Empirical Mode Decomposition to the processed image to get the first IMF. We can determine a suitable threshold to convert the gray level values of the IMF image into black and white image such that the edge microarray image can be extracted. The processed edge image has the thick edge lines and some interior isolated pixels. Then mathematical morphology is applied to remove isolated pixels in the image. The final spot edge microarray image is obtained.

The main steps of the Spot Edge Detection using WBEMD are summed up as follows:

1. To obtain the sharper contrast of a microarray image, we are processing image with Bi Histogram Equalization.
2. Then from obtained image apply WBEMD to get the first IMF.
3. To obtain the gray level values of the First IMF we have to choose suitable thresholds values \( T_1 \) and \( T_2 \), which are helpful to convert the IMF image in to black and white image

\[ I(x,y) = \begin{cases} 0, & T_1 \leq \text{IMF}(x,y) \leq T_2 \\ 1, & \text{else} \end{cases} \quad (6) \]

4. The processed Edge image has thick edge lines and isolated pixels.
5. Perform Mathematical Morphology operations on the resulting image to remove isolated pixels
6. Now we can obtain the ultimate spot edge image.
IV. EXPERIMENTAL RESULTS

The proposed method is used to detect the edge of cDNA microarray image. Processing of a cDNA microarray image performed on a sample microarray slide that has 48 blocks, each block consisting of 110 spots. A sample chosen block has 36 spots of the block have been cropped for simplicity. The sample image is a 198*196 pixel image that consists of a total of 38808 pixels. The microarray image is decomposed by traditional EMD decomposition has the above mentioned defect, because the high-frequency components and the low-frequency components can’t be effectively separated each other. WEMD can effectively deal with the problem. The spot edge detection results of microarray image are presented in figure 2 and the following figure shows the speed of various EMD methods. Suitable thresholds of pixel values -75 and -42 were determined through WBEMD, to convert into black and white image.

<table>
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<tr>
<th>METHOD</th>
<th>BIEMD</th>
<th>MTEM</th>
<th>DEMD</th>
<th>WBEMD</th>
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V. CONCLUSION

In this Article, we presented an edge detection of cDNA Microarray images using WBEMD. The WBEMD approach can separate the spots from the background and it will generate accurate information about the spots such as pixel number and decreases the probability of errors encountered. The microarray edge information obtained by using WBEMD is better than Sobel and Prewitt operators. Experiments prove that our approach is efficient and involves how to optimize the edges.

REFERENCES