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Adaptive Min Max Thresholds Algorithm of Microarray Image Denoising Based on Nonsubsampled Contourlet Transform

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Abstract:- Denoising is one of the major pre-processing steps in microarray image analysis. This paper presents a new method to denoise DNA microarray images. It uses Non subsample Counterlet Transform (NSCT), min-max threshold and a derivative filter to denoise. The proposed method yields promising results for Stanford Microarray Database (SMD), University of North California microarray database (UNC) microarray images. The proposed algorithm is also compared with other existing methods using various performance metrics.

General Terms:- Denoising , Microarray image, Non Subsampled Contourlet Transform.

Keywords:- Microarray Image, Denoising, NSCT, Min-Max Threshold, Derivative filter Introduction.

1. INTRODUCTION

Microarray Technology was fictional in 1995 [1] and since that, it's been used as a crucial technology for cistron study. Deoxyribonucleic acid (DNA) sequence is present in the chip called microarray, which has its own distinctive locations for each every spot. At the same time, these can help in permitting the estimation of expression levels of thousands of genes. The importance of microarray is to unveil hidden biology of biological processes, observation organic phenomenon levels and for drug and treatment development as an example, therapeutic medication for organic phenomenon levels of cancer.

DNA microarray technology [2] plays a major role in several area of application such as identification of human diseases which majorly helps in obtaining the risk factors involved in it, therapy monitoring of disease to determine the stage. These days technology is also been used in agricultural development, drug discovery and also in quantification of genetically changed organisms. Slide noticed contains the group of genetic DNA probes square. There are mainly two population of informational RNA tagged with fluorescent dyes, they are square measure with hybridized slide spots and slide with scanner. The method produces two pictures one for every mRNA population, every of that varies in intensity in line with the extent of hybridization diagrammatic because the amount of absorption indicator contained in every spot.

Microarray Image process consists of the subsequent sequence of 3 main tasks [3]. First step includes gridding which impacts in separating the spots by assignment of image coordinates to that spots. Next step includes segmentation which yields in separation between the foreground and background pixels. Last step includes the signal intensity extraction which basically includes computation of common intensities of both foreground and background for every spot of array. Different sources of errors [4] like electronic noise, mud on slide are contained in microarray image. Mainly different sources of error causes high level of noise which basically propagates through higher image analysis. These may result in distinctive genes which expresses the draw correct biological conclusions by every variety of cells. During the image acquisition, microarray image might get corrupted by noise sources; these might result in difficulty for spot There are also chances of detection of additional bright artifacts as spot of microarray image.

The detailed description of the paper is organized as follows: Section I mainly focuses on the literature survey administrated within the areas of microarray image enhancement. Section II focuses on the approach used to denoise microarray image using NSCT and min-max threshold. Section III focuses on the results obtained in depth experimentation conducted on benchmark images. Finally Section IV focuses on the conclusion of the proposed work.

2. RELATED WORK

It's been ascertained that solely few researchers were dispensed within the space of microarray image enhancement. X.H.Wang, Robert . S. H .Instepanian and Young Hua Song [5] have proposed a new conception as ripple theory for denoising technique by making certain higher phenomenon. This method used by application of stationary ripple remodel for pre-process the microarray images by removing random noises.

RastislavLukac and Bogdan Smolka [6] presents a novel methodology of noise reduction that attenuates each impulse and Gaussian noise, throughout preservation and denoising sharpness the edges of images. R.Lukac et.al [7] explains vector fuzzy filtering framework concept that helps in denoising cDNA microarray images, which basicall determines the weights within the filtering structure by providing totally different filtering structures. Mario [8] has proposed technique for removal of noise by

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smoothening of coefficients of highest sub bands in ripple domain.

K.N.Plataniotis et al [9] describes impulse detection mechanism exploitation coevals the conception in denoise switching system. Harastefanou et.al [10] presented a two stage approach in denoising method by additive and increasing noise element that decomposes signal by multi resolution remodel. Guifang Shao et.al [11] proposed a new conception of denoising those two components as edge noise reduction Ali Zifan at.al [12] presented a approach using decimated and undecimated wavelets.

Tamana Howlader et al [13] proposed a method to denoise microarray images using maximum posterior and minimum linear mean square estimation criteria. J K meher et al [14] proposed a denoising method using optimize spatial resolution and spatial domain filtering. Yogananda Balagurunathan et al [15] developed a technique on simulated microarray images at different noise levels. Chaitragoplappa et.al [16] explained a dual tree complex wavelet to denoise microarray images. Rammmurugesan et.al [17] has described a technique to remove impulse noise based on two phase scheme. Araunakumarkakuni et.al [18] has discussed an algorithm to denoise microarray images using independent component Rastaslavlukac et.al [19] proposed a fuzzy based data adaptive filter to denoise microarray images. Wang Li Qiang et,.al[20] presented a switching scheme to remove the impulse noise present in the microarray image. Nader suffarian et.al [21] introduced sub block bi-histogram technique to enhance microarray image analysis through gridding.

3. PROPOSED WORK

This section focuses on the detailed algorithm used for denoising of microarray image. The proposed work consists of three stages namely 1. NSCT 2.computation of Robust Min-Max Threshold 3.Derivative filter

3.1 Non Subsampled Contourlet Transform

Noise in image is probabilistic functions, which includes impulse, poisson, Gaussian and speckle. It need not to be single mathematical probabilistic but can include more than one type of noise. So removal of noise from the noisy image requires the knowledge of type of noise that is incorporated into the image. To make multiscale, multidirectional expansion and fully shift-invariant, NSCT [22] usually uses two different filter banks to decompose the source image into number of subbands which includes nonsubsampled directional filter banks (NSDFB) and nonsubsampled pyramid (NSP). The decomposition of image results in less contourlet coefficient when compared to original image without decomposition. The screening of coefficient and selection of appropriate threshold value plays a very important role in removal of noise using contourlet. Adaptive threshold for different subbands will provide good removal of noise form source image when compared to static and universal threshold as most of the image will have asymmetric patterns.

Because of its multiscale and fully shift-invariant nature, the NSCT transform can be efficient used in image

denoising and image enhancement. Only with contourlet transform a duplicate representation of discrete images is provided, in this case the contourlet uses laplacian pyramid to accomplish the capturing process of points, later DFB (directional filter bank) is used to append the points together into a linear structure. The laplacian pyramid will have different direction decompositions with contour transform and hence it is more flexible when compared to wavelet transform. When an appropriate threshold value is chosen, the contourlet using LP is a better option when compared to wavelet transform. Moreover the original contourlet transform shows the problem of lagging in shift invariance and may result in pseudo-Gibbs phenomena due to up-sampling and down-sampling. To overcome the above two drawbacks nonsubsampled contourlet transform with nonsubsampled directional filter banks (NSDFB) and nonsubsampled pyramids (NSP) is used.

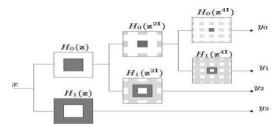


Fig 1: Nonsubsampled three pyramid decomposition structure

Fig 1.shows NonSubsampled three pyramid decomposition structure, Where y_0,y_1,y_2 and y_3 are the co-efficient of pyramid decomposition. Let the output image be named as yrec(x,y). The proposed algorithm works by taking the original image y(x,y) and decomposing it by four levels using NSCT transform.

3.2 Computation of min-max Threshold

To obtain the original image without noise, the inverse transform of reconstructed Nonsubsampled contourlet transform coefficients are processed. The coefficient can be processed by choosing appropriate threshold value, because the lower threshold value may preserve the details of image but noise may not be removed up to the mark. On the contrast the large value of threshold value may remove noise effectively but the crucial information in the image may be lost. So to retain the important information min max threshold is computed. The following parametes are estimated for the computation of min-max threshold from the image yrec(x,y) obtained from the previous section.

1) Mean (m)

2) Standard Deviation (sd)

$$sd = \sqrt{\frac{(yrec(x,y)-m)^2}{n}} \tag{1}$$

Where, x-number of rows, y-number of Columns ,n-total number of pixels

- 3) Determine the maximum (mxl) and minimum (mil) intensity level.
- 4) Calculate the threshold value using the following equation.

$$mmt = \frac{mxl - mil}{sd} \tag{2}$$

Threshold is applied on yrec(x,y) as , if the intensity level is less than mmt replace with zero value otherwise retain the same intensity level. Result image is labeled as st(x,y).

3.3 Derivative Filter

The following derivative filter 3 * 3 filter is used on st(x,y),

0	1	0
1	-4	1
0	1	0

Estimate the sum by multiplying each pixel and its 8 adjacent pixels with the mask and replace the middle pixel with sum. The Resultant image is denoised image which is labeled as df(x,y).

4. RESULTS

The results of proposed work are discussed in this section. The images for testing were taken from SMD, UNC and TBDB database. The performance or quality metrics used here are contrast improvement index (CII), peak signal to noise ratio (PSNR), mean square error (MSE), structure similarity index and mean structure similarity model (SSIM and MSSIM), contrast noise ratio (CNR), weighted peak signal to noise ratio (WPSNR), normalized absolute error (NAE) and normalized cross correlation (NCC)

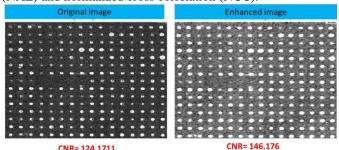


Fig 2a: Original Image with CNR=124.171 Fig 2b: Denoised Image with CNR=146.5176

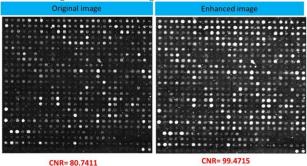


Fig 3a: Original Image with CNR=80.7411 Fig 3b: Denoised Image with CNR=99.4715

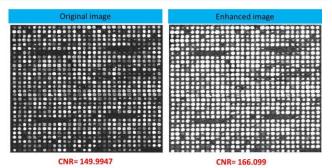


Fig 4a: Original Image with CNR=149.994 Fig 4b: Denoised Image with CNR=166.0999

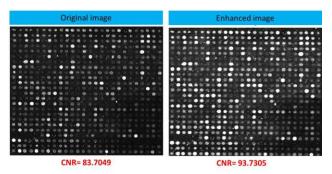


Fig 5a: Original Image with CNR= 83.7049 Fig 5b: Desnoised Image with CNR=93.7305

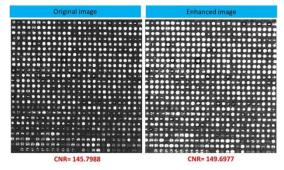


Fig 6a: Original Image with CNR= 145.7988 Fig 6b: Denoised Image with CNR=149.6977

The CNR of the images selected for testing were calculated and shown in the fig 2a, 3a, 4a, 5a, 6a. Later, these images were denoised using the proposed algorithm. From the fig 2b, 3b, 4b, 5b, 6b it is observed that the CNR of the denoised images have been increased which shows that the proposed work is able to remove the noise effectively.

Table 1 shows comparative study for 1) Average Weighted filter 2)Susan filter 3)soft thresholding filter 4) proposed work. From the results it is seen that the proposed work yields promising results.

Table	Ţ٠	Compa	rative	Study
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rable i. Comparative Stady										
	Image	MSE	PSNR	CII	MSSIM	CNR	WPSNR(DB)	200000000	NCC	FSIM
	lmg1	31.69	33.12	0.51	0.44	22.04	9.57	4.31	1.00	0.42
	Img2	14.18	36.61	0.39	0.59	21.69	9.80	2.87	1.02	0.85
1	Img3	13.08	36.96	0.31	0.61	22.51	9.81	2.77	1.05	0.75
	Img4	13.51	36.82	0.50	0.57	23.60	9.40	2.87	0.75	0.75
	Img5	35.67	32.67	0.34	0.40	32.53	9.22	4.63	0.58	0.79
	Img6	35.53	32.62	0.40	0.41	34.39	9.30	4.55	0.64	0.80
	Img7	34.10	32.80	0.44	0.41	21.18	9.25	4.52	0.62	0.81
	Img8	41.46	31.95	0.34	0.37	28.16	9.16	4.91	0.45	0.68
	Img9	40.71	32.03	0.37	0.40	15.68	9.24	4.71	0.61	0.80
	Img10	39.86	32.12	0.66	0.41	21.84	9.56	4.76	0.98	0.69
	Image	MSE	PSNR	CII	MSSIM	CNR	WPSNR(DB)	NAE	NCC	FSIM
	lmg1	55.67	30.67	0.22	0.34	22.74	9.42	5.64	0.92	0.32
	Img2	61.90	30.21	0.18	0.31	25.18	9.53	6.09	0.96	0.75
	Img3	55.00	30.72	0.48	0.34	23.56	9.42	5.70	0.90	0.66
	Img4	55.36	30.69	0.57	0.43	28.94	9.51	5.72	0.98	0.67
	Img5	48.89	31.23	0.21	0.35	27.28	9.44	5.43	1.07	0.74
	Img6	56.67	30.60	0.69	0.34	24.29	9.53	5.72	1.08	0.76
	Img7	54.29	30.78	0.67	0.34	22.87	9.55	5.71	1.11	0.77
	Img8	65.07	29.99	0.70	0.33	29.03	9.62	6.03	0.88	0.67
	Img9	60.44	30.31	0.30	0.33	20.99	9.49	5.97	1.05	0.75
	Img10	55.00	30.72	0.63	0.33	28.17	9.43	5.73	1.09	0.66
3	Image	MSE	PSNR	CII	MSSIM	CNR	WPSNR(DB)	NAE	NCC	FSIM
	lmg1	49.45	24.04	0.79	0.14	33.41	9.49	12.24	1.44	0.45
	Img2	48.76	24.98	0.67	0.15	14.07	9.59	11.09	1.87	0.58
	Img3	47.45	24.71	0.64	0.14	21.84	9.51	11.40	1.81	0.50
	Img4	48.32	24.43	0.60	0.13	26.17	9.52	11.71	1.92	0.48
	Img5	43.34	24.49	0.31	0.23	17.48	9.44	11.67	1.72	0.54
Img6 Img7 Img8 Img9		45.34	24.03	0.85	0.13	25.73	9.62	12.25	1.78	0.53
		42.32	24.24	0.68	0.33	18.95	9.57	12.01	1.98	0.56
		43.39	24.12	0.76	0.15	30.17	9.58	12.22	1.47	0.55
		41.12	24.76	0.77	0.15	23.35	9.58	11.20	1.87	0.58
		42.58	24.69	0.79	0.15	29.03	9.68	11.38	1.99	0.50
4	Image	MSE	PSNR	CII	MSSIM	CNR	WPSNR(DB)	NAE	NCC	FSIM
	lmg1	5.30	40.89	0.54	0.12	146.52	6.45	0.92	1.70	0.59
	Img2	9.04	38.57	0.73	0.29	99.47	15.16	1.02	1.54	0.72
	Img3	18.78	35.39	0.61	0.27	166.10	9.09	0.84	1.43	0.69
	Img4	9.29	38.45	0.74	0.31	93.73	14.81	1.03	1.56	0.49
	Img5	5.52	40.71	0.76	0.38	65.55	15.10	0.99	1.66	0.61
	Img6	12.12	33.06	0.78	0.17	146.63	11.95	1.16	1.06	0.57
			35.57	0.82	0.39	97.72	13.08	0.94	1.32	0.58
	Img7	18.03								
						107.54	11.22	0.93	1.67	0.64
	Img7 Img8 Img9	5.39 15.23	40.81 36.30	0.66	0.32	107.54 129.05	11.22 13.15	0.93	1.67 1.44	0.64

5. CONCLUSION

Noise is inherent in CDNA Microarray images. The presence of noise will affect the subsequent stages of microarray image analysis. So, denoising is one of the important preprocessing steps in microarray analysis. In this paper, a new method for denoising of microarray images is presented. The main advantage of proposed algorithm is that it calculates adaptive min max threshold based on the image parameters which help to retain crucial information, while removing the noise presented in the image. From the results and analysis it is observed that the proposed method produces promising results on microarray images and hence can be efficiently used as pre-processing method in microarray image analysis for accurate profiling of gene expression.

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