DNA Microarray Image Analysis Using Active Contour Model

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1. Introduction

Major contributions of our approach include the followings: (1) We solve the problem of image rotation without manual adjustment. (2) The detection is robust with respect to irregular spot gaps. (3) Our approach is not affected by variations of color and size of spots. (4) Our approach performs well on different numbers of input channels. Besides, the proposed approach can not only handle multiple spots in microarray images, but also find more precise contours of spots. The approach is tested on microarray images obtained from the Stanford Microarray Database. Comprehensive experiments show highly encouraging results.

2. Proposed method

In our approach, a microarray image is first transformed into a gray-level one. Profile analysis is then performed for building orthogonal grid system of the image. Each spot is enclosed within a grid. The boundary of the grid is specified as initial contour of the spot. By shrinking the initial contour through energy conservation, more precise contour of the spot will be located.

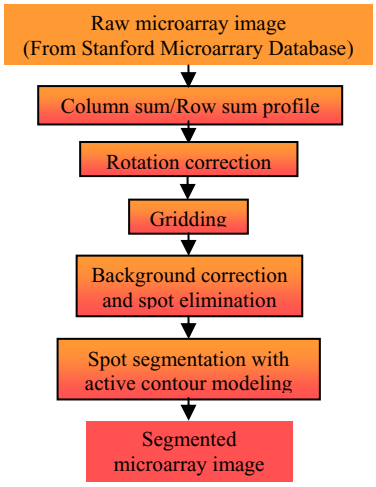

Figure 1. The framework of our approach.

3. Experimental results

A gridding method is proposed based on the valley effect in profiles. Wavelet-based profile analysis is performed for building orthogonal grid system of the image.

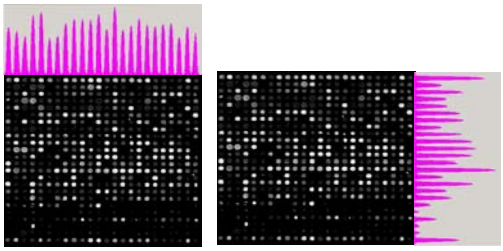

Figure 2. Profile analysis of a microarray image. (a) Vertical profile. (b) Horizontal profile.

Our approach searches for rotation angles that range from $-L^0$ to L^0 in order to rectify the rotated microarray image. The rotation angle can be found by searching for the maxima of the standard deviation of profiles.

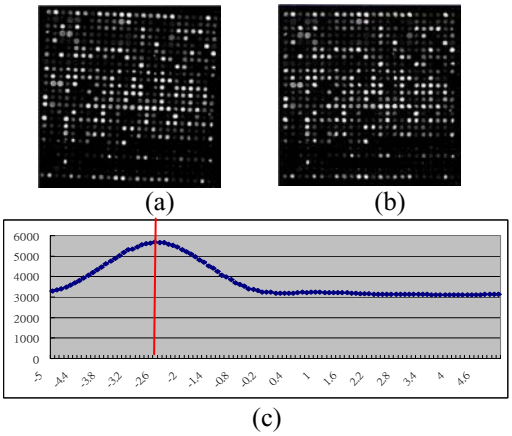

Figure 3. (a)Original image. (b)After correction of rotation. (c) Standard deviation of profiles of rotation degrees from -5^o to 5^o.

Wavelet transformation is performed on both vertical and horizontal profiles. The gridding system of a microarray image can be found by variance analysis of the wavelet coefficients.

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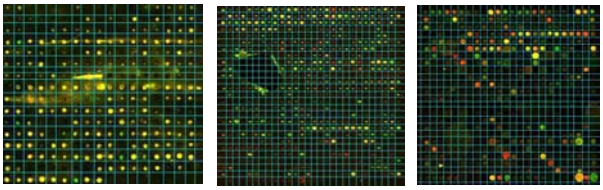

Figure 4. Experimental results of gridding with three kinds of conditions.

The energy function *E* in our active contour model is composed of the following three parts：one external energy and two internal energies. The reason why the energy is composed of different parts is that we use different energy functions to complement each other.

The total energy at a control point c_i is expressed as follows:

$$E(c_i) = \alpha E_{gradient}(c_i) + \beta E_{smooth}(c_i) + \gamma E_{distance}(c_i)$$

, where α, β, γ represent weighting parameters. We can modify the values of these parameters with respect to different conditions.

Although the intensity and size of spots vary greatly, our approach works well for all these spots.

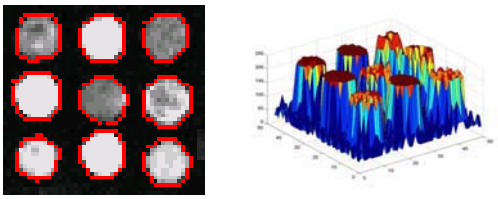

Figure 5. Some normal situations that the shape of spot is mostly regular and near to circle.

Some spots have low expression level because the probes are not hybridized. In spite of this, it will not influence our gridding very much. Thus, we could get better initial contours for the following active contour model.

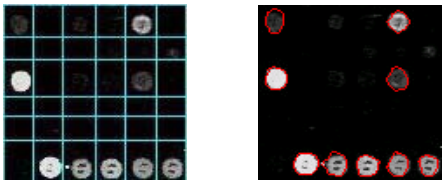

Figure 6. Spots with local low expression levels.

Irregular spots with different sizes and different shapes, such as sickle shape, oval or pear shape and interrupted shape, are shown in Figures 7 (a)-(d). These irregular shapes are usually caused by physical properties of different DNA solutions and the amount of solution captured by the print tip. The experimental results show the robustness of our approach. Figures 7 (e)-(h) show experimental results of the spots of Figures (a)-(d).

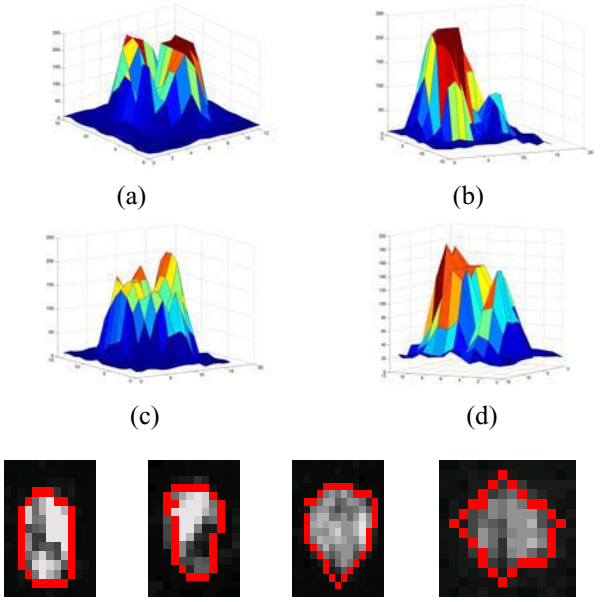

Figure 7. The shape and size of each spot varies greatly.

4. References

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