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IMPROVED WATERSHED ALGORITHM SPOT DETECTION ON PROTEIN 2D GEL ELECTROPHORESIS IMAGES

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ABSTRACT

Two-dimensional gel electrophoresis is one of the most important techniques in proteomics research for subsequent comparison and analysis. Spots identification is among the first things of analyzing Two-dimensional gel electrophoresis images. This paper provides an improved solution to the problem of protein spot detection by applying directed graph watershed transform algorithm. We have developed an adaptive mechanism to adjust the level of detail and determine the threshold value of watershed. The over-segmentation drawback is overcome by applying directed graph version of watershed transform algorithm and morphological opening operation. Labeling and region growing techniques are adopted to extracted individual spots features. The proposed spot detection process has been implemented and tested on 15 protein gel profiles (image size: 1498 x 1544) of porcine testis. The detection results are promising.

KEY WORDS

Improved watershed algorithm, Spots detection, Protein 2D gel images, Segmentation, Morphology operation, Region growing.

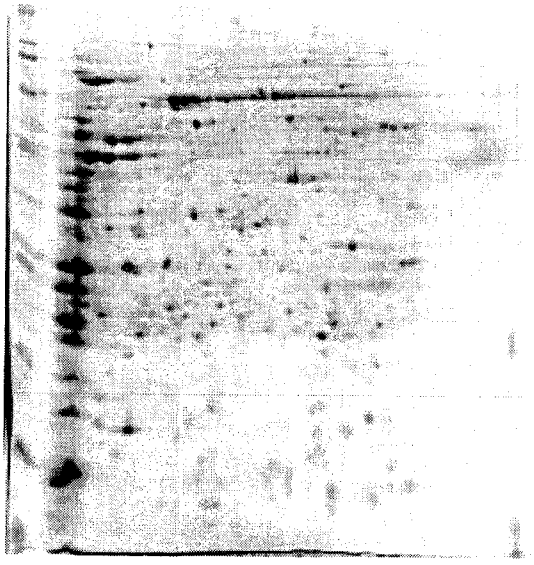

Figure 1. An example of 2DGE image (original size:1498x1544).

1 Introduction

The structure of cells of all living organisms is basically constructed by genetic information. The DNA is a media to carry that information and can be performed by expressing of proteins. In order to gain more information from biological experiments, we always need to obtain the protein in particle and analyze the function of protein. Protein function has been measured by many biologists by using different techniques in many studies [1]. Protein two-dimensional gel electrophoresis is a useful method for proteins quantifying, comparing and characterizing [2]. A strip of gel or a tube gel from isoelectric focusing (the first dimension) is fitted over an SDS-polyacrylamide gel electrophoresis, and the proteins are separated according to molecular weight by electrophoresis. Pre-equilibration of the isoelectric focusing gel in SDS is necessary prior to running the second dimension by isoelectric point (PI). Therefor, we can sort the method into two steps: Isoelectric focusing (IEF), and SDS-polyacrylamide gel electrophoresis (SDS-PAGE). In the first step, the proteins will focused base on their isoelectric point (IEF). After the status is stable, the second step is to separate proteins according to their molecular weights. Finally, different stain methods are applied to make different levels and different kinds of viewing, as shown in Fig. 1.

2DGE is an important tool for investigating different patterns of qualitative and quantitative protein expression. Researchers in the biological field have a need of the automatic data analysis technique of detecting and recognizing the differences simultaneously from thousands of 2DGE images. The key of the comparison of 2D protein profiles lies in the fulfill of a fast and robust protein spot detection, image registration, spot matching, and a database system. There are a few commercial or non-profit software packages have been developed for 2DGE image analysis. They offer various technologies and user interfaces for bi-

ologists. In gel comparison process, there are two different methods focus on image variable and spots distribution. The image registration, a novel technology which first applied in commercial software- Z3 [3], can restore the difference of gel images by using image correlation. Graph theory was also used to deal with the comparison of disordered protein spots, such as CAROL [4]. These two methods have their own advantages and disadvantages. By using the image registration method, we may find the difference between two gel images by overlapping them in two different colors, but we will blemish one. Alternatively, the non-registration method will overcome the drawback but may be failed when comparing non-structure protein spots. After the comparison step, database is a necessary tool to store gel information. Most software packages does not provide database system, like the ImageMaster 2D Elite [5]. In order to construct a powerful analysis system, the database is then builded, e.g. Melanie [6]. Although these packages have different applications, they all can deal with 2DGE images well from their standpoint. In the consideration of integrating these software packages attributes, we have developed a 2DGE images analysis system in a novel way. Issues of 2DGE images analysis have been discussed in many literatures [7, 8, 9, 10, 11]. The problems can be characterized as image registration, spot detection, spot matching, spot analysis, and database processing.

In this paper we provide an analytic framework to deal with one of the key component spots detection. Spot detection is a basic procedure for 2DGE images analysis concerning the identification of excess 3000 spots in a single image [11]. We must segment the possible regions containing spots in the gel image, locate the protein spots coordinates and then record or compare the individual attributes. Many approaches have been developed for detecting the protein spots including: Gaussian fitting [12], Laplacian fitting [3], Histogram [13] and Watershed Transformation [14, 15]. The common features of those algorithms are based on spatial domain processing [16]. The aim of the segmentation process is to define the location, true boundary and intensity for each spot.

We will focus on the spot detection issue in this paper and address the spot detection by using Watershed Transform (WST) Algorithm to segment the protein spots. The reason we use WST is for the sake of processing speed consideration. The segmentation procedure could be avoided for some areas with low intensity. It could also adapt to local area intensity. Other algorithms were not adequate to meet these requirements, e.g. Histogram Equalization [13] may have problem in segmenting protein spots in different intensity area. The over-segmentation drawback is overcome by applying directed graph version of watershed transform algorithm and morphological opening operation. Labelling and region growing techniques are adopted to extracted individual spots features. The proposed spot detection process has been implemented and tested on 15 protein gel profiles (image size: 1498 x 1544) of porcine testis. The detection results are promising.

2 Mathematical Morphology and Watershed Transformation

Mathematical morphology is a very useful technique for image segmentation. Considering the characteristics of gel images, watershed transformation algorithm which is a mathematical morphology methods [16] plays the major role in the proposed spot detection method. WST has been used widely in segmentation. For instance, in gray level images, one of the most important attributes is the morphological gradient of rugged topography. For an image f, the morphological gradient $g(f) = [(\frac{\partial f}{\partial x})^2 + (\frac{\partial f}{\partial y})^2]^{\frac{1}{2}}$ (first derivative) is equivalently defined as:

$$g(f) = (f \oplus B) - (f \ominus B), \tag{1}$$

where f denotes the image, B represents a structure element, and $\oplus$ and $\ominus$ stand for the elementary dilation and erosion operation, respectively [15].

The regions are localized by applying WST on the gradient of images in which the ridges watersheds define the optimal contours of objects. This topographic map contains a lot of contours and we can find the minimum and the maximum gray level pixels in the topography. In one contour cycle region C depicted on Fig 2, the geodesic distance $d(x, y)$ of two points x and y is computed as the length of the shortest path linking x and y inside C:

$$d(x, y) = \ell(C_{xy}), \tag{2}$$

where ℓ denotes shortest path length which is a finite distance. Otherwise, the distance is infinite ($d(x, z) = +\infty$) if points x and z do not reside in the sane region. Hence, the topographic map can be transformed as a hierarchical gray level image. For point sets in some contour cycle sets C shown in Fig. 2, they may be included in different cycles. It is necessary to determine whether these neighbor regions should be merged into one region or not. Let $R_C(Y_i)$ be a set of points whose geodesic distance is finite from any points in the marked set Y_i. $R_C(Y_i)$ can be further divided into subregions $Z_C(Y_i)$ according to the distance measure between desired marker set Y's. The area is computed as follows:

$$Z_C(Y_i) = \{x \in C : \ d_C(x, Y_i) \ is \ finite, \ and \ \forall j \neq i, \ d_C(x, Y_i) < d_C(x, Y_j)\} \tag{3}$$

After we define the areas in C, we can find lots of $Z_C(Y)$'s. Depending on the definition, we can find the

two parameters to adjust the spot detection result. It is worthwhile to develop an intelligent methodology to adapt parameters automatically. Finally, we will provide some image processing tools to handle image merging, spot volume statistics, etc.

5 Conclusion

Two-dimensional gel electrophoresis is one of the most widely used analytical methods to separate complex pictures for subsequent differential comparison and proteomics research [9]. This paper provides an improved solution to the problem of protein spot detection by applying directed graph watershed transform algorithm. We have developed an adaptive mechanism to adjust the level of detail and determine the threshold value of watershed. The over-segmentation drawback is overcome by applying directed graph version of watershed transform algorithm and morphological opening operation. Labelling and region growing techniques are adopted to extracted individual spots features. The proposed spot detection process has been implemented and tested on 15 protein gel profiles (image size: 1498 x 1544) of porcine testis. The detection results are promising. However, there still exist several processing bottlenecks such as rapid throughput in opening operation in order to remove noise or detect smaller size of protein spots. Developing techniques to predict how many protein spots contained in the same regions and conquer the overlapping problem is also fruitful. Meanwhile, it is also useful to constitute an intelligent and automatic analysis tools.

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References

[1] W. F. Patton. Billogist's perspective on analytical imaging systems as applied to protein gel electrophoresis. *Journal of Chromatography*, A, 698:55–87, 1995.

[2] D. M. Bollag, M. D. Rozycki, and S. J. Edelstein. *Protein Methods, Second Edition.* Wiley-Liss, 1994.

[3] Z3. *http://www.compugen.co.il.*

[4] Carol. *http://www.inf.fu-berlin.de.*

[5] ImageMaster 2D Elite Software. *http://www.imsupport.com.*

[6] Melanie. *http://www.genebio.com.*

[7] J. I. Garrels. The quest system for quantitative analysis of two-dimensional gels. *Biol Chem*, 264:5269–5282, 1981.

[8] K-P PleiBner, F. Hoffmann, C. Wenk, S. Wegner, A. Sahlstrom, H. Oswald, H. Alt, and E. Fleck. New algorithmic approach to protein spot detection and pattern matching in two-dimensional electrophoresis gel databases. *Electrophoresis*, 20:755V765, 1999.

[9] B. Raman, A. Cheung, and M. Marten. Quantitative comparison and evaluation of two commercially available, two-dimensional electrophoresis gel image analysis software packages, Z3 and Melanie. *Electrophoresis*, 23:2194V2202, 2002.

[10] A.W. Dowsey, M.J. Dunn, and G.Z. Yang. The role of bioinformatics in two-dimensional gel electrophoresis. *Proteomics.*, 3:1567–1596, 2003.

[11] M. Rogers, J. Graham, and R. Tonge. Statistical methods of shape for the analysis of protein spots in two-dimensional electrophoresis gel images. *Proteomics*, 3:887V896, 2003.

[12] Y. Watanabe K. Takahashi, M. Nakazawa and A. Konagaya. Fully-automated spot recognition and matching algorithms for 2-d gel electrophoretogram of genomic dna. In *Genome Informatics Workshop*, pages 161–172, 1998.

[13] I. R. White P. Culter, G. Heald and J. Ruan. A novel approach to spot detection for two-dimensional gel electrophoresis images using pixel value collection. *Proteomics*, 3:392–401, 2003.

[14] L. Vincent and P. Soille. Watersheds in digital spaces: An efficient algorithm based on immersion simulations. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 13(6):583–598, June 1991.

[15] S. Beucher. The watershed transformation applied to image segmentation. *Cambridge, UK, Scanning Microscopy International*, 6:299–314, 1992.

[16] R. C. Gonzalea and R. E. Woods. *Digital Image Processing.* Prentice Hall International Editions, 2002.

[17] H. J. Noordmans and A. W. M. Smeulders. Detection and characterization of isolated and overlapping spots. *Computer Vision and Image Understanding*, 70(1):23–35, 1998.