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# SEGMENTATION OF 2D-GEL ELECTROPHORESIS IMAGES

E. Kostopoulou, E. Zacharia, and D. Maroulis

Department of Informatics and Telecommunications, University of Athens, Athens, Greece
ikostop@di.uoa.gr, eezacharia@gmail.com, dmaroulis@di.uoa.gr

**Introduction**

Two-Dimensional Gel Electrophoresis technique is a convenient and well-established method to separate thousands of proteins on polyacrylamide gels, according to the differences in their net charge and their molecular mass [1]. Its digital output is an image which depicts proteins as bright or dark spots over a noisy and inhomogeneous background. Each protein is characterized by its vertical and horizontal position on the image, as well as its brightness, size and shape. The process of analyzing 2D-gel images includes the following three main stages [2]: spot detection, spot segmentation and spot quantification. The available software packages [2] for 2D-gel image analysis deal with the problem with a different degree of success and the best solution is far from being reach. In this paper, an original approach for the detection and segmentation of spots on 2D-gel images is presented.

**Method**

The proposed approach has the following four main stages: a) detection of a set $R=\{R_i, i=1,..,N\}$ of regions of 2D-gel image $I$ containing mostly spots (ROIs) based on the 2D histogram of $I$, b) roughly segmentation of each $R_i$ into sub-regions $R_{ij}$ based on groups of local intensity maxima, c) precise segmentation of each $R_{ij}$ based on morphological dilation and thresholding, and d) elimination of spurious spots based on statistical measures. Therefore, both the generation of accurate boundaries that include high and low intensity spot pixels and the elimination of spurious spots are accomplished.

**Results**

Several experiments utilizing both real as well as synthetic 2D-gel image datasets were conducted in order to evaluate the performance of the proposed approach and compare it with two software packages (Melanie 7 [2] and Delta2D [2]) and a recently published method (Scimo [3]). The detection results were statistically evaluated using the weighted harmonic mean of precision and sensitivity, namely *F-measure*. The segmentation results were evaluated using the normalized error measure $E$, as well as the Dice similarity coefficient measure $D$. The proposed approach outperforms the compared software packages and techniques in both spot detection and segmentation. More precisely, regarding spot detection, the proposed approach achieves a high value of *F-measure* (~93%), outperforming Melanie (~89%), Scimo (~83%) and Delta2D (~77%). Considering segmentation, the error value $E$ of the proposed approach is limited to 8.9% and the $D$ value is 93.2%. Melanie 7 (14.6%), Scimo (17.7%) and Delta2D (32.8%) have the second, third and fourth lowest $E$ values, respectively. Additionally, Melanie 7 (88.1%), Scimo (87.8%) and Delta2D (75.3%) have the second, third and fourth highest $D$ values, respectively. Figure 1 depicts the segmentation results of a synthetic 2D-gel sub-image. It can be observed that the proposed approach has segmented the protein spots more accurately in contrary to the other methods, which either exclude a part of the spot area or include background within the spot area.

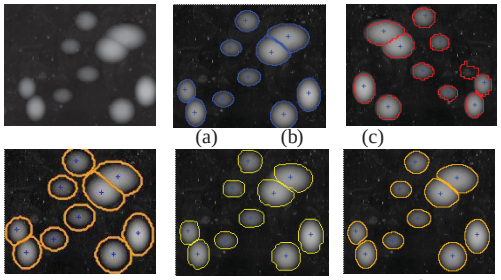


Figure 1: (a) Synthetic 2D-gel sub-image and (b) its ground truth. Segmentation results obtained by: (c) Melanie 7, (d) Delta2D, (e) Scimo, and (f) the proposed approach.

**Conclusions**

In this paper, an original approach for spot-detection and spot-segmentation of 2D-gel images is presented. The experimental results over real and synthetic 2D-gel images demonstrate that it is effective and it outperforms state-of-the-art software packages and techniques.

**References**

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