A SIMPLE METHOD FOR DETECTING PROTEIN SPOTS IN 2D-GE IMAGES USING IMAGE CONTRAST

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ABSTRACT. *The proteomics is a popular bioinformation research. In one specification state, one cell can be presented a kind of proteins, and we say that is a proteome. The proteome can be changed with different situations. In order to analyze the proteomics, the first step is that try to separate the proteins. The 2D-GE (Two-Dimensional Gel Electrophoresis) is an important and useful tool for research. Today, biologists have access to the many image databases that exist online. Biologists are keenly interested in the information that might be discerned from protein spots. Thus, quickly and efficiently finding such spots is an important job. In this paper, we attempt to find these spots based on 2D-GE images' features. We first use the image contrast to find the proteins' edges and then we detect the protein spots by the edges. Our experiments yield good results for detecting protein spots in 2D-GE images.*
Keywords: 2D-GE image, Two-dimensional gel electrophoresis, Protein spots.

1. **Introduction.** One popular technique utilized in biotechnology research is two-dimensional gel electrophoresis (2D-GE) [2, 4, 6, 7, 12, 15]. Researchers use 2D-GE to identify pathogenic proteins, as well as to aid in discovering cures for diseases caused by such proteins.

The 2D-GE utilizes the isoelectric point (PI) of iso-electric focusing (IEF) in the horizontal dimension and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) in the vertical dimension. Using a scanner to scan the 2D-GE, a 2D-GE image can be obtained. First we separate the proteins' sports from 2D-GE images by computer's computation. We can find the interesting spots by comparison gels. Then we obtain the protein information such as protein mass, peptide sequence tag, etc. [9, 17]. Finally, we search the database and know that what is the protein with this spot. For any one disease, we compare 'normal' images with those from patients suffering from a disease. Biologists attempt to find abnormal proteins on the patient's 2D-GE images and compare them to normal ones. Once divergences are identified, a cure can be attempted.

The most important information in a 2D-GE image are the protein spots. Finding these protein spots on a 2D-GE image is thus a critical issue. There are some methods for this job [3, 8, 11]. In Bettens et al.'s [3] method, they use the Watershed method to detect the protein spots in 2D-GE images. In Persson and Bigun's method [11], they use the symmetry features to detect the spots. They are only based on general image processing methods to detect protein spots. They did not use the 2D-GE's features to their scheme. In this paper, we consider the salient features of 2D-GE images and use these features to locate the protein spots. We use the contrast of the image to separate the protein spots and backgrounds. Then we detect and elucidate the spots.