

2D–PAGE Analysis Using Evolutionary Computation

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INTRODUCTION

This paper presents the preliminary studies for the creation of a new tool to assist in medical diagnostic. The tool will help in the analysis of 2D-PAGE images. In order to create a 2D-PAGE image of an ideal patient—the patient could be healthy or ill—the tool will help us in the creation of an image that facilitates and speeds up future diagnostics. The creation of a master image has motivated the development of a tool to alignment gel images. The tool will make easier the correspondence among the proteins into the ideal image and the ones of a new image. Due to the fact that image registering process is quite complex, we use the Intel's library OpenCV which provides functions to calculate optical flow and translation vectors.

This library introduces into the project a set of variables unknown by the facultative. To solve this, an automatic selection of values for this set of variables is necessary. This last task is made with the Evolutionary Computation technique called Particle Swarm Optimization (Kennedy, R. & Eberhart, J. 1995)

BACKGROUND

In the 20th century medicine, the number of medical images has been growing. X-ray photographs, magnetic resonances, 2D gels images, angiographies can be taken as examples. The major difficulty for the physician is to integrate all this information in order to offer a diagnosis.

This way, since computers started being used for analyzing and treating images at the end of the 20th century, one of the most important fields inside the application of computers to image processing has been the treatment of all medical existing images. It is here where technologies of Evolutionary Computation and Neural Networks are necessary, because they facilitate certain processes of adjustment that, in another way, would be extraordinarily complex or laborious. Among the most usual technologies used for the processing of biomedical images there can be pointed out Artificial Neural Networks, Genetic Algorithms, Particle Swarm Optimization, Splines or Growth of Regions.

Amongst some examples, we can emphasize the use of Artificial Neural Networks for the analysis of radiological images, Genetic Algorithms (Holland, J.H., 1975) in the 3D reconstruction of anthropologic models (Santamaría, J., Cordon, O., Damas, S., Alemán, I., Botella, M., 2006) and in the integration of the information obtained by means of different methods—Computed Tomography (CT), Magnetic Resonance Imaging (MRI),...—(Rouet, J. M., Jacq. J. J., Roux, C., 2000), Particle Swarm Optimization for alignment of 2D and 3D biomedical images (Wachowiak, M. P., Smolikova, R., Zheng, Y., Zurada, J. M., Elmaghraby, A. S., 2004) or the use of Splines to 2D-PAGE registering (Seow, N., Sowmya, A., Sun, C., 2005).

In our case, the technology to use will be the Particle Swarm Optimization dedicated to improve the analysis of 2D-PAGE (Seoane, J. A., Mesejo, P., Ruiz-Romero, C., Dorado, J., Pazos, A., Blanco, F. J., 2007).

PSO APPLIED TO THE OPTIMIZATION OF OPENCV PARAMETERS FOR 2D-PAGE ANALYSIS

The aim of this investigation is to help the doctors in process of identification of certain characteristics in the 2D-PAGE images (Ruiz-Romero, C., López-Armada, M. J., Blanco, F. J., 2005). In order to do that the registry image process will consist on the alignment between the master image, which has been labelled for every protein, and an image whose interesting points have been identified by the facultative to study. This registry process will make easier to the medical the study of the presence or absence of a certain kind of protein and its concentration.

2D-PAGE

This work uses the images called 2D-PAGE—*polyacrylamide gel electrophoresis*. The process to obtain these images uses the electrophoresis, which is a well known analytic technique for macromolecules—DNA or Protein—separation. The responsible of this separation is the mobility presented by the electrically charged macromolecules when a differential voltage is applied. The method tries to immobilize the studying molecules into a gelatinous material; in this case the material will be polyacrylamide. This process was well described by (Bueno García, G. 2005) as “A differential voltage is applied to the gel with the biological samples inside during a concrete period of time. Each molecule will migrate through the gel pores with a different speed, which is dependent of the electrical charge and the mass of each molecule.”

On one hand, the resultant gels are classified on X-axis on respect the isoelectric point—PH to which an amphoteric substance has no voltage. On the other hand, on Y-axis gels are sorted by their molecular mass.

The resultant image will help us to detect the presence or absence of a certain protein, or even the more or less protein concentration. This information will assist us to know the existence or inexistence of some illness or characteristic.

OpenCV

OpenCV is an open source library which has been developed in C++ for Computer Vision. This library is optimized to be applied in real time problems inde-

pendently of the platform. It is especially oriented to images manipulation and processing and also to the movement analysis into the image. Some interesting information about this library could be found at (Agam, G., 2006).

To solve the problem, one of the Optical Flow functions, which can be found in the OpenCV library, was used. Specifically we use the function known as *CalcOpticalFlowBM*. This function divides two images into blocks, in order to find the same block of the first one in the second image. After this search process, the function establishes a set of movement vectors which corresponds to the movements of the blocks of the image. For more information about this topic visit (Department of Electrical Engineering, Nara National College of Technology’s Web Page, 2006) and (Intel’s Web Page).

This function is very useful in our problem because we need an alignment image tool for the creation of the proteomic diagnostic image. When we try to align two images, a function that compares these two images and tells us the movement among them will be useful. This function searches the similarities using the statistical correlation among sets of pixels of the two images. The new protein location process will only need the movement vector and the block of that spot.

The function *CalcOpticalFlowBM* has a set of parameters, the ones to be optimized are:

- **blockSize:** the size of comparable blocks in which the image is divided.
- **maxRange:** neighborhood maximum size around a block that would be explore to find the block in the second image.

These parameters will be optimized with an artificial intelligence technique, because, in other case, this process will be done manually by the user.

Particle Swarm Optimization

The Evolutionary Computation technique that has been used in this work is the Particle Swarm Optimization (PSO). Inspired on the social swarm from nature, was developed by Kennedy and Eberhart (Kennedy, J. & Eberhart, R., 1995). In a PSO algorithm a particle swarm explores the search space. Each particle represents a possible solution to the optimization problem. The position of each particle is the result of the best position

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