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Employing Image Processing Techniques for Cancer Detection Using Microarray Images

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Abstract

Microarray technology is a powerful genomic tool for simultaneously studying and analyzing the behavior of thousands of genes. The analysis of images obtained from this technology plays a critical role in the detection and treatment of diseases. The aim of the current study is to develop an automated system for analyzing data from microarray images in order to detect cancerous cases. The proposed system consists of three main phases, namely image processing, data mining, and the detection of the disease. The image processing phase performs operations such as refining image rotation, gridding (locating genes) and extracting raw data from images the data mining includes normalizing the extracted data and selecting the more effective genes. Finally, via the extracted data, cancerous cell is recognized. To evaluate the performance of the proposed system, microarray database is employed which includes Breast cancer, Myeloid Leukemia and Lymphomas from the Stanford Microarray Database. The results indicate that the proposed system is able to identify the type of cancer from the data set with an accuracy of 95.45%, 94.11%, and 100%, respectively.

Keywords: Microarray; Image processing; Data mining; detection of disease.

1. Introduction

In recent years, the use of microarray technology in the form of a small chip has provided to study thousands of genes simultaneously. Microarray technology involves the gene chip, collections of gene sequences in known locations on a solid surface. Each gene on the microarray chip is called a spot. Images obtained from this chip consist of a matrix with several blocks and each block contains a number of rows and columns of spots [1].

Every year, tens of thousands of microarray images of different sizes are produced in biology labs. Thus, the automatic and fast processing of these images and analysis of microarray data are of paramount importance. One of the challenges facing this technology is the mass of data, which calls for the use of statistical techniques, information technology and machine learning approaches. In general, microarray technology consist of two main stages: the operation of clinical trials to produce the microarray images and the analysis of the images [2].

The key phases in microarray analysis include: image processing, data mining and disease identification. The aim of image processing is to quantify microarray images. The quantification of microarray images is usually performed in three steps, namely the gridding, segmentation and calculation of the gene expression. Currently, softwares such as GenePix, ScanAlyze and ImaGene, are available in market to perform microarray analysis. These softwares quantify

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