

Image processing of DNA slide images for disease diagnosis

R.R. SHELKE^{1*} and B.M SHELKE (TATTE)²

¹Department of Information Technology, H.V.P.M's College of Engineering Amravati - 444 605 (India).

²HariOm Colony Kathora Road V.M.V. , Amravati - 444 604 (India).

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ABSTRACT

A DNA microarray also commonly known as gene or genome chip, DNA chip, or gene array is a collection of microscopic DNA spots attached to a solid surface, such as glass, plastic or silicon chip forming an array for the purpose of expression profiling, monitoring expression levels for thousands of genes simultaneously. The affixed DNA segments are known as probes, thousands of which can be placed in known locations on a single DNA microarray.

Measuring gene expression using microarrays is relevant to many areas of biology and medicine, such as studying treatments, disease, and developmental stages. For example, microarrays can be used to identify disease genes by comparing gene expression in diseased and normal cells. In the present work, the 'cell slide images' have been processed to calculate different gene values in the particular slide which in turn maintain the database for cluster analysis and visualization for disease diagnosis .

Key words: Image processing, DNA, Disease diagnosis.

In recent years there has been an explosion in the rate of acquisition of biomedical data. Advances in molecular genetics technologies, such as DNA microarrays¹⁻⁷ allow us for the first time to obtain a "global" view of the cell. For example, one can now routinely investigate the biological molecular state of a cell measuring the simultaneous expression of tens of thousands of genes using DNA microarrays. DNA microarray experiments generate a substantial amount of information about global gene expression. Gene expression profiles can be represented as points in multi-dimensional space. It is essential to identify relevant groups of genes in biomedical research. Clustering is helpful in pattern recognition in gene expression profiles. Some clustering techniques have been introduced. A critical aspect in the analysis of gene expression data is identification of clusters of genes that have similar expression patterns. Clustering techniques transform a large matrix of expression levels for different genes in different conditions into a more organized and informative collection gene sets, which are expected to share similar biological properties. Microarrays are a revolutionary new technology with great potential to provide accurate medical diagnosis which helps to find the right treatment and cure for many diseases and provide a detailed genome-wide molecular portrait of cellular states. The work included in this issue is a good

sample of second generation methodologies and techniques that is being used under development today. As it can be seen from the results , they are very promising and extend the possibilities of applying computational analysis and datamining to aid research in biology and medicine. The present work not only would like to close this introduction with a brief discussion to emphasize the large potential payoff of these analytical efforts but also pointing out the huge challenges ahead.

Now a days ,different diseases are arising which in turn causes an increment in death rate. Different blood testing are available for diagnosis. Though various blood testings or any other testings are available, diagnosis of some diseases is very difficult. Therefore, only blood testing or any other testing (eg. spinal cord fluid testing) is not sufficient. The DNA testing is one of the advanced technique in which affected DNA & normal DNA slides are compared for disease diagnosis. With the software development, it became a very easy and beneficial task. In software development, slide images of patient's DNA and disease affected DNA can be processed and compared. Pixel values of these images stored in the database can be also compared for ultimate result . In the present work, image processing of DNA images is performed in which, slide images of

patient's DNA sample and disease affected DNA sample are processed and compared. The result shows whether the patient is suffering from particular disease or not. In this work, slide images of three diseases viz. cancer, hepatitis, diabetic are considered.

RESULTS AND DISCUSSION

There are several steps in the design & analysis of DNA microarray experiment. Those are 1. DNA type 2. Chip fabrication 3. sample preparation 4. readout 5. software.

The advanced technique (Software) which give the exact result has been used. Once the software is developed, it can be used for different types of DNA. The patient's name whose DNA is to be tested is entered and the record is added and updated for next step. The microdata so added & recorded in the previous case has been viewed in further form along with visualization of the disease affected sample.

The main output form in the present work is as shown in the Fig. 1. In this step, the gray scaling, edge detection, processing, matching has been done. First, the DNA sample image of patient has been selected. The image so selected is gray scaled and edge detections has been done. After that the disease affected sample image is selected (cancer, diabetic or hepatitis). This image is then processed. In processing, gray scaling and edge detection has been done. The processed pattern is then compared with patients image pattern. In comparison, percentage of matching is given which finally gives the result whether the patient is suffering by

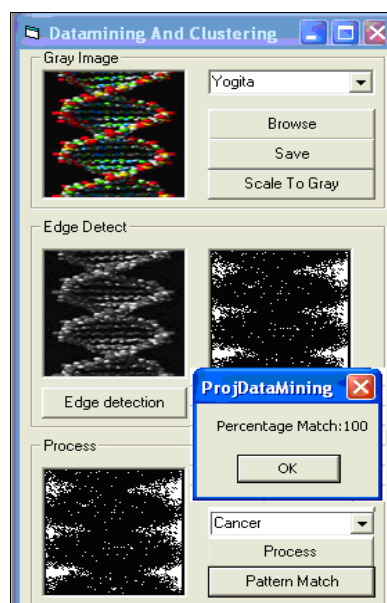


Fig. 1: Comparison of DNA samples and databases

particular disease or not. This is the ultimate result of the present work.

Conclusion

Microarrays are a revolutionary new technology with great potential to provide accurate medical diagnostics. The slide images of patient DNA sample and disease DNA sample has been compared for disease diagnosis which helps to find proper treatment to the patient. There are various possible applications like gene discovery, disease diagnosis, drug discovery, toxicological research etc. These applications can be benefited to the nation as well as society.

REFERENCES

1. Chipping Forecast, The Chipping Forecast. *Sp. Supplement. Nature Genet.* 21, (1999).
2. The Chipping Forecast II. Special Supplement. *Nature Genet.* 32: (2002).
3. Schena, M. et al, Quantitative monitoring of gene expression patterns with a cDNA microarray. *Science* 270: 467-470 (1995).
4. DeRisi, J.L. et al., Exploring the metabolic and genetic control of gene expression on a genomic scale. *Science.*, 278: 680-686 (1997).
5. Chu, S. et al., The transcriptional program of germ cell development in budding yeast. *Science* 282: 699-705 (1998).
6. Iyer, V.R. et al., The transcriptional program in the response of human fibroblasts to serum. *Science* 283: 83-87, (1999).
7. DeRisi J, et al., Use of a cDNA microarray to analyse gene expression patterns in human cancer. *Nat Genet.*, 14(4): 457-60 (1996).
8. J. Quackenbush, Computational analysis of microarray data, *Nature Review Genetics*, 2: 418-427 (2001).
9. D. Dembele, Kastner, P., Fuzzy C-means method for clustering microarray data, *Bioinformatics*, 19: 973-980 (2003).
10. R. Sharan, Maron-Katz, A., and Shamir, R., Click and expander: a system for clustering and visualizing gene expression data, *Bioinformatics*, 19: 1787-1799 (2003).