

Image Processing For Biomedical Application

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Abstract— Karyotyping, a standard method for presenting pictures of the human chromosomes for diagnostic purposes, is a long standing, yet common technique in cytogenetics. Automating the chromosome classification process is the first step in designing an automatic karyotyping system. However, even today, karyotyping is manually performed. Here we intend to automate Karyotyping completely. Karyotyping is a common technique in cytogenetics, to classify human chromosomes into 24 classes. Karyotyping can be used to predict genetic disorders or abnormalities in pre-natal stage which may happen to occur in future generation.

Index Terms— Classification, Feature extraction, Karyotyping, Segmentation, Straightening Algorithm.

1 INTRODUCTION

Chromosomes analysis is an essential procedure for detecting genetic abnormalities in cells. Traditionally, cells are classified according to their karyotype, which is a tabular array where the chromosomes are aligned in pairs. Karyotyping is a useful tool to detect deviations from normal cell structure since abnormal cells may have an excess or a deficit of chromosomes. Normal cells contain 46 chromosomes which consist of 22 pairs of similar, homologous chromosomes and two sex-determinative chromosomes (XY: male and XX: female). Normally, the procedure of assigning each chromosome to a class (karyotyping) is based on the visual scanning of chromosome images by experts (biologists, cytogeneticists). This visual inspection is a time consuming process and expensive. Hence, many attempts have been made to improve visual analysis of chromosomes.

2. THE OBJECTIVES OF THE PROPOSED WORK ARE AS FOLLOWS:

- 2 Perform segmentation of the metaphase image to separate out each chromosome
- 3 Application of the straightening algorithm to each separated chromosomes.. F
- 4 Extract features from each chromosome.
- 5 Classification of chromosomes based on the feature extracted

2.1 Segmentation (Watershed Transform)

The goal of this stage is to create a mask of pixels to be classified. First the image gradient magnitude of the initial image is computed. In order to reduce the number of minima of the gradient magnitude we apply the grayscale transform. The watershed transform is a popular segmentation method originated in the field of mathematical morphology. The image is considered as a topographical relief, where the height of each point is related to its grey level. Imaginary rain falls on the terrain. The watersheds are the lines separating the catchment basins.

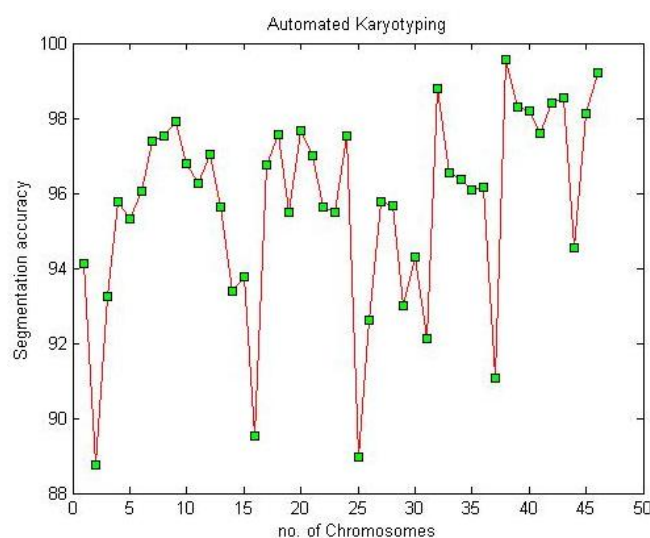


Fig. 1 Shows as the number of chromosomes increases the segmentation accuracy also increases.

2.2 Straighten curved chromosomes

From the segmented image obtained in above step a chromosome is taken at a time. Grayscale chromosome image is one in which an object (chromosome) is lying on a uni-color background with a different gray scale value.. An effective threshold value to separate the object from the background can be determined by locating the global minimum of the histogram Using this threshold all those pixels with a gray value smaller than the threshold are set to 1 (white) and the remaining pixels are set to 0 (black) producing the binary format of the input image. For horizontal projection vector, the pixel values of each row are summed up in the binary image. Considering that the binary image includes only 1s (white pixels) and 0s (dark pixels). The location of the extracted global minimum in the horizontal projection vector of the target image corre-

sponds to the bending centre. The horizontal line passing through the point on the chromosome image represents the bending axis of the chromosome. The most outward intersecting point between the bending axis and the chromosome body is the so called bending centre of the curved chromosome.

The binary image is first separated into two sub-images along the bending axis. The two sub-images must now be rotated so that the two arms to be vertical. Now we apply the same procedure to the real gray scale image rather than its binary version. Next, the two aligned gray scale images of the chromosome arms must be connected to produce the final straightened chromosome picture

2.3 Feature extraction

1. Length
The total length of the chromosome is obtained.
2. Centromeric index:
The centromeric index (C.I.) is the ratio of the length of the short arm to the whole length of a chromosome.
3. Normalized density profile:
Density profile is a one-dimensional graph of the banding pattern property of the chromosome computed at a sequence of points along the possibly curved chromosome medial axis. The density profile for a chromosome is obtained from measurements made along a transverse line, perpendicular to the tangent of the medial axis. It is another significant morphological feature used to identify the chromosome.

2.4 Neural Networks Classification.

Neural Network; it is the second stage of initiation of the Multi-Layer Neural Network with Back-Propagation algorithm and the suitable architecture form, train and transfer functions.

After creating the Neural Network, the typical chromosomes have been inserted in it to be the target in the training process. The output of the segmentation algorithm, which will be an array of objects, will be converted from matrix form into vector form. This vector represents the new input to the Neural Network. This Neural Network uses Back-Propagation algorithm.

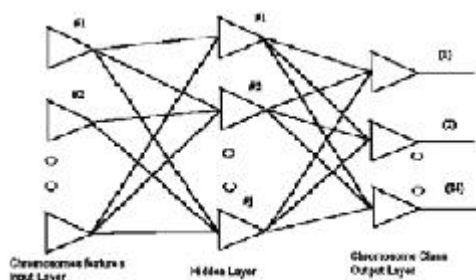


Fig.1 Neural network architecture for multilayer network.

3. RESULTS



Fig.2 Metaphase stage of human chromosomes



Fig.3 Karyotyped image of human chromosome.

4. CONCLUSIONS

By using the following method we found that is an efficient way of classifying the chromosomes. It introduces chromosome imaging and the concept of karyotyping. We studied various characteristics of chromosome images and features of chromosomes that are used for karyotyping and classification

5. ACKNOWLEDGMENT

This work was supported by Birth Right Genetic Clinic, Pune and Denanath Mangeshkar Genetic Lab, Pune

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