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CHROMOSOME IDENTIFICAION USING ARTIFICIAL NEURAL NETWORK

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ABSTRACT: *Cytogenetics plays a central role in the detection of chromosomal abnormalities and in the diagnosis of genetic diseases. The study of human metaphase chromosomes is an important aspect in clinical diagnosis of genetic disorders. A karyogram is representation of human chromosomes where they are arranged in decreasing order of size and Karyotyping is a set of procedures that produces a karyogram during the metaphase step of the cellular division, called mitosis Many image processing techniques have been developed for chromosomal karyotyping to assist in laboratory diagnosis, they fail to provide reliable results in segmenting and extracting the centerline of chromosomes due to their shape variability when placed on microscope slides. Effective identification of the chromosome outline with its center line provides a basis for further operations such as automated chromosome classification and centromere identification. Karyotyping and chromosome analysis are very useful in biological applications, e.g. disease identification. The very first step of karyotyping is the identification of chromosome.Manual karyotyping is tedious, complex and time consuming, as it requires meticulous attention to details and well trained personnel. Automated system gives countless advantages like speed, simplicity and storage.This method is considered simple and, yet, robust for this purpose. In this project, we aim to build an automated karyotyping system for chromosome analysis.*

In this paper we have discusssed the fundamental problems of classification of human chromosomes and have explained the solution to the problem.We have given the introduction about the human chromosomes and the basic theory of the algorithm used.AAN has been implemented to classify the chromosomes.

I. INTRODUCTION

A fundamental problem in computational biology is the classification of proteins into different classes based on evolutionary similarity of protein sequences. Human chromosomes have essential genomic information and chromosome damage causes most abnormalities. Therefore karyotyping, manual chromosome analysis and classification, plays an important role in cancer and genetic syndrome diagnosis, but karyotyping requires a professional geneticist and is expensive. Hence automated *classification has great attraction in this field. Chromosomes exist in cells which contain the genetic information of the human that are* passed on from one generation to the next. Each human cell contains 46 chromosomes: 22 pairs of autosome chromosomes and a pair of sex chromosomes. Chromosome abnormalities are responsible for fetal death, stillbirths and birth imperfections. Chromosome analysis is assigning each chromosome to one of the 24 human chromosome classes. After analysis under the microscope by a trained expert, a picture of the chromosomes is formed according to their sizes and lengths. But this analysis is laborious and time consuming and *also* requires a skilled expert and consequently is expensive. The chromosomes hold the genetic information of all living organisms. In chromosome analysis of different creatures and populations, number, size and shape is of importance. Thus, such evaluations are carried out on microscopic images of a cell's chromosomes. The first step in chromosomes analysis is karyotyping. In this procedure, a microscopic image of the chromosomes contained in a single cell is obtained. Subsequently, each chromosome is classified in one of the 7 known classes called as Denvar classes.[http://astudyinmedicine.blogspot.in/2012/08/denversystem.html]

Chromosome group	A	B	C	D	E	F	G
Chromosome	1,2,3	4,5	6,7,8,9,10, 11,12,X	13,14,15	16,17,18	19,20	21,22,Y

Table.1 Denvar classes of chromosomes

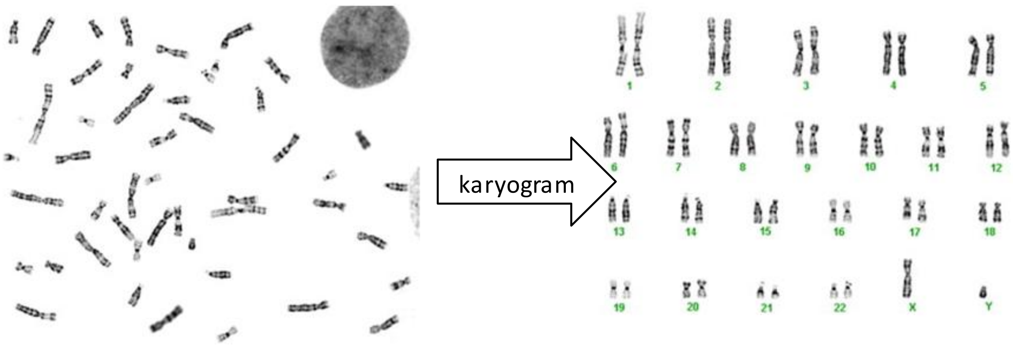

Fig.1 Original Metaphase Image and its Karyotype Image

II. BASIC THEORY

Artificial neural networks (ANN) have been developed as generalizations of mathematical models of biological nervous systems. The basic processing elements of neural networks are called artificial neurons, or simply neurons or nodes. In a simplified mathematical model of the neuron, the effects of the synapses are represented by connection weights that modulate the effect of the associated input signals, and the nonlinear characteristic exhibited by neurons is represented by a transfer function. The neuron impulse is then computed as the weighted sum of the input signals, transformed by the transfer function. The learning capability of an artificial neuron is achieved by adjusting the weights in accordance to the chosen learning algorithm. Artificial Neural Networks (ANN) is the most popular tool owing to its capability of modeling the human brain decision making process to recognize objects based on incomplete or partial information, as well as its simple topographic structure and easier training process[5] . A typical artificial neuron and the modeling of a multilayered neural network are illustrated in Fig.2

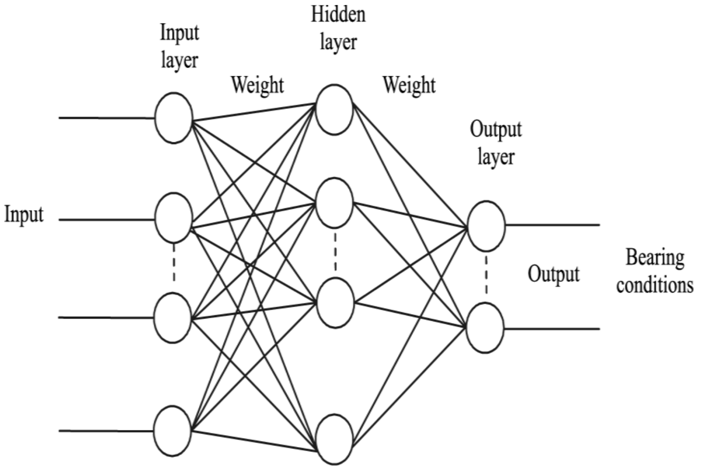

Fig.2[5]

III. PROPOSED METHOD

1.Preprocessing-The chromosomal images were first normalized and then subjected to a global thresholding process Since we are looking for morphological features of a chromosome, the grayscale image contains additional information that is not needed at this stage. Therefore, producing a binary image will make the rest of the process easier.The chromosome images are bimodal images.It means that this images even include the background colour.And the histogram of these images show two peaks consisting one of the background and other of the chromosome image. The preferred threshold value between the background and the object is used. Using this value as a threshold, all the pixels with a gray level below this threshold are set to 1 (white) and the remaining pixels are set to 0 (black) producing the binary format of theinput image.[6,7,8]

2.Feature extraction

A chromosome is described by its length and area of it. Its centromeric index which is the ratio of the short arm of the chromosome to its long arm where they are separated by the centromere that is narrowest part of chromosome.another feature of chromosome is axis which separate pair of long and shortarm from another pair of it.The axis of chromosome is obtained by reducing boundary of chromosome i.e by thinning the image.It will extract the central curve of the chromosomes. The centromere, narrowest part of chromosome is extracted by actually measuring width of chromosome

3.Recognition using classifier

A classifier of type Artificial Neural Network is developed to get the desired output for the given input images of chromosomes.The Neural Network is trained by using set of chromosome images,where for training output and input both are given to adjust weights.Aftertraining,using these weights classifier gives the output for the given input image of chromosome.[8,9]

IV Results and Discussion

In this paper we presented work on the classification of chromosomes based on the algorithm of Artificial Neural Network. Chromosome images were given for training the ANN classifier and based on this trained neural network class of chromosome was achieved.

Length 46
Perimeter 115
Ratio 1
Area 576
CI 0.5
class Class A

Fig.3 Final output obtained on Matlab

IV. CONCLUSION

We have successfully extracted features namely Centromere position, Length of chromosome, Area, Perimeter and Ratio. The results obtained of elongated and curved chromosomes are highly satisfactory and accurate. Satisfactory classification accuracy of individual chromosomes into Denver Class and further classification is achieved.In Neural Network, change in neurons while building network leads to change in accuracy. The implemented MATLAB based tool can be used in hospitals as an preliminary stage for any genetic disorder analysis. The tedious manual and expensive karyotyping procedure is automated by using this tool.

V. FUTURE SCOPE

In this project a method is proposed which can be used to calculate various features of chromosome like centromere, centromeric index, area and perimeter. On this basis chromosomes can be divided into seven major classes. Nowadays too in various hospitals manual karyotyping is done.considering current system this project can give lots of benefits by overcoming various drawbacks.The disentangling of overlapping chromosomes was out of scope for this project. By using segmentation approaches for disentangling of touching and overlapping chromosomes, a complete automated karyotyping system can be developed.

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