SEGMENTATION OF CHROMOSOME IMAGES USING AN ADAPTIVE THRESHOLDING TECHNIQUE AND A WATERSHED ALGORITHM

KANNIKAR KAMOLRAT

With compliments of

A THESIS SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (COMPUTER SCIENCE) FACULTY OF GRADUATE STUDIES MAHIDOL UNIVERSITY 2002

ISBN 974-04-1478-8

COPYRIGHT OF MAHIDOL UNIVERSITY
This research proposes an approach of segmenting chromosome images using an adaptive thresholding technique and a watershed algorithm, focussing on an automatic separation of touching chromosomes from one another. It is well realized that an analysis of laboratory animals' chromosomes is of great significance for genetic toxicology to analyze chromosomes’ abnormality. An essential preliminary process in this regard is karyotyping. Manual karyotyping can be done by segmenting metaphase chromosomes one by one from a chromosome image and then making a pairing of these chromosomes based on their sizes, ranging from large to small, while a centromere position of chromosomes is also taken into account. Afterwards, a pairing of these chromosomes is made again on a standard-form paper. A problem found in manual karyotyping is that it takes a long time since in an analysis of chromosomes, a large number of cells (between 50 and 100) are studied. Furthermore, a chromosome analysis depends on an analyst’s experience and skill, including his or her temper at the time. A lack of experience and skill in an analyst generally results in an erroneous or ineffective analysis.

Based on previous researches and studies, a system of a computerized chromosome analysis encounters a problem of a touching chromosome separation. If this problem arises, it still needs a human being to solve the problem. A current chromosome analytical system is, therefore, not completely automatic. With the above-mentioned problems, this research proposes an approach of segmenting a chromosome image using an adaptive thresholding technique so as to segment chromosomes from the background. This is carried out with a consideration of values of 2 thresholds: global and local. Nevertheless, segmented chromosomes may have some clusters consisting of touching chromosomes. So, there have to be steps to check which cluster consists of such chromosomes. In this research, checking is done with a principle of a multilayer perceptron (MLP) neural network. After checking of touching chromosomes, they are separated from each other with an iterative watershed algorithm.

The experiments in this research utilize 34 image samples of hamsters’ chromosomes. The images are scanned and stored in a bitmap (.bmp) file. There were 3 experiments conducted in this research. The first one was chromosome segmentation using an adaptive thresholding technique. The result was a correct segmentation of 1,336 chromosomes, which is 89.3% of the total number, apart from an emergence of 8 broken and 69 touching chromosomes, which are 0.6% and 10.1% of the total number, respectively. The second experiment was a touching chromosome detection using a neural network. It was found that out of 1,016 samples of single and touching chromosomes, 741 samples were correctly detected, which is 72.43% of the total number, while 275 samples were erroneously detected, which is 27.07% of the total number. Finally, the third experiment was a touching chromosome separation using a watershed algorithm. The outcome was an accurate separation of 63 touching chromosomes out of the total 69 touching ones, which is 91.3% of the total number. There was also an erroneous separation of 6 touching chromosomes done in a wrong position, which was 8.7% of the total number.
In this work, a novel semi-supervised segmentation technique is proposed for chromosome images of hybrid rice using adaptive thresholding and watershed algorithm. This technique improves the accuracy and efficiency of chromosome segmentation compared to existing methods. The proposed method was validated using a dataset of high-quality chromosome images from hybrid rice plants. The results showed a significant improvement in the segmentation accuracy and reliability.