Indian Journal of Science and Technology, *Vol 11(18), DOI: 10.17485/ijst/2018/v11i18/123037,* May *2018*
ISSN (Print) : 0974-6846
ISSN (Online) : 0974-5645

Segmentation and Extraction of Chromosomes from G-Band Metaphase Images

Tha. Sugapriyaa*, P. Kaviyapriya and P. Gomathi

Department of Electronics and Communication Engineering, M. Kumarasamy College of Engineering, Karur, Thalavapalayam – 639113, Tamil Nadu, India; sugapriyaatha.ece@mkce.ac.in, kaviyapriyap.ece@mkce.ac.in, gomathipr.ece@mkce.ac.in

Abstract

Objectives: Genetic problems can be identified by a test called Karyotyping. Karyotyping is used to find the abnormalities and genetic disorders or defects. The automated segmentation and disentangling of chromosomes are the challenging issues. **Methods/Statistical Analysis:** In current systems the separation between touching and overlapping chromosomes need human intervention. Different procedures are proposed to obtain the chromosome from its background. In this paper, an attempt is made to separate the chromosomes for Karyotyping in G-Band metaphase images. As a first step segmentation of chromosomes is done. **Findings:** Thesis carried out by means of local thresholding, region growing and edge detection methods. Then, the chromosome and its clusters are extracted by labelling the connected components. This process successfully separates individual chromosomes. **Application:** Medical image Processing.

Keywords: Chromosome Analysis, Edge Detection, Image Segmentation, Karyotyping, Region Growing

1. Introduction

Chromosomes are located inside the nuclei of eukaryote cells and comprise the DNA double helices. They convey the genetic commands for making living organisms. Genetic defects that affect the chromosome structures are numerous, including chromosome rearrangements, duplications and deletions. Identification of such chromosome aberrations has enormous impact on clinical diagnosis, medicine development and basic research. Nowadays, human chromosome investigation is especially used to distinguish hereditary disarranges in prebirth screening and in disease pathology looks into. The two chromosomes in each pair are called homologous chromosomes: one comes from the egg of the mother (maternal homolog) and the other from the sperm of the father (paternal homolog).

Each chromosome has a constricted region called the centromere. The centromere holds together the two sister chromatids before their separation during the mitotic cell division. On each side of the centromere, are a small and a long arm. Chromosomes are metacentric if they have two arms of equal length. On the contrary, chromosomes are submetacentric if their centromere is not situated in their centre. At last, if the centromere is situated at one furthest point of the Chromosome, the chromosome is acrocentric. The two extremities of the chromosomes are called telomeres. Mitosis is the process of separating the chromosomes into two sets in its cell nucleus. The technique of mitosis is complex and highly regulated. The collection of events is divided into stages, corresponding to the completion of 1 set of activities and begins of the next. These stages are prophase, prometaphase, metaphase, anaphase and telophase.

Prometaphase is the intermediate stage of contraction between prophase and metaphase. Prophase is a stage of mitosis in which the chromatin condenses into a highly ordered structure called a chromosome in which the chromatin becomes visible. Metaphase is a stage of mitosis in the eukaryoticcell cycle in which condensed and

*Author for correspondence

highly coiled chromosomes, carrying genetic information, align in the middle of the cell before being separated into each of the two daughter cells. Chromosome evaluation is completed on dividing cells in their metaphase degree. On this degree, the chromosomes will be recolored such that makes a conventional band-test on them. A chromosome is made of two chromatides, which can be joined all in all on a typical factor named centromere in the metaphase level. A normal human being has 46 chromosomes in which 22 are auto some and remaining are intercourse chromosomes. Whilst there may be a disharmony between this set up, a genetic disease happens. The problem will occur if there are too many chromosomes, lacking chromosomes or combined up bits of chromosomes. Karyotyping is one of the many techniques that facilitate to detect genetic diseases with the help of human genes. Karyotyping comes from the phrase karyotype. Karyotype shows the entire profile of a man or woman's chromosomal set up. A karyotype depicts the information of the chromosomes.

Blood karyotyping is a approach used for analyzing the chromosomes and predicting genetic disease. It counts the variety of chromosomes and identifies the structural modifications in the chromosomes. Karyotyping, or blood chromosome analysis, is a reasonably standard check inside the infertility world. The prefix "karyo" refers back to the fact that the nucleus of the cellular is studied, and the bottom word "kind" refers to the reality that the take a look at is a characterization, or evaluation of the individual. Stage one that should be taken in breaking down a chromosome picture is the division of chromosomes and chromosome bunches from the picture foundation. The methodologies used to investigate cytogenetic pictures depend on the assessment of an overall edge by methods for the Otsu procedure[1,2] on a universal limit with a rethresholding plan[3,4], on k-way grouping[5], or consequently at the watershed change[6,7]. A few endeavors were made to adapt to bunches of touching (however now not covering) chromosomes[8–11] and for clusters of overlapping (but not touching) chromosomes[12] in which combos of geometric and densitometry proof were used to resolve segmentation ambiguities.

A completely automated and efficient method to segment banded chromosomes from its background in G-band metaphase images is proposed in this paper. To attain this, the neighbourhood thresholding, Region growing and edge detection techniques are used to segment chromosome objects from the background. Later the individual chromosomes and clusters are extracted from the segmented image by the usage of labelling the related additives.

2. Methodology

Here we have taken three methods (local thresholding, region growing and edge detection) to segment the chromosomes from its background. Then the output of local thresholding and edge detection methods are used for the extraction of chromosomes and its cluster as shown in Figure 1 and the input G-B and metaphase chromosome image is shown in Figure 2.

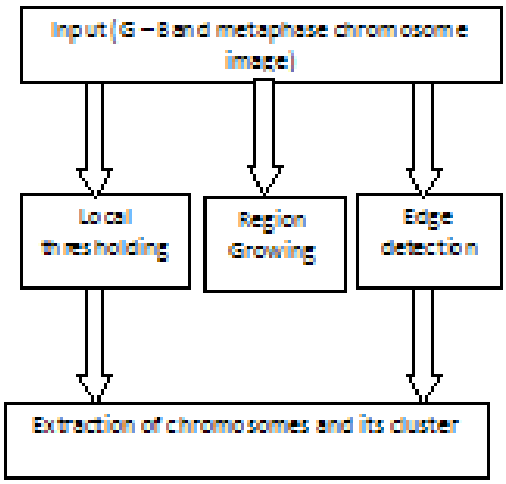


Figure 1. Block diagram of proposed method.

Figure 2. G-Band metaphase chromosome image.

2.1 Segmentation Algorithms

2.1.1 Local Thresholding

Segmentation refers to the system of partitioning a virtual image into multiple segments. The purpose of segmen-

tation is to simplify and/or change the representation of an image into something that is greater meaningful and less complicated to research. The result of image segmentation is a set of segments that together cowl the whole picture. This part ambition is to extract the chromosomes from the background of the metaphase images.

On the off chance that a picture incorporates a question over a uni-shading foundation, the dim level histogram of this picture will display two pinnacles and the perfect edge will be situated at the worldwide least between the two pinnacles. Be that as it may, in metaphase pictures, the foundation pixels dwarf the chromosome pixels. As an outcome a sudden ascent happens in the histogram and it is hard to find the worldwide least. The issue with a straightforward edge is that some dark esteem is regular to the chromosomes and the foundation.

Consequently, the threshold will fragment the chromosomes or highlights noisy area. That is why local thresholding technique[11] is used. A single threshold will not work well. The idea is to partition the image into subimages and then choose a threshold for each subimage. The threshold value is calculated as follows. The global threshold value is calculated for each subimage. Then the largest element in that subimage is computed. Finally the product of global threshold and largest value is used as threshold.

2.1.2 Region Growing

Region growing is one of the method for image segmentation in which neighboring pixels are analyzed and added to a region class if no boundaries are detected. This process is iterated for every boundary pixel in the vicinity. Region growing gives numerous advantages over conventional segmentation techniques. In contrast to gradient and laplacian techniques, the borders of regions observed with the aid of area developing are perfectly thin (because we only add pixels to the outside of the region of interest) and related. The algorithm is likewise very solid with recognize to noise. Region-growing tactics make the most the essential truth that pixels which are close collectively have comparable gray values. Area developing starts with a seed pixel and adds new pixels slowly (i.e.,) it follows the stairs under

- Pick out the seed pixel.
- Test the neighbouring pixels and upload them to the location if they're similar to the seed.
- This system stops when the depth difference between place mean and new pixel emerge as large as a certain threshold.

Choosing the seed depends on the following:

- If relies upon on the character of the problem.
- If objectives need to be detected the use of infrared pictures as an instance, pick out the brightest pixel(s).
- Without a-priori expertise, compute the histogram and select the grey-degree values similar to the most powerful peaks.

2.1.3 Edge Detection

There are many methods to carry out edge detection. But, the maximum of them can be grouped into classes, gradient and laplacian. The gradient method detects the edges by seeking out the maximum and minimal inside the first spinoff of the image. The laplacian technique searches for zero crossings within the second spinoff of the image to discover edges. The gradient techniques are roberts, prewitt, sobel and the laplacian approach is marrs-hildreth.

The sobel technique reveals edges with the usage of the sobel approximation to the derivative. It is simple to use than the other operators. It returns edges at those points in which the gradient of image is maximum.

The sobel detector is especially sensible to noise in images, it efficaciously spotlight them as edges.

2.2 Extraction of Chromosomes and its Clusters

The chromosomes can be extracted using the labelling method. The labelling of chromosomes is applicable to the output of local thresholding and edge detection method. But the labelling of chromosomes is not possible in region growing method. So the chromosomes and its clusters are extracted using the output of local thresholding and edge detection method. First the median filter is used to remove noises in the image. Median filtering is just like the use of an averaging filter, in that each output pixel is set to an average of the pixel values within the neighbourhood of the corresponding input pixel. However, with median filtering, the cost of an output pixel is decided through the median of the neighbourhood pixels, in place of the mean.

3. Results and Discussion

The result of local thresholding is shown in Figure 3(a). The threshold value chosen here to perform region growing is 0.1 and the segmented output is shown in Figure 3(b). It could be in the range between 0.05 to 0.2.Thesobel operator is used to detect the edges of the image and the segmented output is shown in Figure 3c. The chromosomes can be extracted using the labelling method as shown in Figure 4. The output of edge detection and local thresholding methods are given as input to the labelling method. Then the smoothing operation is performed to reduce the number of connected components. The connected components are calculated and labelled. The chromosomes and its cluster can be extracted by giving the label values as shown in Figure 5(a) and 5(b).

(a) (b) (c)

Figure 3. Segmentation of chromosomes from its background using. **(a)** Local thresholding. **(b)** Region growing. **(c)** Edge detection methods.

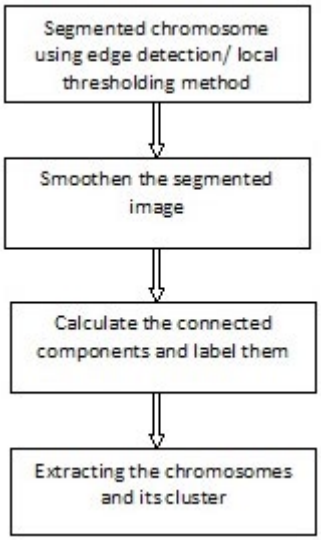


Figure 4. Block diagram of labelling method.

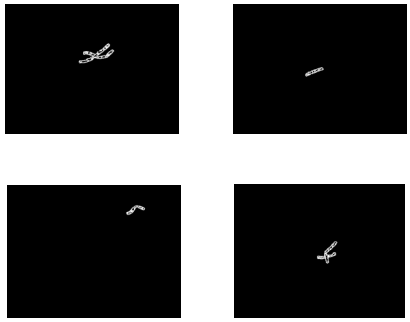
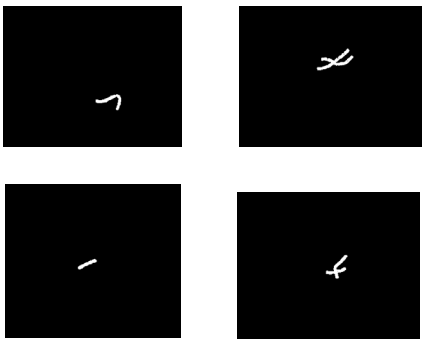


Figure 5. **(a)** Examples of extraction of individual chromosomes and clusters by giving output of edge detection method.



(b) Examples of extraction of individual chromosomes and clusters by giving output of local thresholding method.

4. Conclusion

Thus the segmentation process is done using region growing, local thresholding and edge detection methods. The chromosomes are segmented from its background and the output from the edge detection and local thresholding methods are used for extracting the chromosomes and its clusters. The process can be extended further by disentangling the clusters into individual chromosomes.

5. References

1. Ji L. Intelligent splitting in the chromosome domain. Pattern Recognition. 1989; 22(5):519–32. crossref
2. Guimaraes LV, Schuck A, Elbern A. Chromosome classification for karyotype composing applying shape representation on wavelet packet transforms. Proceedings

25th Silver Anniversary International Conference IEEE Engineering Medical Biology Society; Cancun, Mexico. 2003. p. 941–3. crossref
3. Ji L. Fully automatic chromosome segmentation. Cytometry. 1994; 17:196–208. crossref PMid:7851156
4. Stanley RJ, Keller JM, Gader P, Caldwell CW. Data-driven homologue matching for chromosome identification. IEEE Tranactions Medical Imaging. 1998; 17(3):451–62. crossref PMid:9735908
5. Lerner B. Toward a completely automatic neural-network-based human chromosome analysis. IEEE Transactions on Systems, Man, and Cybernetics, Part B (Cybernetics). 1998; 28(4):544–52. crossref PMid:18255973
6. Karvelis PS, Fotiadis DI, Syrrou M, Georgiou I. Segmentation of chromosome images based on a recursive watershed transforms. 3rd Europe Medical Biology Engineering Conference, EMEBC; Prague, Czech Republic. 2005.
7. Lerner B, Guterman H, Dinstein I. A Classification-driven Partially Occluded Object Segmentation (CPOOS) method with application to chromosome analysis. IEEE Transactions Signal Processing. 1998; 46(10):2841–7. crossref
8. Shunren X, Weidong X, Yutang S. Two intelligent algorithms applied to automatic chromosome incision. Proceedings IEEE International Conference Acoustics, Speech, Signal Process (ICASSP '03); 2003. p. 697–700. crossref
9. Agam G, Dinstein I. Geometric separation of partially overlapping nonrigid objects applied to automatic chromosome segmentation. IEEE Transactions Pattern Analysis. Machine Intelligence. 1997; 19(11):1212–22. crossref
10. Garcıa CU, Rubio AB, Perez FA, Hernandez FS. A curvature-based multiresolution automatic Karyotyping system. Machine Visual Application. 2003; 14:145–56. crossref
11. Grisan E, Poletti E, Ruggeri A. Automatic segmentation and disentangling of chromosomes in Q-Band Prometaphase Images. IEEE Transactions on Information Technology in Biomedicine. 2009; 13(4):575–81. crossref PMid:19193514
12. Shunren X, Weidong X, Yutang S. Two intelligent algorithms applied to automatic chromosome incision. Proc IEEE International Conference Acoustics, Speech, Signal Process, ICASSP; 2003. p. 697–700. crossref