



A NOVEL AND MAXIMUM-LIKELIHOOD SEGMENTATION ALGORITHM FOR TOUCHING AND OVERLAPPING HUMAN CHROMOSOME IMAGES

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ABSTRACT

The chromosome abnormality in human is a vital issue. These abnormalities happen due to touching or overlapping chromosomes in human beings. It may cause breast cancer, improper structure or functions in body metabolism, birth defects, down syndrome, turner syndrome etc. To overcome these problems a stringent screening and diagnosing must be followed during earlier stage of pregnancy. In this paper Novel and Maximum-Likelihood segmentation algorithms were used to segment the overlapping and touching human chromosome images. Either the gray scale image was converted into color image or a color image is directly applied as the input to the Novel as well as Maximum-Likelihood segmentation algorithms. After obtaining threshold from binary, the watershed transform was applied. The output of watershed was improper. So after threshold the iterations were applied, followed by edge detection and corresponding segmentation. The Novel algorithm worked better only for touching chromosomes images but failed to work for overlapping images. Then the segmentation was followed using Maximum-Likelihood segmentation algorithm. By comparing with Novel algorithm, the Maximum-likelihood segmentation algorithm works better for both touching and overlapping chromosome images.

Keywords: chromosome abnormality, down syndrome, turner syndrome, diagnosing, segmentation.

1. INTRODUCTION

Chromosome is a thread-like structure found in the nucleus of each cells. The DNA and histone of proteins are packed to form the chromosome structure. Chromosomes are not visible under the light microscope in non dividing cells. Centromere is the midpoint of each chromosome and it is divided into shorter and longer arms. They are called as p arms and q arms respectively [1].

There are twenty three pairs of chromosomes in each human cell. Twenty two pairs of chromosome, called autosomes, are similar in both male and female. The twenty third pair is called sex chromosome. Males have two distinct chromosomes X and Y whereas females have same chromosomes X and X [2]. The chromosome abnormality in human is a vital issue. These abnormalities happen due to touching or overlapping chromosomes in human beings. It may cause breast cancer, improper structure or functions in body metabolism, birth defects, down syndrome, turner syndrome etc [3].

Birth defects occur in newborn babies and affect the baby's structure, function or body metabolism, which may lead to physical and mental disabilities and may even be fatal sometimes [4]. The Down syndrome will occur due to the extra copy of chromosome twenty one i.e. trisomy twenty one. These are caused by nondisjunction of chromosome when fail to separate during sperm or egg formation. If not diagnosed during the early stage of pregnancy then the offspring will be affected with abnormal shaped ears, a flat face, a small broad nose, a large tongue etc [5]. The Turner syndrome will occur due to incomplete or missing extra chromosomes in women. These also happen due to nondisjunction and if failed to be diagnosed during the early phase, then people will be affected with the disorder like being shorter than the

normal women, a short webbed neck, a receding lower jaw etc [6].

These genetic problems can be detected using karyotyping. The Karyotyping is used to classify the chromosomes into twenty four different classes and also used to examine the chromosomes in the cells and the process involves separating an abnormal chromosome i.e. after diagnosing overlapping and touching chromosomes image. [7].The overlapping and touching chromosome images are clearly visible in metaphase stage. So the G-band metaphase images are used for chromosome image analysis [3, 4], [8 - 10].

2. LITERATURE SURVEY

Enea Poletti *et al.* proposed that automatic segmentation of overlapping and touching chromosome is an open issue. For automatic segmentation of an image, the binary approximation or thresholding an image is the first step. They implemented eleven thresholding methods and compared their performance in segmenting Q-band chromosome images. Among these methods otsu thresholding has been considered as the best [11]. Enrico Grisan *et al.*, proposed that karyotyping analyzing procedure is lengthy, and the automatic segmentation was followed. The author segmented the chromosome automatically using space-variant thresholding scheme by finding the cuts and overlap based on geometric evidence. After segmentation, classification step was followed [12].

Hyohoon Choi *et al.* proposed a Maximum-Likelihood decomposition segmentation method for touching and overlapping chromosomes in M-Fish images. Based on geometric information, pixel classification and size, the hypothesis was chosen to separate the cluster in the image [13]. Khalifa *et al.*, proposed a segmentation



method in left ventricle based on shape. The author also carried out the segmentation based on affine, first order and second order. Based on the intensity value of pixel, they concluded shape based model is best approach for segmenting the left ventricle [14].

Qufa Zhong *et al.* proposed a Novel segmentation algorithm based on watershed and concavities in cluster slender particles. Primarily, the distance and watershed transform was applied to binary image followed by watershed post-processing. Finally, based on the splitting lines the concavities in the un-segmentation were found. This algorithm works well for the cluster slender particles [15].

3. A NOVEL AND MAXIMUM-LIKELIHOOD SEGMENTATION ALGORITHM METHODOLOGY

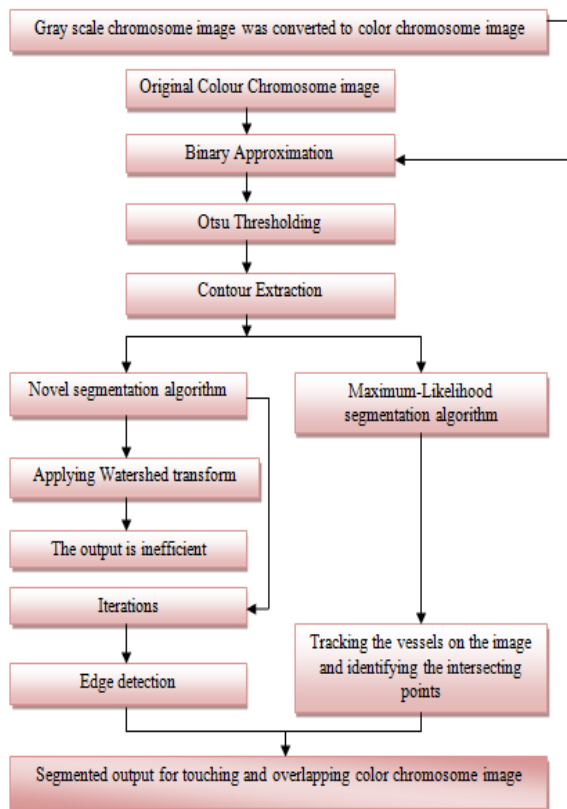


Figure-1. The work flow.

Steps to be considered

- Get the input touching or overlapping color chromosomes image
- Apply binary approximation to the input color image
- Apply Otsu thresholding to the binary approximated image
- Apply contour extraction to the Otsu threshold image
- For Novel segmentation algorithm, apply watershed transform and obtained watershed output

- Apply iterations to the color image
- Obtained edge detection and segmentation output for Novel segmentation algorithm
- For Maximum-Likelihood segmentation algorithm, tracking the vessels on the image and identifying the intersecting points to segment the image
- Obtained segmentation output for Maximum-Likelihood segmentation algorithm

Description

The gray scale image was converted into color image or the color image is taken directly and given as input to the Novel as well as Maximum-Likelihood segmentation algorithm. The Figure-1 shows the work flow. For Novel segmentation algorithm, after obtaining threshold from binary, the watershed transform was applied. The output of watershed was improper. So after threshold the iterations were applied, followed by edge detection and corresponding segmentation. The Novel algorithm worked better only for touching chromosomes images but failed to work for overlapping images. Then the segmentation was followed using Maximum-Likelihood segmentation algorithm. In this algorithm after contour extraction, tracking the vessels on the image and then identifying the intersecting points. These intersecting points help to segment the overlap chromosome images. By comparing with Novel segmentation algorithm, the Maximum-Likelihood segmentation algorithm works better for both touching and overlapping chromosome images.

4. RESULTS AND DISCUSSIONS

A. Pre-processing steps

The gray scale image may be converted into color image or color image by nature is taken and given as input to the Novel as well as Maximum-Likelihood segmentation algorithm. The Figure-2 shows the sample converted color image and Figure-3 shows the sample overlapping and touching color chromosomes image. The process of converting the gray scale image into color image was so complicated. So the original color image can be taken and given as input to the segmentation algorithm. The output will remain same for both converted color image and original color image.

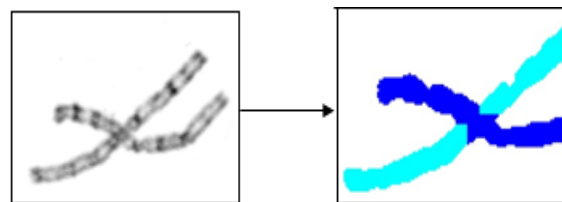


Figure-2. The sample converted gray scale image to color image.



Figure-3. The sample overlapping and touching color chromosomes image.

B. Binary Approximation, Otsu Thresholding and Contour Extraction

On the first hand the touching and overlapping chromosomes image were converted to binary image. In order for binary conversion, proper thresholding method should be selected. In this approach Otsu thresholding was used. The thresholding output was shown in Figure-4. After binary there was some loss of information. For proper segmentation, the information must be fulfilled. The fulfilled information of shape is contained in its threshold. The threshold helps in smoothening the image. For color image segmentation the threshold output was similar to the binary approximation output. This threshold or binary was then extracted by contour. The contour extraction was highlighted with green color as shown in Figure-5.



Figure-4. Binary approximation.



Figure-5. Contour extraction.

C. A Novel segmentation algorithm

After contour extraction, applying distance and watershed transform to an image. In the distance transform there is more loss of information and in watershed it fails to segment the image. The watershed transform output was shown in Figure-6. The watershed output was improper. So the iterations were applied to a color image. These iterations will vary for each image. The iterations output was shown in Figure-7. After proper iterations the edge detection happens as shown in Figure-8 and the corresponding segmentation output for overlapping

chromosomes was shown in Figure-9. By following the same procedure for touching chromosomes image segmentation was obtained as shown in Figure-10. The iterations help to identify the different colors and used to separate the different color images. These algorithms works better only for touching chromosomes but fail to work for overlapped chromosomes i.e. in overlapping chromosomes there is a loss of information as shown in Figure-9.

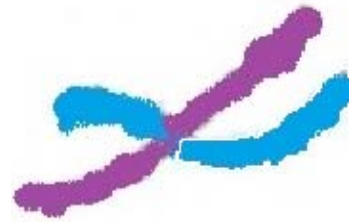


Figure-6. The watershed transform output.

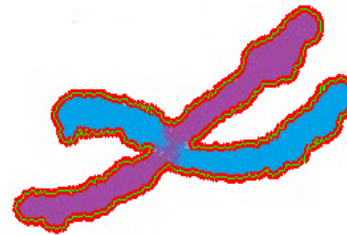


Figure-7. The iterations output.



Figure-8. Edge detection output.



Figure-9. The overlapping chromosomes image segmentation.

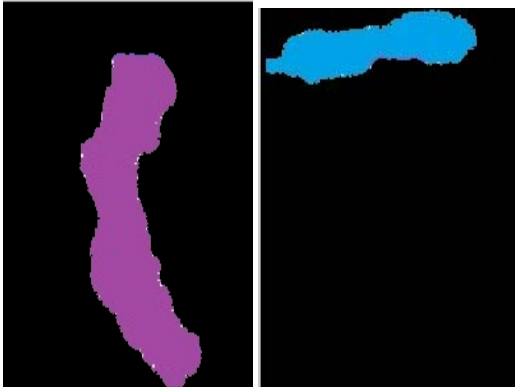


Figure-10. The touching chromosomes image segmentation.

D. Maximum-likelihood segmentation algorithm

After the contour extraction, the vessels were tracked on the threshold image. This vessel tracking was helpful for identifying the intersecting region of overlapping as well as touching chromosomes images. The Figure-11 shows the vessel tracking output. Four cut points were chosen for overlapping chromosomes images. Then connected four cut points represent the intersecting zone for overlapping image as shown in Figure-12. By drawing the hypothesis line from intersecting points it was possible to separate the overlapping chromosome image. The segmentation output for overlapping chromosomes was shown in Figure-13. Similarly by following the same steps for touching chromosomes with two cut points touching chromosomes image was separated. The Segmentation outputs for touching chromosomes were similar to the Novel segmentation algorithm and the segmented output was shown in Figure-10.



Figure-11. Vessel tracking on threshold image.

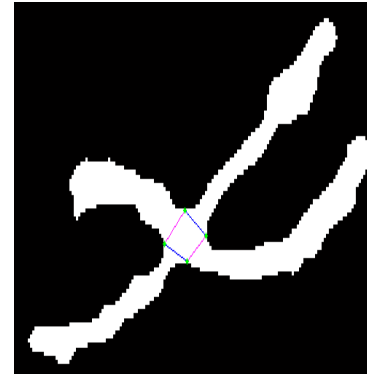


Figure-12. The intersecting zone for overlapping chromosome image.

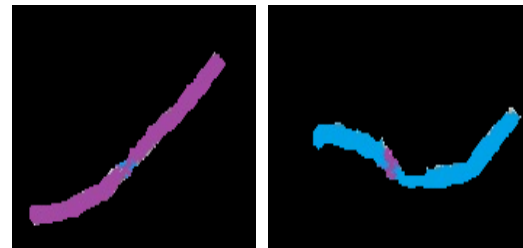


Figure-13. The segmentation output for overlapping chromosomes.

5. CONCLUSIONS

Thus the Novel segmentation algorithm works better only for the touching chromosomes images but fails to work for overlapping chromosomes images. The loss of information occurred in overlapping image will again lead to chromosome abnormality. To get the complete information and for diagnosing the overlapping as well as touching chromosomes a Maximum-Likelihood segmentation algorithm was followed. Finally the Maximum-Likelihood segmentation algorithm proves that this works better for both overlapping and touching chromosome images.

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