Contour based segmentation of chromosomes from metaphase spread: a Make in India initiative

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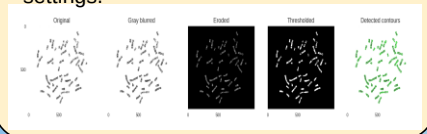
Introduction

Chromosome segmentation from captured metaphase images is the first step towards karyotyping analysis. The laborious manual process of segmentation and identifying the chromosomes from metaphase spread and then compiling a report in accordance with current guidelines takes several hours and skilled workers. The closed source, proprietary, non-extensible, and expensive nature of all available commercial software packages limits their application to medical diagnosis and research purposes; the use of neural networks further reduces their scalability [1] [2].

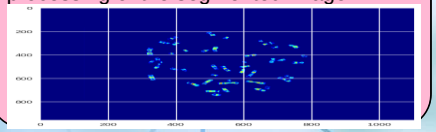
Aim: The aim of the present study was to develop an indigenous low-cost image analysis-based module for segmentation of chromosomes in resource constraint settings.



Materials & Methods

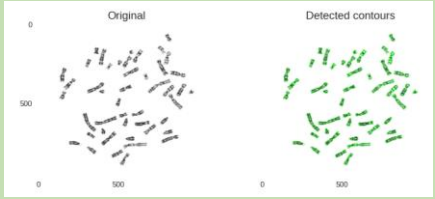
16 (sixteen) Metaphase spread images were converted to grayscale and a Gaussian blur with 3 x 3 kernel was applied. The image was then converted to negative (invert) and an **erosion kernel of size 5 x 5 was applied, to separate the chromosomes that were in contact with each other.** A binary threshold was then applied. Further, the contour finder function from the OpenCV library [3] was used to detect the individual chromosomes. The drawContours function was then used to overlay the contours over the original Image.

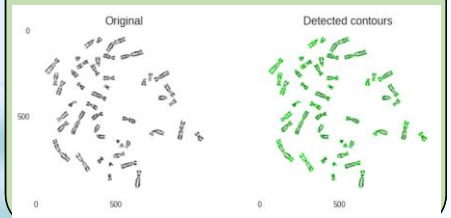
The method can optimally separate chromosome which are in contact at one point; however, it cannot separate overlapping chromosomes. Manual separation step will be required as post-processing of the segmented image.



Results

The segmentation of chromosomes and timing for segmentation were deemed satisfactory by two independent cytogeneticists. While the average time for manual segmentation was 2-3 minutes, the time taken for automated segmentation was less than one second (as measured by the Python timeit() function).





Conclusion

Conventional karyotype segmentation systems have depended on extensive proprietary software, , often utilising resource intensive dense neural networks. The present workflow can be deployed in moderately endowed Desktop computers in an opensource manner, so that further modifications can be made to grow into a full karyotyping software suite. This will contribute to the subsequent development of an affordable paradigm for karyotyping analysis, enabling a wider population to have access to basic genetic testing.

Bibliography

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