Abstract

Since the birth of the automated karyotyping systems by the aid of computers, building a fully automated chromosome analysis system has been an ultimate goal. Along with many other challenges, automating chromosome classification and segmentation has been a major challenge especially due to overlapping and touching chromosomes. The earlier reported
methods have limited success as they are sensitive to scale variations, computationally complex, use only color information in case of multispectral imaging and had challenges in segmentation. The proposed technique addresses the challenge of separating the touching chromosomes using initially the modified snake algorithm to disentangle the cluster of touching chromosomes from the metaphase image and then a greedy approach based on combinatorial computational geometry of the pixels on the boundary of the cluster is used to identify and resolve the set of touching chromosomes. Contribution and novelty of this work lies in the ability of the algorithm to successfully separate the clusters of any number of touching chromosomes. System performance was tested and analyzed using a variety of metaphase images exhibiting various levels of touching chromosomes giving an overall accuracy of 100% for resolving the cluster with 2 touching chromosomes and 95% for separating a cluster of 3, 4 touches. The overall time was 2.4 seconds.

Reference

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Index Terms

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Key words

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