

Segmentation of Pro-Metaphase Chromosome Images

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The need for more information on the structure of chromosomes has led to the increased use of pro-metaphase spreads. These spreads, with more than a 1000 bands in the human genome, present more information than a metaphase spread with about 400 bands.

Automated or semi-automated analysis of pro-metaphase spreads is confounded, however, by the increased number of touching and/or overlapping chromosomes. The segmentation problem – one that has always existed in metaphase spreads – becomes increasingly common and difficult in the presence of the significantly longer pro-metaphase chromosomes. In this research we are examining procedures for analyzing these complex images to see how far we can go in automatic segmentation.

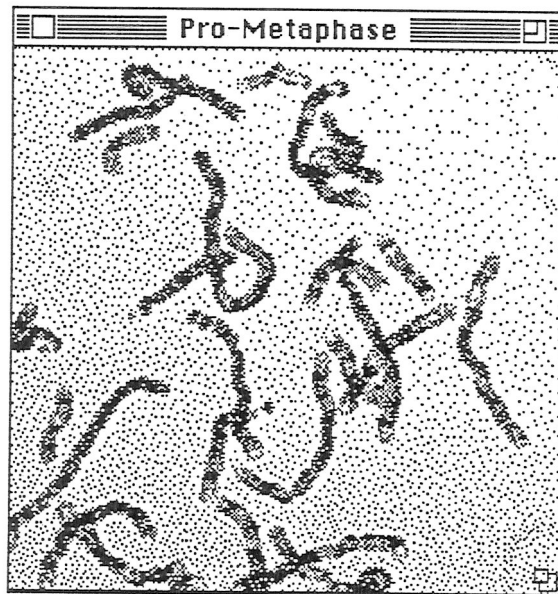


Figure 1: Portion of a pro-metaphase image. The total image contains four times as much area. While the original image consists of grey level information, the picture above has been converted to a "dot pattern" for inclusion in this document.

Our procedure is based upon first obtaining a binary representation of the pro-metaphase image followed by a calculation of the skeleton derived from a Euclidean-distance algorithm. This skeleton image is then approximated by a straight line representation based upon the Wall-Danielsson algorithm. (See Figure 2.)

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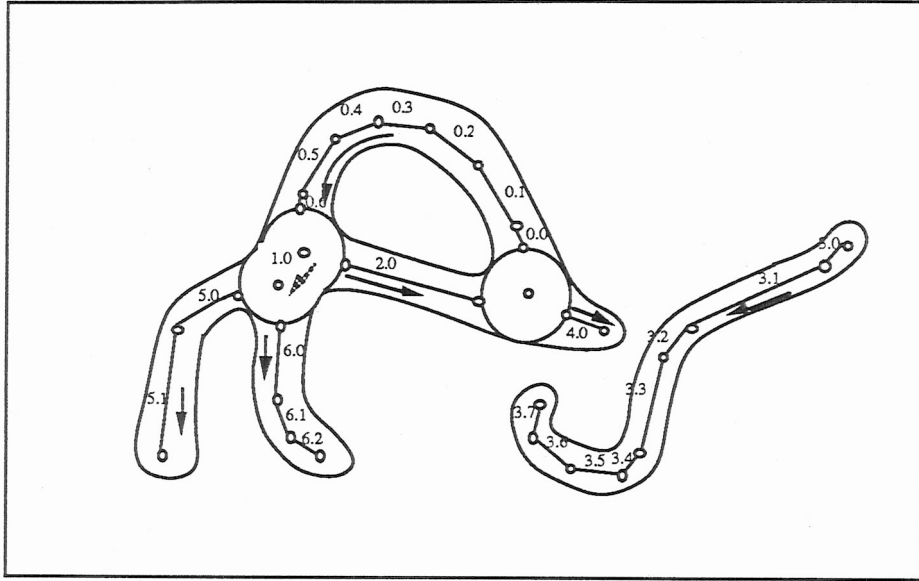


Figure 2: The straight line segment approximation of the skeleton branches. In a circular region around each skeleton branch point the straight line approximation is not performed.

The next step is the syntactic (structural) analysis of the various types of confusion points that may arise in the skeleton. (See Figure 3.) The analysis (or unraveling) of these structures through a set of rules leads to the final decisions as to the "path" of each individual chromosome.

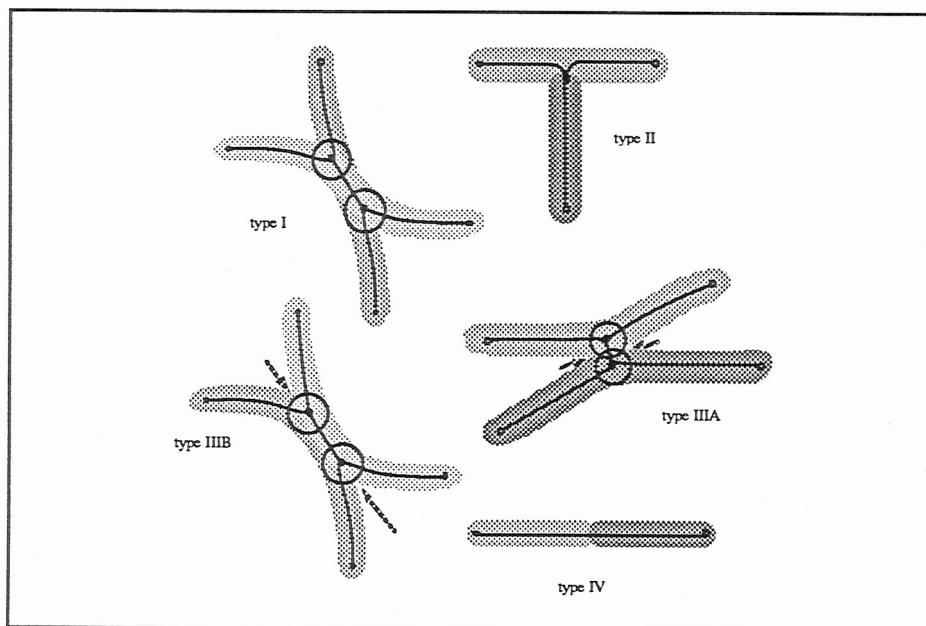


Figure 3: The four types of possible "confusions" - I crossing, II head-to-body touch, III body-to-body touch (A=slight, B=strong), IV head-to-head touch.

The results of this procedure applied to a set of images provided by J. Piper at MRC Edinburgh will be presented and discussed.