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Fully automatic scoring or sister-chromatid ex-changes

Metaphases after differential sister-chromatid staining were found automatically and digitized at X 100 on a Magiscan automatic system. The digitized images were then transferred 10 a Sun-4 for further analysis. Chromosome images were segmented by thresholding, following by automatic shape analysis to reject nuclei and to resolve clusters of touching and overlapping chromosomes. Each chromosome's axis was found automatically, together with the 'shape' profile for centromeric localization, and 'half-profiles' of maximum intensity of either side of the axis for SCE location. Second division cells were selected on the basis of cell-wide properties of the half-profiles. Potential SCEs were found by statistical classification of features of chromosome positions where the half-profiles cross over. In order to validate the system, a pilot project to compare automatic scoring with three-observer visual scoring (two through the microscope and one on the screen) of peripheral human lymphocytes exposed in vitro to four doses of mitomycin-C (2, 8, 12 and 18 ng) and controls has shown comparable dose-response effects between automated and visual scoring.