Structural Similarity and Probabilistic Neural Network Based Human G-Band Chromosomes Classification

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ABSTRACT Chromosome classification has a vital role to play in achieving karyotype. Generally, human chromosomes consists of 46 chromosomes. Karyotyping is the important clinical procedure for screening and diagnosing genetic disorders and cancer. Manual karyotyping is a labor-insensitive and time-consuming task hence, developing automated computer-assisted systems have gained importance. In past decade, chromosome length and centromere positions were considered for classification. In chromosome analysis it is essential to segment the object of interest from the background. This object often consists of two or more chromosomes, either touching, overlapping or multiple overlapping with each other. In this paper, dataset of 1000 touching chromosomes, 1000 overlapping and 500 multiple overlapping chromosomes are taken for the study. SVM and Probabilistic Neural Network (PNN)-based classification is carried out and compared with other classifiers. PNN provides ninety-seven percent of classification accuracy and proves to be better compared to other classifiers.