

Abstracts

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Stochastic Segmentation Models for Array-based Comparative Genomic Hybridization (array-CGH) Data Analysis

Array-based comparative genomic hybridization (array-CGH) is a high-throughput, high-resolution technique for studying the genetics of cancer. Analysis of array-CGH data typically involves estimation of the underlying chromosome copy numbers from the log fluorescence ratios and segmenting the chromosome into regions with the same copy number at each location. We propose for the analysis of array-CGH data a new stochastic segmentation model and an associated segmentation algorithm that has attractive statistical and computational properties. An important benefit of this Bayesian segmentation model is that we can use the posterior distributions of the number and locations of the change-points to provide confidence assessments of the segmentation. Applications to real array-CGH data sets and simulation studies illustrate the advantages of the proposed approach.