GENOMIC INSTABILITY MEASURES FOLLOWING ARRAY CGH

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Array-based comparative genomic hybridization (aCGH) is a powerful, high-throughput tool for whole genome analysis. This technology can be used to determine gains and losses across the genome. Following aCGH data analysis, or "signal processing", it is often of interest to analyze measures of genomic instability. These may be at the clonal or chromosomal or genome level. We propose new measures of instability based on segmentation analysis and based on a new random effects Hidden Markov Modeling approach. We apply them to a comparison of familial and sporadic meningiomas and evaluate them in simulation.