

Statistical assessment of chromosomal aberrations at the cohort level: the CGHSeg package.

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Segmentation methods have been successfully applied to the mapping of chromosomal abnormalities when using CGH microarrays. Most current methods deal with one CGH profile only, and do not integrate multiple arrays, whereas the CGH microarray technology becomes widely used to characterize chromosomal defaults at the cohort level. We present CGHSeg, an R package that is devoted to the analysis of CGH profiles at the individual and at the cohort levels. This package performs segmentation in multiple CGH profiles in the framework of linear models, and multivariate segmentation/clustering for the joint characterization of aberration types (status assignment of regions based on the cohort). Overall, linear models offer a unified framework for the joint analysis of multiple CGH profiles, and we will show how they can be used to link the experience acquired in the field of expression arrays (normalization, experimental design) with array CGH data analysis.