

Summary: Mat-aCGH is an application toolbox for analysis and visualization of microarray-comparative genomic hybridization (array-CGH or aCGH) data which is based on Matlab. Full process of aCGH analysis, from denoising of the raw data to the visualization of the desired results, can be obtained via Mat-aCGH straightforwardly. The main advantage of this toolbox is that it is collection of recent well-known statistical and information theoretic methods and algorithms for analyzing aCGH data. More importantly, the proposed toolbox is developed for multisample analysis which is one of the current challenges in this area. Mat-aCGH is convenient to apply for any format of data, robust against diverse noise and provides the users with valuable information in the form of diagrams and metrics. Therefore, it eliminates the needs of another software or package for multisample aCGH analysis.

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