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## Statistical Analysis of Comparative Genomic Hybridization (CGH) Data: A Segmentation - Clustering Approach

S. Robin INA-PG & INRA Paris, France

Chromosomal aberrations (deletions or amplifications) seem to be responsible for many diseases (diabetes, obesity, etc.). CGH arrays are specific DNA chips that allow to detect such alterations. The detection of the limit of the altered regions appears to be a typical break-point detection problem. The clustering of the different segments into a limited number of classes (normal, amplified, deleted) is a second task that is necessary to derive relevant biological conclusions. We present the aim of the CGH array technology and the kind of signal it provides. We then present a statistical modelling and the corresponding estimation algorithm. The talk is illustrated with application to real data.