

Topological Analysis of Amplicon Structure in Breast Cancer Subtypes

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DNA copy number aberrations (CNAs) play an important role in cancer and can be experimentally detected using aCGH techniques. Amplicons, CNAs that extend over large sections of the genome, are difficult to study since they may contain multiple independent and dependent copy number changes. Here, we propose an algorithm to find the CNAs structure within a given amplicon. Our method relies on the observation that co-occurring CNAs can be encoded as 1-dimensional cycles. We found regions of co-amplifications in Luminal B, ERBB2/HER2/NEU amplified and Basal patients.