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Computational topology in cancer genomics.

Cancer is a polygenic disease in which genomic events are selected in order to produce a sophisticated and coordinated outcome. Determining when two events are co-occurring is an important open question in data science. This work focuses on addressing that question in breast cancer genomics by developing topology-based methods for analyzing how Copy Number Aberrations (CNAs) relate to the breast cancer types and prognosis. (Received September 14, 2020)