

abstract

WORKSHOP ON TOPOLOGY: IDENTIFYING ORDER IN COMPLEX SYSTEMS

Topic:

Speaker:

Affiliation:

Date:

Time/Room:

DNA copy number abnormalities (CNAs) play an important role in cancer, and are associated with tumor progression as well as clinical outcome. Using microarray based comparative genomic hybridization (CGH), analysis of CNAs across large cohorts of cancer patients has led to the discovery of commonly aberrant genes in tumors. Here, we present a new method called Multidimensional Analysis of CGH (MDaCGH), which draws from the theory of computational algebraic homology, to find recurrent CNAs. We show that MDaCGH results on 147 primary glioblastoma tumor samples and 146 normal cell samples mostly agrees with those published by the TCGA network. We further tested MDaCGH on a dataset of 107 stage I and II breast tumor samples to look for regions of CNAs that are associated with cancer recurrence. We found two regions on arms 1q and 6q that have been reported as associated with poor prognosis. In summary, we present a novel method for CNA detection, which has shown to be effective in finding CNAs associated with different tumor characteristics.