Center for Quantum Science and Engineering (CQSE)

Weekly Seminar Sep. 16, 2011 (Friday)

TIME Sep. 16, 14:30 ~ 15:30

TITLE Network theory and application to human cancer and drug

design

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Abstract

We use gene expression data from microarrays of 53 human patients in four conditions, normal control (Nor), adenoma (Ade), inflammatory bowel disease(IBD) and colorectal cancer (CRC), and, in conjunction with protein-protein interaction (PPI) data and gene ontology, to construct functional gene-genenetworks (GGI). We find that both the size and complexity of the GGIsincrease with the severity of the condition. In what we call trend of progression (TOP), the average number of degrees and clustering coefficient in a GGI increase notably in the sequence Nor to Ade to CRC. We find that as a screening tool for biomarkers, or tumorigenic genes, TOP has a significant advantage over conventional methods such as SAM (significant analysis of microarrays). We briefly describe a promising method, based on a combining GGI and TOP developed here with the recently developed gene-set enhanced analysis (GSEA), for designing drug compounds from repurposed drugs for treating systems diseases such as cancer.

