



生物信息学研究中心

Center of Bioinformatics

学术报告

题目： An integrative characterization of recurrent molecular aberrations in glioblastoma

报告人： Chen-Hsiang Yeang (杨振翔)

Institute of Statistical Science,
Academia Sinica

时间： 7月11日（星期三）下午 2:00

地点： 思源楼 1013 室

摘要： Glioblastoma multiform (GBM) is the most common brain tumor in adults. The Cancer Genome Atlas (TCGA) project has mapped many alterations of DNA sequences, copy numbers, methylation states, mRNA and microRNA expressions in GBM cells. Alterations on DNAs may dysregulate gene expressions and drive the malignancy of tumors. It is thus important to uncover causal and statistical dependency between the *effector* molecular aberrations and *target* gene expressions in GBMs. However, despite the rich studies on combining copy number variations and gene expressions, systematic methods to integrate all types of cancer genomic data are relatively scarce.

We propose an algorithm to build association modules linking effector molecular aberrations and target gene expressions and apply the module-finding algorithm to the integrated TCGA GBM datasets. The inferred association modules are validated by six tests using external information and datasets of central nervous system tumors. Besides well-known GBM molecular aberrations, several modules associated with less well-reported molecular aberrations are also validated. In particular, modules constituting trans-acting effects with chromosome 11 CNVs and cis-acting effects with chromosome 10 CNVs manifest strong negative and positive associations with survival times. Functional and survival analyses indicate that immune/inflammatory responses and epithelial-mesenchymal transitions are among the most important processes of prognosis. Finally, we demonstrate that certain molecular aberrations uniquely recur in GBMs but are rare in non-GBM glioma cells. These results justify the utility of an integrative analysis on cancer genomes and provide testable characterizations of effector aberration events in GBMs.