

Weekly Seminar

12pm - 1pm, Friday, November 22, 2019
UWM EMS E237

Statistical analysis for comparison of genomic abnormalities between plasma cell free DNA and tumor tissue DNA

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Abstract:

Circulating cell-free DNA (cfDNA) analysis is emerging as a less invasive approach to assessing tumor genomic alterations in cancer patients. Although high concordance has been reported between tumor tissue NGS and cfDNA in studies investigating specific genetic alterations, the fidelity of cfDNA to tumor tissue DNA in the global genomic scale is largely unknown. In this presentation, whole genome next generation sequencing (NGS) data from a correlative sub study on a prospective clinical trial (NCT# 01953640) will be used to demonstrate how to evaluate correlation of genomic copy number aberrations (CNA) between metastatic tissues and matched plasma cfDNA in patients with advanced prostate cancer. Statistical issues will be discussed regarding data normalization, quantification of DNA copy number change, and estimation of tumor content in cfDNA. Our result identifies significant factors determining the detection sensitivity of CNAs in cfDNA. Furthermore, our finding suggests that cfDNA NGS is a useful tool to investigate clonal evolution associated with cancer progression.