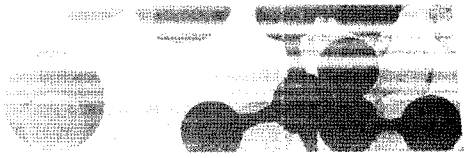

BMS Workshop

LOH and copy number analysis using Illumina Genotyping Arrays

Dr. Richard Shen (Illumina.Inc)

LOH & Copy Number Analysis using SNP-CGH Chip from illumina

The use of genotyping arrays to measure chromosomal aberrations offers a number of advantages over conventional array CGH (comparative genomic hybridization) methods. Array CGH methods are unable to detect LOH since they don't query genomic DNA on an allele-specific basis. whole-genome SNP-based arrays overcome this limitation by generating the industry-leading allelic genotyping data quality which can be used directly to analyze and characterize LOH. In addition, the detection of copy neutral events such as mitotic recombination, gene conversion, and uniparental disomy (UPD) is important for understanding both cancer and genetic disease. These can only be detected using a SNP-based approach. Several recent publications have documented the critical role of copy neutral LOH in tumor samples. Illumina's BeadStudio Genotyping Module enables customers to leverage array-based SNP genotyping data to analyze and visualize DNA copy number changes and to accurately characterize loss of heterozygosity (LOH). These two conditions provide highly informative molecular signposts of cancer development and progression. Genotyping data generated with Infinium-based BeadChips or GoldenGate genotyping products can be used to view LOH and copy number information. This workshop will concentrate the fundamentals of LOH and copy number variation analysis using SNP-based arrays and the data analysis using Illumina's BeadStudio software.