APPLICATION OF COPY NUMBER TRANSITIONS FINDER TO THE ANALYSIS OF THE TUMOR COPY NUMBER DATA AND TO MAPPING SEQUENCE VARIATIONS IN MICE USING BAC ARRAY CGH

J. Fridlyand

UCSF Cancer Research Institute, San Francisco, CA, USA

† E-mail: janef@cc.ucsf.edu

This talk will discuss two different applications of the microarray-based comparative genomic hybridization (array CGH). The development of solid tumors is associated with acquisition of complex genetic alterations, indicating that failures in the mechanisms that maintain the integrity of the genome contribute to tumor evolution. The computational task is to map and characterize the number and types of copy number alterations present in the tumors, and to associate them with known biological markers. We discuss computational approaches leading to copy number phenotypes and the application of the results to testing and classification. We also introduce a connection between copy number and expression profiles. In the second part of the talk we describe a study we conducted on laboratory mice in which we used BAC arrays to map sequence variation among several inbred and outbred mouse strains. We have identified a number of autosomal loci of copy number variation and have shown that these variant loci distinguish laboratory strains. Additionally, we have shown that small ratio changes detected using copy number finder distinguish homozygous and heterozygous regions of the genome in interspecific backcross mice, providing an efficient method for genotyping progeny of backcrosses.