

THE UNIVERSITY



OF HONG KONG

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

Pattern-selection Based Power analysis and Its Application in the Discrimination of High/Low Grade in Myelodysplastic Syndromes Study Using Single Nucleotide Polymorphism Arrays

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on Friday, August 6, 2010 at 10:00am
in Room 206, Run Run Shaw Bldg., HKU

Abstract

Myelodysplastic syndromes (MDS) are a heterogeneous group of clonal hematopoietic disorder characterized by peripheral cytopenia, morphologic dysplasia and susceptibility to leukemic transformation. An important aspect of experimental design is the determination of the number of the samples required in order for the results to be statistically interpretable. By virtue of the heterogeneity of MDS, traditional approaches in the study of power analysis are invalid. A new Constraint Moving Average (CMA) algorithm, which is validated by real time polymerase chain reaction (PCR), is adopted to detect the regions of copy number aberration. An application of our pattern-selection based method is to identify the different MDS grades of patients. Based on the CMA algorithm, the Risk Likelihood Function and General Variant Level (GVL) are defined for each array, which give a uniform measurement to different arrays.

All are welcome
