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ΘΕΜΑ: **MULTI-GENE MOLECULAR DIAGNOSTICS IN CLINICAL ONCOLOGY AND BEYOND: METHODS AND CHALLENGES**

ΤΟΠΟΣ: Αίθουσα Σεμιναρίων ΙΤΕ/ΕΙΧΗΜΥΘ

ΗΜΕΡΟΜΗΝΙΑ: Τετάρτη, 14 Ιουλίου 2004

ΩΡΑ: 17:00

ΠΕΡΙΛΗΨΗ

Several of the technologies that completely transformed molecular biology research in the past several years are now entering a maturity phase that is promising to completely change the practice of clinical medicine. Nowhere is this transformation more apparent than in oncology. Cancer is a complex, multi-gene disease. However, diagnosis and treatment decisions are currently based on population-level risk stratification guidelines mainly derived from pathological and histopathological evaluations, and more recently, on a small number of molecular markers. DNA microarrays have the potential to revolutionize clinical oncology practice, as this technology is capable of measuring the levels of thousands of genes allowing stratification of cancer patients on the basis of multi-gene signatures that are predictive of a patient's disease prognosis or her response to chemotherapy treatment. Whether microarray technology can successfully make the transition from the research lab to clinical diagnostics practice will depend on the development of statistical methodology that can cope effectively with many challenges presented by this type of data, mainly the fact that the number of independent variables or features (10-30 thousands) is orders of magnitude greater than the available samples (typically in the 10's or low 100's). In this seminar, we will present the general statistical methodology and discuss the several issues that are present in diagnostic class prediction from microarray and other "-omic" data. Examples will be drawn from two different domains, a clinical diagnostics application and a toxicity response application.