Istituto Metodi Quantitativi - Università L. Bocconi
Viale Isonzo, 25 - 20135 Milano
Tel. 02-58365632 - Fax 02-58365634

SEMINAR

"Integrating genetic data, disease progression and intermediate response data: an approach via causal graphical models"

Carlo Berzuini
(Università di Pavia and MRC Biostatistics Unit, Cambridge UK)

Thursday, 25th October 2007 – h. 4.30 p.m.
Room 137 – Viale Isonzo 25 - 20135 Milano

Abstract:

Studies of genetic association, favoured by tremendous advances in genotyping technology, are finding convincing links between genetic variation and risk of disease, in various areas of clinical medicine, including cardiovascular disease and diabetes. What is perhaps less clear is that these studies also provide us with an opportunity to 1) clarify the role of epidemiological factors or intermediate phenotypes (e.g. smoking, hypertension, state of coronaries) in the disease generating process, 2) identify the role of specific genetic variants in modulating response to drugs and 3) identifying the molecular pathways which mediate the inheritable components of disease. From a statistical viewpoint, what is required here is an integrated analysis of data at different levels of organization of the biological system. Typically, one wants to perform a combined analysis of genotype data, intermediate markers of disease progression, clinical outcome data and environmental variables. I shall discuss the potential role of probabilistic graphs, specifically directed acyclic conditional independence graphs, in the mentioned analysis framework (as well as in the design stage of the study). In particular, I will consider recent developments in the theory of graphical models for causal reasoning, insisting on problems of identifiability of a causal effect and on the important notion of path-specific effect.