



POLITECNICO  
DI TORINO



Tuesday May 22, 2012 - 3pm

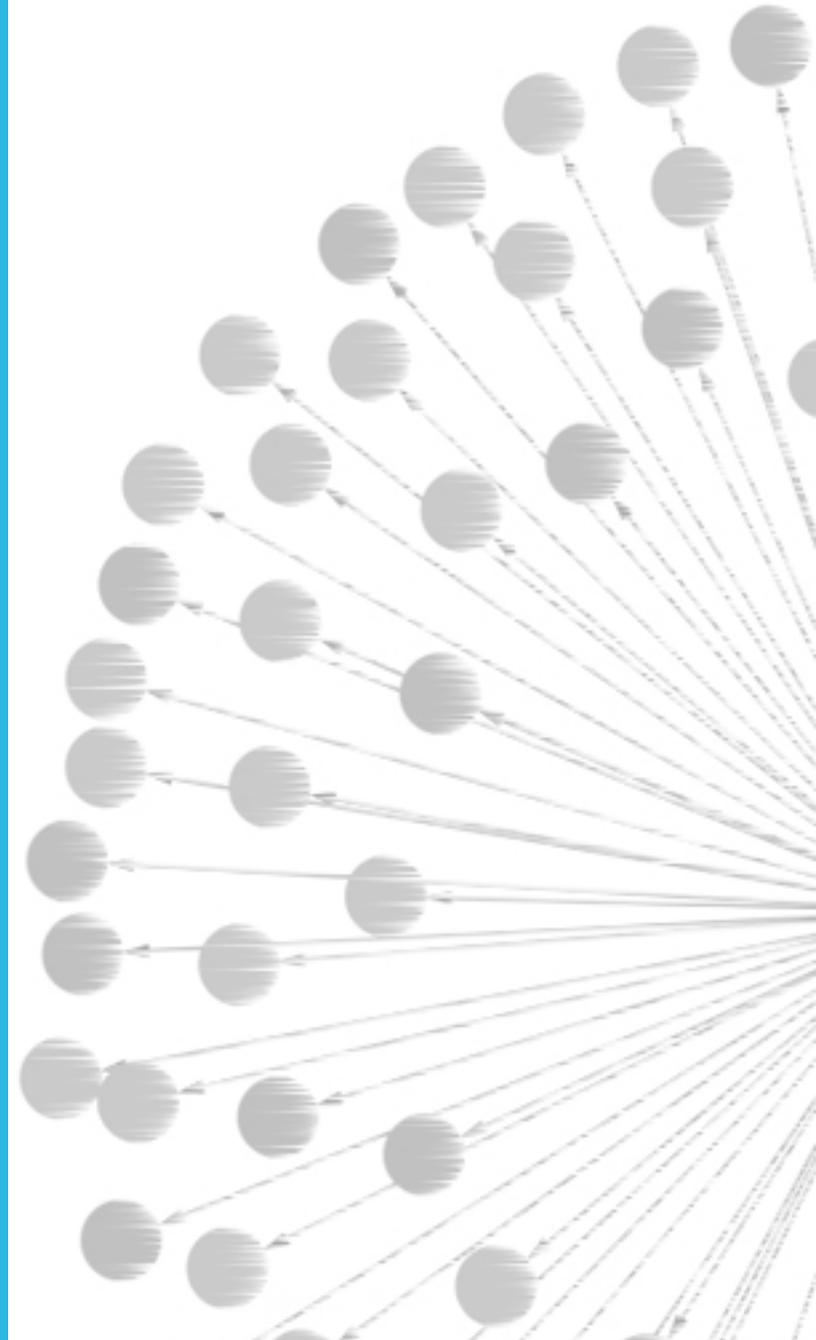
Sala Consiglio di Facoltà  
Politecnico di Torino  
Corso Duca degli Abruzzi, 24  
10129 Torino

# Seminar

"Probabilistic Methods in Cancer Biology"

*Prof. M. Vidyasagar, FRS*

Cecil & Ida Green Chair  
University of Texas at Dallas

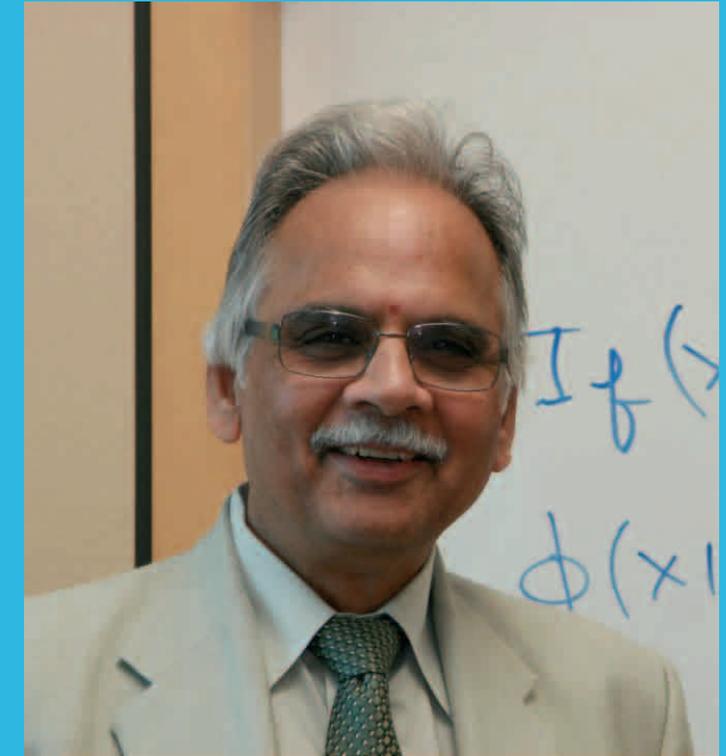
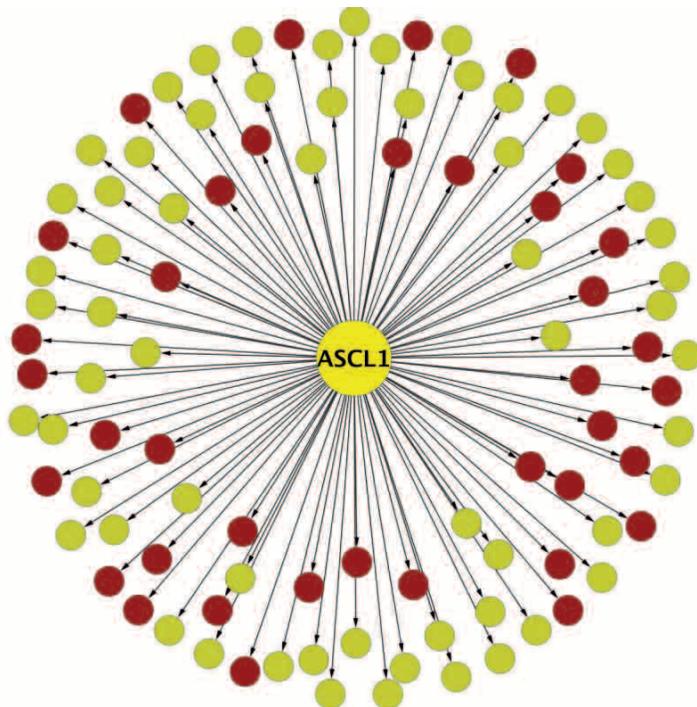


## Abstract

In this talk, I will discuss two problems of great interest in cancer biology.

(1) Reverse-engineering Gene Interaction Networks (GINs) from gene expression data: By treating the expression level of each gene as a random variable, and viewing experimental data as independent measurements of these coupled random variables, infer the underlying dependence structure. It is shown that, by using the so-called phi-mixing coefficient, it is possible to construct a “minimal” network consistent with the data. This approach has been validated in a lung cancer study.

(2) Optimal feature selection for two-class classification: In biology problems, the number of features is many times larger than the number of data points, the inverse of the situation in engineering machine learning problems. A new algorithm, called "lone star", is introduced for choosing just a handful of the most informative features from amongst tens of thousands of features. This approach has been validated in ovarian cancer and endometrial cancer. Some open problems will also be discussed.



Prof. M. Vidyasagar, FRS  
Cecil & Ida Green Chair  
University of Texas at Dallas

Prof. M. Vidyasagar received his Ph.D. from Wisconsin in 1969. During his career, he has worked in many areas including control and system theory, robotics, statistical learning theory, and most recently, computational biology with applications to cancer. He has received numerous awards including the IEEE Control Systems Award and Fellowship of the Royal Society.