



Università degli Studi di Pavia

Dipartimento di Informatica e Sistemistica

## AVVISO DI SEMINARIO

# Identification of approximate metabolic network models from high-throughput data

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### Abstract

*High-throughput measurement techniques for metabolism and gene expression provide a wealth of information for the identification of metabolic network models. Yet, estimation of unknown network parameters remains a challenging problem in many respects. First, metabolic reaction models are large and nonlinear, which makes parameter estimation a hard nonconvex problem. Second, even for structurally identifiable models, practical identifiability from real datasets is not guaranteed and requires better investigation. Third, datasets are noisy and often incomplete due to measurement outliers. Methods for coping with the missing entries exist, but should be further developed to make the most of the available data. In this talk I will discuss identifiability and identification methods for a class of approximate metabolic network models known as lin-log models. I will formalize the notions of structural and practical identifiability, and discuss these properties and open questions also in connection with model reduction. Then, I will describe a maximum likelihood approach to parameter estimation from incomplete datasets. Applications and estimation performance will be illustrated based on artificial examples as well as on a real case study and challenging data from the literature.*

**Martedì 20 Dicembre 2011, ore 14:00,**  
**Aula Seminari, piano D**  
**Dipartimento di Informatica e Sistemistica, V. Ferrata 1, Pavia**

**L'organizzatore**  
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