Hamilton Institute

How to understand the cell by breaking it -
computational inference of cellular networks
from gene perturbation screens

Dr Florian Markowetz
Cancer Research UK,
Cambridge Research Institute

Wednesday, June 11th, 2009

Abstract
Cellular mechanisms are driven by interactions between proteins, DNA and RNA, working together in cellular pathways. Current knowledge of information flow in the cell is still very incomplete and dissection of cellular pathways is one of the major challenges of systems biology. Computational approaches integrating heterogeneous genomic data sources into one joint model promise a comprehensive view on cellular processes. However, to be successful, computational methods need to account for the specific features of each data source.

In this talk I will focus on data from gene perturbation experiments, where individual pathway members are experimentally silenced and effects of these perturbations are measured in genomic assays. I will describe Nested Effects Models, a probabilistic graphical model especially designed to reconstruct signaling pathways from gene perturbation data.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 2.00 - 3.00pm (followed by tea/coffee)

Travel directions are available at www.hamilton.ie

SYSTEMS BIOLOGY
Hamilton Institute