



Hamilton Institute

New 'Dimensions' in Genome Annotation

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Profile

Bernhard Palsson is a Professor of Bioengineering and Adjunct Professor Medicine at the University of California, San Diego. He is the author of over 200 peer reviewed scientific articles and is internationally recognised for his contributions to Systems Biology. His current research at UCSD focuses on 1) the reconstruction of genome-scale biochemical reaction networks, 2) the development of mathematical analysis procedures for genome-scale models, and 3) the experimental verification of genome-scale models with current emphasis on cellular metabolism and transcriptional regulation in *E. coli* and Yeast. He holds a Ph.D. from the University of Wisconsin that he earned in 1984.

Abstract

Traditional Genome annotation involves the enumeration of open reading frames and their functional assignment. Currently, there are on-going efforts to identify all the interactions between these components. The resulting map of interactions effectively represents a two-dimensional annotation. It takes the form of a stoichiometric matrix, if the interactions are described with chemical equations. The formulation and properties of this matrix are detailed and how it can be used as the basis for computing allowable phenotypic functions. The issues associated with the packing of the bacterial genome and the function of the interaction map in three-dimensions will also be discussed. Finally, we will go over the issue of genomes changing in space and time through adaptive evolution and describe the full re-sequencing of bacterial genomes to map all genetic changes that occur during adaptation.

Venue: Lecture Theatre 2, John Hume Building, North Campus
NUI Maynooth

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

Travel directions are available at www.hamilton.ie

