# ICFO Colloquium LUIS SERRANO 'Systems biology analysis of a model organism: what we have learned'

LUIS SERRANO

September 05, 2014

Friday, September 5th, 12:00, ICFO's Auditorium

**LUIS SERRANO**

Leader of the Design of Biological Systems group and Director of the Centre for Genomic Regulation $$ Luis Serrano is the Director of the Centre for Genomic Regulation, CRG and ICREA Professor and the leader of the Design of Biological Systems Group at the CRG. He also directs the EMBL/CRG Systems Biology Research Unit. He has done pioneering work in the field of Systems Biology, an emergent approach in biology that attempts to consider all the components of a biological system and tries to link the properties and interactions of the components with functions performed by the intact system via a computational model. Serrano?s group is aiming at a quantitative understanding of biological systems to an extent that one is able to predict systemic features with the hope to rationally design and modify their behavior.  By achieving this objective he is aiming at new global understanding and

treatment of human diseases in which the target will not be a single molecule but a network. For this purpose he develops on one hand new software and theoretical approximations to understand complex systems and on the other he carries out experiments to validate predictions.

Prof. Serrano received several fellowships (e.g. EMBO fellowship, Marie Curie EU fellowship) is an EMBO member, has founded 4 biotech companies in Germany, Spain and the US, serves as a member of the scientific advisory board of several biotechs and holds 8 international patents

The goal of Systems Biology is to provide a quantitative and predictive description of a living system to the extent that it can be fully simulated in a computer.  We have undertaken such endeavour using as a model the small bacterium, M. pneumoniae.  use Mycoplasma pneumoniae, a human pathogenic bacterium causing atypical pneumonia as model system for our study. Containing a reduced genome with only 690 ORFs, this bacterium is an ideal organism for exhaustive quantitative and systems-wide studies, avoiding technical limitations due to exceeding sample complexity, constrained by limitations in dynamic range and resolution of current generation mass spectrometers. Available data on the transcriptome, on protein complexes, as well as on metabolic pathways facilitate the integration of the data generated for this study into an organism-wide context. Additionally, M. pneumoniae represents a relevant organism to study stochastic noise in living systems. The cells are significantly smaller than other bacteria, such as Eschericha coli (0.05 mm3 and 1 mm3, respectively) resulting in principle in an increased susceptibility to abundance fluctuations of cellular molecules.  Our analysis shows that even apparently simpler organisms have a large hidden layer of complexity and that for every question we have answered we have got two new ones.  We are still far away from having a full understanding of a cell.

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