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ΠΡΟΣΚΕΚΛΗΜΕΝΗ ΟΜΙΛΙΑ ΠΡΟΣΚΕΚΛΗΜΕΝΗ ΟΜΙΛΙΑ

ΟΜΙΛΗΤΕΣ: **Takis Benos**, Associate Professor
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ΥΠΕΥΘ. ΠΡΟΣΚΛΗΣΗΣ: **Dr. Μαρία Κλάπα**, Κύρια Ερευνήτρια ITE/ΕΙΧΗΜΥΘ

ΘΕΜΑ: **From gene expression to disease-specific gene networks**

ΤΟΠΟΣ: Αίθουσα Σεμιναρίων ITE/ΕΙΧΗΜΥΘ

ΗΜΕΡΟΜΗΝΙΑ: **Δευτέρα, 17 Οκτωβρίου 2011**

ΩΡΑ: **12:00**

ΠΕΡΙΛΗΨΗ:

Predicting disease-specific gene networks from gene expression and other data is a major challenge of current computational biology. We have recently developed a new method (mirConnX) that combines gene expression data and prior information to calculate network modules of transcription factors, miRNA genes, and their targets. mirConnX uses sequence (static) information to define interaction priors between genes, which then help reduce the large number of false positives other algorithms generate. We use mirConnX in a pipeline we have developed that can identify gene expression modules that are most relevant to a target disease. In this presentation we will discuss issues related to reverse engineering gene networks and specific cases where miRNA genes seem to play important role in cancer and idiopathic pulmonary fibrosis (IPF).



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ΣΥΝΟΠΤΙΚΟ ΒΙΟΓΡΑΦΙΚΟ

Takis Benos received his undergraduate degree in Mathematics but later he was attracted to Molecular Biology. He earned a PhD degree for his work on the molecular cloning and phylogenetic characterization of alcohol dehydrogenase genes in Diptera. His post-graduate work includes genome analysis and annotation of *Drosophila melanogaster* with **Michael Ashburner** (EMBL-EBI, Cambridge, U.K., <http://www.ebi.ac.uk>) and the development of probabilistic algorithms for modelling protein-DNA interactions with **Gary Stormo** (Washington University in St. Louis, <http://www.wustl.edu/>).

In 2002 he joined University of Pittsburgh (<http://www.pitt.edu>) and he is currently an Associate Professor at the Department of Computational and Systems Biology (<http://www.cccb.pitt.edu>), School of Medicine, while he holds joint appointments at the University of Pittsburgh Cancer Institute (UPCI) and the Department of Biomedical Informatics. He is Co-Director of the Joint CMU-Pitt PhD Program in Computational Biology (CPCB, <http://www.compbio.pitt.edu/>), which is funded by NIBIB-NIH. He is also Co-Director of the Center for Translational Bioinformatics (CTBi), and the Molecular Systems Modeling Core of CTSI (MSM-CTSI).

His research interests are in the area of computational biology and in particular in the study of gene regulatory networks and their evolution. In more recent years, his laboratory has focused efforts on the involvement of non-coding genes in the gene regulatory networks associated with particular diseases.

His work has been published in many peer-reviewed journals such as Nature, Science, PNAS, PLoS Computational Biology, Genome Research, Genome Biology, etc.