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PU	Public	x
PP	Restricted to other programme participants (including the Commission Services)	
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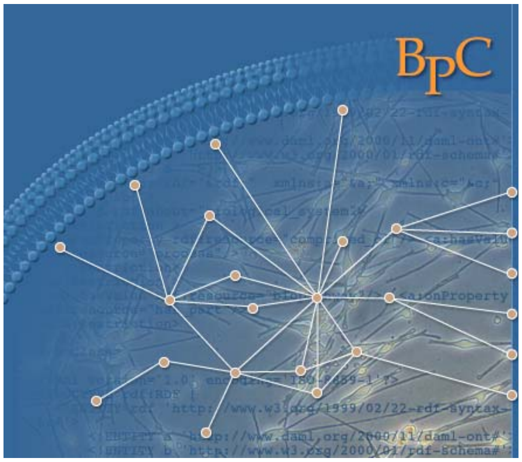

The Eighth Annual BioPathways Meeting

Organized by

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July 19-20, 2007, ISMB-ECCB 2007, Vienna, Austria

The 8th BioPathways meeting was organized by the BioPathways Consortium (www.biopathways.org), an open forum aimed at fostering computational approaches to the modeling, reconstruction, analysis and simulation of biological networks.

Previous BioPathways meeting have focused on a variety of themes, such as computational reconstruction of molecular networks, pathway evolution, integration of models and experiments, models and ontologies for pathways, metabolic pathways on modeling of interactions and regulation on a systems scale.

The special focus this year was on computational design methods for Synthetic Biology and was organised in collaboration with EMERGENCE, an EU-funded consortium aiming at fostering and consolidating the field of Synthetic Biology in Europe (www.emergence.ethz.ch/).

Synthetic Biology addresses the design and fabrication of biological components and systems that do not exist in the natural world as well as the re-design and fabrication of already existing biological systems. Whereas many of the computational methods developed in order to model and analyze natural systems are relevant to the modeling of synthetic living systems, there is also an acute need for new computational methods in order to support the rational design goals and the abstraction/modularity/assembly approach of synthetic biology.

The meeting included as well 3 other plenary sessions, touching on the full spectrum of pathways and networks-related themes and with relevance to Synthetic Biology design tools:

- Network Reconstruction and Analysis
- Database and Software Tools (for pathways and networks)
- Evolution of networks

Each plenary session included several long invited presentations (30’). An open discussion will conclude each day.

The program was as follows:

8th BioPathways Meeting Program

Hall F1, Austria Vienna Center

Day I – July 19th

7:30 – 8:45	**Registration**	
9:00-9:10	Vincent Schachter Genoscope, Evry & BioPathways Consortium	Opening remarks
Session 1: **Computational Methods and Infrastructure for Synthetic Biology** Chairman: Vítor Martins dos Santos		
9:10-09:30	Vitor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig	EMERGENCE: a Foundation for Synthetic Biology in Europe
9:30-10:00	Alfonso Valencia, CNIO, Madrid	Bioinformatics tools to help in the design of biological systems
10:00-10:30	Jörg Stelling, ETH, Zürich	Formal tools for Model-Based Synthetic Biology
10:30-11:00	**Coffee Break**	
11:00-11:30	Randy Rettberg, MIT, Cambridge	The MIT registry of parts and devices
11:30-12:00	Alfonso Jaramillo, Ecole Polytechnique, Paris	Model-based design of genetic circuitry
12:00-13:00	**Lunch**	
Session 2: Network Reconstruction & Analysis (part 1) Chairman: Vincent Schachter		
13:00-13:45	Eric Neumann, Teranode Corp.	A Genome - Phenome Integrated Approach for Mining Disease-Causal Genes using Semantic Web
13:45-14:30	Jason Ernst, Carnegie Mellon University	Reconstructing Dynamic Regulatory Maps

14:30-14:50	Tijana Milenkovic and Natasa Przulj, Irvine, University of California	Uncovering Biological Network Function via Graphlet Degree Signatures
14:50-15:10	Kam Dahlquist, Loyola Marymount University	Mathematical Modeling of the Transcriptional Network Controlling the Environmental Stress Response in Saccharomyces cerevisiae
Session 3: Databases & Software Tools Chairman: Erci Neumann (to be confirmed)		
15:10-15:30	Ozgun Babur, Bilkent University	PATIKAweb Components for Microarray Data Analysis & Advanced Graph-Theoretic Querying
15:30-16:00	**Coffee Break**	
16:00-16:20	Richard Adams, University of Edinburgh	The Edinburgh Pathway Editor
16:20-16:40	Esther Schmidt, EBI, Cambridge	Reactome - a knowledgebase of biological pathways
16:40-17:20	Peter Karp, SRI International	Gene Regulation in EcoCyc and Pathway Tools
Round Table Discussion		
17:20-18:30	**IT Infrastructure & Computational Methods for Systems and Synthetic Biology**	

Day II – July 20th

Session 4 : Network Reconstruction & Analysis (part 2) Chairman: Peter Karp (to be confirmed)		
9:00-9:45	Florence d'Alche-Buc, University of Evry	Supervized Inference of Protein-Protein Interaction Networks
9:45-10:30	Eytan Ruppin, Tel-Aviv University	Genome Scale Studies of Robustness and Annotation of the Yeast Metabolic Network
10:30-11:00	**Coffee Break**	
11:00-11:20	Rainer Koenig, DFKZ, Heidelberg	Using gene expression data and network topology to detect substantial pathways, clusters and switches
11:20-11:40	Hanif Khalak	Microarray-based Class Modeling and Prediction using Set-Enrichment Analysis
11:40-12:00	Sol Efroni, NIH/NCI	Identification of Key Processes underlying Cancer Phenotypes using Biologic Pathway Analysis
12:00-13:00	**Lunch**	
13:00-13:45	Jerzy Turyn, University of Warsaw	Identification of functional modules from ancestral protein-protein interactions
13:45-14:30	Fengzhu Sun, University of Southern California	Network motif identification in stochastic networks
Session 5: Evolution of pathways and networks Chairman: Toni Gabaldón (to be confirmed)		
14:30-15:15	Simon Lovell	Protein-protein interactions and their networks: can they tell us about biology?
15:15-15:35	Natalia Maltsev	Co-evolutionary analysis of Metabolic Pathways and Enzymes in PUMA2 and Chisel systems
15:35-16:00	**Coffee Break**	
16:00-16:45	Toni Gabaldón	Evolution of metabolic systems: insights from comparative genomics

16:45-17:30	Philip Kim	Relating three-dimensional structures to protein networks provides evolutionary insights
Round Table Discussion		
17:30-18:30	**Network Reconstruction and Evolution**	
End of meeting		

Assessment of the results and relevance for the development of novel design tools in Synthetic Biology

The Workshop was organized as a satellite meeting to the Annual Conference on Intelligent Systems in Molecular Biology, the largest world-conference on Bioinformatics. The meeting was attended by about 150 participants, chiefly from a bioinformatics community. The workshop can be considered to have been highly successful. For many of the participants, mainly this was the first time they had contact with Synthetic Biology and the workshop was pivotal in raising awareness and the profile of the field. The discussion profited much form the novel insights and new view points made by the participants not previously exposed to Synthetic Biology.

Many of the tools and methods developed in Systems Biology and Network analysis were considered to be relatively straightforward applicable to SynBio (e.g. genome-scale network analysis for the identification of sensitive intervention points in a regulatory or metabolic network, reverse engineering from high-throughput data, etc.), whereas a number of issues specific to Synthetic Biology were identified.

Indeed, the consistent application of the engineering design paradigm to biological systems is the hallmark of Synthetic Biology. The rational assembly of parts to devices and systems and anticipating and counteracting the impact of their implementation into existing chasses cannot be done without a solid and versatile modelling framework. There is an acute need for an extensive computational infrastructure and new computational methods that specifically support the rational design goals and the abstraction/orthogonality/assembly approach of Synthetic Biology (as opposed, for example, to the currently existing ad hoc systems-oriented computational methods developed to treat and analyze data). This effort must develop in an open-source, user-friendly computational environment that will facilitate collaborative editing, implementation and iterative revision of Synthetic Biology endeavours (part design, circuit building, synthetic genomes, etc.). To fulfil these needs, research in the following topics is strongly warranted:

a) Computational interchange standards, ontologies and collaborative environment: Synthetic biology will generate a large number of components and devices (functions) and systems that need to be catalogued and characterised (e.g. the Registry of Standard Biological Parts at MIT [http://parts.mit.edu/registry] or Biskit (http://biskit.pasteur.fr/), but also have to be made interoperable and embedded in contexts that enable their use as building blocks in system design. This strongly requires

ontologies and appropriated computational resources, model repositories and design frameworks that are currently not available and that should be hence developed.
b) Data mining & integration: Research and tool development are needed for automatic extraction of design-specific information (e.g. from literature and existing biological, chemical and physical databases), and its efficient integration (in a standardised, interoperable way) into the design workflows. These tools demand massive data mining and curation and development of the right query and interface software tools, helped immensely by the implementation of ontologies (see above).
c) Parts design: This includes tools for the (semi-)rational design of parts (such as orthogonal riboswitches and ribosomes, orthogonal sensors, new and orthogonal DNA-protein, protein-protein, and protein-molecule interactions, etc) that complement relevant experimental, directed evolution driven approaches to provide suites of parts with different design parameters and novel functions.
d) Model-based systems design, analysis and optimization: Research is needed on the elements of a comprehensive biological design framework that integrates design tools from the part or minimal function level to the design of complex systems. This involves [i] developing a set of standard modeling objects to describe basic functions of standardized biological parts, [ii] establishing mechanisms for instantiating modeling objects according to the users' selections of parts from the registry, [iii] developing interfaces between registries and repositories and modeling / simulation tools through standardised protocols, and [iv] providing novel methods for computer-assisted circuit design. In particular, the development of design methods will be critical for closing the design cycle. Here, we envisage methods for [i] optimization of circuit layout according to behavioral specifications provided by the user, and [ii] specification of allowable parts characteristics (e.g. binding affinities of TFs) that are consistent with behavioral specifications. These developments should enable, for instance, the potential to combine multiple synthetic operons for construction of complex genetic circuits that can carry out complex synthetic or *in situ* delivery functions.

The discussions and success of the workshop, as well as the recognition of the needs in the development of novel design methods and tools specifically for Synthetic Biology has triggered follow-up initiatives, namely, to the organise a series of this highly successful workshop in the following years and in the scope of the BioPathways initiative (the next meeting will be organised in July 18-19, 2008, in Toronto, again as satelute to the ISMB conference), and a session on Computational Design tool and Modelling at the International Conference on Synthetic Biology, SB4.0, to take place in Hong-Kong in October 2008.