The 9th World Multi-Conference on Systemics, Cybernetics and Informatics

July 10-13, 2005 – Orlando, Florida, USA

Invited Session

Object-oriented modelling in Biology and Medicine

The session is focused on the applications of the object-oriented methodology initially developed in software engineering, to the modelling of the structure and behaviour of biological systems.

Background

Object-oriented modelling aims to describe entities of the real world in order to manage them in a natural manner by merging the data and the operations that can be performed on the data within a single semantic unit: the object. An object is defined by its identifier, its state (attributes) and by its behaviour [changes in attribute values triggered upon the reception of a message from another object or a signal from an external (context) or internal (state) environment]. Objects having the same structure (state) and the same behaviour belong to the same class. Classes can have different interrelationships (specialization, aggregation, association, etc.) that delineate graphs of classes. Modularity allows subdividing a large problem into smaller components, or modules, which can perform well-defined tasks and make it possible to deal with complex systems. Developed with programming languages, database management systems (OODBMS) and software toolkits, the object-oriented paradigm is being extended to new application domains to address specific requirements. Its naturalness supports incremental adoption by non-specialists.

Session topics

As Biology and Medicine enter the Systems Biology age, researchers and physicians approach problems, which are systemic in nature, and need to be solved at the system level rather than the individual component level. Such systemic problems concern multifactorial diseases (for example, cardiovascular diseases, cancer, mental illnesses, infections, etc.), drug design, bio-based industrial products including diagnosis, etc. To achieve this goal, researchers and physicians must struggle with the proliferation of heterogeneous data formats (graphic, text, picture, movie, etc.) and content (sequence, biochemical features, motility, genetics, etc). In addition, different granularities need to be captured (protein, gene, nucleus, cell, organ, etc.) in combination with high-level structural complexity (metabolic networks, genetic networks, microarrays, etc.). Last but not the least, information in data may be different, overlapping, redundant, incomplete, and subject to frequent changes, making data integration an overwhelming task.

In this respect, the object-oriented paradigm can offer a conceptual framework to guide system level representations (structure and behaviour) in Biology and Medicine.

The session will consider:

A. The acquired knowledge: Modeling the individual components

- **Sequence data**
- **Shape (protein, protein complex, etc) data**
- **Network data**
- **High- throughput data**
- **Medical data**

B. The challenge : Data integration and Modeling the biological systems

- **Integrating static data and dynamic processes**
- **Metamodeling,**
- **Schema integration and mediators**
- **UML extension to systems biology**
- **Standardization**

Organizers

Magali ROUX-ROUQUIE, PhD

Informatics Laboratory of Paris 6 (LIP6)
CNRS & University of Pierre and Marie Curie
8, rue du Capitaine Scott
75015 Paris
France

E-mail : magali.roux@lip6.fr

W. Jim Zheng, PhD

Biostatistics, Bioinformatics & Epidemiology
Medical University of South Carolina
135, Cannon street – suite 303
P.O. Box 250835
Charleston, SC 29425 USA

E-mail : zhengw@musc.edu

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Important deadlines

December 18th, 2004: Submission of extended abstracts (500-1500) words or paper drafts (2000-5000) words.
December 18th, 2004: Invited Sessions proposals. Acceptation of invited session proposals will be done in about one week of its registration via the respective conference web form, and final approval will be done after the registration of at least five papers in the respective session
January 28th, 2005: Notifications of Acceptance.
March 23rd, 2005: Submission of camera-ready papers: hard copies and electronic versions.