NETTAB

Network Tools and Applications in Biology

NETTAB 2008
Bioinformatics Methods for Biomedical Complex System Applications
19-21 May 2008, Varenna, Lake Como, Italy

The NETTAB 2008 workshop will focus on all aspects needed to provide the framework for understanding multi-scale, complex biological systems, from the single bio-molecule to the cell, across a wide range of clinical information.

In particular, a special emphasis will be given to combine theory, experiments, informatics, and technologies for an integrative systems approach to biological research, which is becoming increasingly multidisciplinary, multidimensional, information driven.

Chairs

Luciano Milanesi, Institute of Biomedical Technologies, National Research Council, Milan, Italy

Paolo Romano, Bioinformatics, National Cancer Research Institute, Genoa, Italy

Sessions

Opening Keynote Session
Bioinformatics Methods for Complex Systems
Gene networking applications
Poster Session
Mathematical methods for System Biology
Bioinformatics for Oncology

Tutorials

Systems Biology Tools

Systems Biology Standards

Location
Villa Monastero, Via Polvani 2, Varenna, Italy

Important dates
10 April 2008: paper submission
21 April 2008: communication of acceptance
22 April 2008: Registration
19-21 May 2008: Tutorials and Workshop

Abstracts
The guidelines and format and for extended abstract submission is available at the following URL:
http://www.nettab.org/2008/abstract.doc

Registration
Register for the NETTAB 2008 workshop:
http://www.nettab.org/2008/rform.html

General topics
Network Standards, Technologies, Tools, Applications in Bioinformatics
Network standards devoted to bioinformatics needs
Network techmnologies for bioinformatics
Network tools for bioinformatics
Network bioinformatics applications

Focus theme topics
Computational Systems Biology and organic computing
Model-driven system development for system biology
Software methodologies for complex adaptive systems
Self-organization in biological systems
Multi-agent systems and cellular automata
Database integration and data warehouses
Analysis of metabolic and regulatory networks
Genetic association studies and linkage analysis
Proteomics and protein interactions
Microarray modelling and analysis
Integrative approaches for drug design
Grid based and HPC for bioinformatics applications

For the full list of topics please consult the NETTAB website.

Scientific Committee
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