Fourth International Workshop on
NETWORK TOOLS AND APPLICATIONS IN BIOLOGY
(NETTAB 2004)
Models and metaphors from biology to bioinformatics tools

NETTAB

UNICAM
Università di Camerino
1336

Università di Camerino
Dipartimento
di Matematica e Informatica

Camerino (Italy), September 5-7, 2004

Motivation and scope
The post-genomic era can be seen as characterized by two different scenarios: on the one hand, the huge amount of available biological data sets all over the world requires suitable tools and methods both for modelling biological processes and analyzing biological sequences; on the other, many new computational models and paradigms inspired and developed as metaphors of biological systems are ready to be applied in the context of computer science.

It may now be a good time (i) to report on the results achieved in these two areas, (ii) to present some open problems in computational biology, (iii) to advertise novel computational tools successfully applied to biological issues, (iv) to spread the knowledge on computational models inspired by biological processes, and (v) to foster the application of computational models to govern real biological systems.

The workshop intends to bring together bioscientists and computer scientists and to compare their approaches and their ideas for solving computational biology open problems. In particular, we expect the participation of those who are developing novel bioinformatics tools and those who are working towards the vision of biological systems as a model for designing new tools.

The workshop will also aim to inspire future collaboration between the different communities, to strengthen the relationships within the bioinformatics community, to activate a cooperation between bioscientists and computer scientists, to collect the latest ideas, achievements and proposals in computational models and metaphors from biology.

Topics of interest
Topics to be covered will include, but not limited to, the following list:

From Biologists - Open problems in:
- Molecular evolution and theoretical biology
- Gene regulation and expression
- Functional genomics
- Comparative genomics
- Protein structure and interaction
- Gene and enzyme networks
- Metabolic pathways and responses
- Genetic and ecological systems
- Pharmacogenomics and Toxicogenomics

From Bioinformaticians - Novel techniques and computational tools in:
- Bio-information processing systems
- Data Integration
- Ontologies and Knowledge management
- Protein interaction pathways and responses
- Protein structure and modelling
- Gene networks
- Genomics and comparative genomics
- Functional genomics

- Microarrays and gene expression patterns
- Sequence analysis
- Motif finding

From Computer Scientists - Promising models and metaphors in:
- Bioware languages and models
- Data management methods and systems
- Biologically inspired systems
- Evolutionary algorithms
- Machine learning
- Genetic computation
- DNA computing
- Computation in neural systems
- Neural hardware
- Autonomous and evolutionary robotic
- Cellular automata
- Self-organizing, self-repairing and self- replicating systems
- Data mining in bioscience literature
- Concurrent languages for biology
- New technologies and methods

Submission and attendance
NETTAB04 welcomes original contributions, containing new and unpublished results, on both theoretical and practical issues of computational paradigms and novel tools inspired or applied particularly to biological systems.

Submitted papers should normally have at most 12 pages using the Springer LNCS style. Templates (llncs.cls, llncs.sty, or sv-lncs.dot) are available under the "Downloads" heading at: http://www.springeronline.com/sgw/cda/frontpage/0,10735,5-164-2-72376-0,00.html

Posters sessions will be organized as opportunity to exhibit late-breaking results and to discuss these results with conference participants in an informal setting. Abstracts for posters should consist of a 1-2 page summary of the work to be presented.

Proceedings and post-proceedings
All accepted papers will be published in the conference proceedings. Furthermore, the best papers will be published in a special issue of Springer-Verlag 'Transaction on Computational Systems Biology'.

Workshop chairs
- Emanuela Merelli, DMI, Università di Camerino, Italy (emanuela.merelli@unicam.it)
- Pablo Gonzalez, DEIS, Università di Bologna a Cesena, Italy (pgonzalez@ingce.unibo.it)
- Andrea Omicini, DEIS, Università di Bologna a Cesena, Italy (andrea.omicini@unibo.it)

Advisory board
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- Giorgio Valle, Università di Padova, Italy
- Franco Zambonelli, Università di Modena e Reggio Emilia, Italy

Local organizers
Mauro Angeletti, Roberto Ciccocioppo, Emanuela Merelli, Cristina Miceli
Università di Camerino, Italy

Important dates
- Paper submission (full paper): June 29, 2004
- Notifications of acceptance to authors: July 15, 2004
- Final version of accepted papers: August 1, 2004
- Poster submission: June 31, 2004
- Workshop: September 5-7, 2004

Satellite event
Workshop on theory and practice on Gene-Array technology

About Camerino
Camerino is one of the most beautiful little towns of Central Italy, being its medieval historical center one of the oldest in Region Marche. Camerino hosts one of the most ancient university in Italy.

Placed on a spur on the Appennini Mountains at 670 meters high on the sea-level, Camerino achieves its period of greatest splendour under the rule of the Da Varano family. From the top of its rock it dominates the large valleys of the rivers Chienti and Potenza underneath, occupied by towers and fortresses. But if the town might look austere, the countryside, instead, is colourful and offers a lot of farms holidays where to spend a weekend.
http://www.incastro.marche.it/incastro/camerino/eng/default.HTM

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