

# Third International Summer School on Computational Biology (ISSCB 2003)

Warsaw University, August 31 – September 5, 2003

<http://www.mimuw.edu.pl/isscb03/>

**Aims and Scope** The School will be addressed to Ph.D. students and young researchers who want to learn leading experts' coherent view on the area of Computational Biology. No particular knowledge of molecular biology will be assumed from the participants. Hence the school will be accessible to the students/researchers of computer science, mathematics and physics who wish to do research in Computational Biology. It should be also of interest to the students/researchers of biology and chemistry who wish to broaden their understanding of the algorithmic/computational aspects of bioinformatics. Some emphasis will be also put on information-theoretic aspects of bioinformatics. The school will be devoted to the current topics in Computational Biology. These include:

- comparative genomics,
- sequence analysis and string algorithms,
- protein structure – analysis and prediction.

## Registration Fee:

- *before June 30*: 1000 Polish zlotys (~250 euro);
- *after June 30*: 1200 Polish zlotys (~300 euro).

The fee covers reception, lunches, breaks, and social dinner. The number of participants at the school is limited. The participants will be accepted on the bases of the order of their registration.

**Other Details** concerning registration, accomodation, etc. can be found at the home page of the school (<http://www.mimuw.edu.pl/isscb03>).

**Contact:** [isscb03@mimuw.edu.pl](mailto:isscb03@mimuw.edu.pl).

**Organizing Committee:** J. Błażewicz, M. Drabikowski, P. Górecki, K. Grygiel, K. Szafran, J. Tiuryn (chairman), and D. Wójtowicz.

## Scientific program

**Gary Benson** (Mount Sinai School of Medicine, USA)

*Searching for similarity in sequences.*

**Michael Y. Galperin** (National Center for Biotechnology Information, NIH, USA)

*Functional analysis of microbial genomes.*

**Andrzej Kolinski** (Warsaw University, Poland)

*Reduced models of proteins and their applications.*

**Michal Linial** (Hebrew University, Israel)

*From protein sequence to families and to folds.*

**Harold A. Scheraga** (Cornell University, USA)

*Protein folding.*

**Jeffrey Skolnick** (University at Buffalo, USA)

*Prediction of protein structure and function on a genomic scale.*

**Piotr Slonimski** (CNRS, France)

*Non-standard approaches to the analysis of genomes.*

**Martin Tompa** (University of Washington, USA)

*Discovering regulatory motifs in DNA sequences.*

**Jaak Vilo** (EGeen Inc, Tartu, Estonia)

*Mining the functional genomic data.*

**Martin Vingron** (Max Plank Institute for Molecular Genetics, Germany)

*Analysis of DNA microarray data.*

**Piotr Zielenkiewicz** (Institute of Biochemistry and Biophysics, Poland)

*Protein-protein recognition.*