

## Scientific Program BIRD Conference 2008

### Paper Presentations

#### Monday, July 7<sup>th</sup>, 2008

9.00 – 9.30            Opening of BIRD'08

**Session 1:            Gene Expression / Regulation & Micro Arrays**  
9.30 – 10.45

A Tree Index to Support Clustering Based Exploratory Data Analysis  
Christian Martin, Tim W. Nattkemper

XMAS: An Experiential Approach for Visualization, Analysis, and Exploration of  
Time Series Microarray Data  
Ben Dalziel, Hui Yang, Rahul Singh, Matthew Gormley, Susan J. Fisher

Clustering in a Fixed Manifold to Detect Groups of Genes with Similar Expression  
Patterns  
Phuong Nguyen, Tuan Hoang

10.45 – 11.15        Coffee Break

**11.15 – 12.15        Invited Talk Peter Schuster**

12.15 – 13.30        Lunch Break

**Session 2:            Sequence Analysis & Alignment I**  
13.30 – 14.45

Families of FPGA-Based Accelerators for BLAST Algorithm with Multi-seeds  
Detection and Parallel Extension  
Fei Xia, Yong Dou

Fast Structured Motif Search in DNA Sequences  
Mihail Halachev, Nematollaah Shiri

A discriminative method for protein remote homology detection based on N-nary  
profiles  
Bin Liu, Lei Lin, Xiaolong Wang, Qiwen Dong, Xuan Wang

14.45 – 15.15        Coffee Break

**Session 3:            Sequence Analysis & Alignment II**  
15.15 – 16.20

Searching for Supermaximal Repeats in Large DNA Sequences  
Chen Na Lian, Mihail Halachev, Nematollaah Shiri

Motif Location Prediction by Divide and Conquer  
Reda Alhajj

**Poster Session: Start 17.00**

Welcome Reception (18.30 - along with Poster Session)

**Tuesday, July 8<sup>th</sup>, 2008**

**9.00 – 10.00      Invited Talk Tom Slezak**

10.00 – 10.30      Coffee Break

**Session 4: Protein & RNA Structure and Function I**

10.30 – 11.20

Translational Control by RNA-RNA Interaction

Ulrike Mueckstein, Hakim Tafer, Stephan Bernhart, Joerg Vogel, Peter F. Stadler, Ivo Hofacker, Maribel Hernandez-Rosales

A Symmetry-free Subspace for Ab initio Protein Folding Simulations

Xiangchao Gan, Kathleen Steinhofel, Leonidas Kapsokalivas

**11.20 – 12.20      Invited Talk Rudolf Freund**

12.20 – 14.00      Lunch Break

**Session 5: Protein & RNA Structure and Function II**

14.00 – 15.40

Comparative Analysis of Disulfide Bond Determination Using Computational-Predictive Methods and Mass Spectrometry-based Algorithm

Timothy Lee, Rahul Singh

Exploitation of Evolutionary Relations between Protein Structures

Natalja Kurbatova, Juris Viksna

Two local Search Methods for Protein Folding Simulation in the HP and MJ Lattice Models

Leonidas Kapsokalivas, Xiangchao Gan, Andreas Albrecht, Kathleen Steinhofel

A robust class of stable proteins in the 2D HPC model

Alireza Hadj Khodabakhshi, Jan Manuch, Arash Rafiey, Arvind Gupta

15.40 – 16.00      Coffee Break

**Session 6: Machine Learning and Data Analysis**

16.00 – 17.15

A Novel Adaptive Multiple Imputation Algorithm

Veselka Boeva, Elena Tsiporkova

Topological metrics in Blast data mining: plasmid and nitrogen-fixing proteins case studies

Pietro Liò, Matteo Brillì, Renato Fani

Gene Expression Mining for Cohesive Pattern Discovery  
Ramkishore Bhattacharyya, Balaram Bhattacharyya

**20.00 Conference Dinner**

**Wednesday, July 9th, 2008**

**Session 7: Databases and Data Integration I**

9.00 – 10.15

Identifying Subcellular Locations from Images of Unknown Resolution  
Luis Pedro Coelho, Robert Murphy

E-BioFlow: Different Perspectives on Scientific Workflows  
Ingo Wassink, Paul van der Vet, Han Rauwerda, Anton Nijholt, Timo Breit

Knowledge Acquisition Focused Cooperative Development - A Case Study with  
BIO2Me  
Dominic Mainz, Ingo Paulsen, Indra Mainz, Katrin Weller, Jochen Kohl, Arndt von  
Haeseler

10.15 – 10.45 Coffee Break

**Session 8: Pathways, Networks, Systems Biology I**

10.45 – 12.25

Nested q-Partial Graphs for Genetic Network Inference from "Small n, Large p"  
Microarray Data  
Kevin Kontos, Gianluca Bontempi

A computational method for reconstructing gapless metabolic networks  
Esa Pitkänen, Ari Rantanen, Juho Rousu, Esko Ukkonen

Finding Frequent Subgraphs in Biological Networks via Maximal Item Sets  
Hans Zantema, Stefan Wagemans, Dragan Bosnacki

Multi-functional Protein Clustering in PPI Networks  
Clara Pizzuti, Simona Rombo

12.25 – 14.00 Lunch Break

**Session 9: Pathways, Networks, Systems Biology II**

14.00 – 15.40

Protein-protein interaction network querying by a "focus and zoom" approach.  
Valeria Fionda, Luigi Palopoli, Simona Panni, Simona E. Rombo

Matching Spatial Regions with Combinations of Interacting Gene Expression  
Patterns  
Jano van Hemert, Richard Baldock

Combining Molecular and Physiological Data of Complex Disorders  
Emanuel Schwarz, F.Markus Leweke, Sabine Bahn, Pietro Lio

Combining PPI network and sequence attributes for predicting hypertension related proteins

Richard JB Dobson, Patricia B Munroe, Charles A Mein, Mark J Caulfield, Mansoor AS Saqi

15.40 – 16.10      Coffee Break

**Session 10:            Databases and Data Integration II**

16.10 – 17.00

Genome Structure and Characterization of an Endogenous Retrovirus from the Zebrafish Genome Project Database  
Roziyah Kambol, M. Faris Abtholuddin

Bayesian Phylogeny on Grid

Richard van der Wath, Elizabeth van der Wath, Antonio Carapelli, Francesco Nardi, Francesco Frati, Pietro Lio

## **Workshop on Algorithms in Molecular Biology -ALBIO'08**

### **Monday, July 7th, 2008**

**Session 1 (13.30 – 14.45):**

Comparison of Exact String Matching Algorithms for Biological Sequences  
Petri Kalsi, Hannu Peltola, and Jorma Tarhio

Indexing factors in DNA/RNA Sequences

Tomas Flouri, Costas Iliopoulos, M. Sohel Rahman, Ladislav Vagner and Michal Voracek

Implementation of a Swap Matching Algorithm Using a Graph Theoretic Model

Pavlos Antoniou, Costas S. Iliopoulos, Inuka Jayasekera, and M. Sohel Rahman

14.45 – 15.15      Coffee Break

**Session (15:15 - 16:45):**

Suffix Tree Characterization of Maximal Motifs in Biological Sequences  
Maria Federico and Nadia Pisanti

Efficient seeding techniques for protein similarity search

Mikhail Roytberg, Anna Gambin, Laurent Noe, Slawomir Lasota, Eugenia Furltova, Ewa Szczurek, and Gregory Kucherov

An Algorithm for Multiple and Global Alignments

Mourad Elloumi and Ahmed Mokaddem

**Poster Session Start 17.00**

**Tuesday, July 8th, 2008**

**Session 3 (14.00 – 15.40):**

LASA: A tool for non-heuristic alignment of multiple sequences  
Ernst Althaus and Stefan Canzar

SVM-based Local search for Gene selection and classification of microarray data  
Jose Crispin Hernandez Hernandez, Beatrice Duval and Jin-Kao Hao

GENFOCS – a comparative tool on gene finding with sensitivity and specificity  
Lijo Anto M.A

Gene Machine© - A Hardware/Software Platform for Analyzing Genome Data  
Roger Marshall

**Workshop on Dynamical Aspects of Perturbation,  
Intervention and Transition in Biological Systems -  
PETRIN'08**

**Wednesday, July 9<sup>th</sup>, 2008**

**Session 1 (9.00-10.15):**

Complex representation of DNA sequences  
Carlo Cattani

Wavelet Analysis of impulses in axon physiology  
Massimo Scalia, Carlo Cattani

10.15 – 10.45 Coffee Break

**Session 2 (10.45-12.25):**

Acquisition and Algorithms for Fluorescence Applications  
Elena Mocanu, Paul Sterian

Control of the Lasers Dynamics by Pumping Modulation for Biophotonics  
Applications  
Paul Sterian, Octavian Marin, Valerica Ninulescu

Quantum Well Lasers for Medical Industry  
Valerica Ninulescu, Vladut-Bogdan Nicolae, Andreea Sterian

12.25 – 14.00 Lunch Break

**Session 3 (14.00 – 15.15):**

A management infrastructure for improving behavioral patterns  
Trandafir Moisa, Cristian Morarescu

Computational Model for the Study of the Fractal Parameters Characteristic for the  
surface of Titanium Dental Implants  
Stefan Pusca

Practical Test Functions Model for Evaluating the Relationships between the VAC  
in Human Communities  
Codita Irina, Pusca Stefan