

## 25th Symposium On Applied Computing

Sponsored by the  
[ACM Special Interest Group on Applied Computing](#)

Hosted by  
[University of Applied Sciences, Western Switzerland \(HES-SO\) in Sierre](#)  
and  
[Ecole Polytechnique fédérale de Lausanne \(EPFL\) in Lausanne](#)  
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### PROGRAM OF BIOINFORMATICS TRACK

Wednesday March 24, 2010

#### Track Co-Chairs:

Dan Tulpan, National Research Council of Canada, Canada  
Kanagasabai Rajaraman, Institute for Infocomm Research, Singapore  
Paola Lecca, The Microsoft Research - University of Trento CoSBi, Italy

**SESSION BIO-I: Chair Paola Lecca, The Microsoft Research – University of Trento CoSBi, Italy.**

**9:00 – 10:00**

**Invited Talk Getting traction in a wet-lab world; a case study from proteome sequence analysis**

*Paul Horton*

*Leader, Sequence Analysis Team*

*Computational Biology Research Center (CBRC) Japan*

**10:00 – 10:20**

**An Incremental Algorithm for Efficient Unique Signature Discoveries on DNA Databases**

*Hsiao Ping Lee, Chung Shan Medical University, Taiwan*

*Tzu-Fang Sheu, Providence University, Taiwan*

*Chuan Yi Tang, National Tsing Hua University, Taiwan*

**10:20 – 10:40**

**A Framework for Cross-Disciplinary Hypothesis Generation**

*Yue Webster, Eli Lilly, United States*

*Ranga Gudivada, Eli Lilly, United States*

*Ernst Dow, Eli Lilly, United States*

*Jacob Koehler, Eli Lilly, United States*

*Mathew Palakal, IUPUI, United States*

**SESSION BIO-II: Chair Pedro Ribeiro, DCC-FCUP, Universidade do Porto, Portugal.**

**11:10 – 11:30**

**Expression Microarray Classification using Topic Models**

*Manuele Bicego, University of Verona, Italy*

*Pietro Lovato, University of Verona, Italy*

*Barbara Oliboni, University of Verona, Italy*

*Alessandro Perina, University of Verona, Italy*

**11:30 – 11:50**

**An Improved Algorithm to Enumerate All Traces that Sort a Signed Permutation by Reversals**

*Christian Baudet, Institute of Computing - University of Campinas, Brazil*

*Zanoni Dias, Institute of Computing - University of Campinas, Brazil*

**11:50 – 12:10**

**Advanced Querying Interface for Biochemical Network Databases**

*Brendan Elliott, Case Western Reserve University, United States*

*Steve Mayes, Case Western Reserve University, United States*

*Ali Cakmak, Case Western Reserve University, United States*

*Gultekin Ozsoyoglu, Case Western Reserve University, United States*

*Z. Meral Ozsoyoglu, Case Western Reserve University, United States*

**12:10 – 12:30**

**A Stochastic Approach to Candidate Disease Gene Subnetwork Extraction**

*Mohammad Shafkat Amin, Wayne State University, United States*

*Anupam Bhattacharjee, Wayne State University, United States*

*Russell L. Finley Jr., Wayne State University, United States*

*Hasan Jamil, Wayne State University, United States*

**12:30 – 12:50**

**FANGS: High Speed Sequence Mapping for Next generation Sequencers**

*Sanchit Misra, Northwestern University, United States*

*Ramanathan Narayanan, Northwestern University, United States*

*Simon Lin, Northwestern University, United States*

*Alok Choudhary, Northwestern University, United States*

**SESSION BIO-III: Chair Dan Tulpan, National Research Council of Canada, Canada.**

**14:10 – 14:30**

**PROM-OOGLE – Data Mining and Integration of On-line Databases to Discover Gene Promoters**

*Dean Cheng, University of Alberta, Canada*

*John Sheldon, University of Alberta, Canada*

*Marcelo Marcet-Palacios, University of Alberta, Canada*

*Osmar R. Zaiane, University of Alberta, Canada*

**14:30 – 14:50**

**Hypothesis Generation and Ranking Based on Event Similarities**

*Taiki Miyanishi, Kobe University, Japan*

*Kazuhiro Seki, Kobe University, Japan*

*Kuniaki Uehara, Kobe University, Japan*

**14:50 – 15:10**

**G-Tries: An Efficient Data Structure for Discovering Network Motifs**

*Pedro Ribeiro, Universidade do Porto, Portugal*

**15:10 – 15:30**

**Virus DNA-fragment Classification using Taxonomic Hidden Markov Model Profiles**

*Mark Menor, University of Hawaii, United States*

*Kyungim Baek, University of Hawaii, United States*

*Mahdi Belcaid, University of Hawaii, United States*

*Yannick Gingras, Université du Québec à Montréal, Canada*

*Guylaine Poisson, University of Hawaii Manoa, United States*

**15:30 – 15:50**

**A Cytoscape based Integrative Framework for Efficient Sub-graph Isomorphic Protein-Protein Interaction Motif Lookup**

*Mohammad Shafkat Amin, Wayne State University, United States*

*Anupam Bhattacharjee, Wayne State University, United States*

*Hasan Jamil, Wayne State University, United States*