

WABI 08

- preliminary program as of August 29, 2008

September 15, Monday	
9:00 – 9:25	Opening remarks
9:25 – 10:15	Invited Talk <i>Leslie Valiant, Harvard University</i>
10:15 – 10:25	Short break
10:25 – 10:50	ESA 2008 Best Paper Award Better and simpler approximation for the stable marriage problem <i>Zoltan Kiraly</i>
10:50 – 11:15	Multichromosomal Genome median and Halving Problems <i>Eric Tannier, Chunfang Zheng, David Sankoff</i>
11:15 – 11:40	Coffee break
11:40 – 12:05	A Branch-and-Bound Method for the Multichromosomal Reversal Median Problem <i>Meng Zhang, William Arndt, Jijun Tang</i>
12:05 – 12:30	Decompositions of Multiple Breakpoint Graphs and Rapid Exact Solutions to the Median Problem <i>Wei Xu, David Sankoff</i>
12:30 – 14:00	Lunch break
14:00 – 14:25	Read Mapping Algorithms for Single Molecule Sequencing Data <i>Vladimir Yanovsky, Stephen Rumble, Michael Brudno</i>
14:25 – 14:50	Exact Transcriptome Reconstruction from Short Sequence Reads <i>Vincent Lacroix, Michael Sammeth, Roderic Guigo, Anne Bergeron</i>
14:50 – 15:15	Post-Hybridization Quality Measures for Oligos in Genome-Wide Microarray Experiments <i>Florian Battke, Carsten Müller-Tidow, Hubert Serve, Kay Nieselt</i>
15:15 – 15:45	Coffee break
15:45 – 16:10	NAPX: A Polynomial Time Approximation Scheme for the Noah's Ark Problem <i>Glenn Hickey, Paz Carmi, Anil Maheshwari, Norbert Zeh</i>
16:10 – 16:35	Minimum Common String Partition Parameterized <i>Peter Damaschke</i>
16:35 – 17:00	Hardness and Approximability of the Inverse Scope Problem <i>Zoran Nikoloski, Sergio Grimbs, Joachim Selbig, Oliver Ebenhöf</i>
17:00 – 17:10	Short break
17:10 – 17:35	Rapid Neighbour-Joining <i>Martin Simonsen, Christian N.S. Pedersen, Thomas Mailund</i>
17:35 – 18:00	Efficiently Computing Arbitrarily-Sized Robinson-Foulds Distance Matrices <i>Seung-Jin Sul, Grant Brammer, Tiffani Williams</i>
18:15 – ...	Algo 2008 Reception

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September 16, Tuesday	
9:00 – 9:50	Invited Talk <i>Marc Overmars, Universiteit Utrecht</i>
9:50 – 10:00	Short break
10:00 – 10:25	ESA 2008 Best Student Paper Track B Time-Dependent SHARC-Routing <i>Daniel Delling</i>
10:25 – 10:50	Efficient Genome Wide Tagging by Reduction to SAT <i>Arthur Choi, Noah Zaitlen, Buhm Han, Knot Pipatsrisawat, Adnan Darwiche, Eleazar Eskin</i>
10:50 – 11:15	Computing the Minimal Tiling Path from a Physical Map by Integer Linear Programming <i>Serdar Bozdag, Stefano Lonardi, Timothy Close</i>
11:15 – 11:40	Coffee break
11:40 – 12:05	An Efficient Lagrangian Relaxation for the Contact Map Overlap Problem <i>Rumen Andonov, Nicola Yanev, Noel Malod-Dognin</i>
12:05 – 12:30	A Faster Algorithm for RNA Co-folding <i>Michal Ziv-Ukelson, Irit Gat-Viks, Ydo Wexler, Ron Shamir</i>
12:30 – 14:00	Lunch break
14:00 – 14:25	Protein Decoy Generation using Branch and Bound with Efficient Bounding <i>Martin Paluszewski, Pawel Winter</i>
14:25 – 14:50	Fast Target Set Reduction for Large-scale Protein Function Prediction: a Multi-class Multi-label Machine Learning Approach <i>Thomas Lingner, Peter Meinicke</i>
14:50 – 15:15	Multiple Instance Learning Allows MHC Class II Epitope Predictions across Alleles <i>Nico Pfeifer, Oliver Kohlbacher</i>
15:15 – 15:45	Coffee break
15:45 – 16:10	An Algorithm for Orienting Graphs Based on Cause-Effect Pairs and Its Applications to Orienting Protein Networks <i>Alexander Medvedovsky, Vineet Bafna, Uri Zwick, Roded Sharan</i>
16:10 – 16:35	Enumerating Precursor Sets of Target Metabolites in a Metabolic Network <i>Ludovic Cottret, Paulo Vieira Milreu, Vicente Acuña, Alberto Marchetti-Spaccamela, Fábio Viduani Martinez, Marie-France Sagot, Leen Stougie</i>
16:35 – 17:00	Boosting the Performance of Inference Algorithms for Transcriptional Regulatory Networks Using a Phylogenetic Approach <i>Xiuwei Zhang, Bernard Moret</i>
17:00 – 17:10	Short break
17:10 – 17:35	Fast Bayesian Haplotype Inference via Context Tree Weighting <i>Pasi Rastas, Jussi Kollin, Mikko Koivisto</i>
17:35 – 18:00	Genotype Sequence Segmentation: Handling Constraints and Noise <i>Qi Zhang, Wei Wang, Leonard Mcmillan, Fernando Pardo-Manuel de Villena, David Threadgill, Jan Prins</i>

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September 17, Wednesday	
9:00 – 9:50	Invited Talk <i>Eytan Ruppin, Tel Aviv University</i>
9:50 – 10:00	Short break
10:00 – 10:25	ESA 2008 Best Student Paper Track A <i>Deterministic Sampling Algorithms</i> <i>Anke van Zuylen</i>
10:25 – 10:50	Constructing Phylogenetic Supernetworks from Quartets <i>Stefan Grunewald, Andreas Spillner, Kristoffer Forslund, Vincent Moulton</i>
10:50 – 11:15	Summarizing Multiple Gene Trees Using Cluster Networks <i>Daniel Huson, Regula Rupp</i>
11:15 – 11:40	Coffee break
11:40 – 12:05	Fast and Adaptive Variable Order Markov Chain Construction <i>Marcel Schulz, David Weese, Tobias Rausch, Andreas Döring, Knut Reinert, Martin Vingron</i>
12:05 – 12:30	Computing Alignment Seed Sensitivity with Probabilistic Arithmetic Automata <i>Inke Herms, Sven Rahmann</i>
12:30 – 14:00	Lunch break
14:00 – 14:25	The Relation Between Indel Length and Functional Divergence: a Formal Study <i>Raheleh Salari, Alexander Schonhuth, Fereydown Hormozdiari, Artem Cherkasov, S. Cenk Sahinalp</i>
14:25 – 14:50	Detecting Repeat Families in Incompletely Sequenced Genomes <i>José Augusto Amgarten Quitzau, Jens Stoye</i>
14:50 – 15:15	Novel Phylogenetic Network Inference by Combining Maximum Likelihood and Hidden Markov Models <i>Sagi Snir, Tamir Tuller</i>
15:15 – 15:45	Coffee break
15:45 – 16:10	A Local Move Set for Protein Folding in Triangular Lattice Models <i>Hans-Joachim Boeckenhauer, Abu Zafer M Dayem Ullah, Leonidas Kapsokalivas, Kathleen Steinhofel</i>
16:10 – 16:35	An Automated Combination of Kernels for Predicting Protein Subcellular Localization <i>Cheng Soon Ong, Alexander Zien</i>
18:00 – ...	ZKM