



# 1<sup>st</sup> International Conference on Algorithms for Computational Biology

AlCoB 2014, July 1 - 3, 2014

Tarragona, Spain

## Program

Tuesday, July 1	
9:15 – 10:15	Registration
10:15 – 10:25	Opening
10:25 – 11:15 Jason Papin	MICHAEL GALPERIN: <i>Comparative Genomics Approaches to Identifying Functionally Related Genes</i> – Invited Lecture
11:15 – 11:45	Coffee Break
11:45 – 13:00 Erchin Serpedin	LIANA AMAYA MORENO, OZLEM DEFTERLI, ARMIN FÜGENSCHUH, GERHARD-WILHELM WEBER: <i>Vester's Sensitivity Model for Genetic Networks with Time-Discrete Dynamics</i>
	SEBASTIAN WANDEL, ULF LESER: <i>RRCA: Ultra-fast Multiple In-Species Genome Alignments</i>
	DAVID A. ROSENBLUETH, STALIN MUÑOZ, MIGUEL CARRILLO, EUGENIO AZPEITIA: <i>Inference of Boolean Networks from Gene Interaction Graphs using a SAT Solver</i>
13:00 – 14:30	Lunch
14:30 – 15:45 Bhaskar DasGupta	LAURENT LEMARCHAND, REINHARDT EULER, CONGPING LIN, IMOGEN SPARKES: <i>Modeling the Geometry of the Endoplasmic Reticulum Network</i>
	SEAN MAXWELL, MARK R. CHANCE, MEHMET KOYUTÜRK: <i>Efficiently Enumerating All Connected Induced Subgraphs of a Large Molecular Network</i>
	BOGDAN IANCU, DIANA-ELENA GRATIE, SEPINOUD AZIMI, ION PETRE: <i>On the Implementation of Quantitative Model Refinement</i>
15:45 – 16:00	Break
16:00 – 16:50 Annie Chateau	JASON PAPIN: <i>Network Analysis of Microbial Pathogens</i> – Invited Lecture



Cathedral

<b>Wednesday, July 2</b>	
9:00 – 9:50 <i>Michael Galperin</i>	UWE OHLER: <i>Decoding Non-coding Regulatory Regions in DNA and RNA</i> (I) – Invited Tutorial
9:50 – 10:00	Break
10:00 – 11:15 <i>Giuseppe Narzisi</i>	DIMITRIS POLYCHRONOPOULOS, ANASTASIA KRITHARA, CHRISTOFOROS NIKOLAOU, GIORGOS PALIOURAS, YANNIS ALMIRANTIS, GEORGE GIANNAKOPOULOS: <i>Analysis and Classification of Constrained DNA Elements with N-gram Graphs and Genomic Signatures</i> INKEN WOHLERS, MATHILDE LE BOUDIC-JAMIN, HRISTO DJIDJEV, GUNNAR W. KLAU, RUMEN ANDONOV: <i>Exact Protein Structure Classification Using the Maximum Contact Map Overlap Metric</i> TOMOHIKO OHTSUKI, NAOKI NARIAI, KANAME KOJIMA, TAKAHIRO MIMORI, YUKUTO SATO, YOSUKE KAWAI, YUMI YAMAGUCHI-KABATA, TESTUO SHIBUYA, MASAO NAGASAKI: <i>SVEM: A Structural Variant Estimation Method using Multi-Mapped Reads on Breakpoints</i>
11:15 – 11:45	Coffee Break
11:45 – 13:00 <i>Uwe Ohler</i>	CLAIRE LEMAITRE, LIVIU CIORTUZ, PIERRE PETERLONGO: <i>Mapping-free and Assembly-free Discovery of Inversion Breakpoints from Raw NGS Reads</i> GIUSEPPE NARZISI, BUD MISHRA, MICHAEL C. SCHATZ: <i>On Algorithmic Complexity of Biomolecular Sequence Assembly Problem</i> IVO HEDTKE, IOANA LEMNIAN, MATTHIAS MÜLLER-HANNEMANN, IVO GROSSE: <i>On Optimal Read Trimming in Next Generation Sequencing and Its Complexity</i>
13:00 – 14:30	Lunch
14:30 – 15:20 <i>David A. Rosenblueth</i>	ANNIE CHATEAU, RODOLPHE GIROUDEAU: <i>Complexity and Polynomial-Time Approximation Algorithms around the Scaffolding Problem</i> ERNST ALTHAUS, ANDREAS HILDEBRANDT, ANNA KATHARINA HILDEBRANDT: <i>A Greedy Algorithm for Hierarchical Complete Linkage Clustering</i>
15:30	Visit of the City



City Hall



Castellers

Thursday, July 3	
9:00 – 9:50 Michael Galperin	UWE OHLER: <i>Decoding Non-coding Regulatory Regions in DNA and RNA</i> (II) – Invited Tutorial
9:50 – 10:00	Break
10:00 – 11:15 Ulisses Dias	CARLA NEGRI LINTZMAYER, ZANONI DIAS: <i>On Sorting of Signed Permutations by Prefix and Suffix Reversals and Transpositions</i>
	THIAGO DA SILVA ARRUDA, ULISSES DIAS, ZANONI DIAS: <i>Heuristics for the Sorting by Length-Weighted Inversions Problem on Signed Permutations</i>
	ALEXANDER GRIGORIEV, STEVEN KELK, NELA LEKIĆ: <i>On Low Treewidth Graphs and Supertrees</i>
11:15 – 11:45	Coffee Break
11:45 – 13:00 Kaname Kojima	CARLA NEGRI LINTZMAYER, ZANONI DIAS: <i>On the Diameter of Rearrangement Problems</i>
	AMINA NOOR, AITZAZ AHMAD, BILAL WAJID, ERCHIN SERPEDIN, MOHAMED NOUNOU, HAZEM NOUNOU: <i>A Closed-Form Solution for Transcription Factor Activity Estimation using Network Component Analysis</i>
	KANAME KOJIMA, NAOKI NARIAI, TAKAHIRO MIMORI, YUMI YAMAGUCHI-KABATA, YUKUTO SATO, YOSUKE KAWAI, MASAO NAGASAKI: <i>HapMonster: A Statistically Unified Approach for Variant Calling and Haplotyping Based on Phase-Informative Reads</i>
13:00	Closing

We acknowledge the support by:



ALGORITHMS FOR  
MOLECULAR BIOLOGY



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