

Lecture Notes in Bioinformatics

6577

Edited by S. Istrail, P. Pevzner, and M. Waterman

Editorial Board: A. Apostolico S. Brunak M. Gelfand

T. Lengauer S. Miyano G. Myers M.-F. Sagot D. Sankoff

R. Shamir T. Speed M. Vingron W. Wong

Subseries of Lecture Notes in Computer Science

Vineet Bafna S. Cenk Sahinalp (Eds.)

Research in Computational Molecular Biology

15th Annual International Conference, RECOMB 2011
Vancouver, BC, Canada, March 28-31, 2011
Proceedings



Springer

Series Editors

Sorin Istrail, Brown University, Providence, RI, USA
Pavel Pevzner, University of California, San Diego, CA, USA
Michael Waterman, University of Southern California, Los Angeles, CA, USA

Volume Editors

Vineet Bafna
University of California San Diego
EBU3b, #4218
9500 Gilman Drive
La Jolla, CA 92093-0404, USA
E-mail: vbafna@cs.ucsd.edu

S. Cenk Sahinalp
Simon Fraser University
School of Computing Science
8888 University Drive
Burnaby, BC, V5A 1S6, Canada
E-mail: cenk@cs.sfu.ca

ISSN 0302-9743 e-ISSN 1611-3349
ISBN 978-3-642-20035-9 e-ISBN 978-3-642-20036-6
DOI 10.1007/978-3-642-20036-6
Springer Heidelberg Dordrecht London New York

Library of Congress Control Number: 2011923333

CR Subject Classification (1998): J.3, H.2.8, I.2, F.2.2, I.6, F.2

LNCS Sublibrary: SL 8 – Bioinformatics

© Springer-Verlag Berlin Heidelberg 2011

This work is subject to copyright. All rights are reserved, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, re-use of illustrations, recitation, broadcasting, reproduction on microfilms or in any other way, and storage in data banks. Duplication of this publication or parts thereof is permitted only under the provisions of the German Copyright Law of September 9, 1965, in its current version, and permission for use must always be obtained from Springer. Violations are liable to prosecution under the German Copyright Law.

The use of general descriptive names, registered names, trademarks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

Typesetting: Camera-ready by author, data conversion by Scientific Publishing Services, Chennai, India

Printed on acid-free paper

Springer is part of Springer Science+Business Media (www.springer.com)

Preface

This volume contains the papers presented at RECOMB 2011: the 15th Annual International Conference on Research in Computational Molecular Biology held in Vancouver, Canada, during March 28–31, 2011. The RECOMB conference series was started in 1997 by Sorin Istrail, Pavel Pevzner, and Michael Waterman. RECOMB 2011 was hosted by the Lab for Computational Biology, Simon Fraser University, and took place at the Fairmont Hotel Vancouver. This year, 43 papers were accepted for presentation out of 153 submissions. The papers presented were selected by the Program Committee (PC) assisted by a number of external reviewers. Each paper was reviewed by at least three members of the PC, or by external reviewers, and there was an extensive Web-based discussion over a period of two weeks, leading to the final decisions. Accepted papers were also invited for submission to a special issue of the *Journal of Computational Biology*. The Highlights track, first introduced during RECOMB 2010, was continued, and resulted in 53 submissions, of which 5 were selected for oral presentation.

In addition to the contributed talks, RECOMB 2011 featured keynote addresses on the broad theme of Next-Generation Sequencing, and Genomics. The keynote speakers were Evan Eichler (University of Washington), Daphne Koller (Stanford University), Elaine Mardis (Washington University, St. Louis), Marco Marra (BC Genome Sciences Centre), Karen Nelson (J. Craig Venter Institute), and Jun Wang (Beijing Genomics Institute). Finally, RECOMB 2011 featured a special industry panel on Next-Generation Sequencing and Applications, chaired by Inanc Birol.

RECOMB 2011 was made possible by the dedication and hard work of many individuals and organizations. We thank the PC and external reviewers who helped form a high-quality conference program, the Organizing Committee, coordinated by Cedric Chauve, the Organization and Finance Chair and Amanda Casorso, the event coordinator, for hosting the conference and providing the administrative, logistic, and financial support. We also thank our sponsors, including Genome BC, CIHR, SFU, NSERC, BC Cancer Foundation, PIMS, MITACS, Ion Torrent and Pacific Biosystems, as well as our Industrial Relations Chair, Inanc Birol and Sponsorship Chair Martin Ester. Without them the conference would not have been financially viable. We thank the RECOMB Steering Committee, chaired by Martin Vingron, for accepting the challenge of organizing this meeting in Vancouver. Finally, we thank all the authors who contributed papers and posters, as well as the attendees of the conference for their enthusiastic participation.

February 2011

Vineet Bafna
S. Cenk Sahinalp

Conference Organization

Program Committee

Tatsuya Akutsu	Kyoto University, Japan
Can Alkan	University of Washington, USA
Nancy Amato	Texas A&M University, USA
Rolf Backofen	Albert Ludwigs University Freiburg, Germany
Joel Bader	Johns Hopkins University, USA
Vineet Bafna (Chair)	University of California, San Diego, USA
Nuno Bandeira	University of California, San Diego, USA
Vikas Bansal	Scripps Translational Science Institute, USA
Ziv Bar-Joseph	Carnegie Mellon University, USA
Bonnie Berger	Massachusetts Institute of Technology, USA
Jadwiga Bienkowska	BiogenIdec, USA
Mathieu Blanchette	McGill University, Canada
Phil Bradley	Fred Hutchinson Cancer Research Center, USA
Michael Brent	Washington University in St. Louis, USA
Michael Brudno	University of Toronto, Canada
Lenore Cowen	Tufts University, USA
Colin Dewey	University of Wisconsin, Madison, USA
Dannie Durand	Carnegie Mellon University, USA
Eleazar Eskin	University of California, Los Angeles, USA
David Gifford	Massachusetts Institute of Technology, USA
Bjarni Halldorsson	Reykjavik University, Iceland
Eran Halperin	International Computer Science Institute, Berkeley, USA
Trey Ideker	University of California, San Diego, USA
Sorin Istrail	Brown University, USA
Tao Jiang	University of California, Riverside, USA
Simon Kasif	Boston University, USA
Mehmet Koyuturk	Case Western Reserve University, USA
Jens Lagergren	Royal Institute of Technology, Sweden
Thomas Lengauer	Max Planck Institute for Informatics, Germany
Michal Linial	The Hebrew University of Jerusalem, Israel
Satoru Miyano	University of Tokyo, Japan
Bernard Moret	EPFL, Switzerland
William Noble	University of Washington, USA
Lior Pachter	University of California, Berkeley, USA
Ron Pinter	Technion, Israel
Teresa Przytycka	National Institutes of Health, USA
Predrag Radivojac	Indiana University, USA
Ben Raphael	Brown University, USA

Knut Reinert	Freie Universität Berlin, Germany
Marie-France Sagot	INRIA, France
S. Cenk Sahinalp	Simon Fraser University, Canada
David Sankoff	University of Ottawa, Canada
Russell Schwartz	Carnegie Mellon University, USA
Eran Segal	Weizmann Institute of Science, Israel
Roded Sharan	Tel Aviv University, Israel
Adam Siepel	Cornell University, USA
Mona Singh	Princeton University, USA
Donna Slonim	Tufts University, USA
Terry Speed	Walter+Eliza Hall Institute, Australia
Haixu Tang	Indiana University, USA
Anna Tramontano	University of Rome, Italy
Alfonso Valencia	Spanish National Cancer Research Centre, Spain
Martin Vingron	Max Planck Institute for Molecular Genetics, Germany
Tandy Warnow	University of Texas, Austin, USA
Eric Xing	Carnegie Mellon University, USA
Jinbo Xu	Toyota Technology Institute, Chicago, USA
Michal Ziv-Ukelson	Ben Gurion University of the Negev, Israel

Steering Committee

Serafim Batzoglou	Stanford University, USA
Bonnie Berger	Massachusetts Institute of Technology, USA
Sorin Istrail	Brown University, USA
Michal Linial	The Hebrew University of Jerusalem, Israel
Martin Vingron (Chair)	Max Planck Institute for Molecular Genetics, Germany

Organizing Committee

Cedric Chauve (Finance Chair)	Simon Fraser University, Canada
Martin Ester (Sponsorship Chair)	Simon Fraser University, Canada
Inanc Birol (Industry Relations and Panels Chair)	BCGSC, Canada
Fiona Brinkman	Simon Fraser University, Canada
Jack Chen	Simon Fraser University, Canada
Artem Cherkasov	Prostate Centre, VGH, Canada
Colin Collins	Prostate Centre, VGH, Canada
Anne Condon	University of British Columbia, Canada
Steven Jones	BCGSC, Canada
Tamon Stephen	Simon Fraser University, Canada
Stas Volik	Prostate Centre, VGH, Canada
Wyeth Wasserman	University of British Columbia, Canada
Kay Wiese	Simon Fraser University, Canada

Previous RECOMB Meetings

Dates	Hosting Institution	Program Chair	Conference Chair
January 20-23, 1997 Santa Fe, NM, USA	Sandia National Lab	Michael Waterman	Sorin Istrail
March 22-25, 1998 New York, NY, USA	Mt. Sinai School of Medicine	Pavel Pevzner	Gary Benson
April 22-25, 1999 Lyon, France	INRIA	Sorin Istrail	Mireille Regnier
April 8-11, 2000 Tokyo, Japan	University of Tokyo	Ron Shamir	Satoru Miyano
April 22-25, 2001 Montreal, Canada	Université de Montreal	Thomas Lengauer	David Sankoff
April 18-21, 2002 Washington, DC, USA	Celera	Gene Myers	Sridhar Hannenhalli
April 10-13, 2003 Berlin, Germany	German Federal Ministry for Education and Research	Webb Miller	Martin Vingron
March 27-31, 2004 San Diego, USA	University of California, San Diego	Dan Gusfield	Philip E. Bourne
May 14-18, 2005 Boston, MA, USA	Broad Institute of MIT and Harvard	Satoru Miyano	Jill P. Mesirov and Simon Kasif
April 2-5, 2006 Venice, Italy	University of Padova	Alberto Apostolico	Concettina Guerra
April 21-25, 2007 San Francisco, CA, USA	QB3	Terry Speed	Sandrine Dudoit
March 30-April 2, 2008 Singapore, Singapore	National University of Singapore	Martin Vingron	Limsoon Wong
May 18-21, 2009 Tucson, AZ, USA	University of Arizona	Serafim Batzoglou	John Kececiloglu
August 12-15, 2010 Lisbon, Portugal	INESC-ID and Instituto Superior Técnico	Bonnie Berger	Arlindo Oliveira

External Reviewers

Andreotti, Sandro	Costa, Fabrizio
Arndt, Peter	Danko, Charles
Arvestad, Lars	Dao, Phuong
Atias, Nir	DasGupta, Bhaskar
Bebek, Gurkan	DeConde, Robert
Benos, Panayiotis	Del Pozo, Angela
Bercovici, Sivan	Do, Chuong
Bielow, Chris	Donmez, Nilgun
Borgwardt, Karsten	Dutkowski, Janusz
Caglar, Mehmet Umut	Edwards, Matthew
Cai, Yizhi	Ekenna, Chinwe
Cakmak, Ali	Elberfeld, Michael
Chalkidis, Georgios	Emde, Anne-Katrin
Chen, Ken	Erten, Sinan
Chitsaz, Hamid	Frank, Ari
Choi, Jeong-Hyeon	Fujita, Andre
Choi, Sang Chul	Furlanello, Cesare
Clark, Wyatt	Furlotte, Nicholas
Condon, Anne	Gitter, Anthony
Conrad, Tim	Goldenberg, Anna

Gomez, Gonzalo
 Gonzalez-Izarzugaza, Jose Maria
 Gottlieb, Assaf
 Gronau, Ilan
 Haas, Stefan
 Hajirasouliha, Iman
 Han, Buhm
 Hannenhalli, Sridhar
 Hannum, Gregory
 Hansen, Niels
 He, Dan
 He, Xin
 Hildebrandt, Andreas
 Hofree, Matan
 Holtgrewe, Manuel
 Hormozdiari, Fereydoun
 Hosur, Raghavendra
 Hower, Valerie
 Huson, Daniel
 Iqbal, Zam
 Jacob, Arpith
 Jiang, Rui
 Jiao, Dazhi
 Ji, Chao
 Kamisetty, Hetunandan
 Kang, Eun Yong
 Kang, Hyun Min
 Karakoc, Emre
 Kayano, Mitsunori
 Kelleher, Neil
 Kim, Sangtae
 Kim, Sun
 Koller, Daphne
 Krause, Roland
 Kundaje, Anshul
 Kuo, Dwight
 Lacroix, Vincent
 Lan, Alex
 Lange, Sita
 Lasserre, Julia
 Lee, Byoungkoo
 Lee, Seunghak
 Le, Hai-Son
 Lengauer, Thomas
 Lenhof, Hans-Peter

Lin, Tien-ho
 Li, Sujun
 Liu, Xuejun
 Liu, Yu
 Li, Yong
 Loh, Po-Ru
 Lopez, Gonzalo
 Lozano, Jose A.
 Lugo-Martinez, Jose
 Magger, Oded
 Maier, Ezekial
 Manavi, Kasra
 Martins, Andre
 Maticzka, Daniel
 Mayampurath, Anoop
 McPherson, Andrew
 Medvedev, Paul
 Melsted, Pall
 Menconi, Giulia
 Milo, Nimrod
 Milo, Ron
 Möhl, Mathias
 Mongiovì, Misael
 Murali, T.M.
 Nath, Shuvra
 Nibbe, Rod K.
 Niida, Atsushi
 Novembre, John
 O'Donnell, Charles
 Ofra, Yanay
 Owen, Megan
 Patel, Vishal
 Pejavar, Vikas
 Peterlongo, Pierre
 Pevzner, Pavel
 Pinhas, Tamar
 Pisanti, Nadia
 Platts, Adrian
 Pop, Mihai
 Rahman, Atif
 Rausell, Antonio
 Reeder, Christopher
 Reynolds, Sheila
 Ritz, Anna
 Robert, Adam

Roch, Sebastien
Rolfe, Alex
Saglam, Mert
Salari, Raheleh
Schlicker, Andreas
Schulz, Marcel
Schulz, Marcel
Schweiger, Regev
Scornavacca, Celine
Sennblad, Bengt
Shibuya, Tetsuo
Shiraishi, Yuichi
Shlomi, Tomer
Shringarpure, Suyash
Sindi, Suzanne
Singer, Meromit
Singh, Ajit
Singh, Rohit
Siragusa, Enrico
Sjostrand, Joel
Snir, Sagi
Sommer, Ingolf
Spencer, Sarah
Spivak, Marina
Srivasa, Rohith
Steinhoff, Christine
Sul, Jae Hoon
Sutto, Ludovico
Szczyrek, Ewa
Tamada, Yoshinori
Tanaseichuk, Olga

Tesler, Glenn
Thomas, Shawna
Thompson, James
Torda, Andrew
Ulitsky, Igor
Veksler-Lublinsky, Isana
Viksna, Juris
Volouev, Anton
Waldispühl, Jérôme
Wang, Jian
Whitney, Joseph
Will, Sebastian
Wu, Wei
Wu, Yufeng
Xie, Minzhu
Xin, Fuxiao
Yanover, Chen
Ye, Chun
Yeger-Lotem, Esti
Yeh, Hsin-Yi
Yooseph, Shibu
Yosef, Nir
Yu, Chuan-Yih
Zaitlen, Noah
Zakov, Shay
Zakov, Shay
Zhang, Shaojie
Zhang, Xiuwei
Zinmann, Guy
Zotenko, Elena

Table of Contents

Bacterial Community Reconstruction Using Compressed Sensing	1
<i>Amnon Amir and Or Zuk</i>	
Constrained De Novo Sequencing of Peptides with Application to Conotoxins	16
<i>Swapnil Bhatia, Yong J. Kil, Beatrix Ueberheide, Brian Chait, Lemmuel L. Tayo, Lourdes J. Cruz, Bingwen Lu, John R. Yates III, and Marshall Bern</i>	
Metabolic Network Analysis Demystified	31
<i>Leonid Chindelevitch, Aviv Regev, and Bonnie Berger</i>	
Causal Reasoning on Biological Networks: Interpreting Transcriptional Changes (Extended Abstract)	34
<i>Leonid Chindelevitch, Daniel Ziemek, Ahmed Enayetallah, Ranjit Randhawa, Ben Sidders, Christoph Brockel, and Enoch Huang</i>	
Hapsembler: An Assembler for Highly Polymorphic Genomes	38
<i>Nilgun Donmez and Michael Brudno</i>	
Discovery and Characterization of Chromatin States for Systematic Annotation of the Human Genome	53
<i>Jason Ernst and Manolis Kellis</i>	
Disease Gene Prioritization Based on Topological Similarity in Protein-Protein Interaction Networks	54
<i>Sinan Erten, Gurkan Bebek, and Mehmet Koyutürk</i>	
Understanding Gene Sequence Variation in the Context of Transcription Regulation in Yeast	69
<i>Irit Gat-Viks, Renana Meller, Martin Kupiec, and Ron Shamir</i>	
Identifying Branched Metabolic Pathways by Merging Linear Metabolic Pathways	70
<i>Allison P. Heath, George N. Bennett, and Lydia E. Kavraki</i>	
A Probabilistic Model For Sequence Alignment with Context-Sensitive Indels	85
<i>Glenn Hickey and Mathieu Blanchette</i>	
Simultaneous Structural Variation Discovery in Multiple Paired-End Sequenced Genomes	104
<i>Fereydown Hormozdiari, Iman Hajirasouliha, Andrew McPherson, Evan E. Eichler, and S. Cenk Sahinalp</i>	

Variable Selection through Correlation Sifting	106
<i>Jim C. Huang and Nebojsa Jojic</i>	
Weighted Genomic Distance Can Hardly Impose a Bound on the Proportion of Transpositions	124
<i>Shuai Jiang and Max A. Alekseyev</i>	
PSAR: Measuring Multiple Sequence Alignment Reliability by Probabilistic Sampling (Extended Abstract)	134
<i>Jaebum Kim and Jian Ma</i>	
Pedigree Reconstruction Using Identity by Descent	136
<i>Bonnie Kirkpatrick, Shuai Cheng Li, Richard M. Karp, and Eran Halperin</i>	
A Quantitative Model of Glucose Signaling in Yeast Reveals an Incoherent Feed Forward Loop Leading to a Specific, Transient Pulse of Transcription	153
<i>Sooraj Kuttykrishnan, Jeffrey Sabina, Laura Langton, Mark Johnston, and Michael R. Brent</i>	
Inferring Mechanisms of Compensation from E-MAP and SGA Data Using Local Search Algorithms for Max Cut	154
<i>Mark D.M. Leiserson, Diana Tatar, Lenore J. Cowen, and Benjamin J. Hescott</i>	
IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly (Extended Abstract)	168
<i>Wei Li, Jianxing Feng, and Tao Jiang</i>	
Haplotype Reconstruction in Large Pedigrees with Many Untyped Individuals	189
<i>Xin Li and Jing Li</i>	
Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs	204
<i>Tien-ho Lin, Ziv Bar-Joseph, and Robert F. Murphy</i>	
A Geometric Arrangement Algorithm for Structure Determination of Symmetric Protein Homo-oligomers from NOEs and RDCs	222
<i>Jeffrey W. Martin, Anthony K. Yan, Chris Bailey-Kellogg, Pei Zhou, and Bruce R. Donald</i>	
Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers	238
<i>Paul Medvedev, Son Pham, Mark Chaisson, Glenn Tesler, and Pavel Pevzner</i>	
An Optimization-Based Sampling Scheme for Phylogenetic Trees	252
<i>Navodit Misra, Guy Blelloch, R. Ravi, and Russell Schwartz</i>	

Multiplex De Novo Sequencing of Peptide Antibiotics	267
<i>Hosein Mohimani, Wei-Ting Liu, Yu-Liang Yang, Susana P. Gaudêncio, William Fenical, Pieter C. Dorrestein, and Pavel A. Pevzner</i>	
Fractal and Transgenerational Genetic Effects on Phenotypic Variation and Disease Risk (Invited Talk)	282
<i>Joe Nadeau</i>	
AREM: Aligning Short Reads from ChIP-Sequencing by Expectation Maximization	283
<i>Daniel Newkirk, Jacob Biesinger, Alvin Chon, Kyoko Yokomori, and Xiaohui Xie</i>	
Blocked Pattern Matching Problem and Its Applications in Proteomics	298
<i>Julio Ng, Amihood Amir, and Pavel A. Pevzner</i>	
A Three-Dimensional Model of the Yeast Genome	320
<i>William Noble, Zhi-jun Duan, Mirela Andronescu, Kevin Schutz, Sean McIlwain, Yoo Jung Kim, Choli Lee, Jay Shendure, Stanley Fields, and C. Anthony Blau</i>	
Optimization of Combinatorial Mutagenesis	321
<i>Andrew S. Parker, Karl E. Griswold, and Chris Bailey-Kellogg</i>	
Seeing More Is Knowing More: V3D Enables Real-Time 3D Visualization and Quantitative Analysis of Large-Scale Biological Image Data Sets	336
<i>Hanchuan Peng and Fuhui Long</i>	
T-IDBA: A de novo Iterative de Bruijn Graph Assembler for Transcriptome (Extended Abstract)	337
<i>Yu Peng, Henry C.M. Leung, S.M. Yiu, and Francis Y.L. Chin</i>	
Experiment Specific Expression Patterns	339
<i>Tobias Petri, Robert Küffner, and Ralf Zimmer</i>	
Geometric Interpretation of Gene Expression by Sparse Reconstruction of Transcript Profiles	355
<i>Yosef Prat, Menachem Fromer, Michal Linial, and Nathan Linial</i>	
A Ribosome Flow Model for Analyzing Translation Elongation (Extended Abstract)	358
<i>Shlomi Reuveni, Isaac Meilijson, Martin Kupiec, Eytan Ruppin, and Tamir Tuller</i>	

Design of Protein-Protein Interactions with a Novel Ensemble-Based Scoring Algorithm	361
<i>Kyle E. Roberts, Patrick R. Cushing, Prisca Boisguerin, Dean R. Madden, and Bruce R. Donald</i>	
Computing Fragmentation Trees from Metabolite Multiple Mass Spectrometry Data	377
<i>Kerstin Scheubert, Franziska Hufsky, Florian Rasche, and Sebastian Böcker</i>	
Metric Labeling and Semi-metric Embedding for Protein Annotation Prediction	392
<i>Emre Sefer and Carl Kingsford</i>	
Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models	408
<i>Solomon Shenker, Charles W. O'Donnell, Srinivas Devadas, Bonnie Berger, and Jérôme Waldispühl</i>	
Optimally Orienting Physical Networks	424
<i>Dana Silverbush, Michael Elberfeld, and Roded Sharan</i>	
Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences	437
<i>Song Gao, Niranjan Nagarajan, and Wing-Kin Sung</i>	
Increasing Power of Groupwise Association Test with Likelihood Ratio Test	452
<i>Jae Hoon Sul, Buhm Han, and Eleazar Eskin</i>	
Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-loci and Algorithms for Optimal Tagging SNP Selection	468
<i>Ryan Tarpine, Fumei Lam, and Sorin Istrail</i>	
Protein Loop Closure Using Orientational Restraints from NMR Data	483
<i>Chittaranjan Tripathy, Jianyang Zeng, Pei Zhou, and Bruce Randall Donald</i>	
<i>De Novo</i> Discovery of Mutated Driver Pathways in Cancer	499
<i>Fabio Vandin, Eli Upfal, and Benjamin J. Raphael</i>	
An Unbiased Adaptive Sampling Algorithm for the Exploration of RNA Mutational Landscapes under Evolutionary Pressure	501
<i>Jérôme Waldispühl and Yann Ponty</i>	
Nonparametric Combinatorial Sequence Models	516
<i>Fabian L. Wauthier, Michael I. Jordan, and Nebojsa Jojic</i>	

Algorithms for MDC-Based Multi-locus Phylogeny Inference.....	531
<i>Yun Yu, Tandy Warnow, and Luay Nakhleh</i>	
Rich Parameterization Improves RNA Structure Prediction.....	546
<i>Shay Zakov, Yoav Goldberg, Michael Elhadad, and Michal Ziv-Ukelson</i>	
A Bayesian Approach for Determining Protein Side-Chain Rotamer Conformations Using Unassigned NOE Data	563
<i>Jianyang Zeng, Kyle E. Roberts, Pei Zhou, and Bruce R. Donald</i>	
Author Index	579