Lecture Notes in Bioinformatics 7262
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

Benny Chor (Ed.)

Research in Computational Molecular Biology

16th Annual International Conference, RECOMB 2012
Barcelona, Spain, April 21-24, 2012
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 Editor

Benny Chor
Tel-Aviv University
School of Computer Science
69978 Tel-Aviv, Israel
E-mail: benny@cs.tau.ac.il

ISSN 0302-9743 e-ISSN 1611-3349
ISBN 978-3-642-29626-0 e-ISBN 978-3-642-29627-7
DOI 10.1007/978-3-642-29627-7
Springer Heidelberg Dordrecht London New York

Library of Congress Control Number: 2012935493

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

LNCS Sublibrary: SL 8 – Bioinformatics

© Springer-Verlag Berlin Heidelberg 2012
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 2012, the 16th Annual International Conference on Research in Computational Molecular Biology, held in Barcelona during April 21–24, 2012. The RECOMB conference series was started in 1997 by Sorin Istrail, Pavel Pevzner, and Michael Waterman. RECOMB 2012 was hosted by the Centre for Genomic Regulation (CRG), and took place at the Fira Palace hotel, Barcelona. This year, 31 papers were accepted for presentation out of 200 submissions. The papers presented were selected by the Program Committee (PC), with the help of many external reviewers. Each paper was reviewed by at least three members of the PC, or by external reviewers. Following the initial reviews, there was a vivid and extensive e-mail-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, continued. Works published or accepted for publication in a journal during the last 15 months were eligible for submission. There were 42 submissions, and 6 were selected for oral presentation.

In addition to the contributed and highlight talks, RECOMB 2012 featured five keynote addresses on a broad theme of life science and computational biology. The keynote speakers were Richard Durbin (The Wellcome Trust Sanger Institute, UK), Eileen Furlong (Genome Biology Unit, EMBL, Germany), Thomas Gingeras (Cold Spring Harbor Laboratory, USA), Alfonso Valencia (National Cancer Research Centre, Spain), and Ada E. Yonath (Department of Structural Biology, Weizmann Institute of Science, Israel). Finally, RECOMB 2012 featured an NSF-sponsored special session on emerging areas and challenges in computational biology. This session was initiated by Mitra Basu (NSF, USA) and Mona Singh (Princeton University, USA). Five speakers were invited to give talks in this session and participate in a follow-up panel. They were Dirk Evers (UK), Christina Leslie (Memorial Sloan-Kettering Cancer Center, USA), Laxmi Parida (IBM, USA), Teresa Przytycka (NIH–NLM–NCBI, USA), and Amos Tanay (Weizmann Institute of Science, Israel).

RECOMB 2012 would not have been possible without the dedication, hard work, and substantial investment 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 Roderic Guigó, the Organization and Finance Chair, and Blanka Wysocka, the event coordinator, for hosting the conference and providing the administrative, logistic, and financial support. We also thank our sponsors, including the CRG (Centre for Genomic Regulation), the MICINN (Spanish Ministry of Science and Innovation), the ISCB (International Society for Computational Biology), BioMed Central, CRC Press, Cambridge University Press, the INB (Spanish Institute

of Bioinformatics), and the NSF (USA National Science Foundation). Without them the conference would not have been financially viable. We thank all the authors who contributed papers and posters, as well as the attendees of the conference for their enthusiastic participation. Finally, I would like to personally thank Roderic Guigó and Blanka Wysocka for the smooth cooperation we had regarding various organization details, and Michal Linial (Steering Committee), Martin Vingron (Chair of the Steering Committee), Bonnie Berger, and Vineet Bafna (Program Committee Chairs of RECOMB 2010 and 2011, respectively), for numerous discussions, helpful tips, and advice.

February 2012 Benny Chor

Conference Organization

Program Committee

Tatsuya Akutsu	Kyoto University
Rolf Backofen	University of Freiburg, Germany
Vineet Bafna	UC San Diego, USA
Nuno Bandeira	UC San Diego, USA
Vikas Bansal	Scripps Translational Science Institute, USA
Bonnie Berger	Massachusetts Institute of Technology, USA
Mathieu Blanchette	McGill University, Canada
Elhanan Borenstein	University of Washington, USA
Michael Brudno	University of Toronto, Canada
Benny Chor (Chair)	Tel Aviv University, Israel
Lenore Cowen	Tufts University, USA
Eleazar Eskin	UC Los Angeles, USA
Nir Friedman	The Hebrew University of Jerusalem, Israel
David Gifford	Massachusetts Institute of Technology, USA
Bjarni Halldorsson	Reykjavik University, Iceland
Eran Halperin	Tel Aviv University, Israel, and ICSI, Berkeley, USA
Alexander Hartemink	Duke University, USA
Barbara Holland	University of Tasmania, Australia
Katharina Huber	University of East Anglia, UK
Daniel Huson	University of Tübingen, Germany
Sorin Istrail	Brown University, USA
Mehmet Koyuturk	Case Western Reserve University, USA
Jens Lagergren	KTH Royal Institute of Technology, Sweden
Thomas Lengauer	Max Planck Institute for Informatics, Germany
Michal Linial	The Hebrew University of Jerusalem, Israel
Navodit Misra	Max Planck Institute for Molecular Genetics, Germany
Satoru Miyano	University of Tokyo, Japan
Luay Nakhleh	Rice University, USA
William Stafford Noble	University of Washington, USA
Nadia Pisanti	Università di Pisa, Italy
Teresa Przytycka	NIH, USA
Mark A. Ragan	The University of Queensland, Australia
Ben Raphael	Brown University, USA
Knut Reinert	Freie Universität Berlin, Germany
Marie-France Sagot	Université de Lyon, France

S. Cenk Sahinalp	Simon Fraser University, Canada
David Sankoff	University of Ottawa, Canada
Russell Schwartz	Carnegie Mellon University, USA
Charles Semple	University of Canterbury, New Zealand
Ron Shamir	Tel Aviv University, Israel
Mona Singh	Princeton University, USA
Sagi Snir	University of Haifa, Israel
Jens Stoye	Bielefeld University, Germany
Fengzhu Sun	University of Southern California, USA
Amos Tanay	The Weizmann Institute of Science, Israel
Haixu Tang	Indiana University, USA
Anna Tramontano	Sapienza University, Italy
Martin Vingron	Max Planck Institute for Molecular Genetics, Germany
Jerome Waldispuhl	McGill University, Canada
Yufeng Wu	University of Connecticut, USA
Jinbo Xu	Toyota Tech. Inst. at Chicago, USA
Zohar Yakhini	Agilent Technologies and the Technion, Israel
Michal Ziv-Ukelson	Ben-Gurion University, Israel

Steering Committee

Vineet Bafna	UC San Diego, USA
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

Josep F Abril	Universitat de Barcelona, Spain
Francisco Cámara	CRG, Spain
Eduardo Eyras	UPF, Spain
Pedro Ferreira	CRG, Spain
Toni Gabaldón	CRG, Spain
Roderic Guigó (Chair)	CRG, Spain
Cédric Nortedame	CRG, Spain
Gabriel Valiente	Univ. Politècnica de Catalunya, Spain
Blanka Wysocka	CRG, Spain

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 Kececioglu
August 12-15, 2010 Lisbon, Portugal	INESC-ID and Instituto Superior Técnico	Bonnie Berger	Arlindo Oliveira
March 28-31, 2011 Vancouver, Canada	Lab for Computational Biology, Simon Fraser University	Vineet Bafna	S. Cenk Sahinalp

External Reviewers

Akey, Josh
Alkan, Can
Allali, Julien
Altmann, Andre
Ander, Christina
Andreotti, Sandro
Arndt, Peter
Arvestad, Lars
Aviran, Sharon
Ay, Ferhat
Bachmat, Eitan
Backoffen, Rolf
Bader, Gary
Bansal, Mukul
Bar, Amir
Baumbach, Jan
Beiko, Robert
Ben Bassat, Ilan
Ben-Dor, Amir
Ben-Hur, Asa
Benyamini, Hadar
Bernstein, Lars
Berry, Vincent
Birmele, Etienne
Bliven, Spencer
Böcker, Sebastian
Caglar, Mehmet Umut
Capra, Tony
Carmel, Liran
Carr, Rogan
Catanzaro, Daniele
Chen, Quan
Chen, Yang-Ho
Chinappi, Mauro
Chiu, Hsuan-Chao
Cho, Dongyeon
Cho, Sungje
Chowdhury, Salim

Cloonan, Nicole
Cohen, Reuven
Colbourn, Charles
Comin, Matteo
Costa, Fabrizio
Da Fonseca, P.G.S.
Dao, Phuong
Dasgupta, Bhaskar
Daskalakis, Constantinos
David, Matei
Davis, Melissa
Denise, Alain
Diallo, Abdoulaye
Dinitz, Yefim
Donmez, Nilgun
Du, Xiangjun
Dörr, Daniel
Edwards, Matthew
El-Mabrouk, Nadia
Emde, Anne-Katrin
Erten, Sinan
Farahani, Hossein
Ferreira, Rui
Fertin, Guillaume
Frånberg, Mattias
Furlotte, Nicholas
Furman, Ora
Gaspin, Christine
Geiger, Dan
Giegerich, Robert
Goeke, Jonathan
Golan, David
Gophna, Uri
Gorecki, Pawel
Gottlieb, Assaf
Greenblum, Sharon
Grossi, Roberto
Guidoni, Leonardo
Guindon, Stephane
Guthals, Adrian
Habin, Naomi
Hach, Faraz
Hajirasouliha, Iman
Halloran, John
Hamilton, Nicholas
Han, Buhm
Hashimoto, Tatsunori
Hayashida, Morihiro
He, Dan
Hogan, James
Hoinka, Jan
Holtgrewe, Manuel
Hormozdiari, Farhad
Hormozdiari, Fereydoun
Howbert, Jeff
Hu, Jialu
Huang, Yang
Imoto, Seiya
Jaenicke, Sebastian
Joo, Jong Wha
Kamburov, Atanas
Kang, Eun Yong
Kang, John
Kaplan, Tommy
Kato, Yuki
Kayano, Mitsunori
Keasar, Chen
Kenigsberg, Effi
Kim, Sangtae
Kim, Yoo-Ah
Kinsella, Marcus
Kirkpatrick, Bonnie
Klaere, Steffen
Kostem, Emrah
Krause, Roland
Kundu, Kousik
Laframboise, Thomas
Landan, Gilad
Lange, Sita
Lasserre, Julia
Lee, Heewook
Lee, Hyunju
Lee, Su-In
Lempel, Noa
Levin, Alex
Levitt, Michael
Levy, Roie
Li, Jing
Lingjaerde, Ole-Christian
Linial, Nathan

Linz, Simone
Lipson, Doron
Liu, Kevin
Liu, Zhenqiu
Loytynoja, Ari
Lu, Bingwen
Lubling, Yaniv
Luccio, Fabrizio
Mahmoody, Ahmad
Mahony, Shaun
Mandoiu, Ion
Margelevicius, Mindaugas
Maticzka, Daniel
Mayrose, Itay
Mcilwain, Sean
Mckenney, Mark
Mcpherson, Andrew
Medvedev, Paul
Melsted, Pall
Mendelson-Cohen, Netta
Mendes, Nuno
Mezlini, Aziz
Milazzo, Paolo
Milo, Nimrod
Misra, Navodit
Moll, Mark
Mysickova, Alena
Nachman, Iftach
Nair, Nishanth
Navarro, Gonzalo
Navon, Roy
Niida, Atsushi
Numanagic, Ibrahim
O'Donnell, Charles
Oesper, Layla
Oostenbrink, Chris
Ophir, Ron
Orenstein, Yaron
Oshlack, Alicia
Pagli, Linda
Park, Hyun Jung
Parrish, Nathaniel
Pasaniuc, Bogdan
Peng, Jian
Peterlongo, Pierre
Pfeifer, Nico
Picard, Franck
Pinhas, Tamar
Preisner, Robert
Press, Maximilian
Privman, Eyal
Przulj, Natasa
Qi, Yanjun
Rahnenführer, Jörg
Raimondo, Domenico
Rawitz, Droro
Renda, M. Elena
Roch, Sebastien
Rohs, Remo
Rose, Dominic
Roshan, Usman
Rosset, Saharon
Rozov, Roye
Rubinstein, Nimrod
Ruffalo, Matthew
Ruths, Troy
Safer, Hershel
Sankararaman, Sriram
Savel, Daniel
Schlicker, Andreas
Schnall-Levin, Michael
Schoenhuth, Alexander
Scornavacca, Celine
Serin, Akdes
Shatkay, Hagit
Sheridan, Paul
Shibuya, Tetsuo
Shimamura, Teppei
Shomron, Noam
Sindi, Suzanne
Singer, Meromit
Singh, Ajit
Sjöstrand, Joel
Smoly, Ilan
Snedecor, June
Sommer, Ingolf
Souaiaia, Tade
Spivak, Marina
Stacho, Juraj
Steel, Mike

Steinfeld, Israel
Subramanian, Ayshwarya
Sul, Jae Hoon
Swanson, Lucas
Szczurek, Ewa
Sze, Sing-Hoi
Taft, Ryan
Tamada, Yoshinori
Tamura, Takeyuki
Tannier, Eric
Thevenin, Annelyse
Thomaseth, Karl
Timmer, Jens
Tofigh, Ali
Tolosi, Laura
Tompa, Martin
Trappe, Kathrin
Tsourakakis, Charalampos
Tu, Zhidong
Tuller, Tamir
Tzfadia, Oren
Valas, Ruben
Van Iersel, Leo
Vandin, Fabio
Veksler-Lublinsky, Isana
Vialette, Stéphane
Wagner, Allon
Wan, Lin
Wang, Jian
Wang, Mingxun
Wang, Xiaowo
Wang, Zhanyong
Warnow, Tandy
Will, Sebastian
Wittler, Roland
Wojtowicz, Damian
Wolber, Gerhard
Wolf, Lior
Wolfson, Haim
Wu, Yin
Wuchty, Stefan
Xu, Andrew Wei
Yamaguchi, Rui
Yang, Sichun
Yang, Wen-Yun
Yassour, Moran
Yasuda, Tomohiro
Yavas, Gokhan
Yeger- Lotem, Esti
Yeger-Lotem, Esti
Yosef, Nir
Zaitlen, Noah
Zakov, Shay
Zerbino, Daniel
Zhang, Jin
Zhang, Shaojie
Zhou, Wanding
Zhu, Yun
Zimmer, Ralf
Zotenko, Elena
Zwickl, Derrick

Table of Contents

Protein Structure by Semidefinite Facial Reduction 1
Babak Alipanahi, Nathan Krislock, Ali Ghodsi, Henry Wolkowicz, Logan Donaldson, and Ming Li

Ancestry Inference in Complex Admixtures via Variable-Length Markov Chain Linkage Models 12
Sivan Bercovici, Jesse M. Rodriguez, Megan Elmore, and Serafim Batzoglou

Charge Group Partitioning in Biomolecular Simulation 29
Stefan Canzar, Mohammed El-Kebir, Rene Pool, Khaled Elbassioni, Alpesh K. Malde, Alan E. Mark, Daan P. Geerke, Leen Stougie, and Gunnar W. Klau

Increased Methylation Variation in Epigenetic Domains across Cancer Types 44
Hector Corrada Bravo

Estimating the Accuracy of Multiple Alignments and its Use in Parameter Advising 45
Dan F. DeBlasio, Travis J. Wheeler, and John D. Kececioglu

Quantifying the Dynamics of Coupled Networks of Switches and Oscillators 60
Matthew R. Francis and Elana J. Fertig

lobSTR: A Short Tandem Repeat Profiler for Personal Genomes 62
Melissa Gymrek, David Golan, Saharon Rosset, and Yaniv Erlich

Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data 64
Dan He, Buhm Han, and Eleazar Eskin

BALLAST: A Ball-Based Algorithm for Structural Motifs 79
Lu He, Fabio Vandin, Gopal Pandurangan, and Chris Bailey-Kellogg

Evolution of Genome Organization by Duplication and Loss: An Alignment Approach 94
Patrick Holloway, Krister Swenson, David Ardell, and Nadia El-Mabrouk

LoopWeaver – Loop Modeling by the Weighted Scaling of Verified Proteins 113
Daniel Holtby, Shuai Cheng Li, and Ming Li

A Robust Method for Transcript Quantification with RNA-seq Data 127
Yan Huang, Yin Hu, Corbin D. Jones, James N. MacLeod, Derek Y. Chiang, Yufeng Liu, Jan F. Prins, and Jinze Liu

Modeling the Breakage-Fusion-Bridge Mechanism: Combinatorics and Cancer Genomics 148
Marcus Kinsella and Vineet Bafna

TrueSight: Self-training Algorithm for Splice Junction Detection Using RNA-seq 163
Yang Li, Hong-Mei Li, Paul Burns, Mark Borodovsky, Gene E. Robinson, and Jian Ma

Synthetic Sequence Design for Signal Location Search 165
Yaw-Ling Lin, Charles Ward, and Steven Skiena

The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation 180
Marc A. Marti-Renom

Discovery of Complex Genomic Rearrangements in Cancer Using High-Throughput Sequencing 181
Andrew McPherson, Chunxiao Wu, Alexander Wyatt, Sohrab Shah, Colin Collins, and S. Cenk Sahinalp

Network-Based Prediction and Analysis of HIV Dependency Factors 183
T.M. Murali, Matthew D. Dyer, David Badger, Brett M. Tyler, and Michael G. Katze

Structure-Guided Deimmunization of Therapeutic Proteins 184
Andrew S. Parker, Karl E. Griswold, and Chris Bailey-Kellogg

Evidence for Widespread Association of Mammalian Splicing and Conserved Long-Range RNA Structures 199
Dmitri Pervouchine, Ekaterina Khrameeva, Marina Pichugina, Olexii Nikolaienko, Mikhail Gelfand, Petr Rubtsov, and Andrei Mironov

Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly 200
Son K. Pham, Dmitry Antipov, Alexander Sirotkin, Glenn Tesler, Pavel A. Pevzner, and Max A. Alekseyev

Finding Maximum Colorful Subtrees in Practice 213
Imran Rauf, Florian Rasche, François Nicolas, and Sebastian Böcker

Recovering the Tree-Like Trend of Evolution Despite Extensive Lateral Genetic Transfer: A Probabilistic Analysis 224
Sebastien Roch and Sagi Snir

RESQUE: Network Reduction Using Semi-Markov Random Walk Scores for Efficient Querying of Biological Networks (Extended Abstract) 239
Sayed Mohammad Ebrahim Sahraeian and Byung-Jun Yoon

Detecting SNP-Induced Structural Changes in RNA: Application to Disease Studies 241
Raheleh Salari, Chava Kimchi-Sarfaty, Michael M. Gottesman, and Teresa M. Przytycka

A Model for Biased Fractionation after Whole Genome Duplication 244
David Sankoff, Chunfang Zheng, and Baoyong Wang

Exact Pattern Matching for RNA Structure Ensembles 245
Christina Schmiedl, Mathias Möhl, Steffen Heyne, Mika Amit, Gad M. Landau, Sebastian Will, and Rolf Backofen

Reconstructing Boolean Models of Signaling 261
Roded Sharan and Richard M. Karp

Alignment-Free Sequence Comparison Based on Next Generation Sequencing Reads: Extended Abstract 272
Kai Song, Jie Ren, Zhiyuan Zhai, Xuemei Liu, Minghua Deng, and Fengzhu Sun

Differential Oestrogen Receptor Binding is Associated with Clinical Outcome in Breast Cancer 286
Rory Stark

Simultaneous Reconstruction of Multiple Signaling Pathways *via* the Prize-Collecting Steiner Forest Problem 287
Nurcan Tuncbag, Alfredo Braunstein, Andrea Pagnani, Shao-Shan Carol Huang, Jennifer Chayes, Christian Borgs, Riccardo Zecchina, and Ernest Fraenkel

Function-Function Correlated Multi-Label Protein Function Prediction over Interaction Networks 302
Hua Wang, Heng Huang, and Chris Ding

Predicting Protein-Protein Interactions from Multimodal Biological Data Sources via Nonnegative Matrix Tri-Factorization 314
Hua Wang, Heng Huang, Chris Ding, and Feiping Nie

CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping 326
Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin, and Eleazar Eskin

Structure-Based Whole Genome Realignment Reveals Many Novel Non-coding RNAs 341
Sebastian Will, Michael Yu, and Bonnie Berger

Probabilistic Inference of Viral Quasispecies Subject to Recombination 342
Osvaldo Zagordi, Armin Töpfer, Sandhya Prabhakaran, Volker Roth, Eran Halperin, and Niko Beerenwinkel

Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm 355
ZhiZhuo Zhang, Cheng Wei Chang, Willy Hugo, Edwin Cheung, and Wing-Kin Sung

Author Index 371