

Lecture Notes in Bioinformatics

8452

Subseries of Lecture Notes in Computer Science

LNBI 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

LNBI Editorial Board

Alberto Apostolico

Georgia Institute of Technology, Atlanta, GA, USA

Søren Brunak

Technical University of Denmark, Kongens Lyngby, Denmark

Mikhail S. Gelfand

IITP, Research and Training Center on Bioinformatics, Moscow, Russia

Thomas Lengauer

Max Planck Institute for Informatics, Saarbrücken, Germany

Satoru Miyano

University of Tokyo, Tokyo, Japan

Eugene Myers

*Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden, Germany*

Marie-France Sagot

Université Lyon 1, Villeurbanne, France

David Sankoff

University of Ottawa, Ottawa, Canada

Ron Shamir

Tel Aviv University, Ramat Aviv, Tel Aviv, Israel

Terry Speed

*Walter and Eliza Hall Institute of Medical Research,
Melbourne, VIC, Australia*

Martin Vingron

Max Planck Institute for Molecular Genetics, Berlin, Germany

W. Eric Wong

University of Texas at Dallas, Richardson, TX, USA

More information about this series at <http://www.springer.com/series/5381>

Enrico Formenti · Roberto Tagliaferri
Ernst Wit (Eds.)

Computational Intelligence Methods for Bioinformatics and Biostatistics

10th International Meeting, CIBB 2013
Nice, France, June 20–22, 2013
Revised Selected Papers

Editors

Enrico Formenti
University Nice Sophia Antipolis
Sophia Antipolis
France

Ernst Wit
University of Groningen
AG Groningen
The Netherlands

Roberto Tagliaferri
University of Salerno
Fisciano
Italy

ISSN 0302-9743

ISSN 1611-3349 (electronic)

ISBN 978-3-319-09041-2

ISBN 978-3-319-09042-9 (eBook)

DOI 10.1007/978-3-319-09042-9

Library of Congress Control Number: 2014945214

LNCS Sublibrary: SL8 – Bioinformatics

Springer Cham Heidelberg New York Dordrecht London

© Springer International Publishing Switzerland 2014

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed. Exempted from this legal reservation are brief excerpts in connection with reviews or scholarly analysis or material supplied specifically for the purpose of being entered and executed on a computer system, for exclusive use by the purchaser of the work. Duplication of this publication or parts thereof is permitted only under the provisions of the Copyright Law of the Publisher's location, in its current version, and permission for use must always be obtained from Springer. Permissions for use may be obtained through RightsLink at the Copyright Clearance Center. Violations are liable to prosecution under the respective Copyright Law.

The use of general descriptive names, registered names, trademarks, service marks, 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.

While the advice and information in this book are believed to be true and accurate at the date of publication, neither the authors nor the editors nor the publisher can accept any legal responsibility for any errors or omissions that may be made. The publisher makes no warranty, express or implied, with respect to the material contained herein.

Printed on acid-free paper

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

Preface

This volume contains the proceedings of the International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2013), which was in its tenth edition this year. While many past editions were organized in Italy, from last year when the conference took place at the Methodist Research Institute, Houston (USA), the conference started an internationalization process. It coincided with a further enlargement of the spectrum of the scientific domains covered.

Indeed, the main scope of the CIBB meeting series is to provide a forum open to researchers from different disciplines to present and discuss problems concerning computational techniques in bioinformatics, systems biology, and medical and health informatics with a particular focus on neural networks, machine learning, fuzzy logic, and evolutionary computation methods.

This year CIBB was co-located and followed the PRIB (Pattern Recognition In Bioinformatics) conference and there were many authors who contributed to both conferences. As organizers of CIBB we would like to thank all the contributors and organizers of PRIB. There was also a common day between the two conferences. We hope that this was an occasion for new scientific collaborations and exchanges. Many thanks also go to the invited speakers: Sylvain Sené (Aix-Marseille Université, France) Anne Siegel (IRISA CNRS and Inria Rennes, France) and Ernst Wit (University of Groningen, The Netherlands) for their excellent talks.

This year 33 papers were selected for presentation at the conference, and each paper received two reports on average. A further reviewing process took place for the 19 papers that were selected to appear in this volume. The authors are spread over more than ten different countries: Algeria (3), Canada (2), France (18), Islamic Republic of Iran (4), Italy (55), The Netherlands (1), Norway (1), Romania (6), Taiwan (2), Tunisia (2), UK (6), and USA (7).

The editors would like to thank all the Program Committee members and the external reviewers both of the conference and post-conference version of the papers for their valuable work. We are also indebted to the chairs of the very interesting and successful special sessions (“Knowledge-Based Medicine” and “Data Integration and Analysis in Omic-Science”), which attracted even more contributions and attention.

A big thanks also to the munificent sponsors, and in particular to Nice Sophia Antipolis University, which made this event possible. And last but not least, the editors would also like to thank all the authors for the high quality of the papers they contributed and warmly invite them to submit their work to the next edition that will take place in Cambridge.

March 2013

Enrico Formenti
Roberto Tagliaferri
Ernst Wit

Organization

General Chairs

Enrico Formenti
Roberto Tagliaferri
Ernst Wit

Nice Sophia Antipolis University, France
University of Salerno, Italy
University of Groningen, The Netherlands

Special Sessions Chairs

Claudia Angelini
Elia Biganzoli
Clelia Di Serio
Alexandru Floares
Leif Peterson
Alfredo Vellido

IAC-CNR, Italy
Università degli Studi di Milano, Italy
Università Vita-Salute San Raffaele, Italy
Oncological Institute Cluj-Napoca, Romania
Houston Methodist Research Institute, USA
Universitat Politècnica de Catalunya, Spain

Program Committee

Federico Ambrogi
Sansanee Auephanwiriyaikul
Sanghamitra Bandyopadhyay
Gilles Bernot
Chengpeng Bi
Mario Cannataro
Virginio Cantoni
Xue-Wen Chen
Adele Cutler
Paolo Decuzzi
Angelo Facchiano
Leonardo Franco
Christoph Friedrich

Raffaele Giancarlo
Saman K. Halgamuge
Emmanuel Ifeachor
Mika Sato-Ilic
Paulo Lisboa
Vincenzo Manca
Elena Marchiori
Giancarlo Mauri

University of Milan, Italy
Chiang Mai University, Thailand
Indian Statistical Institute, Kolkata, India
Nice Sophia Antipolis University, France
Childrens Mercy Hospital, Kansas City, USA
University of Magna Graecia, Catanzaro, Italy
Università di Pavia, Italy
University of Kansas, Lawrence, USA
Utah State University, Logan, USA
TMHRI, Houston, Texas, USA
Istituto di Scienze dell'Alimentazione - CNR, Italy
University of Malaga, Spain
University of Applied Science and Arts,
Dortmund, Germany
University of Palermo, Italy
The University of Melbourne, Australia
University of Plymouth, UK
University of Tsukuba, Japan
Liverpool John Moores University, UK
Università di Verona, Italy
Radboud University, Nijmegen, The Netherlands
Università degli Studi di Milano-Bicocca, Italy

Luciano Milanese	ITB-CNR, Milan, Italy
Taishin Nomura	Osaka University, Osaka, Japan
Carlos-Andres Pena-Reyes	University of Applied Sciences Western Switzerland, Switzerland
Vassilis Plagianakos	University of Central Greece, Lamia, Greece
Riccardo Rizzo	ICAR-CNR, Palermo, Italy
Paolo Romano	National Cancer Research Institute, Genoa, Italy
Stefano Rovetta	University of Genova, Italy
Jianhua Ruan	University of Texas, San Antonio, USA
Luis Rueda	University of Windsor, Canada
Andrey Rzhetsky	University of Chicago, USA
Jennifer Smith	Boise State University, USA
Giorgio Valentini	University of Milan, Italy
Alfredo Vellido	Universidad Politecnica de Catalunya, Spain
Yanqing Zhang	Georgia State University, Atlanta, USA

Steering Committee

Thomas Back	Leiden University, The Netherlands
Pierre Baldi	University of California, Irvine, USA
Elia Biganzoli	University of Milan, Italy
Alexandru Floares	Oncological Institute Cluj-Napoca, Romania
Jon Garibaldi	University of Nottingham, UK
Nikola Kasabov	Auckland University of Technology, New Zealand
Francesco Masulli	University of Genova, Italy and Temple University, USA
Leif Peterson	TMHRI, Houston, Texas, USA
Roberto Tagliaferri	University of Salerno, Italy

Organizing Committee

Enrico Formenti (Chair)	Nice Sophia Antipolis University, France
Sandrine Julia	Nice Sophia Antipolis University, France
Corinne Jullien	Nice Sophia Antipolis University, France
Bruno Martin	Nice Sophia Antipolis University, France
Christophe Papazian	Nice Sophia Antipolis University, France
Julien Provillard	Nice Sophia Antipolis University, France
Magali Richir	Nice Sophia Antipolis University, France

External Reviewers

Claudia Angelini	Daniela De Canditiis
Gilles Bernot	Angelo Facchiano
Elia Biganzoli	Mario Guarracino

Michele La Rocca
Luca Manzoni
Francesco Masulli
Marco Muselli
Mathilde Noual

Nicolas Pasquier
Giancarlo Raiconi
Riccardo Rizzo
Ernst Wit

Sponsors

We thank very deeply the sponsors that made CIBB 2013 possible (alphabetical order):



Società Italiana di Bioinformatica



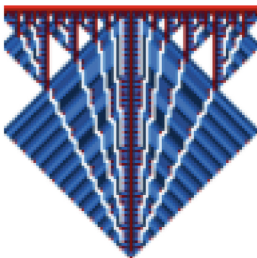
Centre National de la Recherche Scientifique



Dipartimento di Informatica,
Università di Salerno, Italy



Ecole Doctorale STIC



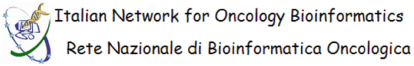
Projet ANR EMC (ANR-09-BLAN-0164)



Laboratoire d'Informatique, Signaux et Systèmes de Sophia Antipolis, France



INNS-SIG on Bioinformatics and Intelligence



Italian Network for Oncology Bioinformatics



Società Italiana REti Neuroniche

Contents

Keynote Speaker

- Dynamic Gaussian Graphical Models for Modelling Genomic Networks 3
Antonio Abbruzzo, Clelia Di Serio, and Ernst Wit

Bioinformatics Regular Session

- Molecular Docking for Drug Discovery: Machine-Learning Approaches
for Native Pose Prediction of Protein-Ligand Complexes. 15
Hossam M. Ashtawy and Nihar R. Mahapatra

- BioCloud Search EnGene: Surfing Biological Data on the Cloud 33
Nicoletta Dessì, Emanuele Pascariello, Gabriele Milia, and Barbara Pes

- Genomic Sequence Classification Using Probabilistic Topic Modeling 49
Massimo La Rosa, Antonino Fiannaca, Riccardo Rizzo, and Alfonso Urso

- Community Detection in Protein-Protein Interaction Networks
Using Spectral and Graph Approaches 62
Hassan Mahmoud, Francesco Masulli, Stefano Rovetta, and Giuseppe Russo

- Weighting Scheme Methods for Enhanced Genomic Annotation Prediction 76
Pietro Pinoli, Davide Chicco, and Marco Masseroli

- French Flag Tracking by Morphogenetic Simulation
Under Developmental Constraints 90
Abdoulaye Sarr, Alexandra Fronville, Pascal Ballet, and Vincent Rodin

Biostatistics Regular Session

- High-Dimensional Sparse Matched Case-Control and Case-Crossover Data:
A Review of Recent Works, Description of an R Tool and an Illustration
of the Use in Epidemiological Studies. 109
*Marta Avalos, Yves Grandvalet, H el ene Pouyes, Ludivine Orriols,
and Emmanuel Lagarde*

- Piecewise Exponential Artificial Neural Networks (PEANN) for Modeling
Hazard Function with Right Censored Data 125
Marco Fornili, Federico Ambrogi, Patrizia Boracchi, and Elia Biganzoli

Writing Generation Model for Health Care Neuromuscular System Investigation. 137
D. Impedovo, G. Pirlo, F.M. Mangini, D. Barbuzzi, A. Rollo, A. Balestrucci, S. Impedovo, L. Sarcinella, C. O'Reilly, and R. Plamondon

Clusters Identification in Binary Genomic Data: The Alternative Offered by Scan Statistics Approach. 149
Danilo Pellin and Clelia Di Serio

Special Session: Knowledge Based Medicine

Reverse Engineering Methodology for Bioinformatics Based on Genetic Programming, Differential Expression Analysis and Other Statistical Methods. 161
Corneliu T.C. Arsene, Denisa Ardevan, and Paul Bulzu

Integration of Clinico-Pathological and microRNA Data for Intelligent Breast Cancer Relapse Prediction Systems. 178
Adriana Birlutiu, Denisa Ardevan, Paul Bulzu, Camelia Pinte, and Alexandru Floares

Superresolution MUSIC Based on Marčenko-Pastur Limit Distribution Reduces Uncertainty and Improves DNA Gene Expression-Based Microarray Classification. 194
Leif E. Peterson

Special Session: Data Integration and Analysis in Omic-Science

Prediction of Single-Nucleotide Polymorphisms Causative of Rare Diseases. 213
Maria Brigida Ferraro and Mario Rosario Guarracino

A Framework for Mining Life Sciences Data on the Semantic Web in an Interactive, Graph-Based Environment 225
Artem Lysenko, Jacek Grzebyta, Matthew M. Hindle, Chris J. Rawlings, and Andrea Splendiani

Combining Not-Proper ROC Curves and Hierarchical Clustering to Detect Differentially Expressed Genes in Microarray Experiments 238
Stefano Parodi, Vito Pistoia, and Marco Muselli

Fast and Parallel Algorithm for Population-Based Segmentation of Copy-Number Profiles. 248
Guillem Rigall, Vincent Miele, and Franck Picard

Identification of Pathway Signatures in Parkinson’s Disease with Gene
Ontology and Sparse Regularization 259
*Margherita Squillario, Grzegorz Zycinski, Annalisa Barla,
and Alessandro Verri*

Author Index 275