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Editorial

ECCB 2014: The 13th European Conference on Computational Biology

This special issue includes the proceeding papers accepted for presentation at the 13th European Conference on Computational Biology (ECCB'14), to be held from September 7 to 10, 2014 at the Congress Center of Strasbourg, France. Details of the conference are available on the conference web site (www.eccb14.org) and will later be archived at eccb.isc-b.org/2014/.

ECCB is the top European conference in computational biology and bioinformatics, and together with ISMB (Intelligent Systems in Molecular Biology) and RECOMB (Research in Computational Molecular Biology), it is one of the major international conference series in this domain. The ECCB conferences gather hundreds of scientists working at the intersection of a broad range of disciplines including computer science, mathematics, biology and medicine. New challenges are now emerging in these fields with the recent advances in low-cost ultra-fast sequencing, bioimaging and bigdata. As a consequence, databases and software are evolving rapidly, and new algorithms are required to improve computational analyses of massive biological or biomedical data sets. Multi-scale integrative analyses are struggling to deal with the enormous complexity of biological systems modeling and the 'data deluge' that results from next-generation sequencing.

ECCB is held annually in a different country or region and incorporates the annual national or regional meeting where it is held. Every other year, it is held jointly with the ISMB conference. This year's conference incorporates the 14th French JOBIM ('Journées Ouvertes Biologie Informatique Mathématiques'), the annual meeting of the French bioinformatics community. Past editions of ECCB have been held in Berlin (Germany, with ISMB), Basel (Switzerland), Vienna (Austria, with ISMB), Ghent (Belgium), Stockholm (Sweden, with ISMB), Cagliari (Italia), Vienna (Austria, with ISMB), Eilat (Israel), Madrid (Spain), Glasgow (United Kingdom, with ISMB), Paris (France) and Saarbrücken (Germany).

The ECCB'14 conference features keynote lectures by distinguished speakers. The opening keynote lecture will be delivered by Nobel Prize laureate Jean-Marie Lehn (Strasbourg University, Nobel Prize in Chemistry in 1987). The following keynote speakers will be Patrick Aloy (Institute for Research in Biomedicine, Barcelona, Spain), Alice McHardy (Heinrich Heine University, Düsseldorf and Helmholtz Center for Infection Biology, Braunschweig, Germany), Ewan Birney (European Bioinformatics Institute, Hinxton, United Kingdom), Nada Lavrač (Jožef Stefan Institute and University of Nova Gorica, Slovenia), Doron Lancet (The Weizmann Institute of Science, Rehovot, Israel) and Eric Westhof (Strasbourg University, France).

The conference topics span all areas of methodological developments for computational biology and innovative applications of computational methods to molecular biology. This year the conference was organized in nine topic areas: 'Sequencing and sequence analysis for genomics'; 'Gene expression'; 'Pathways and molecular networks'; 'Computational systems biology'; 'Structural bioinformatics'; 'Evolution and population genomics'; 'Bioinformatics of health and disease'; 'Biological knowledge discovery from data, texts and bio-images'; 'Methods and technologies for computational biology'. Each topic area was assigned to two area chairs and the different areas were coordinated by the conference chairs.

Following the call for papers, we received 269 submissions, a 20% decrease compared with the record number of 340 submissions received at ECCB'12 in Basel. Within each area, the area chairs assigned papers to expert referees, taking care to avoid any conflict of interest. Together, the program committee (PC) was composed of 274 reviewers and 127 co-reviewers. In general, each paper was reviewed by three PC members. Only in a few cases just two referee reports could be secured. The whole process was carried out using the EasyChair multi-track conference reviewing system (www.easychair.org). This system allows discussion of the papers in cases of divergent reviews. After a consensus had been reached by the reviewers, a final selection was carried out area by area during a phone conference between the area chairs and the conference chairs. A total of 40 papers were conditionally accepted, pending revision. The authors had two weeks to modify their papers according to the suggestions made by the reviewers and to respond to the reviewers' comments. The area chairs examined the modified papers and authors' responses and testified that in all cases the reviewers' recommendations had been taken into account. In many cases, the authors had run confirmation analyses and we wish to thank them for these efforts that contribute to the success and reputation of the ECCB conference. It is worth noting that many authors expressed their gratitude to the reviewers for their comments and suggestions leading to significant improvements in their paper. We therefore wish to acknowledge the hard and painstaking work performed by the reviewers and co-reviewers over a short period of time. This work may seem frustrating when so many papers (about 85%) are refused. In fact, we received very few angry reactions from the authors of refused papers. We believe that in most cases the quality of the reports demonstrated to the authors that despite the final negative decision, their paper had been considered and analyzed carefully. Moreover, the remarks they received will certainly benefit their future work and publications. We also wish to thank all area chairs for their availability throughout the reviewing process, for their very positive attitude in the final selection and for their valuable help in re-examining the modified submissions.

The 40 accepted papers (15% acceptance rate) are included in this special issue. The 173 authors are affiliated with institutions

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from 16 countries across the five continents, with 49 authors from North America, 101 from Europe, 9 from Asia (excluding Israel), 8 from Israel, 5 from Australia and 1 from Saudi Arabia. The conference papers with their supplementary files are available in electronic format via online open access to the journal *Bioinformatics* from August 27, 2014. A unique PDF file containing all papers and supplementary files with an index has been prepared for download by the participants through the *Bioinformatics* web site.

The call for posters (500-word abstracts) was also managed through the EasyChair multi-track conference system. It was kept open until 2 weeks after the notification of the oral presentations so that authors whose manuscript could not be accepted had the opportunity to resubmit their work as a poster. A committee of 54 reviewers looked at the abstracts and accepted about 520 posters from 542 submissions. Accepted posters were distributed as follows: 'Sequencing and sequence analysis for genomics': 93 posters; 'Gene expression': 50 posters; 'Pathways and molecular networks': 37 posters; 'Computational systems biology': 53 posters; 'Structural bioinformatics': 92 posters; 'Evolution and population genomics': 28 posters; 'Bioinformatics of health and disease': 56 posters; 'Biological knowledge discovery from data, texts and bio-images': 45 posters; 'Methods and technologies for computational biology': 68 posters. Unfortunately, and despite their poster acceptance, a few authors were unable to make the trip to Strasbourg owing to visa problems or lack of financial support. The organizing committee deeply regrets this situation, which is beyond its control. All poster abstracts are available on the conference web site.

Highlight presentations were introduced at ISMB/ECCB 2007 in Vienna, and immediately became one of the most popular features of the conference. All papers that had been published in peer-review journals (no book chapters) between January 1, 2013, and the submission deadline of June 2, 2014, were eligible to be presented as a Highlight Talk. The ECCB'14 organizing committee selected 10 proposals out of 55 submissions, mainly on the criteria of compatibility with the proceedings papers, wide impact in the life sciences and the potential for attracting a large audience to the conference.

The industrial and demo track at ECCB'14 provides commercial organizations and academic institutions with the opportunity to present their products or services: software, database, infrastructures, etc. Demo fees give access to two 30-min slots for repeating the demo and reaching a large number of conference attendees. Twelve demos are scheduled, involving among others four ECCB'14 silver sponsors (BioBase, sbv Improver, Koriscale and Totalinux), the French and the Swiss Institutes for Bioinformatics (IFB, SIB), the European Molecular Biology Laboratory (EMBL: Uniprot demo), the French National Institute for Research in Agronomy (INRA: BioMercator demo) and the Galaxy project. A free demo slot was also proposed to several refused paper submissions that described valuable computational methods. Four of them accepted this offer.

Ten exhibitor booths will be open throughout the conference in the conference hall, presenting the latest scientific literature in the field of computational biology, bioinformatics, modeling and simulation, as well as new hardware, software and technology developments.

During the weekend before the conference, two satellite meetings, 10 tutorials and 15 workshops will take place. The Student Council of the International Society for Computational Biology (ISCB) organizes its 3rd European Student Council Symposium (ESCS), chaired by Pieter Meysman (University of Antwerp) and Margherita Francescatto (VU University Medical Center, Amsterdam). ESCS abstracts accepted for oral presentation will be published in a special issue of the BMC Bioinformatics journal. The second satellite meeting is the Junior Principal Investigator (JPI) meeting, which aims to help junior PIs anticipate and manage the challenges of running a research group and to learn from successful examples of established young PIs. It is organized by Virginie Bernard (Curie Institute, Paris), Magali Michaut (Netherlands Cancer Institute, Amsterdam), Lennart Martens (Ghent University and VIB) and Theodore Alexandrov (University of Bremen - University of California San Diego). The ECCB'14 organizing committee congratulates all these dynamic young scientists for their enthusiasm, which is essential to the future of research in computational biology.

The eighth International Workshop on Machine Learning in Systems Biology (MLSB) will take place on Saturday and Sunday, September 6-7, under the direction of Florence d'Alché-Buc (University of Evry) and Pierre Geurts (University of Liège, Belgium). Invited speakers are Pierre Baldi (UCI University, California), Karsten Borgwardt (ETH Zürich), Jean-Loup Faulon (University of Evry) and Nicola Segata (University of Trento).

Most other workshops and tutorials are 1-day events, taking place either on Saturday, September 6, or on Sunday, September 7.

The very active domain of biological network study is covered by three complementary workshops: (1) 'Logical Modelling and Analysis of Cellular Networks', organized on 1½ days by Denis Thieffry (Ecole Normale Supérieure, Paris) and Ioannis Xenarios (Swiss Institute of Bioinformatics, Lausanne); (2) 'BioNetVisA', organized by Ina Kuperstein (Institut Curie, Paris) and colleagues, with the objective of going 'From biological network reconstruction to data visualization and analysis in molecular biology and medicine', and hosting the EMBO lecture by Yosef Yarden (The Weizmann Institute of Science, Rehovot, Israel); and (3) 'Integrative Dynamic Analyses of Large Biomedical Network Data', organized by Natasa Przulj (Imperial College, London) and Tijana Milenkovic (University of Notre Dame, Indiana).

The workshop entitled 'Analysis of differential isoform usage by RNA-seq: statistical methodologies and open software' is organized by Magnus Rattray (University of Manchester) and colleagues. The workshop on 'Computational and Systems Biology for Disease Comorbidities' is organized by Anaïs Baudot (CNRS, Marseille) and Alfonso Valencia (CNIO, Madrid). The workshop entitled 'Drug Development 2.0', organized by Jan Baumbach (University of South Denmark) and colleagues, will address computational integrative biology methods for drug repurposing, target discovery and translational research. The workshop on 'Next Generation Computational Biology for Food Security', organized by Sue Jones (The James Hutton Institute, Dundee) will present novel approaches in crop genomics and computational biology to meet the challenges of food security in a changing climate. The workshop entitled 'Recent

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computational advances in metagenomics' is organized by Sophie Schbath (INRA-MIG, Jouy-en-Josas) and colleagues. The workshop on 'Tools and Techniques for Analysis and Design of Macromolecular Structures' organized by Samuel C. Flores (Uppsala University) and Grzegorz Chojnowski (International Institute of Molecular and Cell Biology, Warsaw) will propose both a lecture session and hands-on exercises. Two workshops will introduce or report on research competitions: (1) the workshop on 'Informatics-based approaches for circular dichroism data' organized by Robert Janes and Lazaros Mavridis from Queen Mary University (London) that will introduce the CIDASE challenge, specifically aimed at the relationship between circular dichroism spectra and information content, and (2) the 'sbv IMPROVER' workshop organized by Manuel Peitsch (Philip Morris International) and colleagues, that will report on the three sbv ('systems biology verification') challenges organized so far. ECCB'14 will also give emerging new scientific communities the opportunity to launch two new workshops: the '1st workshop on Computational Methods for Structural RNAs - CMRS'14' organized by Fabrice Jossinet (University of Strasbourg) and colleagues, and the '1st Unified Workshop on Proteome and Metabolome Informatics' by Andrew Dowsey (University of Manchester) and colleagues. We wish a successful future to these initiatives. Finally and importantly, the sometimes ambiguous relations between bioinformaticians and life scientists will be discussed in the workshop on the 'Dual Benefit of Bioinformatics Training' organized by Vicky Schneider, from the Scientific Training, Education and Learning division at The Genome Analysis Centre (TGAC, Norwich). The ECCB'14 organizing committee wishes to thank all workshop organizers for their efforts in making these workshops high-quality and attractive events.

Tutorials at ECCB'14 will address a wide range of topics: 'Analysis of cis-regulatory motifs from high-throughput sequence set' by Jacques van Helden and Morgane Thomas-Chollier (Ecole Normale Supérieure, Paris); 'Computational tools to define and analyse logical models of cellular networks' (1/2 day) by Claudine Chaouiya (Instituto Gulbenkian de Ciência, Lisbon) and colleagues; 'IMGT, the global reference in immunogenetics and immuno-informatics' (1/2 day) by Véronique Giudicelli & Patrice Duroux (CNRS and University of Montpellier); 'Multivariate projection methodologies for the exploration of large biological data sets - application in R using the mixOmics package' by Kim-Anh Lê Cao (University of Queensland Diamantina Institute, Brisbane) and colleagues; 'Protein evolution analysis: on the use of phylogenetic trees' by Romain Studer (EMBL-EBI, Cambridge) and colleagues; 'Reuse, develop and share biological visualisation with BioJS' by Manuel Corpas (TGAC, Norwich) and Rafael Jimenez (ELIXIR Hub, Hinxton); 'Scientific workflows for analysing, integrating and scaling bioinformatics data: a practical introduction to Galaxy, Taverna and WS-PGRADE' by Sílvia Delgado Olabarriaga (University of Amsterdam) and colleagues; 'Statistics and numerics for dynamical modeling' by Clemens Kreutz and Bernhard Steiert (Freiburg University) and 'TADbit: automated analysis and three-dimensional modeling of genomic domains' by Davide Baù and François Serra (CNAG-CRG, Barcelona). The ECCB'14 organizing committee is grateful to all tutorial organizers and lecturers for their involvement in all these events.

ECCB has a tradition of Art Meets Science that turned into a web art contest this year. We received 14 artistic banner proposals for the web site, and these banners were displayed alternatively in a random manner during the weeks before the conference. The vote for the best banner will be organized during the ECCB conference with a prestigious prize offered by the LORIA (Lorraine Laboratory of Research in Computer Science and its Applications, Nancy). The winning banner will remain associated with the ECCB'14 web site.

Encouraging the participation of young scientists has always been a central goal of ECCB, as this conference is a significant opportunity for education and networking for early-stage scientists. We received more than one hundred applications for travel fellowships from young scientists with an oral or poster presentation. Thanks to our academic and commercial sponsors and to the careful control of conference costs, we could satisfy about two-third of the requests. In addition, all fellowship recipients benefited from a reduction on their registration fees.

It is our pleasure to thank all the people and organizations that are making ECCB'14 a successful and high-quality conference. The crucial and dedicated work performed by the program committee composed of the area chairs, the reviewers and co-reviewers has already been acknowledged above. We are grateful to the regional cross-border organizing committee and to the ECCB steering committee for their support and contribution to the organization of the conference. In particular, the advice and experience shared by Torsten Schwede as organizer of the successful ECCB'12 in Basel was invaluable. Thank you Torsten for your almost constant availability! The cooperation and support of ISCB (International Society for Computational Biology) was much appreciated for diffusing the information about ECCB'14 at the international level and for offering student fellowships.

We thank all those who provided financial support to the conference, especially our five silver sponsors BioBase, sbv IMPROVER, Koriscale, Totalinux and GPB (Genomics, Proteomics and Bioinformatics, The official journal of the Beijing Institute of Genomics, the Chinese Academy of Sciences and the Genetics Society of China). We also acknowledge support from the French Institute of Bioinformatics (IFB), the French Society for Bioinformatics (SFBI), the CNRS research group on Biology, Computer Science and Mathematics (GDR BIM), the European Grid Infrastructure (EGI), the Research Institutes: INRA, Inria (who sponsored the travel expenses of our keynote speakers), EMBI-EBI and the Italian Society for Bioinformatics that offered student fellowships.

We are grateful to the Oxford University Press production team for the preparation of this special issue and to the staff of the CNRS Alsace regional delegation for taking on the administrative and financial burden of the registration process. We wish to thank the staff at the Congress Centre of Strasbourg and Christine Guibert from the University of Strasbourg for their help in preparing the logistics of hosting the conference, and the city of Strasbourg for providing the ECCB'14 welcome cocktail. Moreover, we are pleased to acknowledge the kind support of the Council of Europe which provided the attendee bags and for agreeing to host the gala evening in its nice reception hall and

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gardens along the Ill river. We also especially thank Laurence Lwoff, Head of the Bioethics Unit, for her talk scheduled at the conference opening, in which she will share the Council of Europe's concerns about the bio-ethical challenges raised by the usage of biobanks and biomedical data in research and its applications.

Many people contributed to the local organization of the conference, often much beyond the call of duty, and we owe them a great debt, in particular Anne Ney, Luc Moulinier and all the other members of the LBGI Bioinformatics and Integrative Genomics group from the iCUBE laboratory in Strasbourg, and various administrative and scientific members of the LORIA laboratory and Inria Nancy Grand-Est research center in Nancy.

Finally, all these efforts would be meaningless without the many participants from all over the world. Each of you will bring something to the conference in terms of scientific contributions, oral or poster presentations and discussions. Thank you all for being there and for allowing us to enjoy our science at ECCB'14 in Strasbourg!

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