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The 15th European Conference on Computational Biology

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Editorial

ECCB 2016: The 15th European Conference on Computational Biology

This special issue includes the proceeding papers accepted for presentation at the 15th European Conference on Computational Biology (ECCB 2016), to be held from September 3 to 7, 2016 at the World Forum Convention Center in The Hague, The Netherlands. Details of the conference are available on the conference web site (www.eccb2016.org) and will later be archived at eccb.iscb.org/2016/.

ECCB is the premier 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 are gathering about a thousand scientists and industry staff 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, bio-imaging and big data. Computational analysis platforms are challenged by the enormous complexity of biological systems and the sheer amount of data resulting from high-throughput measuring techniques, such as single-cell or single-molecule measurements. As a consequence, databases and software are evolving rapidly, and new algorithms are required to improve computational analyses of massive biological or biomedical datasets. Recent advances are presented at the conference in the field of data interoperability and machine learning, in particular ‘deep learning’ and network-based analysis techniques. The impact on the field of public data repositories such as TCGA (Weinstein *et al.*, 2013), ENCODE (ENCODE Project Consortium, 2012) and GDSC (Yang *et al.*, 2013) is palpable with many submissions revolving around these resources.

ECCB is held annually in a different country, while it is held jointly with the ISMB conference biennially. Going back in time, the fourteen previous editions of ECCB have been held in: Dublin, Ireland, together with ISMB (Moreau and Beerenwinkel, 2015); Strasbourg, France (Devignes, 2014); Berlin, Germany, together with ISMB (Ben-Tal, 2013); Basel, Switzerland (Schwede and Iber, 2012); Vienna, Austria, together with ISMB (Gaasterland and Vingron, 2011); Ghent, Belgium (Moreau and Heringa, 2010); Stockholm, Sweden, together with ISMB (Gusfield and Tramontano, 2009); Cagliari, Italy (Tramontano, 2008); Vienna, Austria, together with ISMB (Lengauer *et al.*, 2007); Eilat, Israel (Wolfson and Safer, 2007); Madrid, Spain (Guigo *et al.*, 2005); Glasgow, United Kingdom, together with ISMB (Thornton *et al.*, 2004); Paris, France (Lenhof and Sagot, 2003); and Saarbrücken, Germany (Lengauer, 2002).

The ECCB 2016 edition features keynote lectures by distinguished speakers. The opening keynote lecture will be delivered by the 2013 Breakthrough Prize-winner Hans Clevers (Hubrecht Institute and Princess Maxima Centre for Pediatric Oncology,

Utrecht, The Netherlands). Further keynote presentations will be given by Amos Tanay (Weizmann Institute, Tel Aviv, Israel), John Marioni (EMBL-EBI, Hinxton, UK), Nuria Lopez-Bigas (Universitat Pompeu Fabra, Barcelona, Spain), Benedict Paten (UCSC, Santa Cruz, USA), Pauline Hogeweg (Utrecht University, Utrecht, The Netherlands) and Christina Leslie (Memorial Sloan Kettering Cancer Center, New York, USA).

The conference topics span all areas of methodological developments for computational biology and innovative applications of computational methods to molecular biology and biomedicine. To present a more unified view of where the science has gone over recent years, new to ECCB this year is that the conference presentations are divided over five broad themes: (i) *Data* (organization, management, categorization, integration, analysis of data, knowledge discovery); (ii) *Genome* (sequence analysis, alignment, evolution, phylogeny, genetics, epigenetics, 3D conformation); (iii) *Genes* (expression, function, regulation, transcription, translation, geno/phenotype); (iv) *Proteins* (structure, function, alterations, assemblies, interactions, design, proteomics) and (v) *Systems* (systems biology, pathways, molecular networks, dynamics, signalling, multi-scale modelling).

This year four different tracks were created for ECCB: two scientific and two application-oriented ones. On the scientific side, the Proceedings Track presents novel scientific contributions, while the Highlights Track showcases already published high-impact science in computational biology. These two tracks were coordinated and managed across the five themes by a board of $5 \times 4 = 20$ co-chairs, both overseen by a dedicated track chair.

A novelty of ECCB this year is that we have given a prominent platform to applications in the new Application and ELIXIR tracks. The Application Track is an initiative to promote application of computational biology in industry and other fields beyond academia. Submissions to this track should cross the boundaries of traditional academic science, or show developments that are directly relevant beyond academia or have potential for it. Consequently, submissions relating to (pure) research were deemed out of scope. The ELIXIR Track, running for the first time at ECCB 2016, is managed by ELIXIR and focuses on developments relating to services and infrastructure within the ELIXIR nodes. ELIXIR is the pan-European life science infrastructural network (‘Data for the Life Sciences’). It coordinates, integrates and sustains bioinformatics resources across its member states, enabling users in academia and industry to access vital data, tools, standards, compute and training services for research. ELIXIR has chosen ECCB as their major dissemination platform, acting as co-organising sponsor.

Following the call for Proceedings papers, we received 150 submissions. Submission authors were asked to rank the five themes for

fit of their paper. These rankings were subsequently used to assign papers to themes and to arrive at an optimally balanced distribution of submissions over the themes. Within each theme, the theme co-chairs assigned papers to expert referees, taking care to avoid any conflict of interest. Together, the Programme Committee (PC) was composed of 217 reviewers and 35 co-reviewers. The reviewing and selection process was carried out using the EasyChair multi-track conference reviewing system (www.easychair.org). The review form explicitly differentiated between impact and suitability for ECCB on the one hand, and scientific quality and reproducibility on the other. This distinction was intended to create more clarity for both the reviewers and authors; the reviewing criteria were therefore explicitly stated in the submission guidelines. The added focus on reproducibility resulted in many authors opting to make their methods open source. After the reviewers reached a consensus, a final ranking and selection for each theme was carried out by the theme (co-)chairs. A total of 48 papers were conditionally accepted (acceptance ratio of 32%) based on a predefined number of acceptances per theme based on the distribution of initial assignments over the themes. The authors had two weeks to modify their papers according to the suggestions made by the reviewers and to respond to the reviewers' comments, which was checked by the theme (co-)chairs. We thank the authors for incorporating these suggestions as they were given little time to carry out (minor) revisions. Essentially, these efforts 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. We also gratefully acknowledge the hard and diligent work performed by the reviewers over a short period of time. We believe that for all of the rejected submissions, the reviewers provided high-quality reports. We hope that authors of rejected manuscripts will benefit from these remarks in their future research. We thank all theme co-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 48 accepted papers are included in this special issue. The Proceedings Track papers with their supplementary files are available free-for-view in electronic format from Oxford's press journal *Bioinformatics* from September 1st, 2016.

Highlight presentations were introduced at ISMB/ECCB 2007 in Vienna (Lengauer *et al.*, 2007), and immediately became one of the most popular features of the conference. All original research papers that had been published in peer-review journals between 1 March, 2015, and the submission deadline of 29 March 2016, were eligible to be presented as a Highlight talk. After thorough consideration and discussion, the ECCB 2016 theme (co-)chairs selected 24 proposals out of 71 submissions, mainly on the criteria of compatibility with the ECCB objectives, wide impact in the life sciences and the potential for attracting a large audience to the conference.

The Applications Track features 11 presentations, which were selected out of 31 submissions. At the time of writing, three Sponsored Talks will be delivered as part of the Applications Track by respectively The Hyve, Keygene and Data Computing. Sponsored Talks enable sponsors to showcase their innovations in computational biology and to highlight their scientific value. Finally, the ELIXIR track proved to be a very popular addition, with 50 high-quality submissions for only 12 presentation slots.

Submissions to the Poster Track were evaluated based on a 250-word abstract and will be shown at the conference along the five main conference themes. In line with the new Application and ELIXIR tracks, there will also be special Application and ELIXIR poster tracks. A dedicated Education Poster Track was created to devote in-depth attention to education that is so crucial for the next

generation of bioinformaticians. All poster abstracts are available on the conference web site. We also arranged with F1000Research (<http://f1000research.com/>) to publish the posters via a new ECCB2016 channel; submission is on a voluntary basis.

At least sixteen exhibitor booths will be open throughout the conference in the central conference hall, which is well connected to the other activities at ECCB: The Hyve, EMBL-EBI, TimeLogic, Springer, ISCB Student Council, Goblet, ELIXIR, ISCB, Oxford University Press, ENPICOM, Data Computing, CRC Press, SIB, ELIXIR Denmark and Cambridge University Press. They will be presenting the latest scientific literature in the field of computational biology, bioinformatics, data stewardship, modeling and simulation, as well as new hardware, software and technology developments. The Hague Tourist Office, and the four organizing institutions (DTL, Netherlands Bioinformatics and System Biology Research School (BioSB), VU University Amsterdam and Delft University of Technology) will also be represented.

During the weekend before the conference, a satellite meeting, 14 workshops and nine tutorials will take place. The Student Council of the International Society for Computational Biology (ISCB) organizes its 4th European Student Council Symposium (ESCS), chaired by Annika Jacobsen (Vrije Universiteit Amsterdam) and Kevin Schwahn (Universität Potsdam, Max Planck Institute of Molecular Plant Physiology). ESCS highlights will be published in F1000Research via the ISCB Student Council channel. The ECCB 2016 organizing committee congratulates all these dynamic young scientists for their enthusiasm, which is essential to the future of research in computational biology.

The 14 workshops preceding the ECCB 2016 main meeting were selected out of a total of 29 applications, showing how popular ECCB has become as a venue for dissemination of computational biology research. The workshops, running all but one for a single day, provide participants with an informal setting to discuss technical issues, exchange research ideas, and to share practical experiences on a range of focused or emerging topics in computational biology. Taken together, the workshops demonstrate how extensively technologies have found their way into large-scale practical applications:

- (W1) The 10th International Workshop on Machine Learning in Systems Biology, organised by (Juho Rousu, Aalto University, Finland), Dick de Ridder (Wageningen University, The Netherlands), Harri Lähdesmäki (Aalto University, Finland) and Aalt—Jan van Dijk (Wageningen University, The Netherlands), is a two-day workshop with its own proceedings track, where accepted papers will be published in *BMC Bioinformatics*,
- (W2) Network Inference: New Methods and New Data, organised by Anagha Joshi (Roslin Institute, University of Edinburgh, UK), Tom Michoel (Roslin Institute, University of Edinburgh, UK) and Eric Bonnet (Centre National de Génotypage, CEA, Paris, France)
- (W3) Getting the Most out of Your Methods and Algorithms: A Workshop on How to Use Existing Datasets to Gain Novel Insight, chaired by Morris Swertz and Lude Franke (both at University Medical Centre Groningen, The Netherlands),
- (W4) Digital Pathology Meets Bioinformatics, organised by Yves Sucaet (Vrije Universiteit Brussel, Belgium), Jeroen Van der Laak (UMC Radboud, Nijmegen, The Netherlands), Marius Nap (HistoGeneX, Belgium and Rigshospitalet Copenhagen, Denmark), Zev Leifer (New York College of Podiatric Medicine, USA), Yukako Yagi (Harvard Medical School, Cambridge and Massachusetts General Hospital, Boston, USA) and Raphaël Marée (Université de Liège, Belgium),

- (W5) RepSeq 2016: Immune Repertoire Sequencing—Bioinformatics and Applications in Hematology and Immunology, organised by Jack Bartram (University College London, UK), Eva Froňková (Charles University Prague, Czech Republic), Mathieu Giraud, (CNRS, Lille, France—program co-chair), Peter N. Robinson (Charité Berlin, Germany), Mikael Salson (Université de Lille, France—proceedings chair), Mikhail Shugay (Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, Moscow, Russia—program co-chair) and Andrew P. Stubbs (Erasmus MC, Rotterdam, The Netherlands),
 - (W6) FAIR Data and Data Stewardship, organised by Erik Schultes, Mark Thompson Marco Roos (all three at Leiden University Medical Centre, The Netherlands), Mark Wilkinson (Universidad Politecnica de Madrid, Spain), Luiz Olavo Bonino da Silva Santos (Dutch Techcentre for Life Sciences and Vrije Universiteit Amsterdam, The Netherlands),
 - (W7) Challenges and Approaches in Comprehensive and Informative Complex Network Analysis for Precision Medicine, organised by Igor Jurisica (University of Toronto, Canada), Natasa Przulj (University College London, UK) and Tijana Milenkovic (University of Notre Dame, USA),
 - (W8) Computing a Tissue: Modeling Multicellular Systems, organised by Walter de Back (TU Dresden, Germany), Sara Montagna (University of Bologna, Italy) and Roeland Merks (Center for Mathematics and Computer Science (CWI), Amsterdam and Leiden University, The Netherlands),
 - (W9) Computational Pan-Genomics, organised by Zamin Iqbal (University of Oxford, UK), Tobias Marschall (Saarland University and Max Planck Institute for Informatics, Saarbrücken, Germany) and Benedict Paten (3UC Santa Cruz Genomics Institute, Santa Cruz, CA, USA),
 - (W10) BioNetVisA: from Biological Network Reconstruction to data visualisation and analysis in Molecular Biology and Medicine, organised by Inna Kuperstein, Emmanuel Barillot, Andrei Zinovyev (all three at Institut Curie, Paris, France), Hiroaki Kitano (Okinawa Institute of Science and Technology Graduate University, RIKEN Center for Integrative Medical Sciences, Japan), Minoru Kanehisa (Kyoto University, Japan), Samik Ghosh (Systems Biology Institute, Tokyo, Japan), Nicolas Le Novère (Babraham Institute, Cambridge, UK), Robin Haw (Ontario Institute for Cancer Research, Canada), Alfonso Valencia (Spanish National Bioinformatics Institute, Madrid, Spain) and Lodewyk Wessels (Netherlands Cancer Institute, Amsterdam, and Technical University Delft, The Netherlands),
 - (W11) Recent Computational Advances in Metagenomics, organised by Sophie Schbath, Valentin Loux and Mahendra Mariadassou (all at INRA, Jouy-en-Josas, France),
 - (W12) BioExcel: Advanced Simulations for Biomolecular Research, a SIG workshop organised by Rossen Apostolov (KTH, Stockholm, Sweden), Alexandre Bonvin (Utrecht University, The Netherlands), Cath Brooksbank (EMBL-EBI, Hinxton, UK) and Ian Harrow (Ian Harrow Consulting, Whitstable, UK),
 - (W13) Clinical Bioinformatics as a Service, organised by Niko Beerenwinkel (ETH Zurich, and SIB Swiss Institute of Bioinformatics, Switzerland), Wolfgang Huber (EMBL, Heidelberg), Simon Tavaré (Cancer Research UK Cambridge Institute, UK) and Daniel Stekhoven (NEXUS Personalized Health Technologies, ETH Zurich and SIB Swiss Institute of Bioinformatics, Switzerland),
 - (W14) Computational Challenges of Third Generation DNA Sequencing Data Analysis, organised by Leon Mei (Leiden University Medical Center, The Netherlands), Wigard Kloosterman (UMC Utrecht, The Netherlands) and Hans Jansen (ZFScreens, Leiden, The Netherlands).
- The purpose of the ECCB tutorial program is to provide participants with lectures and hands-on training, covering topics relevant to the field of bioinformatics. Each tutorial will offer participants an opportunity to learn about new areas of bioinformatics research, to get an introduction to important established topics, or to develop advanced skills in areas they are already familiar with. A total of nine ECCB 2016 tutorials running for half or a full day will be held at ECCB 2016, which were selected out of 21 applications:
- (T1) Scalable Data Analysis with Apache Spark and Hadoop, organised by Mathijs Kattenberg, Jeroen Schot and Machiel Jansen (SURFSara, The Netherlands),
 - (T2) Scientific Workflows under Galaxy—use case: Multiple Genome Comparison, organised by Michael Krieger (RISC Software GmbH, Austria), Óscar Torreño (University of Malaga, Spain) and Jose Arjona (University of Malaga, Spain),
 - (T3) Protein Interactomes: Build and Explore Protein-Protein Interaction Networks, organised by Javier De Las Rivas (University of Salamanca, Spain),
 - (T4) Genome-wide Association Analysis and Post-analytic Interrogation with R, organised by Andrea S. Foulkes (Mount Holyoke College, MA, United States),
 - (T5) Modern Software Tools and Standards for Modeling Biological Systems, organised by Frank Bergmann (University of Heidelberg, Germany) and Dagmar Waltemath (University of Rostock, Germany),
 - (T6) R2: Easy Online Analysis and Visualization Platform for High-Throughput Data, organised by Jan Koster (Academic Medical Center, Amsterdam and University of Amsterdam, The Netherlands),
 - (T7) DisGeNet: A Discovery Platform to Support Translational Research on Human Diseases, organised by Laura I. Furlong and Janet Piñero (both at University Pompeu Fabra, Barcelona, Spain),
 - (T8) Bio-Ontologies and their Role in Analyzing Personal Genome Data, organised by Paul N. Schofield (University of Cambridge, UK), Robert Hoehndorf (King Abdullah University of Science and Technology, Thuwal, Saudi-Arabia) and Georgios V. Gkoutos (University of Birmingham, UK),
 - (T9) Introduction into Mixed Linear Programming and its Applications in Bioinformatics and in Particular Network Analysis, organised by Rainer König and Marcus Oswald (both at Hans Knöll Institute, Jena and Jena University Hospital, Germany).
- Encouraging the participation of young scientists has always been a central goal of ECCB, and also at this year's conference there is significant opportunity for education and networking for early-stage scientists. We received more than eighty 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-thirds of the requests.
- It is our pleasure to thank all the people and organizations that are making ECCB 2016 a successful and high-quality conference. First of all, we are indebted to the program committee composed of the theme (co-)chairs and reviewers for their crucial and dedicated work. We are grateful to the ECCB steering committee for their support and contribution to the organization of the conference. In particular, the advice and experience shared by Anna Tramontano

(Chair Steering Committee and Chair ECCB 2008), Anne-Marie Devignes (Chair ECCB 2014), Yves Moreau (Chair ECCB 2010, Co-chair ECCB 2014) and Torsten Schwede (Chair ECCB 2012) were invaluable. Thank you Anna, Anne-Marie, Yves and Torsten for your continuous and prompt availability! The cooperation and support of ISCB (International Society for Computational Biology) in spreading the information about ECCB 2016 at the international level and for offering student fellowships were much appreciated.

We thank all those who provided financial support to the conference. In addition to the co-organising sponsor ELIXIR, we gratefully acknowledge our Gold sponsors The Hyve (The Netherlands and USA) and the National Centre for Scientific Research (CNRS, France). We also thank, as our further supporting sponsors, Gemeentemuseum Den Haag, where also the opening reception will be held, the Municipality of The Hague, Bayer (sponsoring the morning run) and The Utrecht Bioinformatics Centre (sponsoring the Poster Award).

We are grateful to the Oxford University Press production team for preparing the ECCB 2016 special issue. The F1000Research foundation is thanked for hosting and showcasing the ECCB 2016 posters on their web interface.

The ECCB 2016 science has been in the able hands of the following individuals, whose painstaking efforts have been vital: Celia van Gelder (Netherlands Bioinformatics and Systems Biology Research School; Dutch Techcentre for Life Sciences), ECCB 2016 Tutorials Chair, for handling the tutorial selection process; Thomas Abeel (TU Delft, The Netherlands), ECCB 2016 Workshops Chair, for carrying out the workshop selection process; Theodore Alexandrov (EMBL, Heidelberg, Germany), ECCB 2016 Applications Track Chair, for pioneering and overseeing the new Applications Track; Niklas Blomberg, Andrew Smith and Premysl Velek (all at ELIXIR Hub, Hinxton, UK) for taking independent care (but in close consultation) of the first ELIXIR Applications Track; and Matti Nykter (University of Tampere, Finland), ECCB 2016 Poster Track Chair, for evaluating and selecting the ECCB 2016 posters.

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 Femke Francissen and Jacintha van Beemen, both at the Dutch Techcentre for Life Sciences (DTL) for their relentless logistic and organizational support. Thanks in this regard are also due to Miranda Schouten-Motshagen and Nicolette van Erven of Congress by design (The Netherlands), our ECCB 2016 Professional Congress Organiser. Ruben Kok (Dutch Techcentre for Life Sciences) had a decisive role in the Local Steering Committee, while Celia van Gelder is thanked once more for her support also in organisational matters.

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, applications, oral or poster presentations and discussions. Thank you all for being there and for allowing us to enjoy our science at ECCB 2016 in The Hague!

On behalf of the ECCB 2016 Local Steering Committee

*Jaap Heringa (ECCB 2016 Conference Chair)
Vrije Universiteit, Amsterdam, The Netherlands*

*Marcel Reinders (ECCB 2016 Co-Chair and Programme Committee Chair)
Delft University of Technology, Delft, The Netherlands*

*Sanne Abeln (ECCB 2016 Proceedings Chair and Programme Committee Co-chair)
Vrije Universiteit, Amsterdam, The Netherlands*

*Jeroen de Ridder (ECCB 2016 Highlights Chair and Programme Committee Co-chair)
University Medical Centre Utrecht, The Netherlands*

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