Yves Moreau and Jaap Heringa, on behalf of the ECCB10 organizing and steering committees

This special issue of Bioinformatics contains the proceedings of the ninth European Conference on Computational Biology 2010 (ECCB10), which was held from September 26 to 29 at the International Conference Center in Ghent, Belgium. Details of the conference are available through the conference web site (www.eccb10.org) and will later be archived at eccb.iscb.org/2010. This year's conference also served as the sixth Benelux Bioinformatics Conference (BBC10), the annual meeting of the regional computational biology community.

ECCB is the top European conference in computational biology and bioinformatics, and a major international conference series in computational biology, alongside ISMB and RECOMB. It covers computational methods for analysis and modeling of an explosively increasing volume and variety of data for molecular biology, medicine and pharmaceutical research. The scope of the conference evolves each year to accommodate the latest developments in biological applications of mathematical modeling and computational methods.

ECCB is held in a different country or region each year, and incorporates the annual national or regional meeting where it is held. It is currently held jointly with the Intelligent Systems in Molecular Biology every other year. Past editions of ECCB have been held in Stockholm (SE) (joint with ISMB), Cagliari (IT), Vienna (AT) (with ISMB), Eilat (IL), Madrid (ES), Glasgow (UK) (with ISMB), Paris (FR) and Saarbrücken (DE).

The conference papers are available in open access electronic-only format, both through online open access to the journal *Bioinformatics* and through the conference CD. Poster abstracts are available both through the conference CD and the conference web site.

The conference topics span all areas of methodological developments for computational biology and innovative applications of computational methods to molecular biology. They were divided into nine areas, ranging from sequence analysis to text mining and from comparative genomics to molecular networks.

The selected contributions are included in this special issue. A Scientific Program Committee of 208 reviewers and 114 co-reviewers selected full manuscript submissions from those nine areas. Each of the nine areas was coordinated by two area chairs and all nine areas were coordinated by the Proceedings and Conference Chairs. We received a record 215 submissions, of which 36 papers (17%) were accepted for oral presentation and publication in *Bioinformatics*. The area chairs distributed the papers among the referees within each area. Each paper was assigned to three or four reviewers and we received three reports for most of the papers, with a few cases where we could only secure two referee reports. The whole process was carried out through the EasyChair conference reviewing system. The same system was used for discussing papers in cases where the reviewers had different opinions about the relevance or quality of the contribution. After consensus was reached by the

reviewers, a final selection was carried out by the area chairs and the proceedings chairs.

Poster submission closed shortly after the selection of the oral presentations, so that authors whose manuscript could not be accepted had the opportunity to resubmit their work as poster. After evaluation of the abstracts for scientific relevance and quality, 392 posters were accepted. Those abstracts are available through the conference CD and web site. A call for late-breaking poster abstracts was also opened shortly before the conference to give researchers a final opportunity to submit their work. This process has not been completed at the time of writing. Those abstracts will be available only at the conference web site.

The conference featured keynote lectures by distinguished speakers: Peer Bork (European Molecular Biology Laboratory, Heidelberg, Germany), Elaine Mardis (Washington University Genome Center, St Louis, MO, USA), Michael J. E. Sternberg (Imperial College, London, UK), Yves Van de Peer (Flemish Institute of Biotechnology and University of Ghent, Belgium) and Hans Westerhoff (University of Manchester, UK and VU University Amsterdam, The Netherlands).

One-day workshops and tutorials were held on Sunday, September 25. The International Society for Computational Biology Student Council (www.iscbsc.org) organized its first European Student Council Symposium (ESCS1). The meeting gave students the opportunity to present their work to an international audience and to build a network and exchange ideas and knowledge within the computational biology community. It was organized under the coordination of Magali Michaut, Thomas Abeel, and Jeroen De Ridder.

Two full-day workshops were organized as well. The workshop 'Learning from perturbation effects' focused on computational methods to leverage perturbation techniques (such as target-specific inhibitors and RNA interference) toward reverse engineering biological networks. It was chaired by Holger Fröhlich [Bonn-Aachen International Center for IT (B-IT), Bonn, Germany)] The second workshop 'Annotation, Interpretation and Management of Mutations (AIMM)' focused on extraction and reuse of genotype–phenotype knowledge from scientific literature and databases. It was chaired by Christopher Baker (University of New Brunswick, Saint John, Canada), Dietrich Rebholz-Schuhmann (European Bioinformatics Institute, Cambridge, UK) and René Witte (Concordia University, Montreal, Canada).

Four tutorials were presented: (i) 'Working with next-generation sequencing data' by Thomas Keane and Jan Aerts (Sanger Institute, Cambridge, UK), (ii) 'Use of semantic web resources in computational biology and bioinformatics' by Paolo Romano (National Cancer Research Institute of Genoa, Italy) and Andrea Splendiani [Rothamsted Research (BBSRC), Harpenden, UK], (iii) 'Current methods and applications for regulatory sequence analysis' by Jacques Van Helden (Free University

of Brussels, Belgium) and Stein Aerts (University of Leuven, Belgium) and (iv) 'Protein structure validation' by Robbie Joosten (Dutch cancer institute—NKI, Amsterdam, The Netherlands) and Jurgen Doreleijers, Hanka Venselaar and Gert Vriend (Radboud University Nijmegen, The Netherlands).

In addition to the main keynote and proceedings track, a technology track included 14 demos and presentations of commercial and academic software, databases and biological applications by sponsors, exhibitors and academic institutions. Eighteen exhibitor stands were open throughout the conference in the main conference halls.

ECCB also has a tradition of *Art Meets Science*. This year's event was a joint lecture by Koen Vanmechelen and Jean-Jacques Cassiman, an artist versus a geneticist. Belgian artist Koen Vanmechelen makes iconoclastic sculpture, paintings, glasswork and installations questioning contemporary science, philosophy and ethics. By manipulating chicken breeds from all over the world, his Cosmopolitan Chicken Project aims to create a universal, cosmopolitan chicken as a metaphor for multiculturalism and globalization. In an associated research project, Prof. Jean-Jacques Cassiman ties art and science together by studying the genetic diversity of chicken breeds and Cosmopolitan Chicken hybrids.

Encouraging the participation of young scientists has always been a central goal of the ECCB conference because the conference is a significant opportunity for education and networking for early stage scientists. Thanks to contributions from previous editions of ECCB and from our commercial and academic sponsors (including the International Society for Computational Biology), we could provide 62 travel fellowships to PhD and postdoc applicants from all over the world. Presenters and contributors to oral presentations were given priority. We also aimed to strike a balance across geographical locations. Unfortunately, many deserving applicants had to be turned down; we ask for their understanding since we were faced with the limitations of available resources.

It is our pleasure to thank all the people and organizations that made ECCB10 possible.

Our first thanks go to the program committee of reviewers and co-reviewers, and in particular the area chairs. A swift and effective review process is at the heart of a conference like ECCB. Reviewing 215 manuscripts in just a few weeks is truly challenging, especially since many members of the program committee had been involved in reviewing for ISMB shortly before. The dedication and hard work of the program committee was quite simply the key to the high quality of the conference.

We are grateful to the local organizing committee and ECCB steering committee for their support and contributions to the organization of the conference. In particular, the advice and guidance from Anna Tramontano, Michal Linial and Hershel Safer as organizers of previous editions of ECCB was invaluable. Anna: your instant answers to our many urgent requests were truly a blessing—Thank you!

We thank all those who provided financial support for the conference. We especially thank our Platinum Sponsor, IBM. The list of sponsors is included in this issue and at the conference web site, as well as the list of exhibitors. We also acknowledge our academic sponsors, the two communities of the Fund for Scientific Research Belgium (FWO, Flanders and FNRS) and institutional support from the interuniversity network on computational biology (IUAP BioMaGNet) and the university centers SymBioSys and BioSCENTer at the Katholieke Universiteit Leuven.

Logistics is crucial for a successful conference. We are grateful to the Oxford University Press production team for the preparation of this special issue, to the International Convention Center Ghent for the venue organization and to the professional conference organizer Momentum for registration support.

Many people contributed to the local organization of the conference, often much beyond the call of duty, and we owe them a great debt: Mimi Deprez, Sonia Leach, Lieven Thorrez, Peter Konings, Ernesto Iacucci, Peter Van Loo, Sylvain Brohée, Leo Tranchevent, Ilse Pardon, John Vos and Liesbeth Van Meerbeek, as well as several others. Your act of kindness, as well as your professionalism, will not be forgotten.

Finally, a conference is only as good as those who contribute to it, so we are grateful to the authors of all submitted manuscripts, keynote speakers, presenters of selected papers, tutorial lecturers, workshop organizers and contributors, poster authors and to all the participants. Thank you for making this conference a success.

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