German Conference on Bioinformatics 2012

GCB'12, September 19–22, 2012, Jena, Germany

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Preface

This volume contains papers presented at the German Conference on Bioinformatics (GCB 2012) held in Jena, Germany, September 19 – 22, 2012. The German Conference on Bioinformatics is an annual, international conference, which provides a forum for the presentation of current research in bioinformatics and computational biology. The GCB 2012 was organized by the Jena Center of Bioinformatics (JCB) in cooperation with the German Society for Chemical Engineering and Biotechnology (DECHEMA) and the Society for Biochemistry and Molecular Biology (GBM). The conference was open to all fields of bioinformatics and theoretical systems biology.

Five satellite workshops that took place on 19 September 2012 placed thematic emphasis on diverse aspects of systems biology: "Systems Biology of Aging" organized by J. Sühnel, "Organ-oriented Systems Biology" by D. Driesch and R. Mrowka, "Network Reconstruction and Analysis in Systems Biology" by W. Wiechert and T. Lengauer, "Computational Proteomics and Metabolomics" by S. Böcker, and "Image-based Systems Biology" by M.T. Figge.

Six leading scientists accepted our invitation to give keynote lectures at the conference:

- Claude dePamphilis (Pennsylvania State University, University Park, USA)
  The draft genome sequence of *Amborella trichopoda* sheds light on the ancestral angiosperm genome
- Oliver Fiehn (University of California, Davis, USA)
  Comprehensive metabolomic databases and annotation workflows: The U.S. West Coast Metabolomics Center
- Arndt von Haeseler (Max F. Perutz Laboratories, Vienna, Austria)
  Exploring the sampling universe of RNA-seq
- Tom Kirkwood (Newcastle University, Newcastle, GB)
  Probing the deep complexity of ageing
- Erik van Nimwegen (University of Basel, Basel, Switzerland)
  A democracy of transcription factors: Inferring transcription regulatory interactions from high-throughput data
- Ruth Nussinov (National Cancer Institute, Frederick, USA)
  Structural proteome scale prediction of protein-protein interactions using interfaces

With the topics of these talks the meeting indeed succeeded in '***J***oining ***E***volution, ***N***etworks, and ***A***lgorithms', according to this year's conference motto.

From 39 submissions, the program committee selected 10 highlight papers and 11 regular papers as contributed talks for the conference. Additionally, about 95 poster abstracts were accepted for presentation. All regular papers are collected in this volume. The highlight papers, the abstracts from the invited speakers, and the poster abstracts are collected in a separate volume available online (www.gcb2012-jena.de).

We thank all members of the program committee as well as all local organizers and helpers for their efforts. We are also very grateful to the participants who presented their work at the lively panel sessions and poster party. Our special thanks go to the sponsors who supported the conference financially.

August 2012,
Sebastian Böcker, Franziska Hufsky, Kerstin Scheubert, Jana Schleicher, and Stefan Schuster

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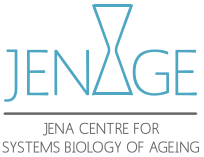

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