
4th INTERNATIONAL CONFERENCE ON ALGORITHMS FOR COMPUTATIONAL BIOLOGY

AlCoB 2017

Aveiro, Portugal

June 5-6, 2017

Organized by:

Center for Research & Development in Mathematics and Applications (CIDMA)
Institute of Electronics and Informatics Engineering of Aveiro (IEETA)
University of Aveiro

Research Group on Mathematical Linguistics (GRLMC)
Rovira i Virgili University

<http://grammars.grlmc.com/AlCoB2017/>

AIMS:

AlCoB aims at promoting and displaying excellent research using string and graph algorithms and combinatorial optimization to deal with problems in biological sequence analysis, genome rearrangement, evolutionary trees, and structure prediction.

Previous events were held in Tarragona, Mexico City, and Trujillo.

The conference will address several of the current challenges in computational biology by investigating algorithms aimed at:

- 1) assembling sequence reads into a complete genome,
- 2) identifying gene structures in the genome,
- 3) recognizing regulatory motifs,
- 4) aligning nucleotides and comparing genomes,
- 5) reconstructing regulatory networks of genes, and
- 6) inferring the evolutionary phylogeny of species.

Particular focus will be put on methodology and significant room will be reserved to young scholars at the beginning of their career.

VENUE:

AlCoB 2017 will take place in Aveiro, an industrial city with an important seaport on the Atlantic Ocean, and known as "the Portuguese Venice" due to its network of canals. The venue will be:

Department of Mathematics
University of Aveiro
Campus Universitário de Santiago
3810-193 Aveiro

SCOPE:

Topics of either theoretical or applied interest include, but are not limited to:

Exact sequence analysis
Approximate sequence analysis
Pairwise sequence alignment
Multiple sequence alignment
Sequence assembly
Genome rearrangement
Regulatory motif finding
Phylogeny reconstruction
Phylogeny comparison
Structure prediction
Compressive genomics
Proteomics: molecular pathways, interaction networks
Transcriptomics: splicing variants, isoform inference and quantification, differential analysis
Next-generation sequencing: population genomics, metagenomics, metatranscriptomics
Microbiome analysis
Systems biology

STRUCTURE:

ALCoB 2017 will consist of:

invited lectures
peer-reviewed contributions
posters

INVITED SPEAKERS:

Michael Biehl (University of Groningen), Prototype-based Models for the Analysis of Biomedical Data

Benedict Paten (University of California, Santa Cruz), The Human Genome Variation Map Project

Marie-France Sagot (INRIA, Villeurbanne), Algorithmically Exploring and Exploiting Interspecific Interactions

PROGRAMME COMMITTEE:

Can Alkan (Bilkent University, Ankara, TR)
Stephen Altschul (National Institutes of Health, Bethesda, US)
Yurii Aulchenko (PolyOmica, Groningen, NL)
Timothy L. Bailey (University of Nevada, Reno, US)
Bonnie Berger (Massachusetts Institute of Technology, Cambridge, US)
Philipp Bucher (Swiss Federal Institute of Technology, Lausanne, CH)
Ken Chen (University of Texas MD Anderson Cancer Center, Houston, US)
Julio Collado-Vides (National Autonomous University of Mexico, Cuernavaca, MX)
Eytan Domany (Weizmann Institute of Science, Rehovot, IL)
Dmitrij Frishman (Technical University of Munich, DE)
Terry Furey (University of North Carolina, Chapel Hill, US)
Olivier Gascuel (Pasteur Institute, Paris, FR)
Debashis Ghosh (University of Colorado, Denver, US)
Susumu Goto (Kyoto University, JP)
Osamu Gotoh (Institute of Advanced Industrial Science and Technology, Tokyo, JP)
Artemis Hatzigeorgiou (University of Thessaly, Volos, GR)
Javier Herrero (University College London, UK)
Karsten Hokamp (Trinity College Dublin, IE)
Fereydoun Hormozdiari (University of California, Davis, US)
Kazutaka Katoh (Osaka University, JP)
Lukasz Kurgan (Virginia Commonwealth University, Richmond, US)
Gerton Lunter (University of Oxford, UK)
Carlos Martín-Vide (Rovira i Virgili University, Tarragona, ES, chair)
Zemin Ning (Wellcome Trust Sanger Institute, Hinxton, UK)
William Stafford Noble (University of Washington, Seattle, US)
Cedric Notredame (Center for Genomic Regulation, Barcelona, ES)
Christos Ouzounis (Centre for Research & Technology Hellas, Thessaloniki, GR)
Manuel C. Peitsch (Philip Morris International, Bern, CH)
Matteo Pellegrini (University of California, Los Angeles, US)
Graziano Pesole (University of Bari, IT)
David Posada (University of Vigo, ES)
Knut Reinert (Free University of Berlin, DE)
Peter Robinson (The Jackson Laboratory, Farmington, US)
Julio Rozas (University of Barcelona, ES)
David Sankoff (University of Ottawa, CA)
Alejandro Schäffer (National Institutes of Health, Bethesda, US)
Xinghua Shi (University of North Carolina, Charlotte, US)
Nicholas D. Socci (Memorial Sloan Kettering Cancer Center, New York, US)
Alexandros Stamatakis (Heidelberg Institute for Theoretical Studies, DE)
Granger Sutton (J. Craig Venter Institute, La Jolla, US)
Kristel Van Steen (University of Liège, BE)
Arndt von Haeseler (Center for Integrative Bioinformatics Vienna, AT)
Kai Wang (Columbia University, New York, US)
Ioannis Xenarios (Swiss Institute of Bioinformatics, Lausanne, CH)
Jinn-Moon Yang (National Chiao Tung University, Hsinchu City, TW)
Shibu Yooseph (University of Central Florida, Orlando, US)
Mohammed J. Zaki (Rensselaer Polytechnic Institute, Troy, US)
Daniel Zerbino (European Bioinformatics Institute, Hinxton, UK)

Weixiong Zhang (Washington University in St. Louis, US)

Zhongming Zhao (University of Texas Health Science Center at Houston, US)

ORGANIZING COMMITTEE:

Diana Costa (Aveiro, CIDMA)

Daniel Figueiredo (Aveiro, CIDMA, co-chair)

Carlos Martín-Vide (Tarragona, co-chair)

Manuel A. Martins (Aveiro, CIDMA)

Manuel Jesús Parra Royón (Granada)

Armando J. Pinho (Aveiro, IEETA)

Diogo Pratas (Aveiro, IEETA, co-chair)

David Silva (London)

Miguel A. Vega-Rodríguez (Cáceres)

SUBMISSIONS:

Authors are invited to submit non-anonymized papers in English presenting original and unpublished research. Papers should not exceed 12 single-spaced pages (including eventual appendices, references, proofs, graphics, etc.) and should be prepared according to the standard format for Springer Verlag's LNCS series (see <http://www.springer.com/computer/lncs?SGWID=0-164-6-793341-0>).

Submissions have to be uploaded to:

<https://easychair.org/conferences/?conf=alcob2017>

PUBLICATIONS:

A volume of proceedings published by Springer in the LNCS/LNBI series will be available by the time of the conference.

A special issue of the Journal of Computational Biology (2015 JCR impact factor: 1.537) will be later published containing peer-reviewed substantially extended versions of some of the papers contributed to the conference. Submissions to it will be by invitation.

REGISTRATION:

The registration form can be found at:

<http://grammars.grlmc.com/AlCoB2017/Registration.php>

DEADLINES (all at 23:59 CET):

Paper submission: January 29, 2017 – EXTENDED –

Notification of paper acceptance or rejection: February 25, 2017

Final version of the paper for the LNCS/LNBI proceedings: March 9, 2017

Early registration: March 9, 2017

Late registration: May 22, 2017

Submission to the journal special issue: September 7, 2017

COLLOCATED EVENTS:

AlCoB 2017 will be collocated with the Fourth Workshop on Molecular Logic:

<http://molecularlogic2017.weebly.com/>

QUESTIONS AND FURTHER INFORMATION:

david.silva409 (at) yahoo.com

POSTAL ADDRESS:

AlCoB 2017
Research Group on Mathematical Linguistics (GRLMC)
Rovira i Virgili University
Av. Catalunya, 35
43002 Tarragona, Spain

Phone: +34 977 559 543

Fax: +34 977 558 386

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Universidade de Aveiro
Universitat Rovira i Virgili