



Programme

Wednesday, October 4th

18:00 - 20:00 Welcome Cocktail (PRBB building - Terrace on the 5st floor)

Thursday, October 5th (Marie Curie room – Ground floor)

- 09:00 09:30 Registration
- 09:30 09:40 Opening Remarks by Tomàs Marquès and Roderic Guigó
- Chair: Roderic Guigó, Centre for Genomic Regulation, ES
- 09:40 10:30 **Keynote: Iria Fernández**, School of Biology, University of Vigo, ES Genome sequencing and the future of coral reefs
- 10:30 11:00 Coffee break
- 11:00 11:15 *TreeShrink: efficient detection of outlier tree leaves* Siavash Mir Arabbaygi, University of California, US
- 11:15 11:30 *Inferring Local Genealogies on Closely Related Genomes* Ryan Elworth, Rice University, US
- 11:30 12:45 **The similarity distribution of paralogous gene pairs created by recurrent alternation of polyploidization and fractionation** Yue Zhang, University of Ottawa, CA
- 11:45 12:00 Fast Heuristics for Resolving Weakly Supported Branches using Duplication, Transfers, and Losses Maureen Stolzer, Carnegie Mellon University, US
- 12:00 12:50 Keynote: Iñaki Ruiz-Trillo, Institute of Evolutionary Biology (CSIC-IBE), ES Investigating animal origins with the genomes of their closest unicellular relatives

12:50 - 14:30 Lunch

- Chair: Tomàs Marquès, Institute of Evolutionary Biology (CSIC-IBE), ES
- 14:30 14:45 *Generation and Comparative Genomics of Synthetic Dengue Viruses* Tamir Tuller, Tel Aviv University, IL
- 14:45 15:00 *A tractable variant of the Single Cut or Join distance with duplicated genes* Aniket Mane, Simon Fraser University, CA
- 15:00 15:15 Algorithms for Computing the Family-Free Genomic Similarity under DCJ Jens Stoye, Bielefeld University, DE
- 15:15–15:30 A Unified ILP Framework for Genome Median, Halving, and Aliquoting Problems under DCJ Pavel Avdeyev, George Washington University, US
- 15:30 18:00 Poster Session
- 20:00 22:00 Conference Dinner (not included in the registration fee previous registration required). Place: Llamber restaurant, Calle de la Fusina, 5, 08003 Barcelona http://llamber.com/en/





Friday, October 6th

Chair: Luay Nakhleh, Rice University, US

- 09:30 10:20 Keynote: Toni Gabaldón, Centre for Genomic Regulation, ES Recent genome evolution in the emerging fungal pathogen Candida glabrata
- 10:20 10:35 *Enhancing Searches for Optimal Trees using SIESTA* Pranjal Vachaspati, UIUC, US
- 10:35 10:50 ASTRAL-III: increased scalability and impacts of contracting low support branches

Siavash Mir Arabbaygi, University of California, San Diego, US

10:50 - 11:30 Coffee break

Chair: Siavash Mir Arabbaygi, UCSD, US

11:30 – 11:45 Statistical Consistency of Coalescent-based Species Tree Methods under Models of Missing Data Michael Nute, University of Illinois at Urbana Champaign, US

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- 11:45– 12:00 *New Algorithms for Genomic Duplication Problem* Jarosław Paszek, University of Warsaw, PL
- 12:00 12:15 **On the Rank-Distance Median of 3 Permutations** Leonid Chindelevich, Simon Fraser University, CA
- 12:15 14:00 Lunch and poster session

Chair: To be determined

14:00 – 15:00 **Keynote: Wes Warren**, McDonnell Genome Institute, Washington University School of Medicine US

The genetic odyssey of the African green monkey

- 15:00 15:15 *Finding Teams in Graphs and its Application to Spatial Gene Cluster Discovery* Tizian Schulz, Bielefeld University, DE
- 15:15 15:30 *Orientation of Ordered Scaffolds* Max Alekseyev, George Washington University, US
- 15:30 15:45 *Rearrangement Scenarios Guided by Chromatin Structure* Sylvain Pulicani, LIRMM, IGH, FR

Closing remarks