

Algorithms for Computational Biology: Fifth Edition

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THIS special section of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics* presents extended versions of some of the best papers presented at the Fifth International Conference on Algorithms for Computational Biology, AlCoB 2018, held in Hong Kong on June 25-26, 2018. The conference was organized by the Department of Computing of Hong Kong Polytechnic University and the Research Group on Mathematical Linguistics (GRLMC) from Rovira i Virgili University, Tarragona, Spain.

AlCoB 2018 was the fifth event in a series dedicated to 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.

Out of 25 submissions to the conference, 11 papers were accepted (which represents an acceptance rate of 44%). Among them, the authors of three papers were invited to submit to this special section. Each submission was reviewed by three experts and, based on their comments, the guest editors decided to accept two papers for this special section (which represents an acceptance rate of about 8% out of the submissions to the conference).

Next, we briefly present the papers included in this special section.

In their paper “Heuristics for the Reversal and Transposition Distance Problem,” Klairton Lima Brito, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias approach the Sorting Signed Permutations by Reversals and Transpositions Problem in its classical and somehow restricted versions and propose three related heuristics able to cope with the problem better. These heuristics seem to have a wider range of applicability to other areas of genome rearrangement. Each of them shows an advantage if one looks for improving time, quality, or flexibility of the solution.

Leo van Iersel, Remie Janssen, Mark Jones, Yukihiro Murakami, and Norbert Zeh, in their paper “Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation,” consider three variants of the known problem of inference of a species phylogeny from gene trees. One consists of inferring based on a model using

speciation and duplication, with duplications clustered in the minimum possible number of duplication episodes. The second utilizes speciation and reticulation, with the minimal number of reticulation events. The third variant optimizes the first one by minimizing the duplication episode depth. The authors show that all three variants of the inference problem can be solved in polynomial time.

We thank the authors for their contributions, the reviewers for their valuable work, and the editorial team of the journal for their professional support and collaboration.

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Guest Editors



Carlos Martín-Vide is a full professor with Rovira i Virgili University, Tarragona. His research interests include automata and language theory, molecular computing, theoretical computer science, and mathematical and computational linguistics. He has authored or coauthored more than 300 papers. He has been involved in the definition, operation, and monitoring of several European funding initiatives in support of fundamental research in mathematics and computer science.



Miguel A. Vega-Rodríguez received the PhD degree in computer engineering from the University of Extremadura, Spain, in 2003. He is currently an associate professor (accredited as full professor) of computer architecture with the Department of Computer and Communications Technologies, University of Extremadura. He has authored or co-authored more than 690 publications including journal papers (more than 150 JCR-indexed journal papers), book chapters, and peer-reviewed conference proceedings, for which he got several awards (such as best paper awards). He has edited more than 15 special issues of JCR-indexed journals. His main research interests include parallel and distributed computing, multiobjective optimization, evolutionary and bio-inspired computation, bioinformatics, and reconfigurable and embedded computing.

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