Algorithms for Computational Biology: Third Edition

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THIS special section of the journal *IEEE/ACM Transactions on Computational Biology and Bioinformatics* offers extended versions of some of the best papers presented at the 3rd International Conference on Algorithms for Computational Biology, AlCoB 2016, held in Trujillo, Spain, on June 21-22, 2016. The conference was organized by the Computer Architecture and Logic Design Group (ARCO) from the University of Extremadura, the Extremadura Centre for Advanced Technologies (CETA-CIEMAT), and the Research Group on Mathematical Linguistics (GRLMC) from Rovira i Virgili University, Tarragona, Spain.

AlCoB 2016 was the third event in a series dedicated to 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 29 submissions to the conference, 13 papers were accepted (which represents an acceptance rate of about 45 percent). Among them, the authors of 11 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 four papers for this special section (which represents an acceptance rate of about 14 percent out of the submissions to the conference).

Next, we briefly present the papers included in this special section. For each paper, we mention the most important results.

In their paper “Gibbs/MCMC Sampling for Multiple RNA Interaction with Sub-Optimal Solutions,” Syed Ali Ahmed and Saad Mneimneh formulate the Multiple RNA Interaction problem in a combinatorial optimization way with approximation algorithms to handle various interaction patterns. When this is combined with Gibbs sampling and MCMC, optimal and sub-optimal solutions are efficiently produced. In front of structures far from an optimal solution, one can explore dependences among parts of the interaction and cluster the solutions in order to obtain possible alternative structures.

Agnieszka Mykowiecka and Paweł Górecki, in their paper “Credibility of Evolutionary Events in Gene Trees,” propose a novel bootstrap method to define support for gene duplication and speciation events in phylogenetic trees. Support for evolutionary events can be calculated by comparing bootstrap gene trees to the original gene tree. A linear time algorithm for the computation of bootstrap values is presented. Finally, two experiments are described, one of them supporting the fact that species trees inferred from gene trees having highly supported events are more biologically consistent.

In order to resolve the occurrence of speciation and whole genome duplication in phylogenetic analysis, David Sankoff, Chunfang Zheng, Yue Zhang, João Meidanis, Eric Lyons, and Haibao Tang, in their paper “Models for Similarity Distributions of Syntenic Homologs and Applications to Phylogenomics,” revise the notions of gene divergence and fractionation. They propose an algorithm for resolving data on local peaks in the distributions of duplicate gene similarities for a number of related genomes and illustrate this in a particular family.

Laura Urbini, Blerina Sinaimeri, Catherine Matias, and Marie-France Sagot, in their paper “Exploring the Robustness of the Parsimonious Reconciliation Method in Host-Symbiont Cophylogeny,“ approach the issue of robustness of the parsimonious host-symbiont tree reconciliation method under special circumstances. On the one hand, editing of the input involves making selections of unique symbiont mapping to a host when multiple associations exist, which is something tree reconciliation is unable to do. On the other hand, small perturbations can happen which are re-rootings of the symbiont tree to deal with a wrong placement of the root in fast evolution. The authors design a simulation scheme for host-symbiont cophylogeny and also a measure to compare sets of tree reconciliations.

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