

Preface

These proceedings contain the papers that were presented at the Second International Conference on Algorithms for Computational Biology (AlCoB 2015), held in Mexico City, Mexico, during August 4–5, 2015.

The scope of AlCoB includes topics of either theoretical or applied interest, namely:

- 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

AlCoB 2015 received 23 submissions. Most papers were reviewed by three and some by two Program Committee members. There were also two external reviewers consulted; we acknowledge all the reviewers in the next section. After a thorough and lively discussion phase, the committee decided to accept 11 papers (which represents an acceptance rate of 47.83 %). The conference program also included three invited talks and some presentations of work in progress.

The excellent facilities provided by EasyChair allowed us to successfully manage the conference submissions and to handle and check the proceedings preparation.

We would like to thank all invited speakers and authors for their contributions, the Program Committee and the reviewers for their cooperation, and Springer for its very professional publishing work.

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