

# Preface

These proceedings contain the papers that were presented at the Third International Conference on Algorithms for Computational Biology (AICoB 2016), held in Trujillo, Spain, during June 21–22, 2016.

The scope of AICoB 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

AICoB 2016 received 23 submissions. Most papers were reviewed by three Program Committee members. There were also several external reviewers consulted. After a thorough and lively discussion phase, the committee decided to accept 13 papers (which represents an acceptance rate of about 56 %). The conference program included three invited talks and some presentations of work in progress as well.

The excellent facilities provided by the EasyChair conference management system allowed us to deal with the submissions successfully and handle the preparation of these proceedings in time.

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

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