

Preface

We are proud to present the papers selected for the fourth edition of the IWBBIO conference “International Work-Conference on Bioinformatics and Biomedical Engineering” held in Granada (Spain) during April 20–22, 2016.

IWBBIO 2016 sought to provide a discussion forum for scientists, engineers, educators, and students on the latest ideas and realizations in the foundations, theory, models, and applications for interdisciplinary and multidisciplinary research encompassing the disciplines of computer science, mathematics, statistics, biology, bioinformatics, and biomedicine.

The aims of IWBBIO 2016 were to create a friendly environment that could lead to the establishment or strengthening of scientific collaborations and exchanges among attendees, and, therefore, IWBBIO 2016 solicited high-quality original research papers (including significant work-in-progress) on any aspect of bioinformatics, biomedicine, and biomedical engineering.

New computational techniques and methods in machine learning, data mining, text analysis, pattern recognition, data integration, genomics and evolution, next-generation sequencing data, protein and RNA structure, protein function and proteomics, medical informatics and translational bioinformatics, computational systems biology, modelling and simulation, and their application in the life science domain, biomedicine, and biomedical engineering were especially encouraged. The list of topics in the successive Call for Papers also evolved, resulting in the following list for the present edition:

1. **Computational proteomics.** Analysis of protein–protein interactions. Protein structure modelling. Analysis of protein functionality. Quantitative proteomics and PTMs. Clinical proteomics. Protein annotation. Data mining in proteomics.
2. **Next-generation sequencing and sequence analysis.** De novo sequencing, re-sequencing, and assembly. Expression estimation. Alternative splicing discovery. Pathway analysis. Chip-seq and RNA-Seq analysis. Metagenomics. SNPs prediction.
3. **High performance in bioinformatics.** Parallelization for biomedical analysis. Biomedical and biological databases. Data mining and biological text processing. Large-scale biomedical data integration. Biological and medical ontologies. Novel architecture and technologies (GPU, P2P, Grid, etc.) for Bioinformatics.
4. **Biomedicine.** Biomedical computing. Personalized medicine. Nanomedicine. Medical education. Collaborative medicine. Biomedical signal analysis. Biomedicine in industry and society. Electrotherapy and radiotherapy.
5. **Biomedical engineering.** Computer-assisted surgery. Therapeutic engineering. Interactive 3D modelling. Clinical engineering. Telemedicine. Biosensors and data acquisition. Intelligent instrumentation. Patient monitoring. Biomedical robotics. Bio-nanotechnology. Genetic engineering.
6. **Computational systems for modelling biological processes.** Inference of biological networks. Machine learning in bioinformatics. Classification for biomedical

data. Microarray data analysis. Simulation and visualization of biological systems. Molecular evolution and phylogenetic modelling.

7. **Health care and diseases.** Computational support for clinical decisions. Image visualization and signal analysis. Disease control and diagnosis. Genome-phenome analysis. Biomarker identification. Drug design. Computational immunology.
8. **E-health.** E-health technology and devices. E-health information processing. Telemedicine/e-health application and services. Medical image processing. Video techniques for medical images. Integration of classical medicine and e-health.

After a careful peer-review and evaluation process (286 submission were submitted and each submission was reviewed by at least three, and on average 3.2, Program Committee members or additional reviewer), 69 papers were accepted to be included in the LNBI proceedings.

During IWBBIO 2016, several special sessions were carried out. Special sessions are a very useful tool with which to complement the regular program with new and emerging topics of particular interest for the participating community. Special sessions that emphasize multi-disciplinary and transversal aspects as well as cutting-edge topics are especially encouraged and welcomed, and in this edition of IWBBIO 2016 they were the following:

1. **SS1: Tools for Next-Generation Sequencing Data Analysis.** Next-generation sequencing (NGS) is a broadly used term to describe the most recent sequencing technologies, including Illumina, Roche/454, Ion Torrent, SOLiD, and Pacific Biosciences. These technologies allow for the quick and cost-effective sequencing of DNA and RNA, opening new ways for the study of genomics, transcriptomics, gene expression, and systems biology, among others.
The continuous improvements in these technologies (longer read length, fewer base calling errors, greater throughput, etc.) and the broad application of NGS in many research fields are producing a continuous increase of data requiring improved bioinformatics tools. Therefore, we invite authors to submit original research, pipelines, and review articles on topics helping in the study of NGS data, such as (but not limited to):
 - (a) Tools for data pre-processing (quality control and filtering)
 - (b) Tools for sequence mapping
 - (c) Tools for de novo assembly
 - (d) Tools for quality check of sequence assembling
 - (e) Tools for the analysis of genomic data: identification and annotation of genomic variants (variant calling, variant annotation)
 - (f) Tools for functional annotation: identification of domains, orthologues, genetic markers, controlled vocabulary (GO, KEGG, InterPro, etc.)
 - (g) Tools for biological enrichment in non-model organisms
 - (h) Tools for the analysis of transcriptomic data: RNA-Seq analyses (quantification, normalization, filtering, differential expression) and distinguishing transcripts, alleles, and paralogs
 - (i) Tools for Chip-Seq data

- (j) Tools for big-data analyses
- (k) Tools for handling and editing complex workflows and pipelines

Organizers: Prof. M. Gonzalo Claros Diaz, PhD, Department of Molecular Biology and Biochemistry, University of Malaga (Spain)

Dr. Javier Perez Florido, PhD, Genomics and Bioinformatics Platform of Andalusia (GBPA), Seville, (Spain).

2. **SS2: Fundamentals of Biological Dynamics.**

Motivation: For a proper description of the dynamic phenomenon it is necessary to discriminate between the trajectory of the evolution toward the limit set and the properties of the limit set. The limit set is the final state that may be dynamic, i.e., oscillating or following the trajectory of deterministic chaos. Concrete examples relevant to the proposed session are, for example, the living cycle of one living organism from the connection of gametes to death — this is the trajectory of the evolution of a partly discrete self-organized system — or behavior of the unconstrained fish shoal in free space — this is possible for assessing a limit set. Structured systems on the trajectory to the limit set prevail in nature.

Objectives: The objective of the session is to gather researchers active in discrete dynamic systems research, i.e., multilevel cellular automata or agent-based models, researchers in qualitative dynamics, and the relevant experimentalists, namely, behavioral science researchers, cell dynamic researchers etc. Experimenters on relevant model systems such as chemical self-organization are also welcome. Such meetings occur only seldom and are never balanced in attendance; often producers of primary datasets do not have a sufficient audience.

The session should contribute to answering following questions:

- (a) Which primary time and space element is predicted by the dynamic model?
- (b) Which are the experimental limits of behavioral and cell dynamic experiment and how well do they reproduce model predictions?

Only with the merging of these two aspects can an answer on the proper setting and interpretation of biological measurements be provided.

Organizer: Prof. Dalibor Stys, PhD, Head of Laboratory of Experimental Complex Systems, Institute of Complex Systems, University of South Bohemia (Czech Republic).

3. **SS3: Maximization of Information Extraction from the Experiments in the Biological Systems.**

Interpretation of experimental results depends on the proper evaluation of the measured data, their comparison, and their classification. The experimental set-up, conditions, and measurement device attributes are also of importance. The significance of the interpretation could be optimized via experimental design. The collection of all settings requires the approach of catalogization and protocol databases. In this way, there could be an emphasis on the requirements necessary to obtain the best possible information, in the maximal relevant content, so as to assure nonbiased interpretation and knowledge extraction. There are, of course, specific details presented in bioinformatical cases. On the other hand, there are

already solved methods in different fields, which could serve in several bioinformatic cases as well.

In this special section we describe broad examples from experimental design through information tuning and data standardization to real implementation using optical sensors, image processing and analysis, and distributed knowledge database. The aim of this section is to present the potential increase of data interpretation and related methods.

Organizer: Dr. Jan Urban, PhD, Head of Laboratory of Signal and Image Processing, Institute of Complex Systems, University of South Bohemia (Czech Republic)

4. **SS4: Using Quantitative Systems Pharmacology for Novel Drug Discovery: A “Systems-level” Perspective to Reduce Toxicity and Increase the Therapeutic Effect of Drugs towards ‘precision medicine’.**

Over the past three decades, the predominant paradigm in drug discovery was designing selective ligands for a specific target to avoid unwanted side effects. However, in the last 5 years, the aim has shifted to take into account the biological network in which they interact. Quantitative and systems pharmacology (QSP) is a new paradigm that aims to understand how drugs modulate cellular networks in space and time, in order to predict drug targets and their role in human pathophysiology.

The goal of this symposium is to go through the current computational and experimental QSP approaches such as polypharmacology techniques combined with systems biology information and consider the use of new tools and ideas in a wider systems-level context in order to design new drugs with improved efficacy and fewer unwanted off-target effects.

The use of network biology produces valuable information such as new indications for approved drugs, drug–drug interactions, proteins–drug side effects and pathways–gene associations. However, we are still far from the aim of QSP, both because of the huge effort needed to model precisely biological network models and the limited accuracy that we are able to reach with those. Hence, moving from “one molecule for one target to give one therapeutic effect” to the “big systems-based picture” seems obvious moving forward although whether our current tools are sufficient for such a step is still under debate. We will discuss all these issues in this symposium.

Organizer: Dr. Violeta I. Perez-Nueno, PhD, Inria Nancy Grand Est (LORIA), Villers les Nancy (France).

5. **SS5: High-Performance Computing in Bioinformatics, Computational Biology, and Computational Chemistry.**

The goal of this special session is to explore the use of emerging parallel computing architectures as well as high-performance computing systems (supercomputers, clusters, grids) for the simulation of relevant biological systems in the context of structural bioinformatics, computational biology, and computational chemistry. We welcome papers, not submitted elsewhere for review, with a focus on topics of interest on:

- (a) Programming models and systems for multicore, manycore, and clusters of multicore/manycore
- (b) Parallel stochastic simulation
- (c) Biological and numerical parallel computing
- (d) Parallel and distributed architectures
- (e) Emerging processing architectures (e.g., GPUs, Intel Xeon Phi, FPGAs, mixed CPU-GPU or CPU-FPGA, etc.)
- (f) Parallel model-checking techniques
- (g) Parallel algorithms for biological analysis
- (h) Cluster and grid deployment for systems biology
- (i) Soft computing algorithms in bioinformatics, computational biology, and computational chemistry
- (j) Application of HPC developments in structural bioinformatics, computational biology, and computational chemistry
- (k) Biological and chemical databases for big data management
- (l) Automated verification in computational biology
- (m) System infrastructure for high-throughput analysis
- (n) Biomolecular structure prediction and large molecular systems
- (o) Molecular visualization of biological big data
- (p) Large-scale proteomics

Organizers: Dr. Horacio Perez-Sanchez

Dr. Jose M. Cecilia, Universidad Catolica San Antonio de Murcia (UCAM), (Spain).

6. SS6: Advances in Drug Discovery.

We welcome research papers, not submitted elsewhere for review, with a focus on topics of interest ranging from but not limited to:

- (a) Target identification and validation
- (b) Computational chemistry: modelling biological processes through quantum chemistry and hybrid QM:MM approaches, interpreting ligand–protein binding sites with novel non-covalent interactions analysis, applying density functional theory (DFT) for predicting drug reactivity towards protein fragments and DNA, computing excited states to disclose the in vivo action of DNA/sensitizers and related molecules.
- (c) Chemoinformatics: methodological basis and applications to drug discovery of: QSAR, Docking, CoMFA-like methods, high-performance computing (HPC), cloud computing, biostatistics, artificial intelligence (AI), machine learning (ML), and bio-inspired algorithms like artificial neural networks (ANN), genetic algorithms, or swarm intelligence
- (d) Multidimensional QSAR. Applications and recent advances in QSAR concepts exploring higher dimensions related to their benefit in the drug-discovery process
- (e) Bioinformatics biosystems: methodological basis and applications to drug design, target or biomarkers discovery of: alignment tools, pathway analysis, complex networks, non-linear methods, microarray analysis, software and Web servers

- (f) High-throughput screening (HTS) of drugs; fragment-based drug discovery; combinatorial chemistry and synthesis

Organizers: Dr. Horacio Perez-Sanchez, Dr. Alfonso Perez-Garrido

Dr. Jose Pedro Ceron, Universidad Catolica San Antonio de Murcia (UCAM), (Spain).

7. SS7: Human Behavior Monitoring, Analysis, and Understanding (HBMAU).

Most prevalent diseases are partly caused or aggravated by lifestyle choices that people make in their everyday life. Accordingly, there is an urgent need for mechanisms to automatically and autonomously identify and eventually change people's unhealthy behaviors. This special session aims at showcasing the latest achievements in the monitoring, analysis, and understanding of human behavior through smart technologies. We welcome novel, innovative, and exciting contributions in areas including but not limited to:

- (a) Applications for cognitive and physical health
- (b) Ambient-assisted living applications
- (c) Smart coaching systems
- (d) Mobile social networks
- (e) Behavioral grouping
- (f) Participatory sensing (crowd-sensing)
- (g) Behavior analysis for alerts and recommendations
- (h) Behavior sensing and personalization of mobile devices
- (i) Context-awareness and semantic modeling
- (j) Affective computing (emotion recognition)
- (k) Activity and action recognition
- (l) User mobility modeling (location tracking)
- (m) User-centric computing
- (n) Benchmarking, databases, and simulation tools

Organizers: Dr. Oresti Banos, Biomedical Signals and Systems Group (BSS), University of Twente (UT) - Enschede, (The Netherlands)

Dr. Hector Pomares, University of Granada (Spain).

8. SS8: Pattern Recognition and Machine Learning in the -omics Sciences.

The biological sciences are quickly becoming data-centered sciences and, as a result, they are, more than ever, one of the key targets for data scientists, particularly from the viewpoints of pattern recognition (PR) and machine learning (ML). Nowhere else this is more evident than in the -omics sciences, spanning the fields of genomics, proteomics, metabolomics, and transcriptomics. In all of these, the advances in data acquisition are creating a true deluge of information and, with it, new challenging scenarios related to data management in all forms, compounded by privacy and legal issues.

In this scenario, PR and ML methods hold the promise of opening new avenues for transforming raw and unstructured -omics information into usable knowledge for the biomedical and bioinformatics domains.

Topics that are of interest to this session include (but are not necessarily limited to):

- (a) Applications of PR and ML methods to problems in the -omics sciences (including genomics, proteomics, metabolomics, and transcriptomics)
- (b) Development of novel PR and ML methods suitable for application to -omics problems
- (c) PR- and ML-based methods for decision support in the -omics sciences
- (d) PR and ML for data processing, preparation, and transformation in -omics
- (e) Scalable PR and ML models for big data problems in -omics, including online and stream learning, as well as parallel and high-performance computing approaches

More information is available at

<http://www.cs.upc.edu/~avellido/research/conferences/IWBBIO16-PRML-Omics.html>

Main Organizer: Alfredo Vellido, PhD, Department of Computer Science, Universitat Politècnica de Catalunya, BarcelonaTECH (UPC), Barcelona (Spain).

Co-organizers: Jesus Giraldo, PhD, Institut de Neurociències and Unitat de Bioestadística, Universitat Autònoma de Barcelona (UAB), Cerdanyola del Valles, Barcelona (Spain).

Rene Alquezar, PhD, Department of Computer Science, Universitat Politècnica de Catalunya, BarcelonaTECH (UPC), Barcelona (Spain).

9. SS9: Resources for Bioinformatics.

From dealing with the complex storage and accessibility requirements, to the challenge of organizing and extracting meaningful information from big data, resources have a key role in today's research workflows. Bioinformatics support involves very different domains: from the creation of standards and rules to enable data exchange and representation to the maintenance of sustainable and efficient hardware and software infrastructures where data can be hosted and analyzed. Although recognized by the research community, this support role often does not find a devoted discussion forum in scientific events.

In this special session we want to provide an opportunity to share the latest ideas and developments on how different resources provide service to bioinformatics research. We welcome contributions focused on all aspects of bioinformatics and biomedicine support, roughly divided into the following topics:

- (a) Data providers: Creating and maintaining databases hosting organized data enabling research involves some serious issues, from raw data hosting to curation and organization of the information to enable users' accessibility.
- (b) Tool development: Analyzing and integrating data needs for the creation of tools and algorithms that help users make sense of the current overflow of information.
- (c) Computing and infrastructure: Data organization and analysis is not possible without specific infrastructure and technical support enabling storage and accessibility, while ensuring sustainability and scalability.
- (d) Standards and integration: Information integration is one of the most demanding challenges we face in bioinformatics research. Developing

standards and common guidelines is the way forward to eliminate current barriers for data exchange and re-use.

Organizers: Dr. Pablo Porras Millan, PhD, European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI) (UK)

Dr. Rafael Jimenez, PhD, ELIXIR Chief Technical Officer (UK).

10. **SS10: Assistive Technology for People with Neuromotor Disorders.**

The motivation for this special session arises from the limitations caused by neuromotor disorders in the fundamental areas of life: mobility, communication, manipulation, orientation, and cognition. This special session collects publications about the newest advances and trends in assistive technologies for people with motor disorders. The term motor disorder includes pathologies with some common patterns such as spinal cord injury, cerebral palsy, and stroke.

According to the Association for the Advancement of Assistive technology in Europe (AAATE), assistive technology (AT) is any item, piece of equipment, or product system, whether acquired commercially off the shelf, modified, or customized, that is used to increase, maintain, or improve the functional capabilities of children with disabilities. AT is used in the context of the whole life of a person with a disability, to function as a part of an individual's total system of support, and not just in one role, setting, or functional application.

AT frequently uses methods and knowledge developed in other technological (robotics, informatics, telecommunications, artificial intelligence, etc.) or humanistic (psychology, pedagogy, sociology, etc.) fields. The main objective of AT (equipments and services) is to contribute to a better quality of life of the many persons affected by disabilities worldwide, through the integration of technological aspects in equipment, services, and contexts.

These technologies must be adapted to the special features of the users affected by disabilities. Human-computer interaction, for instance, can contribute significantly to AT. Rehabilitation robotics is also an emerging field focused on recovering physical and cognitive skills.

The main topics of this special session are:

- (a) Mobility and manipulation technical aids
- (b) Human-computer interaction
- (c) Rehabilitation robotics
- (d) Physiological sensors
- (e) Biofeedback and virtual reality

Organizers: Dr. Rafael Raya, PhD, Department of Information Technologies and Researcher, Bioengineering Laboratory, Universidad CEU San Pablo (Spain).

Dr. Gabriel Caffarena, PhD, Department of Information Technologies and Researcher, Bioengineering Laboratory, Universidad CEU San Pablo (Spain).

11. **SS11: Toward an Effective Telemedicine: An Interdisciplinary Approach.**

In the last 20 years, many resources have been spent in experimentation and marketing of telemedicine systems, but — as pointed by several researchers - no

real product has been fully realized — neither in developed nor in underdeveloped countries. Many factors could be detected:

- (a) Lack of a decision support system in analyzing collected data
- (b) The difficulty of using the specific monitoring devices;
- (c) The caution of patients and/or doctors toward e-health or telemedicine systems
- (d) The passive role imposed to the patient by the majority of experimented systems
- (e) The limits of profit-driven outcome measures
- (f) A lack of involvement of patients and their families as well as an absence of research on the consequences in the patient's life

The constant improvement of ICT tools should be taken into account: at-home and mobile monitoring are both possible; virtual visits can be seen as a new way of performing an easier and more accepted style of patient–doctor communication (which is the basis of a new active role of patients in monitoring symptoms and evolution of the disease). The sharing of this new approach could be extended from patients to healthy people, obtaining tools for a real preventive medicine: A large amount of data could be gained, stored, and analyzed outside the sanitary structures, contributing to a low-cost approach to health.

The goal of this session is to bring together interdisciplinary experts to develop (discuss about) these topics:

- (a) Decision support systems for the analysis of collected data
- (b) Customized monitoring based on the acuteness of the disease
- (c) Integration of collected data with e-health systems
- (d) Attitudes of doctors and sanitary staff
- (e) Patient–doctor communication
- (f) Involvement of patients and of their relatives and care-givers
- (g) Digital divide as an obstacle/hindrance
- (h) Alternative measurements on the effectiveness of telemedicine (quality of life of patients and care-givers, etc.)
- (i) Mobile vs. home monitoring (sensors, signal transmissions, etc.)

Organizer: Maria Francesca Romano, Institute of Economics, Scuola Superiore Sant Anna, Pisa (Italy)

12. **SS12: Medical Planning: Sterilization Department Design.**

Since the sterilization department is one of the most sophisticated and complex sections inside health-care facilities and hospitals, creation of this department is a very important task. Sterilization departments should satisfy special requirements and conditions to comply with infection control. These conditions reflect the department space area, department location inside the hospital, functional relation to the operating rooms department and intensive care unit, as well as devices capacities. In this section, we will introduce the minimum requirements and needs from location selection, minimum required area, device capacities, and how to comply with the quality and infection control. These requirements have been

applied to many hospitals and centers and we have recorded some improvements and enhancements for work flow and infection control.

Organizers: Dr. Khaled S. Ahmed, PhD, Department of Bio-Electronics, Modern University for Technology and Information (Egypt).

13. SS13: Biological Sequence Modeling with Computational Algorithms as HMMs.

Sequence modeling is one of the most important problems in bioinformatics. In the sequential data modeling, the computational algorithms can be used for modeling and comparing biological sequences. Hidden Markov models (HMMs) have been widely used to find similarity between sequences, since the performance of HMMs is suitable for the handling of sequence patterns with various lengths. Some of the most important topics in this session are:

- (a) Modeling of biological sequences in bioinformatics
- (b) The application of hidden Markov models (HMM)
- (c) HMM in modeling of sequential data
- (d) The advantages of HMM in biological sequence modeling compare with other algorithms
- (e) The new algorithms of training HMM
- (f) Gene sequence modeling with HMM

Organizer: Dr. Mohamad Soruri, PhD, Ferdows Faculty of Engineering, University of Birjand, (Iran).

14. SS14: Information Security Optimization and Big Data in Bioinformatics and Biomedical Engineering (ISOBD).

The challenge of handling big data is considered one of the main hot topics that concerns most organizations especially in the medical sector. Nowadays, the usage of information systems and strategic tools has been applied to various fields. Through time a vast amount of data is generated. Although there are several data processing tools to extract knowledge and various visualization tools to present these data, the overarching challenge of the current big data paradigm is to encourage researchers to develop novel data processing and computational algorithms. Furthermore, securing these data is still a challenge that leads to competitions aimed at developing and applying a number of new promising security algorithms.

The aim of this special session is to bring scientists, researcher scholars, and students from academia and industry to present recent and ongoing research activities related to the advances in securing data and applying optimization techniques, especially in medical applications as well as to allow the exchange and sharing of ideas and algorithm experiences. Topics of interest include but are not limited to:

- (a) Big data analytics modeling
- (b) Bioinformatics and biomedical applications
- (c) Data mining and knowledge representation
- (d) Machine learning for medical data analysis
- (e) Information security and biometrics

- (f) Supervised and unsupervised learning of big data
- (g) IOT applications
- (h) Optimization algorithms

More information is available at:

Information Security Optimization and Big Data (ISOBD)

Organizers: Dr. Kareem Kamal A. Ghany, PhD, Faculty of Computers Information, Beni-Suef University, Egypt. Director of Intelligent Systems and Informatics Research Lab.

Eng. Hossam M. Zawbaa, Research Assistant, Faculty of Mathematics and Computer Science, Babes-Bolyai University, Romania.

Eng. Heba Ayeldeen, Assistant Lecturer, Akhbar El-Yom Academy, Egypt.

Plenary Talks

In this edition of IWBBIO, we were honored to have the following invited speakers:

- (a) Prof. Rita Casadio, Group Leader of the Bologna Biocomputing Unit, University of Bologna (UNIBO), Bologna (Italy)
- (b) Prof. Ferran Sanz, Director Research Programme on Biomedical Informatics (GRIB), Hospital del Mar Medical Research Institute (IMIM), Department of Health and Life Sciences, Universitat Pompeu Fabra (Spain)
- (c) Dr. Andreas Bender, Department of Chemistry, Centre for Molecular Informatics, Group Leader: Bender Group, University of Cambridge (UK)

It is important to note, that for the sake of consistency and readability the presented papers are classified under 12 chapters including contributions on:

- (a) Bioinformatics for healthcare and diseases
- (b) Biomedical image analysis
- (c) Biomedical signal analysis
- (d) Computational systems for modelling biological processes
- (e) E-health
- (f) Tools for next-generation sequencing data analysis
- (g) Assistive technology for people with neuromotor disorders
- (h) Fundamentals of biological dynamics and maximization of information extraction from experiments in biological systems
- (i) High-performance computing in bioinformatics, computational biology, and computational chemistry
- (j) Human behavior monitoring, analysis, and understanding
- (k) Pattern recognition and machine learning in the -omics sciences
- (l) Resources for bioinformatics

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in-Chief of different international journals for their interest in publishing special issues of the best papers of IWBBIO.

We would also like to express our gratitude to the members of the different committees for their support, collaboration, and good work. We especially thank the Local Committee, Program Committee, the reviewers, and special session organizers. Finally, we want to thank Springer, and in particular Alfred Hofmann and Anna Kramer for their continuous support and cooperation.

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