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FOREWORD

Biological sciences have been developing rapidly in the last decades and will continue to develop in the foreseeable future. An already enormous and still growing body of data calls for the development of algorithms for data storage and processing, and for massive computational resources for this purpose. Computational resources are even more needed to study the molecular origin of cellular processes, a topic of importance in the development of medical sciences. On the other end stand studies of entire cells, organisms, populations and ecosystems. These are the subject of system biology in which mechanistic details are omitted in favor of investigation of how dependencies and interactions between individual components contribute to the functioning and behavior of a system. A variety of theories and algorithms are being developed and it is difficult, even for a specialist, to keep up with the state-of-the-art approaches.

The "From Computational Biology to System Biology" conference series, first held in 2006 in Forschungszentrum Jülich, Germany, and subsequently held in Jülich and in various locations in the U.S. attempts to make scientists aware of what is happening in the field. The CBSB14 conference found home in the historic city of Gdansk, Poland. The conference was held in the Intercollegiate Faculty of Biotechnology of the University of Gdansk and the Medical University of Gdansk, with the historic Old Town across the street. The conference attracted over 150 participants from all over the world. The topics included protein folding and aggregation, multi-protein complexes and assemblies, cellular environments and interaction networks, models, algorithms, and use of computers in biosciences, and many more. The three keynote speakers: Harold Scheraga (Cornell University, U.S.A.), an icon of protein chemistry, John Moult (University of Maryland, U.S.A.) who has run the Community Wide Experiments on the Critical Assessment of Techniques for Protein Structure Prediction (CASP) since 1994, and Andrzej Koliński (University of Warsaw, Poland) a pioneer of protein simulations, as well as 11 invited speakers, each a renowned scientist, assured a high level of science and sparked vivid debates during panel discussions and poster sessions.

Continuing the tradition of the first CBSB conferences held in Jülich, the Academic Computer Center in Gdansk (TASK) offered its journal, TASK Quarterly, to publish the conference proceedings. The two subsequent issues of TASK Quarterly contain 6 papers from keynote and invited speakers and 13 papers from other participants.

In addition to TASK and the staff of TASK Quarterly, including the editor-in-chief, Prof. Jarosław Rybicki, we would like to thank the institutions that financed the conference or supported it in other ways: the Polish Ministry of Science and Higher Education, the Intercollegiate Faculty of Biotechnology, the University of Gdansk and the Medical University of Gdansk, the Faculty of Chemistry, the University of Gdansk, the Academic Computer Center in Gdansk (CI TASK) and the University of Oklahoma. We would also like to thank ProScience, and in particular Mr Andrzej Sieradzan, for organizing the logistics and all the faculty and graduate students of the Chair of Theoretical Chemistry, Faculty of Chemistry, University of Gdansk, who helped to run the conference.

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U. H. E. Hansmann
A. Liwo
C. Czaplewski