Editorial

The German Conference on Bioinformatics 2001

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The **German Conference on Bioinformatics (GCB) 2001** was held between October 7–10 in Braunschweig, Germany. It was the 17th meeting in a long series which started in the middle of the eighties as a workshop series on "Computers in Bioscience", established by Dietmar Schomburg at the GBF, the German Research Centre for Biotechnology, in Braunschweig which during the first years routinely was the hosting institution. Subsequently, the event became a national bioinformatics conference, but since it was one of the first in Europe it attracted interest of colleagues from all over Europe as well as from overseas, so it was natural that English became soon the conference language and the GCB an international meeting. This year, the GCB came back to its roots, to the campus of the GBF, where it was organized by the Research Group Bioinformatics (headed by E. Wingender) together with the Research Group Bioinformatics and Medical Informatics of the Magdeburg University (R. Hofestaedt; now University of Bielefeld).

The conference program comprised 5 sessions:
- Network Modelling and Simulation
- Molecular Structures
- Ontologies, Classifications & Data Sources
- Gene Expression & Regulation
- Gene Prediction

Five keynote lectures marked the highlights of this conference which clearly focussed on the distinct aspects of the bioinformatics for functional genomics for which modelling and simulation of metabolic and regulatory networks are central topics. Thus, Masaru Tomita from Keio University reported on the status of his pioneering E-cell project and guided the audience to the front of the research in this field. Because of the extraordinary importance of this area, a second keynote lecture was appointed: John Reinitz (Stony Brook University, New York) introduced the functional genomics of the larval development of *Drosophila* and how to describe the accompanying gene regulation processes with a

theoretical model. There is no contribution by John to this GCB Special, but interested readers may wish to have a look at the paper describing his collaborative work with the group of Maria Samosonova in St. Petersburg which has recently been published in this journal [1].

Another field of increasing importance is the generation of ontologies. The question of what an ontology really is has been answered in the scientific literature by a number of definitions, some of which may appear rather abstract, perhaps too abstract to be applicable to simply daily problems. Even restricting the view to one of the most commonly accepted definitions does not prevent from arguing whether a certain ordered list, catalogue, classification, deserves to be called an ontology or not. But nevertheless nearly everybody intuitively agrees with the opinion that ontologies have the great potential to help us to sort out the flood of data the genomic era brings about. In his keynote lecture, Steffen Schulze-Kremer from the German Resource Center for Genome Research gave a stimulating introduction into this upcoming field in bioinformatics research by gently guiding the audience through his view of this matter [2].

The computational analysis of transcriptional regulation represents a bridge between network research on the one and genome sequence-oriented, "classical" bioinformatics on the other side. How to interpret genomic DNA sequences with regard to their regulatory potential and, thus, to identify promoter regions in them is still far from being a trivial task. In his keynote lecture, Thomas Werner (National Research Center for Environment and Health and Genomatix Software GmbH) gave an overview of the state of the art as well as a fascinating report on the progress of his own group and its latest breakthroughs in promoter analysis [3].

The basis of all research initiatives that proclaim the dawn of the "post-genomic era" is a profound representation of the (human) genome itself. This field of still very active research and development was introduced by Ewan Birney in his keynote lecture. He presented the status and the latest progress of the Ensemble project at the European Bioinformatics Institute (EBI) in Hinxton.

A delegation of four scientists from the P.R. China was invited to provide "Insights into Bioinformatics in China" in a special session. This series of talks was introduced by a fascinating presentation of Chun-Ting Zhang from the Tianjin University who explained and demonstrated his approach to gene finding using Z curves. The talks by Z.-P. Feng (also Tianjin University) about the predictability of subcellular protein location and J. Luo about the bioinformatics services at the Peking University are subject of two papers in this Special [4, 5].

Recently, six so-called Competence Centers for Bioinformatics have been installed in Germany. They are funded by the Federal Ministry of Education and Research (BMBF). The concept of the whole program as well as the aims of the individual centers were presented in a separate evening session which is reviewed by Dietmar Schomburg and Martin Vingron [6].

There is neither enough space in this short Editorial to report on all the interesting talks given on the GCB'01, nor is it the place to emphasize individual talks, and it is nearly impossible to qualify any of the 60 posters presented at the conference. Instead, the following selection of full articles, short communications, reviews and reports, some of them being based on talks, others on posters, provide a representative insight into the themes the GCB'01 was focussing on. Altogether, this Special will probably comprise 25 articles, among them 1 editorial (this one), 2 reports [5, 6], 2 reviews [2, 3], 18 full articles and 2 short communications. "Probably" because the specific advantages of online publishing allow us to issue the first papers while some of the envisaged manuscripts are still under revision or even in the reviewing procedure so that the final number of contributions may still vary. Nevertheless, we tried to arrange them in an order that makes scientific sense, but that means that at the end the articles of this Special may not appear in the chronological order of their submission. However, the exact publication dates will be included in all articles from now on.

REFERENCES

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