

Meeting report

Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology

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Abstract

In this meeting report we give an overview of the 3rd International Society for Computational Biology Student Council Symposium. Furthermore, we explain the role of the Student Council and the symposium series in the context of large, international conferences.

Introduction

The Student Council of the International Society for Computational Biology (ISCB) is a student-led, worldwide network of young researchers in computational biology and bioinformatics. The ISCB Board of Directors officially approved the Student Council in July 2004 at the joint European Conference on Computational Biology (ECCB) and Intelligent Systems for Molecular Biology (ISMB) conference in Glasgow, Scotland. The major aims of the Student Council are to organize events and facilitate networking opportunities for Student Council members while nurturing soft skills to complement the normal academic program, such as organizational, teamwork and networking skills. Since its inception, the Student Council has organized an annual student symposium for the benefit of the student community in the field of computational biology and bioinformatics. This year the 3rd ISCB

Student Council Symposium was held in Vienna on 21st July, again as a satellite meeting of the joint conference ISMB/ECCB 2007 [1], with the participation of over 110 delegates.

Several distinguished scientists were invited to the symposium, including Janet Thornton (European Bioinformatics Institute) who presented the opening keynote on "Comparative Functional Genomics of Ageing" and Anna Tramontano (University of Rome, La Sapienza) who gave a keynote lecture on the "Advances and Pitfalls of Structural Bioinformatics". ISCB Vice President Reinhard Schneider (European Molecular Biology Laboratory) delivered the closing remarks.

For students and young scientists it is crucial to be aware of the directions in which the field is moving to make the

right career decisions. The symposium addressed this challenge by providing two different perspectives on bioinformatics: During two presentation sessions and a poster session student delegates were given the opportunity to learn about the latest research of their peers. Another, more comprehensive, view on the development of the field was provided through aforementioned keynote lectures and a panel discussion on "The Future of Bioinformatics" moderated by Thomas Lengauer (Max Planck Institute for Informatics). Several accomplished senior scientists were on the panel, namely Rita Casadio (University of Bologna), Tan Tin Wee (National University of Singapore), Janet Thornton (European Bioinformatics Institute) and Anna Tramontano (University of Rome, La Sapienza). The discussion was highly interactive, providing delegates with the opportunity to actively contribute and to ask questions. In addition, attendees were able to learn first-hand about personal experiences of some of the scientists that have shaped the field of computational biology.

Proceedings summary

The goal of the proceedings of the symposium is to present a selection of the best abstracts selected from a total of 69 submissions. The abstracts that have been selected for this supplement comprise 6 abstracts chosen for oral presentation plus the abstracts of the 8 best-rated posters. Two rounds of rigorous peer-review were carried out by members of the program committee, which was comprised of an international group of students and young researchers. The first round included review and rating of every abstract by at least 2 program committee members, from which the top 25 abstracts were chosen for the second round. The second round consisted in re-scoring of the top 25 abstracts by 4 experienced members of the program committee to identify abstracts for oral presentation, ensuring a sufficiently broad and balanced representation of topics.

The research work selected for the proceedings can be broadly grouped into the following five major themes:

1. Microarrays

Since microarray technology became available roughly a decade ago it has been applied in almost every sub-discipline of biology from organism-level studies to tissue-specific gene expression variations to disease analysis. In line with the community efforts to improve this high-throughput technology, Nielsen and co-workers [2] presented a new oligonucleotide array design algorithm with increased genome coverage and reduced noise. Margolin *et al.* [3] presented a statistical method for inferring true transcription factor – target gene interactions from ChIP-on-chip data. Finally, Blanco *et al.* [4] presented a classification scheme integrating diverse dissimilarity patterns to

identify disease associated genes from cancer gene expression data.

2. Bioinformatics of health and disease

Most of the work presented in this section dealt with genotype-phenotype association studies for inferring disease-associated scenarios from a variety of resources. In particular, Rasche and Herwig [5] presented a web-resource for meta analysis and marker identification to predict approximately 200 genes relevant to type 2 diabetes, while Fisher and co-workers [6] combined quantitative trait loci and microarray data to aid the search for candidate genes responsible for phenotypic variation. In another related work, Steinfeld, Navon and colleagues [7] presented a semi-supervised class discovery method to quantify disease parameters, showing their method's performance on cardiovascular disease putative risk factors.

3. Sequence analysis, structure and function prediction

In the sequence analysis section Lindgreen *et al.* [8] presented a novel approach for the prediction of RNA structure by integrating several parameters like covariation, basepair probabilities and log-likelihood of the alignment into their scoring system. In another systematic study Karaman *et al.* [9] addressed the effect of various parameters like hydrophobicity, van-der-Waals forces and electrostatic potential on the variation of the ligand and binding pocket shape. They showed a correlation between ligand and binding site for the shape and hydrophobicity parameters. In another homology modelling study conducted by Goncarenco and co-workers [10] the authors built a model for the voltage-gated potassium channel and assessed it using experimental data.

4. Systems biology and networks

This section comprised a wide variety of works including modelling and simulation, alignment of networks and integration of diverse data sources to study system-level properties. Among the highlighted works are the identification of the repertoire of genes in plants that act in response to drought conditions by Ashkenazi *et al.* [11] (presentation of this work was supported by a travel fellowship to the first author provided by the ISCB Student Council through funding from the European Bioinformatics Institute) and the modelling and analysis of the budding yeast cell cycle by Fauré and colleagues [12]. A study on mining functional modules in the human genome by integration of datasets of static protein-protein interactions and expression data was presented by Georgii *et al.* [13].

5. Miscellaneous

Barbarini *et al.* [14] presented a procedure to decompose high-resolution SELDI- and MALDI-TOF mass spectra obtained from complex mixtures of peptides based on

computation of correlation coefficients. In another study, Peixoto and Roos [15] showed that about 15% of the metabolic enzymes in *Toxoplasma gondii* are likely to have been acquired by lateral gene transfer (LGT) events in apicomplexan parasites. Using a rigorous method the authors were able to identify a highly probable list of LGT events and showed that most of the high-confidence predictions point to the phylogenetic affinity of apicomplexa to plants. This is consistent with the algal origin of the apicoplast organelle present in these parasites.

Conclusion

A total of 69 abstracts were received for this symposium. All abstracts were rigorously reviewed by at least two referees to select the best abstracts for oral presentation. Eventually 8 authors were invited to give oral presentations of their abstracts, one was rejected and the remaining were asked to present their work as posters. The research presented covered a wide variety of scientific themes including (1) Microarrays, (2) Bioinformatics of Health and Disease, (3) Sequence Analysis, Structure and Function Prediction as well as (4) Systems Biology and Networks. A selection of 14 outstanding abstracts has been compiled for this supplement.

A survey [1] conducted among the delegates at the symposium showed that nearly all of them believe that it is definitely important to have activities focussed on their needs at large conferences such as ISMB and ECCB. For almost 50% of the delegates the student talks or the poster session were the most important aspect of the symposium. More than a third would like to have more student talks and roughly half of all delegates asked for an extended poster session. The latter was perceived to be of good to very good scientific quality. The survey also showed that there is a great demand for career-related events organized by students for students. The evaluation of the survey is available at <http://www.iscb.org/scs3/evaluation.pdf>.

The outcome of the survey, the feedback we received from the delegates after the symposium as well as the increasing number of participants makes us confident that the Student Council Symposium series and related events are a necessary and well-received addition to the program of major conferences in our field. The Student Council leadership is determined to continue and expand its efforts to promote the career-development of the next generation of computational biologists.

Outlook

The 4th ISCB Student Council Symposium will be held in Toronto, Canada in conjunction with the annual conference on Intelligent Systems for Molecular Biology (ISMB) in July 2008. Further information about the Student

Council Symposium will be available on our web site at the address <http://www.iscb.org/scs4>.

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