

# The European Conference on Computational Biology

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The first European Conference on Computational Biology (ECCB 2002) was held in conjunction with the German Conference on Bioinformatics (GCB 2002) [6–9 October 2002, Saarbrücken, Germany (<http://www.zbi.uni-saarland.de/ECCB2002>)]. The conference was followed by a two-day mini-satellite workshop on bioinformatics and statistical physics [1]. This marks the launch of a new, annual computational biology conference in the tradition of the International Conference on Intelligent Systems for Molecular Biology (ISMB) or the International Conference on Research in Computational Molecular Biology (RECOMB), with a focus on computational methods for molecular biology, molecular medicine and pharmaceuticals, each year in conjunction with a different national bioinformatics conferences in Europe. With 26 talks, eight invited lectures and approximately 460 participants, the conference was immediately well-accepted and attracted international interest.

ECCB 2002 was organized in eight tracks including protein networks, expression data, DNA sequence analysis, sequence algorithms, phylogeny, gene and protein function, protein classification and genome analysis. The talks covered a wide range of topics, including algorithms, bioinformatics tools and life science applications and were of high quality; however, because of space restrictions, we will summarize only general trends and the invited lectures.

## Dawn of the post-genome era

Even at the rise of the post-genome era, the classical problems of sequence management and analysis are far from being resolved, a fact that was reflected by a huge number of contributed talks in this area. As a representative of the pre-genome era, Tim Hubbard (Head of Human Sequence Analysis, Sanger Institute; <http://www.sanger.ac.uk>) reported on the status of the Human Genome Project, which is on course for providing a complete assembly in 2003. He also reviewed the status of ENSEMBL (<http://www.ensembl.org/>), a joint project by the Sanger Institute and the European Bioinformatics Institute (EMBL–EBI: <http://www.embl-heidelberg.de>; <http://www.ebi.ac.uk>;) to develop an open source software system as a framework for storing, automatically annotating and integrating complete eukaryotic genomes. Hubbard concluded by emphasizing both the importance and benefits of free access and open source concepts, culminating in the appeal ‘no patents any more!’

Being in the possession of the human genome immediately poses new questions. How can we boil down the large gene set to a handful of promising candidates for further investigation? How can we extract relevant information about diseases? Who is better placed to answer this question than the company that sped up the sequencing of the human genome so tremendously? Scott Patterson (Vice President Proteomics, Celera Genomics; <http://www.celera.com>) gave an enlightening talk illustrating Celera’s

proteomic-driven strategy to find disease-relevant genes by searching proteins that are differentially expressed in disease tissue using chromatography-MS. Specifically, he focused on finding serum markers, discovering targets for small-molecule drugs and identifying cell-surface proteins for therapeutic antibody intervention.

A complementary approach to learn about diseases relies on investigating genetic differences between individuals. Andres Metspalu (Head of the Estonian Genome Project, University of Tartu; <http://www.ut.ee>) described the efforts to collect data from 1,000,000 individuals for high-density single nucleotide polymorphism (SNP) mapping. This could be an invaluable basis for finding disease genes and personalized medicine, but it also bears the danger of stigmatizing individuals and could cause severe ethical and legal problems.

With increasing amounts of sequence data, comparing whole genomes to infer functional properties became a key bioinformatical technique. In this conference, this technique was applied to quite different problems, including transcription factor binding-site detection and protein function or interaction prediction. Laurent Duret (Laboratoire de Biométrie et Biologie Évolutive, Lyon; <http://biomserv.univ-lyon1.fr>) compared frequencies of synonymous codons to detect selection in sequence evolution. Siv Anderson (Uppsala University; <http://www.uu.se>) described her work on comparative genomics of microbial pathogens and

symbionts, highlighting pitfalls in phylogenetic tree construction and arguing that many statements about horizontal gene transfer might be wrong because of artifacts.

Although the genome is an organism's blueprint, the biologist's main interest is to understand proteins, the actual building blocks of life. More and more scientists try to shift into this direction, and following this trend there were three invited, and a large number of contributed, talks focusing on this subject. Douglas Brutlag (Stanford University; <http://www.stanford.edu>) described a new approach that uses robotic motion and roadmap planning techniques for protein folding and ligand docking.

Sarah Teichmann (MRC Laboratory of Molecular Biology, Cambridge; <http://www.mrc-lmb.cam.ac.uk>) investigated principles and types of protein-protein interactions and their evolutionary conservation. Peer Bork (Head of the Comparative Sequence

Analysis Group, EMBL Heidelberg) focused on the analysis of protein interaction networks and described STRING (<http://www.bork.embl-heidelberg.de/STRING/>), a search tool for retrieval of interacting genes or proteins. He warned that there is no solid ground to build on – our knowledge of gene prediction remains provisional. He then reviewed different approaches to infer functional association and pointed out that, to build protein interaction networks, we have to combine results of different methods because no single approach could reliably cover the complete set of interactions. This combination of methods requires careful benchmarking and quantification, because the error rates of these methods might be quite different. Surprisingly, the result of this benchmarking showed that the performance of *in silico* methods (e.g. phylogenetic profiling, the Rosetta Stone approach, gene order comparison) is comparable to wet lab

approaches, an encouraging result for further research.

### Summary

ECCB 2002 was a great success! The conference was well-organized and provided an ideal environment in which to interact with the main European players. The talks and invited lectures were well-balanced, but a surprising trend towards sequence analysis and (less surprising) towards whole genome applications and systems biology was noticeable. We are looking forward to next year's ECCB, which will be held in conjunction with the French National Bioinformatics conference, Journée Ouvertes Biologie Informatique Mathématiques (JOBIM) (27 September–1 October 2003, Paris).

### Reference

- 1 Lengauer, T. and Lenhof, H.P., eds (2002) ECCB 2002 – Proceedings of the European Conference on Computational Biology 2002 in conjunction with the German Conference on Bioinformatics (GCB 2002). Bioinformatics 18, Suppl. 2, Oxford University Press

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# The TNF superfamily is on the TRAIL to BlyS

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The 9th (Biennial) International Congress on TNF-Related Cytokines (30 October–2 November 2002; The Manchester Grand Hyatt, San Diego, CA, USA) covered recent advances in the understanding of these biologically and clinically important molecules. Organized by Carl Ware (La Jolla Institute for Allergy and Immunology; <http://www.liai.org>), this conference series dates back nearly two decades.

The plethora of new discoveries highlighted in 76 presentations over three days testifies to the complexity of the TNF ligand and receptor families and their biological and clinical relevance. The conference further revealed the history of this growing family of proteins by recapitulating scientific progress from clinical trials and therapeutic developments from transgenic mouse models, cell biology, biochemistry and

the genetics/genomics of the tumor necrosis factor (TNF) superfamily.

### Core TNF superfamily members

TNF has been clinically validated as an important driver of both acute and chronic inflammation, therefore, there was a refocus on the role of TNF in the innate immune system toward the effects of TNF on the adaptive immune response and dissection of the dual