

Andrew Torda, Stefan Kurtz, Matthias Rarey (eds.)

**German Conference on  
Bioinformatics 2005**

**GCB 2005**

**October 5-7, 2005, Hamburg, Germany**

Gesellschaft für Informatik 2005

**Lecture Notes in Informatics (LNI) - Proceedings**

Series of the Gesellschaft für Informatik (GI)

Volume P-71

ISBN 3-88579-400-4

ISSN 1617-5468

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## Preface

This volume contains the papers presented at the German Conference on Bioinformatics, GCB 2005, held in Hamburg, October 5–7, 2005. GCB is an annual international conference providing a forum for the presentation of research results in Bioinformatics and Computational Biology. It is run on behalf of the Fachgruppe “Informatik in den Biowissenschaften (BIOINF)” of the German Society of Computer Science (GI), the AG “Computereinsatz in den Biowissenschaften” of the German Society of Chemical Technique and Biotechnology (DECHEMA), and the Studiengruppe “Bioinformatik” of the German Society for Biological Chemistry and Molecular Biology (GBM).

GCB 2005 was preceded by three tutorials in the morning of October 5, 2005: “Experiences with Integrated Databases” given by Ines Liebich, “Solutions for Grid Computing in Life Sciences” given by Ulrich Meier, and “Computational Inference of Cellular Networks” given by Florian Markowetz.

The technical program consisted of 19 contributed talks and seven invited lectures ranging from evolutionary theory to Chemogenomics. Peter Schuster (Vienna) gave a presentation on “Landscapes in RNA folding and evolution”; Tom Slezak (Livermore) on “A large-scale application of comparative genomics for biodefense”. This year, a regional focus was given to China. Guo-Ping Zhao (Chinese National Genome Center, Shanghai) and Li Jin (Fudan University, Shanghai) gave keynote lectures on “SARS molecular epidemiology and SARS-CoV evolution: Combating an emerging infectious disease with the regimen of genomics and bioinformatics” and “Linkage Disequilibrium Sharing and TagSNP Portability Between Populations”. Due to the increasing role of molecular structure in bioinformatics, further invited talks were given by Rolf Hilgenfeld (Lübeck), David Case (La Jolla), and Hugo Kubinyi (Heidelberg) on “Proteins of SARS coronavirus— experimental and theoretical studies”, “Macromolecular Simulations Using Continuum Solvent Models”, and “Chemistry meets Biology: Chemogenomics in Drug Discovery”.

After refereeing 73 submissions, five “discovery notes” and 14 “regular papers” were accepted. The “discovery notes” report on recent biological findings using established computational methods. Additionally, about 125 poster abstracts were accepted for presentation at the poster sessions. This volume contains the regular papers and short abstracts from the invited speakers. The poster abstracts appear in a special abstract book together with the discovery notes.

Obviously, with so many submissions and so few speaking slots, many good submissions were not included. Thanks to the members of the program committee and their colleagues who gave their time to referee the submissions. We are also very grateful to the large number of members of the community who presented their work at the lively panel and poster sessions.

Hamburg, August 2005  
Andrew Torda  
Stefan Kurtz  
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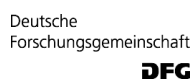
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