Bioconsensus

DIMACS Working Group Meetings on Bioconsensus, October 25–26, 2000 and October 2–5, 2001
DIMACS Center
M. F. Janowitz
F.-J. Lapointe
F. R. McMorris
B. Mirkin
F. S. Roberts
Editors

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Volume 61

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Center for Discrete Mathematics and Theoretical Computer Science
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Foreword

This volume is based on two DIMACS working group meetings on “Bioconsensus” held on October 25–26, 2000 and October 2–5, 2001. We would like to express our appreciation to Mel Janowitz, François-Joseph Lapointe, Fred R. McMorris, Boris Mirkin and Fred Roberts for their efforts to organize and plan these two successful meetings.

The meetings were part of the Special Focus on Computational Molecular Biology. We extend our thanks to Martin Farach-Colton, Craig Nevill-Manning, Wilma Olson and Fred Roberts for their work as special focus organizers.

A “working group” is a new concept at DIMACS, and the Bioconsensus meetings constituted our very first effort at organizing such an activity. A working group is typically interdisciplinary, as was this one. Its meetings stress informal presentations (with a few more formal ones mixed in, possibly an associated “public workshop”) and a lot of time for interaction. The group or subgroups come back to DIMACS for further meetings, discussions, and collaborations. This particular working group emphasized the uses in the biological sciences of methods of consensus and social choice originally developed mostly by mathematical social scientists. Because of the biological content of the meeting and the level of activity in the field, emphasis was placed on phylogenetic trees. Attention was also given to the role that ideas from bioconsensus might apply back to problems in the social sciences.

The group brought together mathematical scientists (mathematicians, computer scientists, statisticians) and biological scientists for a pair of lively meetings that have come a long way toward establishing the new field of “bioconsensus.” This volume, however, is more than just a report of two meetings. In particular, it includes some historical background, as well as a substantial introduction to the axiomatic foundations of the field of bioconsensus, some practical applications of consensus methods to real data, and it includes papers by some individuals who were not present at the group meetings.

DIMACS gratefully acknowledges the generous support that makes these programs possible. The special focus on Computational Molecular Biology has been primarily supported by the Alfred P. Sloan Foundation and the National Science Foundation, with supplementary support from the New Jersey Commission on Science and Technology, Celera Genomics, SmithKline Beecham, and IBM, and was also supported by DIMACS’s partners at Rutgers, Princeton, AT&T Labs-Research, Bell Labs, NEC Laboratories America, and Telcordia Technologies.

Fred S. Roberts
Director

Robert Tarjan
Co-Director for Princeton
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Preface

Consensus methods developed in the context of voting, decision making, and other areas of the social and behavioral sciences have begun to have a variety of applications in the biological sciences, originally in taxonomy and evolutionary biology, and more recently in molecular biology. Typically, several alternatives (such as alternative phylogenetic trees, molecular sequences, or alignments) are produced using different methods or under different models and then one needs to find a consensus solution. There are, already, several hundred papers in this developing field of “Bioconsensus.” We hope that this volume will provide a valuable introduction and reference to various aspects of the subject.

This volume has its genesis in two working group meetings on Bioconsensus that were held at DIMACS on October 25–26, 2000 and October 2–5, 2001. The goals of the meetings were to gather together a diverse group of researchers from Mathematics, Statistics, Biology, and Computer Science with the idea of exploring which biological concepts could benefit from concepts and methods of consensus theory, as well as the extent to which consensus methods from social choice theory might apply to problems in evolutionary biology and other areas of the biological sciences. The formal sessions were kept to a minimum so as to allow ample time for discussions and actual research. We should mention, however, that this volume is more than just a Proceedings of two workshops. It includes invited papers that were not part of the working group meetings, as well as expansions of talks that were presented at the two meetings. It is anticipated that the two survey papers will provide a valuable guide to the already vast literature in this area.

Issues such as the following were typical of those that were discussed: computational complexity of various consensus algorithms, the role of supertrees in evolutionary biology, the extent to which techniques from social choice theory can be modified to be useful in molecular biology, study of axiomatic properties of consensus methods, the importance of choosing consensus methods based on biological rather than mathematical properties, the extent to which consensus methods even make sense in connection with the reconstruction of evolutionary history.

There are a total of 16 papers in the volume. They are difficult to classify by area of author expertise because many of them are joint papers written by authors from different fields. We chose instead to divide them into three general areas. The section on axiomatic considerations is more theoretical than the rest of the volume, and contains five papers. The papers leaning toward computer science approaches can be found in the next section on data analysis, and consists of another five papers. The final part deals more with phylogenetic techniques and has in it the remaining six papers.
The working group meetings that formed the basis for this volume were part of the DIMACS 2000–2003 Special Focus on Computational Molecular Biology. Funding was provided by the Alfred P. Sloan Foundation, Celera Genomics, the National Science Foundation, the New Jersey Commission on Science and Technology, IBM, and SmithKline Beecham. The editors wish to express their thanks for this support.

Melvin F. Janowitz
François-Joseph Lapointe
Fred R. McMorris
Boris Mirkin
Fred S. Roberts
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This volume is based on two DIMACS meetings on "Bioconsensus". It provides a valuable introduction and reference to the various aspects of this rapidly developing field.

The book includes some historical background, as well as a substantial introduction to the axiomatic foundations of the field of bioconsensus and some practical applications of consensus methods to real data. Also included are contributed papers from experts who were not at the meetings. The book is intended for mathematical biologists, evolutionary biologists, and computer scientists.