

Editors

T. J. Barth, Moffett Field, CA

M. Griebel, Bonn

D. E. Keyes, Norfolk

R. M. Nieminen, Espoo

D. Roose, Leuven

T. Schlick, New York

3rd International Workshop on Algorithms for Macromolecular Modeling

Organizing Committee

Peter Deuffhard, ZIB, Berlin

Hin Hark Gan, New York University

Jan Hermans, University of North Carolina, Chapel Hill

Benedict Leimkuhler, University of Leicester, UK

Alan E. Mark, University of Groningen, The Netherlands

Sebastian Reich, Imperial College, London

Tamar Schlick, New York University

Robert Skeel, University of Illinois at Urbana-Champaign

Springer-Verlag Berlin Heidelberg GmbH

Tamar Schlick
Hin Hark Gan
Editors

Computational Methods for Macromolecules: Challenges and Applications

Proceedings of the 3rd International Workshop
on Algorithms for Macromolecular Modeling,
New York, October 12–14, 2000

With 128 Figures, 14 in Color, and 55 Tables



Springer

Editors

Tamar Schlick
Hin Hark Gan

Department of Chemistry
Courant Institute of Mathematical Sciences
New York University
and Howard Hughes Medical Institute
251 Mercer Street
New York, NY 10012, USA
e-mail: schlick@nyu.edu
hgan@biomath.nyu.edu

Cataloging-in-Publication Data applied for

Die Deutsche Bibliothek - CIP-Einheitsaufnahme

Computational methods for macromolecules : challenges and applications ;
proceedings of the 3rd International Workshop on Algorithms for Macromolecular Modeling,
New York, October 12 - 14, 2000 ; with 55 tables / Tamar Schlick ; Hin Hark Gan, ed.. -
Berlin ; Heidelberg ; New York ; Barcelona ; Hong Kong ; London ; Milan ; Paris ; Tokyo :
Springer, 2002

(Lecture notes in computational science and engineering ; Vol. 24)

Cover figure: Washington Square Arch, Greenwich Village, New York City
(photo by Hin Hark Gan)

Mathematics Subject Classification (2000):

92-XX, 34-XX, 35-XX, 41-XX, 60-XX, 70-XX, 82-XX

ISSN 1439-7358

ISBN 978-3-540-43756-7

ISBN 978-3-642-56080-4 (eBook)

DOI 10.1007/978-3-642-56080-4

This work is subject to copyright. All rights are reserved, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilm or in any other way, and storage in data banks. Duplication of this publication or parts thereof is permitted only under the provisions of the German Copyright Law of September 9, 1965, in its current version, and permission for use must always be obtained from Springer-Verlag. Violations are liable for prosecution under the German Copyright Law.

<http://www.springer.de>

© Springer-Verlag Berlin Heidelberg 2002

Originally published by Springer-Verlag Berlin Heidelberg New York in 2002

The use of general descriptive names, registered names, trademarks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

Cover Design: Friedhelm Steinen-Broo, Estudio Calamar, Spain

Cover production: *design & production*

Typeset by the authors using a Springer T_EX macro package

Printed on acid-free paper

SPIN: 10859427

46/3142/LK - 5 4 3 2 1 0

Preface

The workshop on Methods for Macromolecular Modeling (M^3), held at New York University on 12–14 October 2000, attracted 187 participants from Europe, Asia, the Americas, and the Middle East. (see monod.biomath.nyu.edu/~hgan/conf00.html for more information). The exciting program was made possible by the dedicated work of the international advisory committee whose members were P. Deuffhard, J. Hermans, B. Leimkuhler, A. E. Mark, S. Reich, T. Schlick, and R. Skeel. We are indebted to the following agencies and institutions for their generous support: the Burroughs Wellcome Fund, Department of Energy, National Science Foundation, National Institutes of Health, Computational Biomedicine Initiative at Mount Sinai School of Medicine, and NYU's Courant Institute of Mathematical Sciences, Department of Chemistry, and Science Council.

This volume is a collection of 19 review and original articles by the speakers and participants of the M^3 workshop. The topics covered include molecular dynamics methods, Monte Carlo methods, other conformational sampling methods, free energy methods, long range interactions and fast electrostatics, and statistical approaches to protein structures. A perspective article introduces the contributions in this volume and reflects on future prospects in macromolecular modeling.

Tamar Schlick and Hin Hark Gan
New York
November 20, 2001

Table of Contents

INTRODUCTION

Methods for Macromolecular Modeling (M^3): Assessment of Progress and Future Perspectives.....	3
<i>H. H. Gan and T. Schlick</i>	

I BIOMOLECULAR DYNAMICS APPLICATIONS

Mathematics and Molecular Neurobiology	31
<i>N. A. Baker, K. Tai, R. Henchman, D. Sept, A. Elcock, M. Holst, and J. A. McCammon</i>	
Structural and Dynamical Characterization of Nuclei Acid Water and Ion Binding Sites	61
<i>P. Auffinger, B. Masquida, and E. Westhof</i>	

II MOLECULAR DYNAMICS METHODS

A Test Set for Molecular Dynamics Algorithms	73
<i>E. Barth, B. Leimkuhler, and S. Reich</i>	
Internal Coordinate Molecular Dynamics Based on the Spectroscopic B-Matrix.....	104
<i>S.-H. Lee, K. Palmo, and S. Krimm</i>	
The Sigma MD Program and a <i>Generic</i> Interface Applicable to Multi-Functional Programs with Complex, Hierarchical Command Structure.....	129
<i>G. Mann, R. H. Yun, L. Nyland, J. Prins, J. Board, and J. Hermans</i>	
Overcoming Instabilities in Verlet-I/r-RESPA with the Mollified Impulse Method	146
<i>J. A. Izaguirre, Q. Ma, T. Matthey, J. Willcock, T. Slabach, B. Moore, and G. Viamontes</i>	

III MONTE CARLO METHODS

On the Potential of Monte Carlo Methods for Simulating Macromolecular Assemblies.....	177
<i>M. Mezei</i>	

Structure Calculation of Protein Segments Connecting Domains with Defined Secondary Structure: A Simulated Annealing Monte Carlo Combined with Biased Scaled Collective Variables Technique	197
<i>S. A. Hassan, E. L. Mehler, and H. Weinstein</i>	

IV OTHER CONFORMATIONAL SAMPLING METHODS

Hierarchical Uncoupling-Coupling of Metastable Conformations.....	235
<i>A. Fischer, C. Schütte, P. Deufhard, and F. Cordes</i>	
Automatic Identification of Metastable Conformations via Self-Organized Neural Networks	260
<i>T. Galliat, P. Deufhard, R. Roitzsch, and F. Cordes</i>	

V FREE ENERGY METHODS

Equilibrium and Non-Equilibrium Foundations of Free Energy Computational Methods	287
<i>C. Jarzynski</i>	
Free-Energy Calculations in Protein Folding by Generalized-Ensemble Algorithms	304
<i>Y. Sugita and Y. Okamoto</i>	
<i>Ab Initio</i> QM/MM and Free Energy Calculations of Enzyme Reactions	333
<i>Y. Zhang, H. Liu, and W. Yang</i>	

VI LONG RANGE INTERACTIONS AND FAST ELECTROSTATICS METHODS

Treecode Algorithms for Computing Nonbonded Particle Interactions..	359
<i>R. Krasny and Z.-H. Duan</i>	
A New Reciprocal Space Based Method for Treating Long Range Interactions in <i>Ab Initio</i> and Force-Field Based Calculations for Surfaces, Wires, and Clusters.....	381
<i>M. E. Tuckerman, P. Minary, K. Pihakari, and G. J. Martyna</i>	
Efficient Computational Algorithms for Fast Electrostatics and Molecular Docking	411
<i>B. Sandak</i>	

**VII STATISTICAL APPROACHES TO PROTEIN
STRUCTURES**

Fold Recognition Using the OPLS All-Atom Potential and the Surface Generalized Born Solvent Model.....	445
<i>A. K. Felts, A. Wallqvist, E. Gallicchio, D. Bassolino, S. R. Krystek, and R. M. Levy</i>	
Identification of Sequence-Specific Tertiary Packing Motifs in Protein Structures using Delaunay Tessellation	477
<i>S. A. Cammer, C. V. Carter, Jr., and A. Tropsha</i>	
Appendix: Color Plates	495