

Methods in Enzymology

Volume 321

*Numerical Computer
Methods*

Part C

EDITED BY

Michael L. Johnson

CENTER FOR BIOMATHEMATICAL TECHNOLOGY
UNIVERSITY OF VIRGINIA HEALTH SYSTEM
CHARLOTTESVILLE, VIRGINIA

Ludwig Brand

JOHNS HOPKINS UNIVERSITY
BALTIMORE, MARYLAND



ACADEMIC PRESS

San Diego London Boston New York Sydney Tokyo Toronto

Table of Contents

CONTRIBUTORS TO VOLUME 321	vii
PREFACE	ix
VOLUMES IN SERIES	xi
1. Physiological Modeling with Virtual Cell Framework JAMES C. SCHAFF, BORIS M. SLEPCHENKO, AND LESLIE M. LOEW	1
2. Kinetic Analysis of Dynamics of Muscle Function JULIEN S. DAVIS	23
3. Molecular Parameters from Sedimentation Velocity Experiments: Whole Boundary Fitting Using Approximate and Numerical Solutions of Lamm Equation BORRIES DEMELER, JOACHIM BEHLKE, AND OTTO RISTAU	38
4. Sedimentation Velocity Analysis of Macromolecular Assemblies LENNY M. CARRUTHERS, VIRGIL R. SCHIRF, BORRIES DEMELER, AND JEFFREY C. HANSEN	66
5. Analysis of Weight Average Sedimentation Velocity Data JOHN J. CORREIA	81
6. Sedimentation Equilibrium Analysis of Mixed Associations Using Numerical Constraints to Impose Mass or Signal Conservation JOHN S. PHILO	100
7. Optimal Data Analysis Using Transmitted Light Intensities in Analytical Ultracentrifuge EMILIOS K. DIMITRIADIS AND MARC S. LEWIS	121
8. Ultracentrifugal Analysis of Molecular Mass of Glycoproteins of Unknown or Ill-Defined Carbohydrate Composition MARC S. LEWIS AND RICHARD P. JUNGHANS	136
9. Irregularity and Asynchrony in Biologic Network Signals STEVEN M. PINCUS	149
10. Distribution Methods and Analysis of Nonlinear Longitudinal Data MICHELLE LAMPL AND MICHAEL L. JOHNSON	182
11. Distinguishing Models of Growth with Approximate Entropy MICHAEL L. JOHNSON, MICHELLE LAMPL, AND MARTIN STRAUME	196
12. Approximate Entropy as Indication of Goodness-of-Fit MICHAEL L. JOHNSON AND MARTIN STRAUME	207

13. Kinetic Models and Data Analysis Methods for Fluorescence Anisotropy Decay	EDWARD L. RACHOFSKY AND WILLIAM R. LAWS	216
14. Analysis of Nonequilibrium Facets of Pulsatile Sex-Steroid Secretion in Presence of Plasma-Binding Proteins	JOHANNES D. VELDHUIS AND MICHAEL L. JOHNSON	239
15. Monte Carlo Simulations of Lateral Membrane Organization	MADS C. SABRA AND OLE G. MOURITSEN	263
16. Hydrodynamic Bead Modeling of Biological Macromolecules	OLWYN BYRON	278
17. Bayesian Hierarchical Models	CHRISTOPHER H. SCHMID AND EMERY N. BROWN	305
18. Monte Carlo Applications to Thermal and Chemical Denaturation Experiments of Nucleic Acids and Proteins	D. JEREMY WILLIAMS AND KATHLEEN B. HALL	330
19. Analysis of Drug-DNA Binding Data	XIAOGANG QU AND JONATHAN B. CHAIRES	353
20. Neural Network Techniques for Informatics of Cancer Drug Discovery	WILLIAM W. VAN OSDOL, TIMOTHY G. MYERS, AND JOHN N. WEINSTEIN	369
21. Dynamic Network Model of Glucose Counterregulation in Subjects with Insulin-Requiring Diabetes	BORIS P. KOVATCHEV, MARTIN STRAUME, LEON S. FARHY, AND DANIEL J. COX	396
22. Association of Self-Monitoring Blood Glucose Profiles with Glycosylated Hemoglobin in Patients with Insulin-Dependent Diabetes	BORIS P. KOVATCHEV, DANIEL J. COX, MARTIN STRAUME, AND LEON S. FARHY	410
23. Outliers and Robust Parameter Estimation	MICHAEL L. JOHNSON	417
24. Parameter Correlations while Curve Fitting	MICHAEL L. JOHNSON	424
AUTHOR INDEX		447
SUBJECT INDEX		461