

Contents

Preface	v
Editorial Board of the BIOMAT Consortium	vii

Biological Modeling

Modelling aspects of vascular cancer development. <i>Philip K. Maini, Tomás Alarcón and Helen M. Byrne</i>	1
Cellular automaton modelling of biological pattern formation. <i>Andreas Deutsch</i>	13
A mathematical analysis of cylindrical shaped aneurysms. <i>Tor A. Kwembe, Shatondria N. Jones</i>	35
On the origin of metazoans. <i>Frederick W. Cummings</i>	49
A software tool to model genetic regulatory networks: Applications to segmental patterning in <i>Drosophila</i> . <i>Filipa Alves, Rui Dilão</i>	71
The mitochondrial Eve in an exponentially growing population and a critique to the out of Africa model for human evolution. <i>Armando G. M. Neves, Carlos H. C. Moreira</i>	89
A neurocomputational model of the role of cholesterol in the process of Alzheimer's disease. <i>Gizelle K. Vianna, Artur Emílio S. Reis, Fábio Barreto, Luis Alfredo V. Carvalho</i>	103
Theoretical study of a biofilm life cycle: Growth, nutrient depletion and detachment. <i>Galileo Dominguez-Zacarías, Erick Luna, Jorge X. Velasco-Hernández</i>	119
Optimal control of distributed systems applied to the problems of ambient pollution. <i>Santina F. Arantes, Jaime E. M. Rivera</i>	131

Epidemiology and Immunology

Modeling the in vivo dynamics of viral infections. <i>Ruy M. Ribeiro</i> ...	153
Short and long-term dynamics of childhood diseases on dynamic small-world networks. <i>José Verdasca</i>	171
Clonal expansion of cytotoxic T cell clones: The role of the immunoproteasome. <i>Michal Or-Guil, Fabio Luciani, Jorge Carneiro</i>	199
Modeling plague dynamics: Endemic states, outbreaks and epidemic waves. <i>Francisco A. B. Coutinho, Eduardo Massad, Luiz F. Lopez, Marcelo N. Burattini</i>	213

The basic reproductive rate in the Malaria model. <i>Ana Paula Wyse, Luiz Bevilacqua, Marat Rafikov</i>	231
Epidemiological model with fast dispersion. <i>Mariano R. Ricard, Celia T. González González, Rodney C. Bassanezi</i>	245

Protein Structure

Structure prediction of alpha-helical proteins. <i>Scott R. McAllister, Christodoulos A. Floudas</i>	265
Quality and effectiveness of protein structure comparative models. <i>Domenico Raimondo, Alejandro Giorgetti, Domenico Cozzetto, Anna Tramontano</i>	289
Steiner minimal trees, twist angles, and the protein folding problem. <i>James MacGregor Smith</i>	299
Steiner trees as intramolecular networks of the biomacromolecular structures. <i>Rubem P. Mondaini</i>	327

Bioinformatics

Exploring chemical space with computers: Informatics challenges for AI and machine learning. <i>Pierre Baldi</i>	343
Optimization of between group analysis of gene expression disease class prediction. <i>Florent Baty, Michel P. Bihl, Aedín C. Culhane, Martin Brutsche, Guy Perrière</i>	351
On biclustering with features selection for microarray data sets. <i>Panos M. Pardalos, Stanislav Busygin, Oleg Prokopyev</i>	367
Simple and effective classifiers to model biological data. <i>Rogério L. Salvini, Inês C. Dutra, Viviana A. Morelli</i>	379
Index	395