Research Articles in Peer-Reviewed Journals from Past BIOMATH conferences

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http://dx.doi.org/10.3217/jucs-002-02-0058


http://dx.doi.org/10.3217/jucs-002-02-0070

D. Lavenier, Dedicated Hardware for Biological Sequence Comparison, Journal of Universal Computer Science (J. UCS), vol. 2, no. 2 (1996), 77–86

http://dx.doi.org/10.3217/jucs-002-02-0077

1 Citation: T. Ivanov, Research Articles in Peer-Reviewed Journals from Past BIOMATH conferences. Biomath Communications 1/2 (2014) http://dx.doi.org/10.1145/j.bmc.2015.03.101
http://dx.doi.org/10.3217/jucs-002-02-0087

Mathematical Biosciences 156(1–2), pp. 1–338
http://www.sciencedirect.com/science/journal/00255564/156

http://dx.doi.org/10.1016/S0025-5564(98)10058-5

http://dx.doi.org/10.1016/S0025-5564(98)10059-7

http://dx.doi.org/10.1016/S0025-5564(98)10060-3

http://dx.doi.org/10.1016/S0025-5564(98)10061-5

http://dx.doi.org/10.1016/S0025-5564(98)10062-7

http://dx.doi.org/10.1016/S0025-5564(98)10063-9

http://dx.doi.org/10.1016/S0025-5564(98)10064-0

http://dx.doi.org/10.1016/S0025-5564(98)10065-2

Mario Markus, Dominik Böhm, Malte Schmick, Simulation of vessel morphogenesis using cellular automata, Mathematical Biosciences 156 (12),
http://dx.doi.org/10.1016/S0025-5564(98)10067-6

R. Díaz-Sierra, B. Hernández-Bermejo, V. Fairén, Graph-theoretic description of the interplay between non-linearity and connectivity in biological systems, Mathematical Biosciences 156 (12), 1999, 229–253.
http://dx.doi.org/10.1016/S0025-5564(98)10068-8

Andreas Deutsch, Anna T. Lawniczak, Probabilistic lattice models of collective motion and aggregation: from individual to collective dynamics, Mathematical Biosciences, 156 (12), 1999, 255–269.
http://dx.doi.org/10.1016/S0025-5564(98)10069-X

http://dx.doi.org/10.1016/S0025-5564(98)10070-6

http://dx.doi.org/10.1016/S0025-5564(98)10071-8

Eckhard Finke, Gottfried Jetschke, How inbreeding and outbreeding influence the risk of extinction a genetically explicit model, Mathematical Biosciences 156 (12), 1999, 309314.
http://dx.doi.org/10.1016/S0025-5564(98)10072-X

http://dx.doi.org/10.1016/S0025-5564(98)10073-1

Mathematical Biosciences 157(1-2), pp. 1–372
http://www.sciencedirect.com/science/journal/00255564/157

http://dx.doi.org/10.1016/S0025-5564(98)10074-3

Jacek Waniiewski, Wojciech Jedruch, Individual based modeling and parameter estimation for a LotkaVolterra system, Mathematical Biosciences

Tanya Kostova, Jia Li, Mark Friedman, Two models for competition between age classes, Mathematical Biosciences 157 (12), 1999, 65–89.


Luís Sanz, Rafael Bravo de la Parra, Variables aggregation in a time discrete linear model, Mathematical Biosciences 157 (12), 1999, 111–146.


R.G. Seigneuric, J.-L. Chassé, P.M. Auger, A.L. Bardou, Role of the dispersion of refractoriness on cardiac reentries, Mathematical Biosciences
Sergej V. Aksenov, Dynamics of the inducing signal for the SOS regulatory system in Escherichia coli after ultraviolet irradiation, Mathematical Biosciences 157 (12), 1999, 269–286.

http://dx.doi.org/10.1016/S0025-5564(98)10086-X


http://dx.doi.org/10.1016/S0025-5564(98)10087-1


http://dx.doi.org/10.1016/S0025-5564(98)10088-3


http://dx.doi.org/10.1016/S0025-5564(98)10089-5


http://dx.doi.org/10.1016/S0025-5564(98)10090-1


http://dx.doi.org/10.1016/S0025-5564(98)10091-3

Serdica Journal of Computing, Volume 4, Number 1, 2010


Mikhail Ivanov Krastanov, High-Order Control Variations and Small-Time Local Controllability, Serdica Journal of Computing 4, 1, 2010, 85–92
Noël Malod-Dognin, Rumen Andonov, Nicola Yanev, Solving Maximum Clique Problem for Protein Structure Similarity, Serdica Journal of Computing 4, 1, 2010, 93–100

http://dx.doi.org/10.1016/S0898-1221(96)00193-9
http://dx.doi.org/10.1016/S0898-1221(96)00194-0


Alicia Prieto-Langarica, Hristo V. Kojouharov, Benito M. Chen-Charpentier, Discrete and continuous approaches to modeling cell movement in the presence of a foreign stimulus, Computers & Mathematics with Applications 64
http://dx.doi.org/10.1016/j.camwa.2011.12.040

http://dx.doi.org/10.1016/j.camwa.2011.12.053

Michael Chapwanya, Jean M.-S. Lubuma, Ronald E. Mickens, From enzyme kinetics to epidemiological models with Michaelis-Menten contact rate: Design of nonstandard finite difference schemes, Computers & Mathematics with Applications 64 (3), 2012, 201–213.
http://dx.doi.org/10.1016/j.camwa.2011.12.053

http://dx.doi.org/10.1016/j.camwa.2012.01.044

http://dx.doi.org/10.1016/j.camwa.2012.01.047

http://dx.doi.org/10.1016/j.camwa.2012.01.049

http://dx.doi.org/10.1016/j.camwa.2012.01.058

http://dx.doi.org/10.1016/j.camwa.2012.01.059


http://dx.doi.org/10.1016/j.camwa.2012.02.068


http://dx.doi.org/10.1016/j.camwa.2013.02.009


http://dx.doi.org/10.1016/j.camwa.2013.02.009


http://dx.doi.org/10.1016/j.camwa.2013.01.046


http://dx.doi.org/10.1016/j.camwa.2013.01.039


http://dx.doi.org/10.1016/j.camwa.2012.12.003


http://dx.doi.org/10.1016/j.camwa.2013.02.002


http://dx.doi.org/10.1016/j.camwa.2013.03.008

http://dx.doi.org/10.1016/j.camwa.2013.02.010


http://dx.doi.org/10.1016/j.camwa.2013.02.010


http://dx.doi.org/10.1016/j.camwa.2013.03.019


http://dx.doi.org/10.1016/j.camwa.2013.04.008


http://dx.doi.org/10.1016/j.camwa.2013.04.007


http://dx.doi.org/10.1016/j.camwa.2013.04.002


http://dx.doi.org/10.1016/j.camwa.2013.04.010


http://dx.doi.org/10.1016/j.camwa.2013.03.024

Elena Nikolova, Ivan Jordanov, Nikolay K. Vitanov, Dynamical features of the quasi-stationary microRNA-mediated protein translation pro-
http://dx.doi.org/10.1016/j.camwa.2013.04.021


http://dx.doi.org/10.1016/j.camwa.2014.05.018

http://dx.doi.org/10.1016/j.camwa.2014.05.001

http://dx.doi.org/10.1016/j.camwa.2014.06.010

http://dx.doi.org/10.1016/j.camwa.2014.04.009

http://dx.doi.org/10.1016/j.camwa.2014.03.006

http://dx.doi.org/10.1016/j.camwa.2014.02.026

http://dx.doi.org/10.1016/j.camwa.2014.04.006

E. D. Popova, Improved enclosure for some parametric solution sets with linear shape, Computers & Mathematics with Applications, Vol. 68,

http://dx.doi.org/10.1016/j.camwa.2014.04.005


http://dx.doi.org/10.1016/j.camwa.2014.03.007


http://dx.doi.org/10.1016/j.camwa.2014.04.019


http://dx.doi.org/10.1016/j.camwa.2014.03.009


http://dx.doi.org/10.1016/j.camwa.2014.03.010


http://dx.doi.org/10.1016/j.camwa.2014.04.010


http://dx.doi.org/10.1016/j.camwa.2014.04.021

Biotechnology & Biotechnological Equipment vol 2 (2) (2012), 3242–3320, BIOINFORMATICS (selected papers from BioMath 2011)


http://dx.doi.org/10.5504/bbeq.2012.0061

http://dx.doi.org/10.5504/bbeq.2012.0063


http://dx.doi.org/10.5504/bbeq.2012.0064


http://dx.doi.org/10.5504/bbeq.2012.0066


http://dx.doi.org/10.5504/bbeq.2012.0065


http://dx.doi.org/10.5504/bbeq.2012.0062


http://dx.doi.org/10.5504/bbeq.2012.0073


http://dx.doi.org/10.5504/bbeq.2012.0069


http://dx.doi.org/10.5504/bbeq.2012.0068


http://dx.doi.org/10.5504/bbeq.2012.0071

Simeonova V., I. Popov, D. Vassilev, Estimation of Sequencing Error
http://dx.doi.org/10.5504/bbeq.2012.0070

http://dx.doi.org/10.5504/bbeq.2012.0072

http://dx.doi.org/10.5504/bbeq.2012.0074

Nikolov S., J. V. Gonzalez, M. Nenov, O. Wolkenhauer, Dynamics of a Mirna Model with Two Delays, Biotechnology & Biotechnological Equipment, 26(5), 2012, 3315–3320.
http://dx.doi.org/10.5504/bbeq.2012.0067

Journal Biomath vol. 1/1 (2012)

A. Prieto-Langarica, H. Kojouharov, L. Tang, Constructing One-Dimensional Continuous Models from Two-Dimensional Discrete Models of Medical Implants, Biomath 1 (2012), 1209041,
http://dx.doi.org/10.11145/j.biomath.2012.09.041

C. Timofte, Multiscale Analysis of Composite Structures, Biomath 1 (2012), 1209021,
http://dx.doi.org/10.11145/j.biomath.2012.09.021

P. Hingley, Exploring Family Relations between International Patent Applications, Biomath 1 (2012), 1209031
http://dx.doi.org/10.11145/j.biomath.2012.09.031

N. Al-Asuoad , R. Anguelov, K. Berven, M. Shillor, Model and Simulations of a Wood Frog Population, Biomath 1 (2012), 1209032,
http://dx.doi.org/10.11145/j.biomath.2012.09.032

N. Filmann, E. Herrmann, Modeling of Viral Dynamics after Liver Transplantation in Patients with Chronic Hepatitis B and D, Biomath 1 (2012), 1209022,
http://dx.doi.org/10.11145/j.biomath.2012.09.022

D. Bon, C. Stephan, O. Keppler, E. Herrmann, Viral Dynamic Model of Antiretroviral Therapy Including the Integrase Inhibitor Raltegravir in
Patients with HIV-1, Biomath 1 (2012), 1209251,
http://dx.doi.org/10.11145/j.biomath.2012.09.251

H. Umeo, A. Nomura, A State-Efficient Zebra-Like Implementation of Synchronization Algorithms for 2D Rectangular Cellular Arrays, Biomath 1 (2012), 1209022,
http://dx.doi.org/10.11145/j.biomath.2012.09.022

G. Toole, M. Hurdal, Growth in a Turing Model of Cortical Folding, Biomath 1 (2012), 1209252,
http://dx.doi.org/10.11145/j.biomath.2012.09.252

N. Vitanov, Z. Dimitrova, On Waves and Distributions in Population Dynamics, Biomath 1 (2012), 1209253,
http://dx.doi.org/10.11145/j.biomath.2012.09.253

Y. Coudiere, M. Saad, A. Uzureau, An Upstream Finite Volume Scheme for a Bone Healing Model, Biomath 1 (2012), 1209254,
http://dx.doi.org/10.11145/j.biomath.2012.09.254

D. Knipl, G. Röst, Multiregional SIR Model with Infection during Transportation, Biomath 1 (2012), 1209255,
http://dx.doi.org/10.11145/j.biomath.2012.09.255

A. Denes, G. Röst, Structure of the Global Attractors in a Model for Ectoparasite-Borne Diseases, Biomath 1 (2012), 1209256,
http://dx.doi.org/10.11145/j.biomath.2012.09.256

Journal Biomath vol. 1/2 (2012)

http://dx.doi.org/10.11145/j.biomath.2012.10.043

O. Roeva, T. Trenkova, Modelling of a Fed-batch Culture Applying Simulated Annealing, Biomath 1 (2012), 1211114,
http://dx.doi.org/10.11145/j.biomath.2012.11.114

N. Pesheva, J. Brankov, Position-Induced Phase Change in a TASEP with a Double-Chain Section (a Model of Biological Transport), Biomath 1 (2012), 1211211,
http://dx.doi.org/10.11145/j.biomath.2012.11.211


16


Journal Biomath vol. 2/1 (2013)


http://dx.doi.org/10.11145/j.biomath.2013.03.027

http://dx.doi.org/10.11145/j.biomath.2013.05.155

Samuel Bowong, Yves Dumont, Jean Jules Tewa, A patchy model for Chikungunya-like diseases, Biomath 2 (2013), 1307237,
http://dx.doi.org/10.11145/j.biomath.2013.07.237

Marc R Roussel, On the Distribution of Transcription Times, Biomath 2 (2013), 1307247,
http://dx.doi.org/10.11145/j.biomath.2013.07.247

Laurens Bakker, Andrew Poelstra, Calculating Hyphal Surface Area in Models of Fungal Networks, Biomath 2 (2013), 1309087,
http://dx.doi.org/10.11145/j.biomath.2013.09.087

Sorana D. Bolboaca, Lorentz Jäntschi, Quantitative Structure-Activity Relationships: Linear Regression Modelling and Validation Strategies by Example, Biomath 2 (2013), 1309089,
http://dx.doi.org/10.11145/j.biomath.2013.09.089

Journal Biomath vol. 2/2 (2013)

Jan Harm van der Walt, The Linear Space of Hausdorff Continuous Interval Functions, Biomath 2 (2013), 1311261,
http://dx.doi.org/10.11145/j.biomath.2013.11.261

Claire Dufourd, Christopher Weldon, Roumen Anguelov, Yves Dumont, Parameter Identification in Population Models for Insects Using Trap Data, Biomath 2 (2013), 1312061,
http://dx.doi.org/10.11145/j.biomath.2013.12.061

Georges Chamoun, Mazen Saad, Raafat Talhouk, Mathematical and Numerical Analysis of a Modified Keller-Segel Model with General Diffusive Tensors, Biomath 2 (2013), 1312071,
http://dx.doi.org/10.11145/j.biomath.2013.12.071

Diána H Knipl, Gergely Röst, Backward Bifurcation in SIVS Model with Immigration of Non-Infectives, Biomath 2 (2013), 1312051,
http://dx.doi.org/10.11145/j.biomath.2013.12.051


Journal Biomath vol. 3/1 (2014)


Elena Nikolova, Ivan Jordanov, Nikolay Vitanov, On Nonlinear Dynamics of the STAT5a Signaling Protein, Biomath 3 (2014), 1404131, http://dx.doi.org/10.11145/j.biomath.2014.04.131


Daniel Coffield, Anna Maria Spagnuolo, Steady State Stability Analysis of a Chagas Model, Biomath 3 (2014), 1405261,
Nadja Radchenkova, Margarita Kambourova, Spasen Vassilev, Rene Alt, Svetoslav Markov, On the Mathematical Modelling of EPS Production by a Thermophilic Bacterium, Biomath 3 (2014), 1407121,
http://dx.doi.org/10.11145/j.biomath.2014.07.121

Mamadou Diouf, Abderrahman Iggidr, Mamadou Sy, Global Stability of an Epidemic Model with two Infected Stages and Mass-Action Incidence, Biomath 3 (2014), 1407211,
http://dx.doi.org/10.11145/j.biomath.2014.07.211

Journal Biomath vol. 3/2 (2014)

http://dx.doi.org/10.11145/j.biomath.2014.07.191

Svetoslav G. Nikolov, Modelling and Analysis of miRNA Regulation, Biomath 3 (2014), 1407231,
http://dx.doi.org/10.11145/j.biomath.2014.07.231

Olaposi Idowu Omotuyi, Hiroshi Ueda, Descriptor-based Fitting of LPA3 Inhibitors into a Single Predictive Mathematical Model, Biomath 3 (2014), 1410061,
http://dx.doi.org/10.11145/j.biomath.2014.10.061

Ana Vivas-Barber, Carlos Castillo-Chavez, Ernest Barany, Dynamics of an SAIQR Influenza Model, Biomath 3 (2014), 1409251,
http://dx.doi.org/10.11145/j.biomath.2014.09.251

http://dx.doi.org/10.11145/j.biomath.2014.11.041

Daniel J. Coffield Jr., Ken Kuttler, Xianggui Qu, Jorge Rabinovich, Meir Shillor, Anna Maria Spagnuolo, Alexandra Zetye, A Model for the Transmission of Chagas Disease with Random Inputs, Biomath 3 (2014), 1411071,
http://dx.doi.org/10.11145/j.biomath.2014.11.071

Peter Rashkov, Regular and Discontinuous Solutions in a Reaction-Diffusion Model for Hair Follicle Spacing, Biomath 3 (2014), 1411111,
Kharananda Sharma, Bradley J. Roth, How Compressibility Influences the Mechanical Bidomain Model, Biomath 3 (2014), 1411171,