Integrated Evolutionary Algorithms for Michaelis-Menten Model Parameter Identification

Tuan, Ngo Anh、吳幸珍

E-mail: 360071@mail.dyu.edu.tw

ABSTRACT

The proposed research centers on the development a parameter identification method for Michaelis-Menten (M-M) model in Biological System by Evolution Algorithms. The inference of M-M model without knowledge of system parameters is a complicated task due to its nonlinearity and derivation. In this research, a parameter estimation algorithm is proposed for inferring M-M model parameters. This algorithm combines two parameter estimation methods: Genetic algorithm (GA) and Particle Swarm Optimization (PSO) in the strategy of parallel hybridization. The decoupling method is applied to predefine the parameter values in order to improve the accuracy estimation. The performance of the proposed algorithm is evaluated on two aspects: the parameter estimation error and structure identification accuracy. The proposed algorithm is applied to three different M-M models with simulated data. The results show that the proposed algorithm has lower estimation error and higher identification accuracy than the existing method although it processed in a wider search space (from 0 to 5,000).

Keywords : Parameter Identification, System Estimation, Evolutionary Algorithms

Table of Contents

REFERENCES

[1]. P. K. Liu, F. S. Wang, Inverse problems of biological systems using multi-objective optimization, Journal of the Chinese Institute of Chemical Engineers 39; pp.339-406 (2008).
[2]. D. Juki?, R. Scitovski, K. Sabo, A review of existence criteria for parameter estimation of the Michaeils – Menten regression model, Annali dell'Universita' di Ferrara. Vol.53, No.2, pp.281-291 (2007).
[3]. C.Darwin, On the Origin of Species. London: John Murray, (1859), http://embryology.med.unsw.edu.au/pdf/Origin_of_Species.pdf [4]. J. T. Alander, On Optimal Population Size of Genetic Algorithms, IEEE, (1992).
[5]. W. S. M. Elshamy, Using Artificial Intelligence Models in System Identification, (M.S thesis), (2007).
[6]. A. H. Wright, Genetic algorithms for real parameter optimization, in: G. J. E. Rawlins (Ed.), Foundations of Genetic Algorithms I, Morgan Kaufmann, San Mateo, pp.205 – 218. (1991).
[7]. K. Deep, M. Thakur, A new mutation operator for real coded genetic algorithms, Applied Mathematics and Computation N.193, pp.211-230 (2007).
[8]. Z. Michalewicz, Genetic Algorithms + Data Structures = Evolution Programs, Springer-Verlag, New York (1992).
[9]. J. Kennedy, R. C. Eberhart, and Y. Shi, Swarm Intelligence, ser. Evolutionary Computation Series. San Francisco: Morgan Kaufman (2001).
[10]. J. Kennedy, The particle swarm: social adaptation of knowledge. Proceedings of IEEE International Conference on Evolutionary Computation. pp.303 – 308 (1997). -38- [11]. J. J. Liang, A. K. Qin, P. N. Suganthan and S. Baskar, Comprehensive Learning Particle Swarm Optimizer for Global Optimization of Multimodal Functions, IEEE Transaction on Evolutionary Computation, Vol.10, No.3, (Jun 2006).
[12]. M. S. Voss and X. Feng, " Emergent system identification using particle swarm optimization " in Procceedings of SPIE: Complex Adaptive Structures, W. B. Spillman, Ed., vol. 4512, pp.193 – 202, (Oct. 2001), http://citeseer.ist.psu.edu/voss01emergent.html.
[13]. M. Silva, Ferreira, E. N. Antonio, A. M. Tomas, C. Cordeiro, and A. P. Freire, Quantitative assessment of the Glyoxalase pathway in Leishmania infantum as a Therapeutic Target by Modeling and Computer and Simulation, The FEBS J., 270, 2388 (2005).
[14]. B. Robertson and R. D. Astumian, Michaelis – Menten equation for an enzyme in an oscillating electric field, Biophysical Journal, V.58, pp.969-974 (1990).
[15]. ode45 parameter solver for ordinary differential equations (ODEs) guideline: http://www.weizmann.ac.il/matlab/techdoc/ref/ode45.html
[16]. N. M. Abbasi, Using Matlab ode45 to solve differential equations, (2012). http://12000.org/my_notes/matlab_ODE/document.pdf [17]. E. O. Voit, Computational Analysis of Biochemical Systems, p.91, Cambridge University Press, Cambridge, U.K. (2000).
[18]. Rate equations for M-M model 2 (metabolic pathway with branch points) http://jjj.biochem.sun.ac.za/database/silva/index.html [19]. C. G. Moles, P. Mendes, and J. R. Banga, Parameter Estimation in Biochemical Pathways: A Comparison of Global Optimization Methods, Genome Research, 13(11), pp.2467-2474 (Nov 2003). http://www.ncbi.nlm.nih.gov/pmc/articles/PMC403766/?tool=pubmed [20]. T. P. Runarsson and X. Yao, Stochastic ranking for constrained evolutionary optimization, IEEE Trans Evol Comput, pp.284-294 (2000).