A hybrid of Cuckoo Search and Minimization of Metabolic Adjustment to optimize metabolites production in genome-scale models

Muhammad AzharuddinArif[a]*; Mohd SaberiMohamad*[bc]*; Muhammad ShafieAbd Latif*[d]*SafaaiDeris*[bc]*; Muhammad AkmalRemli*[e]*KautharMohd Daud*[a]*; ZuwairieIbrahim*[f]*; SigeruOmatu*[g]*; Juan ManuelCorchado*[h]
[a]Artificial Intelligence and Bioinformatics Research Group, School of Computing, Universiti Teknologi Malaysia, 81310, Skudai, Johor, Malaysia
[b]Institute for Artificial Intelligence and Big Data, Universiti Malaysia Kelantan, City Campus, Pengkalan Chepa, 16100, Kota Bharu, Kelantan, Malaysia
[c]Faculty of Bioengineering and Technology, Universiti Malaysia Kelantan, Jeli Campus, Lock Bag 100, 17600, Jeli, Kelantan, Malaysia
[d]Pervasive Computing Research Group, School of Computing, Universiti Teknologi Malaysia, 81310, Skudai, Johor, Malaysia
[e]Faculty of Computer Systems & Software Engineering, Universiti Malaysia Pahang, Kuantan, Pahang, 26300, Malaysia
[f]Faculty of Electrical and Electronic Engineering, Universiti Malaysia Pahang, Pekan, Pahang, Malaysia
[g]Department of Electronics, Information and Communication Engineering, Osaka Institute of Technology, Osaka, 535-8585, Japan
[h]University of Salamanca, Biomedical Research Institute of Salamanca/BISITE Research Group, Salamanca, Spain

ABSTRACT

Metabolic engineering involves the modification and alteration of metabolic pathways to improve the production of desired substance. The modification can be made using *in silico*gene knockout simulation that is able to predict and analyse the disrupted genes which may enhance the metabolites production. Global optimization algorithms have been widely used for identifying gene knockout strategies. However, their productions were less than theoretical maximum and the algorithms are easily trapped into local optima. These algorithms also require a very large computation time to obtain acceptable results. This is due to the complexity of the metabolic models which are high dimensional and contain thousands of reactions. In this paper, a hybrid algorithm of Cuckoo Search and Minimization of Metabolic Adjustment is proposed to overcome the aforementioned problems. The hybrid algorithm searches for the near-optimal set of gene knockouts that leads to the overproduction of metabolites. Computational experiments on two sets of genome-scale metabolic models demonstrate that the proposed algorithm is better than the previous works in terms of growth rate, Biomass Product Couple Yield, and computation time.

KEYWORDS:

Artificial intelligence; Bioinformatics; Metabolic engineering; Cuckoo Search; Minimization of Metabolic Adjustment; Gene knockout