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## Integration of omics into metabolic flux distribution by complementary elementary mode analysis for large-scale metabolic networks

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Metabolic pathway analysis becomes a core method for constructing a mathematical model that predicts the flux distribution for large-scale metabolic networks. Elementary mode (EM) analysis is potentially effective in integrating omics data into metabolic network analyses and tooffer great opportunities for studying functional and structural properties of metabolic pathways. The principal drawback of the ordinary EM analysis is that the number of EMs in a network suffers from a combinatorial explosion; huge computational time and use of a complete set of EMs gives rise to a scalability problem when applied to large-scale network models. To overcome such existing problems, we proposed a fast and efficient EM analysis named cEM analysis by implementing the EM decomposition method that generates major EMs responsible for a flux distribution. The  $\alpha$ -spectrum method based on flux balance analysis (FBA) is used to determine possible ranges of metabolic flux distributions necessary for the EM decomposition method. The maximum entropy principle (MEP) is used as an objective function for optimizing the EM coefficients (EMCs). To demonstrate the feasibility of the cEM analysis, we predicted the flux distributions of two large-scale metabolic networks of E. coli. The cEM analysis optimized the flux distribution much faster than the ordinary EM analysis without deteriorating the prediction accuracy. The cEM analysis will expose a new window for a genome-scale metabolic network, greatly reducing the computational time and memory cost. It enables to plan a genetic engineering strategy for large-scale metabolic networks, enhancing production of useful metabolites.

## Biography

Md. Bahadur Badsha was born in 1985. He received the BSc and MSc degrees from the Department of Statistics, Rajshahi University, Bangladesh, with top position in 2008 and 2009, respectively. He was a lecturer at the Department of Mathematics and Natural Science (MNS), BRAC University, Bangladesh, in 2012. Currently he isa Ph.D. scholar at Department of Bioscience and Bioinformatics, Kyushu Institute ofTechnology, Japan. He has published 15 articles in various indexed journals and conference proceedings. His research interests in metabolic engineering and mathematical model of CHO cells for producing antibody.

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