

欠定和不确定条件下胞内代谢通量的最大熵原理估算

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摘要: 在代谢工程和系统生物学领域, 计算机模拟比以往更为有效的应用于生物过程的分析 and 优化。胞内代谢通量可以用代谢通量分析和基元模式分析来估算。由于测定数据的不足和误差, 以及基元途径的冗余, 经常很难得到准确的代谢通量分布数据。本研究提出一种基于最大熵原理的算法来计算基元模式系数。欠定和不确定条件下, 通过胞外代谢通量数据估算胞内代谢通量分布。为了检验算法的可行性, 对杂交瘤细胞、枯草芽孢杆菌和大肠杆菌的胞内代谢通量分布做了估算。本研究提出的基于最大熵原理的优化算法避免了对细胞状态的生理学假设。与其他目标函数相比, 可以更为可靠和可行的估算胞内代谢通量分布。

关键词: 基元模式, 酶控制通量, 最大熵原理, 代谢通量分析

Estimation of Intracellular Flux Distribution under Underdetermined and Uncertain Conditions by Maximum Entropy Principle

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Abstract: *In silico* simulation is much more powerful and reliable than before for the bioprocess analysis and optimization in the fields of metabolic engineering and systems biology. The intracellular flux distribution could be estimated by Metabolic Flux Analysis (MFA) and Elementary Mode Analysis (EMA). It is always difficult to obtain an accurate flux distribution due to the insufficiencies, the measurement errors of the experimental data and the redundancy of EMs. An algorithm has been proposed to determine the Elementary Mode Coefficients (EMCs) by the maximum entropy principle (MEP). The intracellular flux distribution is calculated from the extracellular fluxes under underdetermined and uncertain conditions. To demonstrate the feasibility of this algorithm, it is used to estimate of the intracellular flux distribution for hybridoma, *Escherichia coli* and *Bacillus subtilis*. The MEP algorithm avoids any physiological hypotheses for the cellular states. It is reliable and feasible for the estimation of the intracellular flux distribution compared with other objective functions.

Keywords: elementary mode, enzyme control flux, maximum entropy principle, metabolic flux analysis

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