

91. Identification of Conserved Metabolic Moieties by Graph Theoretical Analysis of Atom Transition Networks

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Project Goals: We aim to develop scalable algorithms for estimation of reaction kinetic parameters in metabolic networks from nonstationary isotope labeling experiments [1]. Computational modeling is essential for the design and analysis of isotope labeling experiments. Current modeling frameworks are limited to small metabolic networks as they require algorithms that scale poorly with network size. We propose to simplify these models by reducing the number of atoms that need to be considered for labeling. To achieve this we will take advantage of the fact that not all atoms traverse metabolic networks independently of each other. Groups of atoms, known as conserved moieties, remain intact through all reactions of a network [2]. Atoms belonging to the same moiety do not have to be modeled separately but can be represented as a single model variable.

All conserved moieties in a metabolic network can be represented as nonnegative integer vectors in the left null space of the network's stoichiometric matrix. Algorithms exist for computing such vectors based on reaction stoichiometry [3, 4, 5] but none are globally convergent. Moreover, existing algorithms give no information about moiety structure and may return vectors that do not correspond to any moieties. Here, we present a novel algorithm for computing conserved moieties in metabolic networks by graph theoretical analysis of the corresponding atom transition networks. Our algorithm returns the exact group of atoms belonging to each moiety as well as the corresponding vector in the left null space of the input stoichiometric matrix. Computation time appears to scale linearly with network size. Computation of conserved moieties in a large metabolic network with more than 4,000 internal reactions completed in approximately two hours.

References

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This work was supported by the U.S. Department of Energy, Offices of Advanced Scientific Computing Research and the Biological and Environmental Research as part of the Scientific Discovery Through Advanced Computing program, grant #DE-SC0010429.