Comparison of atom mapping algorithms for metabolic reactions

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Project Goals: We aim to represent metabolic reactions at atomic resolution by saturating metabolic databases with structural formulas for metabolites and atom mappings for reactions. Atom level representations of metabolites and reactions extend the range of applications for metabolic network reconstructions to include, for example, estimation of thermodynamic parameters [1], identification of conserved moieties [2], and stable isotope assisted metabolic flux analysis [3].

Metabolic reactions conserve mass and elements. Each instance of a reaction must therefore map every substrate atom to a specific product atom of the same element. Realisable atom mappings are determined by organic chemistry and reaction mechanisms. Atom mapping data for metabolic reactions open the door to a growing list of applications [3, 4, 5, 2] that are not available with data at the level of reaction stoichiometry. Until recently, acquiring atom mapping data for genome-scale metabolic network reconstructions was a labour intensive prospect. However, a number of algorithms to predict atom mappings have now become available. Here, we compare four recently published algorithms on criteria including accuracy, speed, and availability. The algorithms are DREAM [6], Pathway Tools [7], ICMAP [8] and CLCA [9]. Accuracy was determined by comparison to a set of manually curated atom mappings. We discuss common issues including hydrogen atom mapping and molecular symmetry. We conclude with an effective strategy to increase the coverage of high quality atom mapping data in the metabolic databases.

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