Highlighting Metabolic Strategies using Network Analysis over Strain Optimization Results

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Abstract

The field of Metabolic Engineering has been growing, supported by the increase in the number of annotated genomes and genome-scale metabolic models. In silico strain optimization methods allow to create mutant strains able to overproduce certain metabolites of interest in Biotechnology. Thus, it is possible to reach (near-) optimal solutions, i.e. strains that provide the desired phenotype in computational phenotype simulations. However, the validation of the results involves understanding the strategies followed by these mutant strains to achieve the desired phenotype, studying the different use of reactions/pathways by the mutants. This is quite complex given the size of the networks and the interactions between (sometimes distant) components. The manual verification and comparison of phenotypes is typically impossible.

Here a methodology to validate in silico results though the use network topology analysis is proposed, our method is based in two algorithms the first, called simulation filtering, uses a metabolic and the results of a in silico to create a smaller network which is a "snapshot" of the metabolism in the simulated conditions, the second, called multiple topological network comparison, compares one metabolic network with a set of similar networks in order to identify the more common differences.

Our method identifies the more commune alterations that occur from the wildtype when an organism is manipulated thus highly contributing to elucidate the strategies that lead to successful mutants.

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