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Tailoring the metabolism against mutations NATALI GULBAHCE, Northeastern University, ADILSON E. MOTTER, Northwestern University, EIVIND ALMAAS, Lawrence Livermore National Laboratory, ALBERT LASZLO BARABASI, Northeastern University — In the post-genomic era, organisms can be modelled at the whole-cell level in silico via steady state methods to describe their metabolic capabilities. We use two such methods, Flux Balance Analysis and Minimization of Metabolic Adjustment to explore the behavior of cells (of E. coli and S. cerevisiae) after severe mutations. We propose experimentally feasible ways of modifying the underlying biochemical reaction network of a mutant cell such that cell functionality, in particular growth rate, is significantly improved.

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