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Poster presentation

Thermodynamically constrained steady state solution space of the *E. coli* metabolic network

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Metabolic engineering can be accelerated using a comprehensive mass & charge balanced stoichiometric reconstruction of an organism-specific metabolic network. Boundary constraints, representing growth in a defined medium, allow the characterisation of candidate metabolic steady states of a metabolic network. Each steady state is represented by a time invariant flux through each reaction and the concentration of each metabolite in the network. Markov-chain, monte-carlo algorithms are used to uniformly sample the steady state solution space, i.e. the volume occupied by the set of feasible solutions. This work presents the first attempt to explicitly include the conservation of energy and the second law of thermodynamics as constraints in a novel sampling algorithm. In *E. coli* the intersection of the thermodynamically feasible solution space with the mass & charge balanced solution space represents a minute fraction of the latter's volume. Constraints based modelling can differentiate feasible from infeasible states in a binary fashion. In reality, infeasible represents the infinitely improbable, whereas not all feasible solutions are equally probable. At equilibrium, extremal principles are used to predict the most probable solutions within the set of feasible. However, *E. coli* metabolism represents an evolved non-equilibrium system and no clear evidence exists as to what, if any, extremal principal applies to living systems. Here we apply candidate extremal principals to predict the probability of non equilibrium steady state solutions. Understanding how thermodynamic driving forces manifest in a particular metabolic phenotype is aimed at predicting the phenotype of genetically engineered *E. coli* strains.