

Title: MONGOOSE - a new approach to metabolic network analysis

Constraint-based metabolic models are currently the only methodology that allows metabolic network analysis on a genome-scale. Curiously, the results of flux balance analysis may vary with the software being run. We introduce MONGOOSE (MetabOlic Network GrOwth Optimization Solved Exactly), an algorithmic pipeline for analyzing the structure of constraint-based metabolic models in exact rational arithmetic. When applying the pipeline to 98 existing genome-scale metabolic network models we find that the biomass reaction is surprisingly blocked in nearly half of them. We propose a new principled approach for unblocking these reactions and extend it to other important problems: identifying essential and synthetic lethal reactions and designing minimal media.