SLIMEr: probing flexibility of lipid metabolism in yeast with an improved constraint-based modeling framework

Background

A recurrent problem in genome-scale metabolic models (GEMs) is to correctly represent lipids as biomass requirements, due to the numerous of possible combinations of individual lipid species and the corresponding lack of fully detailed data. In this study we present SLIMEr, a formalism for correctly representing lipid requirements in GEMs using commonly available experimental data. Results

SLIMEr enhances a GEM with mathematical constructs where we Split Lipids Into Measurable Entities (SLIME reactions), in addition to constraints on both the lipid classes and the acyl chain distribution. By implementing SLIMEr on the consensus GEM of Saccharomyces cerevisiae, we can represent accurate amounts of lipid species, analyze the flexibility of the resulting distribution, and compute the energy costs of moving from one metabolic state to another. Conclusions

The approach shows potential for better understanding lipid metabolism in yeast under different conditions. SLIMEr is freely available at https://github.com/SysBioChalmers/SLIMEr.

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