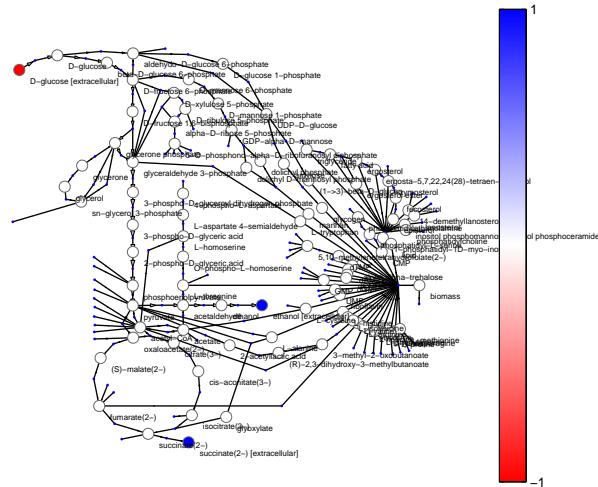
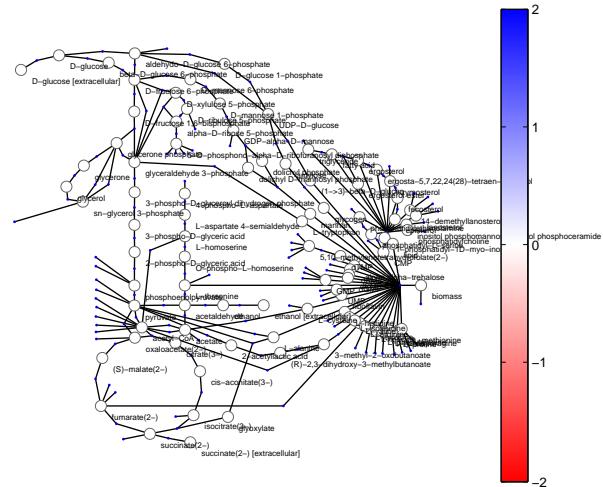


# Saccharomyces cerevisiae (Stanford et al.)

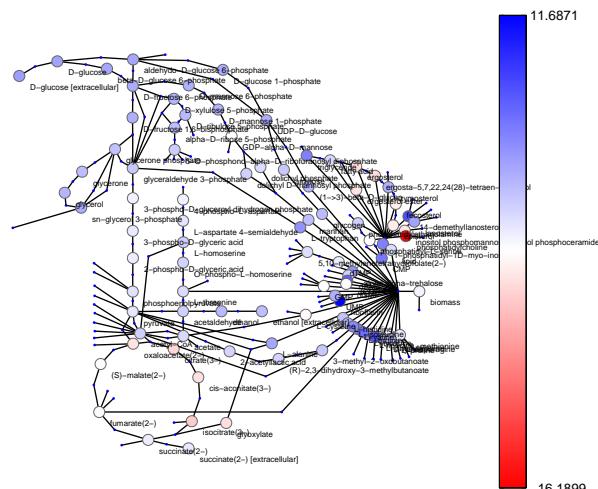
(a) Metabolic fluxes (mM/s)



(b) Concentrations (mM)



(c) Chemical potentials (kJ/mol)



(d) Thermodynamic forces (kJ/mol)

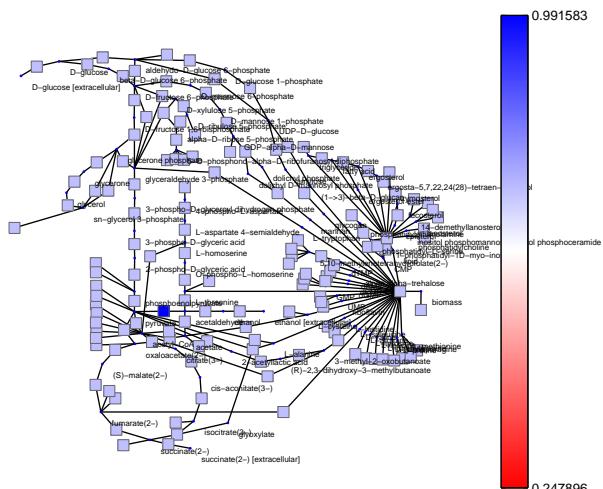


Figure 1: Model construction step by step. (a) Thermodynamically feasible flux distribution (grey arrows). (b) Metabolite levels. (c) Chemical potentials. (d) Thermodynamic driving forces.

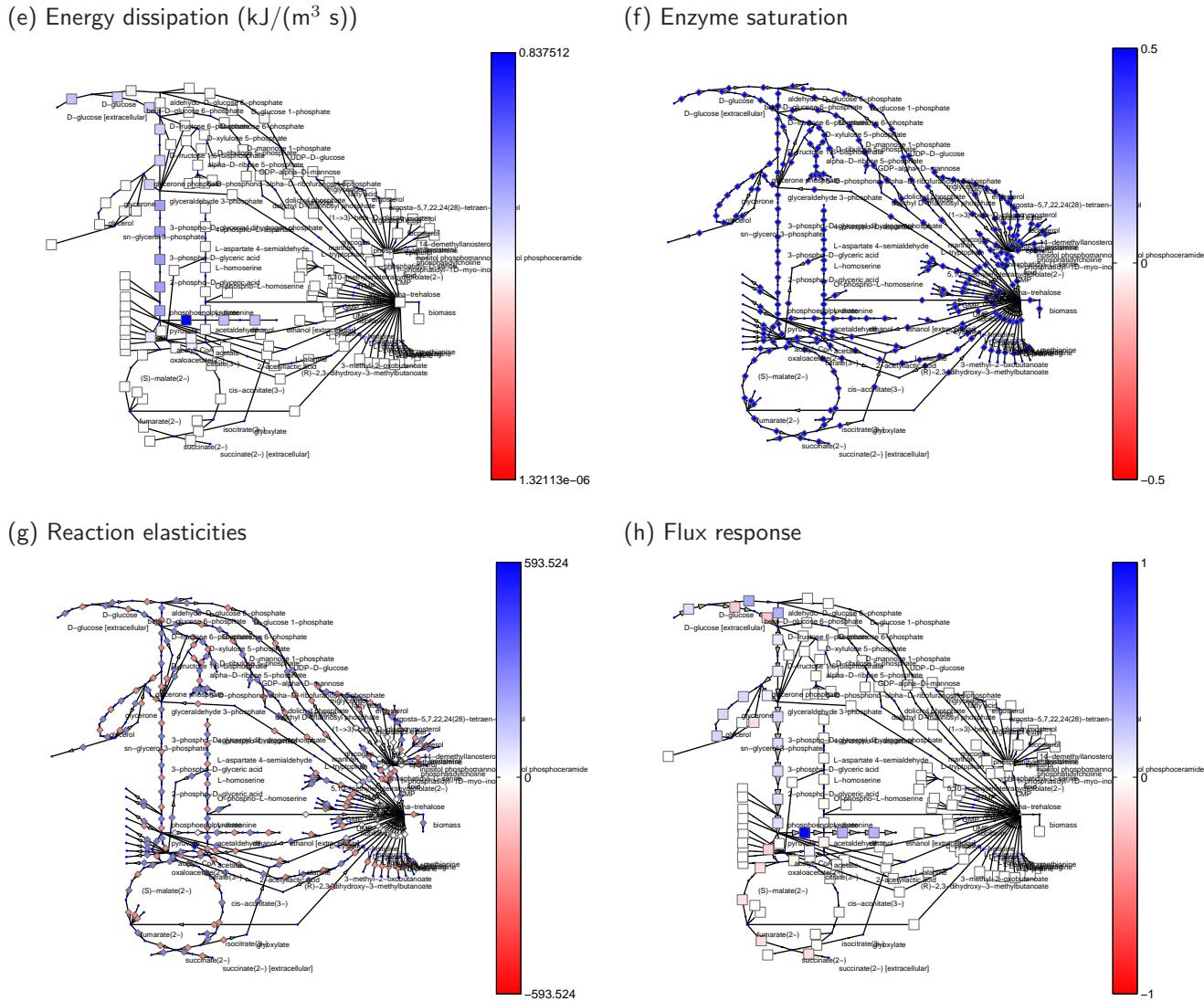
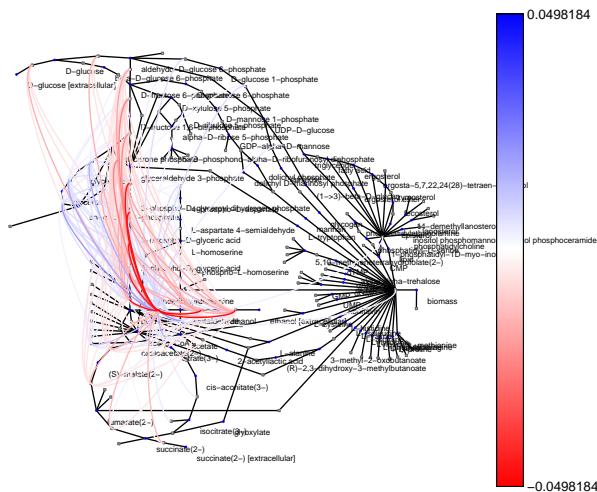
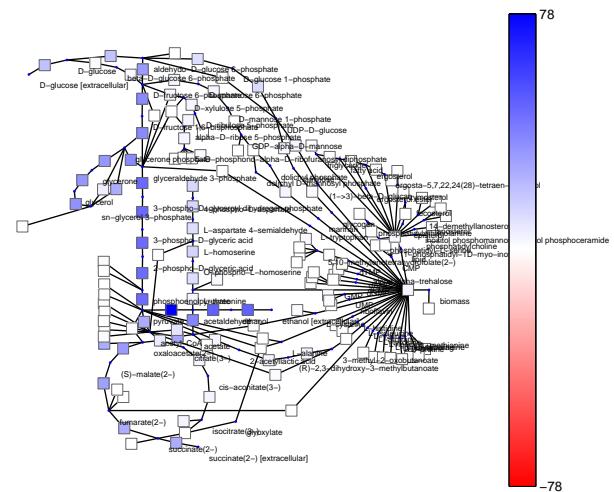


Figure 2: Model construction step by step (continued). (e) Local dissipation of Gibbs free energy (driving force multiplied by flux). (f) Saturation values. (g) Scaled elasticities. (h) Scaled enzyme response coefficients, predicted by elasticity sampling. Positive values are shown in blue, negative values in red, zero values in white.

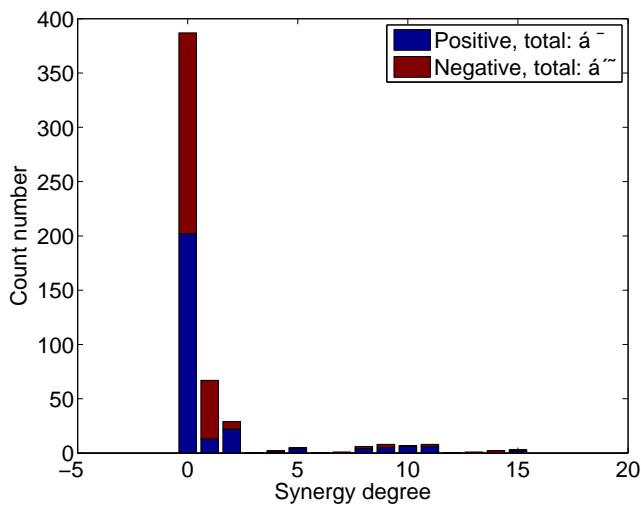
Synergies (2nd order scaled control)



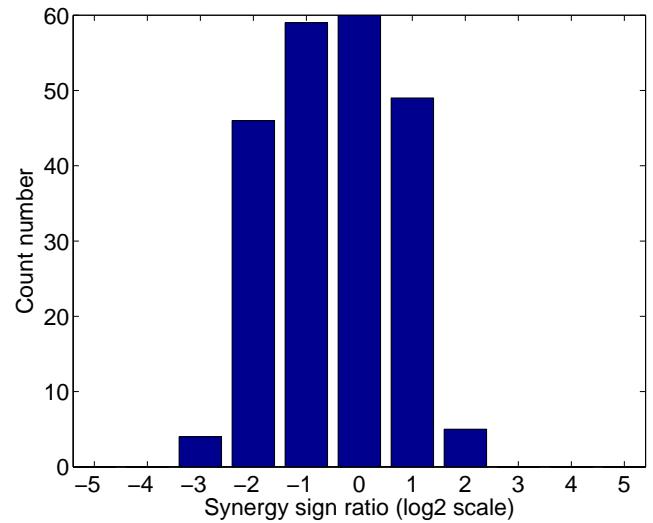
Synergy degrees



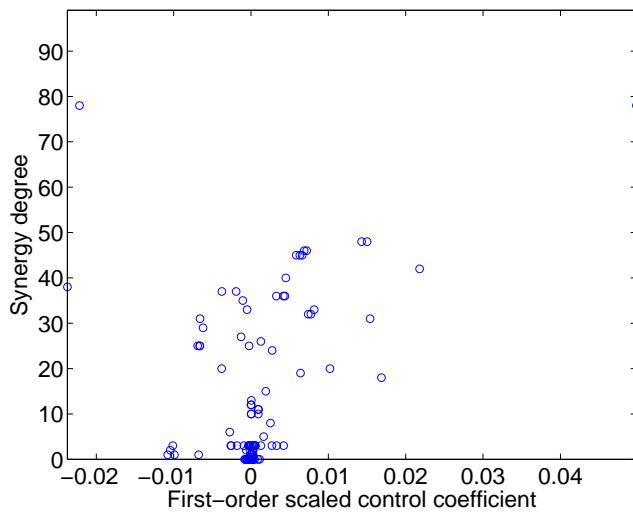
Synergy degree distribution



Fraction syn. deg. (positive) / syn. deg. (negative)



Synergy degrees and scaled control



Synergy clusters

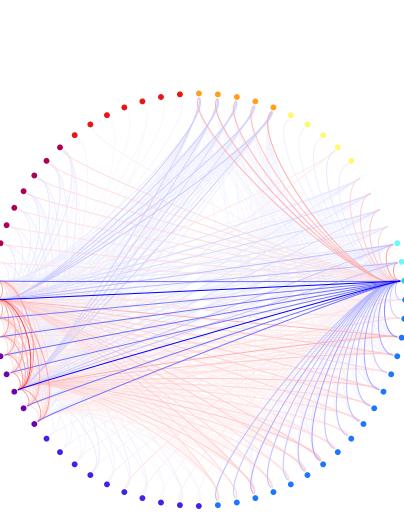


Figure 3: Synergies: statistics

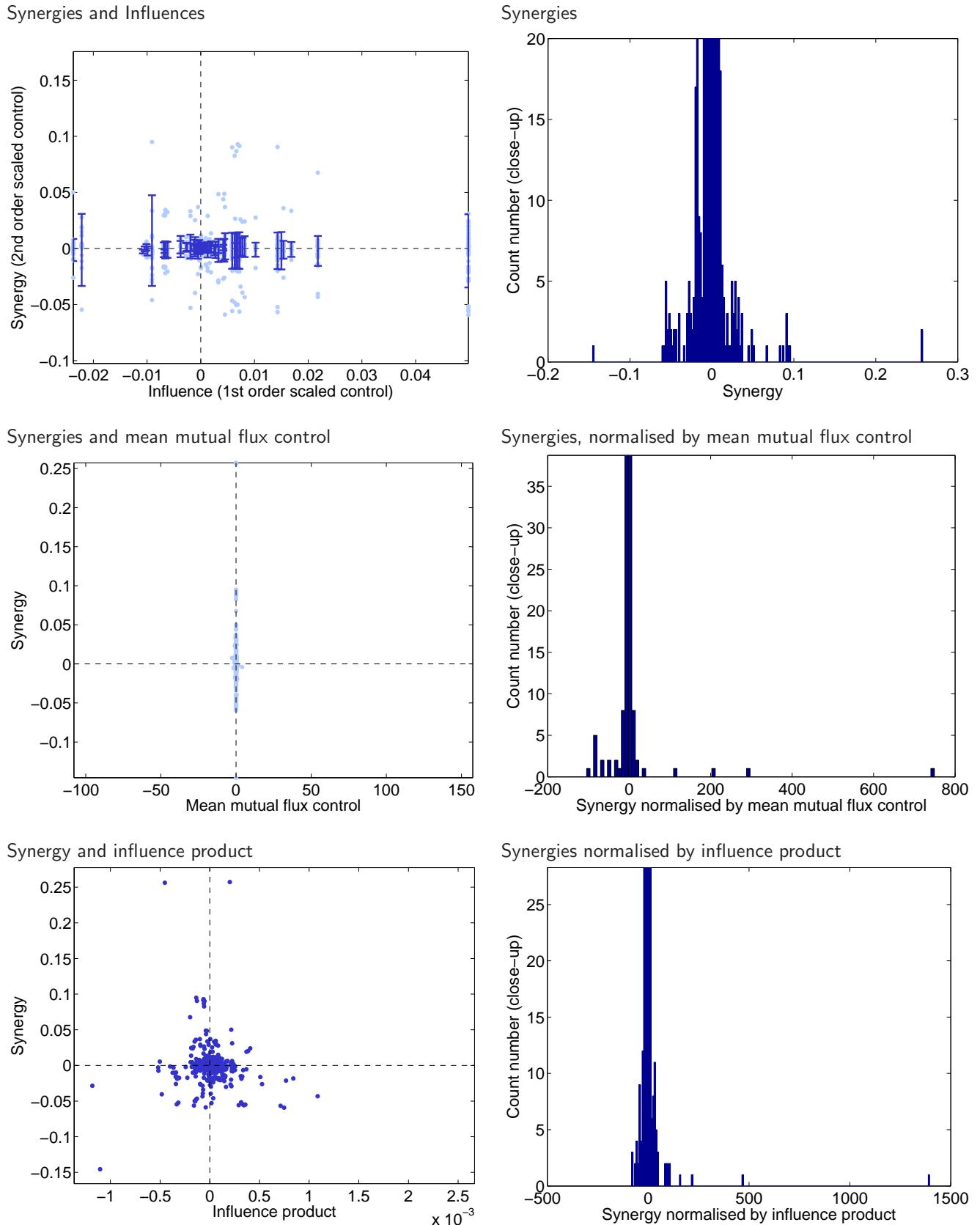


Figure 4: Synergies: correlations to other quantities

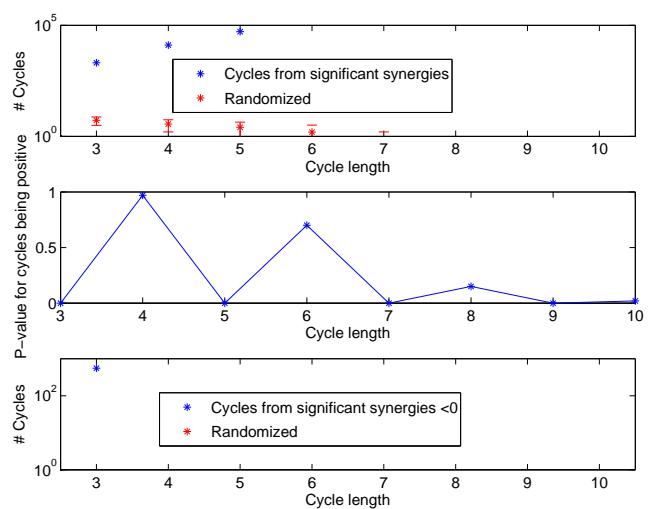


Figure 5: Statistics of synergy cycles