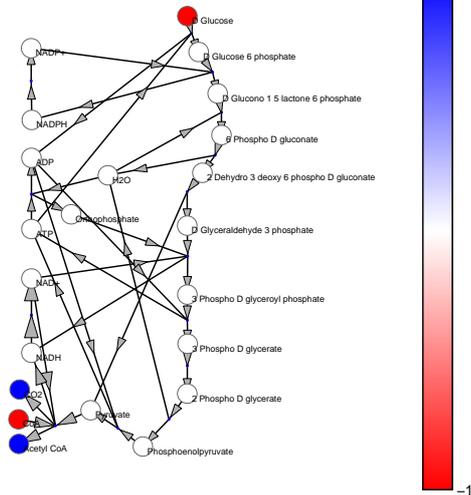
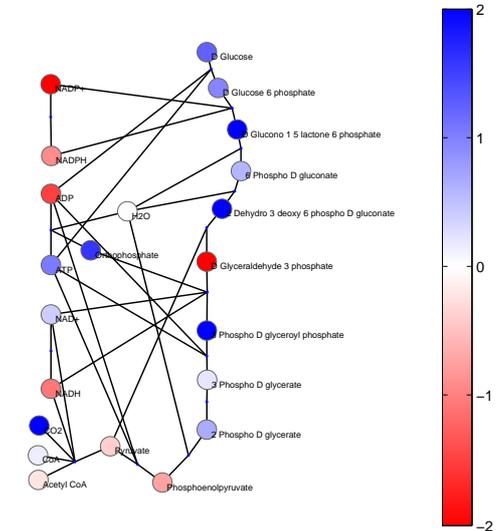


Escherichia coli Entner-Doudoroff pathway

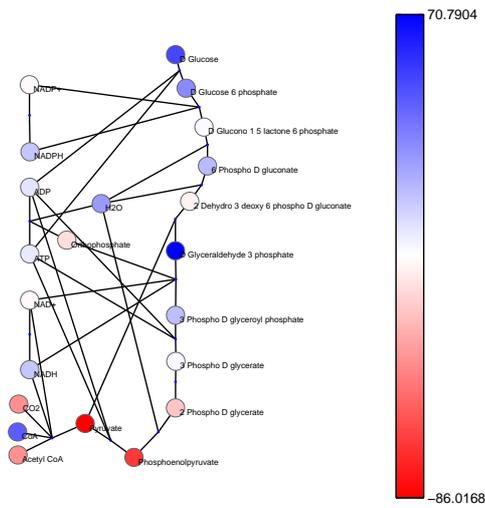
(a) Metabolic fluxes (mM/s)



(b) Concentrations (mM)



(c) Chemical potentials (kJ/mol)



(d) Thermodynamic forces (kJ/mol)

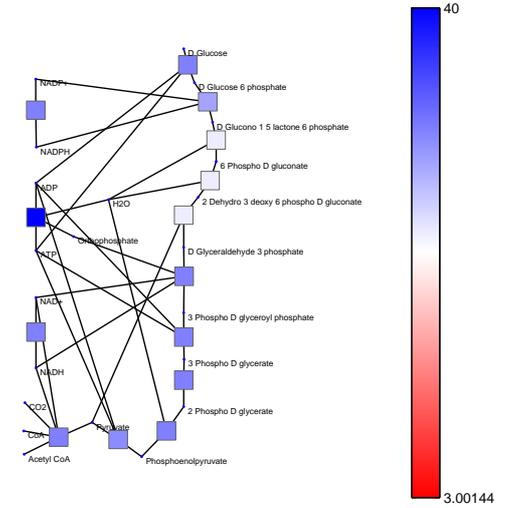
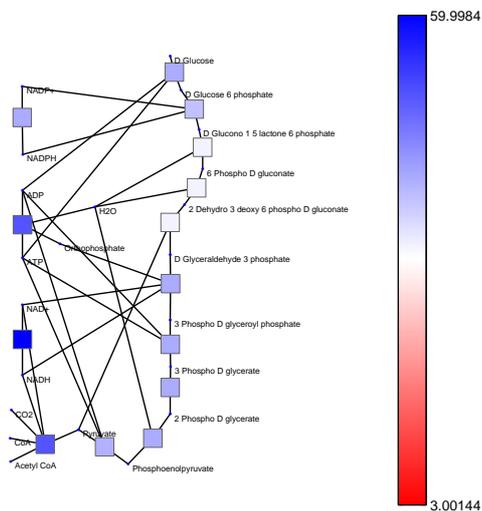
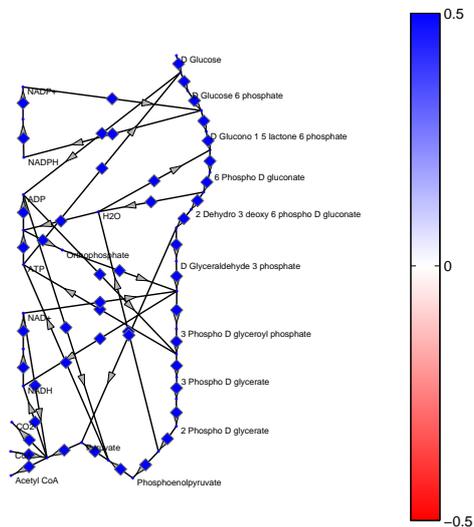


Figure 1: Model construction step by step. (a) Thermodynamically feasible flux distribution (grey arrows). (b) Metabolite levels. (c) Chemical potentials. (d) Thermodynamic driving forces.

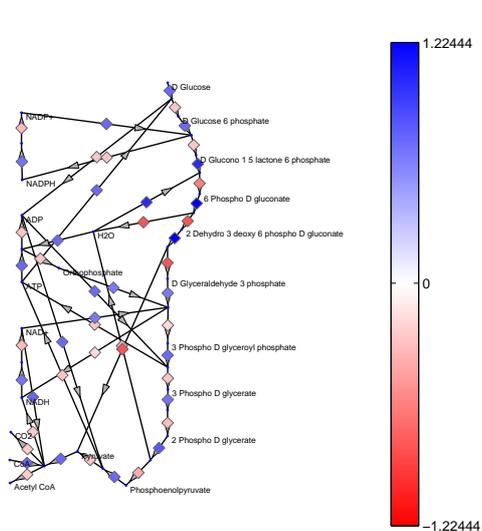
(e) Energy dissipation ($\text{kJ}/(\text{m}^3 \text{ s})$)



(f) Enzyme saturation



(g) Reaction elasticities



(h) Flux response

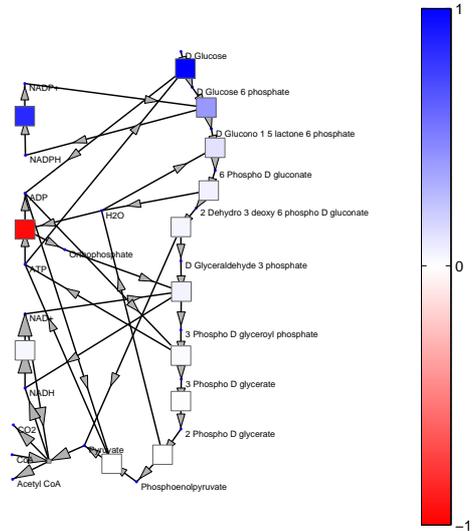
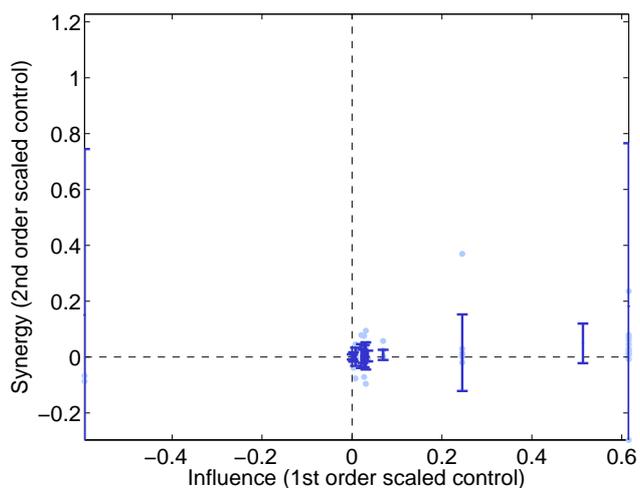
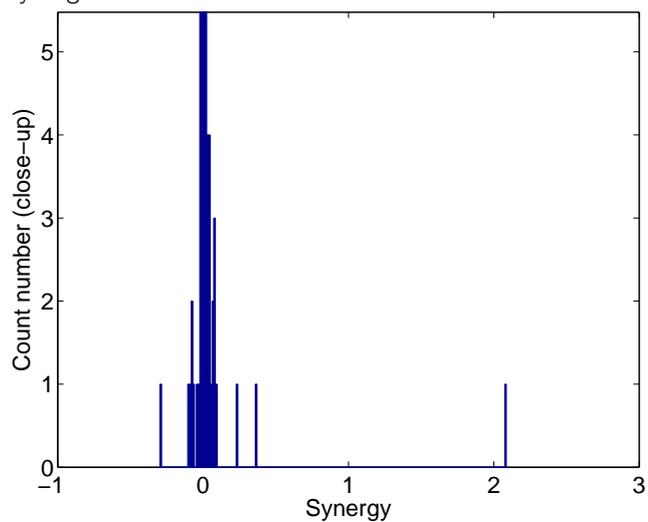


Figure 2: Model construction step by step (continued). (e) Local dissipation of Gibbs free energy (driving force multiplied by flux). (f) Saturation values. (g) Scaled elasticities. (h) Scaled enzyme response coefficients, predicted by elasticity sampling. Positive values are shown in blue, negative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

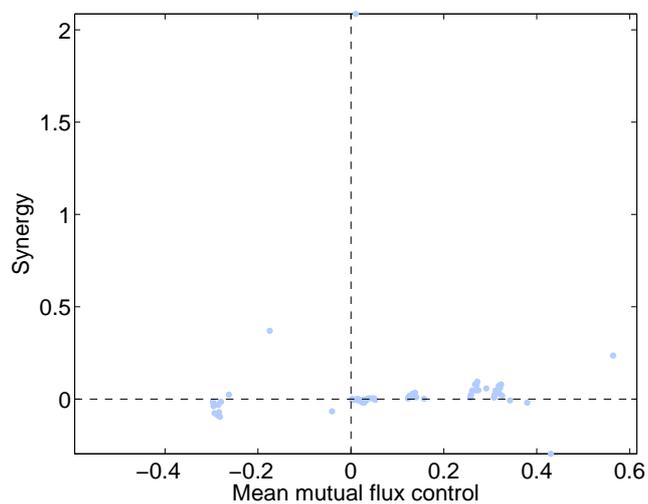
Synergies and Influences



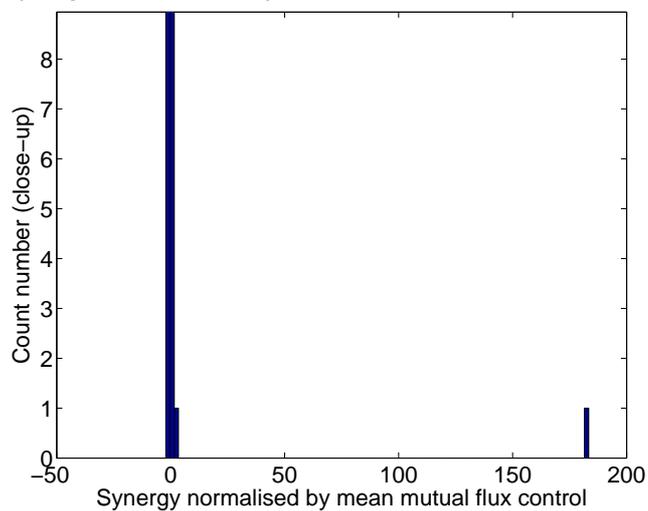
Synergies



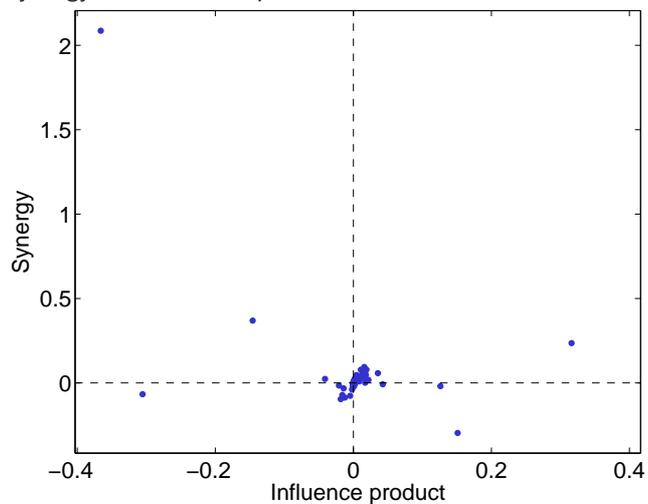
Synergies and mean mutual flux control



Synergies, normalised by mean mutual flux control



Synergy and influence product



Synergies normalised by influence product

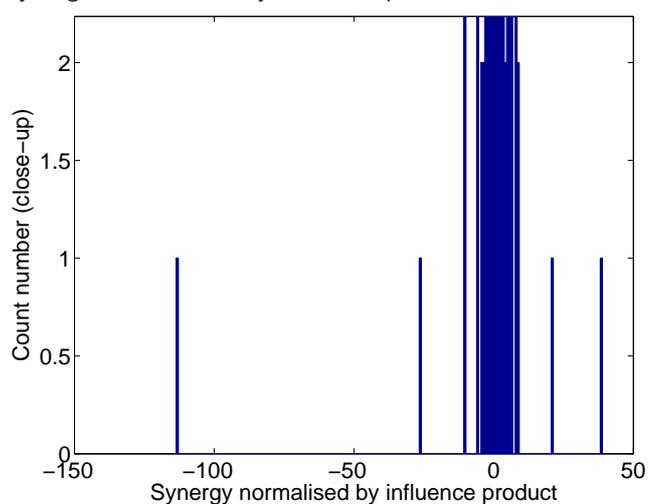


Figure 4: Synergies: correlations to other quantities

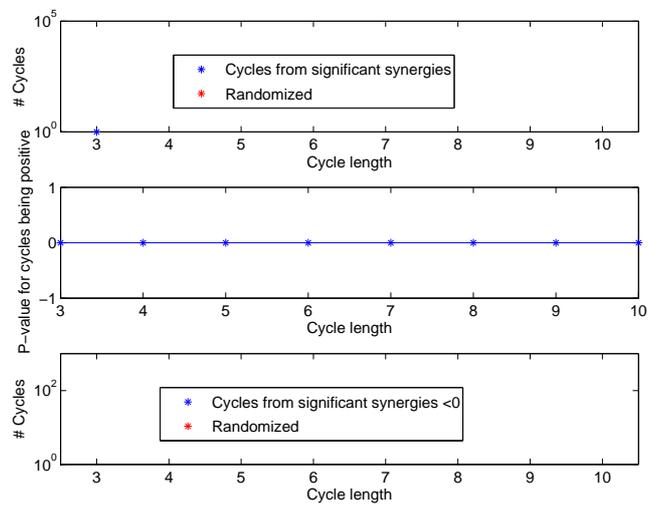


Figure 5: Statistics of synergy cycles