Enzyme rhythms in model linear_chain4.speedy

Model name: linear_chain4

o Optimisation problem
- Protein turnover time 1 s = 0.0167 min
- Perturbed parameter(s) : x1
- Perturbation frequency f : 0.0333/s (period 30 s)
- Scored quantity: v4
- Fitness-averaged fitness
- No posttranslational rhythms allowed
- Standard frequency considered f : 0.0333/s (period 30 s)

o Model properties:
- inactive_enzymes: 0
- balanced_reference_state: 1
- consider_external_rhythm: 1
- adaptive_rhythm: 1
- spontaneous_rhythm: 0
- spontaneous_rhythm_at_omega: 0
- has_spontaneous_rhythm_and_inactive_enzymes: 0

o No beneficial autonomous oscillation found

o Fitness changes after external perturbation at frequency f=0.0333/s
- Change by perturbation alone (xx): -1.25e-09
- Change by adaption synergies (xu): 0.00348
- Change by periodic enzyme (uu): -0.0012
- Change by enzyme mean shift (u): 7.04e-10
- Total fitness change : 0.00228
- Fitness gain by adaption : 0.00228
- Maximum adaptive fitness found (in tested range) at frequency f =0.0891/s (period 11.2 s)
- Predicted max. fitness change (adaptive, num. opt, full ampl. constraints) at frequency f =0.0891: 0.00282

o autonomous oscillations?
- No beneficial autonomous oscillations (2nd order, amplitude below 1/2 of mean) found at frequency f = 0.0333/s (principal synergy = -0.0501): Predicted fitness change -0.000389

o Numerical calculation (responsive, f=0.0333)
- Fitness change (fitness-averaged): -2.68e-09
- Fitness change (state-averaged): -1.43e-09
o Numerical calculation (adaptive, f=0.0333)
- Fitness change (fitness-averaged): 0.00235
- Fitness change (state-averaged): 0.00297

o Numerical calculation (autonomous rhythm, amplitude below 1/2 of mean, f=0.0333)
- Fitness change (fitness-averaged) : 5.47e-06
- Fitness change (state-averaged): 5.47e-06

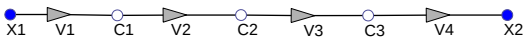

Figure 1: Network and reference flux

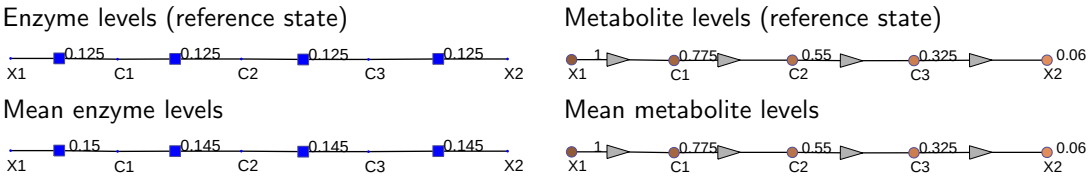

Figure 2: Reference state (top) and mean state during oscillation (bottom).

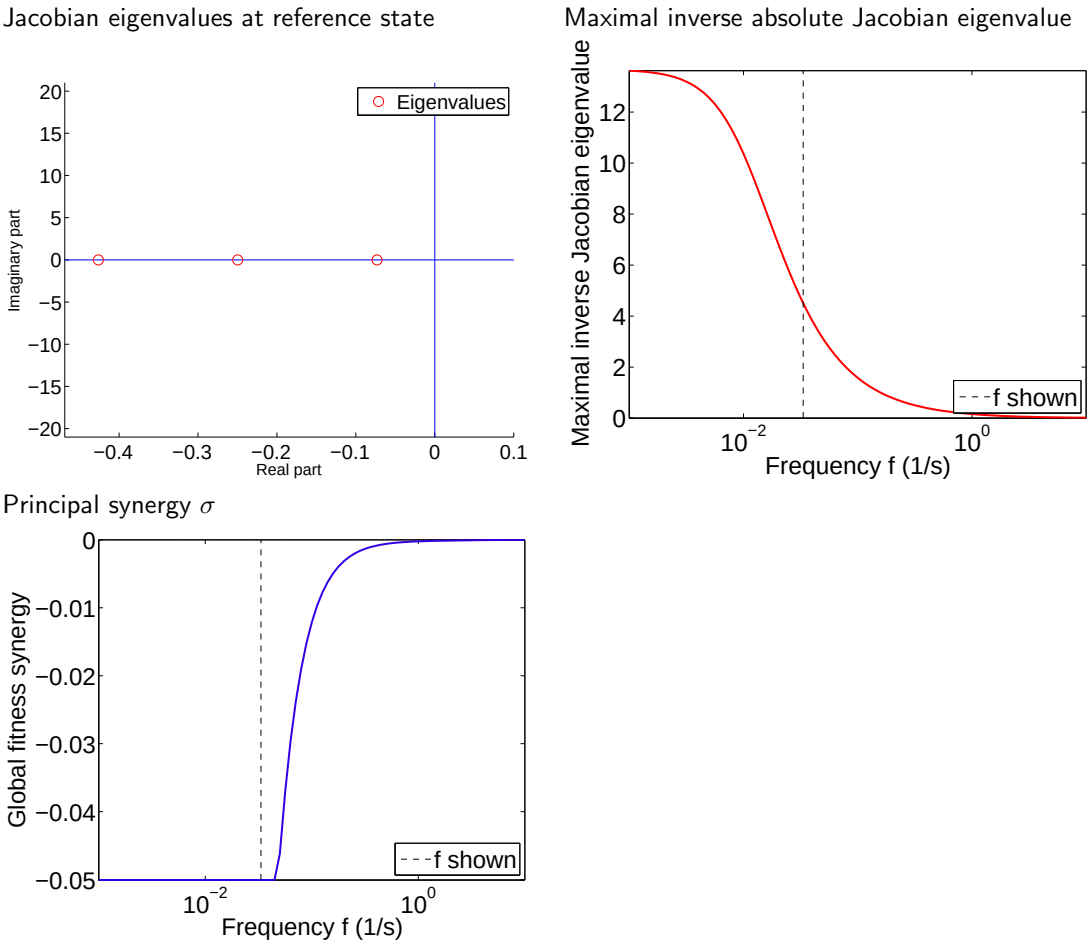

Figure 3: Control analysis. Left: Global fitness synergy (maximal fitness curvature eigenvalue), as a function of the frequency. Right: Relative amplitudes of individual enzymes for the least wasteful enzyme mode (components of the leading fitness curvature eigenvector).

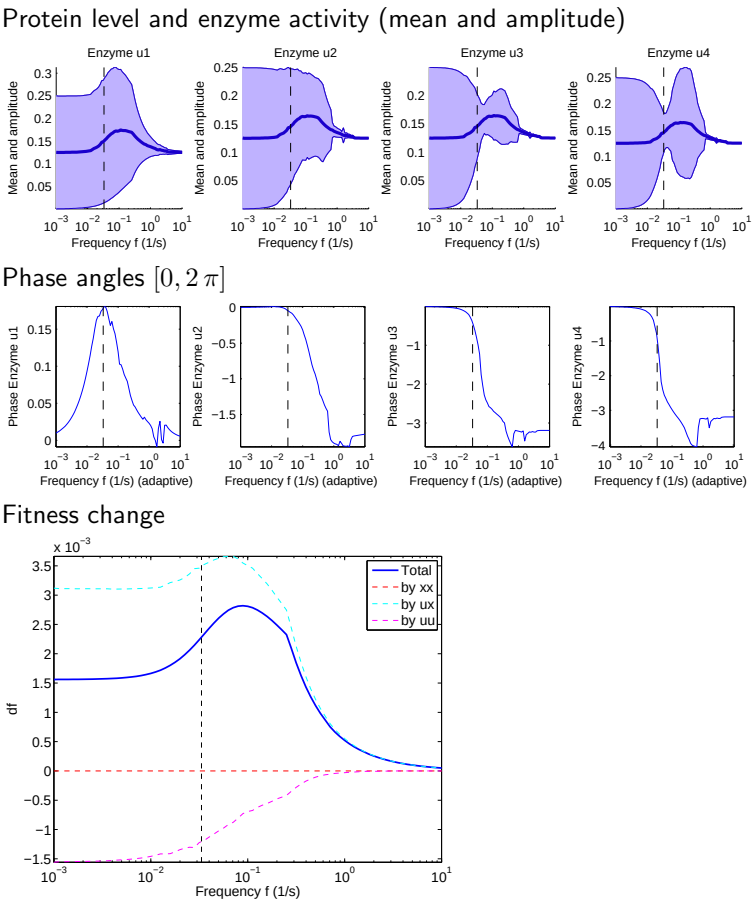

Figure 4: Adaptive oscillations. Left: amplitudes of protein levels (blue) and modification (grey). Right: phase shifts.

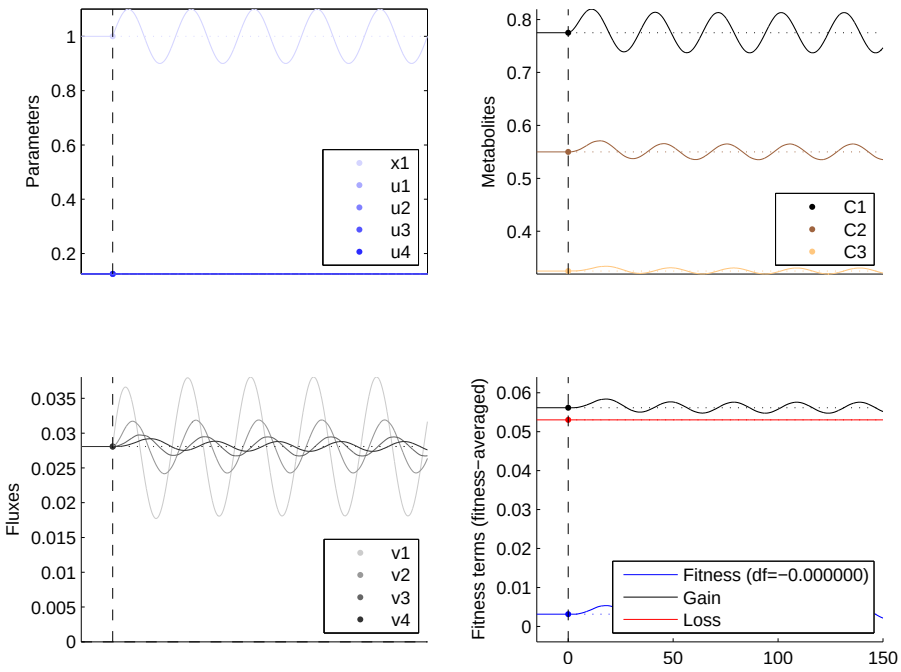

Figure 5: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first page.

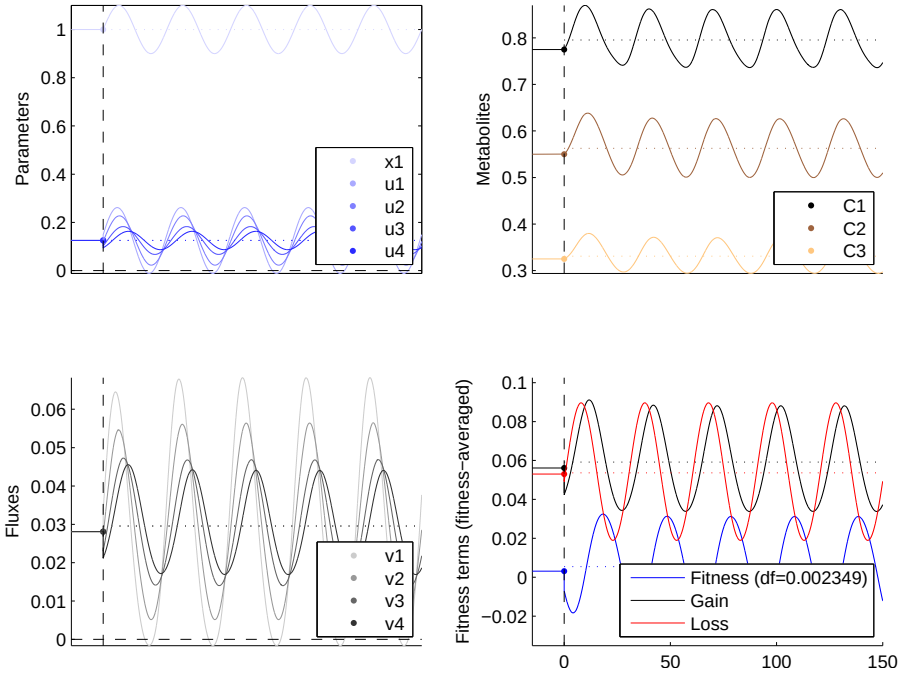

Figure 6: Numerical calculations: adaptive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first page.

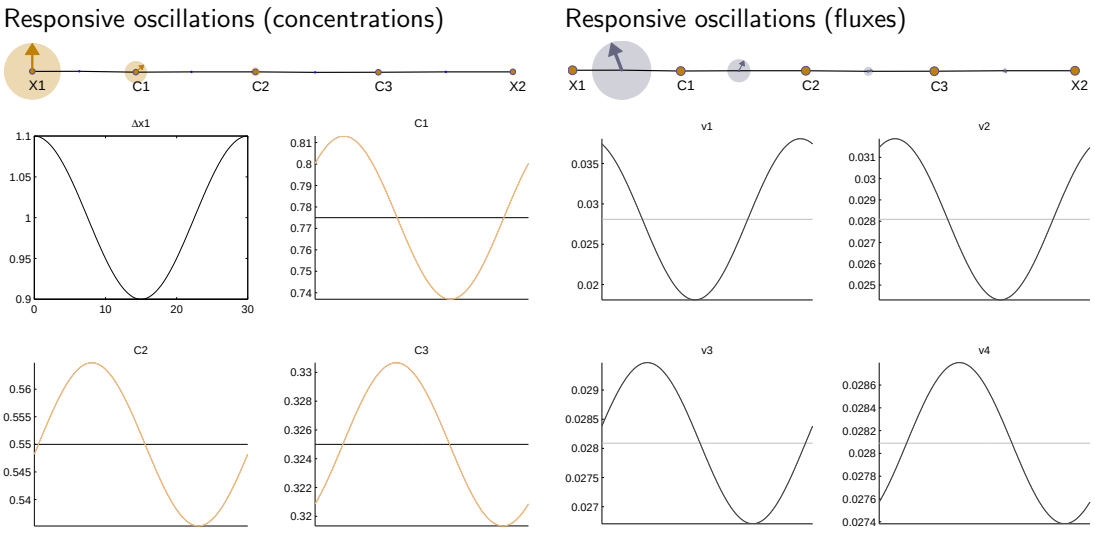

Figure 7: Responsive oscillations (local expansion; arrows: absolute changes) Perturbation frequency see first page.

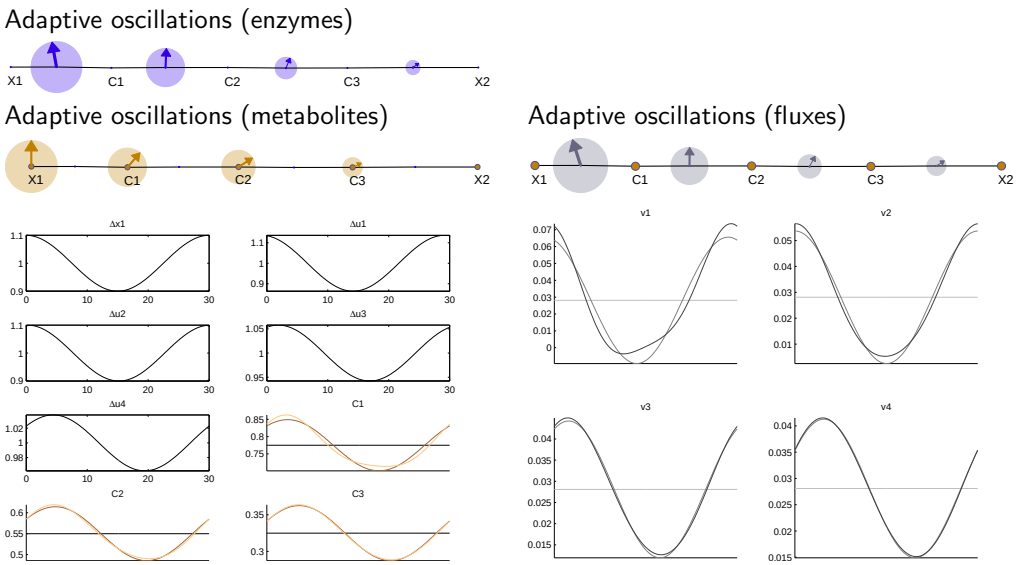

Figure 8: Adaption to forced oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

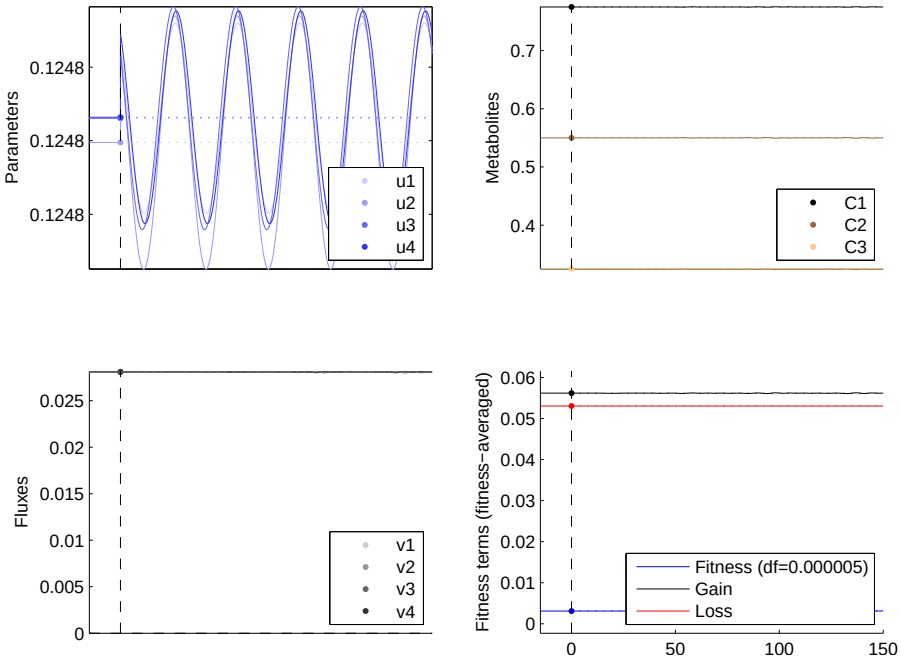

Figure 9: Tentative spontaneous oscillations. Perturbation frequency see first page.

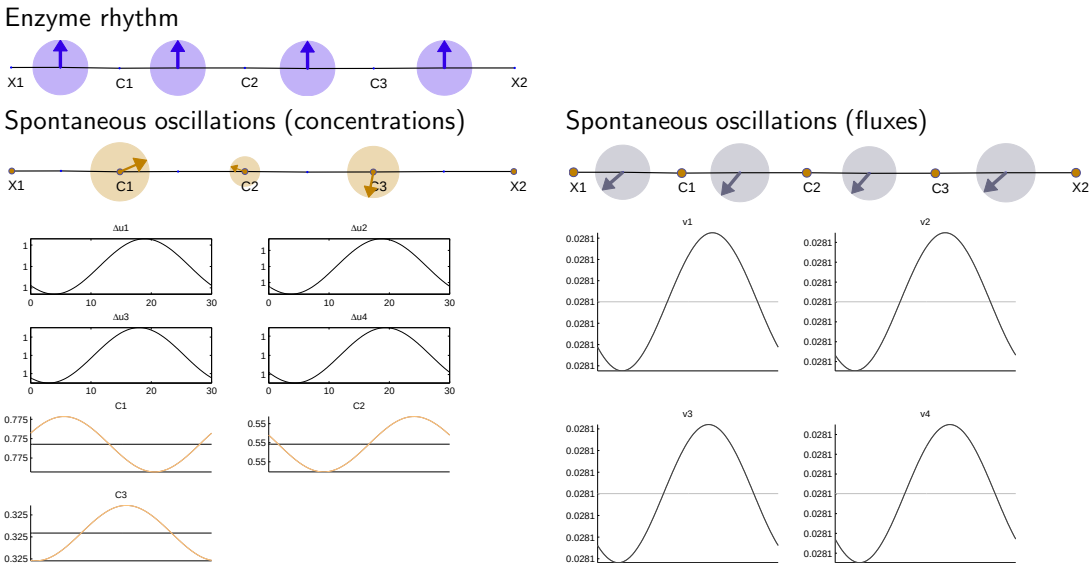

Figure 10: Tentative spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

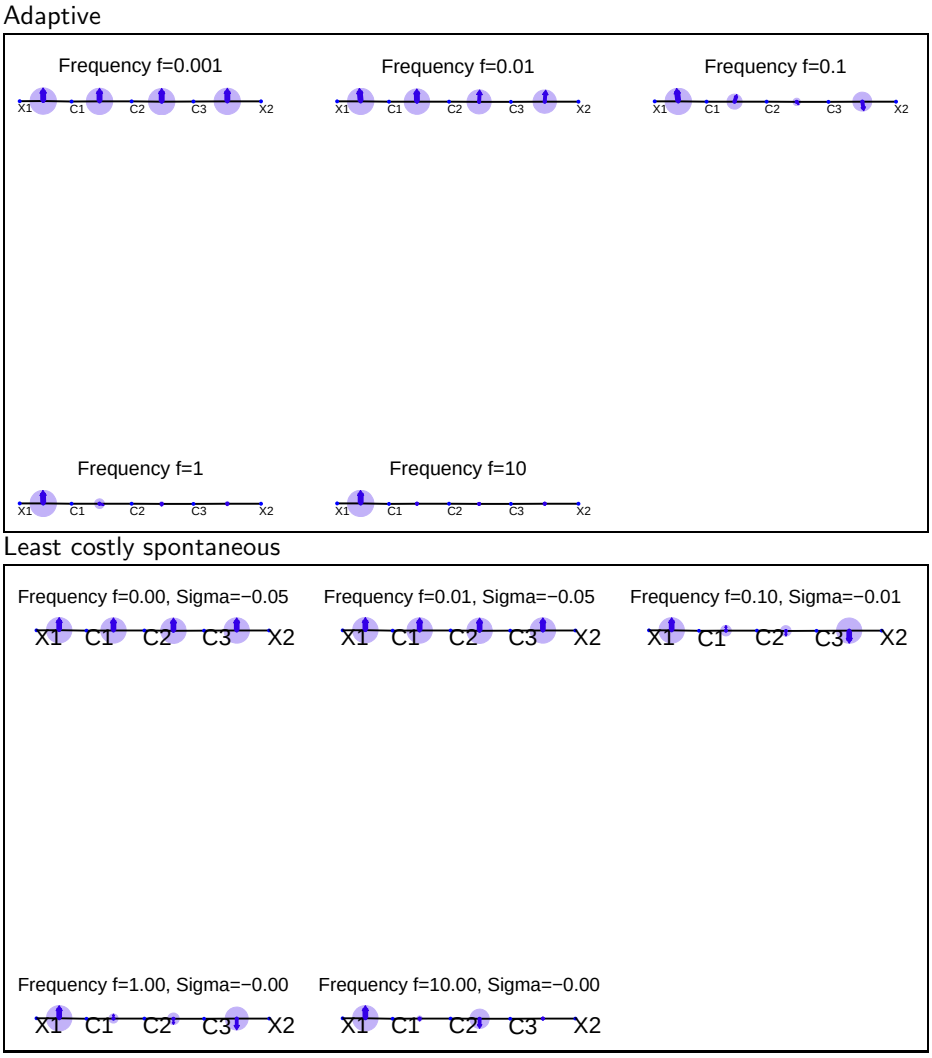

Figure 11: Potential oscillations at various frequencies (local expansion).

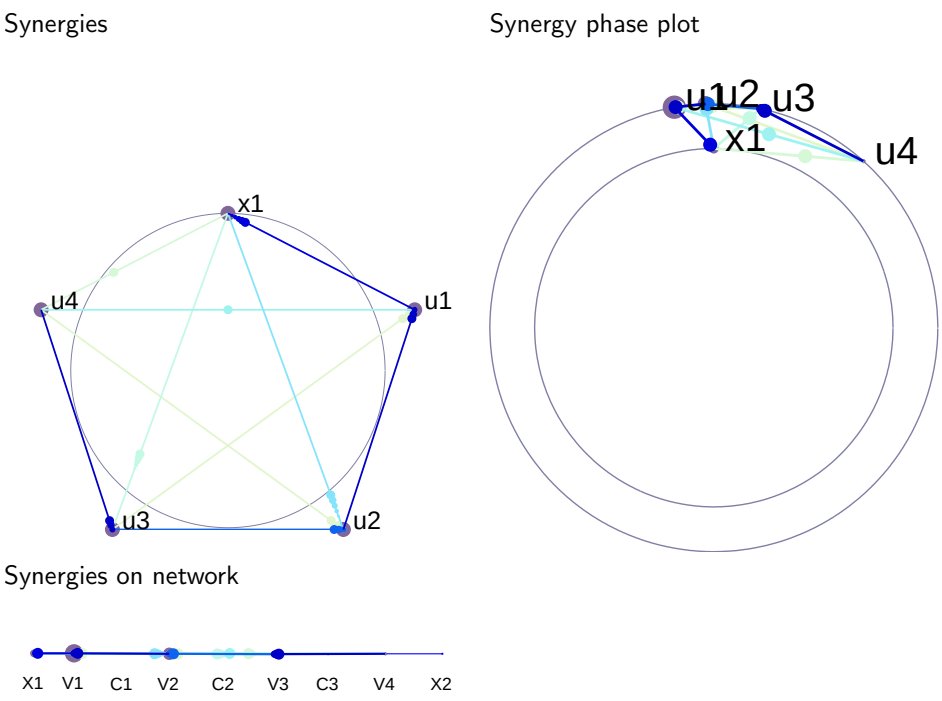

Figure 12: Periodic economic potentials and direct enzyme values.