## Enzyme rhythms in model cost\_coupling.speedy

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Model name: cost_coupling
o Optimisation problem
- Protein turnover time 1 s = 0.0167 min
- Perturbed parameter(s) : x1
- Perturbation frequency f: 0.1/s (period 10 s)
- Scored quantity: v1
- Scored quantity: v2
- Fitness-averaged fitness
- No posttranslational rhythms allowed
- Standard frequency considered f: 0.1/s (period 10 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 self-induced oscillation found
o Fitness changes after external perturbation at frequency f=0.1/s
- Change by perturbation alone (xx): -0.0418
- Change by adaption synergies (xu): 1.73
- Change by periodic enzyme (uu): -0.413
- Change by enzyme mean shift (u): -3.82e-09
- Total fitness change: 1.28
- Fitness gain by adaption: 1.32
- Maximum adaptive fitness found (in tested range) at frequency f = 0.01/s (period 100 s)
- Predicted maximal fitness change (adaptive, numeric opt, full amplitude constraints) at frequency f =0.01: 1.5
o Self-induced oscillations?
- No beneficial self-induced oscillations (2nd order, amplitude below 1/2 of mean) found at frequency f = 0.1/s
(principal synergy = -0.005): Predicted fitness change -0.0837
o Numerical calculation (responsive, f=0.1)
- Fitness change (fitness-averaged): -0.0418
- Fitness change (state-averaged): 1.06e-12
o Numerical calculation (adaptive, f=0.1)
- Fitness change (fitness-averaged): 1.31
- Fitness change (state-averaged): 1.88
o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=0.1)
- Fitness change (fitness-averaged): 9.11e-13
- Fitness change (state-averaged): -3.02e-14
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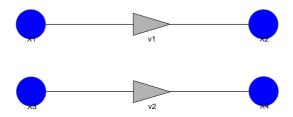


Figure 1: Network and reference flux

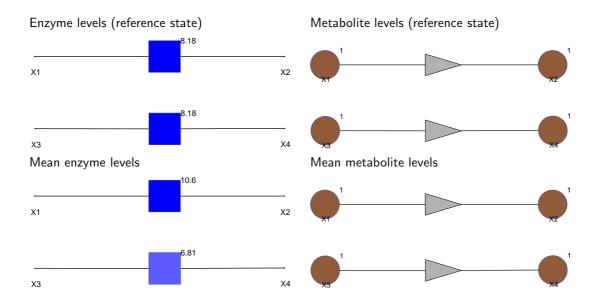
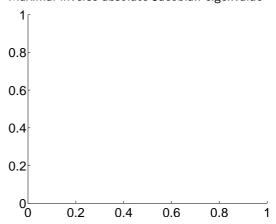
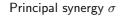


Figure 2: Reference state (top) and mean state during oscillation (bottom).









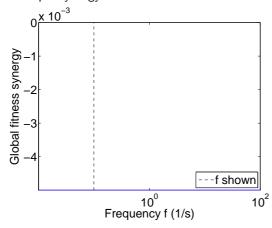
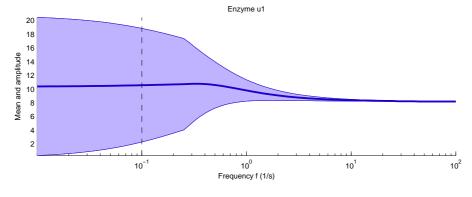
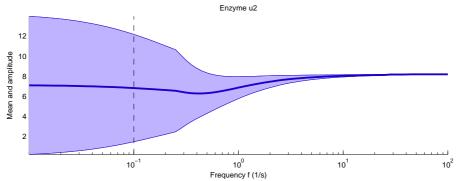


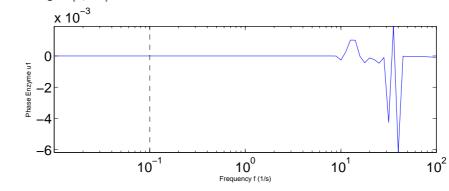
Figure 3: Control analysis. Left: Global fitness synergy (maximal fitness curvature eigenvalue), as a function of the frequency. Right: Relative amplitudes of individual enzymes for the least wasteful enzyme mode (components of the leading fitness curvature eigenvector).

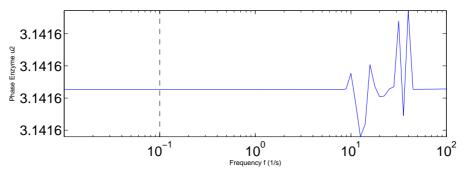
## Protein level and enzyme activity (mean and amplitude)



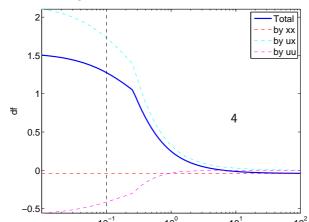


## Phase angles $[0,2\,\pi]$





## Fitness change



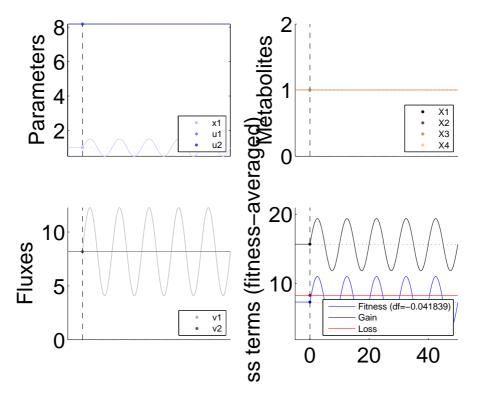


Figure 5: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first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

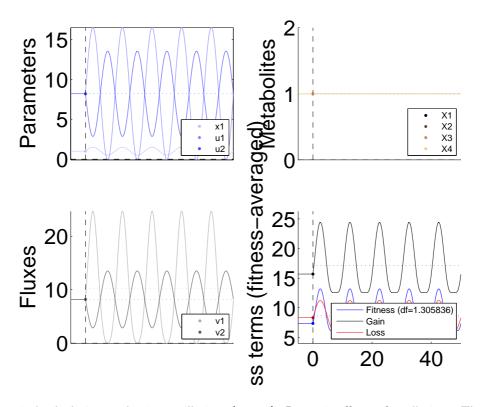


Figure 6: Numerical calculations: adaptive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first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

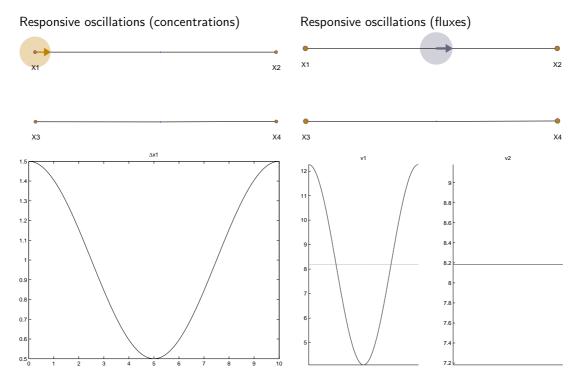


Figure 7: Responsive oscillations (local expansion; arrows: absolute changes) Perturbation frequency see first page.

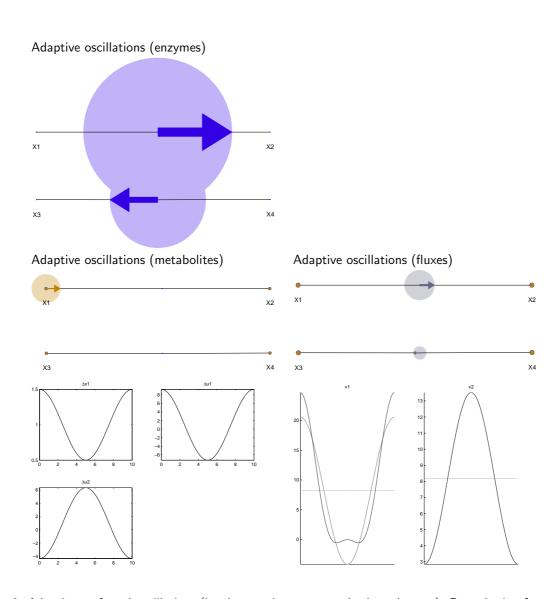


Figure 8: Adaption to forced oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

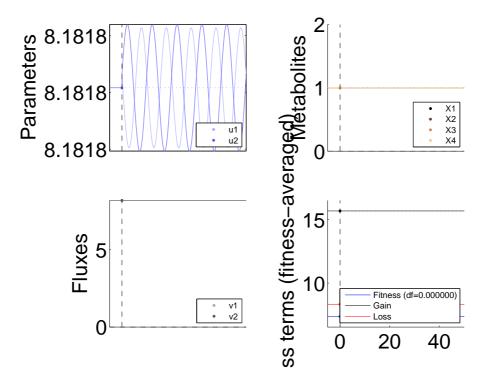


Figure 9: Tentative spontaneous oscillations. Perturbation frequency see first page.

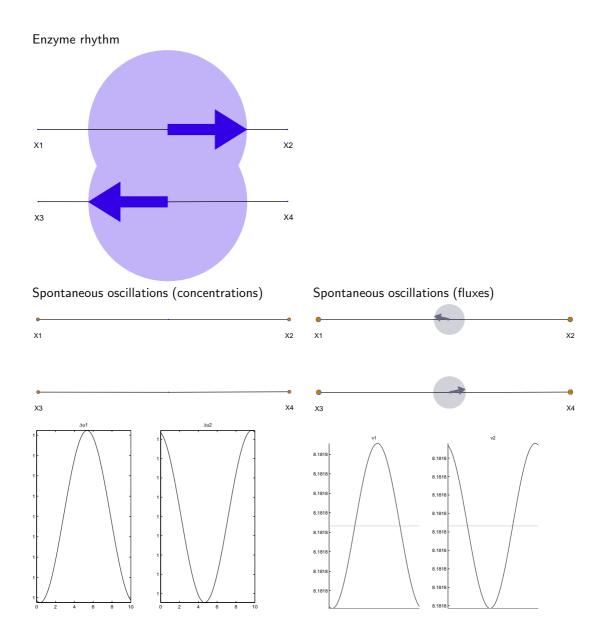
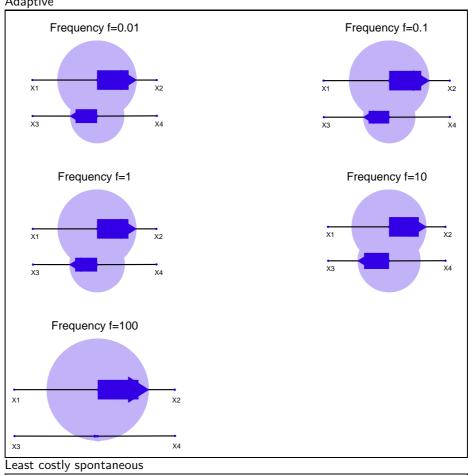


Figure 10: Tentative spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.





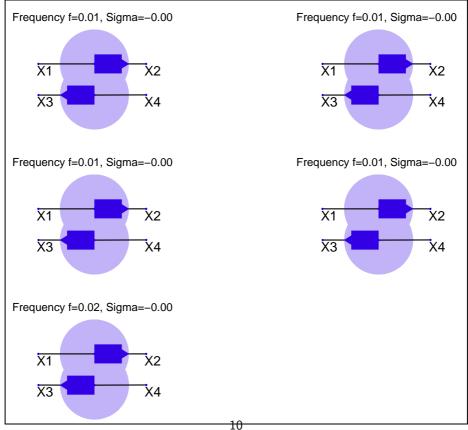


Figure 11: Potential oscillations at various frequencies (local expansion).