Enzyme rhythms in model linear_chain4_irrev.speedy

Model name: linear_chain4_irrev o Optimisation problem - Protein turnover time 1 s = 0.0167 min- Perturbed parameter(s) : x1 - Perturbation frequency f: 0.25/s (period 4 s) - Scored quantity: v4 - Fitness-averaged fitness - No posttranslational rhythms allowed - Standard frequency considered f: 0.25/s (period 4 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=0.25/s - Change by perturbation alone (xx): -0.00639 - Change by adaption synergies (xu): 2.13 - Change by periodic enzyme (uu): -0.992 - Change by enzyme mean shift (u): -4.46e-10 - Total fitness change: 1.14 - Fitness gain by adaption: 1.14 - Maximum adaptive fitness found (in tested range) at frequency f =0.282/s (period 3.55 s) - Predicted max. fitness change (adaptive, num. opt, full ampl. constraints) at frequency f =0.282: 1.14 o Self-induced oscillations? - No beneficial self-induced oscillations (2nd order, amplitude below 1/2 of mean) found at frequency f = 0.25/s(principal synergy = -0.0241): Predicted fitness change -0.5o Numerical calculation (responsive, f=0.25) - Fitness change (fitness-averaged): -0.0136 - Fitness change (state-averaged): -0.00723 o Numerical calculation (adaptive, f=0.25) - Fitness change (fitness-averaged): 1.12 - Fitness change (state-averaged): 2.05

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=0.25)

- Fitness change (fitness-averaged): -2.72e-06
- Fitness change (state-averaged): -2.72e-06

Figure 1: Network and reference flux

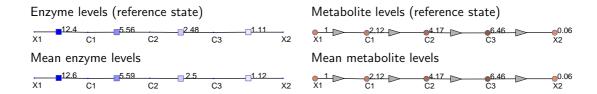


Figure 2: Reference state (top) and mean state during oscillation (bottom).

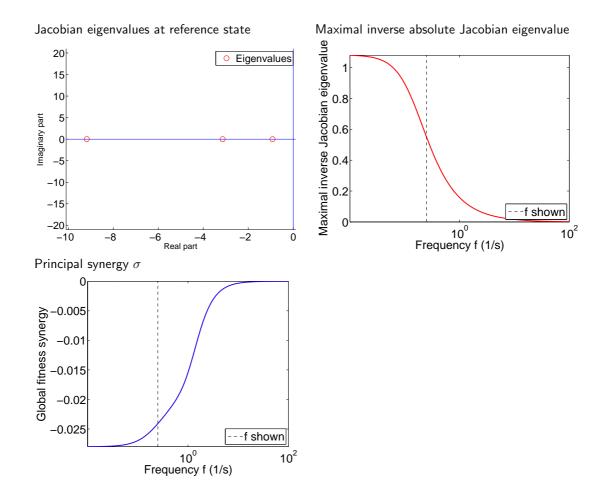


Figure 3: Control analysis. Left: Global fitness synergy (maximal fitness curvature eigenvalue), as a function of the frequency. Right: Relative amplitudes of individual enzymes for the least wasteful enzyme mode (components of the leading fitness curvature eigenvector).

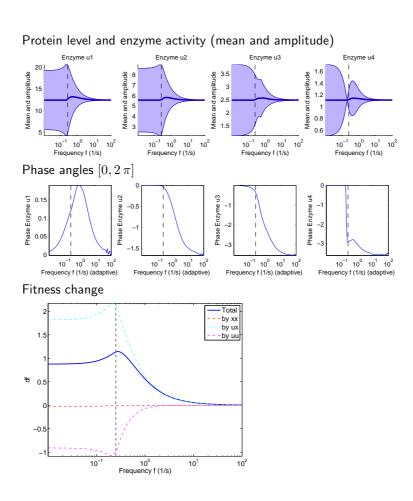


Figure 4: Adaptive oscillations. Left: amplitudes of protein levels (blue) and modification (grey). Right: phase shifts.

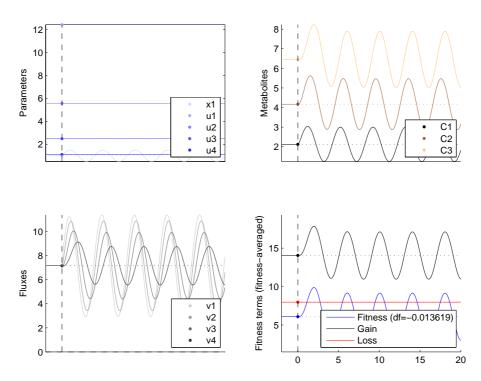


Figure 5: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first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

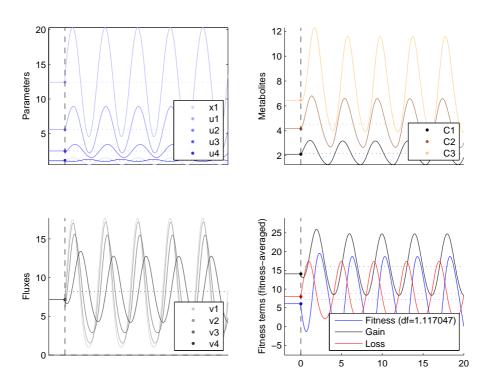


Figure 6: Numerical calculations: adaptive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first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

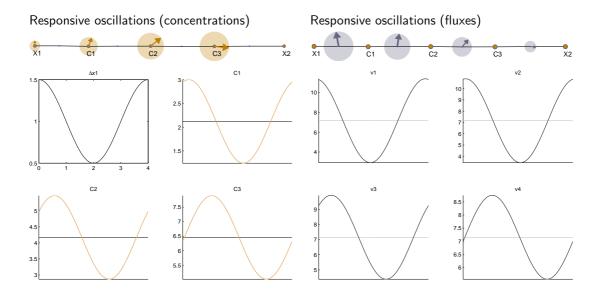


Figure 7: Responsive oscillations (local expansion; arrows: absolute changes) Perturbation frequency see first page.

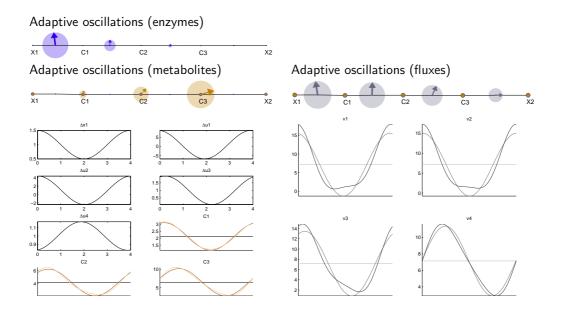


Figure 8: Adaption to forced oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

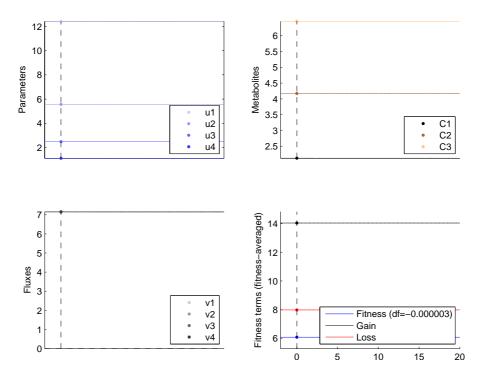


Figure 9: Tentative spontaneous oscillations. Perturbation frequency see first page.

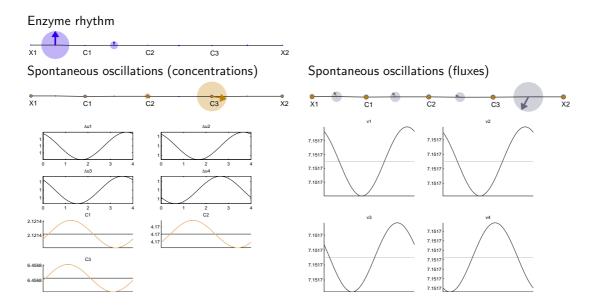


Figure 10: Tentative spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

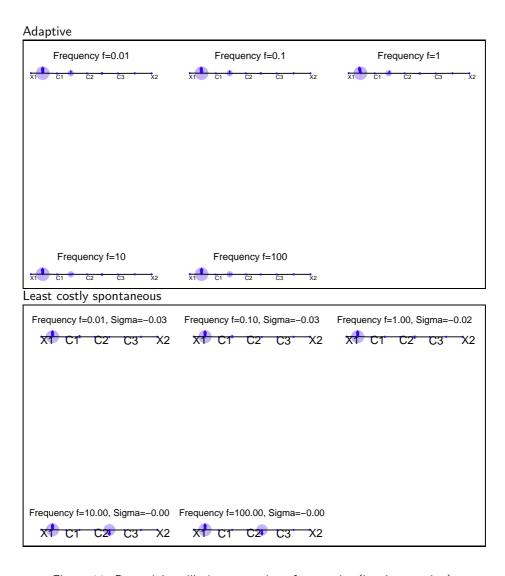


Figure 11: Potential oscillations at various frequencies (local expansion).