Enzyme rhythms in model time_gap2 - spontaneous oscillations

Model name: time_gap2

o Optimisation problem
- Protein turnover time 1.8e+03 s = 30 min
- Perturbed parameter(s) : X0
- Perturbation frequency f : 0.1/s (period 10 s)
- Scored quantity: v4
- Fitness-averaged fitness
- 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: 1
- spontaneous_rhythm_at_omega: 0
- has_spontaneous_rhythm_and_inactive_enzymes: 0

o Beneficial self-induced oscillation found
- Maximum principal synergy found (in tested range) at frequency f =0.794/s (period 1.26 s)
- Maximum fitness found (in tested range) at frequency f =0.501/s (period 2 s)

o Fitness changes after external perturbation at frequency f=0.1/s
- Change by perturbation alone (xx): 2.06e-05
- Change by adaption synergies (xu): 0.00015
- Change by periodic enzyme (uu): -0.000239
- Change by enzyme mean shift (u): -5.49e-11
- Total fitness change : -6.86e-05
- Fitness gain by adaption : -8.92e-05
- Maximum adaptive fitness found (in tested range) at frequency f =0.00178/s (period 562 s)
- Predicted maximal fitness change (adaptive, numeric opt, full amplitude constraints) at frequency f =0.00178: 0.000114

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 = -0.00706): Predicted fitness change -0.00418

o Numerical calculation (responsive, f=0.1)
- Fitness change (fitness-averaged): 1.76e-05
- Fitness change (state-averaged): 1.78e-05
o Numerical calculation (adaptive, f=0.1)
- Fitness change (fitness-averaged): 8.67e-05
- Fitness change (state-averaged): 0.000108

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=0.1)
- Fitness change (fitness-averaged) : -2.72e-08
- Fitness change (state-averaged): -2.71e-08

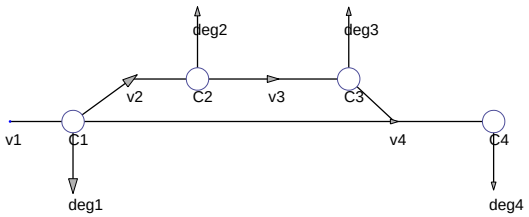


Figure 1: Network and reference flux

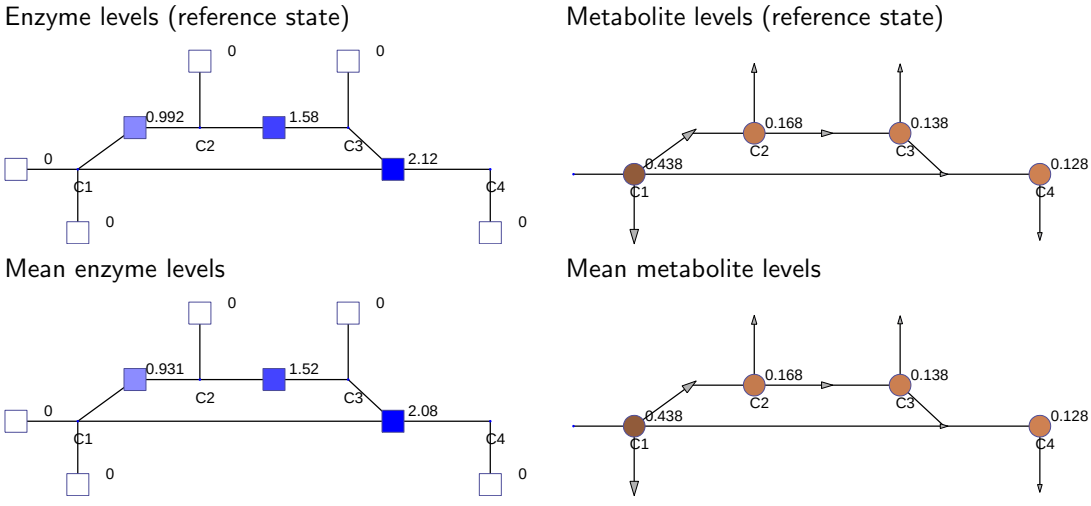


Figure 2: Reference state (top) and mean state during oscillation (bottom).

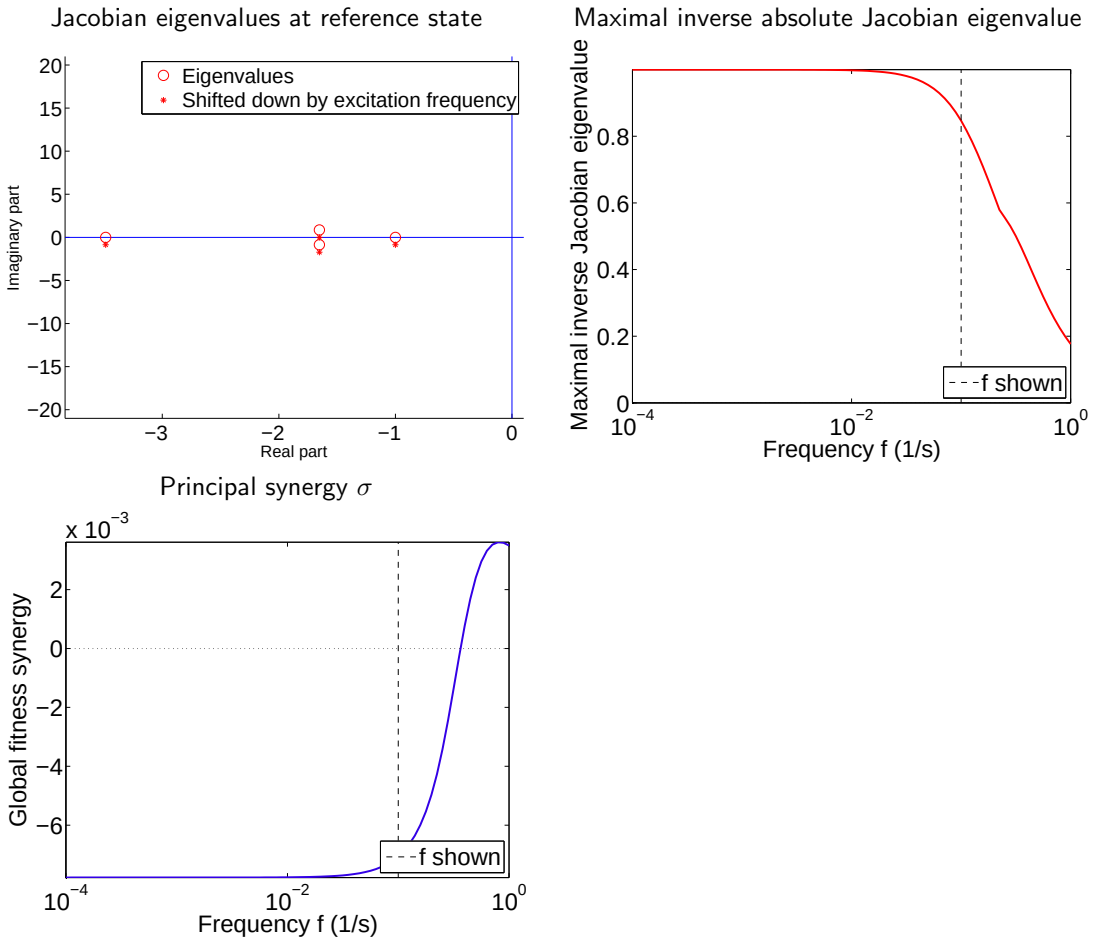
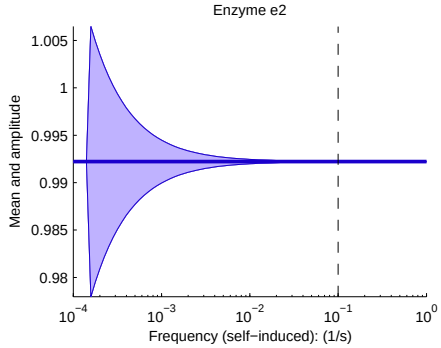
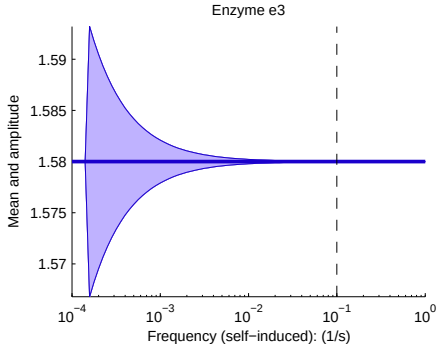
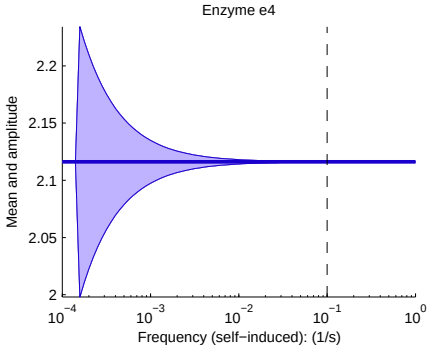


Figure 3: Control analysis: fitness curvatures. Left: Frequency-dependent fitness curvature eigenvalues. Right: relative sizes and phases of the individual enzyme levels (components of the leading fitness curvature eigenvector).

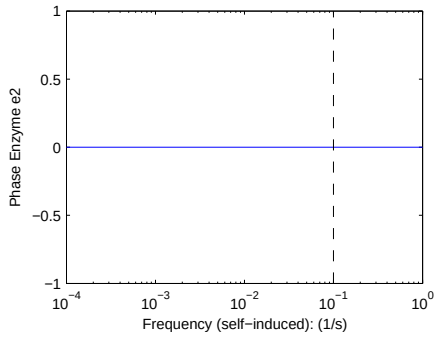
Protein level and enzyme activity (mean and amplitude)

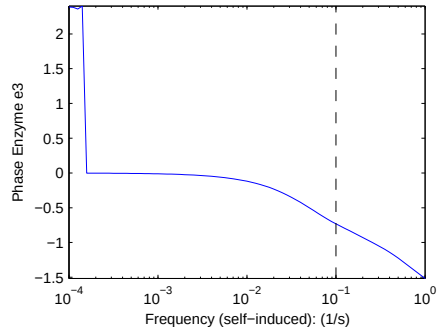


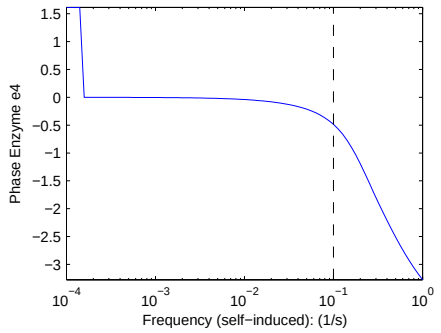




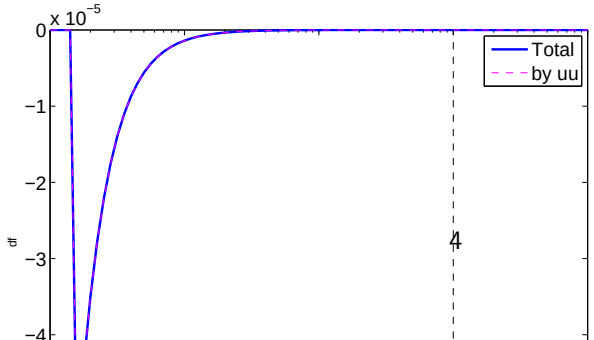
Phase angles $[0, 2\,\pi]$







Fitness change



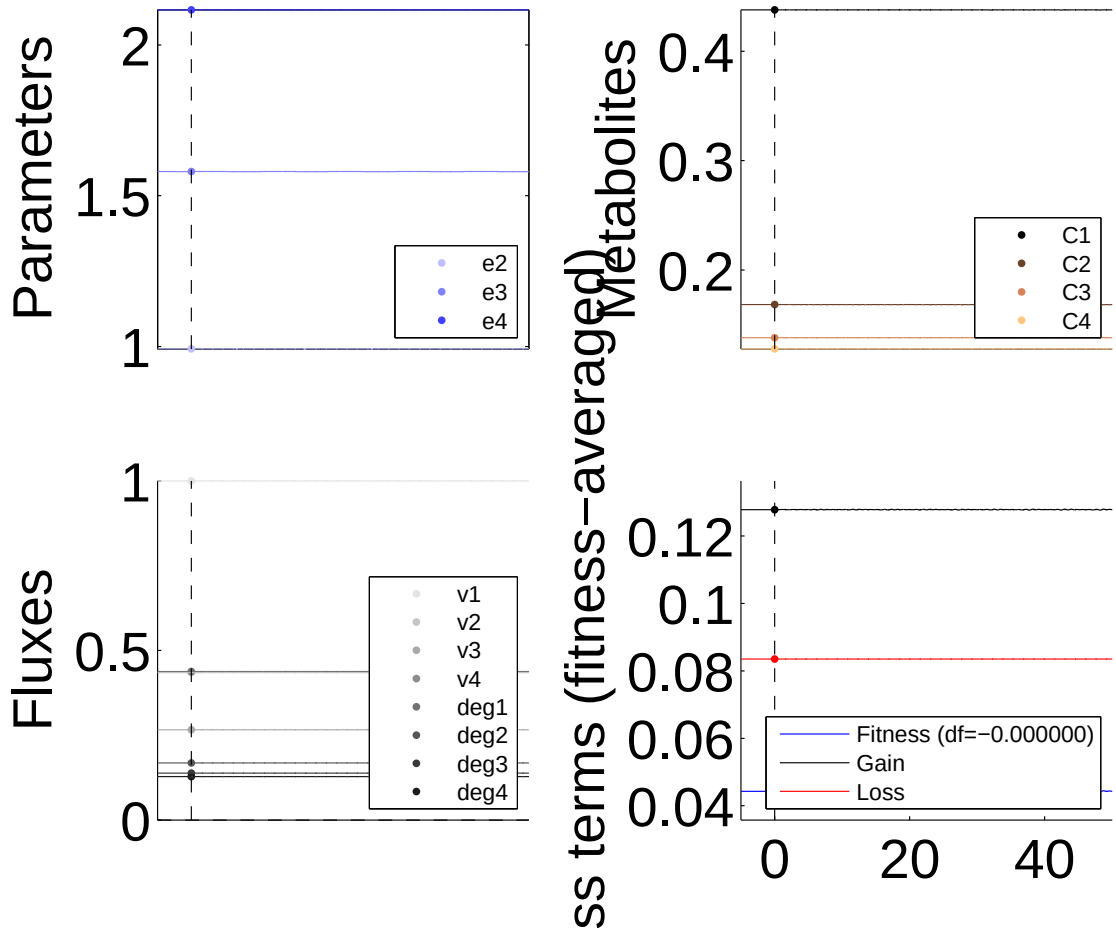


Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.

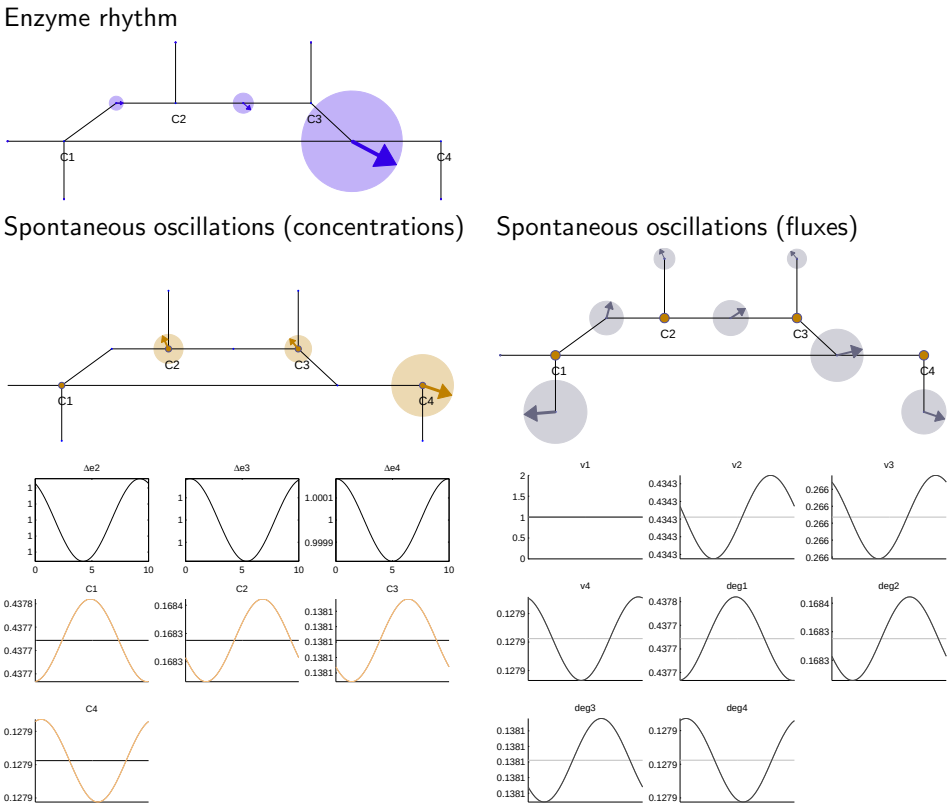


Figure 6: Spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

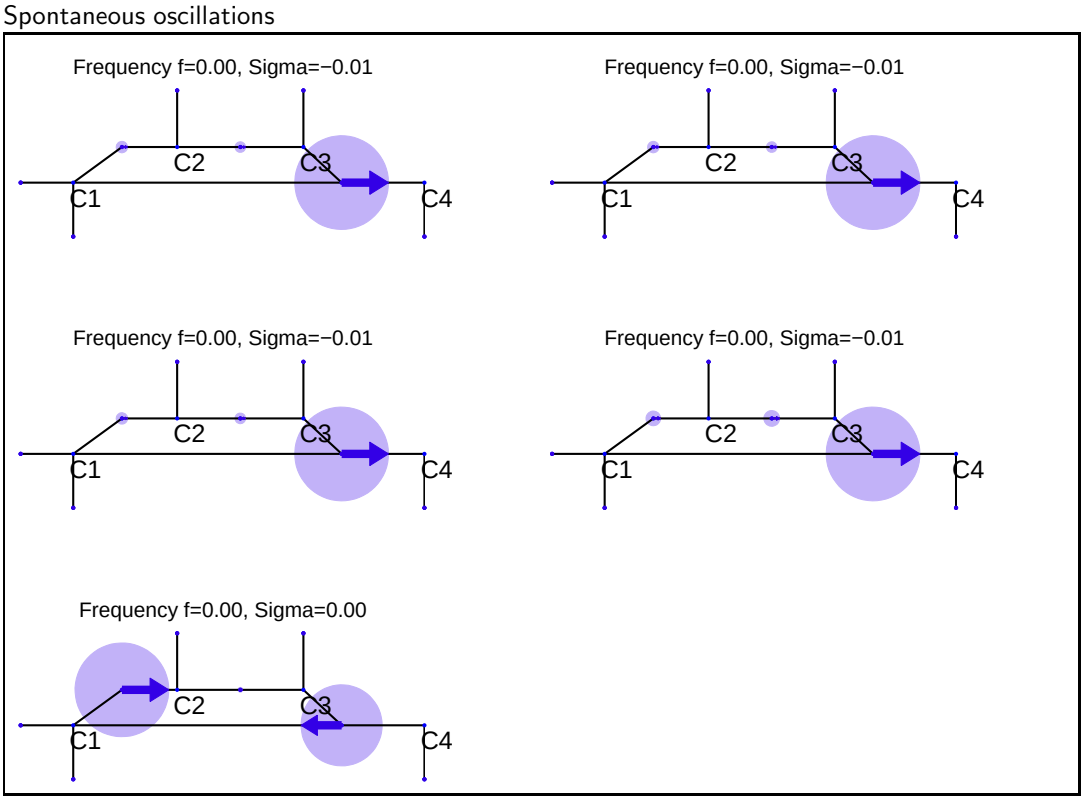


Figure 7: Spontaneous oscillations (or tendencies towards them) for various circular frequencies ω. If the maximal fitness curvatures λ is positive, the rhythm is beneficial (local expansion; arrows: absolute changes).