Enzyme rhythms in model time_gap2.speedy - spontaneous oscillations

Model name: time_gap2

o Optimisation problem
- Protein turnover time 1 s = 0.0167 min
- Perturbed parameter(s) : X0
- Perturbation frequency f : 0.1/s (period 10 s)
- Scored quantity: v4
- 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: 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): 0.00206
- Change by adaption synergies (xu): 0.0194
- Change by periodic enzyme (uu): -0.00969
- Change by enzyme mean shift (u): 0
- Total fitness change : 0.0118
- Fitness gain by adaption : 0.00969
- Maximum adaptive fitness found (in tested range) at frequency f =0.224/s (period 4.47 s)
- Predicted maximal fitness change (adaptive, numeric opt, full amplitude constraints) at frequency f =0.224: 0.0133

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): 0.00208
- Fitness change (state-averaged): 0.0021
o Numerical calculation (adaptive, f=0.1)
- Fitness change (fitness-averaged): 0.0113
- Fitness change (state-averaged): 0.0158

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=0.1)
- Fitness change (fitness-averaged) : -3.8e-07
- Fitness change (state-averaged): -3.8e-07

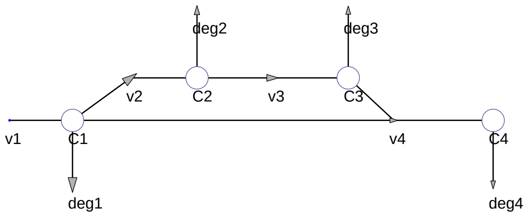
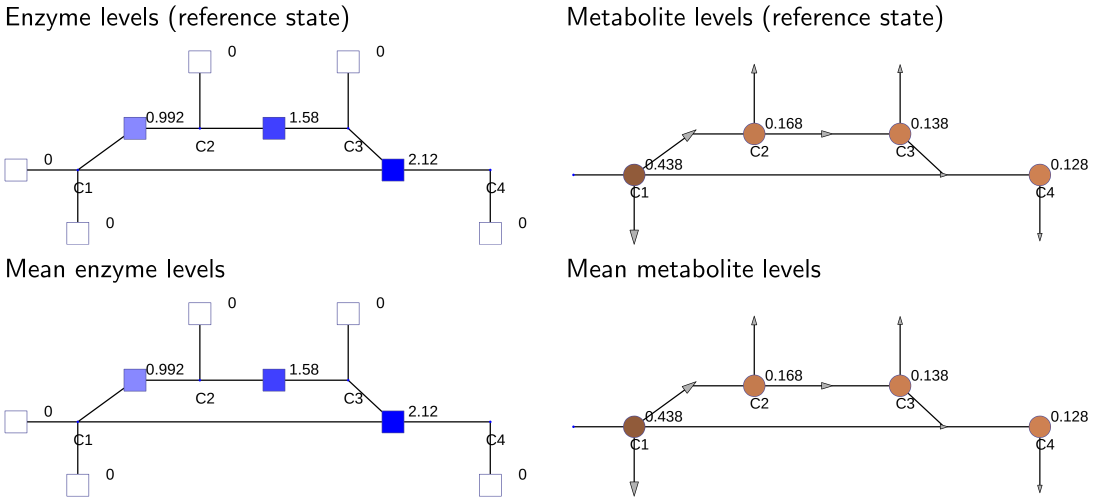


Figure 1: Network and reference flux


Enzyme levels (reference state)

Metabolite levels (reference state)

Mean enzyme levels

Mean metabolite levels

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

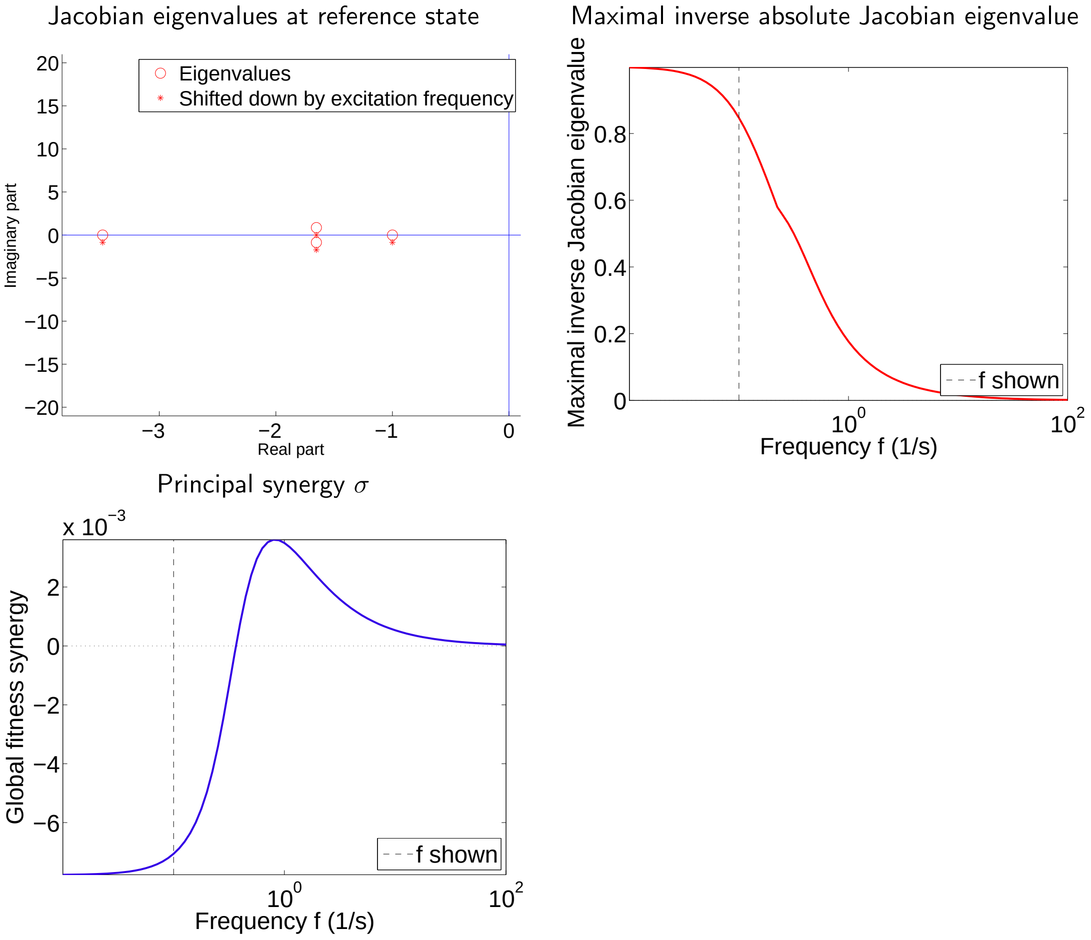
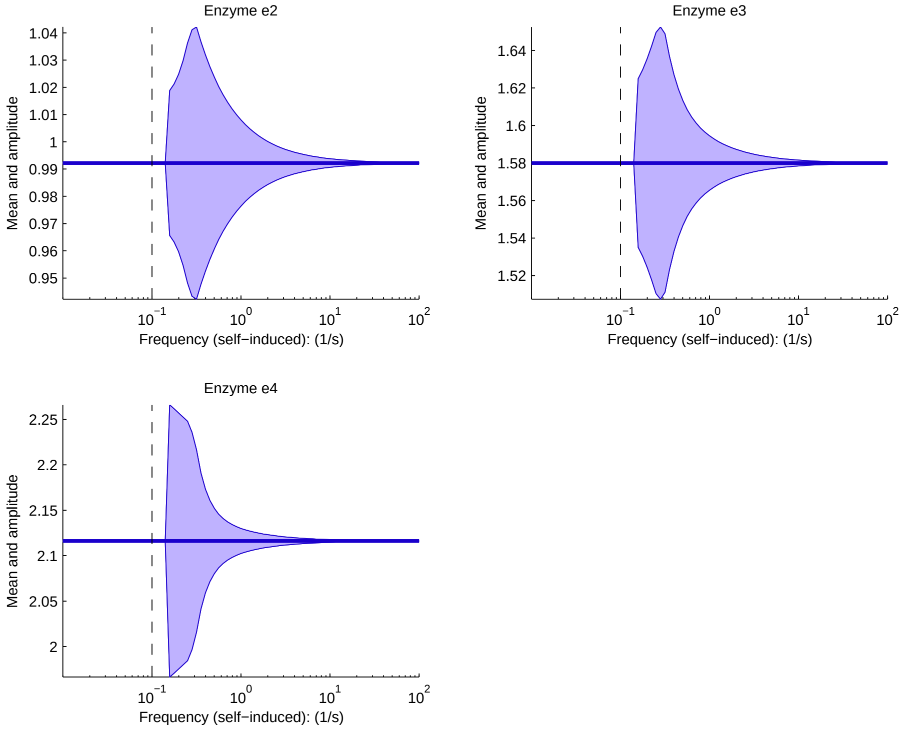
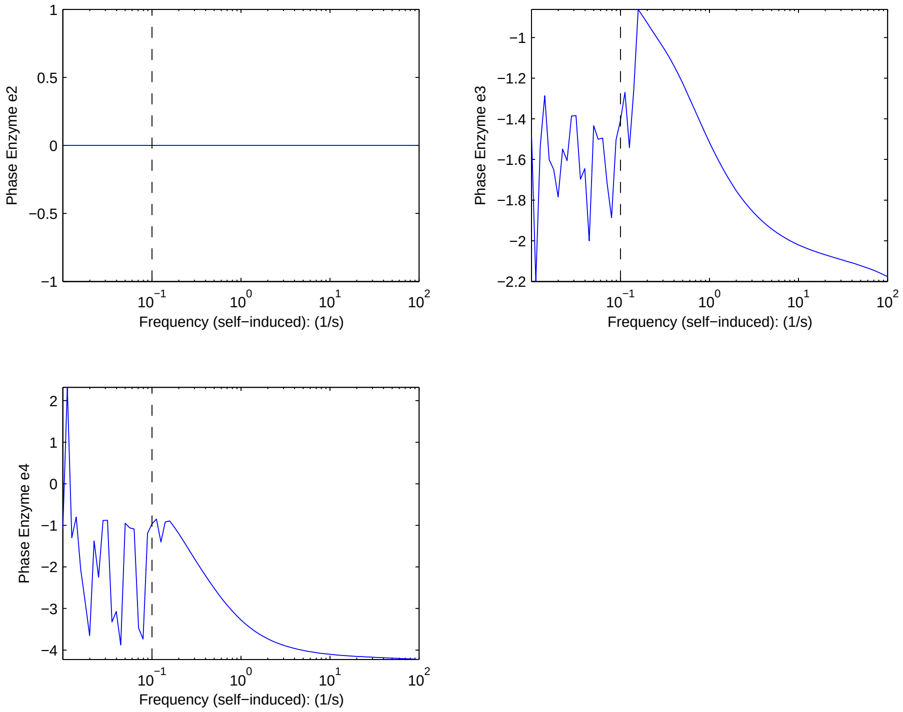


Figure 3: Control analysis: fitness curvatures. Left: Frequency-dependent fitness curvature eigenvalues. Right: relative sizes and phases of the individual enzyme levels (components of the leading fitness curvature eigenvector).

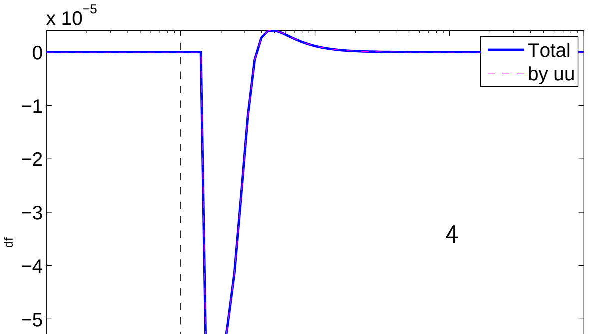
Protein level and enzyme activity (mean and amplitude)



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



Fitness change



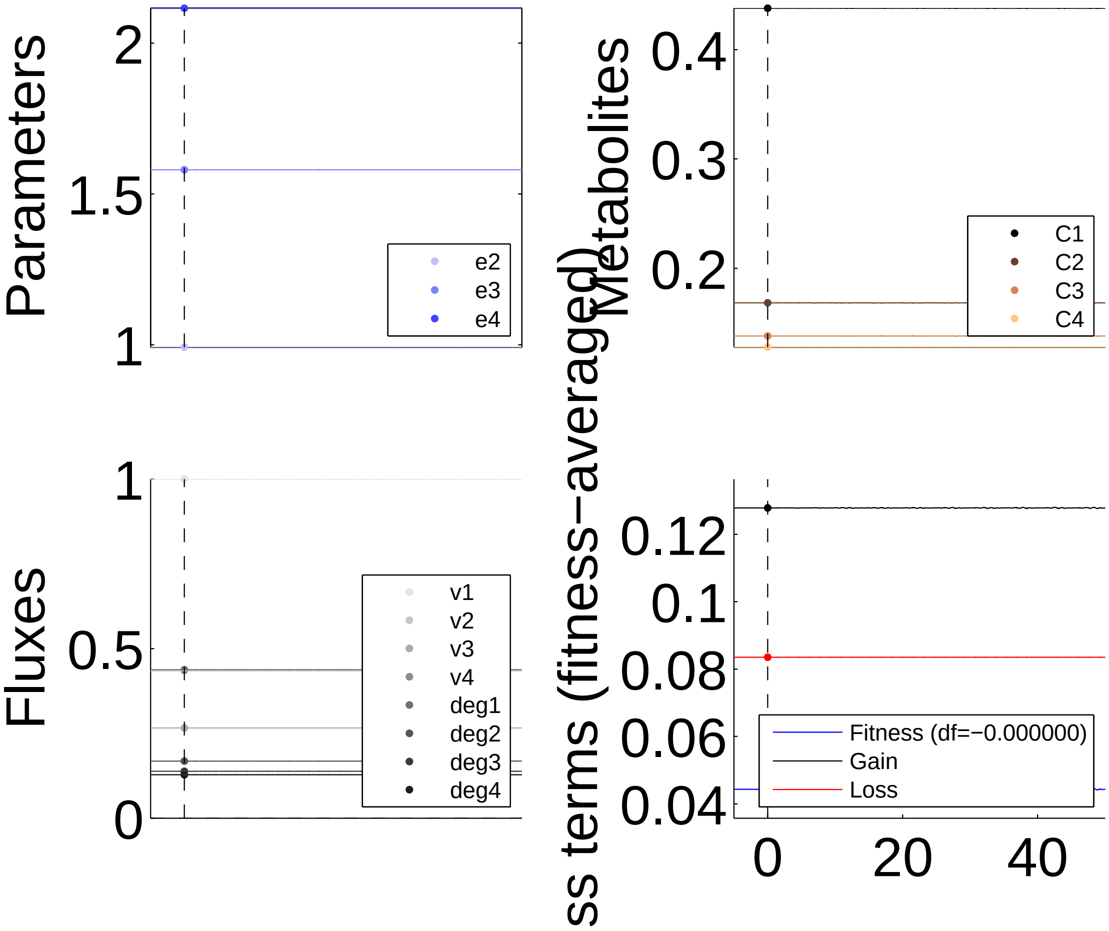
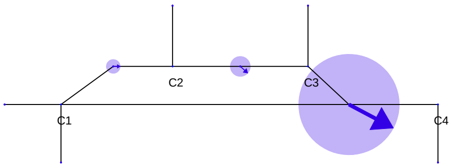
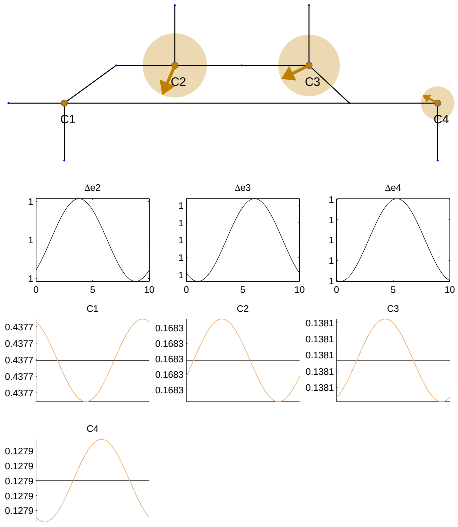


Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.

Enzyme rhythm



Spontaneous oscillations (concentrations)



Spontaneous oscillations (fluxes)

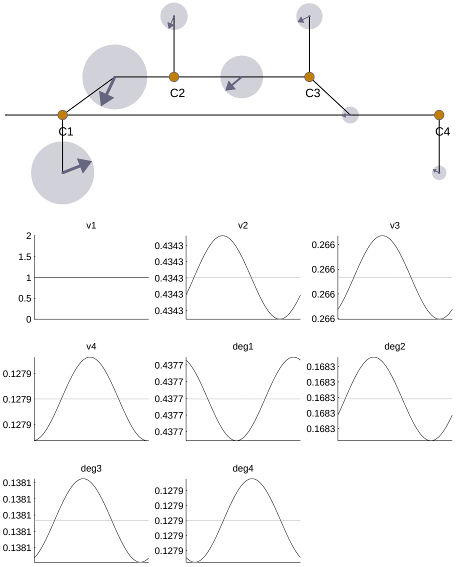
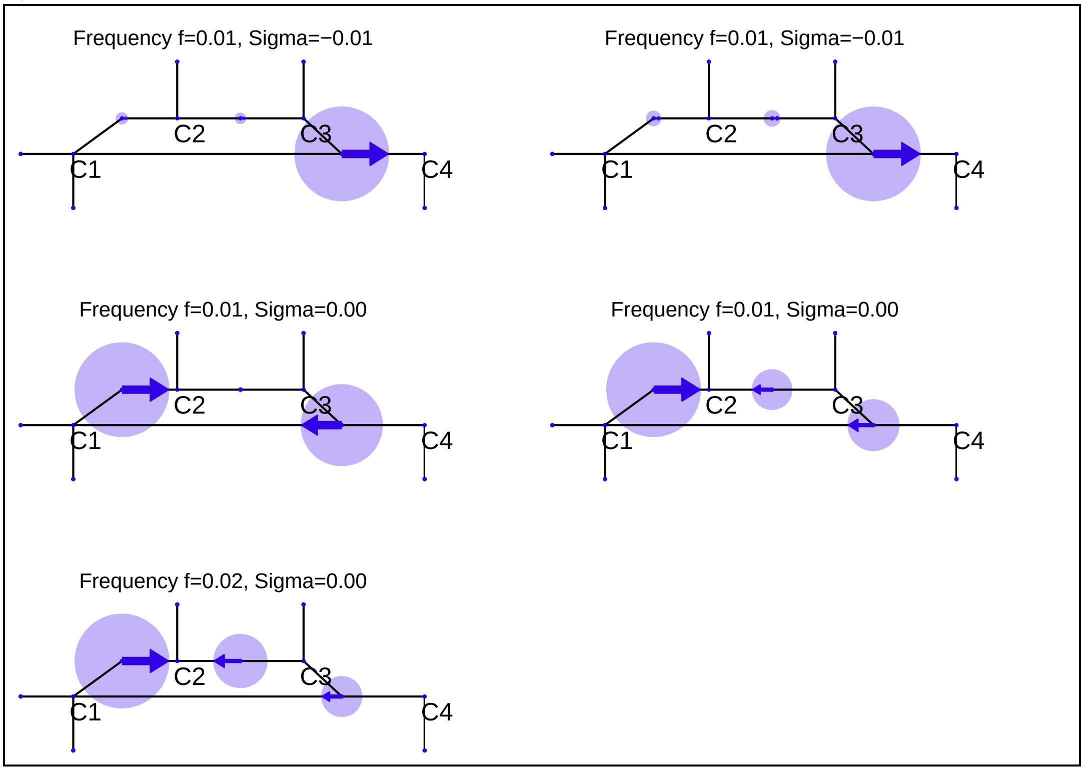


Figure 6: Spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

Spontaneous oscillations



Frequency f=0.01, Sigma=−0.01

Frequency f=0.01, Sigma=−0.01

Frequency f=0.01, Sigma=0.00

Frequency f=0.01, Sigma=0.00

Frequency f=0.02, Sigma=0.00

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).