Enzyme rhythms in model linear_chain_dilution - spontaneous oscillations

Model name: linear_chain_dilution

o Optimisation problem
- Protein turnover time 1.8e+03 s = 30 min
- Perturbed parameter(s) : x1
- Perturbation frequency f : 0.0167/s (period 60 s)
- Scored quantity: v4
- State-averaged fitness
- Posttranslational rhythms allowed
- Standard frequency considered f : 0.0167/s (period 60 s)

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

o Beneficial autonomous oscillation found
- Maximum principal synergy found (in tested range) at frequency f =0.0001/s (period 1e+04 s)
- Maximum fitness found (in tested range) at frequency f =0.0001/s (period 1e+04 s)

o Fitness changes after external perturbation at frequency f=0.0167/s
- Change by perturbation alone (xx): -3e-13

o Autonomous oscillations?
- Maximally autonomous oscillations (in tested range) at f = 0.0001, principal synergy 0.0014
- Beneficial autonomous oscillations found at frequency f = 0.0167/s (principal synergy = 0.00139)
- Predicted fitness change (autonomous, 2nd order, amplitude below 1/2 of mean) at frequency f =0.0167: 0.0863
- Predicted maximal fitness change (autonomous, numeric opt, full amplitude constraints) at frequency f =0.0001: 0.726
WARNING: an external rhythm is given and an autonomous rhythm has been found

o Numerical calculation (responsive, f=0.0167)
- Fitness change (fitness-averaged): -3.73e-05
- Fitness change (state-averaged): -1.29e-05

o Numerical calculation (autonomous rhythm, amplitude below 1/2 of mean, f=0.0167)
- Fitness change (fitness-averaged) : 2.04e-06
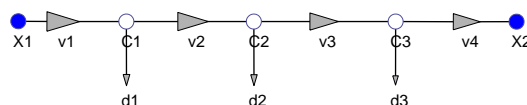- Fitness change (state-averaged): 2.28e-06

Figure 1: Network and reference flux

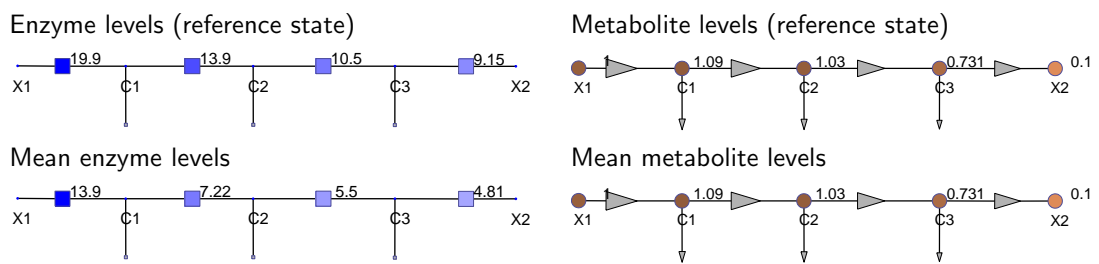Figure 2: Reference state (top) and mean state during oscillation (bottom).
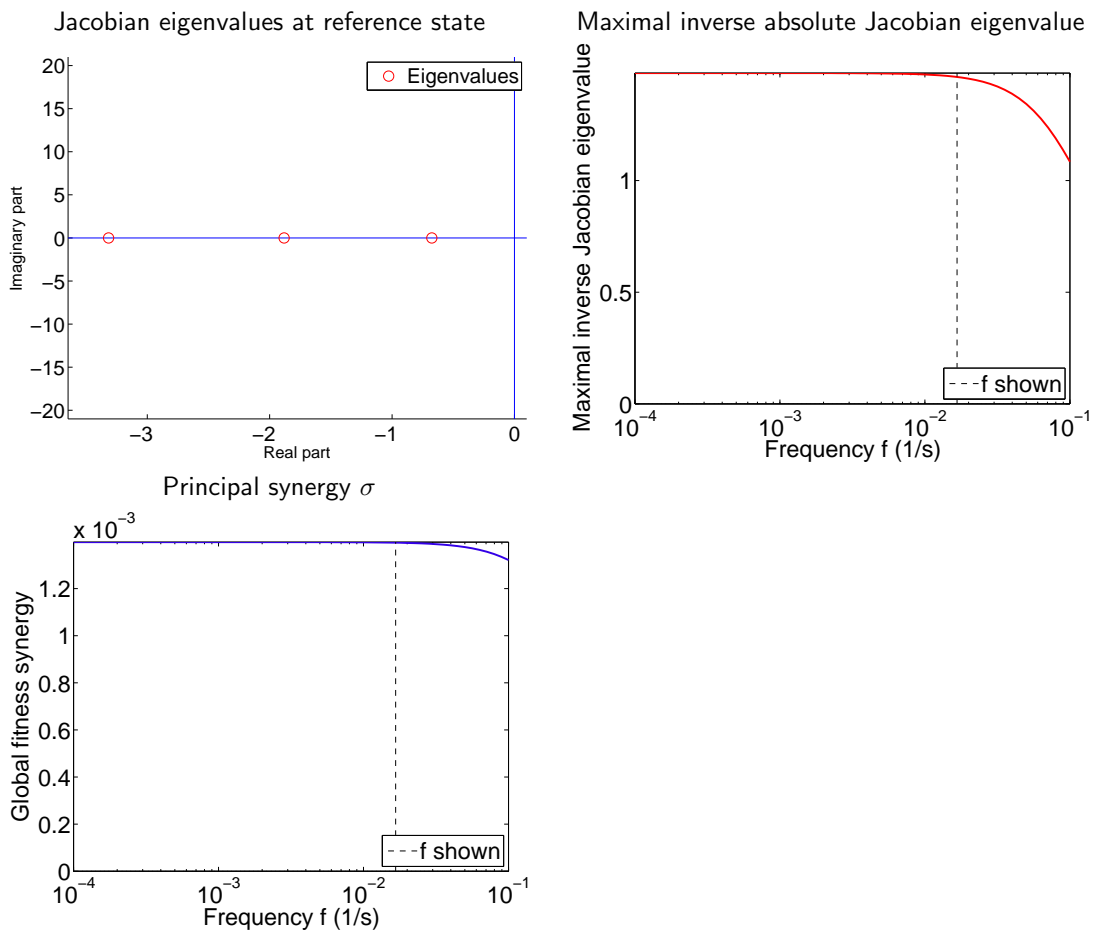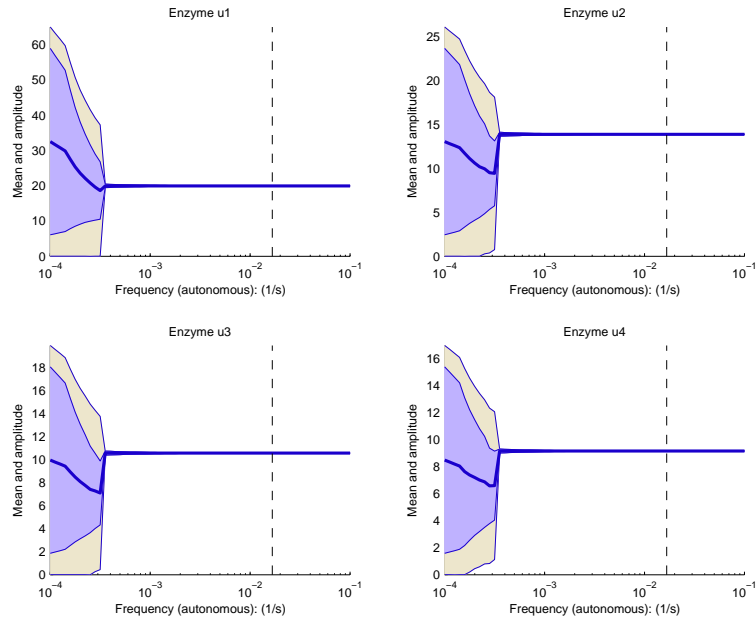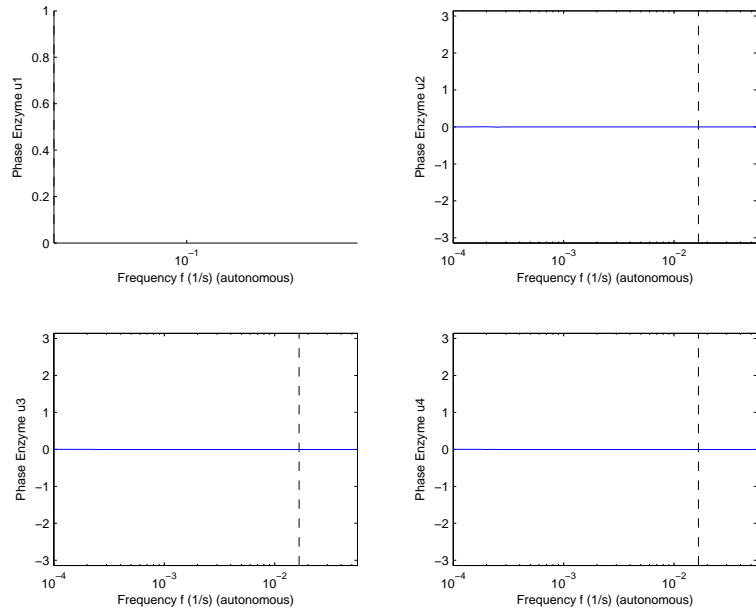
Figure 3: Control analysis: fitness curvatures. Left: Frequency-dependent fitness curvature eigenvalues. Right: relative sizes and phases of the individual enzyme levels (components of the leading fitness curvature eigenvector).

Protein level and enzyme activity (mean and amplitude)

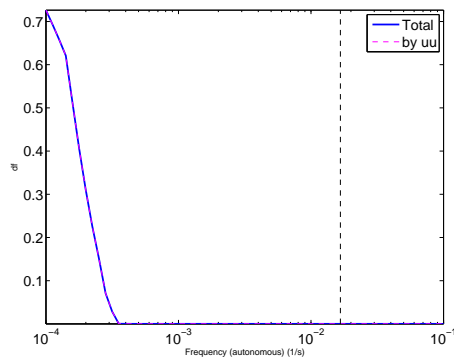## Phase angles $[0, 2\pi]$

Fitness change

Figure 4: Self-promoting oscillations. Left: amplitudes of protein levels (blue) and modification (grey). Right: phase shifts.
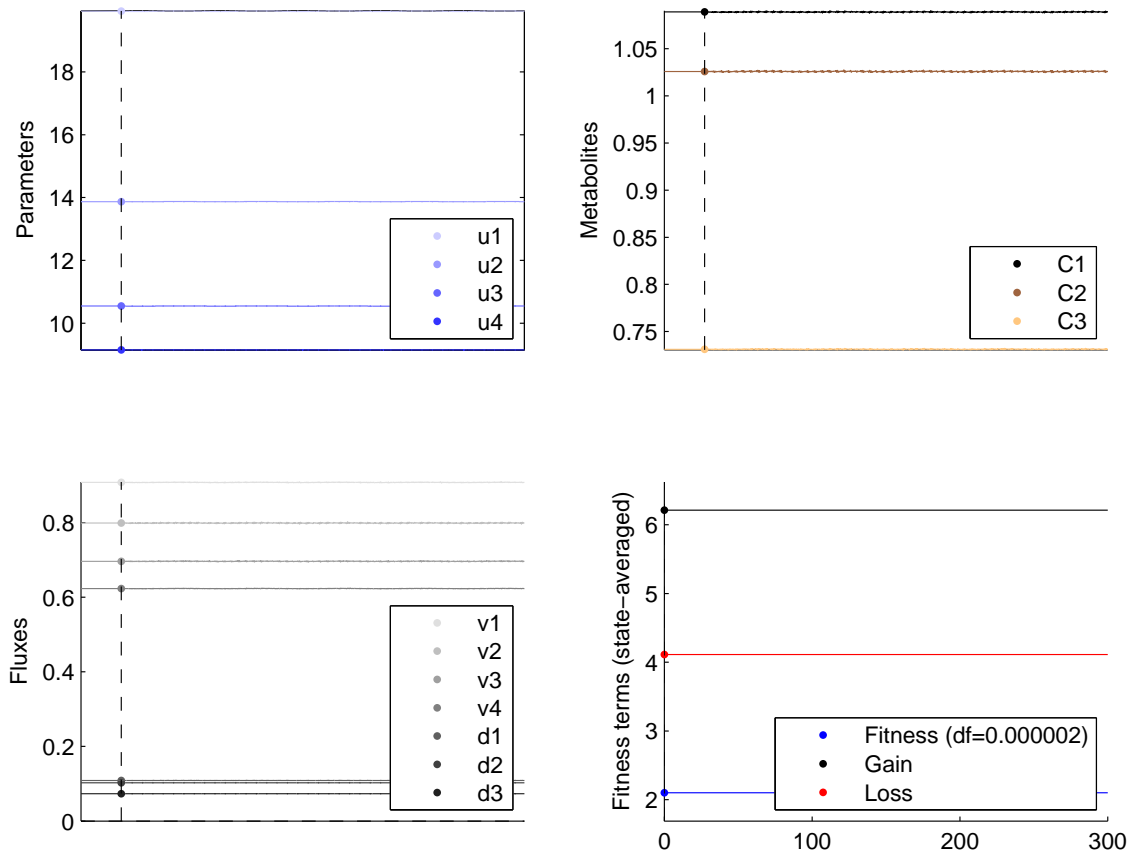
Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.
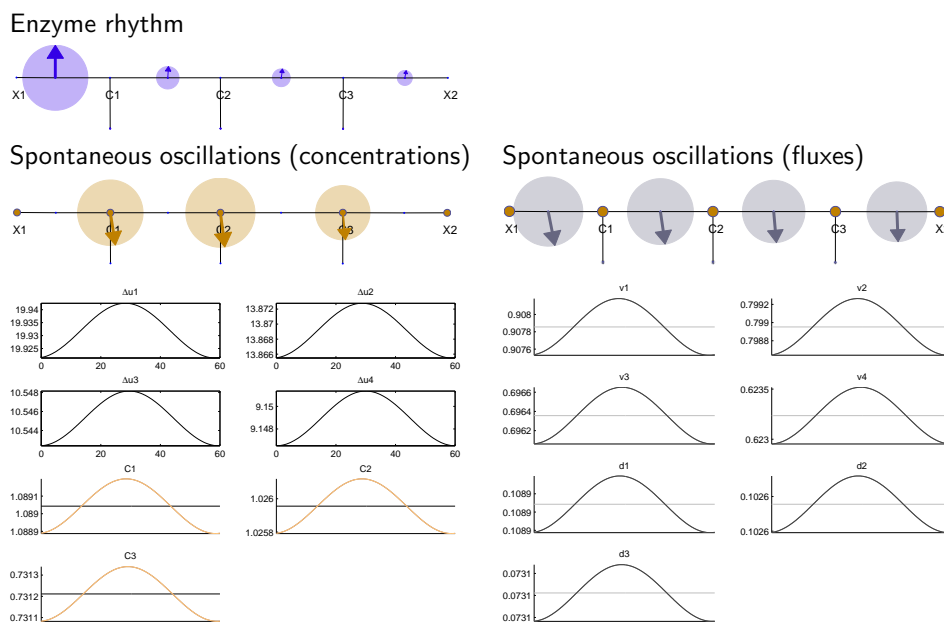

Figure 6: Spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.
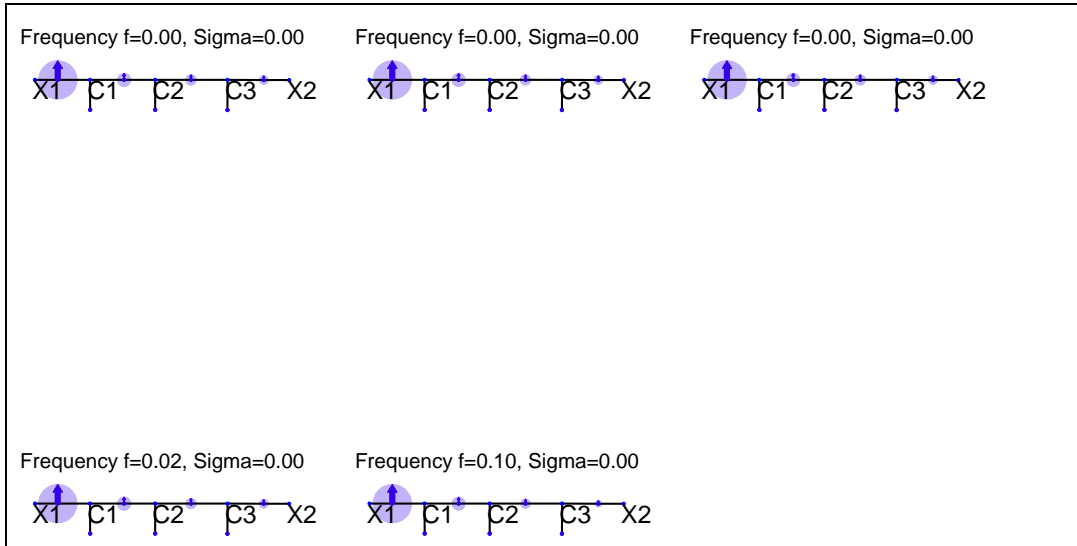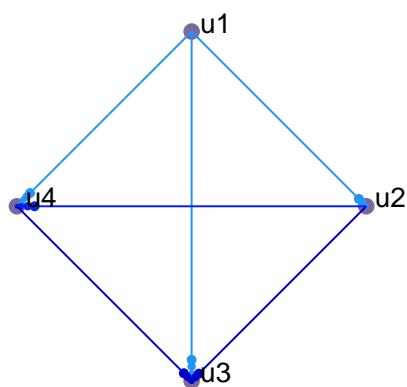
Spontaneous oscillations

Frequency f=0.00, Sigma=0.00   Frequency f=0.00, Sigma=0.00   Frequency f=0.00, Sigma=0.00

X1 C1   C2   C3   X2   X1 C1   C2   C3   X2   X1 C1   C2   C3   X2

Frequency f=0.02, Sigma=0.00   Frequency f=0.10, Sigma=0.00
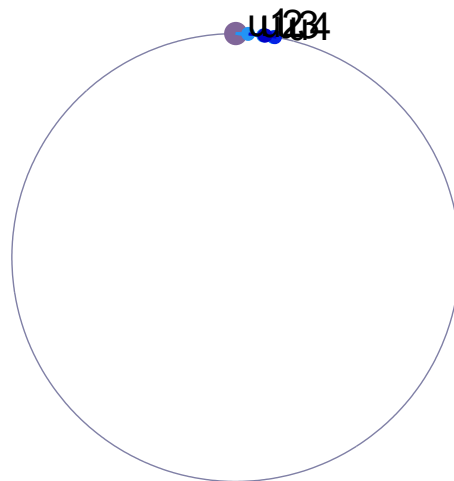
X1 C1   C2   C3   X2   X1 C1   C2   C3   X2

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).

Synergies   Synergy phase plot

u1

u4   u2

u3

Synergies on network

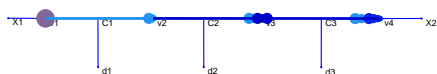X1   v1   C1   v2   C2   v3   C3   v4   X2

d1   d2   d3

Figure 8: Periodic economic potentials and direct enzyme values.