Enzyme rhythms in model repressilator - spontaneous oscillations

Model name: repressilator

o Optimisation problem
- Protein turnover time 1.8e+03 s = 30 min
- No external perturbation considered
- Scored quantity: v1
- Scored quantity: v2
- Scored quantity: v3
- State-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: 0
- adaptive_rhythm: 0
- spontaneous_rhythm: 1
- spontaneous_rhythm_at_omega: 1
- has_spontaneous_rhythm_and_inactive_enzymes: 0

o Beneficial self-induced oscillation found
- Maximum principal synergy found (in tested range) at frequency f =0.112/s (period 8.91 s)
- Maximum fitness found (in tested range) at frequency f =0.0001/s (period 1e+04 s)

o Self-induced oscillations?
- Maximally self-induced oscillations (in tested range) at f = 0.112, principal synergy 0.663
- Beneficial self-induced oscillations found at frequency f = 0.1/s (principal synergy = 0.663)
- Predicted fitness change (self-induced, 2nd order, amplitude below 1/2 of mean) at frequency f =0.1: 0.0422
- Predicted maximal fitness change (self-induced, numeric opt, full amplitude constraints) at frequency f =0.0001: 0.0795

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=0.1)
- Fitness change (fitness-averaged) : -1.1e-05
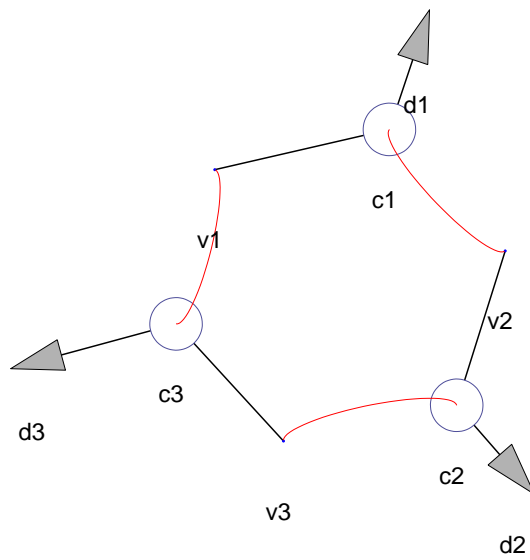- Fitness change (state-averaged): -1.1e-05

Figure 1: Network and reference flux

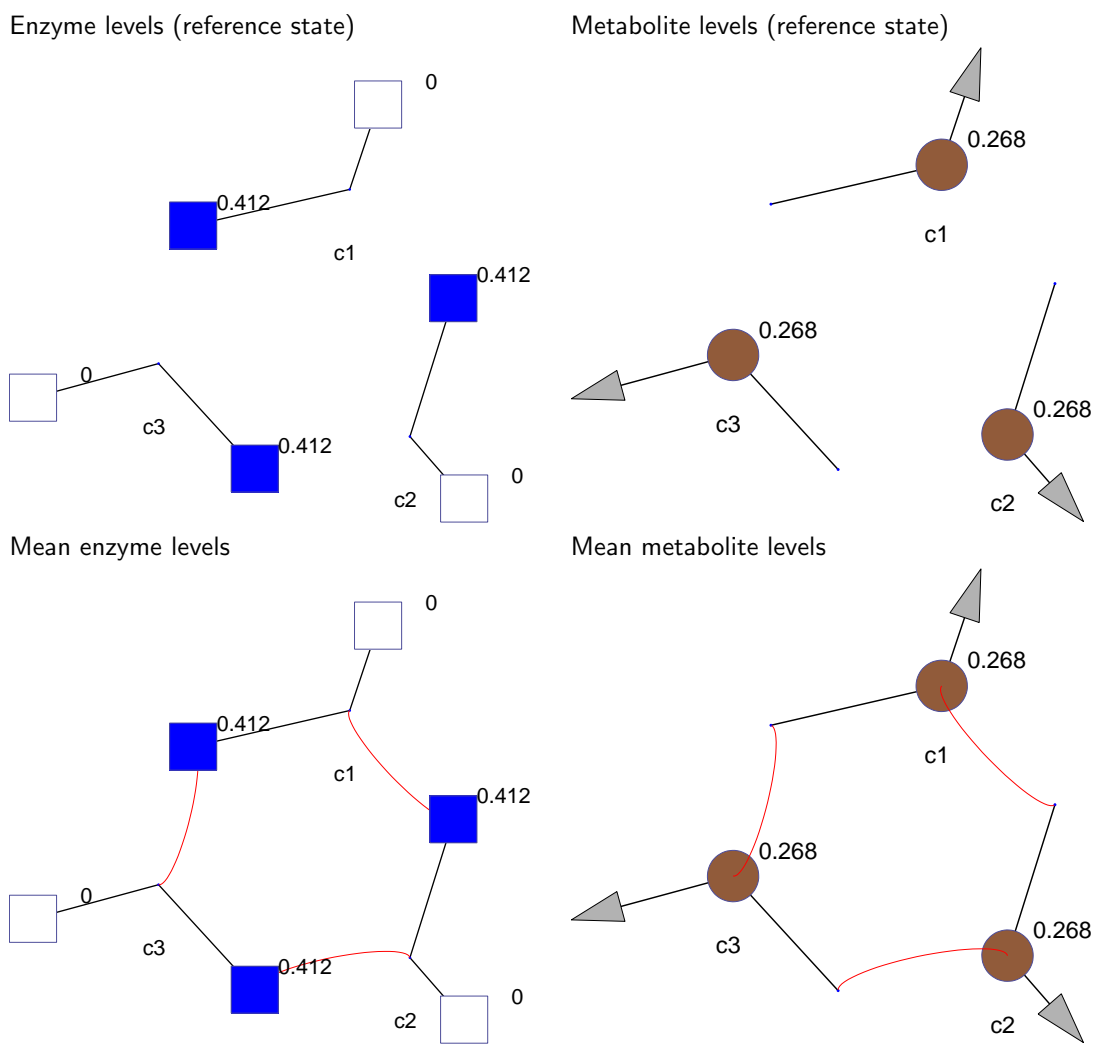Enzyme levels (reference state)

Metabolite levels (reference state)

0

0.412

c1

0.412

0

c3

0.412

0.268

c1

0.268

c3

0.268

c2

Mean enzyme levels

Mean metabolite levels

0

0.412

c1

0.412

0

c3

0.412

c2

0.268

c1

0.268

c3
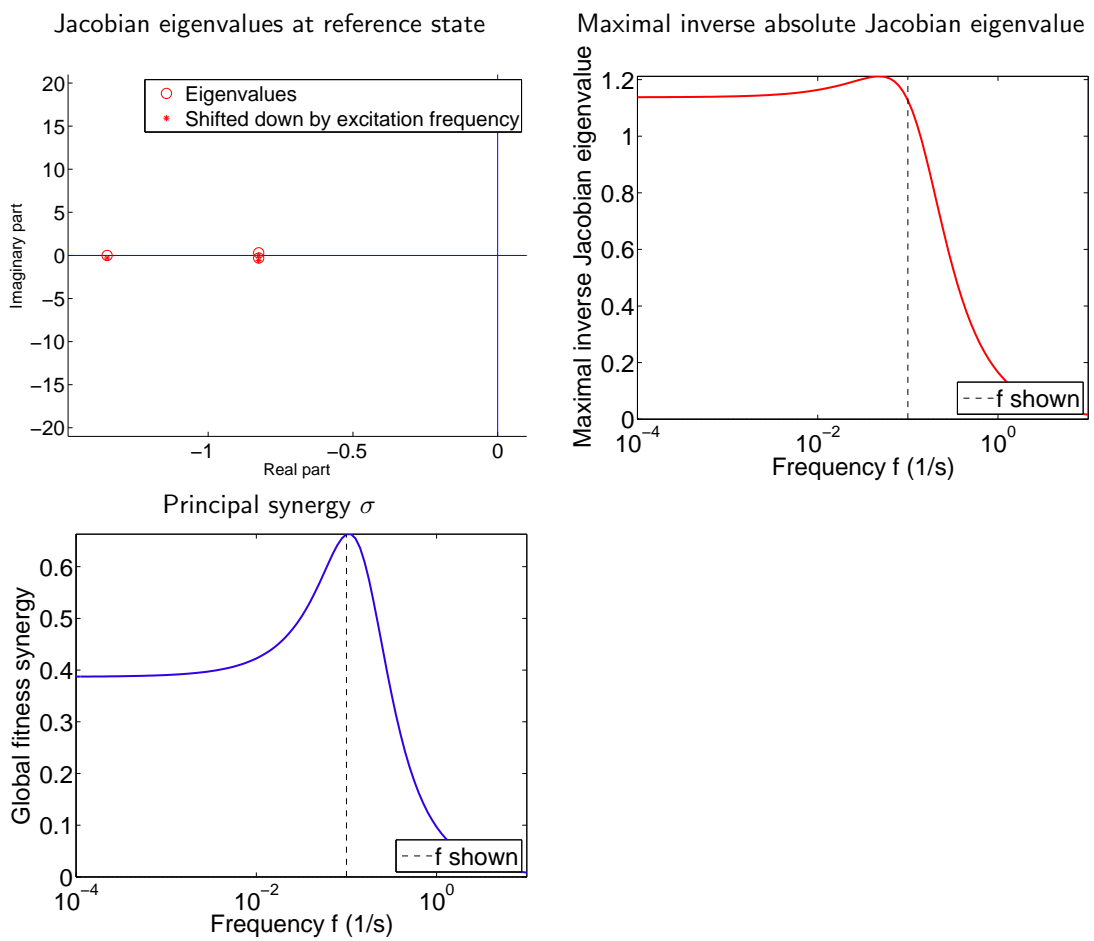
0.268

c2

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).
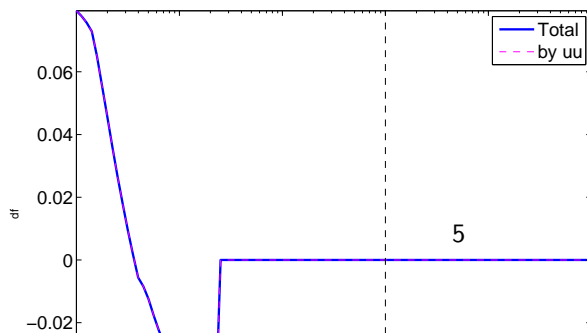
Protein level and enzyme activity (mean and amplitude)
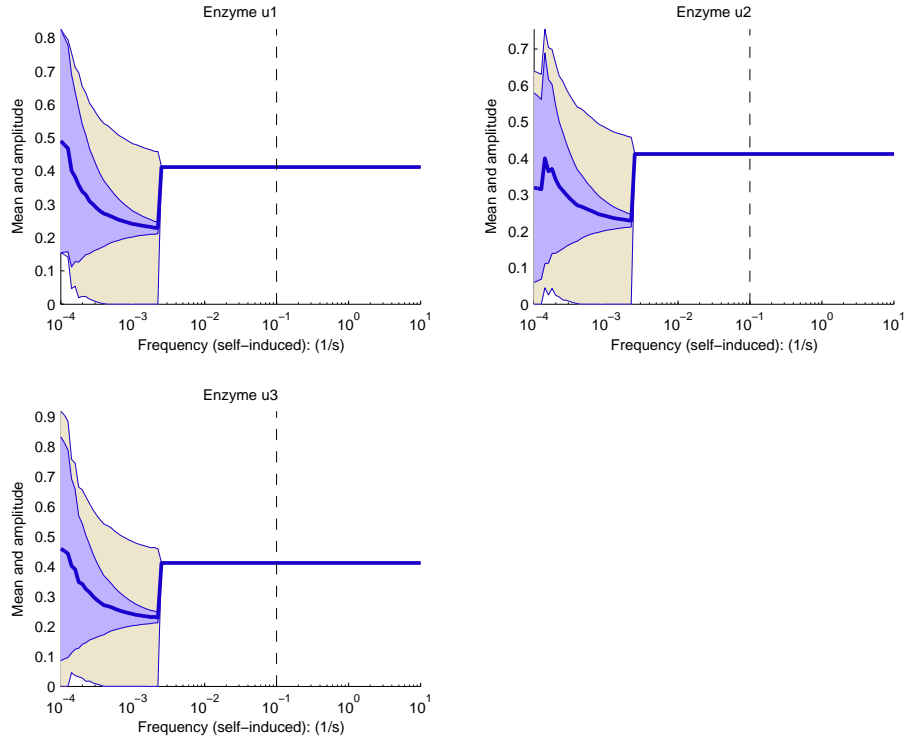
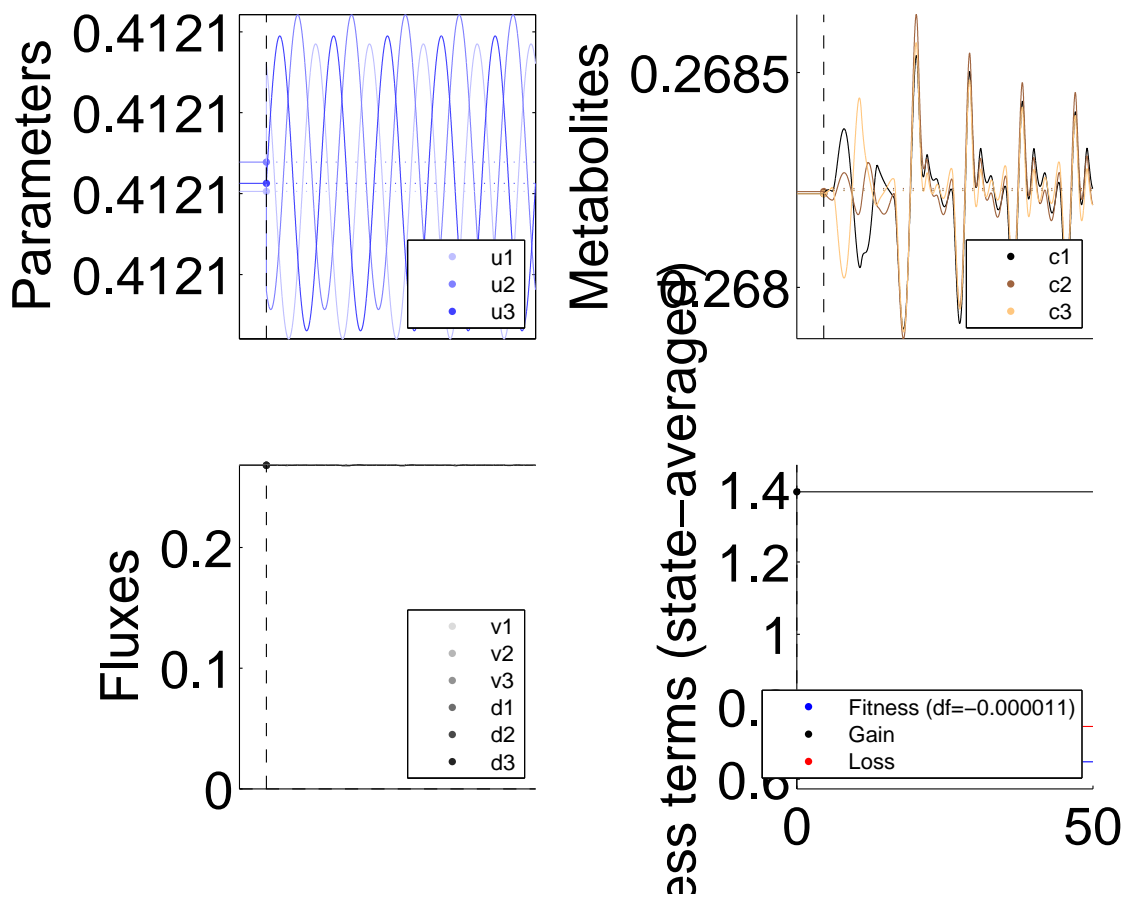
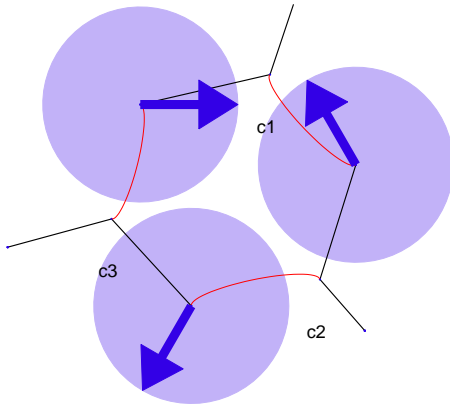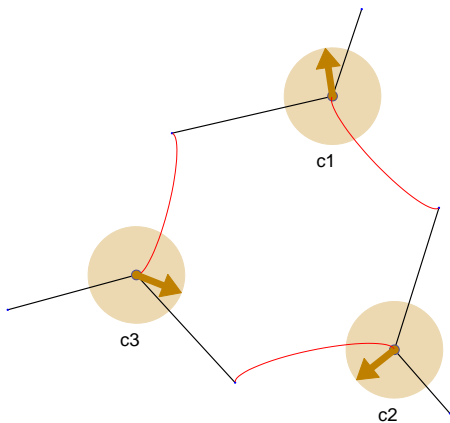## Phase angles $[0, 2\pi]$

Fitness change

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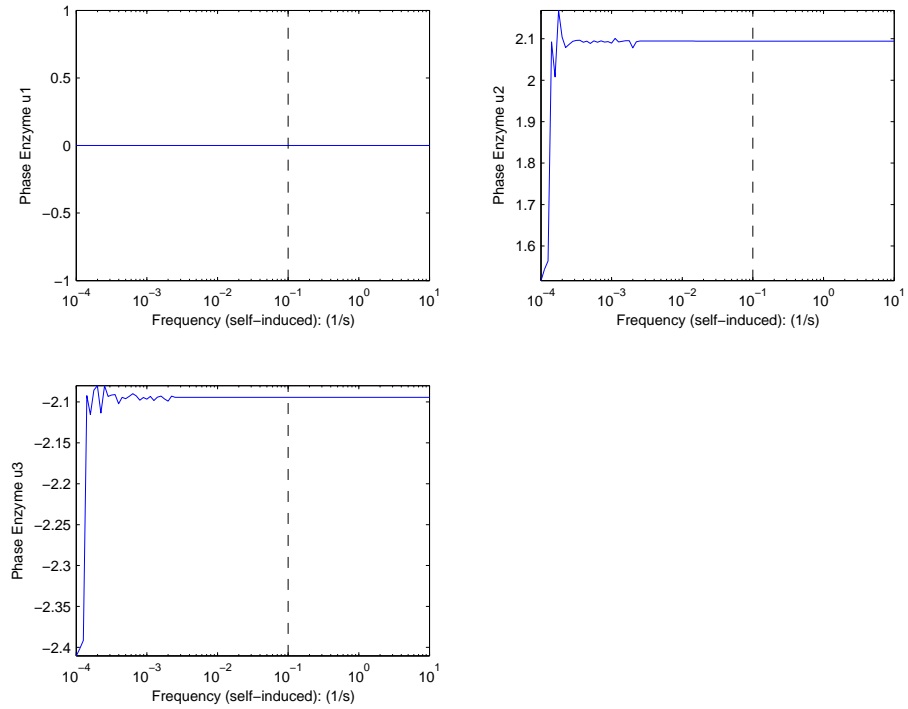
Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.

Enzyme rhythm

Spontaneous oscillations (concentrations)

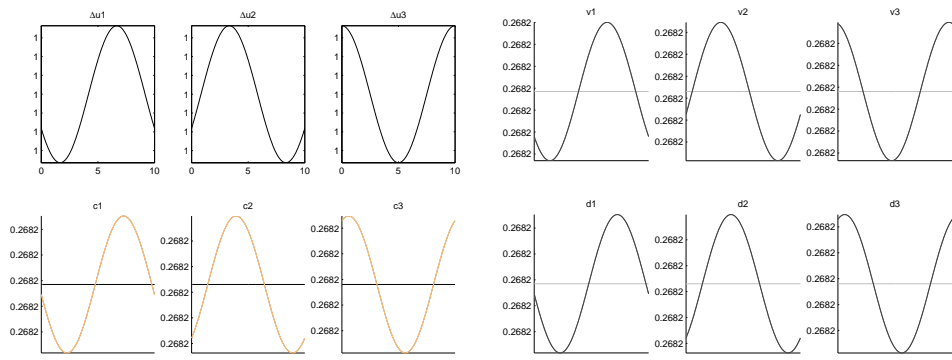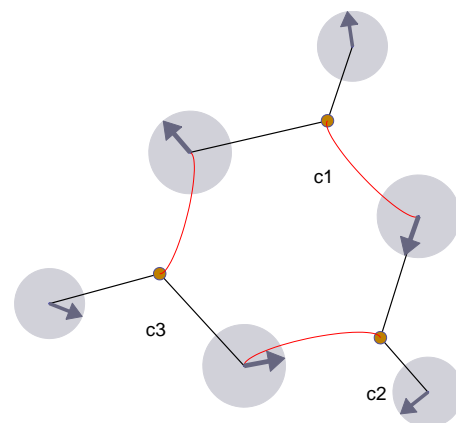Spontaneous oscillations (fluxes)

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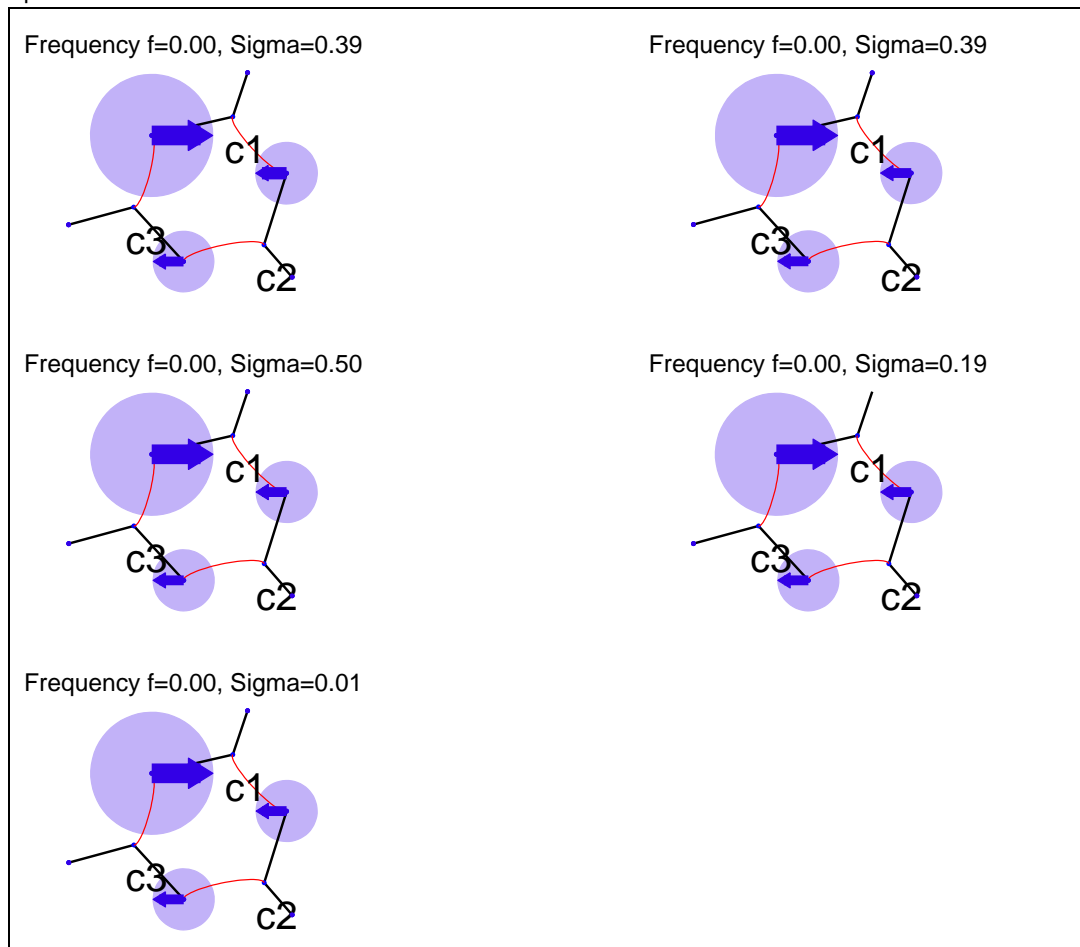
Spontaneous oscillations

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).