

Enzyme rhythms in model ros_simple.speedy - spontaneous oscillations

Model name: ros_simple

o Optimisation problem

- Protein turnover time $1 \text{ s} = 0.0167 \text{ min}$
- Perturbed parameter(s) : x1
- Perturbation frequency $f : 6.25/\text{s}$ (period 0.16 s)
- Scored quantity: v3
- Fitness-averaged fitness
- No posttranslational rhythms allowed
- Standard frequency considered $f : 6.25/\text{s}$ (period 0.16 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 self-induced oscillation found

- Maximum principal synergy found (in tested range) at frequency $f = 12.6/\text{s}$ (period 0.0794 s)
- Maximum fitness found (in tested range) at frequency $f = 6.31/\text{s}$ (period 0.158 s)

o Fitness changes after external perturbation at frequency $f=6.25/\text{s}$

- Change by perturbation alone (xx): 0.00202

o Self-induced oscillations?

- Maximally self-induced oscillations (in tested range) at $f = 12.6$, principal synergy 0.00189
- Beneficial self-induced oscillations found at frequency $f = 6.25/\text{s}$ (principal synergy = 0.00112)
- Predicted fitness change (self-induced, 2nd order, amplitude below 1/2 of mean) at frequency $f = 6.25$: 0.0577
- Predicted maximal fitness change (self-induced, numeric opt, full amplitude constraints) at frequency $f = 6.31$: 1.49×10^{-6}

WARNING: an external rhythm is given and a self-induced rhythm has been found

o Numerical calculation (responsive, $f=6.25$)

- Fitness change (fitness-averaged): 0.00301
- Fitness change (state-averaged): 0.00322

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, $f=6.25$)

- Fitness change (fitness-averaged) : 7.63×10^{-5}
- Fitness change (state-averaged): 8.11×10^{-5}

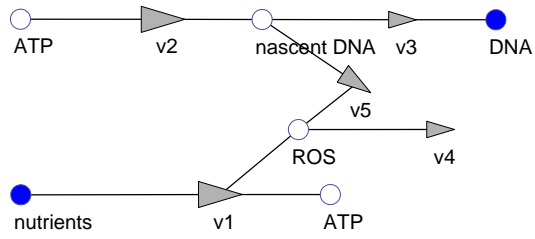


Figure 1: Network and reference flux

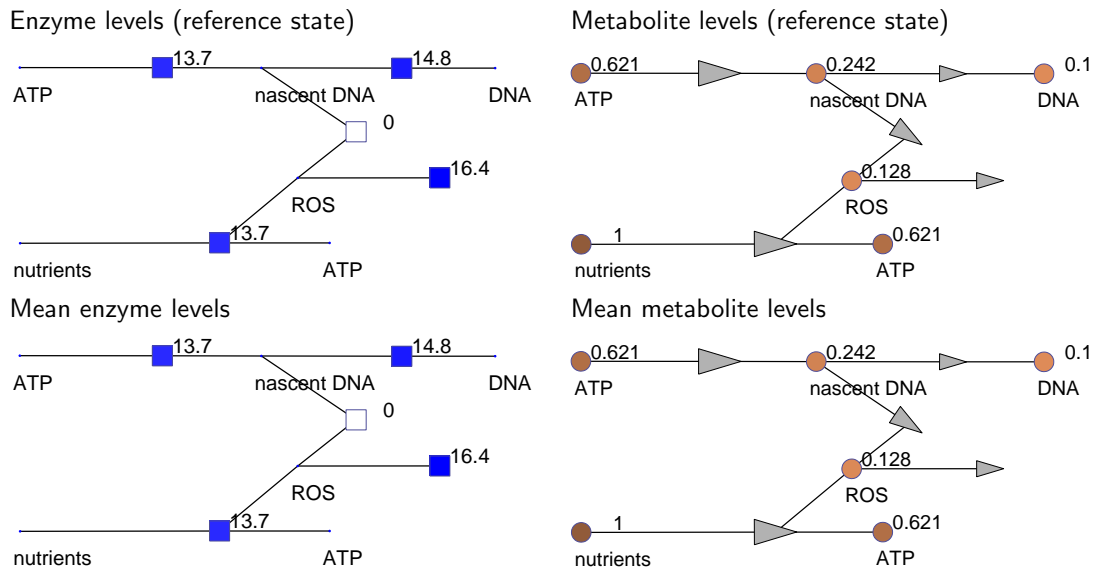


Figure 2: Reference state (top) and mean state during oscillation (bottom).

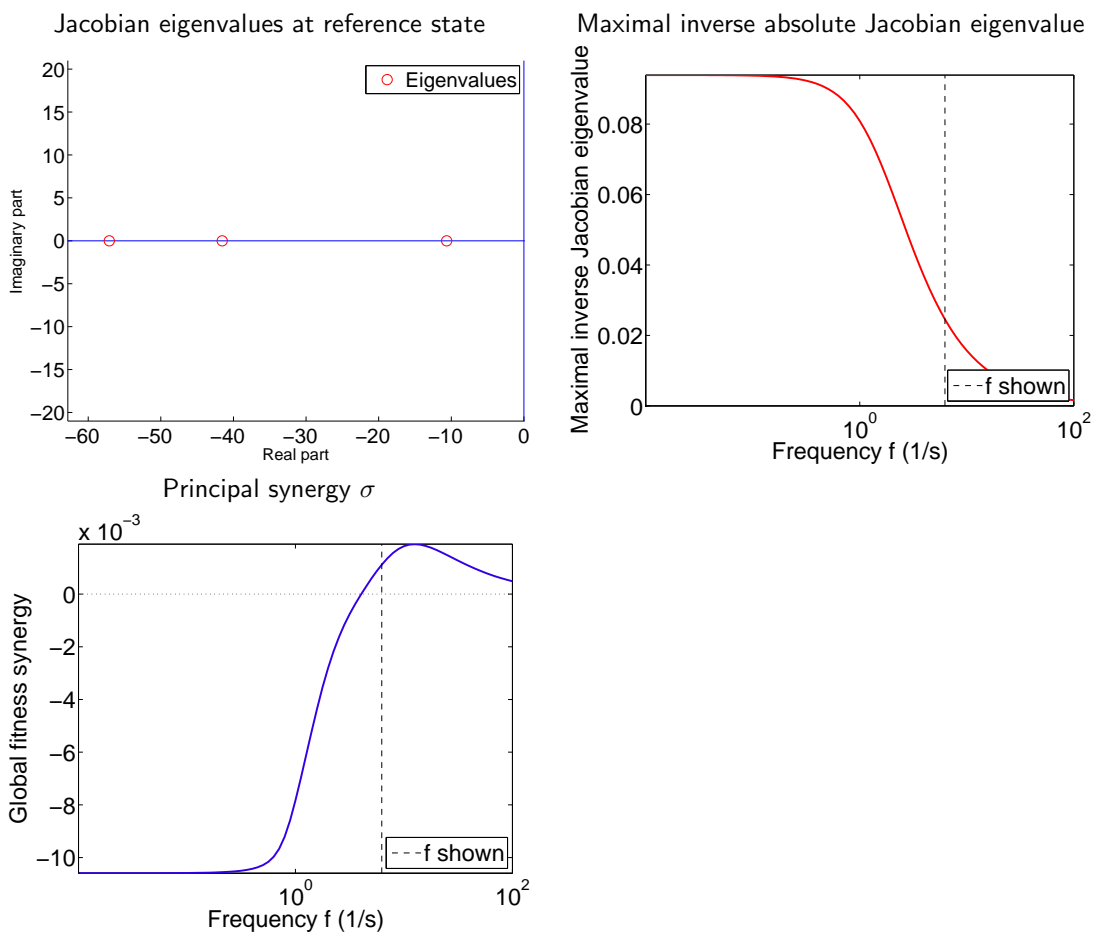
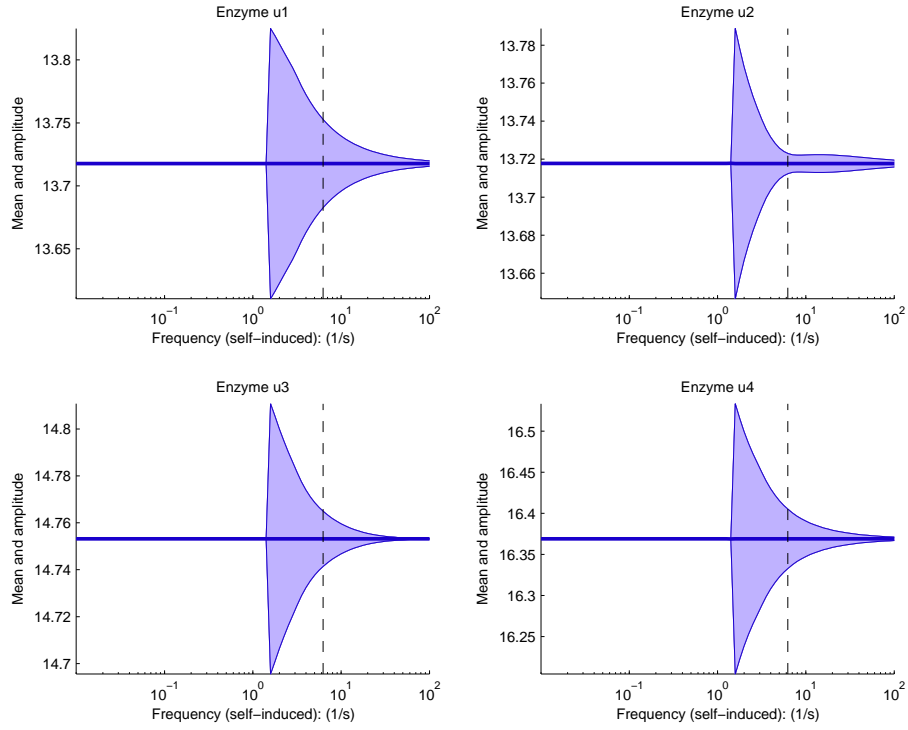
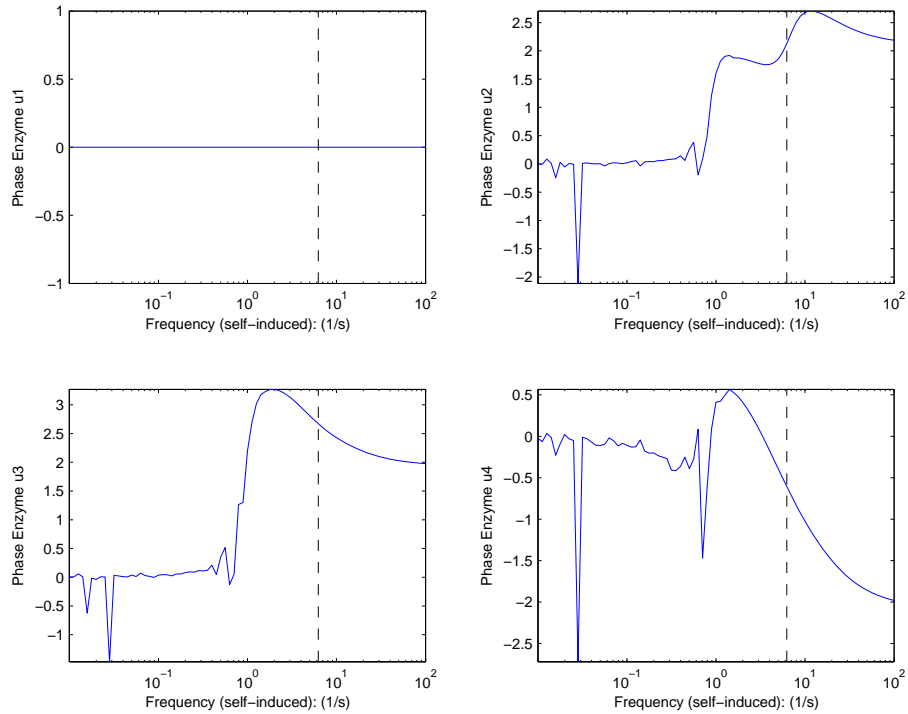


Figure 3: Control analysis: fitness curvatures. Left: Frequency-dependent fitness curvature eigenvalues. Right: relative sizes and phases of the individual enzyme levels (components of the leading fitness curvature eigenvector).

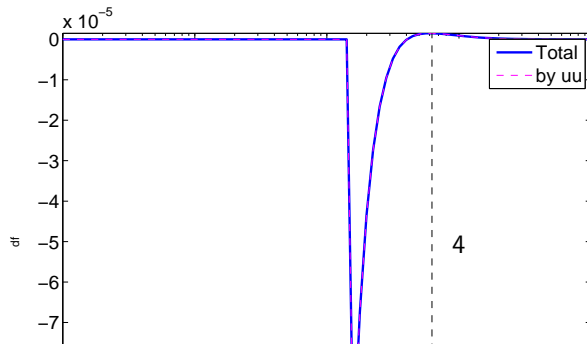
Protein level and enzyme activity (mean and amplitude)



Phase angles $[0, 2\pi]$



Fitness change



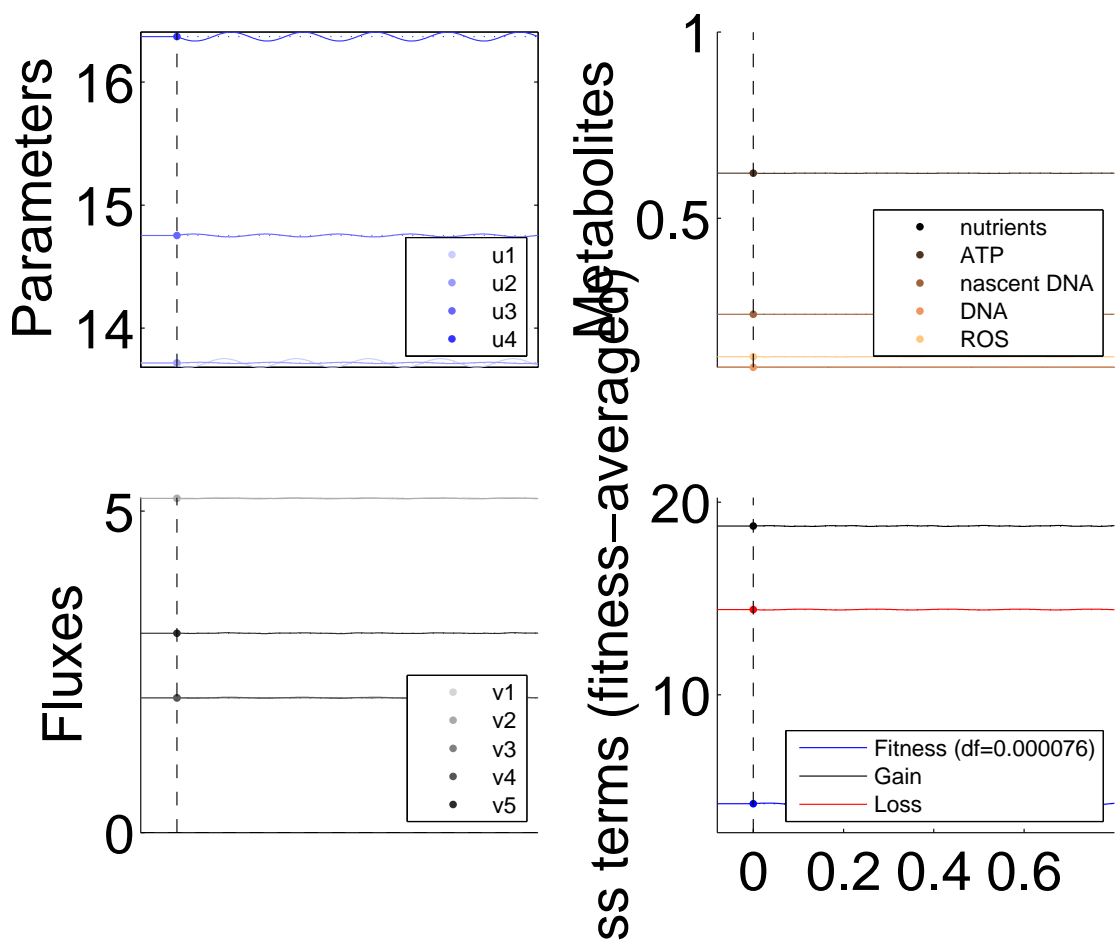
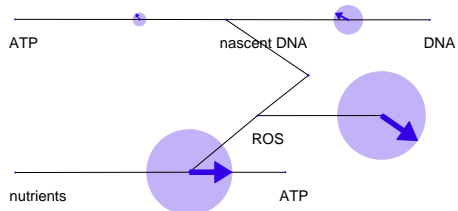
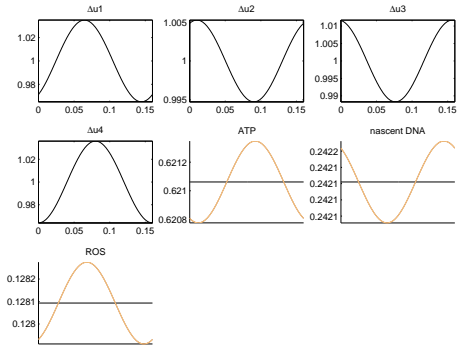
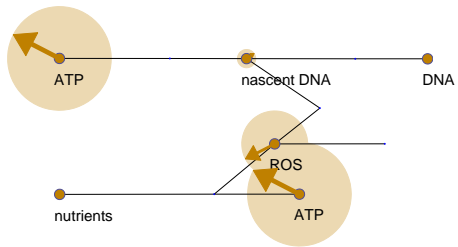


Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.

Enzyme rhythm



Spontaneous oscillations (concentrations)



Spontaneous oscillations (fluxes)

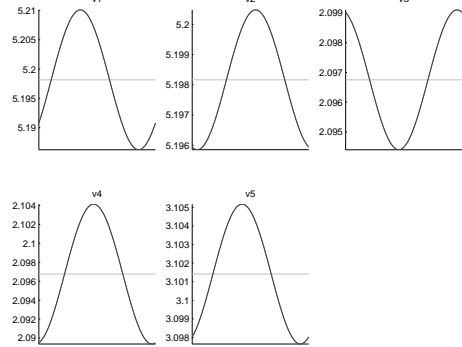
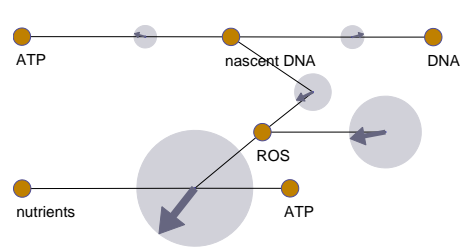


Figure 6: Spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

Spontaneous oscillations

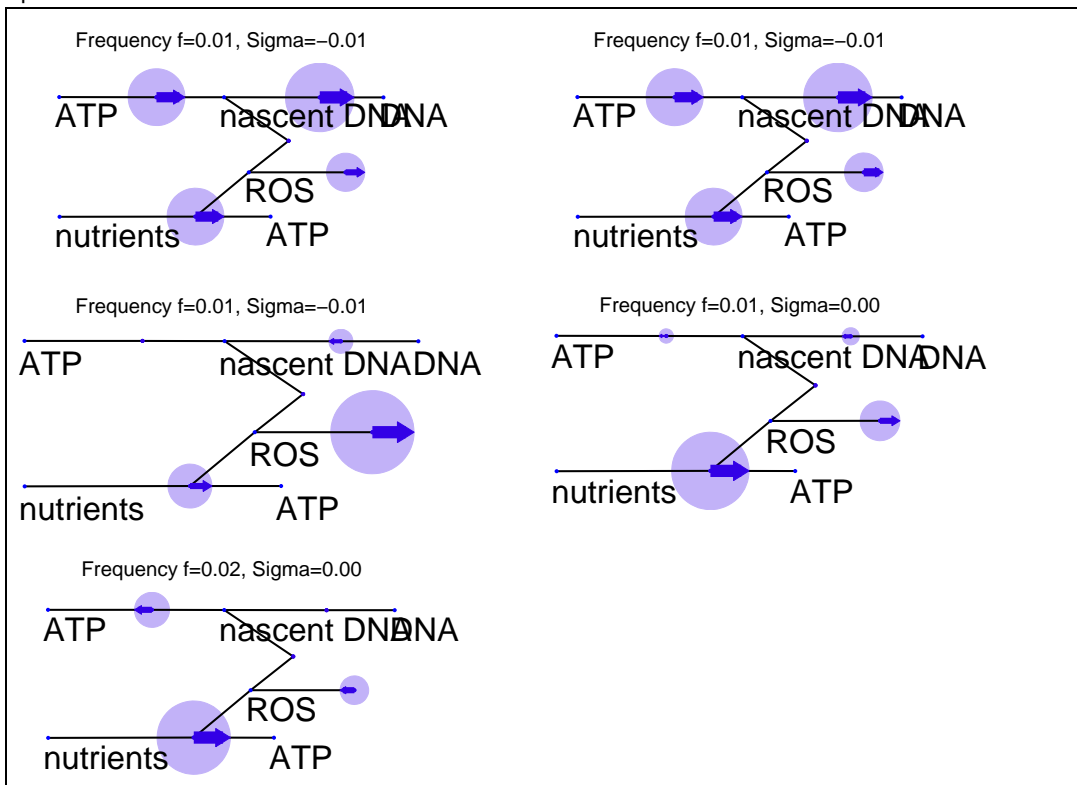


Figure 7: Spontaneous oscillations (or tendencies towards them) for various circular frequencies ω . If the maximal fitness curvatures λ is positive, the rhythm is beneficial (local expansion; arrows: absolute changes).