

Enzyme rhythms in model ros_simple - spontaneous oscillations

Model name: ros_simple

o Optimisation problem

- Protein turnover time $1.8e+03$ s = 30 min
- Perturbed parameter(s) : x1
- Perturbation frequency f : 0.0333/s (period 30 s)
- Scored quantity: v3
- Fitness-averaged fitness
- Posttranslational rhythms allowed
- Standard frequency considered f : 0.0333/s (period 30 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 $f = 12.6/s$ (period 0.0794 s)
- Maximum fitness found (in tested range) at frequency $f = 6.31/s$ (period 0.158 s)

o Fitness changes after external perturbation at frequency $f=0.0333/s$

- Change by perturbation alone (xx): -0.00549
- Change by adaption synergies (xu): 0.00448
- Change by periodic enzyme (uu): -0.00196
- Change by enzyme mean shift (u): -1.14e-07
- Total fitness change : -0.00297
- Fitness gain by adaption : 0.00252
- 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 $f = 0.00178/s$: 0.0024

o Self-induced oscillations?

- No beneficial self-induced oscillations (2nd order, amplitude below 1/2 of mean) found at frequency $f = 0.0333/s$ (principal synergy = -0.0106): Predicted fitness change -0.774

o Numerical calculation (responsive, $f=0.0333$)

- Fitness change (fitness-averaged): -0.0055
 - Fitness change (state-averaged): -0.00347
- ### o Numerical calculation (adaptive, $f=0.0333$)
- Fitness change (fitness-averaged): -0.00171
 - Fitness change (state-averaged): 0.00274

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, $f=0.0333$)

- Fitness change (fitness-averaged) : $1.18e-05$
- Fitness change (state-averaged): $1.31e-05$

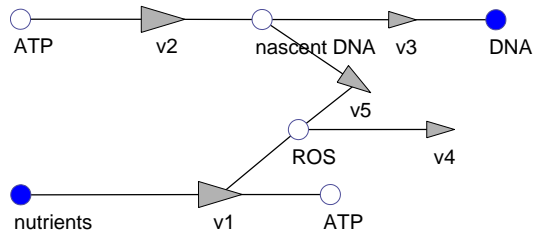


Figure 1: Network and reference flux

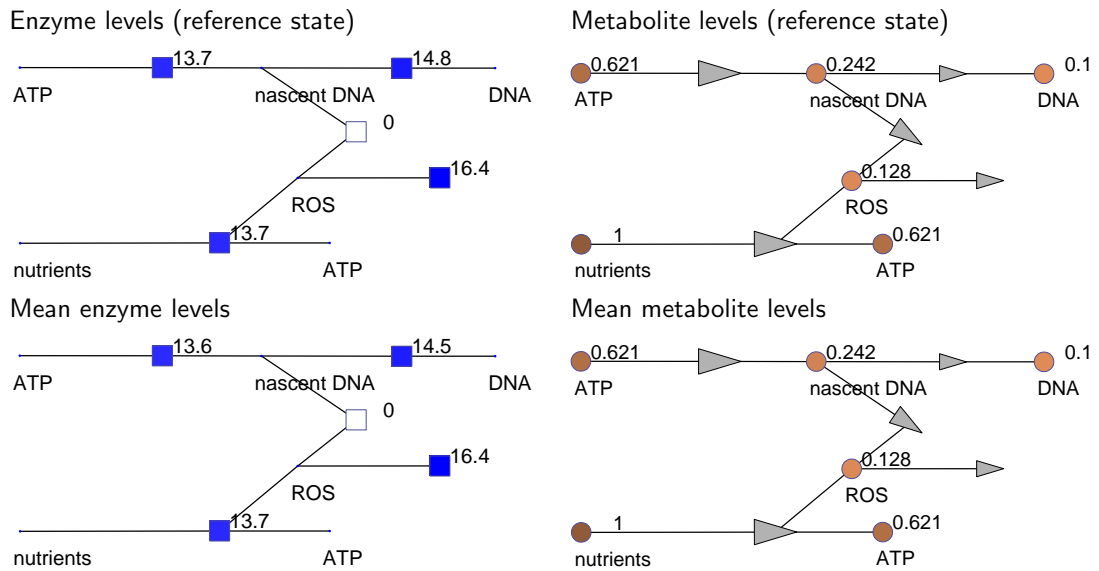


Figure 2: Reference state (top) and mean state during oscillation (bottom).

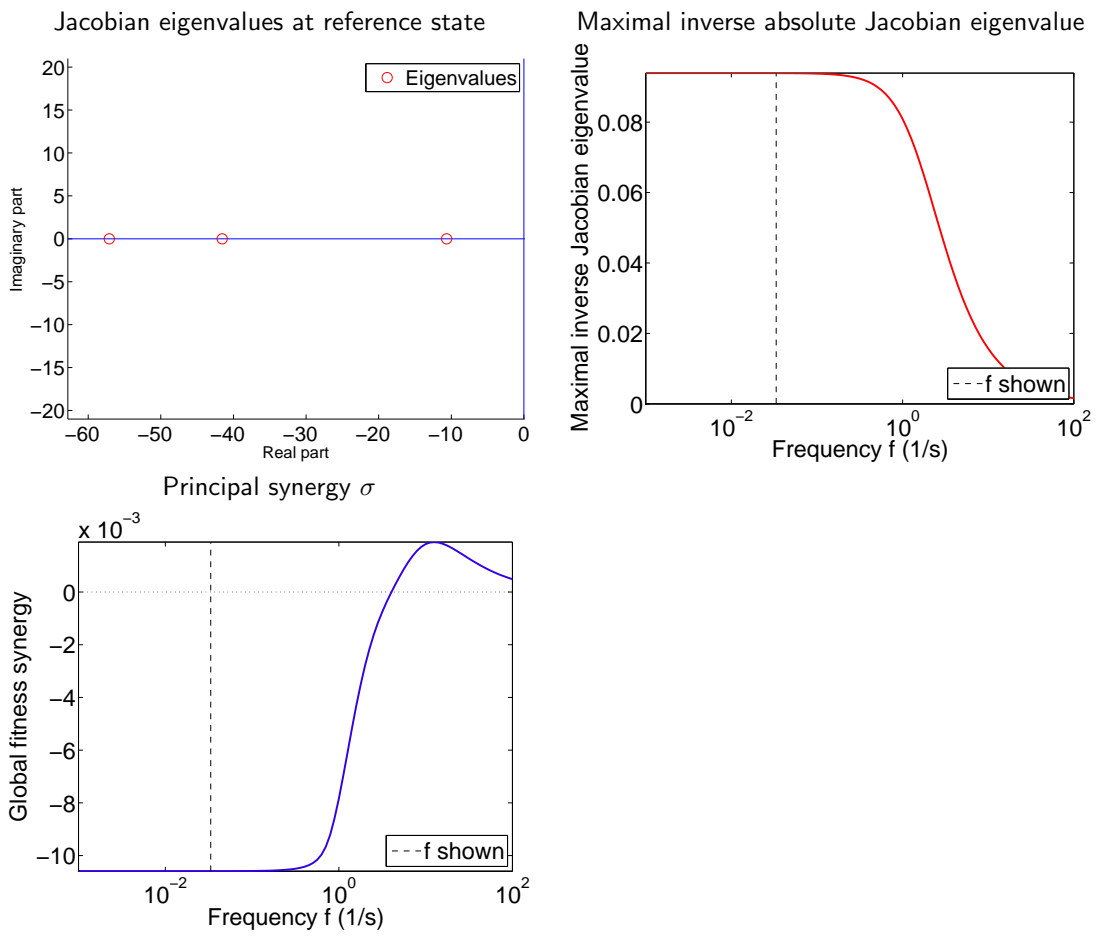
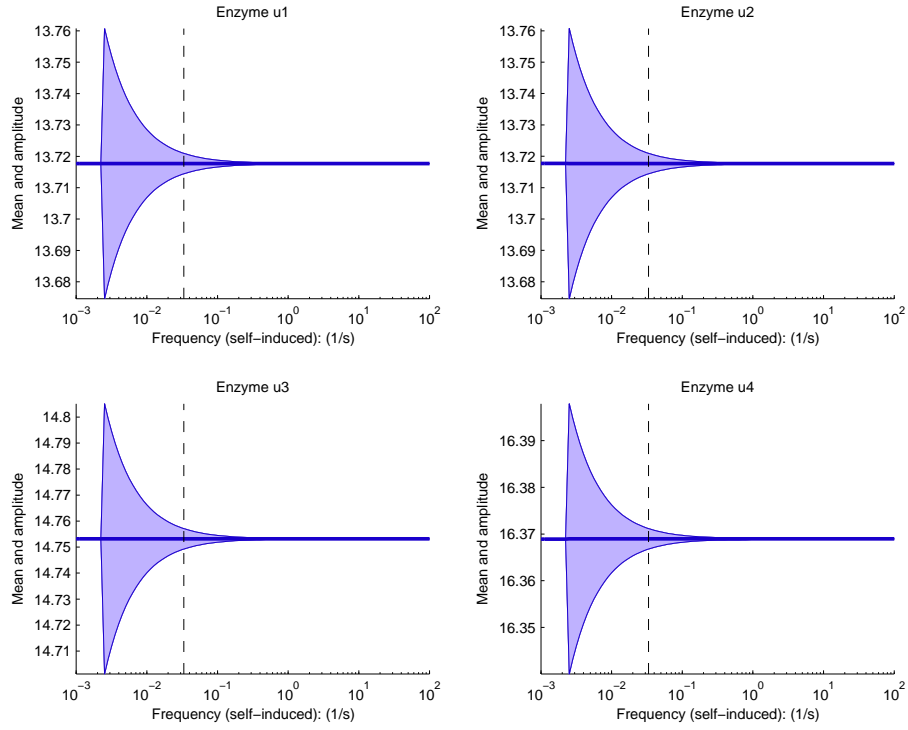
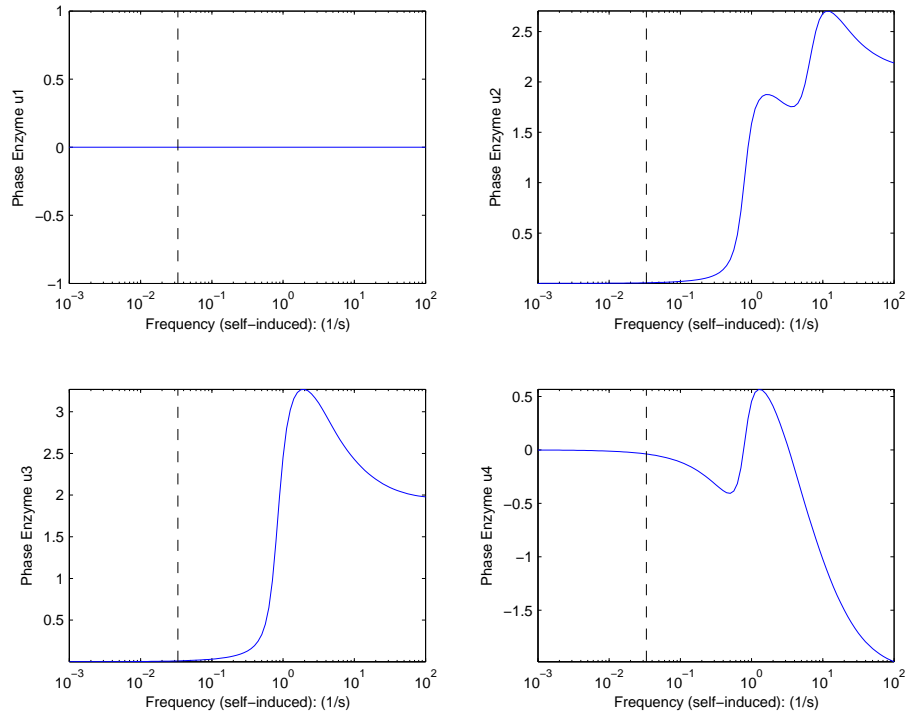


Figure 3: Control analysis: fitness curvatures. Left: Frequency-dependent fitness curvature eigenvalues. Right: relative sizes and phases of the individual enzyme levels (components of the leading fitness curvature eigenvector).

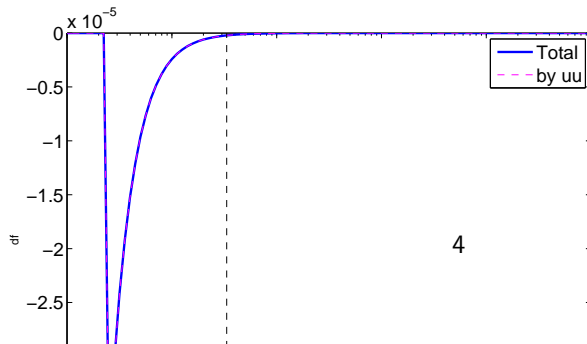
Protein level and enzyme activity (mean and amplitude)



Phase angles $[0, 2\pi]$



Fitness change



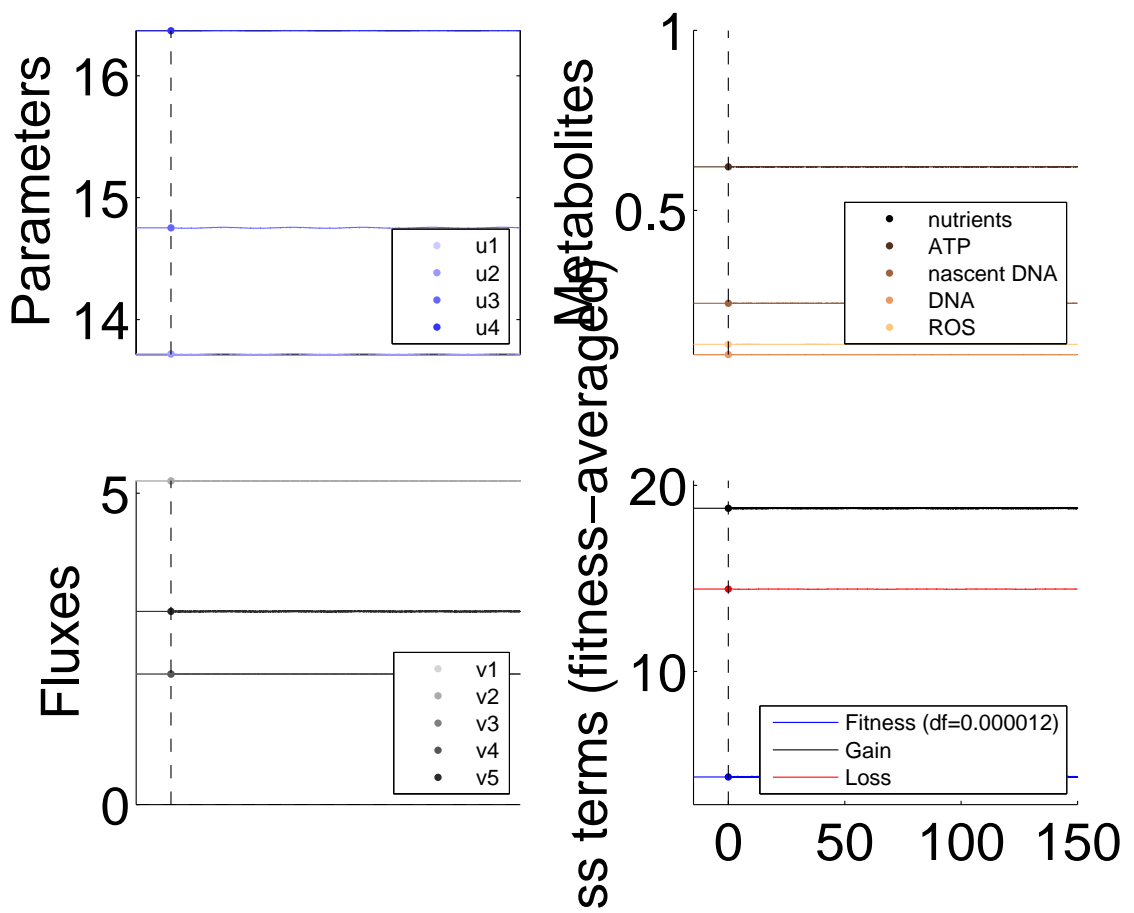
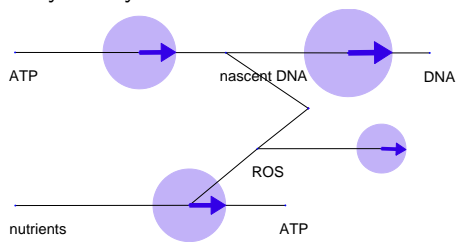
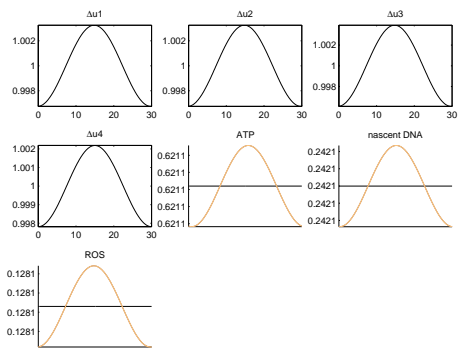
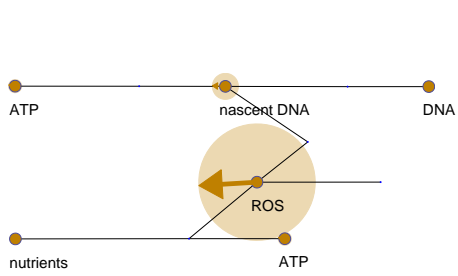


Figure 5: Numerical calculations: spontaneous oscillations. Perturbation frequency see first page.

Enzyme rhythm



Spontaneous oscillations (concentrations)



Spontaneous oscillations (fluxes)

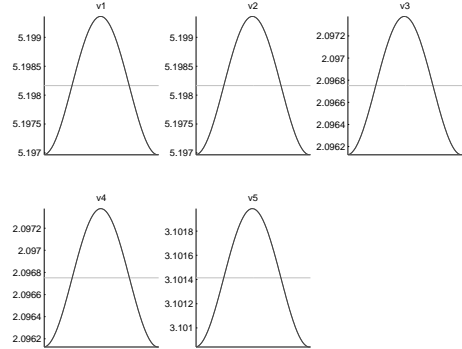
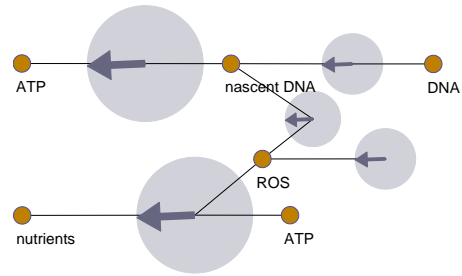


Figure 6: Spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

Spontaneous oscillations

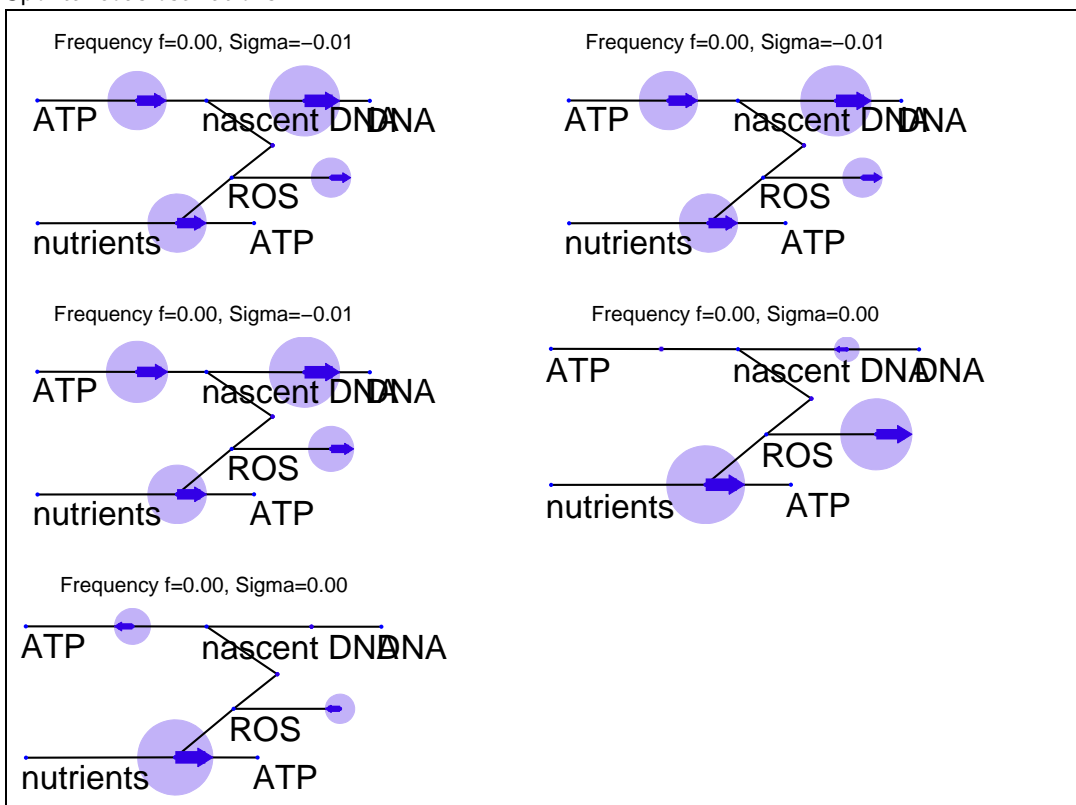


Figure 7: Spontaneous oscillations (or tendencies towards them) for various circular frequencies ω . If the maximal fitness curvatures λ is positive, the rhythm is beneficial (local expansion; arrows: absolute changes).