

## Enzyme rhythms in model glycogen\_storage\_dilution - enzymes are activated

Model name: glycogen\_storage\_dilution

### o Optimisation problem

- Protein turnover time  $1.8e+03$  s = 30 min
- Perturbed parameter(s) : x1
- Perturbation frequency f : 0.00333/s (period 300 s)
- Scored quantity: glucose
- Scored quantity: v4
- Fitness-averaged fitness
- Posttranslational rhythms allowed
- Standard frequency considered f : 0.00333/s (period 300 s)

### o Model properties:

- inactive\_enzymes: 1
- balanced\_reference\_state: 0
- consider\_external\_rhythm: 1
- adaptive\_rhythm: 1
- spontaneous\_rhythm: 0
- spontaneous\_rhythm\_at\_omega: 0
- has\_spontaneous\_rhythm\_and\_inactive\_enzymes: 0

### o No beneficial autonomous oscillation found

### o Fitness changes after external perturbation at frequency $f=0.00333/s$

- Change by perturbation alone (xx): -19.7
  - Change by adaption synergies (xu): 30.4
  - Change by periodic enzyme (uu): -17
  - Change by enzyme mean shift (u):  $-3.66e-07$
  - Total fitness change : -6.3
  - Fitness gain by adaption : 13.4
  - Maximum adaptive fitness found (in tested range) at frequency  $f=3.16e-05/s$  (period  $3.16e+04$  s)
  - Predicted max. fitness change (adaptive, num. opt, full ampl. constraints) at frequency  $f=3.16e-05$ : -0.471
- Inactive enzymes found; computing adaptive rhythms with shifted mean values in 1st order approximation

### o Autonomous oscillations?

#### o Numerical calculation (responsive, $f=0.00333$ )

- Fitness change (fitness-averaged): -19.7
- Fitness change (state-averaged):  $-2.86e-07$

#### o Numerical calculation (adaptive, $f=0.00333$ )

- Fitness change (fitness-averaged): -17.4
- Fitness change (state-averaged): -12.7

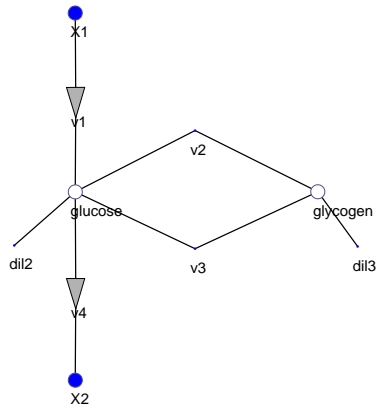


Figure 1: Network and reference flux

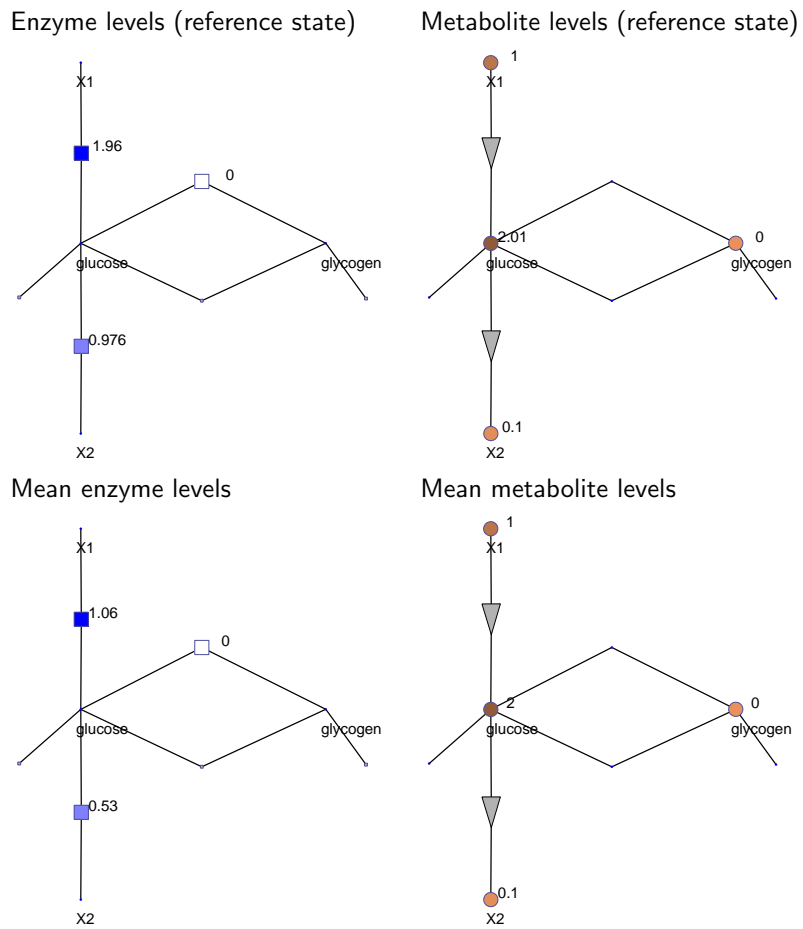
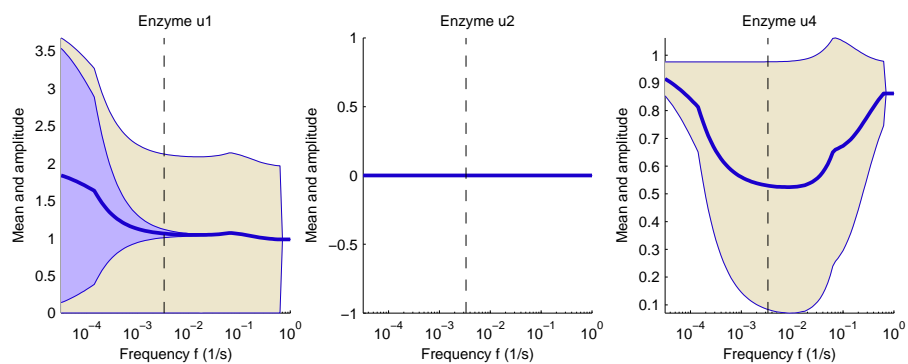
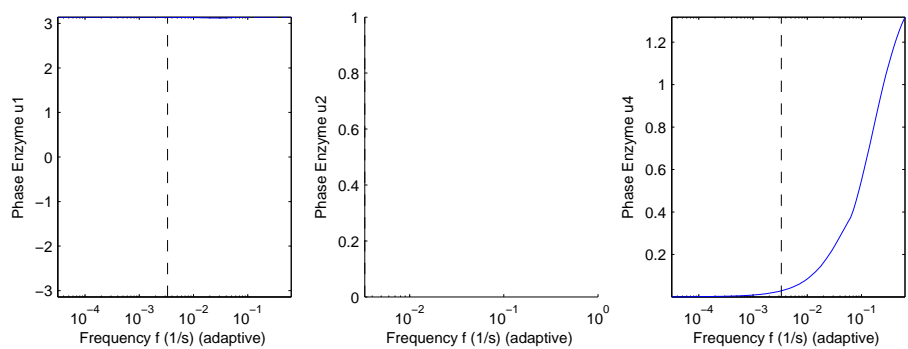


Figure 2: Reference state (top) and mean state during oscillation (bottom).

Protein level and enzyme activity (mean and amplitude)



Phase angles  $[0, 2\pi]$



Fitness change

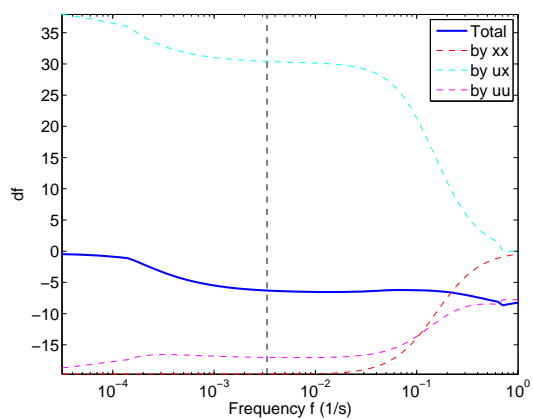


Figure 3: Adaptive oscillations. Left: amplitudes of protein levels (blue) and modification (grey). Right: phase shifts.

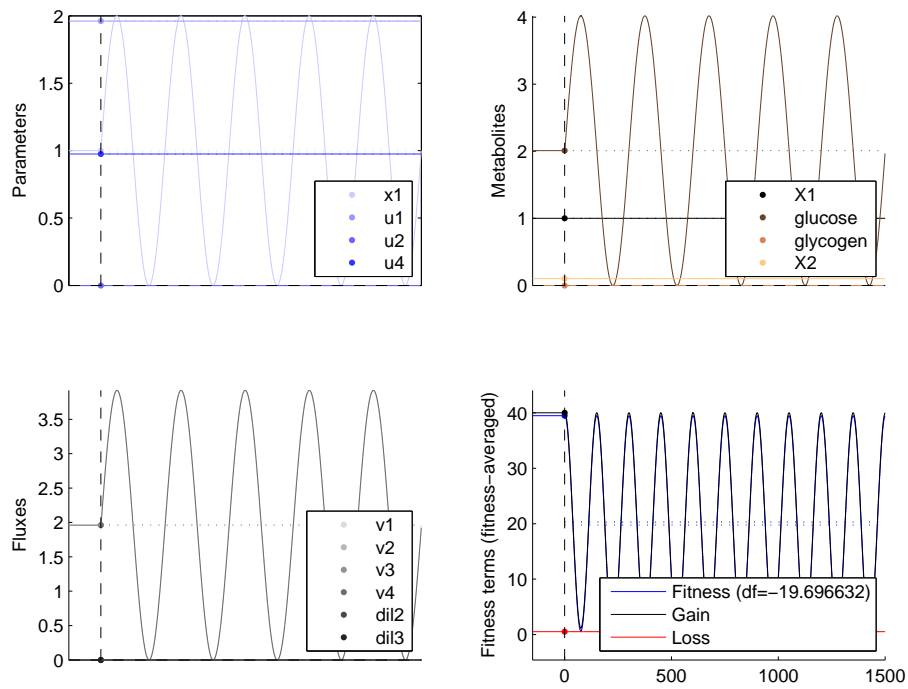


Figure 4: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost.

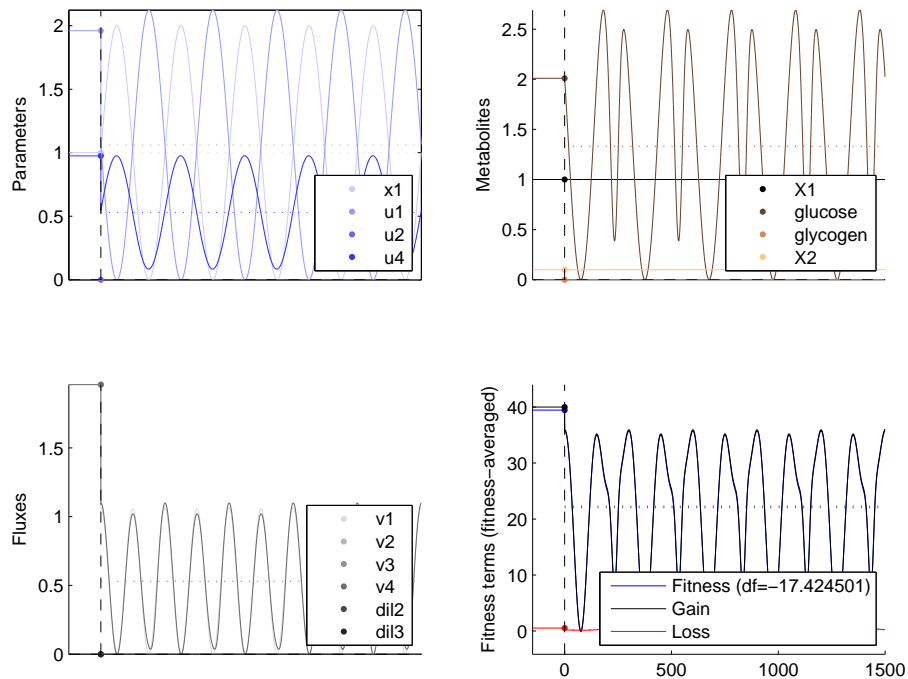
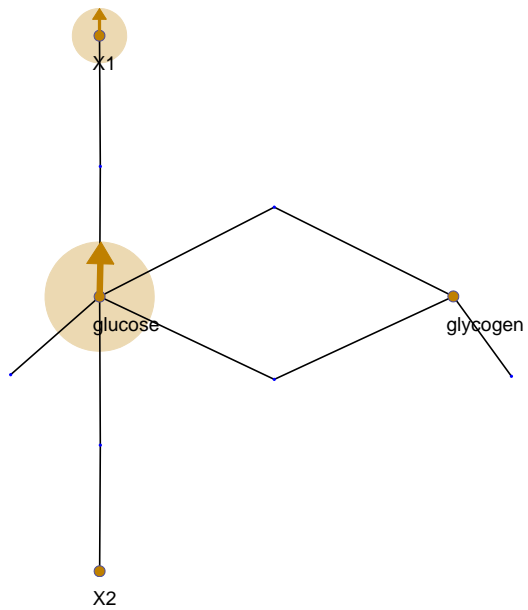


Figure 5: Numerical calculations: adaptive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost.

Responsive oscillations (concentrations)



Responsive oscillations (fluxes)

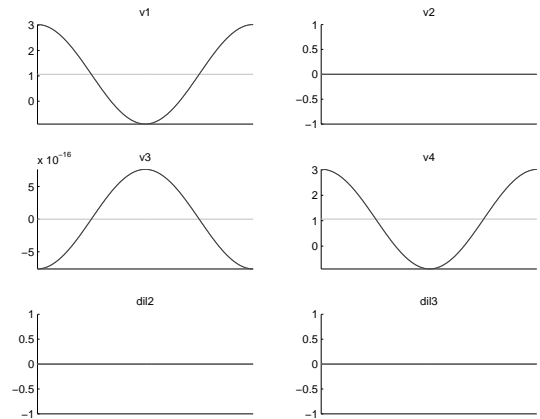
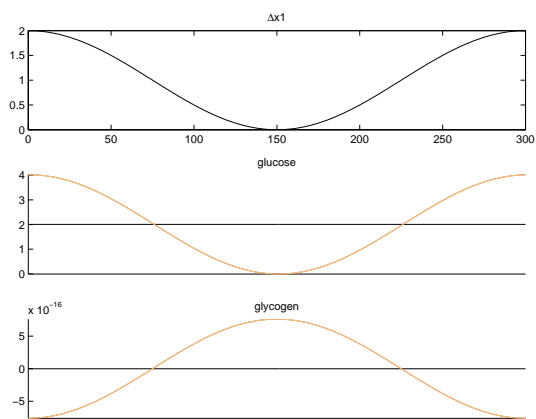
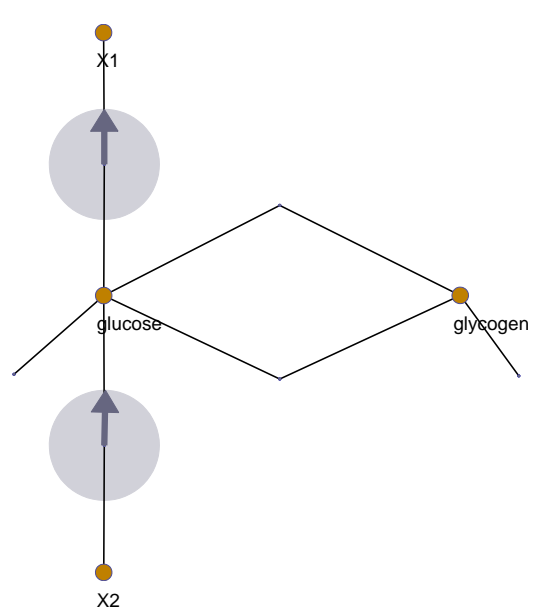
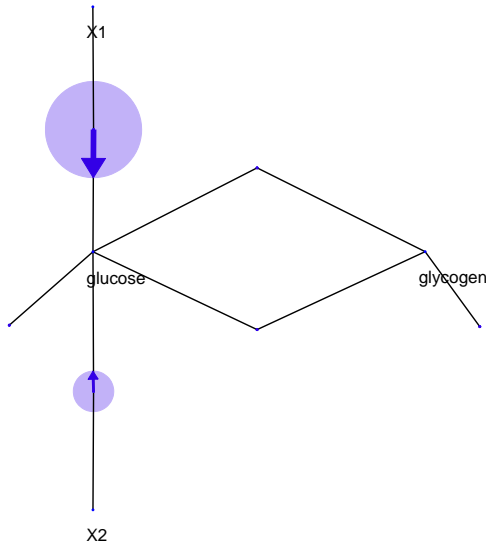
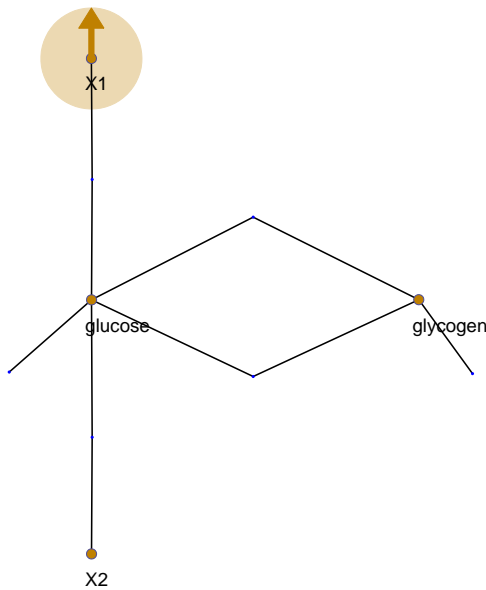


Figure 6: Responsive oscillations (local expansion; arrows: absolute changes)

Adaptive oscillations (enzymes)



Adaptive oscillations (metabolites)



Adaptive oscillations (fluxes)

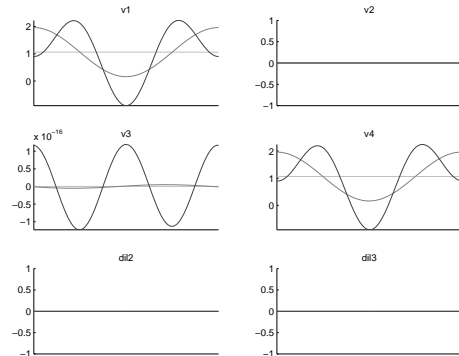
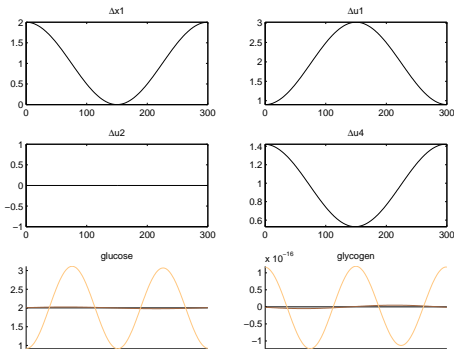
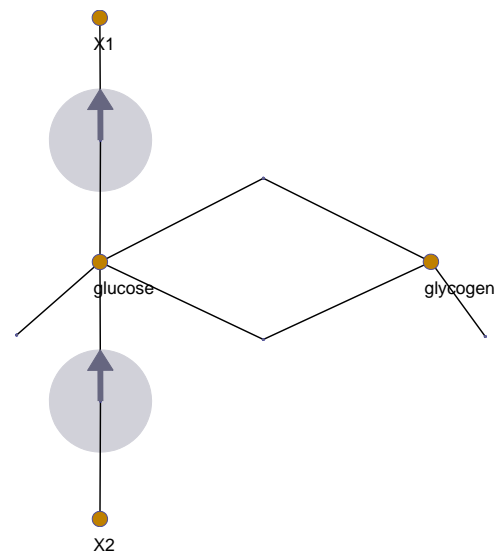


Figure 7: Adaption to forced oscillations (local expansion; arrows: absolute changes)

Adaptive

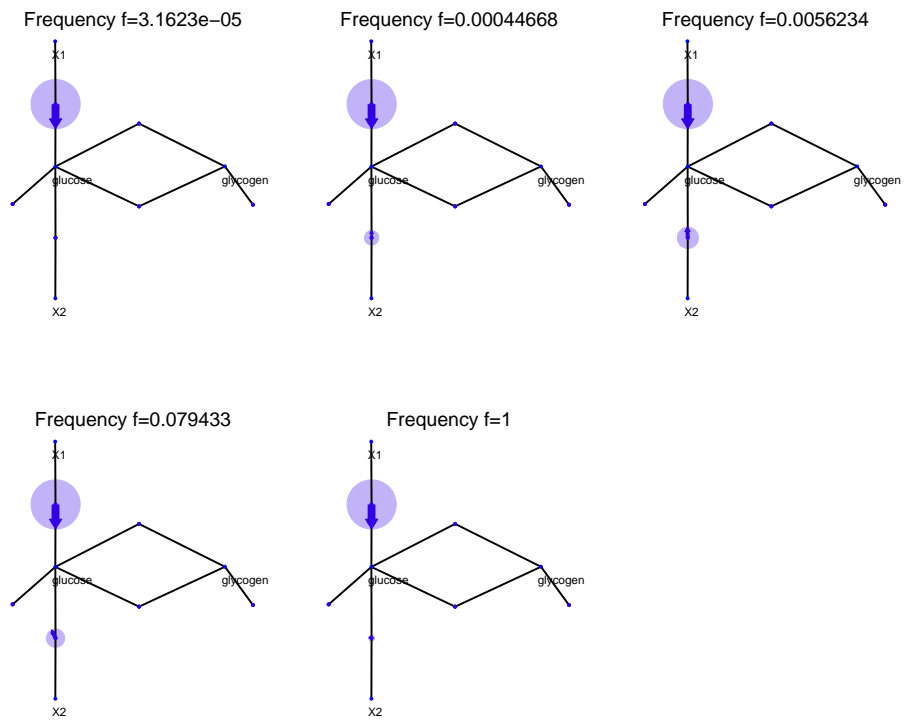
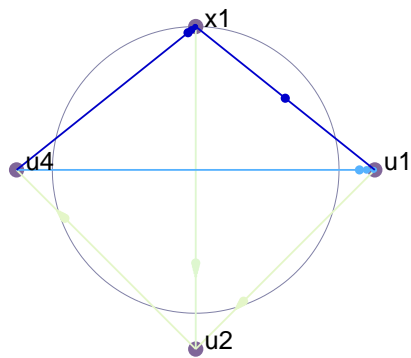
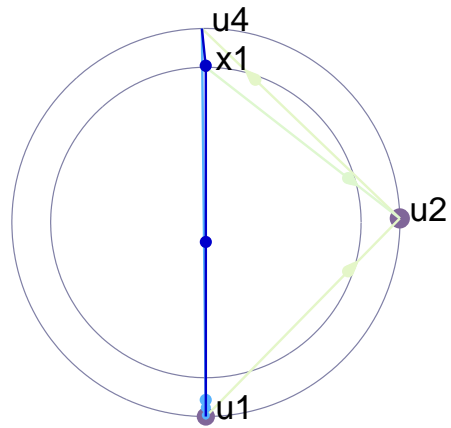


Figure 8: Adaptive oscillations for several frequencies (from local expansion).

Synergies



Synergy phase plot



Synergies on network

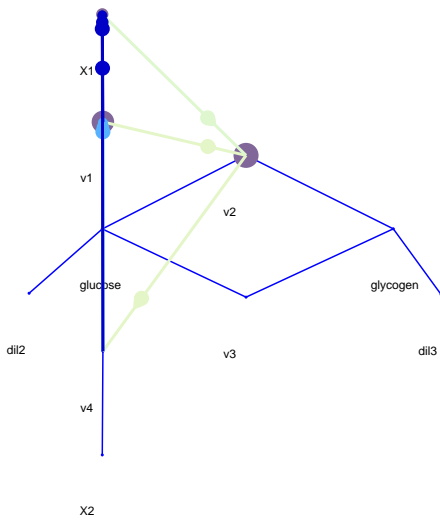


Figure 9: Periodic economic potentials and direct enzyme values.