

## Enzyme rhythms in model ycm\_oxygen.speedy

Model name: ycm\_oxygen

- o Optimisation problem

- Protein turnover time 1 s = 0.0167 min
- Perturbed parameter(s) : x11
- Perturbation frequency f : 0.2/s (period 5 s)
- Scored quantity: R00200
- Scored quantity: R01512
- Scored quantity: R01600
- Scored quantity: R04779
- Scored quantity: R00235
- Scored quantity: GTP\_irrev\_ATP
- Scored quantity: Oxphos\_Reduced\_Acceptor\_irrev\_ATP
- Scored quantity: Oxphos\_NADH\_irrev\_ATP
- Fitness-averaged fitness
- No posttranslational rhythms allowed
- Standard frequency considered f : 0.2/s (period 5 s)

- o Model properties:

- inactive\_enzymes: 0
- balanced\_reference\_state: 1
- 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 self-induced oscillation found

- o Fitness changes after external perturbation at frequency f=0.2/s

- Change by perturbation alone (xx): 0.000117
- Change by adaption synergies (xu): 0.35
- Change by periodic enzyme (uu): -0.146
- Change by enzyme mean shift (u): -4.75e-10
- Total fitness change : 0.205
- Fitness gain by adaption : 0.205
- Maximum adaptive fitness found (in tested range) at frequency f = 0.01/s (period 100 s)
- Predicted max. fitness change (adaptive, num. opt, full ampl. constraints) at frequency f = 0.01: 0.242

- o Self-induced oscillations?

- No beneficial self-induced oscillations (2nd order, amplitude below 1/2 of mean) found at frequency f = 0.2/s (principal synergy = -0.636): Predicted fitness change -0.00083

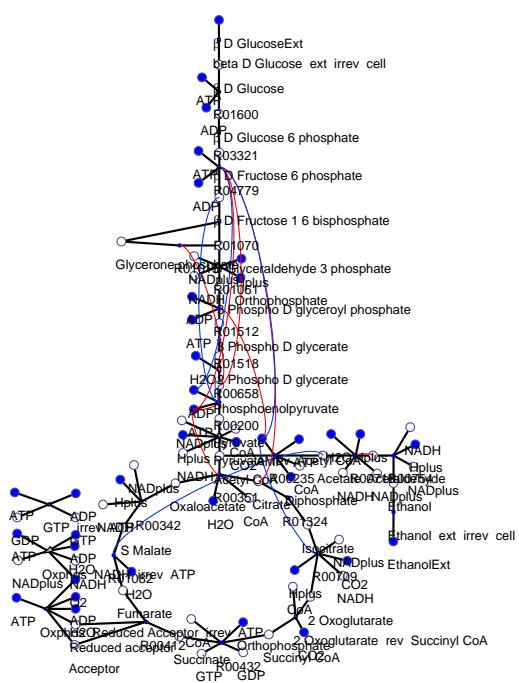
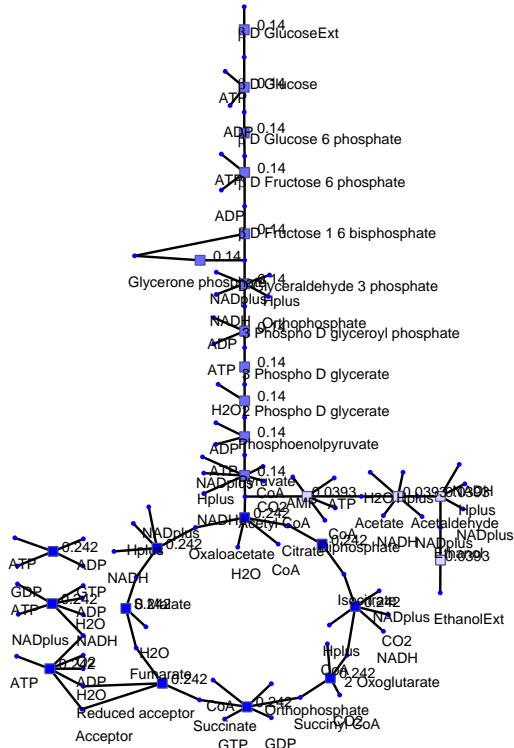
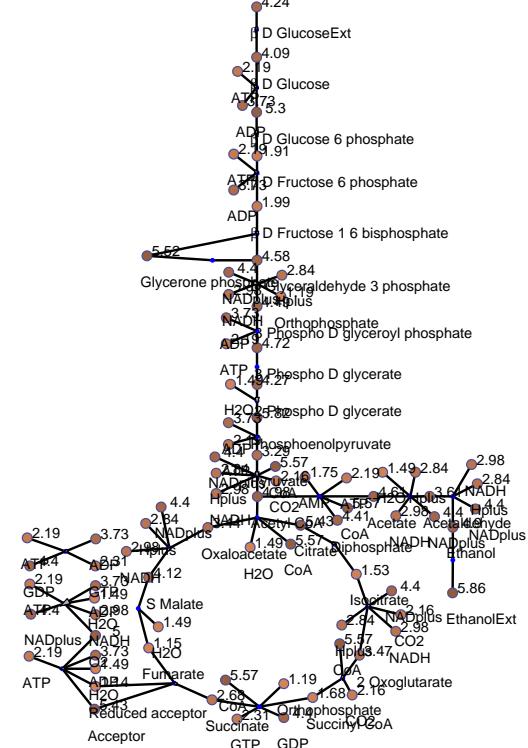


Figure 1: Network and reference flux

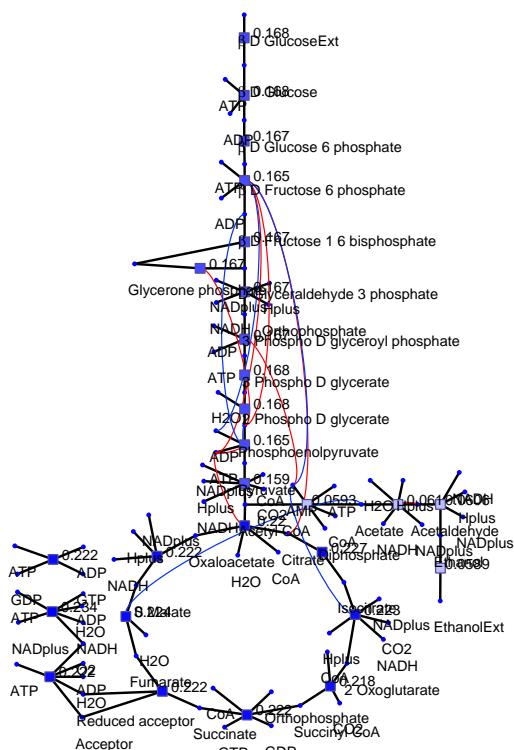
Enzyme levels (reference state)



Metabolite levels (reference state)



Mean enzyme levels



Mean metabolite levels

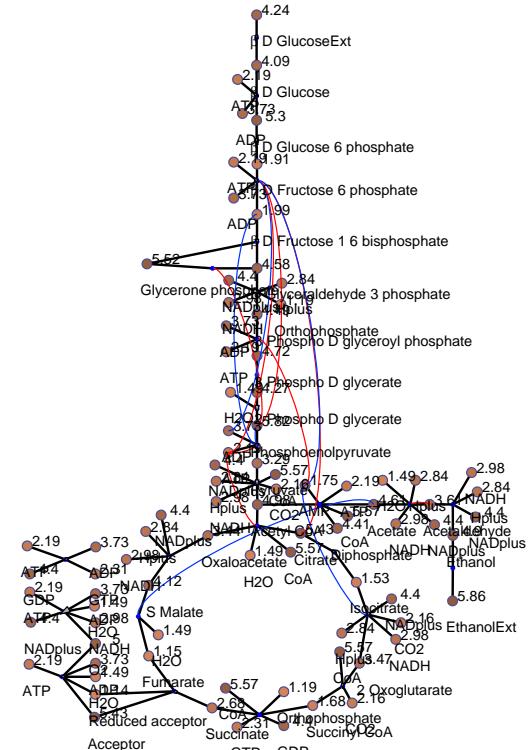


Figure 2: Reference state (top) and mean state during oscillation (bottom).

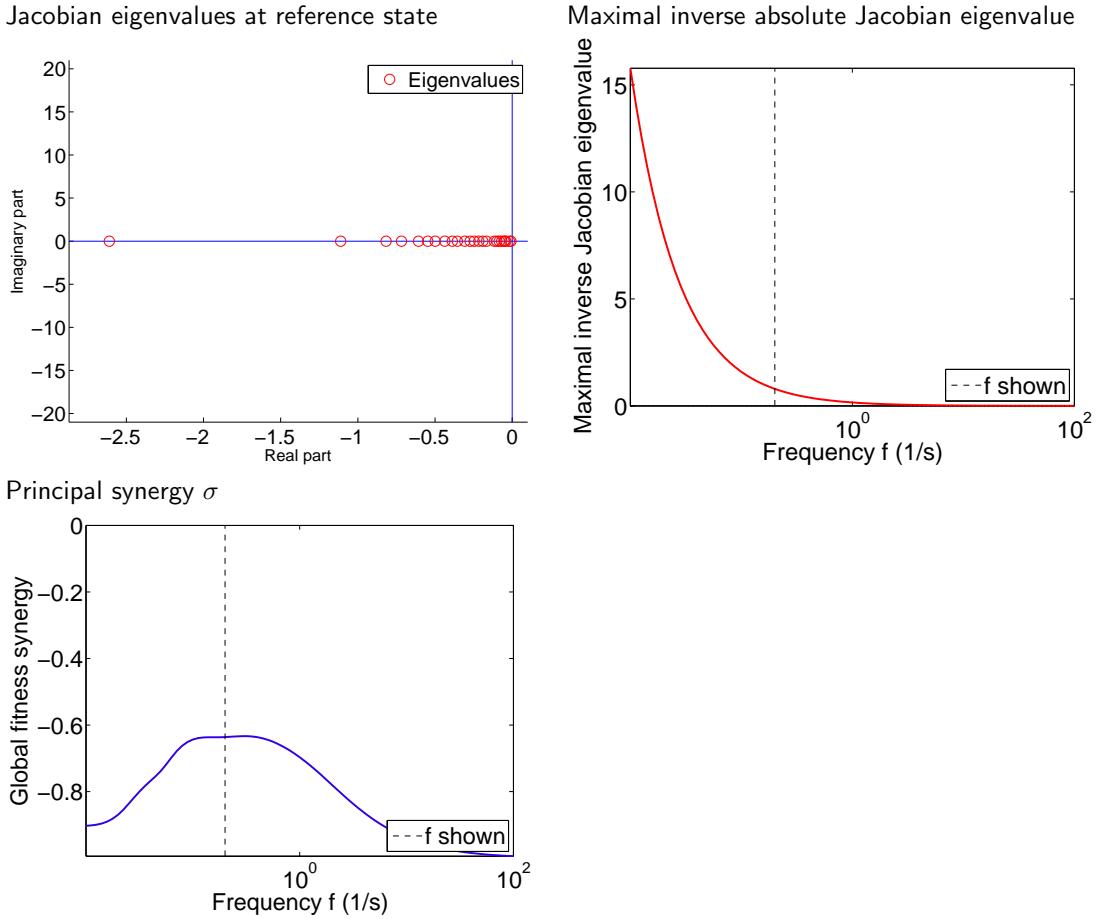
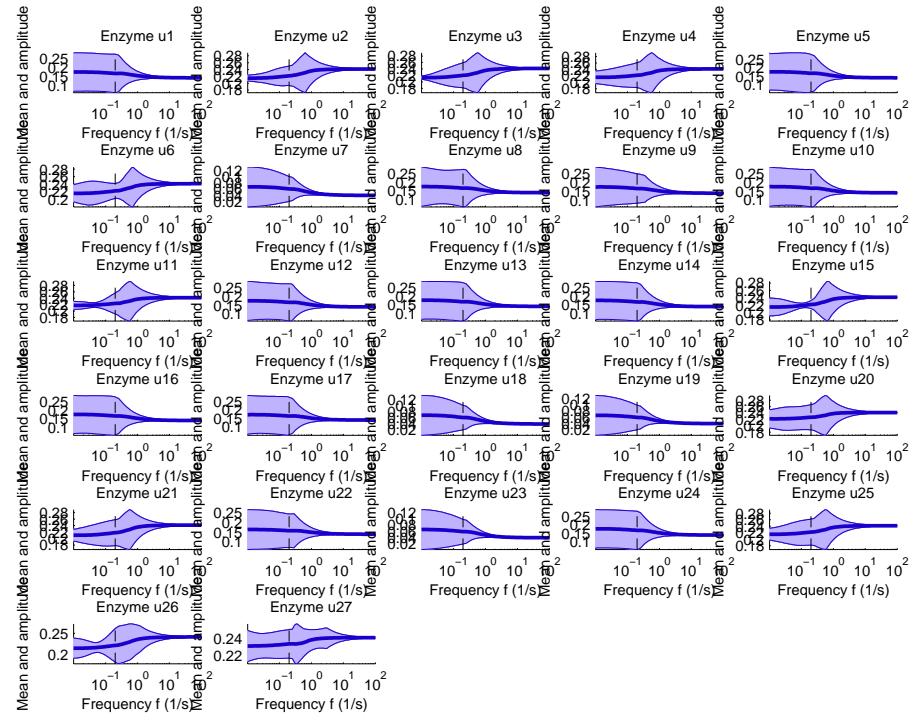
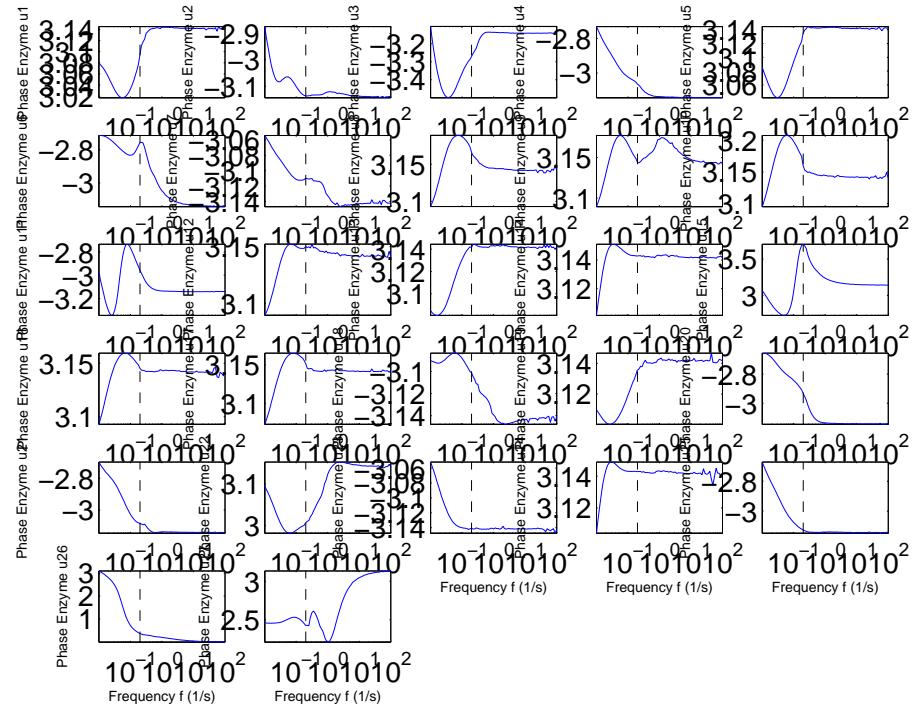


Figure 3: Control analysis. Left: Global fitness synergy (maximal fitness curvature eigenvalue), as a function of the frequency. Right: Relative amplitudes of individual enzymes for the least wasteful enzyme mode (components of the leading fitness curvature eigenvector).

### Protein level and enzyme activity (mean and amplitude)



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



### Fitness change

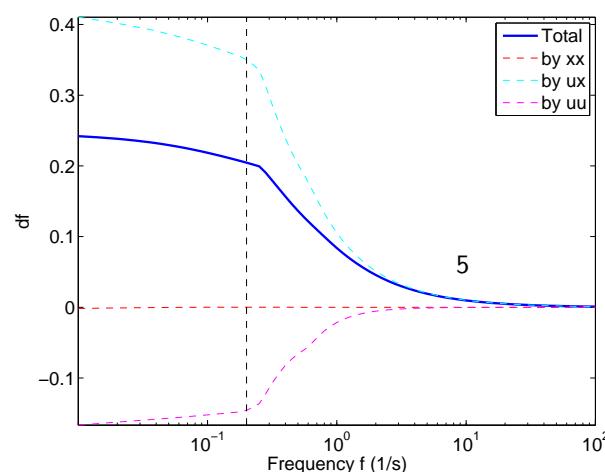
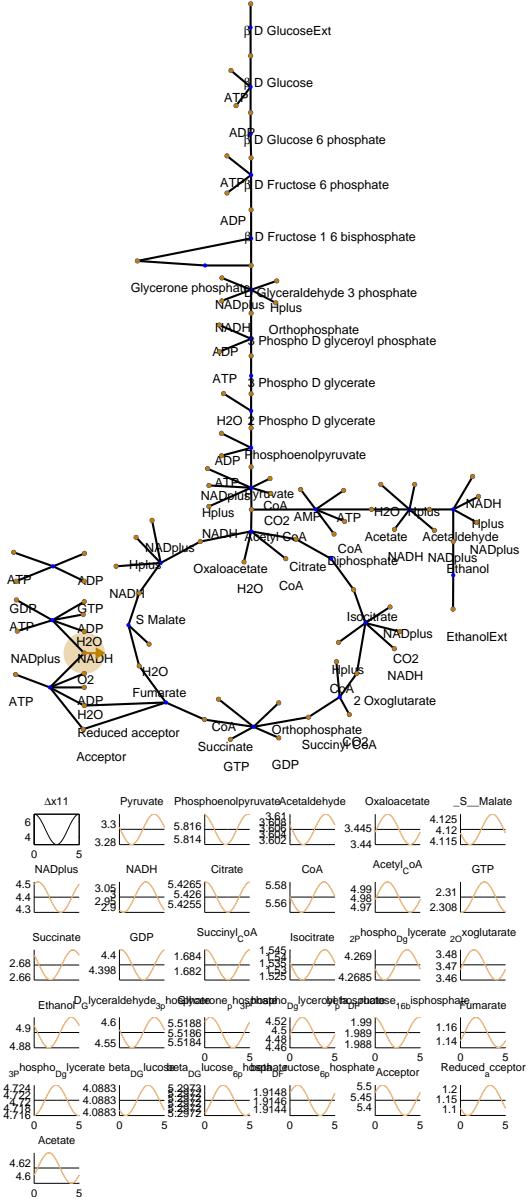


Figure 5: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first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

Figure 6: 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. Perturbation frequency see first page.

### Responsive oscillations (concentrations)



### Responsive oscillations (fluxes)

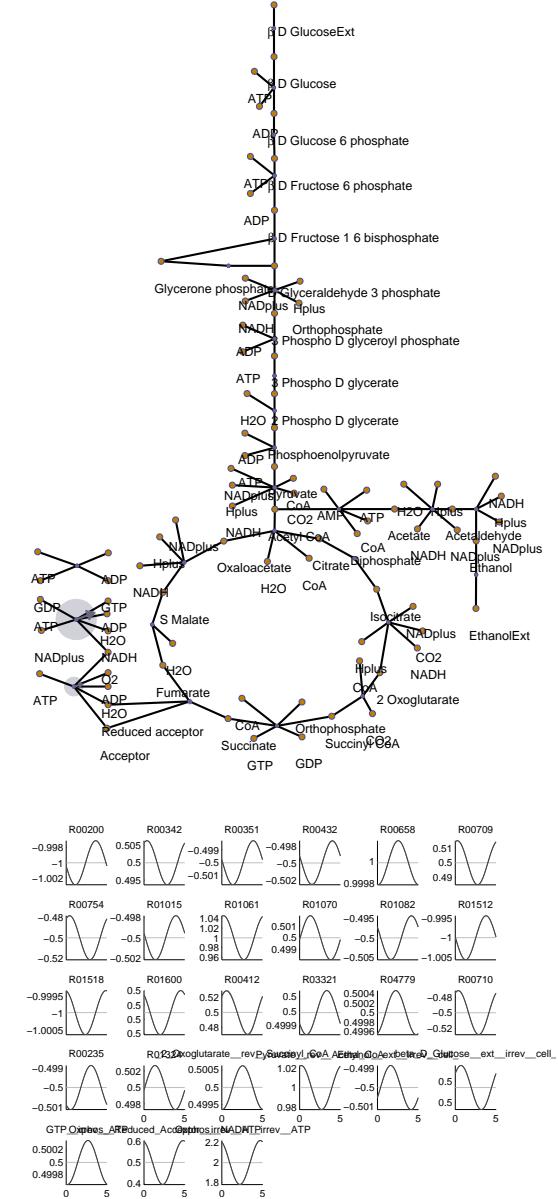
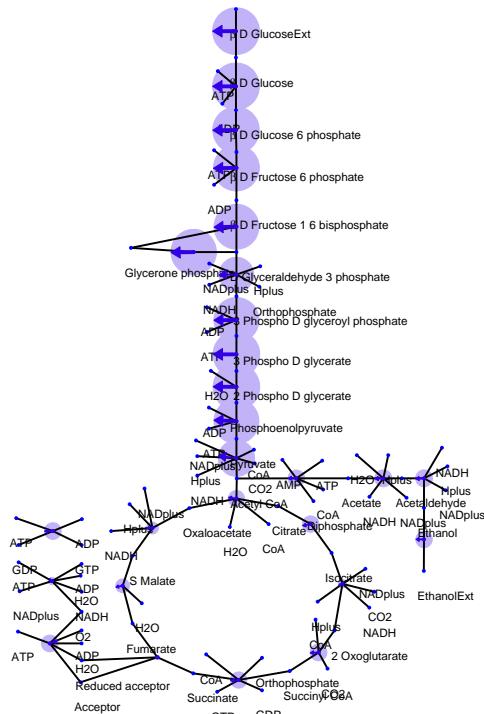
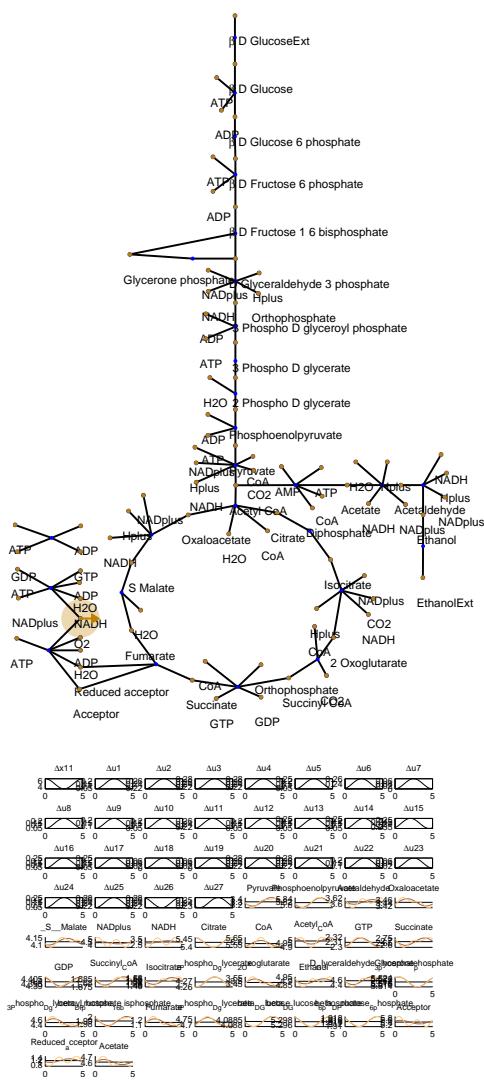


Figure 7: Responsive oscillations (local expansion; arrows: absolute changes) Perturbation frequency see first page.

### Adaptive oscillations (enzymes)



### Adaptive oscillations (metabolites)



### Adaptive oscillations (fluxes)

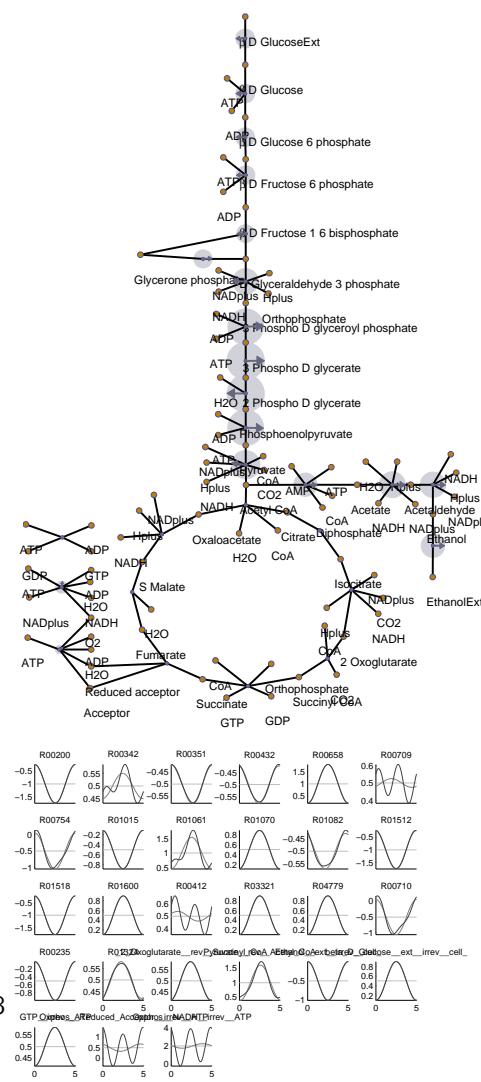
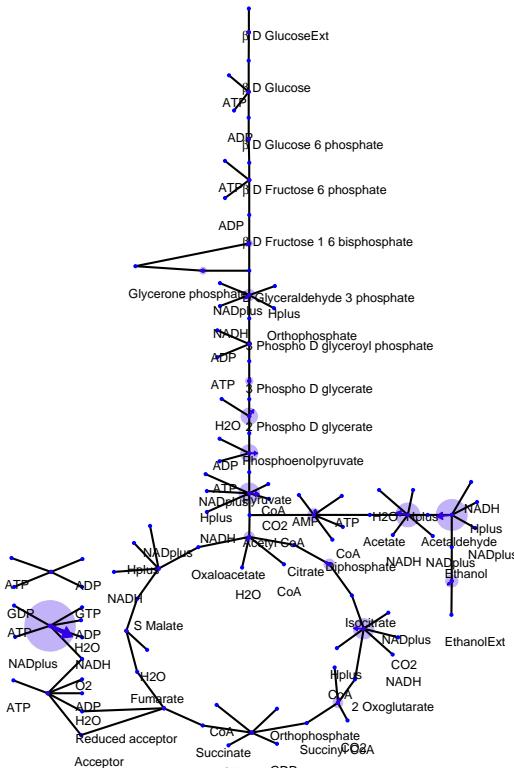


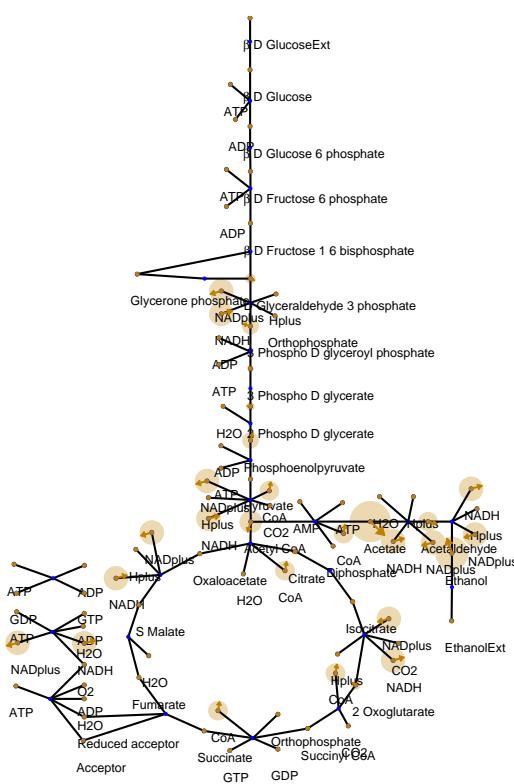
Figure 8: Adaption to forced oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

Figure 9: Tentative spontaneous oscillations. Perturbation frequency see first page.

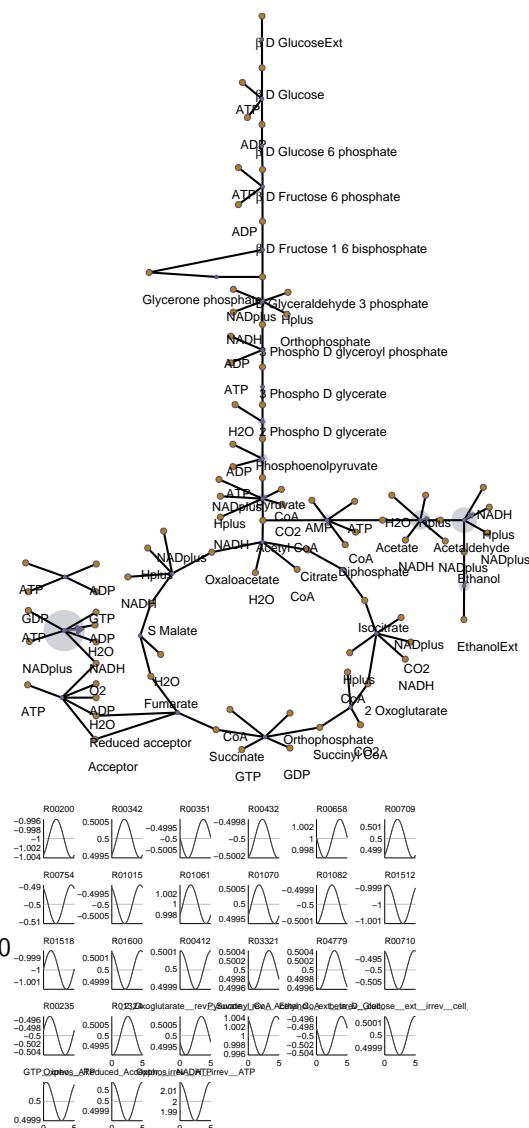
## Enzyme rhythm



## Spontaneous oscillations (concentrations)



## Spontaneous oscillations (fluxes)



	Δμ1	Δμ2	Δμ3	Δμ4	Δμ5	Δμ6	Δμ7	Δμ8
Δμ9	0	5	0	5	0	5	0	5
Δμ10	0	5	0	5	0	5	0	5
Δμ11	0	5	0	5	0	5	0	5
Δμ12	0	5	0	5	0	5	0	5
Δμ13	0	5	0	5	0	5	0	5
Δμ14	0	5	0	5	0	5	0	5
Δμ15	0	5	0	5	0	5	0	5
Δμ16	0	5	0	5	0	5	0	5
Δμ17	0	5	0	5	0	5	0	5
Δμ18	0	5	0	5	0	5	0	5
Δμ19	0	5	0	5	0	5	0	5
Δμ20	0	5	0	5	0	5	0	5
Δμ21	0	5	0	5	0	5	0	5
Δμ22	0	5	0	5	0	5	0	5
Δμ23	0	5	0	5	0	5	0	5
Δμ24	0	5	0	5	0	5	0	5
Pyruvate kinase / Pyruvate kinase_rev	0	5	0	5	0	5	0	5
NADP plus	4.495	-2.98	5.57	-4.885	4.995	-3.001	4.999	-3.001
NADH	-0.4995	0.4995	-0.5001	0.4999	-0.4995	0.4995	-0.4995	0.4995
Citrate	0	5	0	5	0	5	0	5
CoA	0	5	0	5	0	5	0	5
Acetyl CoA	4.495	-2.98	5.57	-4.885	4.995	-3.001	4.999	-3.001
GTP	4.495	-2.98	5.57	-4.885	4.995	-3.001	4.999	-3.001
Succinate	0	5	0	5	0	5	0	5
GDP	4.495	-2.98	5.57	-4.885	4.995	-3.001	4.999	-3.001
Succinyl-CoA	0	5	0	5	0	5	0	5
Orthophosphate	0	5	0	5	0	5	0	5
Isocitrate	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
β-hydroxyisocitrate	0	5	0	5	0	5	0	5
β-hydroxysuccinate	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
Glyceraldehyde 3 phosphate	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
β-hydroxybutyrate	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
H2O	0	5	0	5	0	5	0	5
Acetate	0	5	0	5	0	5	0	5

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## Adaptive

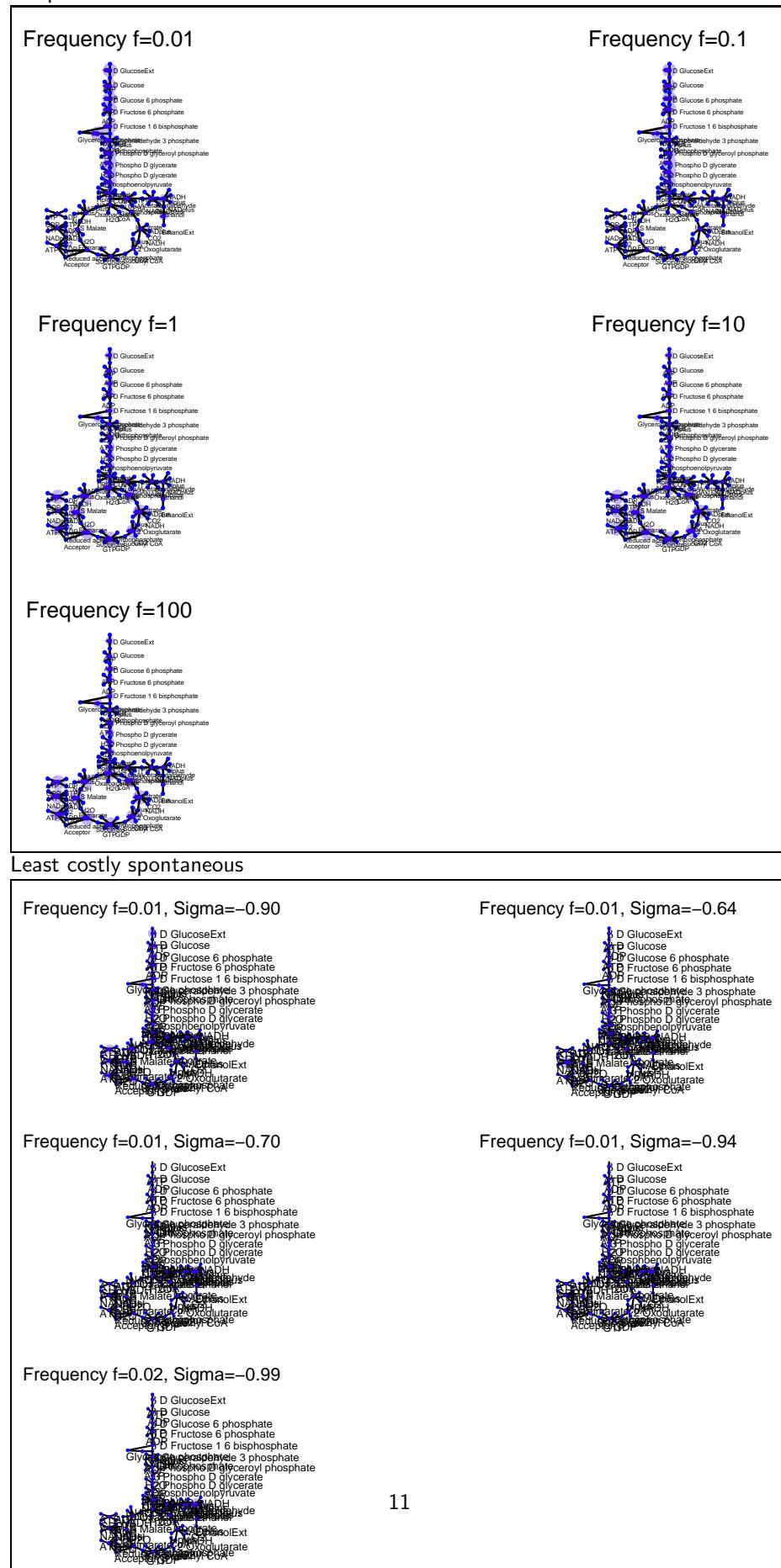


Figure 11: Potential oscillations at various frequencies (local expansion).