

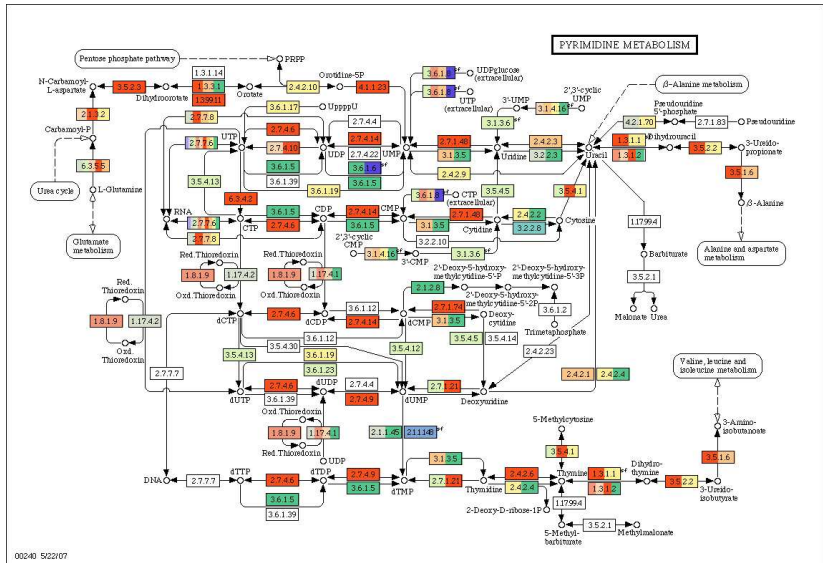
Robustness and Modularity in Metabolic Networks

Alexander Ullrich

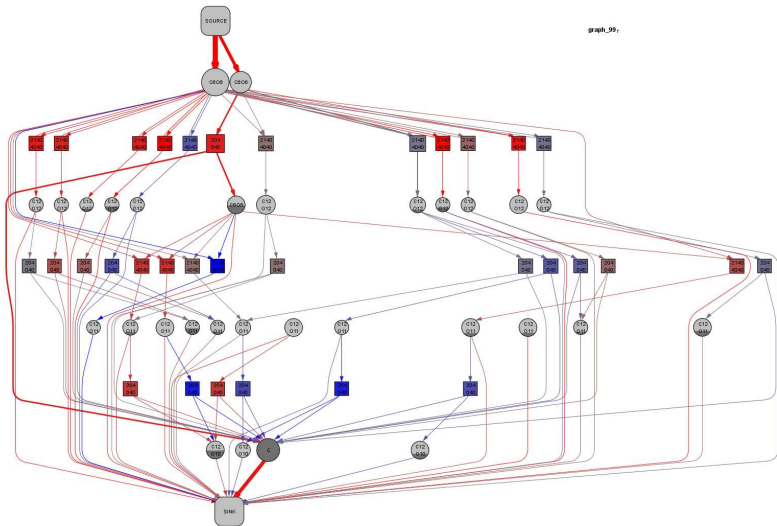
Bioinformatics
University of Leipzig

Bled, February 17

Metabolic Networks

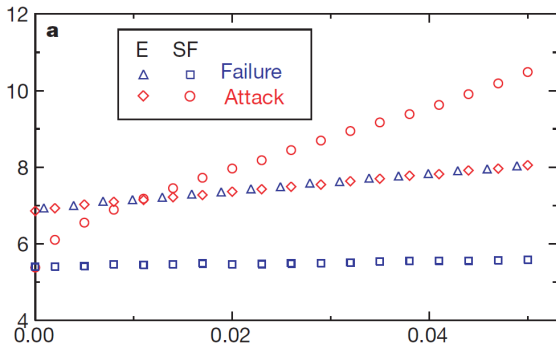


Metabolic Networks



Robustness

- Ability to function despite changes
- Genetic Changes: Mutations,...
- Epigenetic Changes: Fluctuations in Molecule concentrations
- Complex Systems are highly robust
- Scale-free Networks are particularly robust



Modularity

- Module: (structural) subsystem with distinct function
- Key organizing principle of biological networks
- High Clustering Coefficient suggests Modularity
- However, Origin and Preservation of Modularity not understood
- Changing Goals or Environments

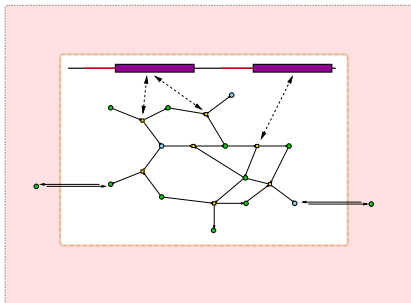
Motivation

- Biological systems develop desired properties
 - Robustness, Flexibility, Modularity, Evolvability, ...
 - Properties are connected
- Well studied, but their emergence is less well understood
 - Investigate the evolution of metabolic networks
 - Analyse network structure and metabolic functions
- Answers beyond analyzing real-world data

→ a multi-scale computational model of early metabolism

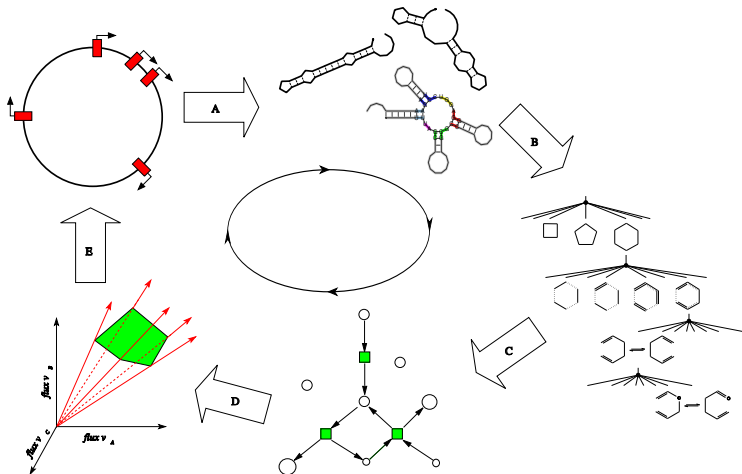
→ appropriate measures for network properties

Simulation

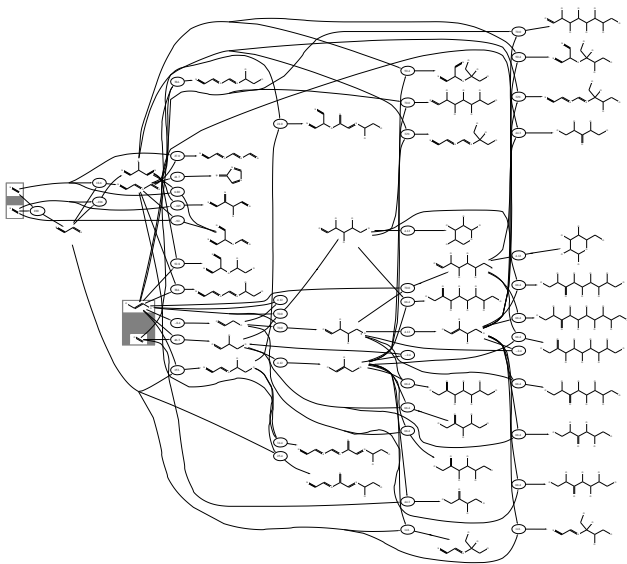


- Protocellular entity
- Bag of ribozymes
- Algebraic chemistry model
- Exchange of molecules with the environment

Simulation - Overview

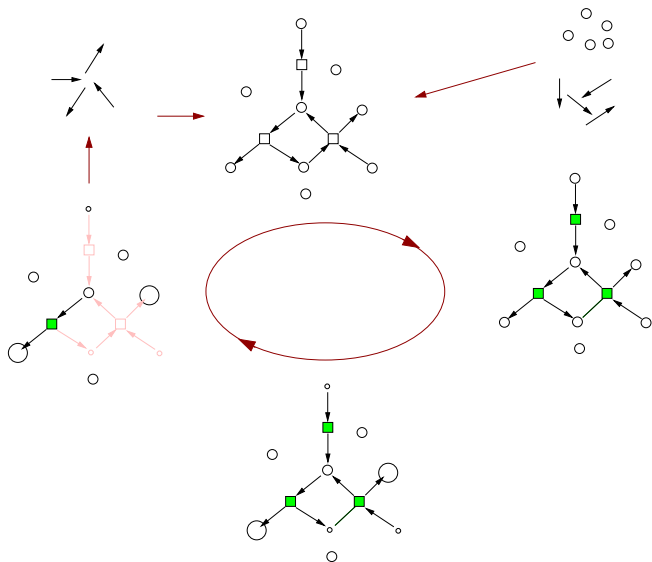


Simulation - Growth



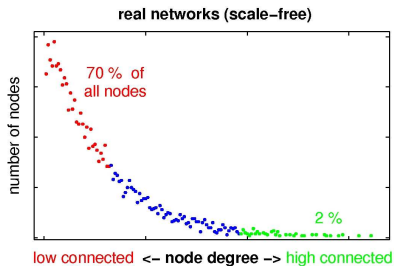
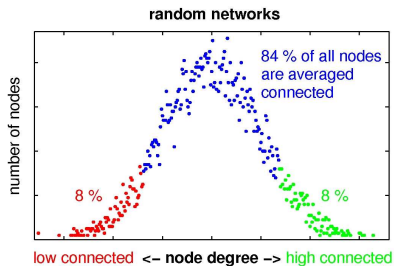
cyanide, formaldehyde glycol; aldolcondensation, tautomerization

Simulation - Stochastic Network Generator

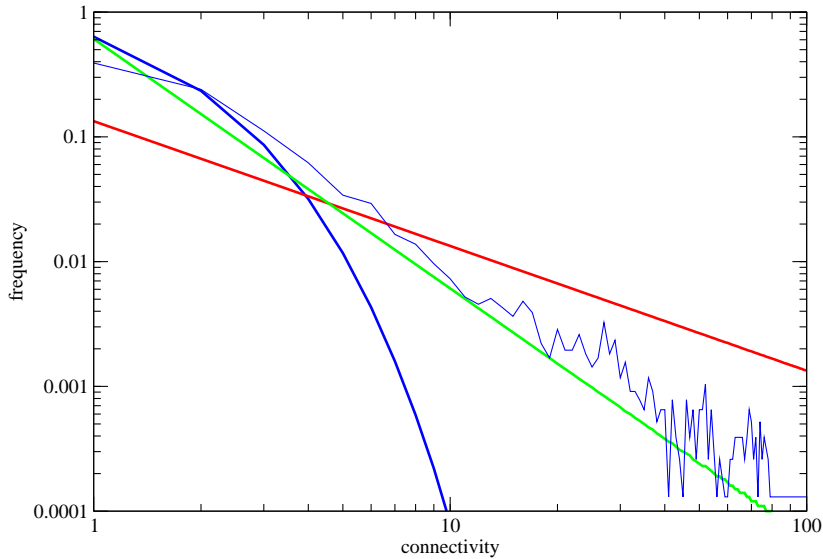


General network analysis

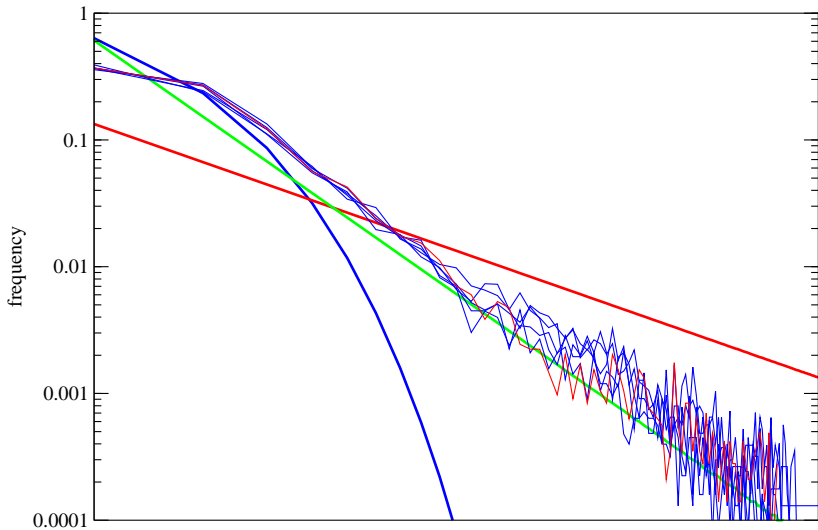
- Connectivity Distribution
 - small vs big
 - early vs evolved
- Clustering Coefficient, Centrality, Entropy, ...
 - simulated vs real world



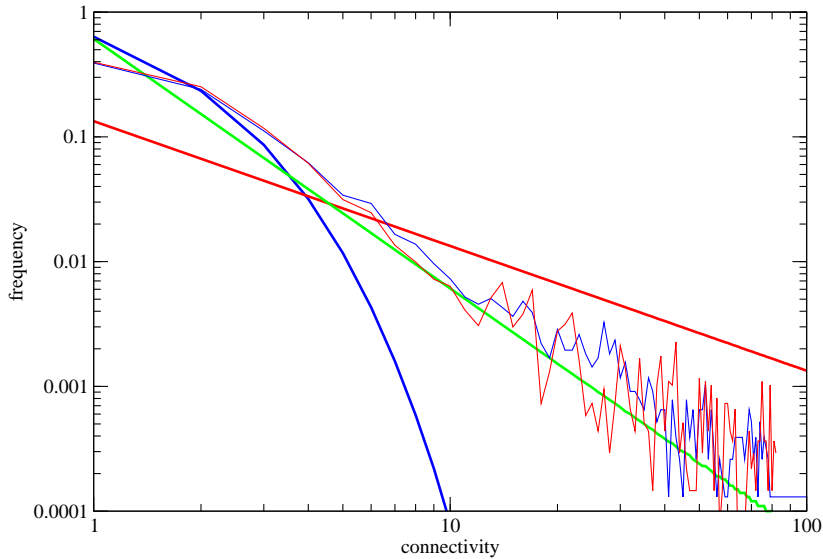
after 10 Generations



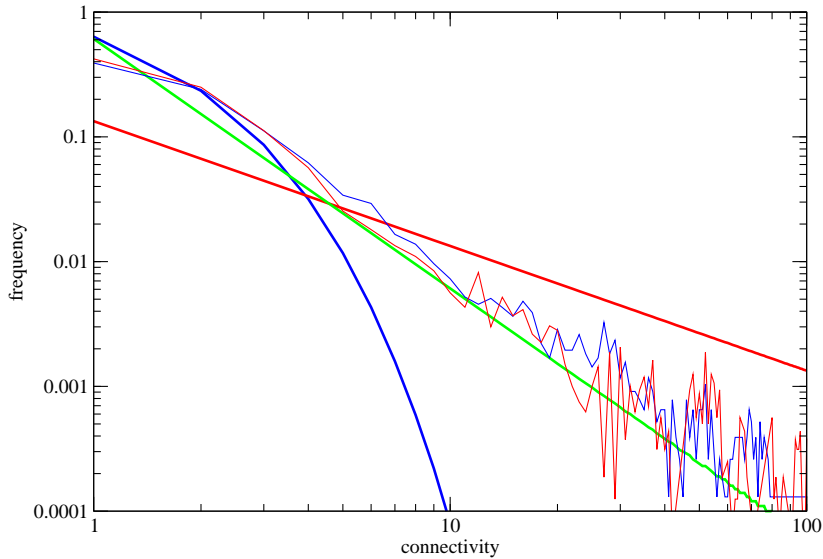
after 50 Generations



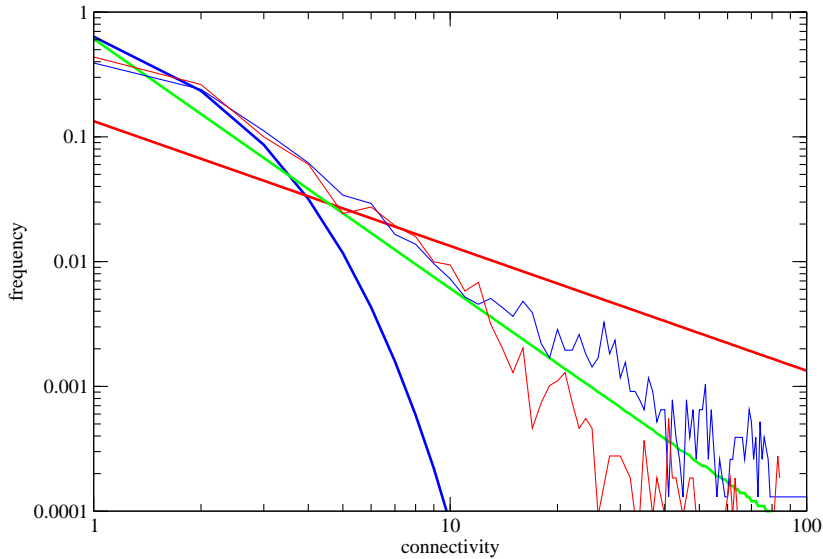
after 100 generations



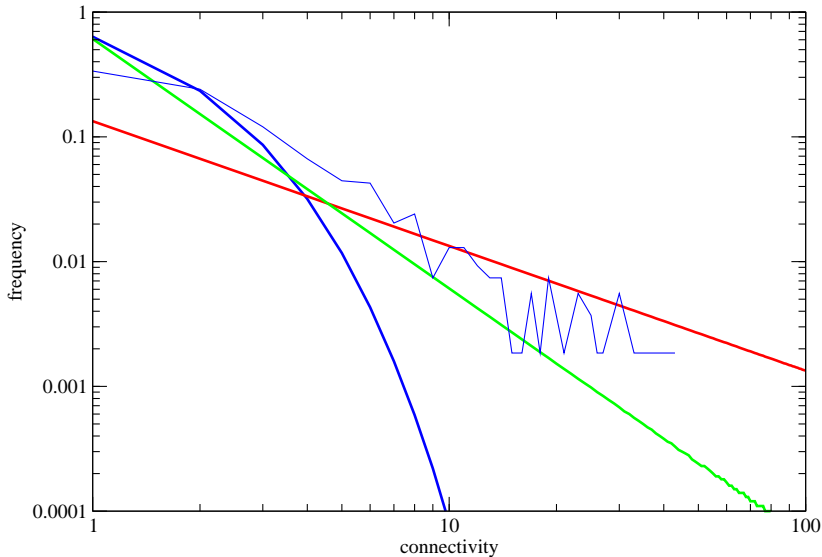
after 250 generations



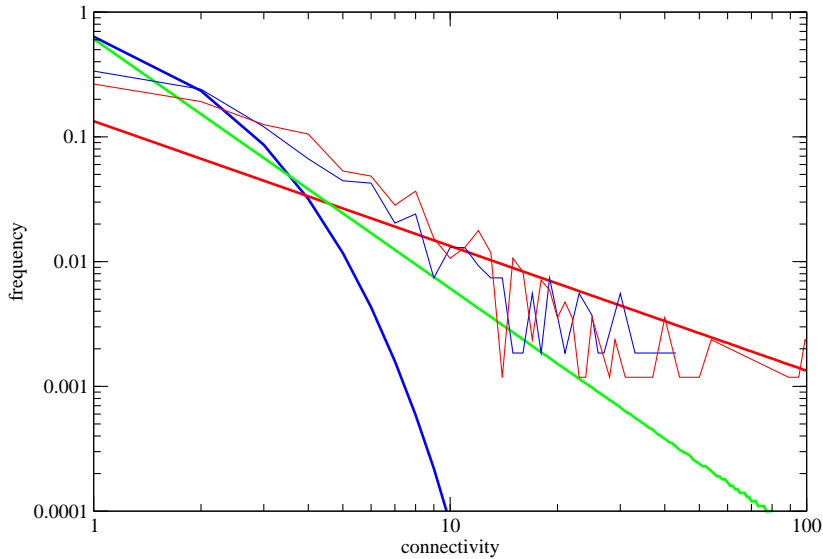
after 500 generations



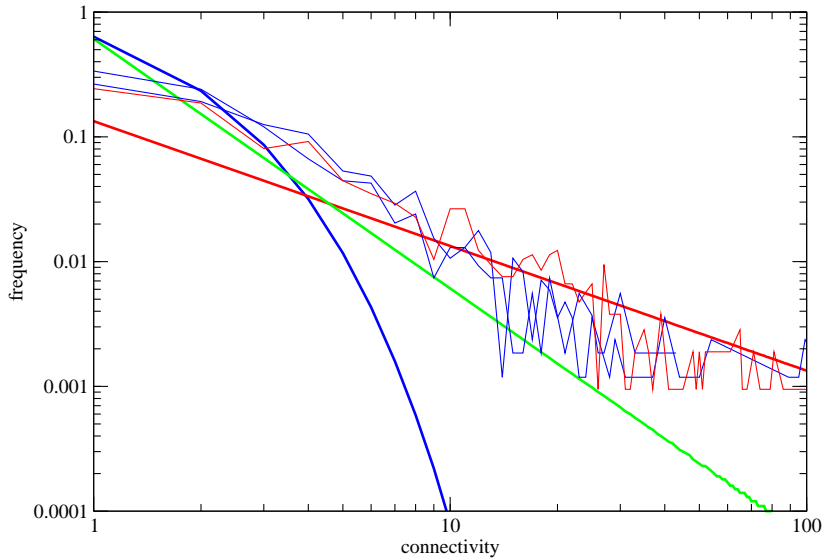
Changing Environment - after 100 generations



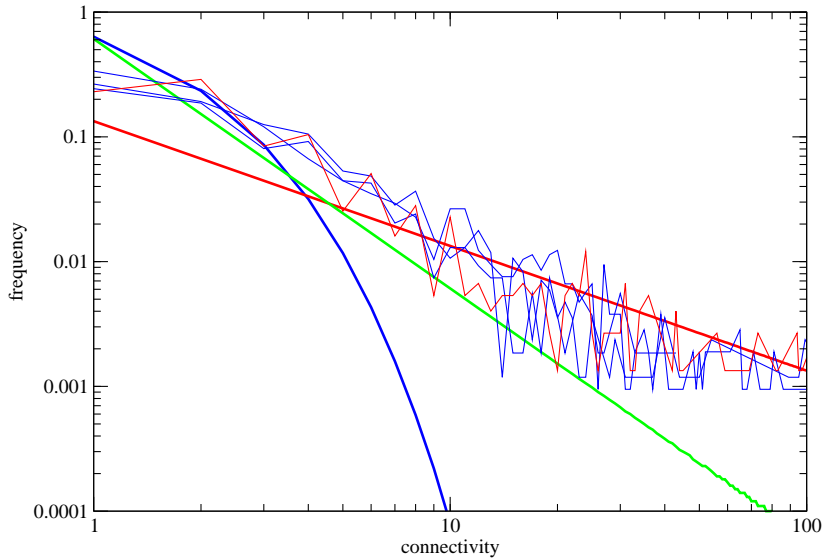
after 250 generations



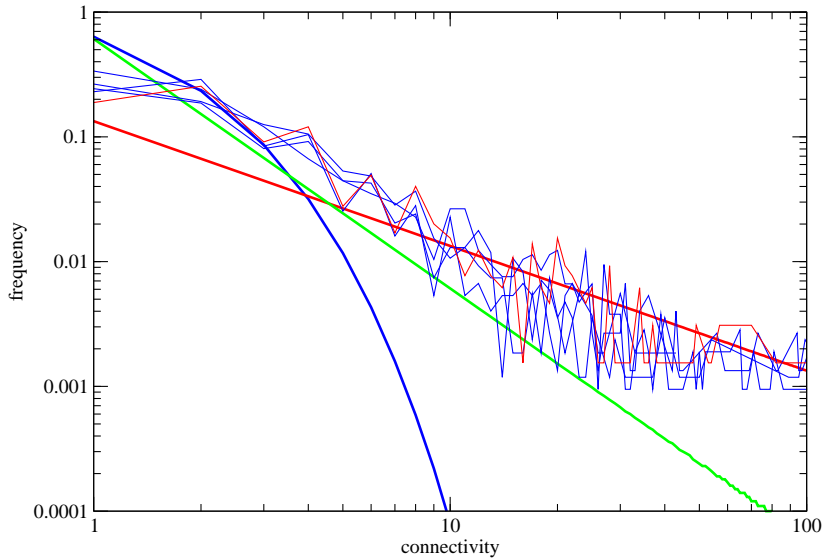
after 500 generations



after 750 generations



after 1000 generations



Metabolic network analysis

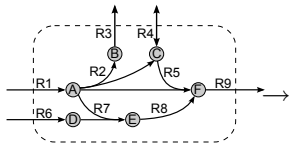
We have sets of edges forming meaningful complex entities



pathways

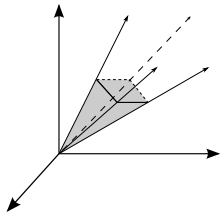
- number of pathways → flexibility
- change in case of single/multiple knockouts → robustness
- number of acceptable knockouts → robustness

Metabolic Pathway Analysis



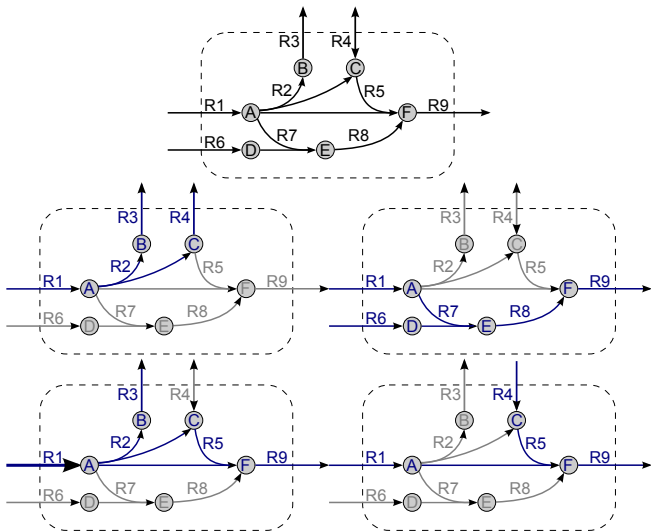
$$\begin{array}{c}
 A \\
 B \\
 C \\
 D \\
 E \\
 F
 \end{array}
 \begin{array}{c}
 R1 \\
 R2 \\
 R3 \\
 R4 \\
 R5 \\
 R6 \\
 R7 \\
 R8 \\
 R9
 \end{array}
 \begin{pmatrix}
 1 & -1 & 0 & 0 & -1 & 0 & -1 & 0 & 0 \\
 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\
 0 & 1 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\
 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\
 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 \\
 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & -1
 \end{pmatrix}$$

↓



$$\begin{array}{c}
 R1 \\
 R2 \\
 R3 \\
 R4 \\
 R5 \\
 R6 \\
 R7 \\
 R8 \\
 R9
 \end{array}
 \begin{array}{c}
 v_1 \\
 v_2 \\
 \dots \\
 v_{n-1} \\
 v_n
 \end{array}
 \begin{array}{c}
 S * v_i = 0 \\
 \begin{pmatrix}
 2 & -1 & \dots & 0 & 0 \\
 1 & -1 & \dots & -1 & -1 \\
 1 & -1 & \dots & -1 & -1 \\
 0 & 1 & \dots & 1 & 0 \\
 1 & 0 & \dots & 0 & -1 \\
 0 & 0 & \dots & 1 & 2 \\
 0 & 0 & \dots & 1 & 2 \\
 0 & 0 & \dots & 1 & 2 \\
 1 & 0 & \dots & 1 & 1
 \end{pmatrix}
 \end{array}$$

Metabolic Pathway Analysis



Knockout effects

single $R_1 = \frac{\sum_{i=1}^r z^i}{r * z}$

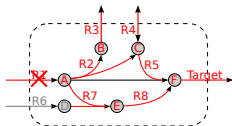
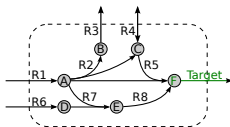
depletion $R_2 = \frac{\sum_{i=1}^n R_1^i}{n}$

multiple $R_3(k) = \frac{\sum_{i=1}^{s(k)} z^i}{s(k) * z}$

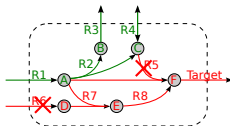
overall $R_3(\leq K) = \sum_{k=1}^K R_3(k) p_k$

Example system		Number of reactions	Number of elementary modes	$R_1(1)$	$R_1(2)$	$R_1(3)$	$R_1(\leq 3)$
1		4	2	1/2 = 0.5	1/6 ≈ 0.167	0	0.414
2		4	2	1/2 = 0.5	1/4 = 0.25	1/8 = 0.125	0.436
3		4	2	3/8 = 0.375	1/12 ≈ 0.083	0	0.302
4		4	2	1/4 = 0.25	0	0	0.189
5		8	2	7/16 ≈ 0.438	3/8 = 0.375	5/16 ≈ 0.313	0.418
6		8	2	1/2 = 0.5	3/14 ≈ 0.214	1/14 ≈ 0.071	0.416
7		5	4	13/20 = 0.65	3/8 = 0.375	7/40 = 0.175	0.573
8		5	3	2/3 ≈ 0.667	2/5 = 0.4	1/5 = 0.2	0.592

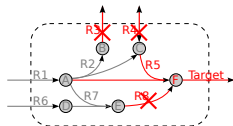
Minimal Knockout sets



{R1}

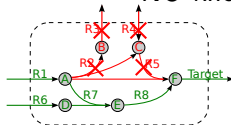


{R5, R6}

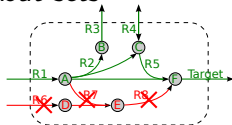


{R3, R4, R8}

NO knockout sets



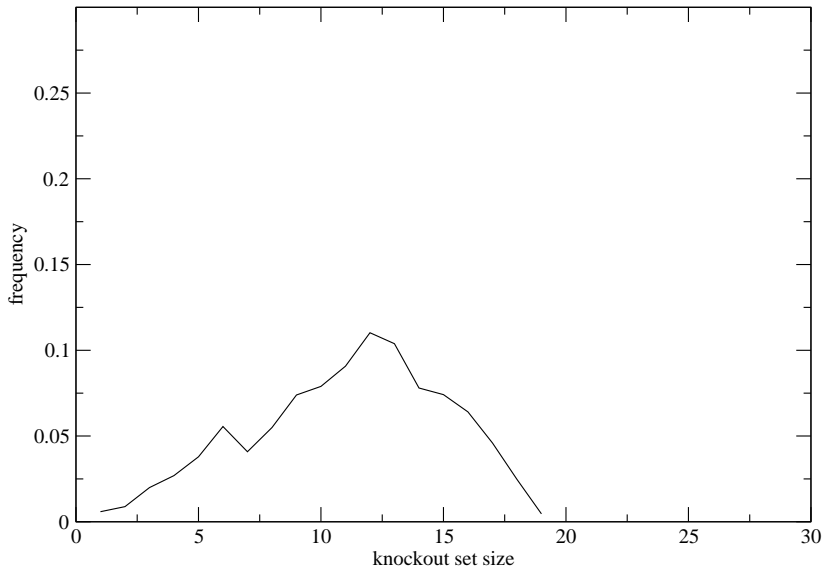
{R2, R3, R4, R5}



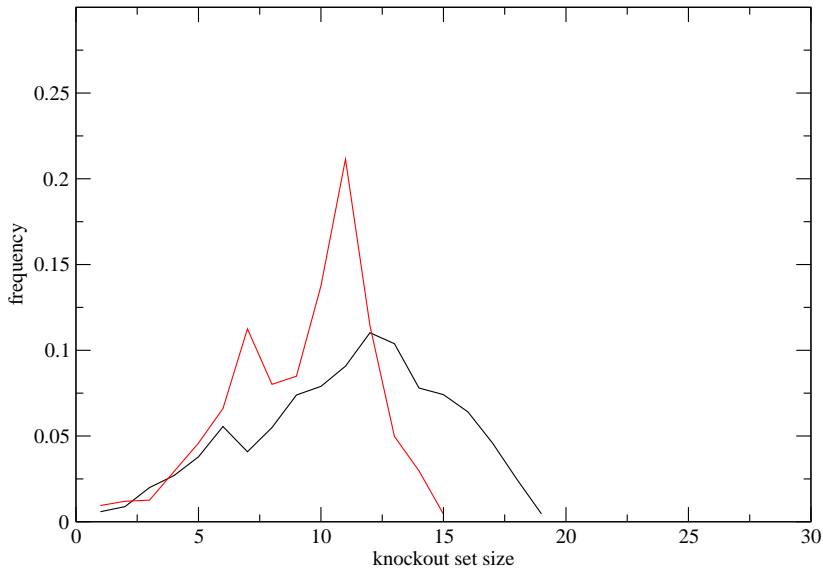
{R6, R7, R8}

Knockout set size distribution \rightarrow Robustness (bigger is better)

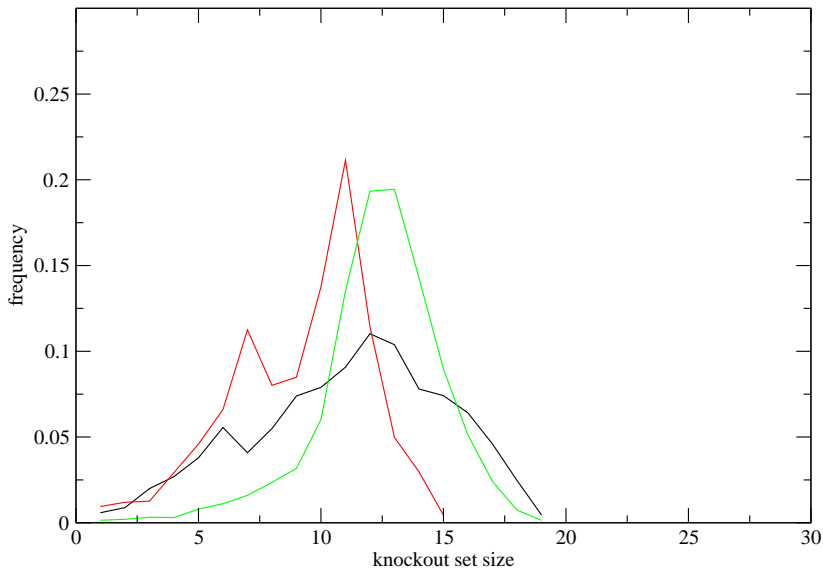
after 10 generations



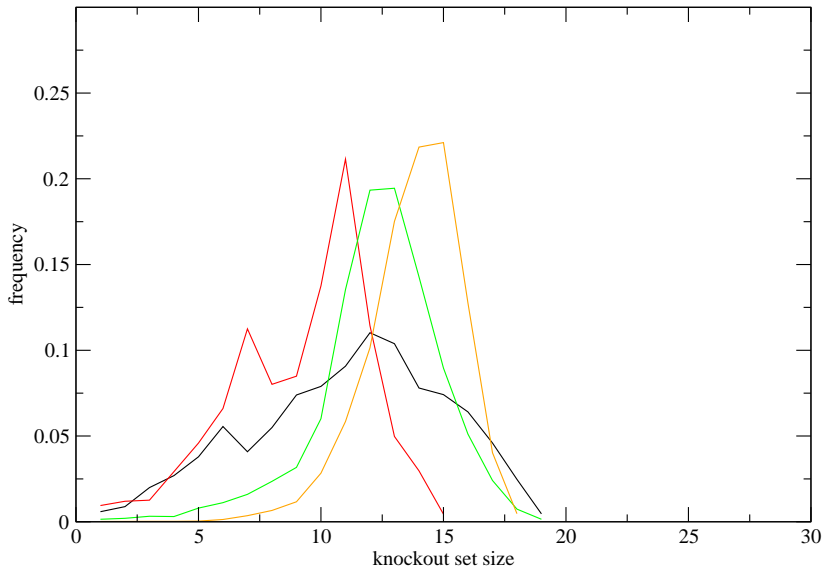
after 20 generations



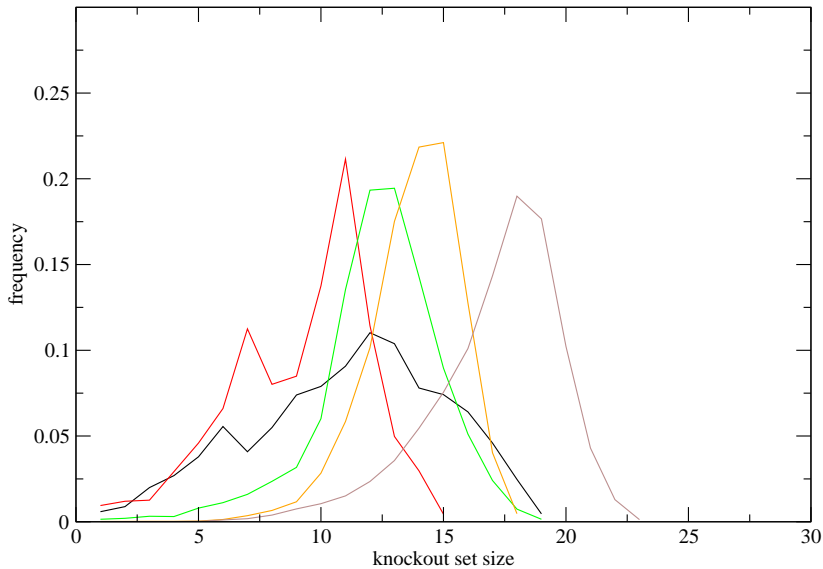
after 50 generations



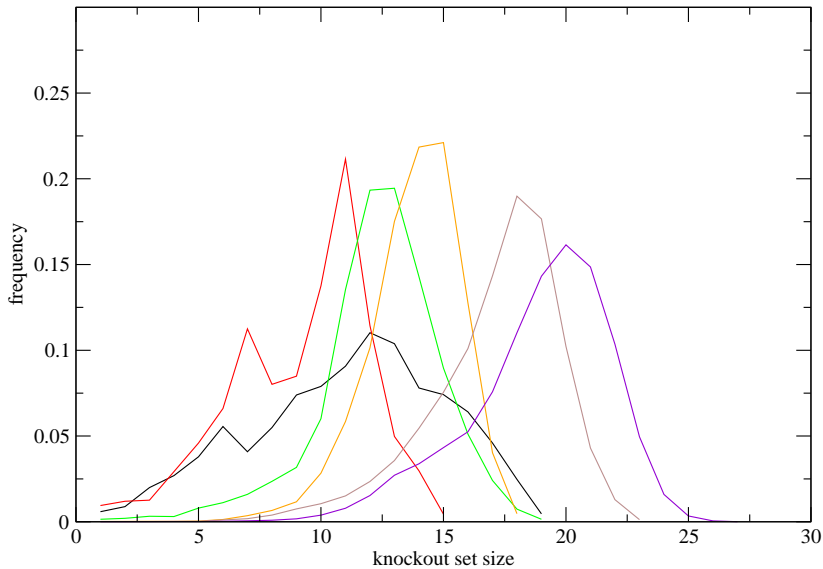
after 100 generations



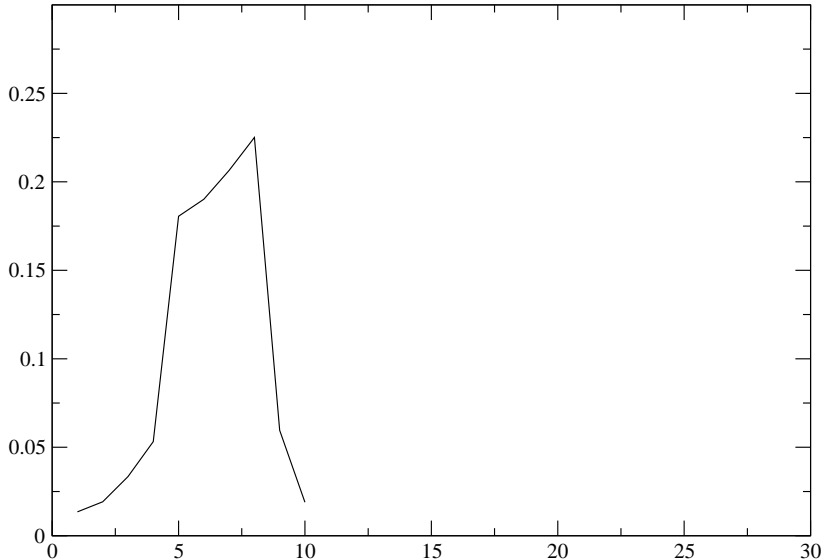
after 250 generations



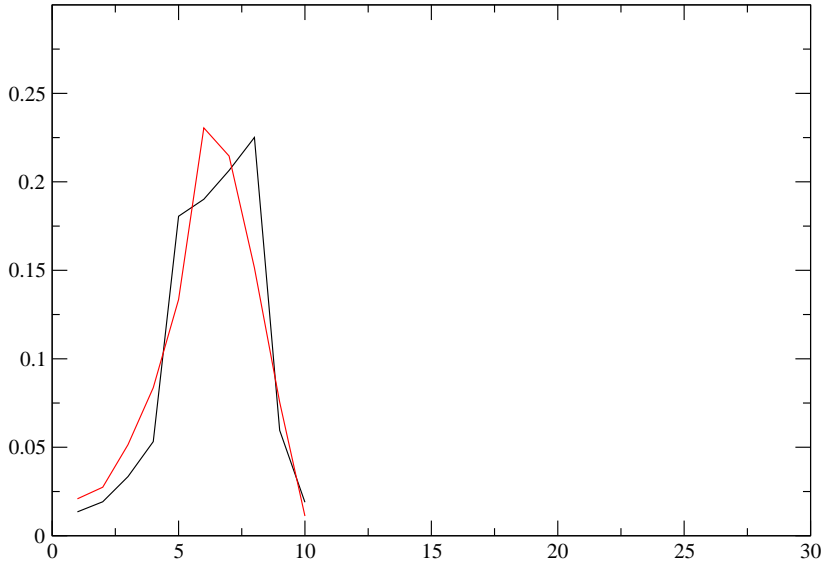
after 500 generations



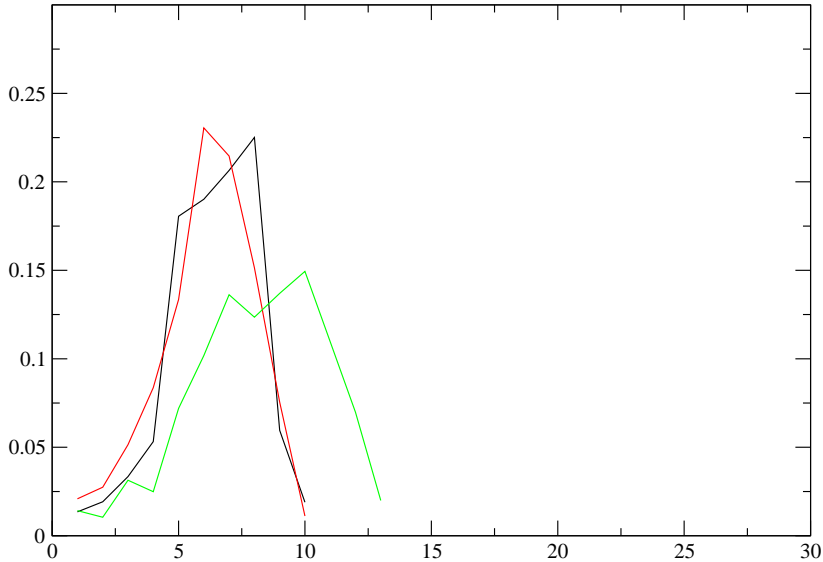
Changing Environment - after 10 generations



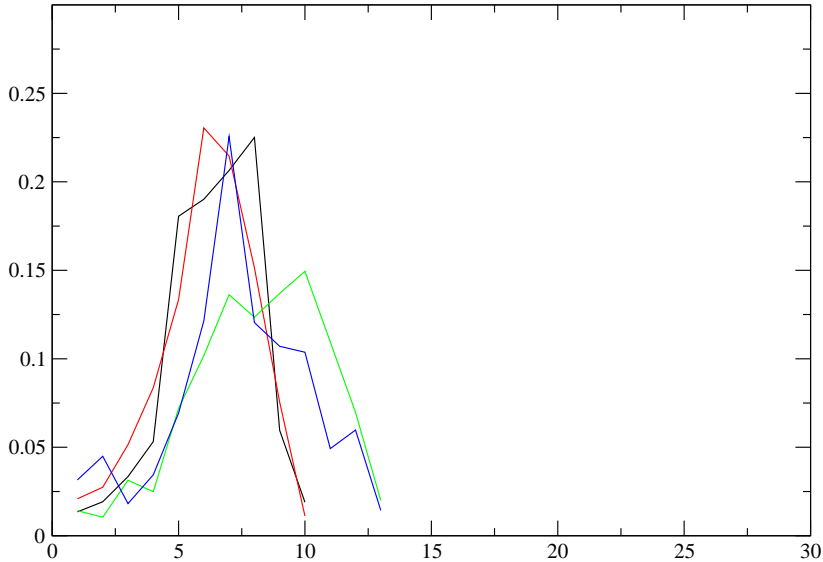
after 50 generations



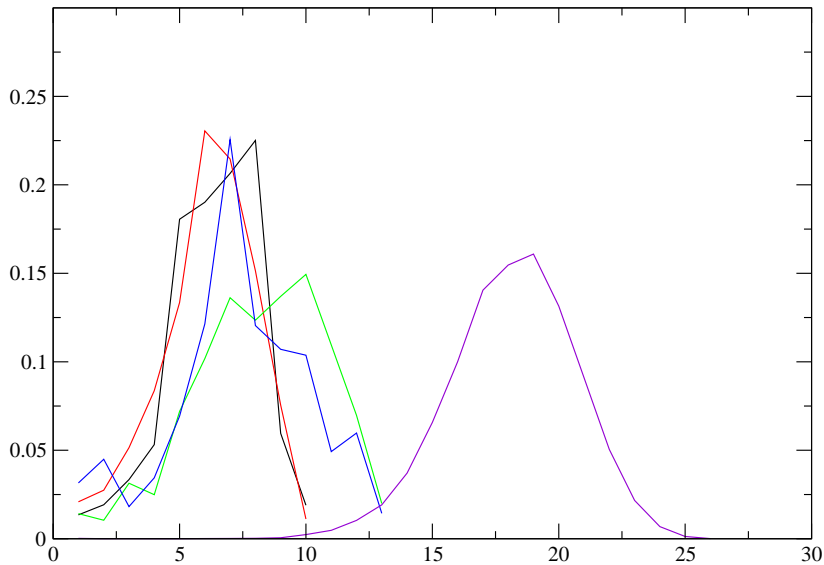
after 250 generations



after 500 generations



after 1000 generations



Chemical Organizations

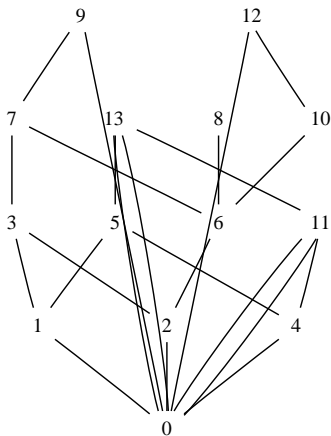
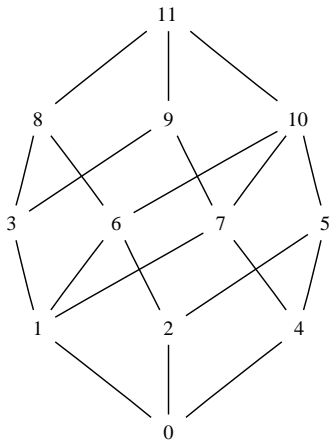
Self-maintaining and closed sets of molecules and reactions



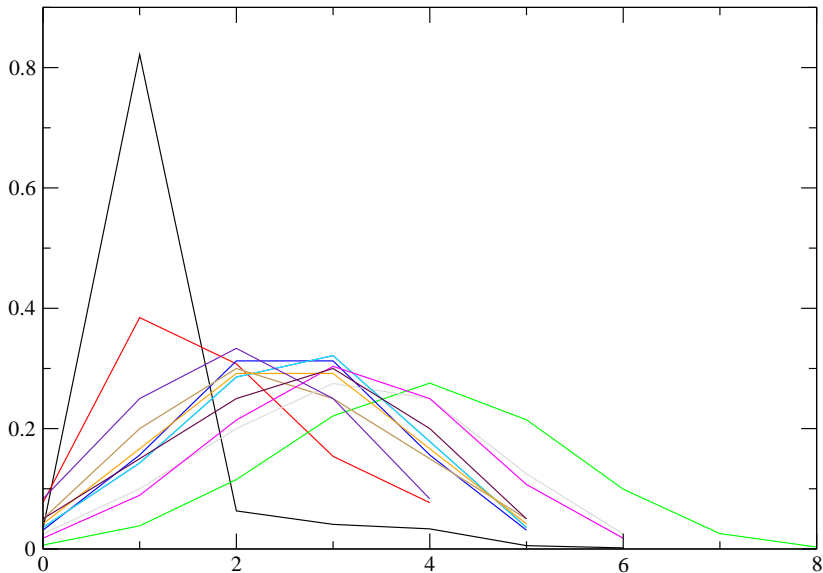
chemical organizations

- Hierarchies of organizations
- Shape of Hierarchies → robustness
- Size distribution of organizations → robustness, modularity

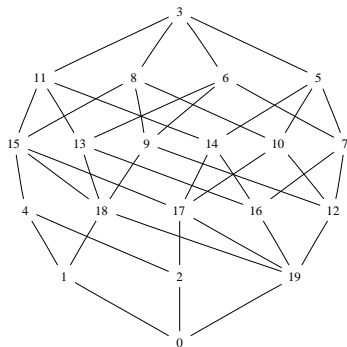
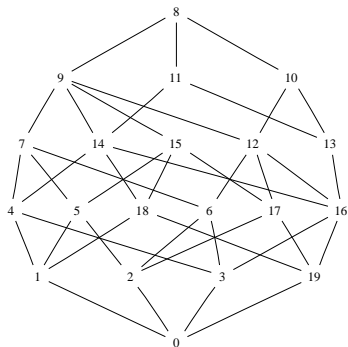
Chemical Organizations



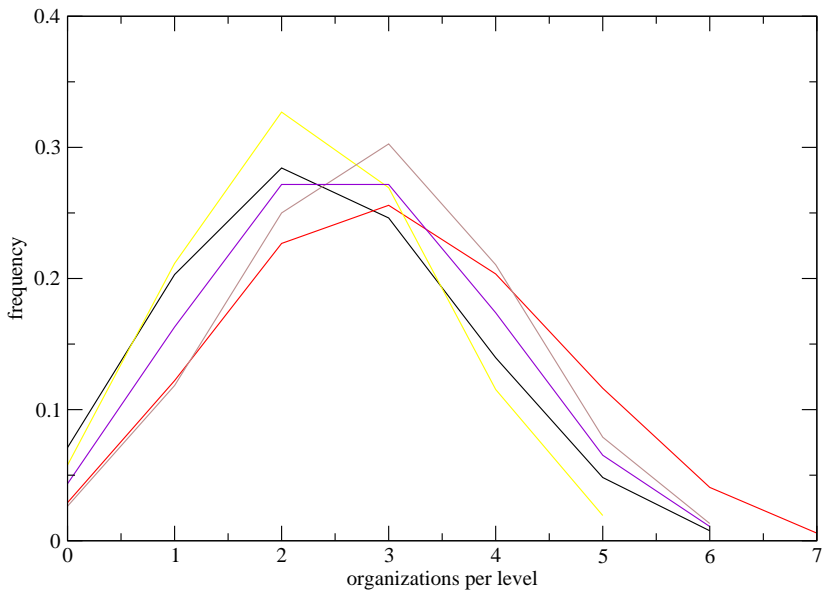
Level Size Distribution - after 500 generations



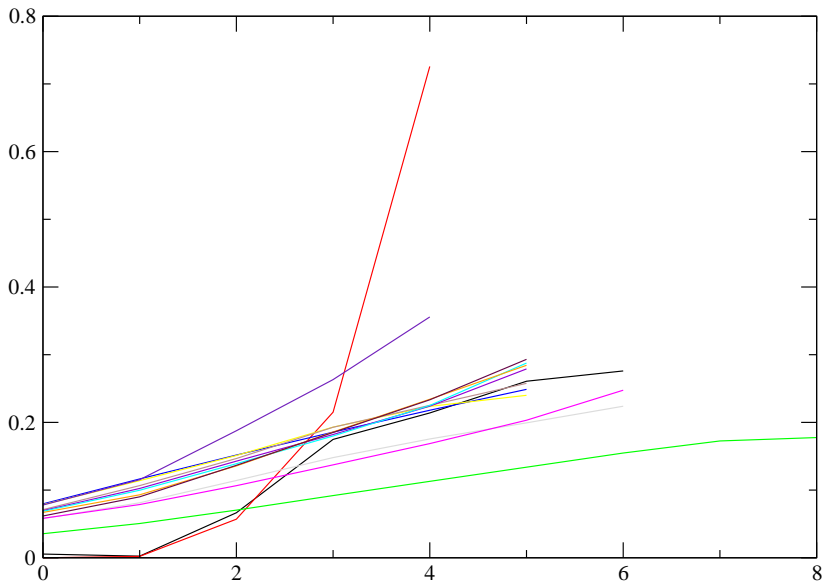
Chemical Organizations



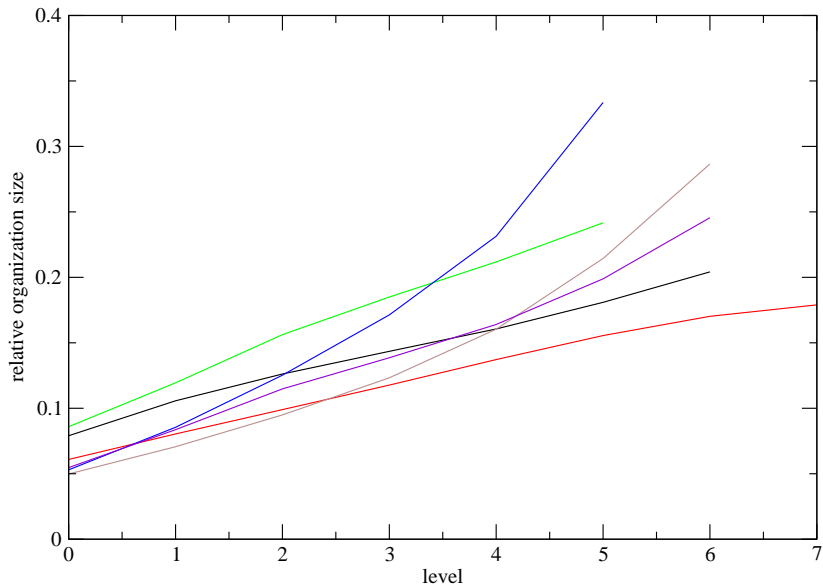
Changing Environment - after 500 generations



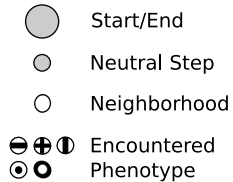
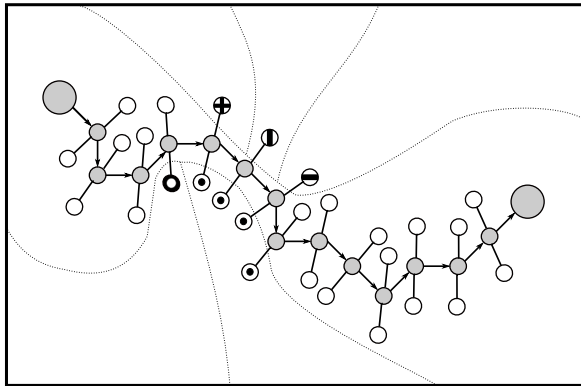
Organization Size Distribution - after 500 generations



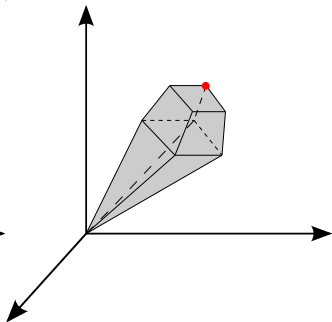
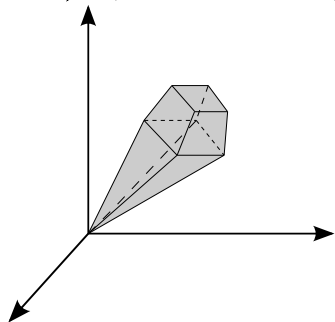
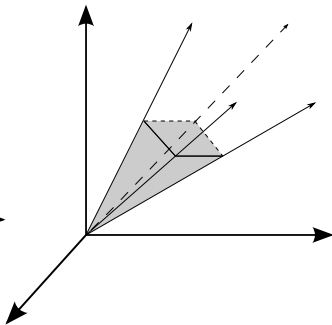
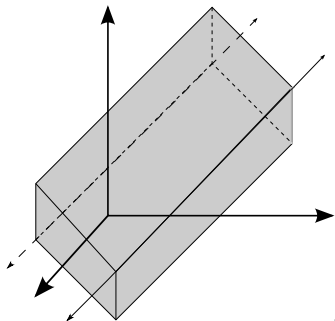
Changing Environment - after 1000 generations



Work in Progress

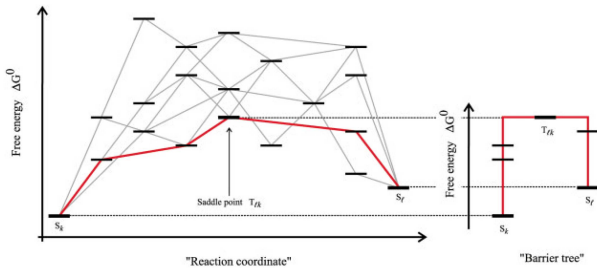


FBA



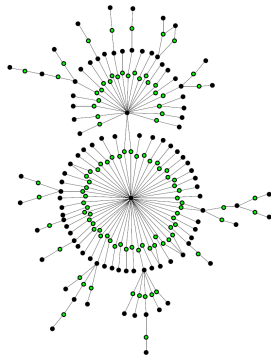
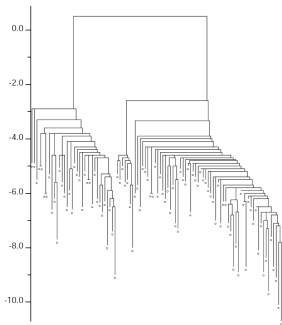
Flux barrier analysis

- linear optimization: EMs modeled as system of linear equations
- constraints: limits on reactions, exclusion of combinations of EMs
- barrier tree



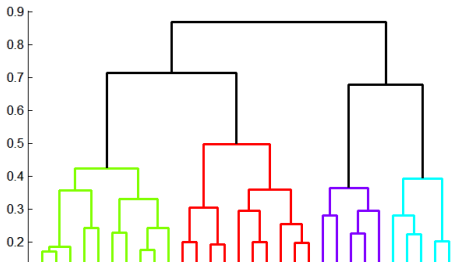
Reaction barrier analysis

- linear optimization: stoichiometric matrix
- constraints: limits on reactions, exclusion of combinations of reactions
- barrier tree



Flux similarity

- Compute pairwise similarity of elementary modes
- similarity between metabolites (in+out / all) through topological indices
- similarity between enzymes/reactions by comparing transition state structure



Conclusion

- Summary
 - Structural and Functional measures for Robustness and Modularity
 - Follow the Law (Connectivity Distribution)
 - Size Matters (Knockout set Size)
 - Shape too (Chemical organization Hierarchy)
- Outlook
 - Investigate single networks (flux barriers, flux similarity)
 - Different scenarios (Horizontal Gene Transfer)
 - Structural modularity (Clustering Coefficient)

Acknowledgements

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Dennis Goerlich