

# Analysis of Metabolic Networks

## Structure, Properties, Visualization

Alexander Ullrich

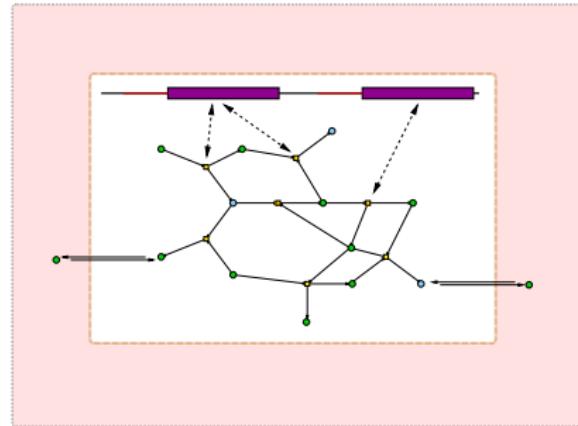
Chair for Bioinformatics  
University of Leipzig

TBI-Winterseminar, Bled, February 14-21

# Outline

- Simulation
- Motivation
- Visualization
- General network analysis
- Metabolic network analysis
- Outlook

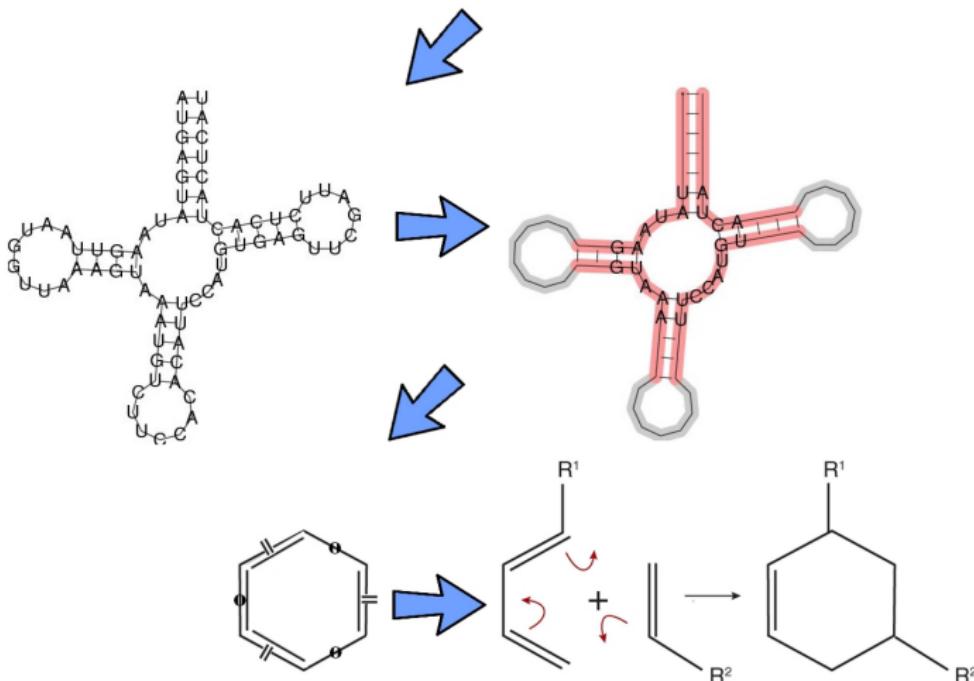
# Simulation



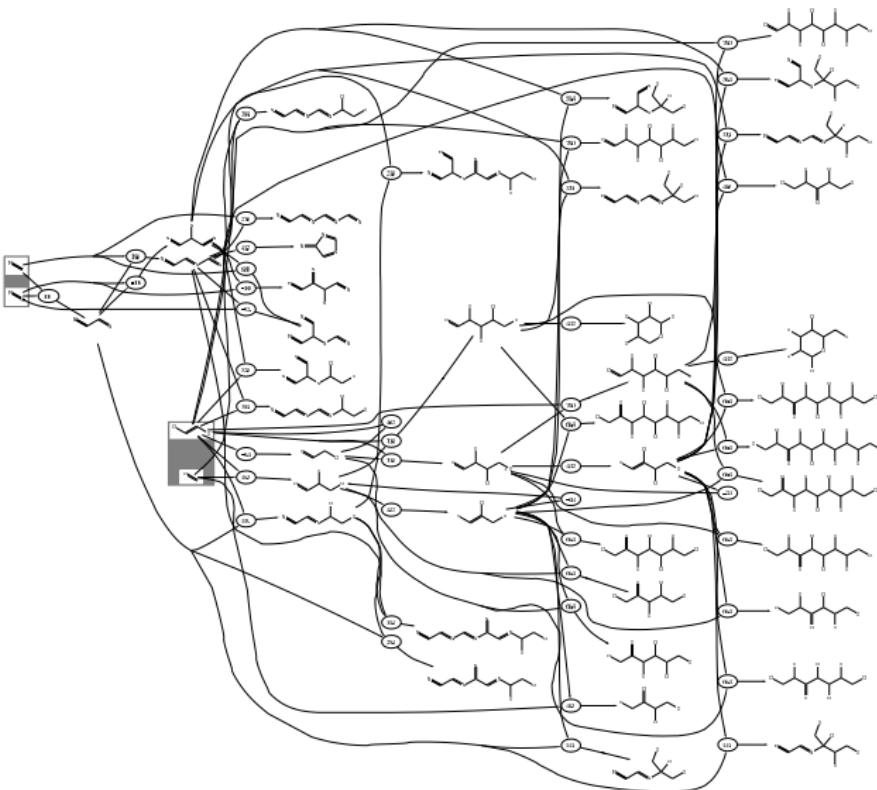
- Bag of ribozymes.
- Algebraic chemistry model.
- Exchange of molecules with the environment.

# Simulation

AUGAGUAUAAGUUAAUGGUAAAAGUAAAUGUCUUCACACAUUCGAUGUGAGUUCGAAUUCAGUACUAU

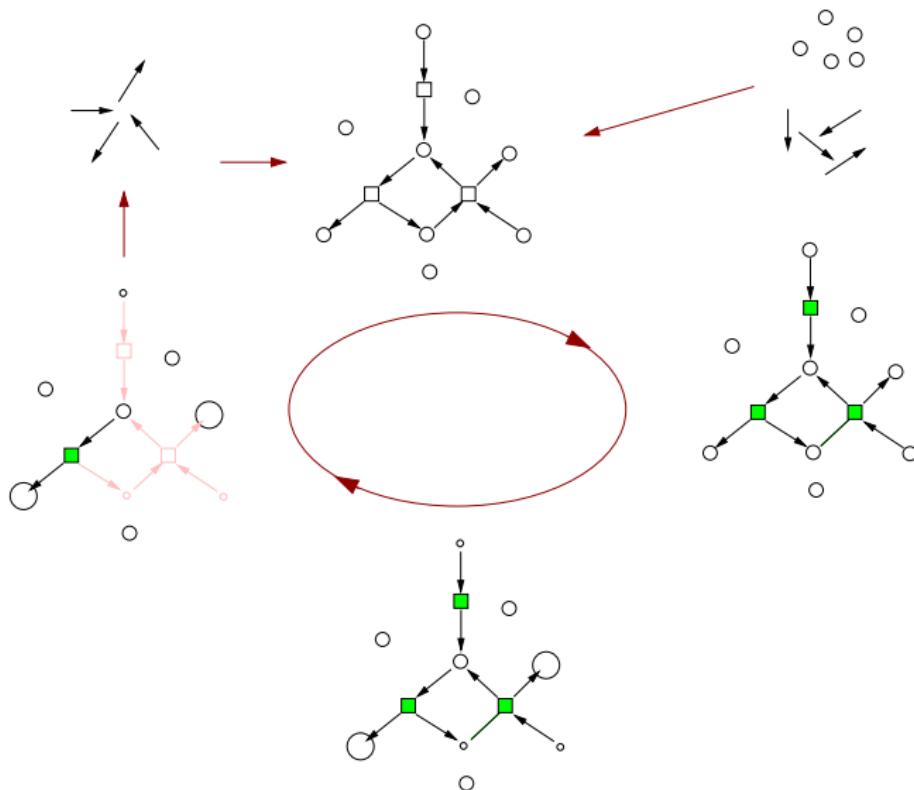


# Simulation



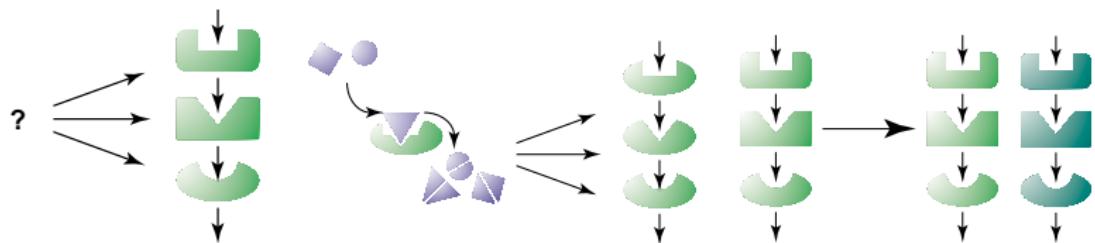
cyanide, formaldehyde glycol; aldolcondensation, tautomerization

# Simulation



# Motivation

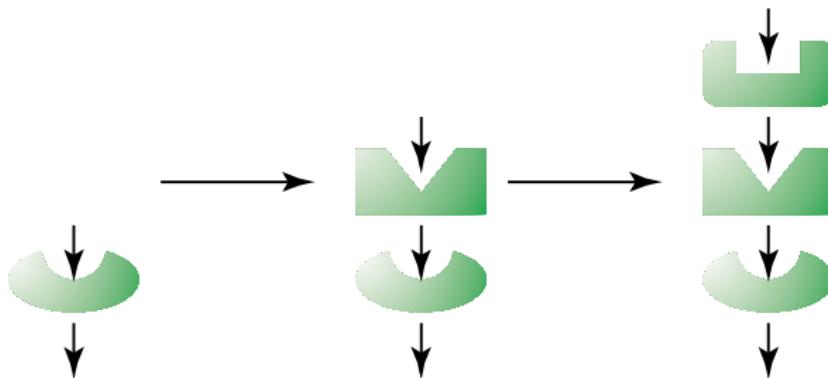
- Study the early development of metabolism
  - Evolution of pathways (different scenarios)



- Analysis of the metabolic networks
  - network structure
  - network properties

# Pathway Evolution

## Retrograde Evolution

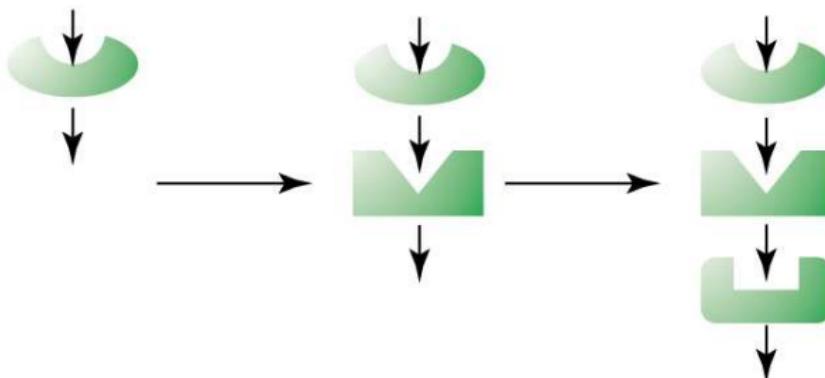


End-product can be derived from more and more distant metabolites

Example: glycolytic pathway, histidine biosynthesis

# Pathway Evolution

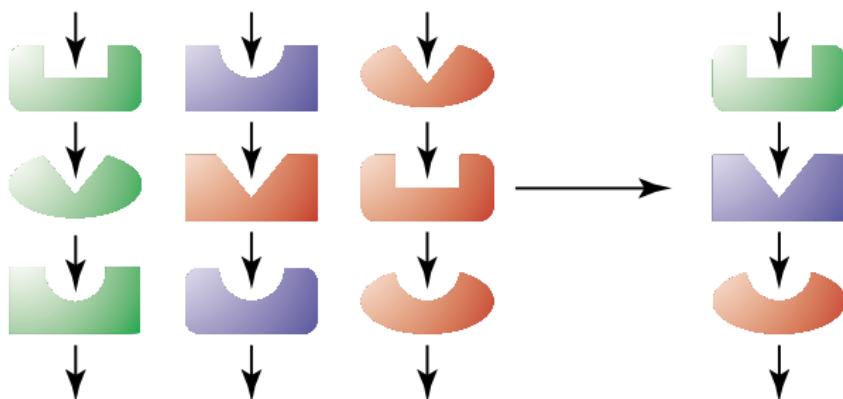
## Forward Evolution



more efficient extraction through deeper break-down of metabolites  
Example: isoprene lipid pathway

# Pathway Evolution

## Patchwork Evolution



Enzyme Recruitment from other Pathways

# Pathway Evolution

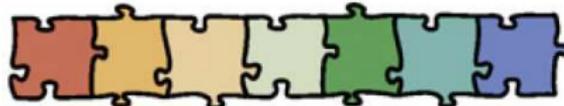
Comparison

red = older, blue = younger

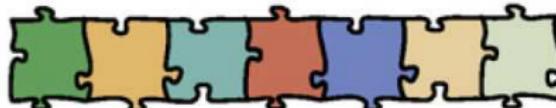
Retrograde Evolution



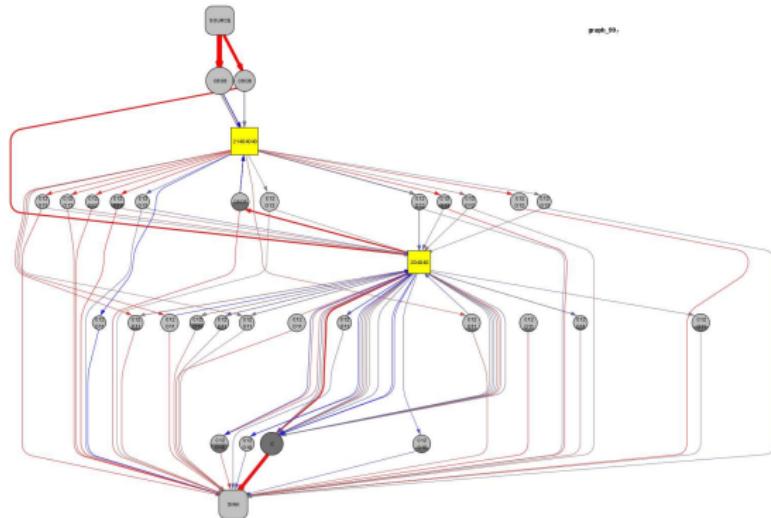
Forward Evolution



Patchwork Evolution



# Visualization



- bidirectional, bipartite graph
- nodes: metabolites, enzymes/reactions
- edges: participation in the same reaction
- dot layout: flow of mass downwards in the graph (if possible)

## Visualization

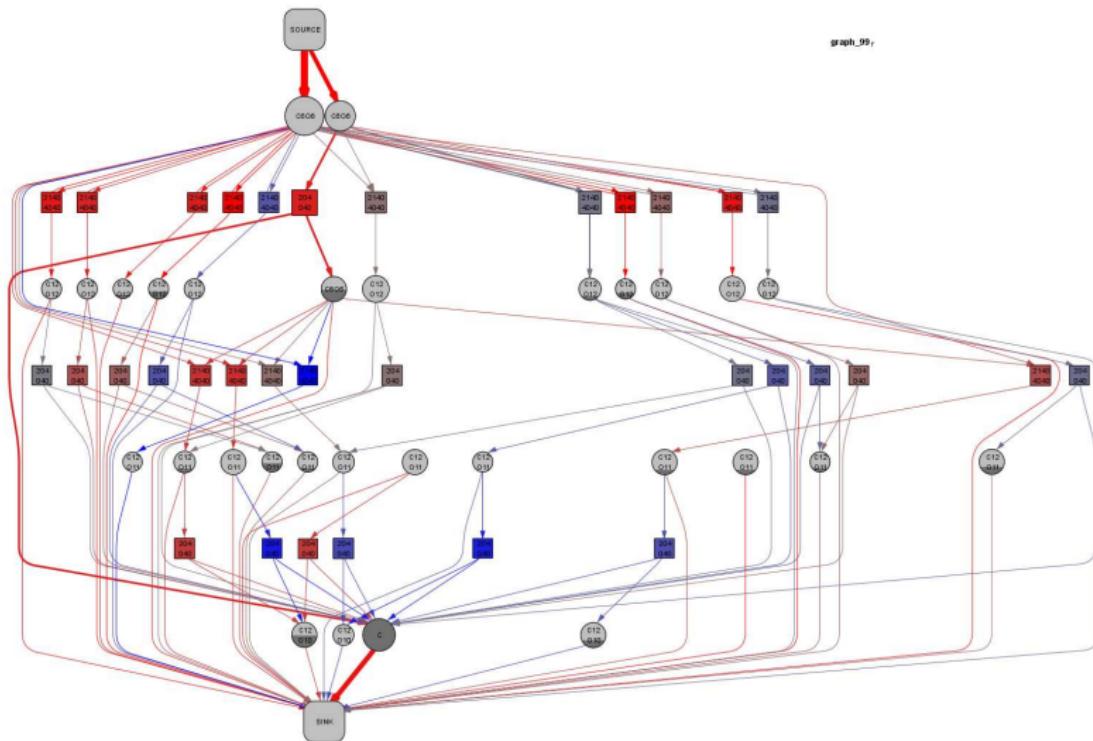
## Retrograde Evolution



## Forward Evolution

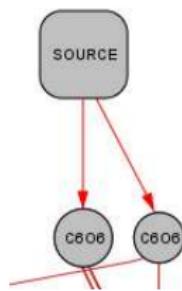


## Patchwork Evolution

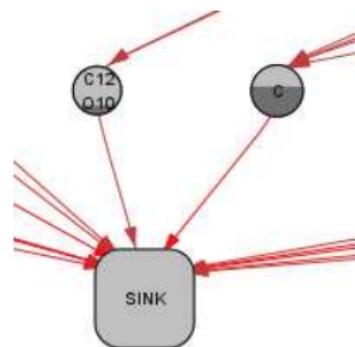


# Visualization

Flow

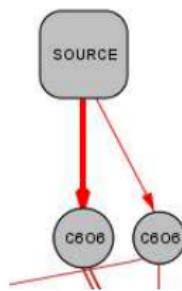


Concentration

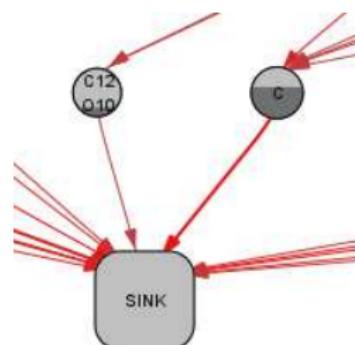


# Visualization

Flow

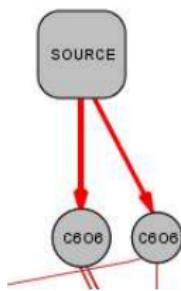


Concentration

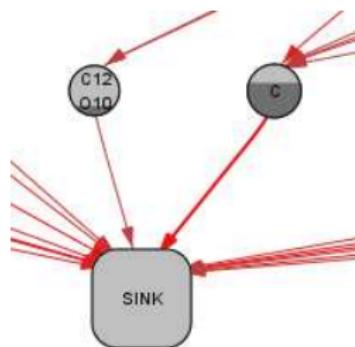


# Visualization

Flow

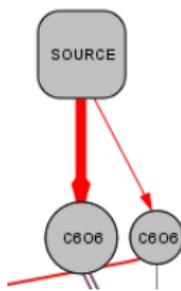


Concentration

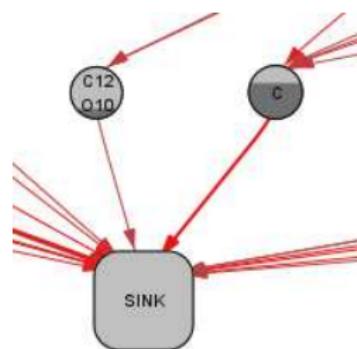


# Visualization

Flow

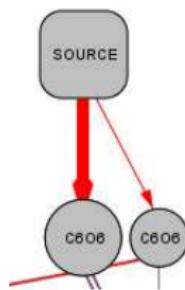


Concentration

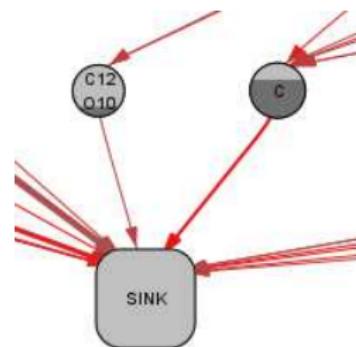


# Visualization

Flow

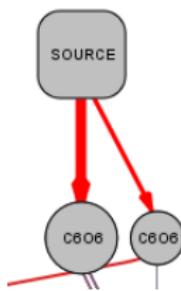


Concentration

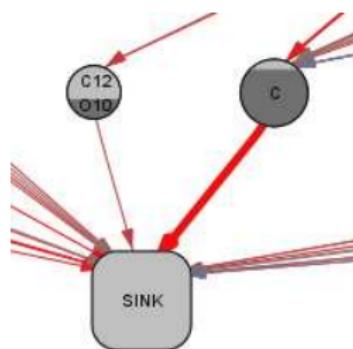


# Visualization

Flow



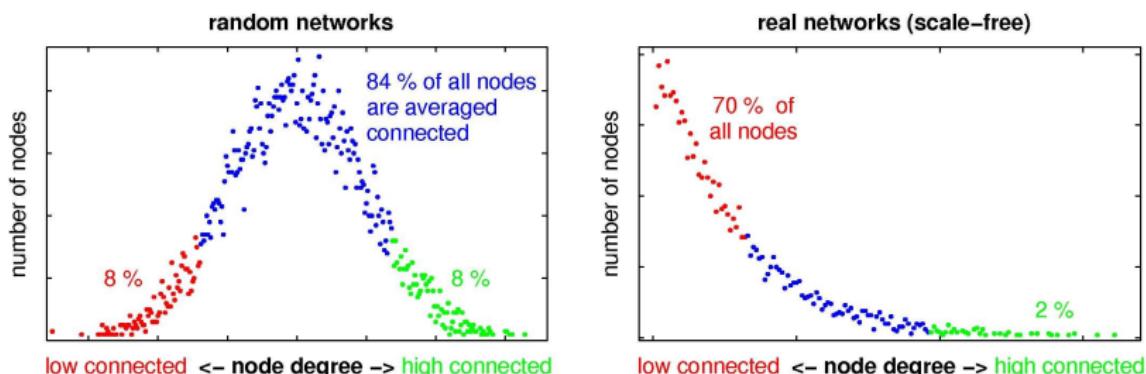
Concentration



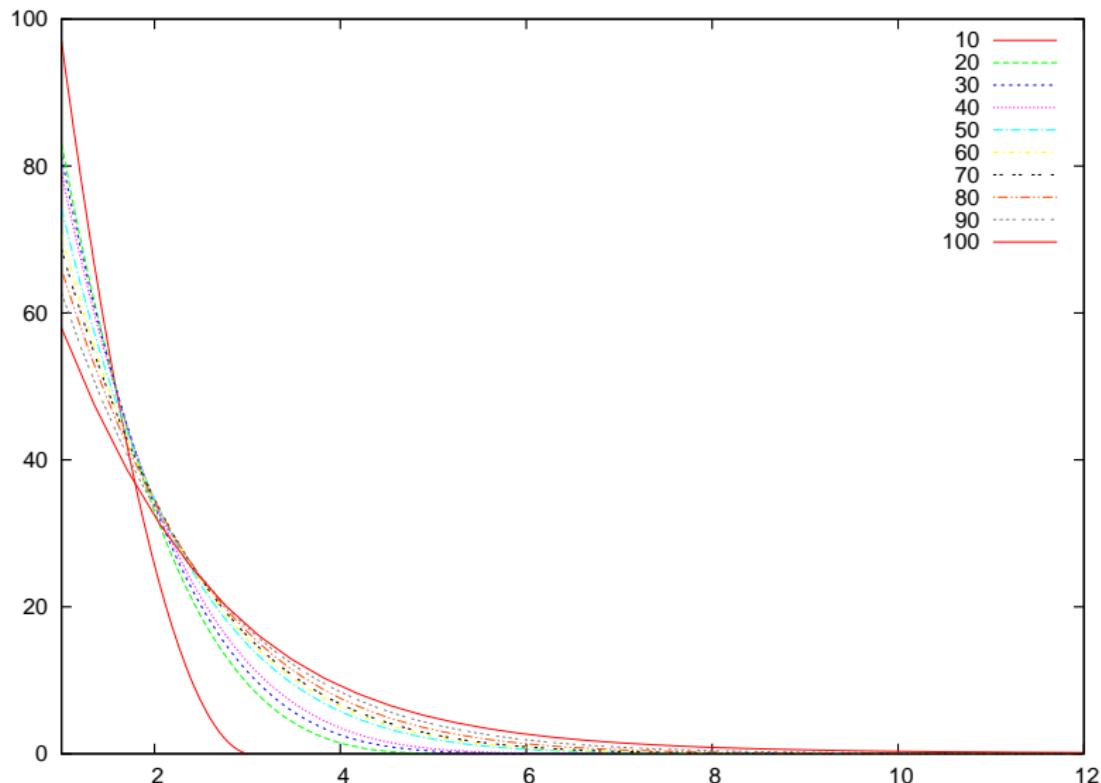
# Animation

# General network analysis

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



# Connectivity Distribution



# Metabolic network analysis

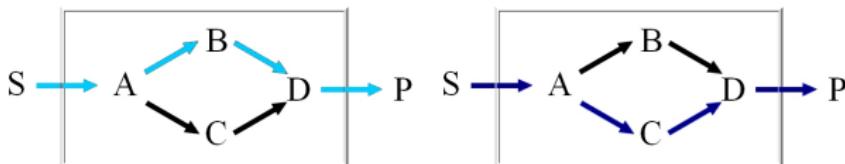
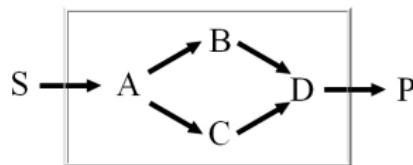
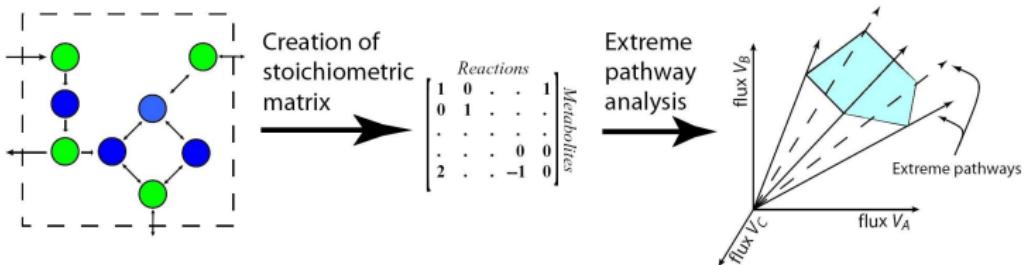
We have sets of edges forming meaningful complex entities



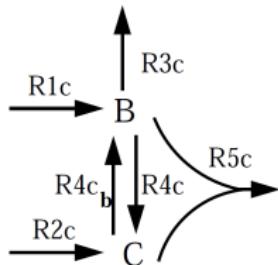
pathways

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

# Metabolic Pathway Analysis



# Metabolic Pathway Analysis



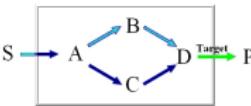
$$N_C = \begin{pmatrix} 1 & 0 & -1 & 1 & -1 & -1 \\ 0 & 1 & 0 & -1 & 1 & -1 \end{pmatrix} \begin{matrix} R1c & R2c & R3c & R4c_b & R4c & R5c \end{matrix}$$

$$K_C' = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0.5 & -0.5 & -0.5 & 1 \\ 0.5 & 0.5 & -0.5 & 0 \end{pmatrix} \begin{matrix} R1c \\ R2c \\ R3c \\ R4c_b \\ R4c \\ R5c \end{matrix}$$

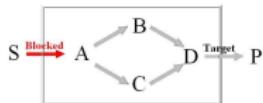
$$R^5 = \begin{pmatrix} \times & 0 & \times & \times & 0 & 0 \\ 0 & 0 & \times & 0 & \times & \times \\ 0 & 0 & 0 & 0 & \times & 0 \\ 0 & \times & 0 & 0 & 0 & \times \\ \frac{\times}{0.5} & \frac{\times}{0} & \frac{0}{1} & \frac{0}{0} & \frac{0}{1} & \frac{0}{-1} \end{pmatrix} \begin{matrix} R1c \\ R2c \\ R3c \\ R4c_b \\ R4c \\ R5c \end{matrix}$$

$$R^6 = \begin{pmatrix} \times & 0 & \times & \times & 0 & 0 \\ 0 & 0 & \times & 0 & \times & \times \\ 0 & 0 & 0 & \times & 0 & \times \\ 0 & \times & 0 & 0 & \times & \times \\ \times & \times & 0 & 0 & 0 & 0 \\ \times & 0 & \times & 0 & \times & 0 \end{pmatrix} \begin{matrix} R1c \\ R2c \\ R3c \\ R4c_b \\ R4c \\ R5c \end{matrix}$$

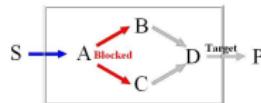
# Acceptable Knockouts



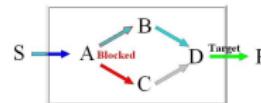
## Minimal Knockout sets



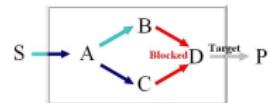
$\{S \rightarrow A\}$



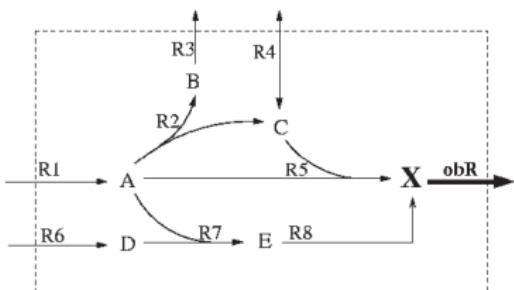
$\{A \rightarrow B, A \rightarrow C\}$



$\{A \rightarrow C\}$  is not a MKS



$\{B \rightarrow D, C \rightarrow D\}$

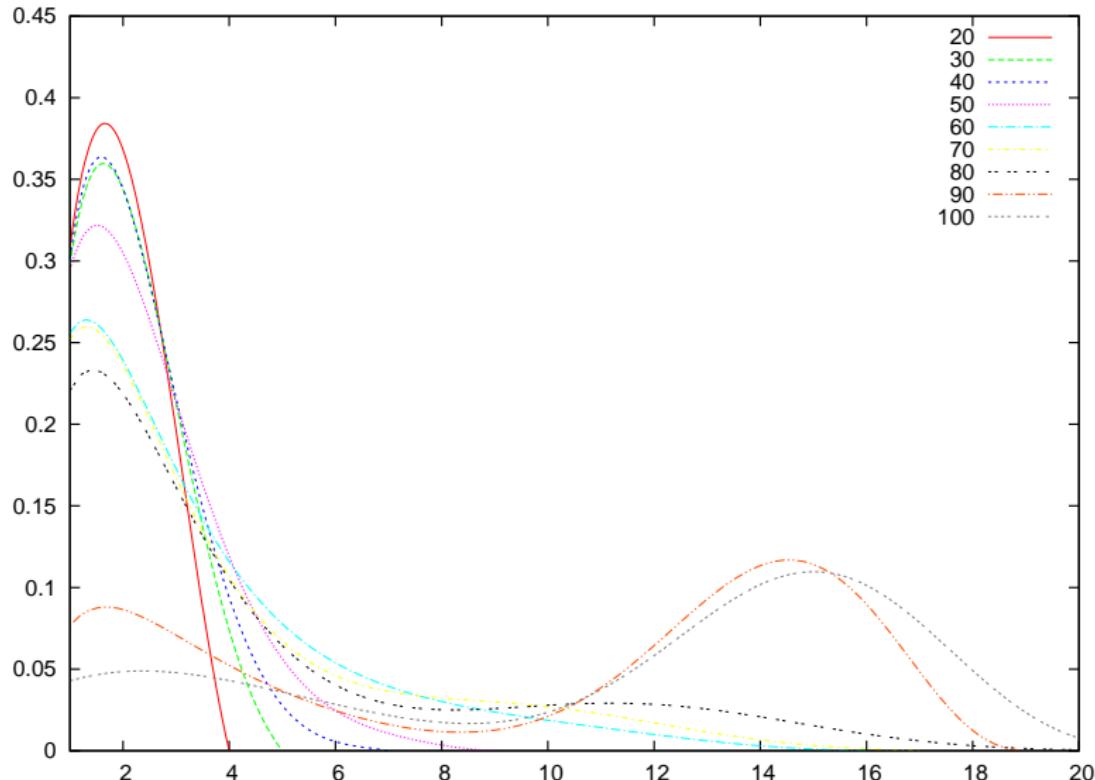


	R1	R2	R3	R4	R5	R6	R7	R8	obR
Elementary modes									
EM1	1	1	1	-1	0	0	0	0	0
EM2	1	0	0	0	0	1	1	1	1
EM3	2	1	1	0	1	0	0	0	1
EM4	1	0	0	1	1	0	0	0	1

### Minimal cut sets (objective reaction: obR)

MCS0									x
MCS1	x								
MCS2			x			x		x	
MCS3			x				x		
MCS4			x					x	
MCS5		x		x			x		
MCS6			x	x			x		
MCS7	x		x					x	
MCS8		x	x				x		
MCS9	x		x					x	
MCS10		x	x					x	
$F_i$	1	1/3	1/3	1/3	1/2	3/8	3/8	3/8	1

# Knockout set size distribution



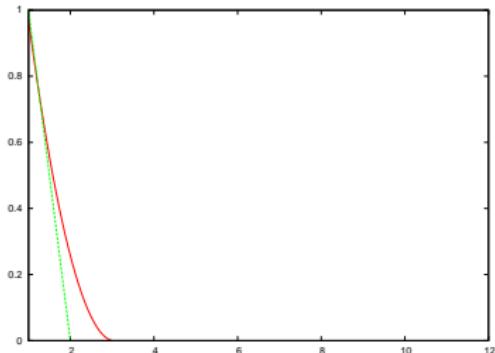
# Knockout effects

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

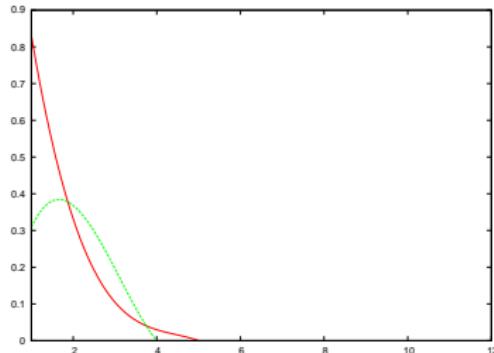
Example system	Number of reactions	Number of elementary modes	$R_1(1)$	$R_1(2)$	$R_1(3)$	$R_3(\leq 3)$
1	4	2	$1/2 = 0.5$	$1/6 \approx 0.167$	0	0.414
2	4	2	$1/2 = 0.5$	$1/4 = 0.25$	$1/8 = 0.125$	0.436
3	4	2	$3/8 = 0.375$	$1/12 \approx 0.083$	0	0.302
4	4	2	$1/4 = 0.25$	0	0	0.189
5	8	2	$7/16 \approx 0.438$	$3/8 = 0.375$	$5/16 \approx 0.313$	0.418
6	8	2	$1/2 = 0.5$	$3/14 \approx 0.214$	$1/14 \approx 0.071$	0.416
7	5	4	$13/20 = 0.65$	$3/8 = 0.375$	$7/40 = 0.175$	0.573
8	5	3	$2/3 \approx 0.667$	$2/5 = 0.4$	$1/5 = 0.2$	0.592

# Robustness

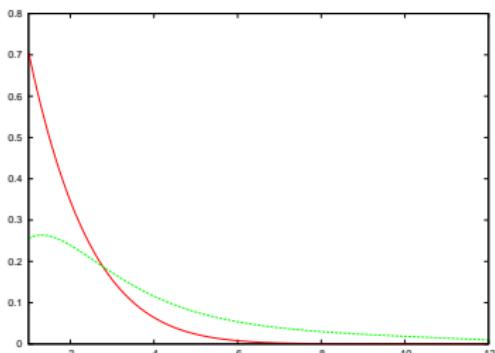
Robustness = 0.51



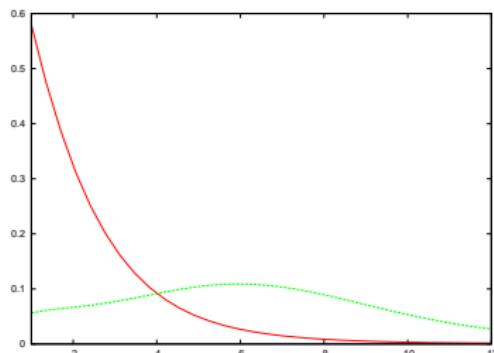
Robustness = 0.67



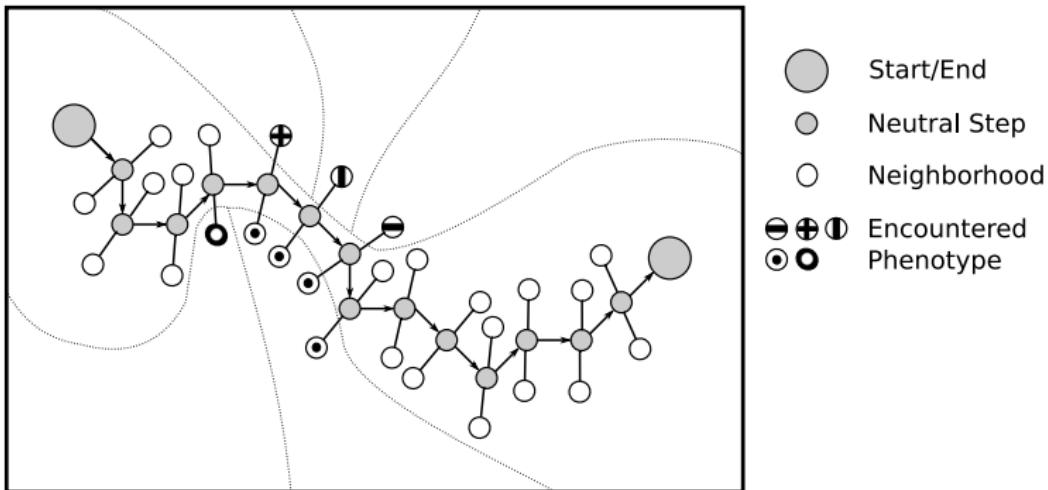
Robustness = 0.75



Robustness = 0.81



## Future analysis methods



- Neutral network of a metabolic network (see RNA, GRN)
- Barrier trees of flux distributions (see xtof)

## Acknowledgements

Christoph Flamm

Peter Stadler

Konstantin Klemm

Martin Mann

Markus Rohrschneider