

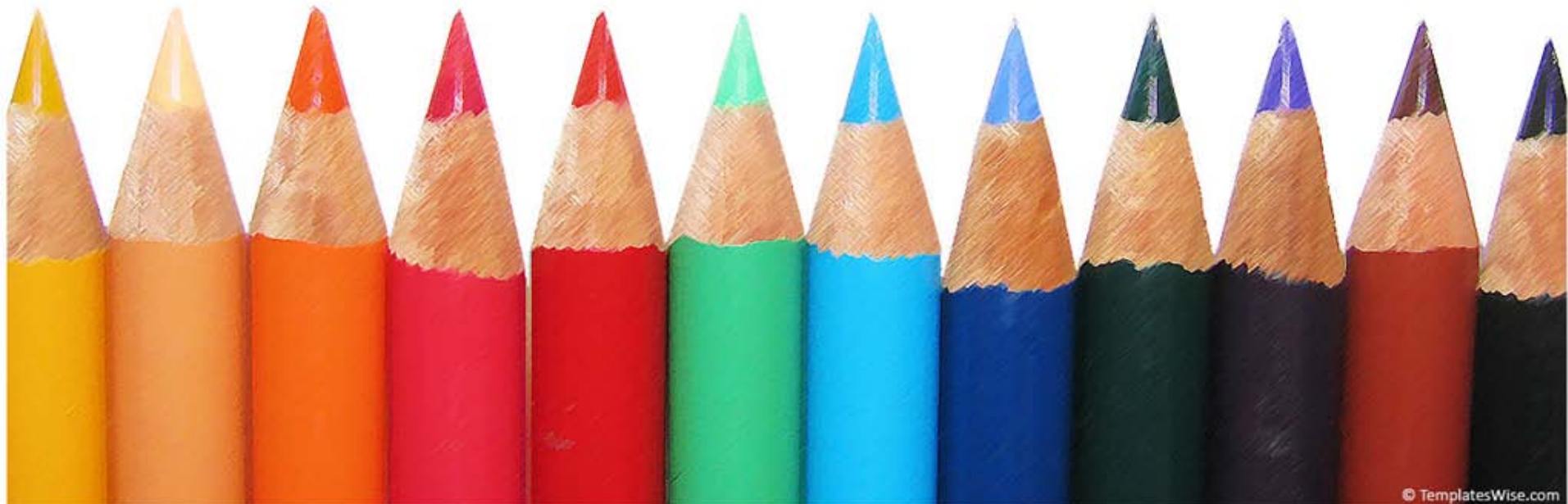
Impact of individual nodes in Boolean network dynamics

Fakhteh Ghanbarnejad, Konstantin Klemm

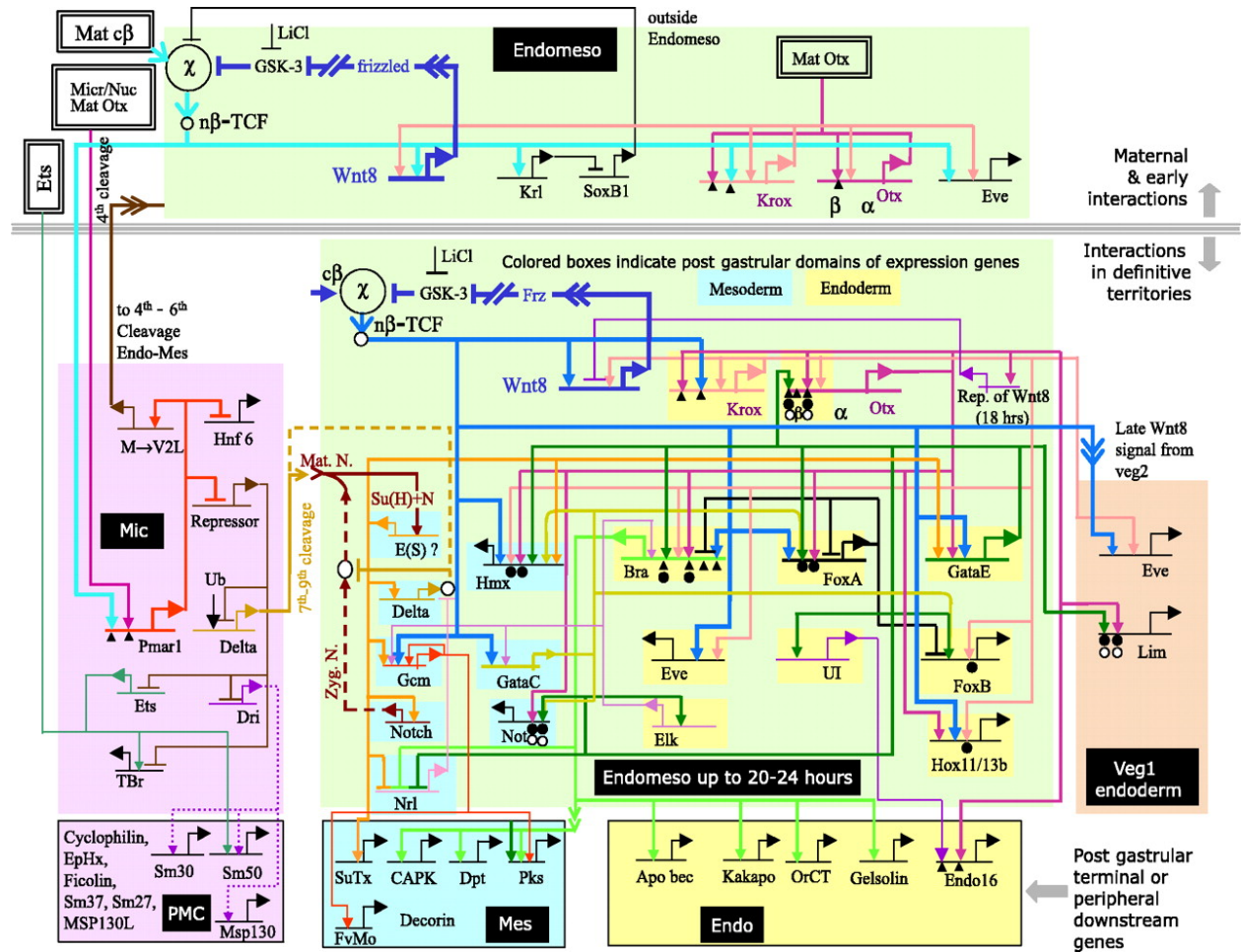
Bioinformatics group, Universität Leipzig, Germany

[arXiv:1111.5334v1](https://arxiv.org/abs/1111.5334v1)

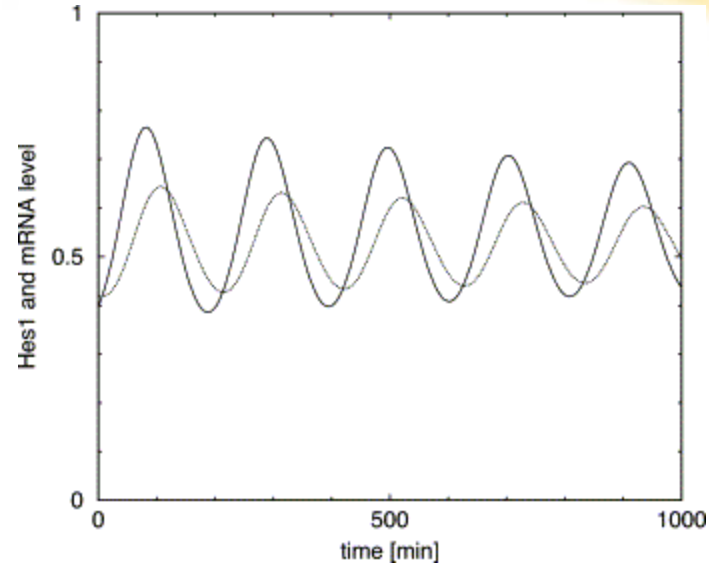
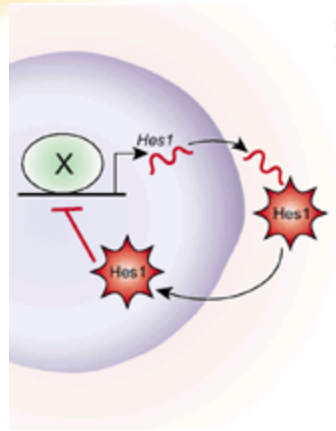
Dresden, May 2012



Impact of individual nodes in Boolean network dynamics



Regulatory Dynamics



$$\frac{d[mRNA(t)]}{dt} = \frac{\alpha k^h}{k^h + [Hes1(t - \tau)]^h} \frac{[mRNA(t)]}{\tau_{rna}}$$

$$\frac{d[Hes1(t)]}{dt} = \beta [mRNA(t)] - \frac{[Hes1(t)]}{\tau_{hes1}}$$

Regulatory Dynamics

$$\frac{d[mRNA(t)]}{dt} = \frac{\alpha k^h}{k^h + [Hes1(t - \tau)]^h} - \frac{[mRNA(t)]}{\tau_{rna}}$$
$$\frac{d[Hes1(t)]}{dt} = \beta [mRNA(t)] - \frac{[Hes1(t)]}{\tau_{hes1}}$$

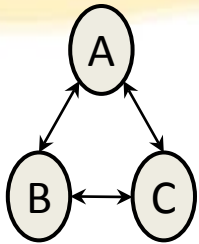
- parameters: production delay, production rates, binding threshold, characteristic degradation times Hes1 & rna
- six parameters for a single gene
- larger systems?!!!

Discrete Abstract Model

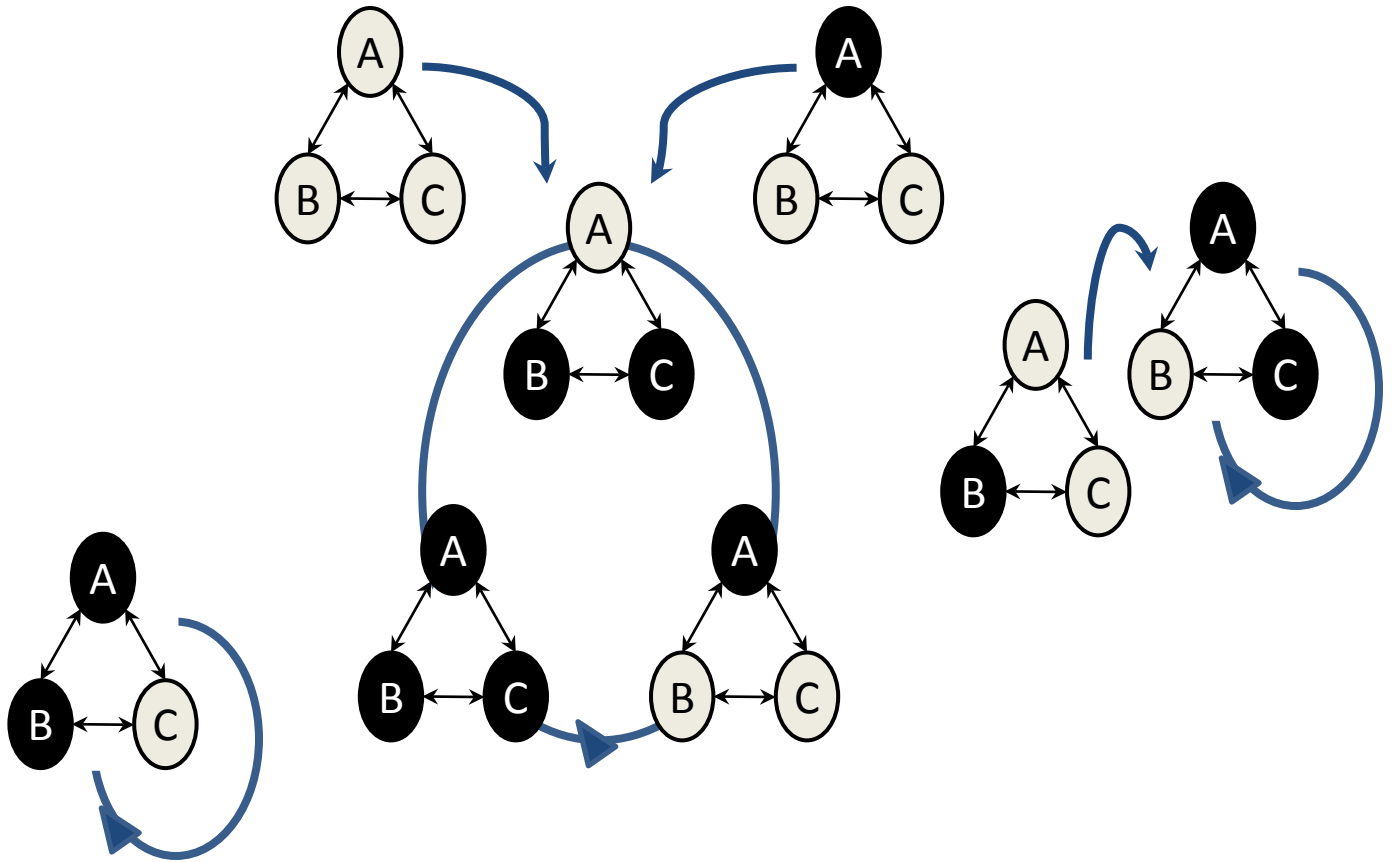
- ON/Off States
- Interactions Network
- Dynamics (time evolution of states):
Logical Operators

Boolean Networks

Attractors



	ABC
00	011
01	011
10	011
11	100



Activity & Sensitivity

	F
00	0 F ₀
01	0 F ₁
10	1 F ₂
11	1 F ₃

	F
10	F ₂
11	F ₃
00	F ₀
01	F ₁

	F
00	1 F ₀
01	0 F ₁
10	1 F ₂
11	1 F ₃

	F
10	F ₀
11	F ₃
00	F ₂
01	F ₁

$$a(f_i) = 2^{-n} \sum_{x \in \{0,1\}^n} |f(x) - f(x^{\uparrow j})|$$

$$s(f_i) = \sum_{j=1}^n 2^{-n} \sum_{x \in \{0,1\}^n} |f(x) - f(x^{\uparrow j})|$$

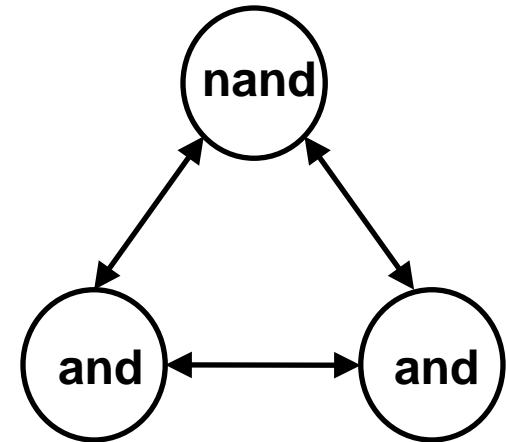
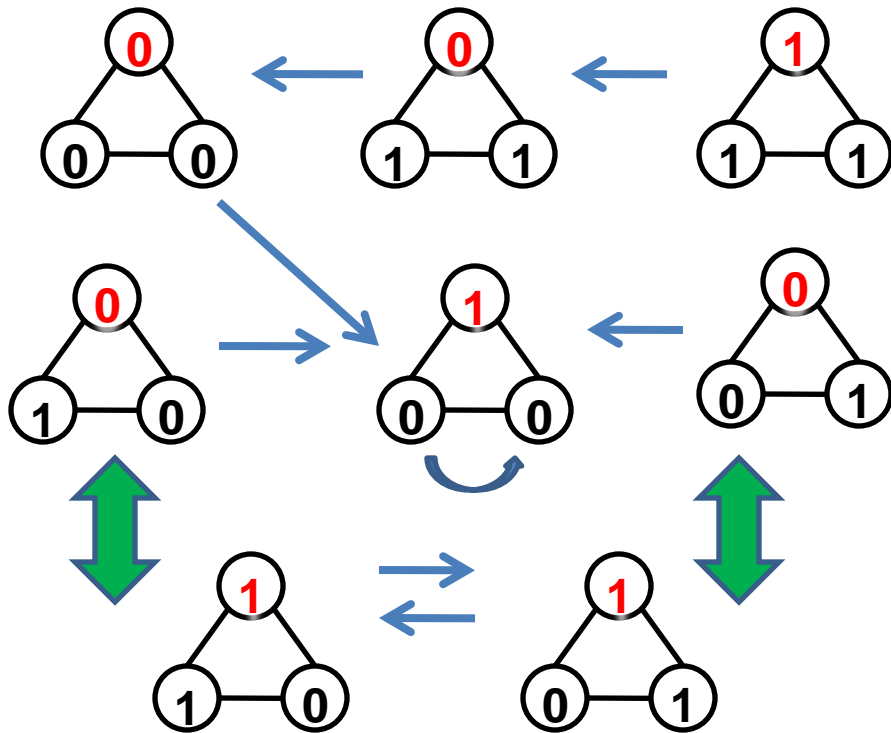
Impact of individual nodes in Boolean network dynamics

Short term

Long term



Computing the dynamical impact of nodes

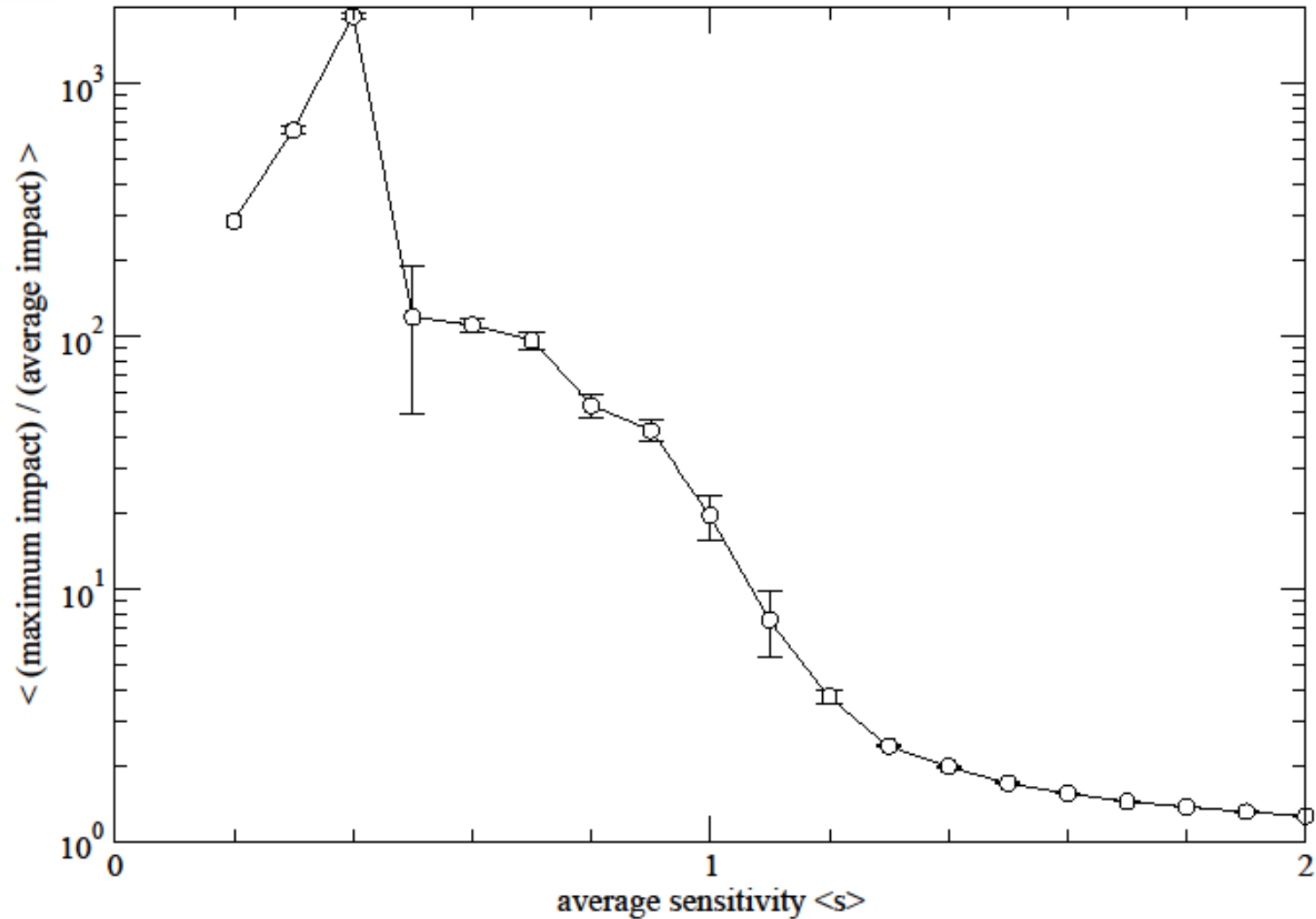


Flip:

0→1

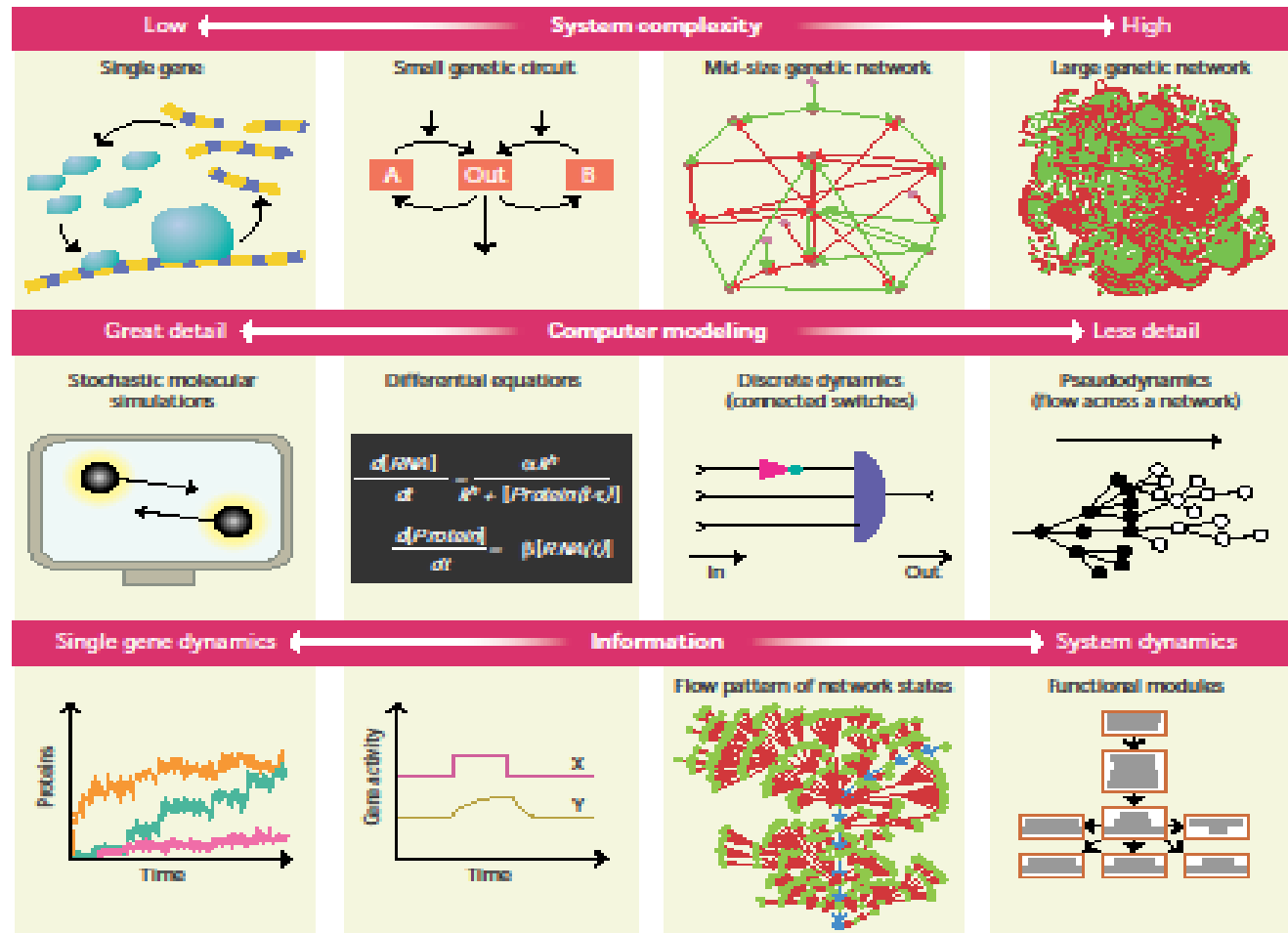
1→0

Variation of dynamical impact across nodes in random Boolean networks



Predicting of dynamical impact

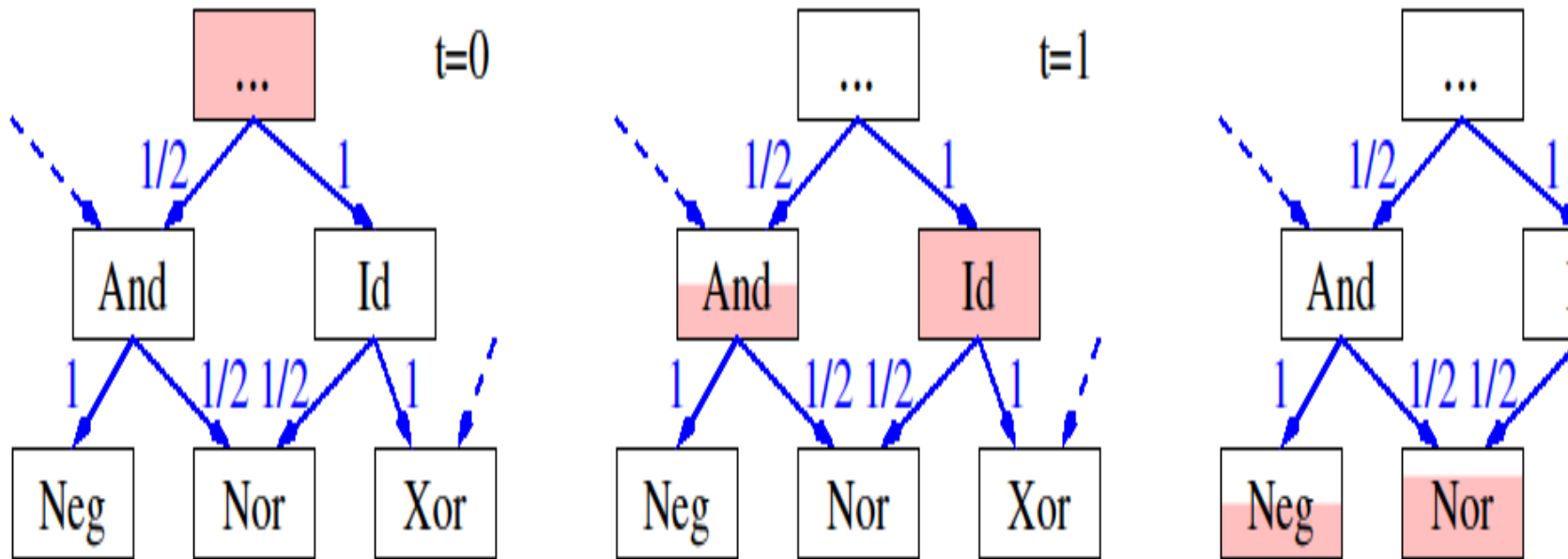
- Why ?



Predicting of dynamical impact

- How ?

Probabilistic description of damage spreading in a Boolean dynamics



$$p_j(t) \propto \sum_{i=1}^N \alpha_{ji} p_i(t-1)$$

$$p(t) = \mathcal{N}^T p(t-1)$$

$$p(t) = (\mathcal{N}^T)^t p(0)$$

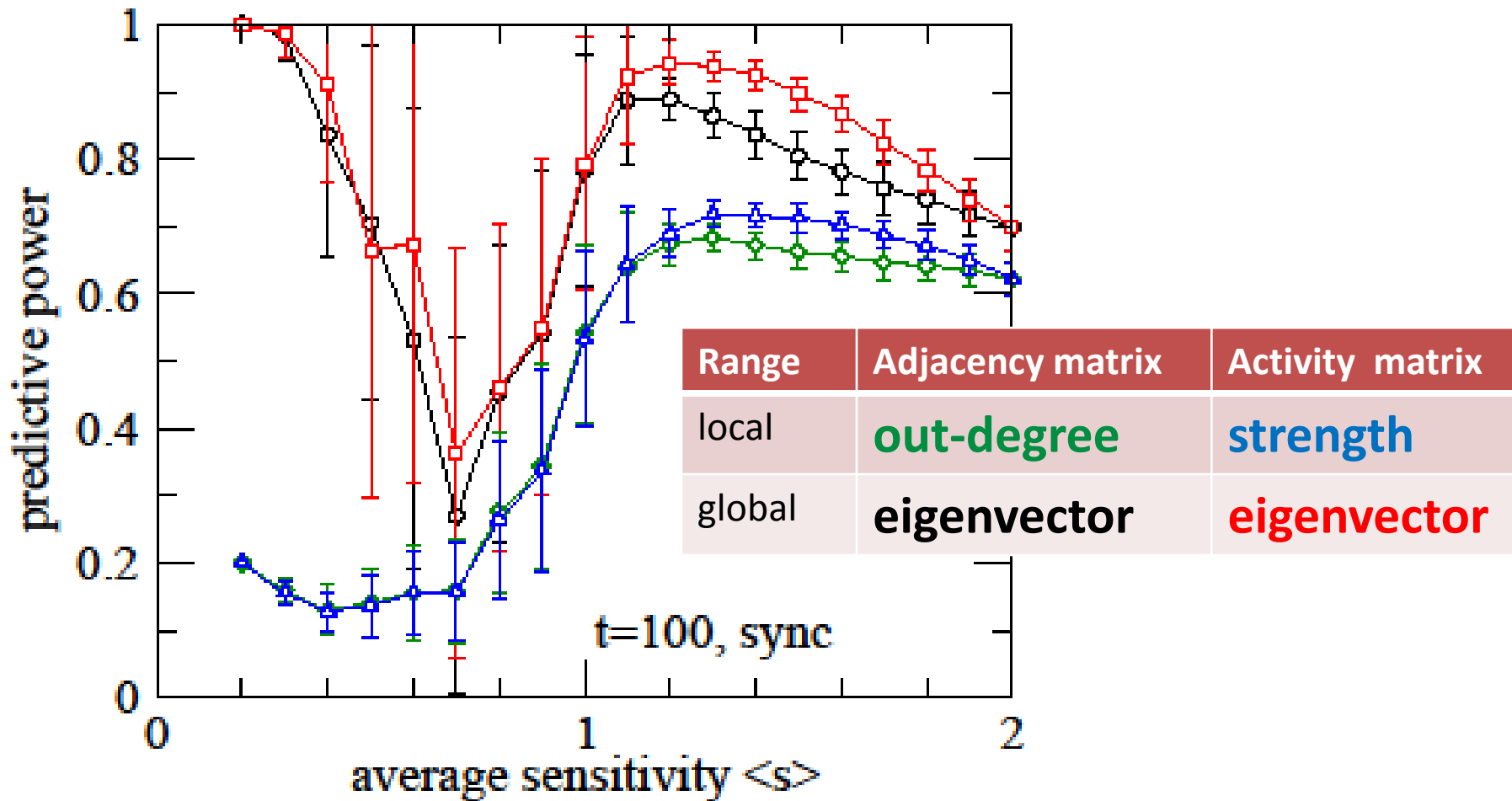
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Centrality measures considered as predictors for the dynamical impact

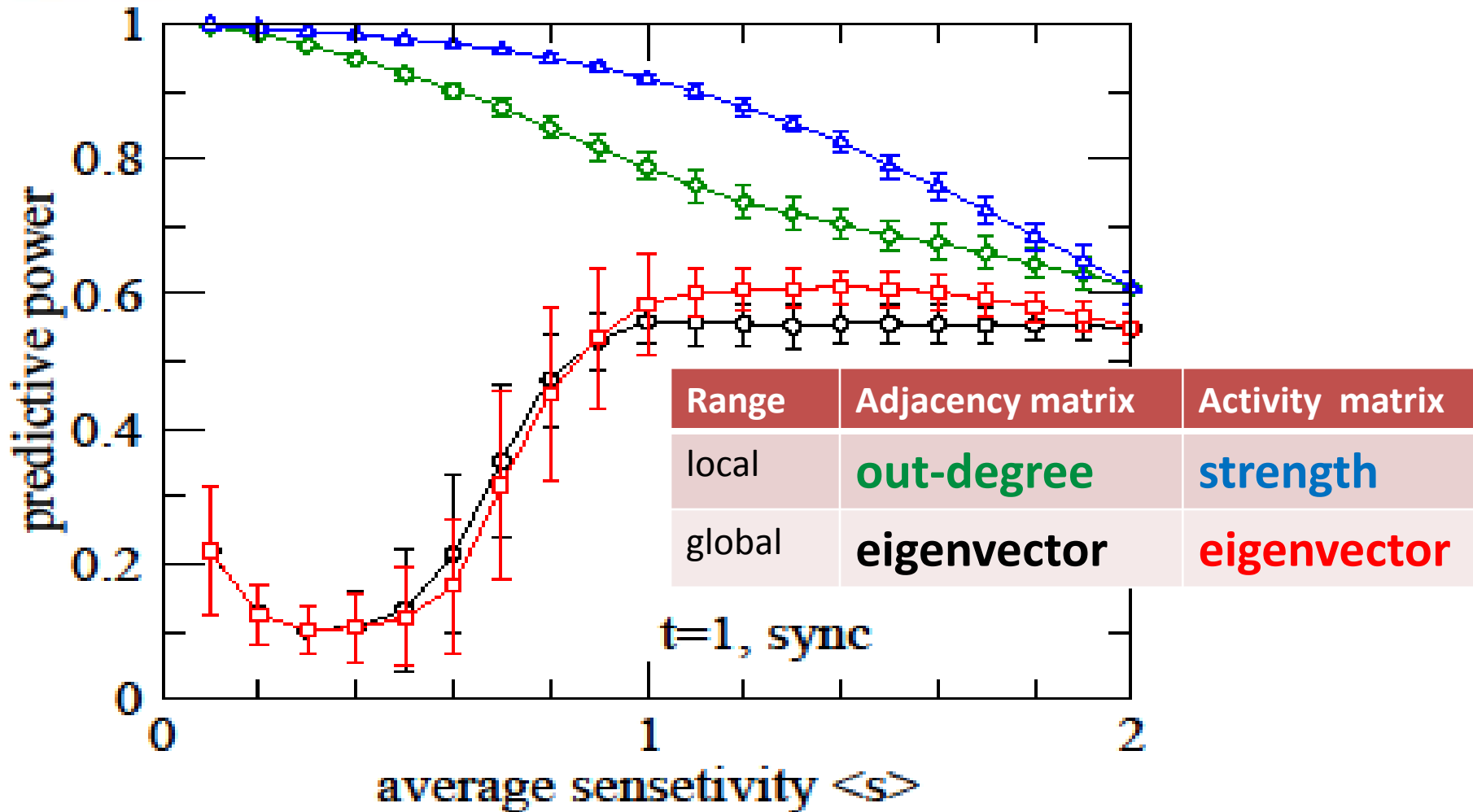
Range	Adjacency matrix	Activity matrix
local	out-degree	strength
global	eigenvector	eigenvector



Results for random Boolean networks

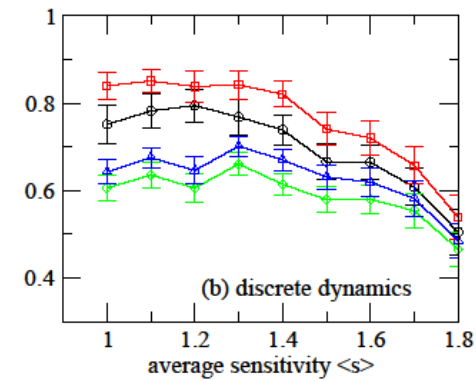
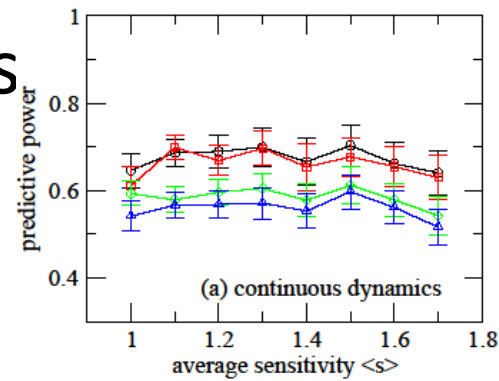
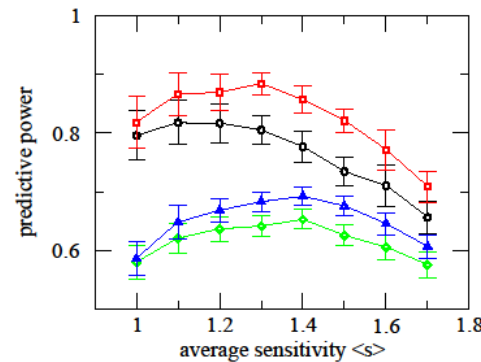
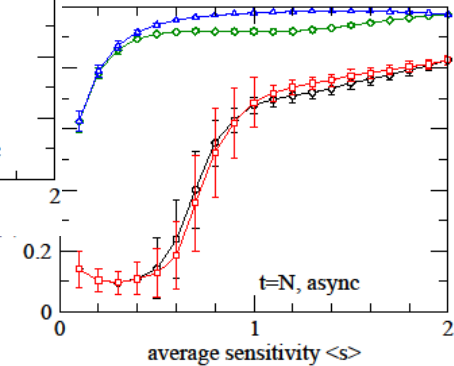
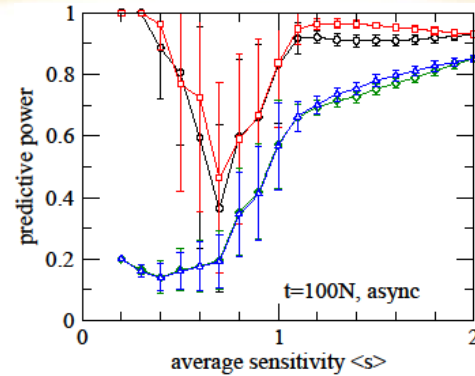


Results for random Boolean networks











More cases

- Asynchronous updating
- Attractor switching
- With small perturbations



Dynamical impact in a real network

		all nodes			
		\mathcal{P}_ϵ 	\mathcal{P}_e 	\mathcal{P}_σ 	\mathcal{P}_d 
synchronous	$t = 1$	0.671	0.454	0.930	0.455
	$t = 100$	0.920	0.734	0.746	0.523
asynchronous	$t = N$	0.706	0.528	0.904	0.564
	$t = 100N$	0.854	0.694	0.748	0.542
		only core nodes			
		\mathcal{P}_ϵ 	\mathcal{P}_e 	\mathcal{P}_σ 	\mathcal{P}_d 
synchronous	$t = 1$	0.633	0.467	0.946	0.528
	$t = 100$	0.911	0.777	0.738	0.611
asynchronous	$t = N$	0.658	0.543	0.919	0.656
	$t = 100N$	0.834	0.731	0.741	0.631

fibroblast signal transduction

Impact of individual nodes in Boolean network dynamics

- Linear algebra
- Random Boolean networks
- Empirical Boolean networks

Range	Adjacency matrix	Activity matrix
local	out-degree	strength
global	eigenvector	eigenvector





Thanks!
To be continued ...

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Stability of Boolean and continuous dynamics

[Phys. Rev. Lett. 107.188701](https://doi.org/10.1103/PhysRevLett.107.188701)

