

Automata Networks

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Boolean Automata Networks: discrete deterministic dynamical systems over a graph only with states 0 or 1 on the vertices.

A vertex updates its state following a boolean rule depending of the states of its graph's neighbors.

The dynamics

Parallel or synchronous update: Every site is updated at the same time.

Sequential update: sites are updated one by one in a prescribed order.

Block- sequential updates:

Consider a partition $\{I_1, \dots, I_p\}$ of the set $\{1, \dots, n\}$

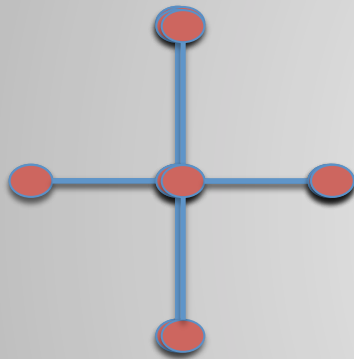
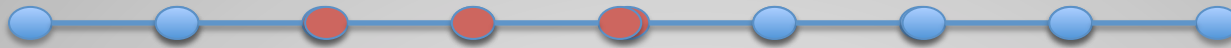
We update the blocks one by one:

To update the k -th block we consider the new state of every sites belong to previous blocks.

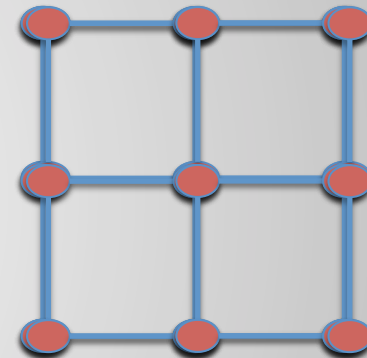
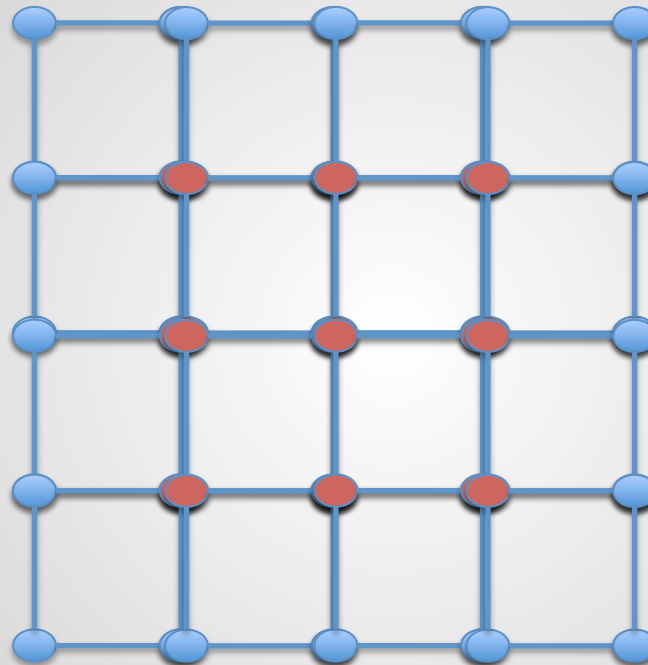
Particular cases

Cellular Automata: on d-dimensional grids with the same local function in every site, updated (usually) in parallel.

Arbitrary finite graph modelling regulatory genetic networks



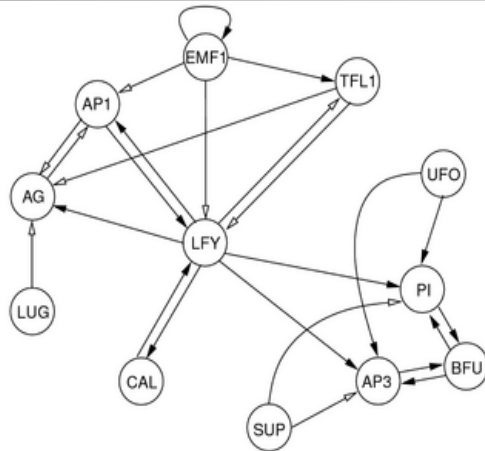
Von Neumann neighborhood



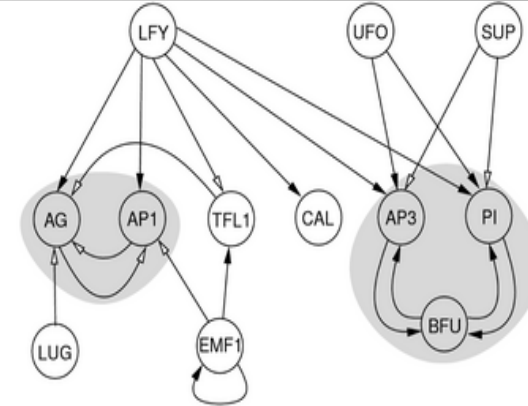
Moore neighborhood

One and two-dimensional grids

Arabidopsis regulation threshold network



$$W = \begin{pmatrix} & \text{EMF1} & \text{TFL1} & \text{LFY} & \text{AP1} & \text{CAL} & \text{LUG} & \text{UFO} & \text{BFU} & \text{AG} & \text{AP3} & \text{PI} & \text{SUP} \\ \text{EMF1} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{TFL1} & 1 & 0 & -2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{LFY} & -2 & -1 & 0 & 2 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{AP1} & -1 & 0 & 5 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ \text{CAL} & 0 & 0 & 2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{LUG} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{UFO} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{BFU} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ \text{AG} & 0 & -2 & 1 & -2 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{AP3} & 0 & 0 & 3 & 0 & 0 & 0 & 2 & 1 & 0 & 0 & 0 & -2 \\ \text{PI} & 0 & 0 & 4 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & -1 \\ \text{SUP} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad \Theta = \begin{pmatrix} 0 \\ 0 \\ 3 \\ -1 \\ 1 \\ 0 \\ 0 \\ 1 \\ -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$



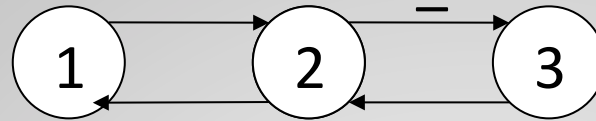
$$\tilde{W} = \begin{pmatrix} & \text{EMF1} & \text{TFL1} & \text{LFY} & \text{AP1} & \text{CAL} & \text{LUG} & \text{UFO} & \text{BFU} & \text{AG} & \text{AP3} & \text{PI} & \text{SUP} \\ \text{EMF1} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{TFL1} & 1 & 0 & -2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{LFY} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{AP1} & -2 & 0 & 5 & 0 & 0 & 0 & 0 & 0 & -2 & 0 & 0 & 0 \\ \text{CAL} & 0 & 0 & 2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{LUG} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{UFO} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{BFU} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ \text{AG} & 0 & -2 & 1 & -2 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{AP3} & 0 & 0 & 3 & 0 & 0 & 0 & 2 & 1 & 0 & 0 & 0 & -2 \\ \text{PI} & 0 & 0 & 4 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & -1 \\ \text{SUP} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad \tilde{\Theta} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ -2 \\ 1 \\ 0 \\ 0 \\ 1 \\ -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

Bioinformatics. 1999 Jul-Aug;15(7-8):593-606.

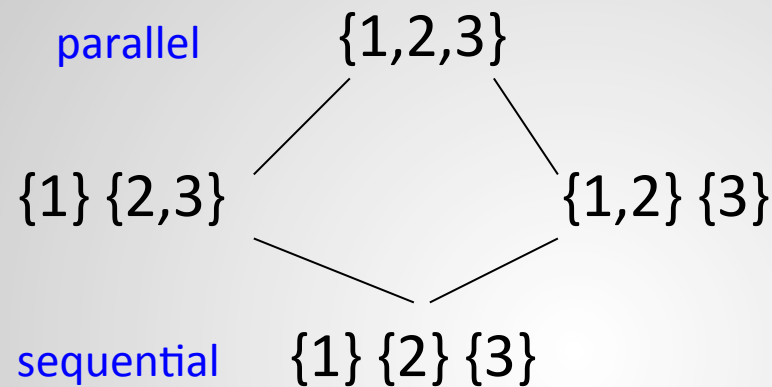
Genetic control of flower morphogenesis in *Arabidopsis thaliana*: a logical analysis. Mendoza L, Thieffry D, Alvarez-Buylla ER.

Demongeot J, G. E, Morvan M, Noual M, Sené S (2010) Attraction Basins as Gauges of Robustness against Boundary Conditions in Biological Complex Systems. PLoS ONE 5(8): e11793. doi:10.1371

The(directed) graph



EXAMPLE



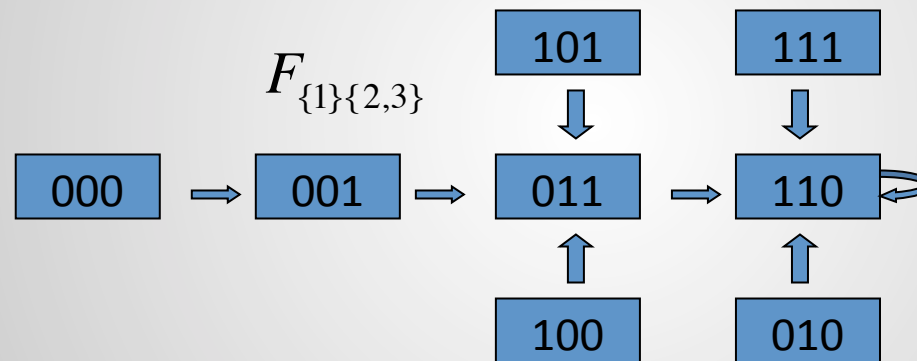
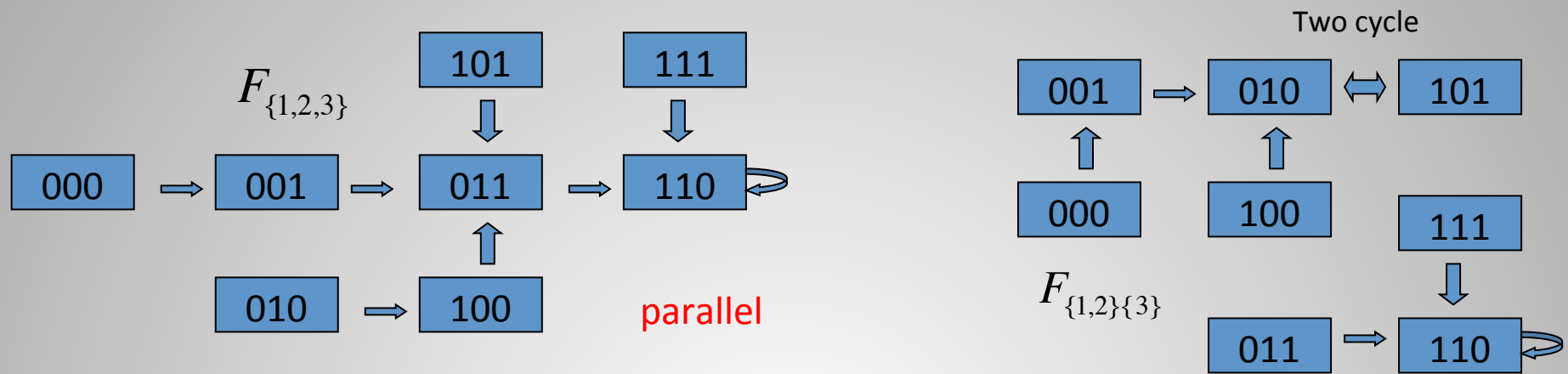
Some Block-Sequential
partitions for three
sites

$$F_{\{1,2,3\}}(x_1, x_2, x_3) = (x_2, x_1 + x_3, \neg x_2)$$

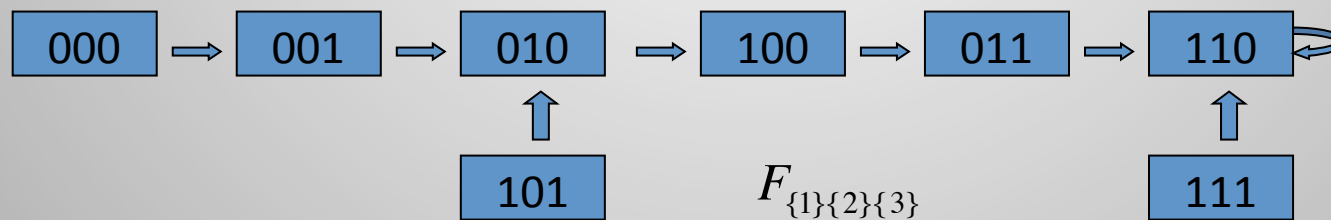
$$F_{\{1,2\}\{3\}}(x_1, x_2, x_3) = (x_2, x_1 + x_3, (\neg x_1)(\neg x_3))$$

$$F_{\{1\}\{2,3\}}(x_1, x_2, x_3) = (x_2, x_2 + x_3, \neg x_2)$$

$$F_{\{1\}\{2,3\}}(x_1, x_2, x_3) = (x_2, x_2 + x_3, (\neg x_2)(\neg x_3))$$



Block
sequential
diagrams



sequential

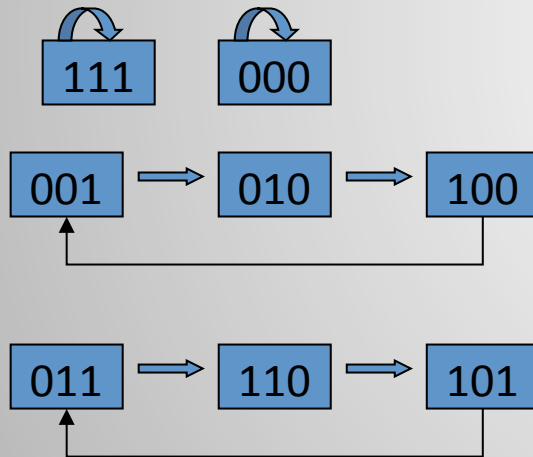
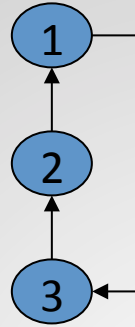
Cycles for synchronous and sequential updates

$$F : \{0,1\}^3 \rightarrow \{0,1\}^3$$

$$f_1(x_1, x_2, x_3) = x_2$$

$$f_2(x_1, x_2, x_3) = x_3$$

$$f_3(x_1, x_2, x_3) = x_1$$



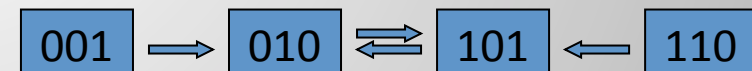
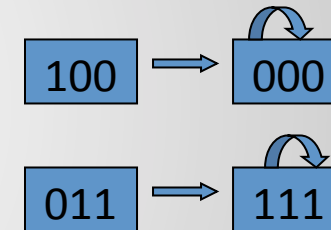
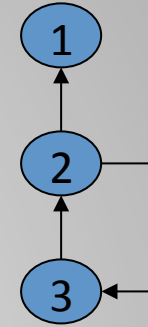
Parallel update: 3-cycles

$$G : \{0,1\}^3 \rightarrow \{0,1\}^3$$

$$g_1(x_1, x_2, x_3) = x_2$$

$$g_2(x_1, x_2, x_3) = x_3$$

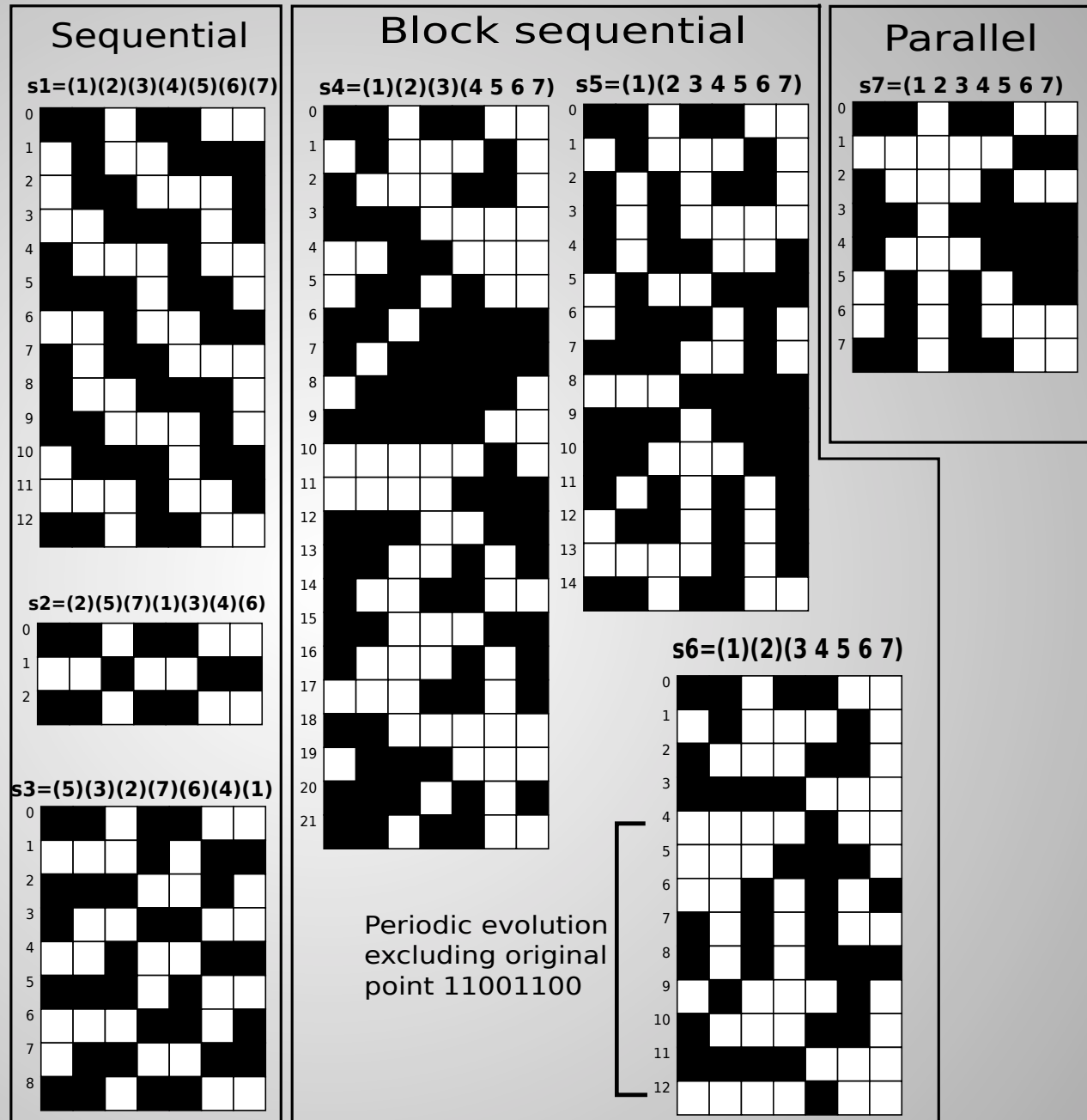
$$g_3(x_1, x_2, x_3) = x_2$$



Sequential update: 2-cycle

Elementary one dimensional
Automaton with periodic
conditions and the linear
local rule 150

000 0
001 1
010 1
011 0
100 1
101 0
110 0
111 1



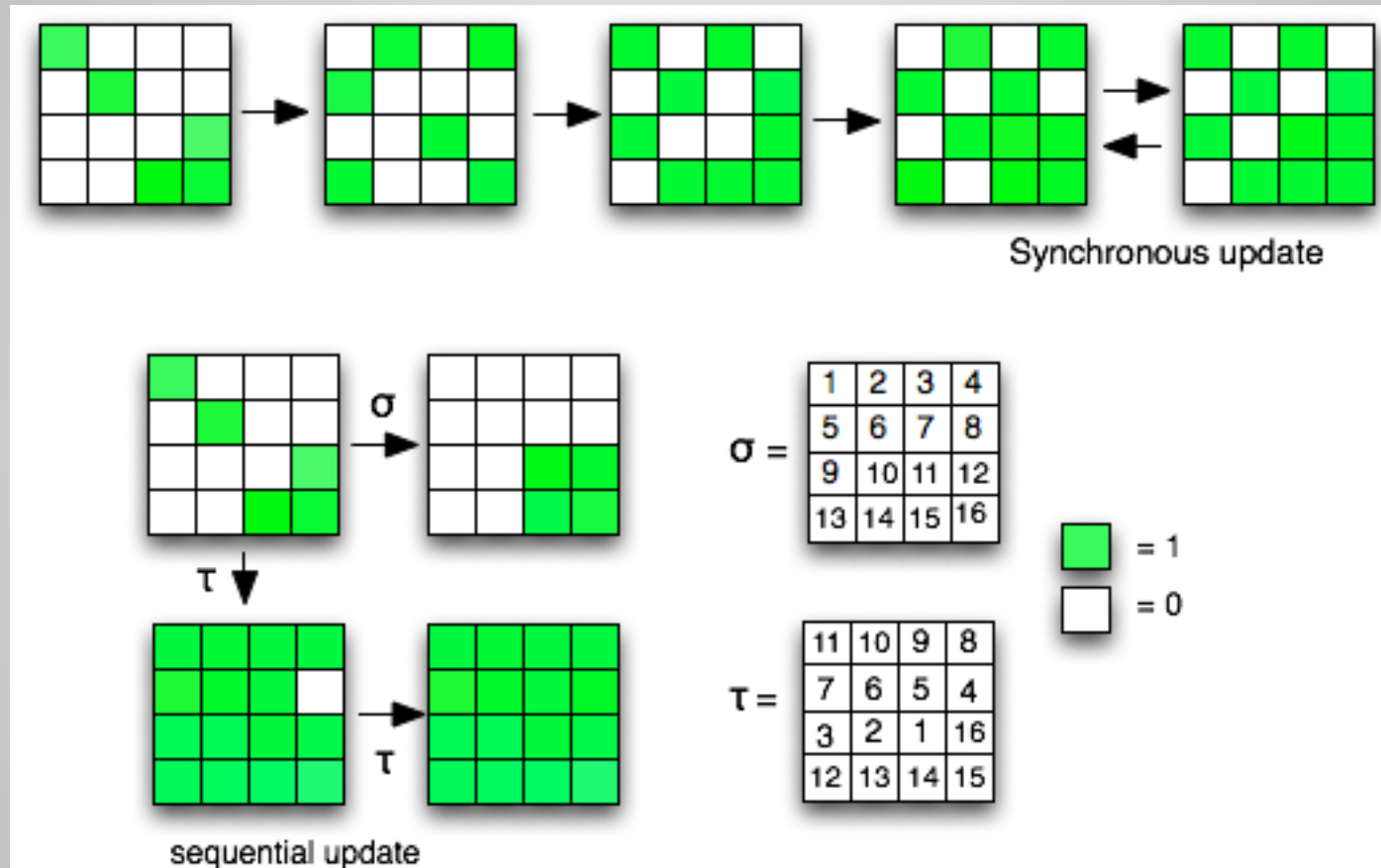
dynamics for the majority rule in a two dimensional grid

We consider a 4x4 lattice with periodic conditions, nearest interactions, states 0 or 1, and the local majority function:

If the number of ones is bigger or equal to the number of zeros then the site takes the value 1

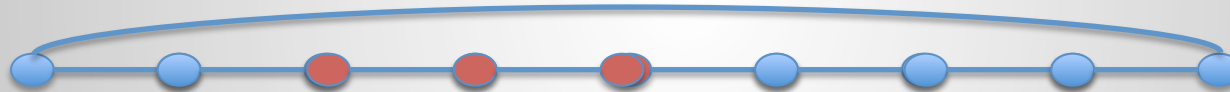
$$x'_{ij} = 1 \quad \text{iff} \quad x_{i-1,j} + x_{i+1,j} + x_{i,j-1} + x_{i,j+1} \geq 2$$

Dynamics: two cycles and fixed points; different behavior for different updates



Different updates give
different
dynamic behavior

Different updates schemes on one dimensional elementary periodic CAs



$n \geq 3$ sites

An ECA is sequential invariant If and only if for $n > 3$ and any permutation (sequential update), the set of attractors is the same.

Clearly, if the ECA admits only fixed points it is trivially sequential invariant

Theorem (Macauley, Mcammond, Morveit (JCA2013))

There exists 41 non-equivalent sequential-invariant ECA

Rule	$f_i(u, v, w)$	Rule	$f_i(u, v, w)$
0	0	108	$u\bar{v}w + v\bar{w} + \bar{u}v$
1	$\bar{u}\bar{v}\bar{w}$	128	uvw
4	$\bar{u}v\bar{w}$	129	$\bar{u}\bar{v}\bar{w} + uvw$
5	$\bar{u}\bar{w}$	132	$\bar{u}v\bar{w} + uvw$
8	$\bar{u}vw$	133	$uvw + \bar{u}\bar{w}$
9	$\bar{u}\bar{v}\bar{w} + \bar{u}vw$	136	vw
12	$\bar{u}v$	137	$\bar{u}\bar{v}\bar{w} + vw$
13	$\bar{u}\bar{w} + \bar{u}v$	140	$\bar{u}v + vw$
28	$u\bar{v}\bar{w} + \bar{u}v$	141	$\bar{u}\bar{w} + vw$
29	$\bar{v}\bar{w} + \bar{u}v$	150	$u\bar{v}\bar{w} + \bar{u}v\bar{w} + \bar{u}\bar{v}w + uvw$
32	$u\bar{v}w$	152	$u\bar{v}\bar{w} + vw$
40	$u\bar{v}w + \bar{u}vw$	156	$u\bar{v}\bar{w} + \bar{u}v + vw$
51	$\bar{v}$	160	uw
54	$\bar{u}v\bar{w} + u\bar{v} + \bar{v}w$	164	$\bar{u}v\bar{w} + uw$
57	$\bar{u}vw + \bar{v}\bar{w} + u\bar{v}$	168	$uw + vw$
60	$u\bar{v} + \bar{u}v$	172	$\bar{u}v + uw$
72	$uv\bar{w} + \bar{u}vw$	184	$u\bar{v} + vw$
73	$\bar{u}\bar{v}\bar{w} + uv\bar{w} + \bar{u}vw$	200	$uv + vw$
76	$v\bar{w} + \bar{u}v$	204	v
77	$\bar{u}\bar{w} + v\bar{w} + \bar{u}v$	232	$uv + uw + vw$
105	$\bar{u}\bar{v}\bar{w} + uv\bar{w} + u\bar{v}w + \bar{u}vw$		

TABLE 1

The 41 representative rules π -independent of [5] and its minimal disjunctive normal form representations. At each time step, the value x_i is updated according to the rule $x'_i = f_i(u, v, w)$ where $u = x_{i-1}$, $v = x_i$ and $w = x_{i+1}$.

Between those 41 rules we are interested
To characterize those which are invariant for every
Block Sequential update

For instance the rule 5 is not block-sequential invariant

It is enough to consider $n=4$

Rule 5

And the updates $(3,4)(1,2)$ and $(4)(3)(1,2)$

$f(0,0,0)=1$
 $f(x,y,z)=0$ else

The attractors for $(3,4)(1,2)$ are: 0000; 0011; 1100; i.e., 0, 3, 12

3-cycle

0000
0011
1100
0000

The attractors for $(4)(3)(1,2)$ are: 0000 and 0101, i.e. 0 and 5

0000
0101
0000

Theorem (Montalva, Morveit, Ramirez, EG)

For $n > 3$, there are 15 non-equivalent rules

block-sequential invariants.

0, 4, 8, 12, 28, 51, 72, 76, 128, 132, 136, 140, 141, 200, 204

Theorem (Montalva, Morveit, Ramirez, EG)

For $n > 3$, there are 15 non-equivalent rules

block-sequential invariants.

0, 4, 8, 12, 28, 51, 72, 76, 128, 132, 136, 140, 141, 200, 204

consider for instance the rule 32 which is not block-invariant
But it is for n odd.

000 0
001 0
010 0
011 0
100 0
101 1
110 0
111 0

Clearly * 00* remains stable. And at each step
0s are added at both sides ...

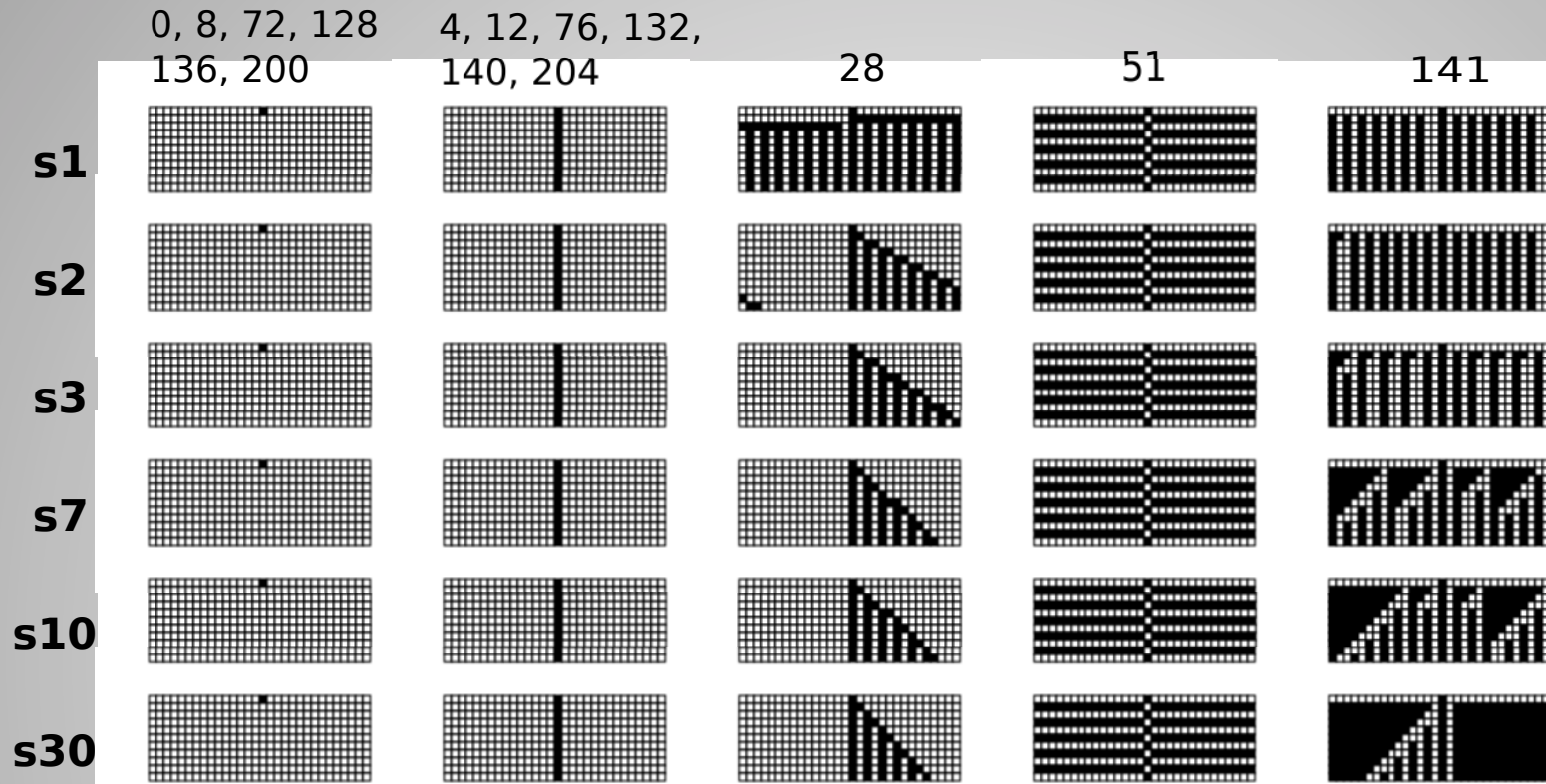
The other case: 10101010
is a two cycle only for n even

If there are two 1's together every update create a block 00

So the rule 32 is block- invariant only for n odd

(9n parallel the 2-cycle exist only for n even).

Block invariant rules



Evolution of the 15 block invariant Wolfram's rules starting with a single one in the 16th position, under the block updates $s_1 = (1)(2) \cdots (30)$, $s_2 = (1, 2)(3, 4) \cdots (29, 30)$, $s_3 = (1, 2, 3)(4, 5, 6) \cdots (28, 29, 30)$, $s_7 = (1, \dots, 7)(8, \dots, 14) \cdots (22, \dots, 28)(29, 30)$, $s_{10} = (1, \dots, 10) \cdots (21, \dots, 30)$ and $s_{30} = (1, \dots, 30)$.

Threshold networks

$$x'_i = H\left(\sum_{j=1}^n w_{ij}x_j - b_i\right) \text{ for } 1 \leq i \leq n \quad x \in \{0,1\}^n$$

$W = (w_{ij})$ the weight integral matrix

$b = (b_i)$ the threshold vector

$$H(u) = \begin{cases} 1 & \text{if } u \geq 0 \\ 0 & \text{otherwise} \end{cases}$$

E.G and G. Ruz, Dynamics of Neural Networks over undirected graphs,
Neural Networks, Vol 63, 156-169, 2015

For arbitrary matrices W previous model may accept,
Iterated in parallel or sequentially, long period cycles
and transients ...

But when W is symmetric the network converges to
fixed point or two periodic cycles (parallel update),

And, if $\text{diag}(W) \geq 0$ to fixed point (sequential update).

E.G, J. Olivos, Periodic behaviour of generalized threshold functions,
Discrete mathematics, vol 30, pp 187-189, 1980.

E.G., Fixed Point behavior of threshold functions on a finite set, SIAM Journal on
Alg. And Discrete Methods, vol 3(4), pp 2554-2558, 1982.

Further for W symmetric the network admits an energy:

Parallel update:

$$E(x(t)) = -\sum_{i=1}^n x_i(t) \sum_{j=1}^n w_{ij} x_j(t-1) + \sum_{i=1}^n b_i (x_i(t) + x_i(t-1))$$

If $\text{diag}(W) \geq 0$, Sequential update:

$$E(x) = -\frac{1}{2} \sum_{i=1}^n \sum_{j=1}^n w_{ij} x_i x_j + \sum_{i=1}^n b_i x_i$$

Which implies that:

1) for the parallel updating the attractors are only Fixed points or two cycles.

2) For the sequential updating and $\text{diag}(W) \geq 0$ there are only fixed points.

3) In both situations transients are bounded by $\alpha ||W|| ||x|| ||b||$

$$x' \neq x$$

$$\Delta E = E(x(t)) - E(x(t-1)) < 0 \quad \text{if and only if} \quad x(t) \neq x(t-2)$$

And for the sequential iteration

$$\Delta E = E(x') - E(x) < 0 \quad \text{iff} \quad x' \neq x$$

The most general dynamical result about Threshold networks:

Consider the block-sequential scheme $s = \{I_1, \dots, I_p\}$

The symmetrical threshold network $T = (W, b, s)$

Let $W(I_k)$ the sub-matrix associated to the k -th block

If for every $k \in \{1, \dots, p\}$ $W(I_k)$ is non-negative-definite

The network converges to fixed points

E. G., F. Fogelman-Soulie, D. Pellegrin, Decreasing energy functions as a tool

For studying threshold networks, Discrete Applied Mathematics, vol 12, pp261-277, 1985.

Sketch of the proof:

The update of the k-th block:

$$x' = (x_{I_1}, \dots, x_{I_{k-1}}, x'_{I_k}, x_{I_{k+1}}, \dots, x_{I_p})$$

$$\Delta E = - \sum_{i \in I_k} (x'_i - x_i) \left(\sum_{j=1}^n w_{ij} x_j - b_i \right) - \frac{1}{2} \sum_{i \in I_k} (x'_i - x_i) \sum_{i \in I_k} (x'_i - x_i)$$

$$\Delta E = \sum_{i \in I_k} \delta_i - \frac{1}{2} y^t W(I_k) y - \frac{1}{2} y^t W(I_k) y \quad \text{where} \quad y = (x' - x) \in \{-1, 0, 1\}^n$$

$$\delta_i = -(x'_i - x_i) \left(\sum_{j=1}^n w_{ij} x_j - b_i \right)$$

Since $W(I)$ is non-negative definite $-\frac{1}{2} y^t W y \leq 0$

and $x' \neq x \Rightarrow$ there exists $i \in \{1, \dots, n\}$ such that $\delta_i \leq -\frac{1}{2}$

(since W is an integral matrix)

Then

$$\Delta E < 0$$

We will suppose now that every matrix W is the incidence matrix of an undirected graph $G=(V,E)$, so their entries belong to the set $\{0,1\}$

$W=W(G)= (w_{ij})$ eventually with loops $(w_{ii} = 1)$

Consider the quantity:

$$\alpha(G) = -n - k + 2m - 4p$$

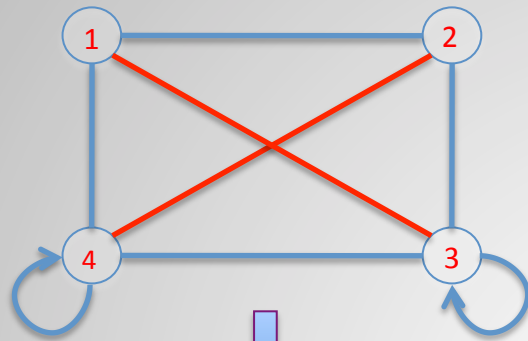
$n = |V|,$

$m = |E|,$ (without loops)

$K =$ the number of loops,

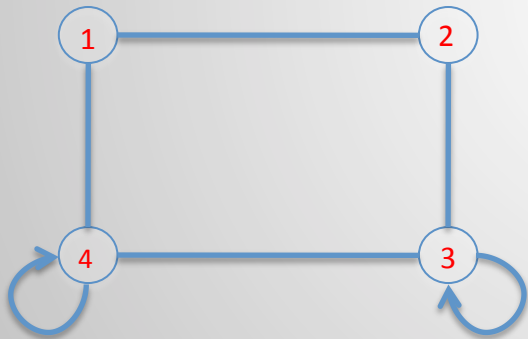
$p =$ the minimum number of edges to remove
such that the sub-graph is bipartite.

Example



$$|V| = 4 \quad k = 2$$

$$|E| = 6 \quad p = 2$$



Maximum bipartite sub-graph

$$\alpha(G) = -4 - 2 + 2 \times 6 - 4 \times 2 = -2 < 0$$

Theorem-1

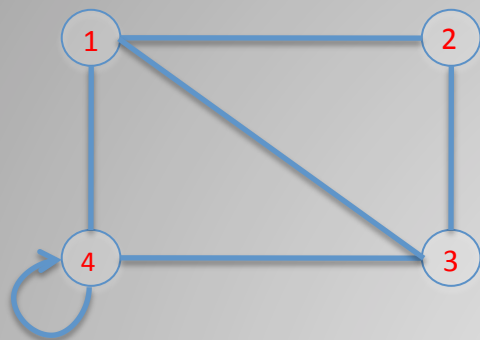
Consider an undirected graph $G=(V,E)$, $W=W(G)$, b a threshold vector.

and the network updated in **parallel**, $N= (W, b, \{1, \dots, n\})$

$\alpha(G') < 0$ For any G' sub-graph of G (by deleting vertices) $\Rightarrow$ Fixed points for any threshold vector

$\alpha(G') \geq 0 \Rightarrow$

There exists a threshold vector such that two cycles appears



$$f_1(x) = H(x_2 + x_1 + x_4 - \frac{3}{2})$$

$$f_2(x) = H(x_1 + x_2 + x_3 - \frac{3}{2})$$

$$f_3(x) = H(x_2 + x_3 + x_4 - \frac{3}{2})$$

$$f_4(x) = H(x_1 + x_4 + x_3 - \frac{3}{2})$$

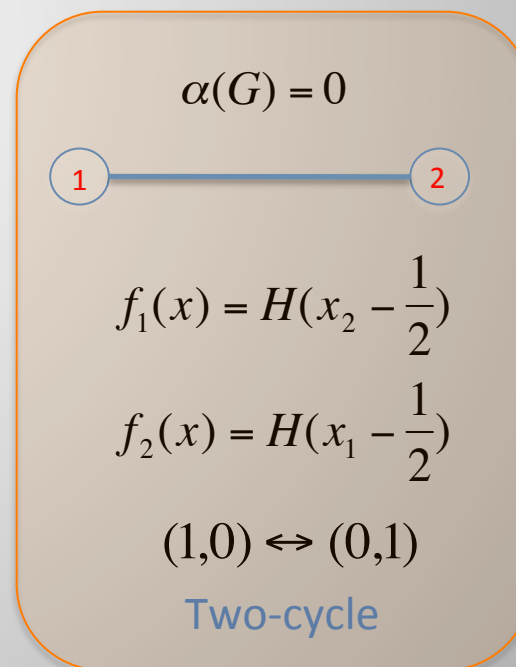
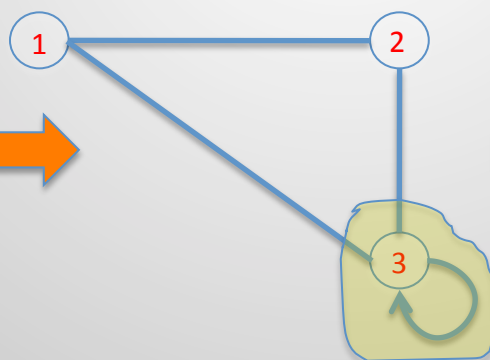
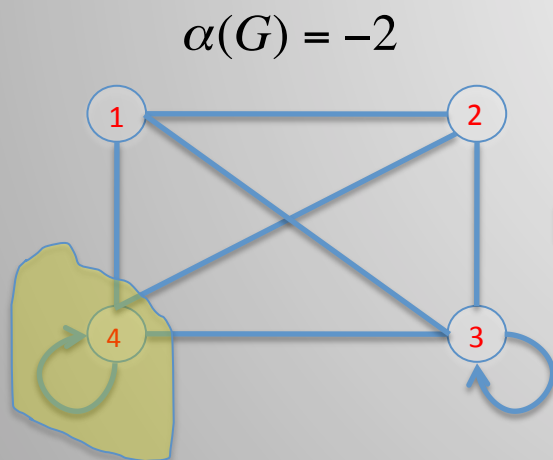
$\Rightarrow$

Two-cycle

$$(x_1, x_2, x_3, x_4) = (1, 0, 1, 0) \leftrightarrow (0, 1, 0, 1)$$

$$\alpha(G) = -4 - 1 + 2 \times 5 - 4 = 1 \geq 0 \quad \text{So there exists a two-cycle.}$$

There exists a strict sub-graph with $\alpha(G) \geq 0$



Parallel updating on two families of graphs

Bipartite graphs ($k=0$)
with n loops
($\text{diag}(W)=(1,\dots,1)$)



$$\alpha(G) = -2n + 2m$$

If G is a forest) then $n > m$
(with loops)



Only fixed points

Complete graphs with n loops

In this situation, the minimum number of edges to remove to obtain a bipartite graph

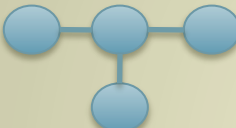
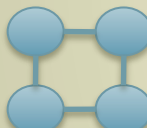
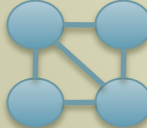
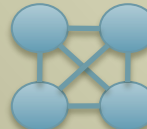
$$p = 2q(q-1) \quad \text{for } n=2q$$

$$p = 2q^2 \quad \text{for } n=2q+1$$

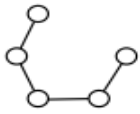
$$\alpha(K_n) < 0 \Rightarrow$$

Complete graphs updated in
Parallel converges to fixed points

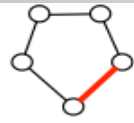
Parallel Updating

n=4	Fixed points	Two-Cycles
	$3 \leq k \leq 4$	$0 \leq k \leq 2$
	$1 \leq k \leq 4$	$k=0$
	$\emptyset$	$0 \leq k \leq 4$
	$3 \leq k \leq 4$	$0 \leq k \leq 2$
	$1 \leq k \leq 4$	$k=0$

k=number
of loops



$$(a) p = 0 \implies -5 + 4 < 0$$



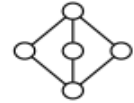
$$(b) p = 1 \implies -5 + 5 - 2 < 0$$



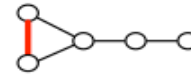
$$(c) p = 0 \implies -5 + 4 < 0$$



$$(d) p = 0 \implies -5 + 5 = 0$$



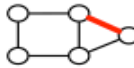
$$(e) p = 0 \implies -5 + 6 > 0$$



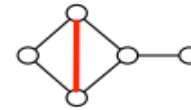
$$(f) p = 1 \implies -5 + 5 - 2 < 0$$



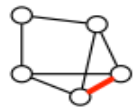
$$(g) p = 1 \implies -5 + 5 - 2 < 0$$



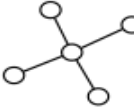
$$(h) p = 1 \implies -5 + 6 - 2 < 0$$



$$(i) p = 1 \implies -5 + 6 - 2 < 0$$



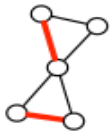
$$(j) p = 1 \implies -5 + 7 - 2 = 0$$



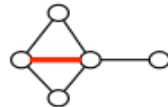
$$(k) p = 0 \implies -5 + 4 < 0$$



$$(l) p = 1 \implies -5 + 5 - 2 < 0$$



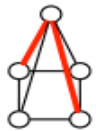
$$(m) p = 2 \implies -5 + 6 - 4 < 0$$



$$(n) p = 1 \implies -5 + 6 - 2 < 0$$



$$(o) p = 2 \implies -5 + 7 - 4 < 0$$



$$(p) p = 2 \implies -5 + 8 - 4 < 0$$



$$(q) p = 2 \implies -5 + 7 - 4 < 0$$



$$(r) p = 2 \implies -5 + 7 - 4 < 0$$



$$(s) p = 3 \implies -5 + 8 - 6 < 0$$



$$(t) p = 3 \implies -5 + 9 - 6 < 0$$

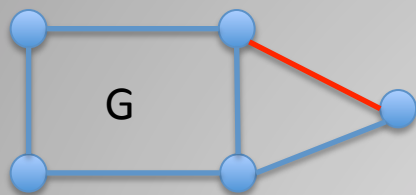


$$(u) p = 4 \implies -5 + 10 - 8 < 0$$

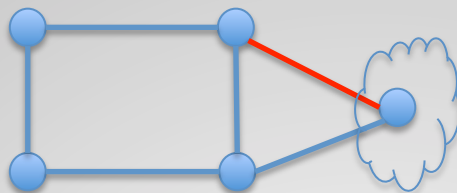
Connected
graphs for
 $n=5$ with 5
loops.

$$\frac{\alpha(G)}{2} = -n + m - 2p$$

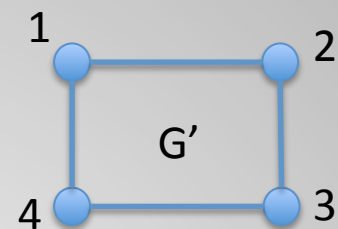
In red the edges to be
removed for a maximum
bipartite graphs



$$\alpha(G) = -5 - 5 + 2x6 - 4 = -2$$



(delete)



$$\alpha(G) = -5 - 5 + 2x6 - 4 = -2$$

(Each vertex has a loop)

$(1,0,1,0) \longleftrightarrow (0,1,1,0)$

Two-cycle

$$f_1(x) = H(x_2 + x_1 + x_4 - \frac{3}{2})$$

$$f_2(x) = H(x_1 + x_2 + x_3 - \frac{3}{2})$$

$$f_3(x) = H(x_2 + x_3 + x_4 - \frac{3}{2})$$

$$f_4(x) = H(x_1 + x_4 + x_3 - \frac{3}{2})$$

Theorem-II: attractors for every block-sequential update.

Consider the block-sequential scheme $s = \{I_1, \dots, I_p\}$

The symmetrical threshold network $T=(W, b, s)$

Let $G(I_k)$ the graph associated to the k-th block

$\forall k \in \{1, \dots, p\} \quad \alpha(G') < 0 \quad \forall G' \subseteq G(I_k) \Rightarrow$

fixed points

$\exists k \in \{1, \dots, p\}$ and $G' \subseteq G(I_k)$ such that $\alpha(G') \geq 0 \Rightarrow$

cycles

Corollary

No more than three sites at each block

Consider an undirected graph $G=(V,E)$ with every loop and the

the block-sequential scheme $s = \{I_1, \dots, I_p\}$

$\forall k \in \{1, \dots, p\} \quad |I_k| \leq 3 \Rightarrow$

Fixed points

Otherwise, there exists graphs and threshold vectors such that cycles appear

Sketch of the proof:

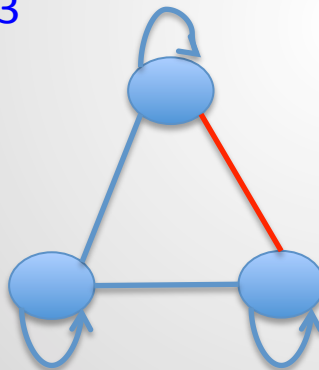
Partition size = 1 directly from the fact that $\text{diag}(W) \geq 0$

Partition size = 2

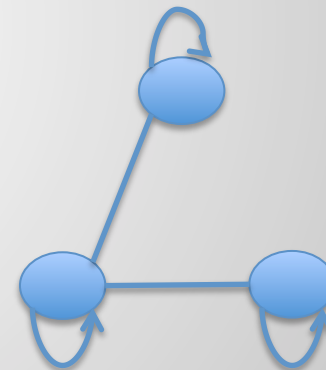


$$\alpha(G) = -2$$

Partition size = 3

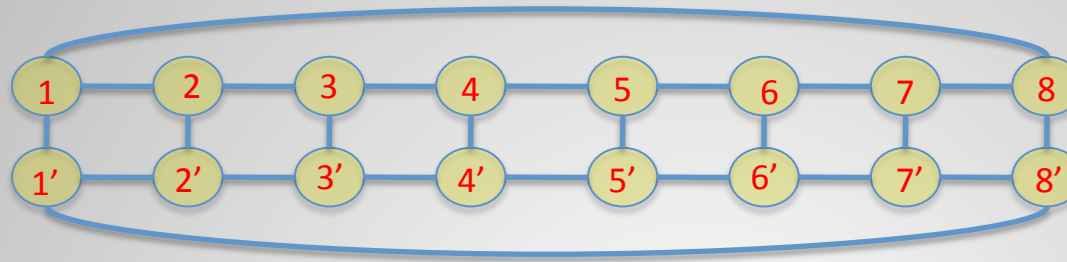


$$\alpha(G) = -4$$

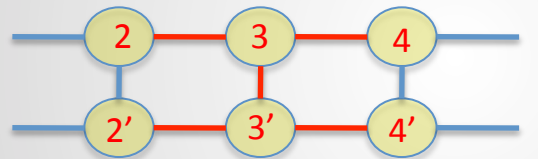


$$\alpha(G) = -2$$

Non-Polynomial Cycles



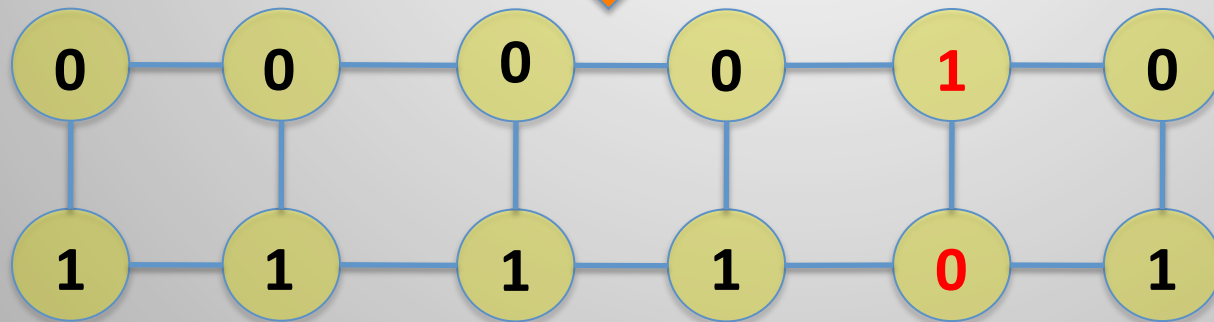
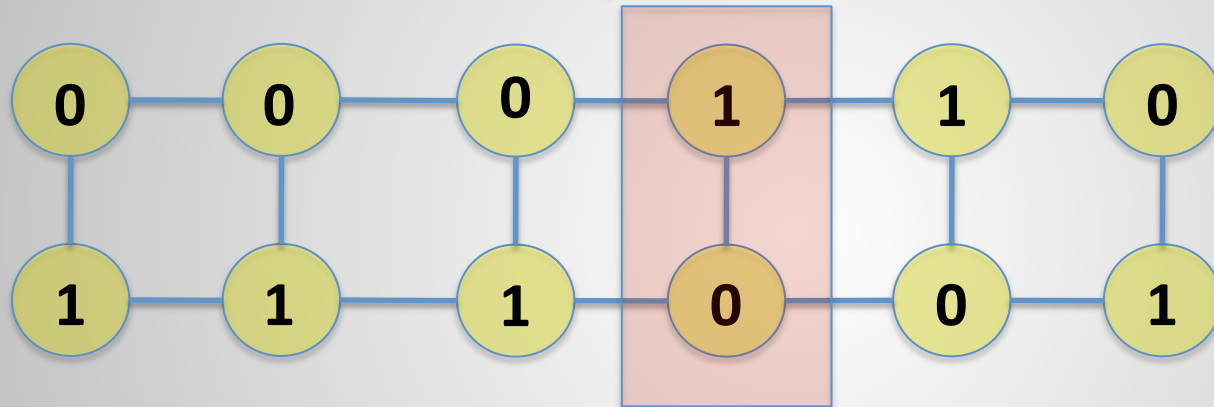
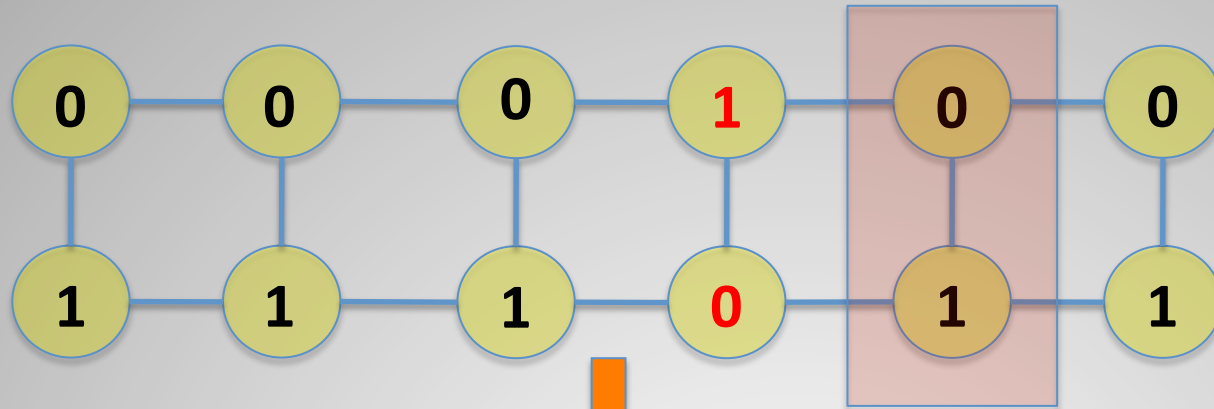
staircase



Local majority at
each vertex

$$f_3(x) = H(x_2 + x_{3'} + x_4 - \frac{3}{2})$$

$$f_{3'}(x) = H(x_{2'} + x_3 + x_{4'} - \frac{3}{2})$$



Local Majority



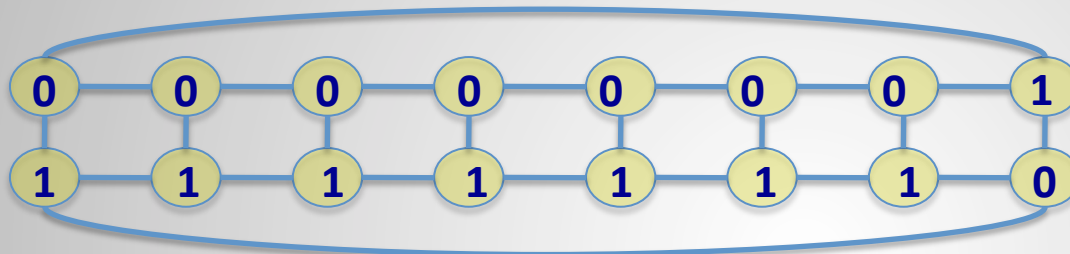
= Updated vertices



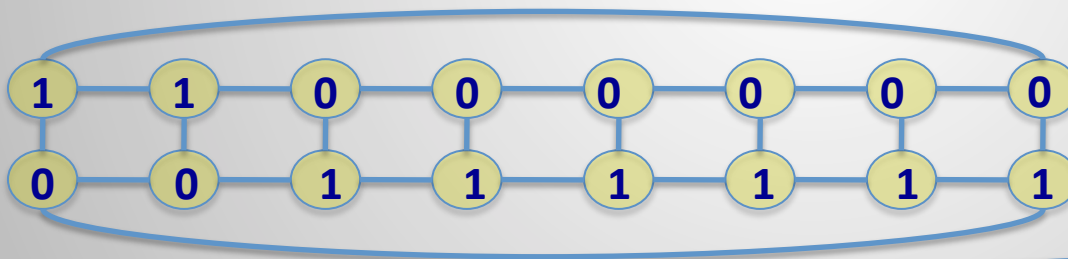
Travel to
The right

Block-Sequential updating

$$\tau = \{\{1,1'\},\{n,n'\},\{n-1,(n-1)'\},\dots,\{3,3'\},\{2,2'\}\}$$

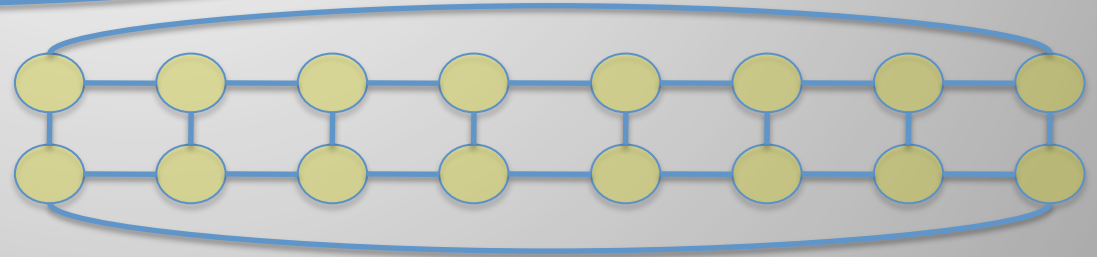


$X(0)$



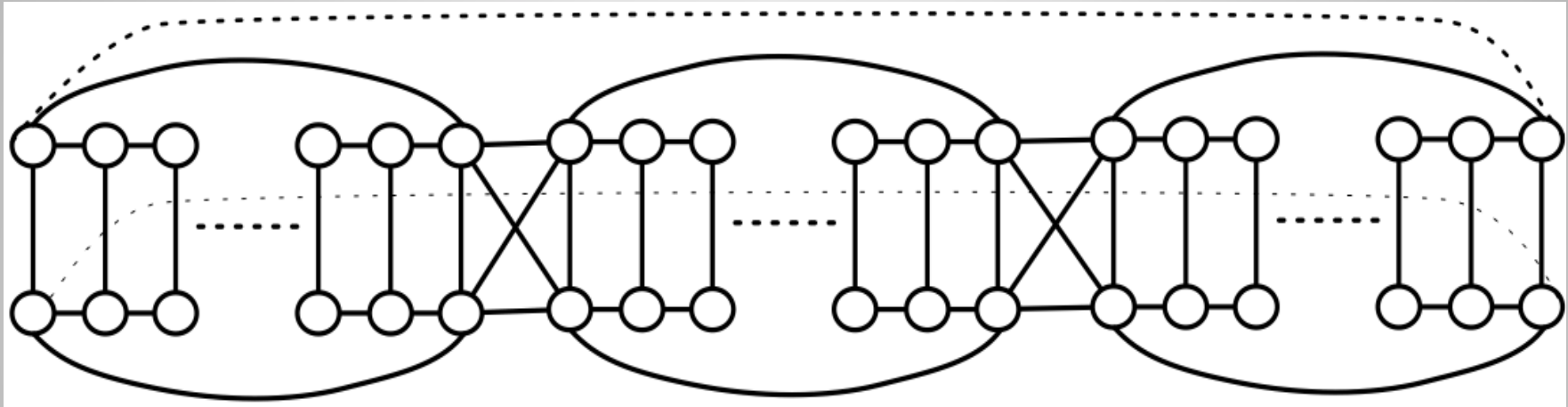
$X(1)$

Cycle of period $T=n-1$



Union of the first l prime number's staircases of size

$$p_1 + 1 = 3; p_2 + 1 = 4; p_3 + 1 = 6, p_4 + 1 = 8, \dots, p_l + 1$$



So by considering the global partition

$$\tau = \bigcup_{k=1}^l \tau_k$$

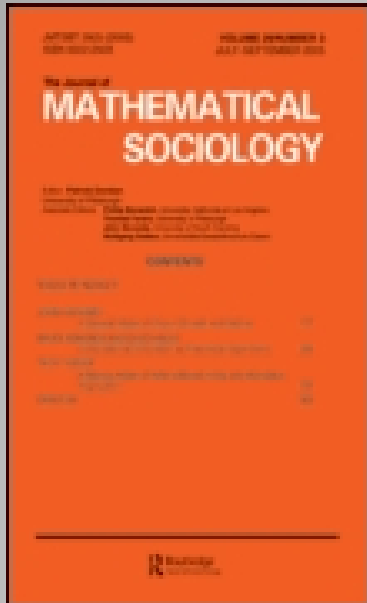
The period of the network is

$$T \geq \prod_{k=1}^l p_k = e^{\Omega(\sqrt{|V(G)| \log |V(G)|})}$$

Same arguments can be done for the transient time.

The SAKODA's model of social Interactions

Complexity2017 (Medina, E.G., R. Zarama, S. Rica)



The Journal of Mathematical Sociology

Publication details, including instructions for authors and subscription information:

<http://www.tandfonline.com/loi/gmas20>

The checkerboard model of social interaction

James M. Sakoda ^a

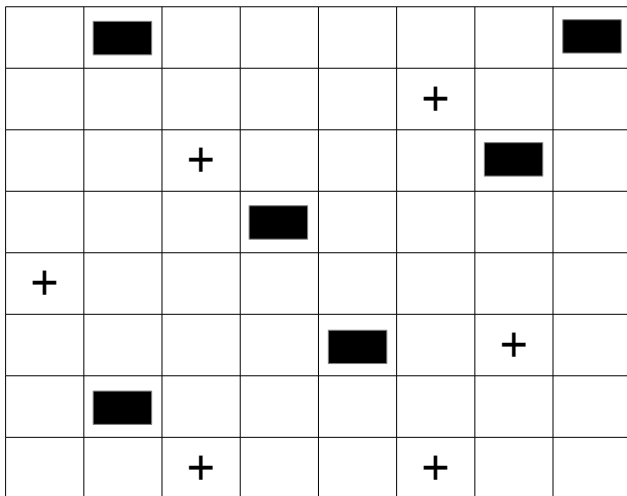
^a Brown University

Published online: 26 Aug 2010.

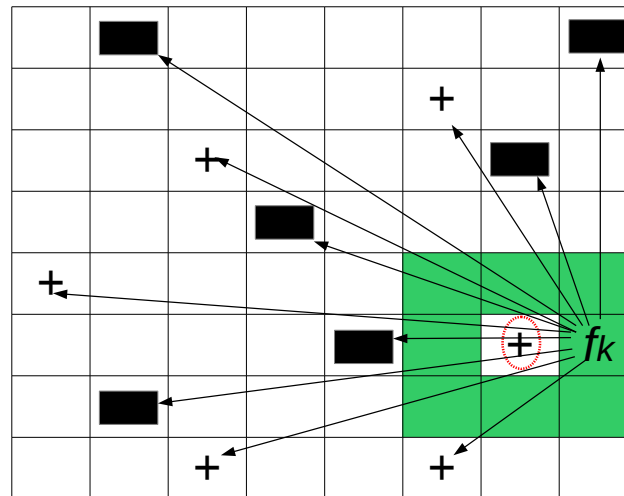
To cite this article: James M. Sakoda (1971) The checkerboard model of social interaction, The Journal of Mathematical Sociology, 1:1, 119-132, DOI: [10.1080/0022250X.1971.9989791](https://doi.org/10.1080/0022250X.1971.9989791)

To link to this article: <http://dx.doi.org/10.1080/0022250X.1971.9989791>

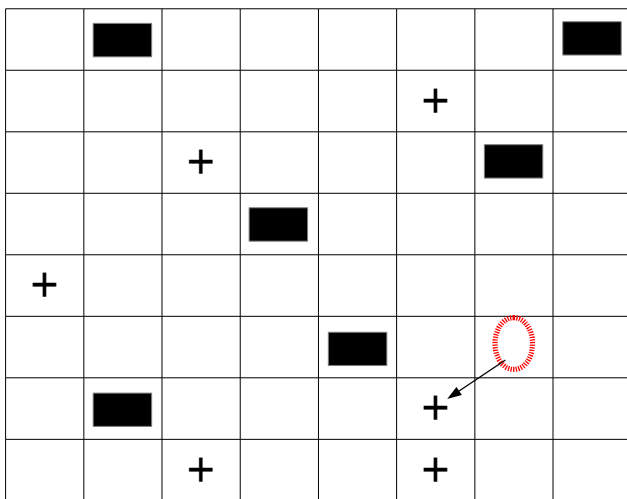
Pablo Medina PhD student , U. Andes. Bogotá, Colombia
,Sergio Rica (Físico, Universidad Adolfo Ibáñez, Santiago, Chile
Roberto Zarama , Ingeniería Industrial, Universidad de los Andes, Bogotá
EG., Matemático, Universidad Adolfo Ibáñez, Santiago, Chile.



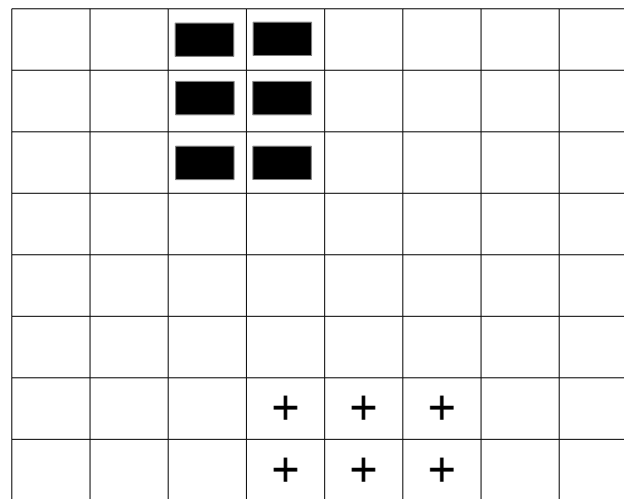
(a)



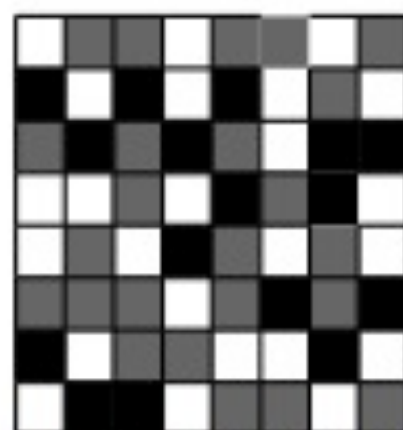
(b)



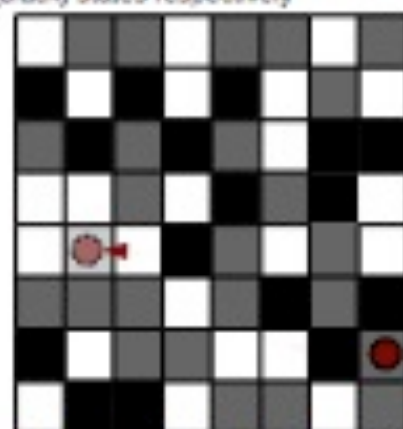
(c)



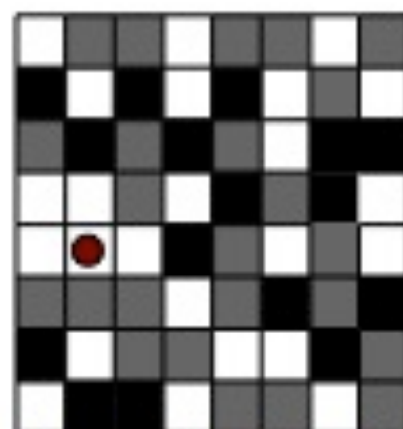
(d)



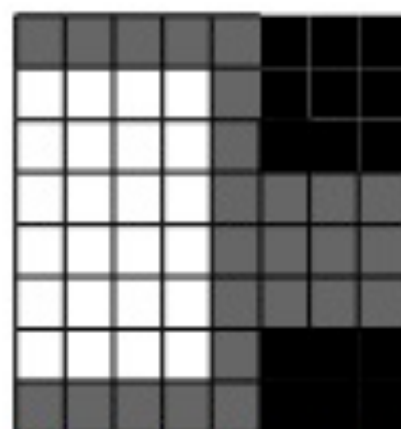
1. The simulation starts with a random configuration with a fraction ϕ_v of empty nodes (gray nodes) and fraction ϕ_{+1}, ϕ_{-1} of occupied nodes in +1 (white) and -1 (black) states respectively



2. An individual moves different empty node considering a long move (all network) or short movement (neighborhood) move and evaluate the potential f_k considering long influence or short influence



3. The individual move to the position in its neighborhood that improves the value of the potential f_k



4. The steps two and three are applied to all individuals recursively many times. The system converges to an attractor after various iterations of these steps.

Nodes and states: A node k occupied by an individual at state $x_k = +1, -1$

Fract. vaccancy and occupancy: Vaccancy ϕ_v , occupancy $1 - \phi_v$
With $1 - \phi_v = \phi_{+1} + \phi_{-1}$ and $\phi_{\pm 1}$ the fraction of states ± 1 respectively ($\phi_{+1} = \phi_{-1}$)

The S-matrix

$$S = \begin{bmatrix} s_{11} & s_{12} \\ s_{21} & s_{22} \end{bmatrix}; \quad s_{\alpha\beta} = \begin{cases} -1 & \text{repulsion between } x_k, x_j \\ 0 & \text{neutrality between } x_k, x_j \\ +1 & \text{attraction between } x_k, x_j \end{cases}$$

The potential f_k

$$f_k = \sum_j^N \delta(x_k, x_j) v(r_{kj}); \quad \delta(x_k, x_j) = \begin{cases} s_{\alpha\beta} & \text{for } x_k, x_j \neq 0 \\ 0 & \text{otherwise} \end{cases}$$

$v(r_{kj})$ A function that depends on the distance between node k and j

Sakoda's attitude matrices

$$S = \begin{matrix} & \circ(+1) & \bullet(-1) \\ \begin{matrix} \circ(+1) \\ \bullet(-1) \end{matrix} & \begin{pmatrix} s_{11} & s_{12} \\ s_{21} & s_{22} \end{pmatrix} \end{matrix}$$

-1, 0, 1 entries

There are 81 matrices. By diagonal symmetries (changing blacks and whites) only 45 different.

$$= \begin{pmatrix} \begin{pmatrix} -1 & -1 \\ -1 & -1 \end{pmatrix} & \begin{pmatrix} -1 & -1 \\ -1 & 0 \end{pmatrix} & \cdots & \begin{pmatrix} -1 & -1 \\ 1 & 1 \end{pmatrix} \\ \begin{pmatrix} 0 & -1 \\ -1 & -1 \end{pmatrix} & \begin{pmatrix} 0 & -1 \\ -1 & 0 \end{pmatrix} & \cdots & \\ \vdots & \vdots & \ddots & \vdots \\ \begin{pmatrix} 1 & 1 \\ -1 & -1 \end{pmatrix} & \begin{pmatrix} 1 & 1 \\ -1 & 0 \end{pmatrix} & \cdots & \begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix} \end{pmatrix}.$$

Fig.1 CROSSROADS .

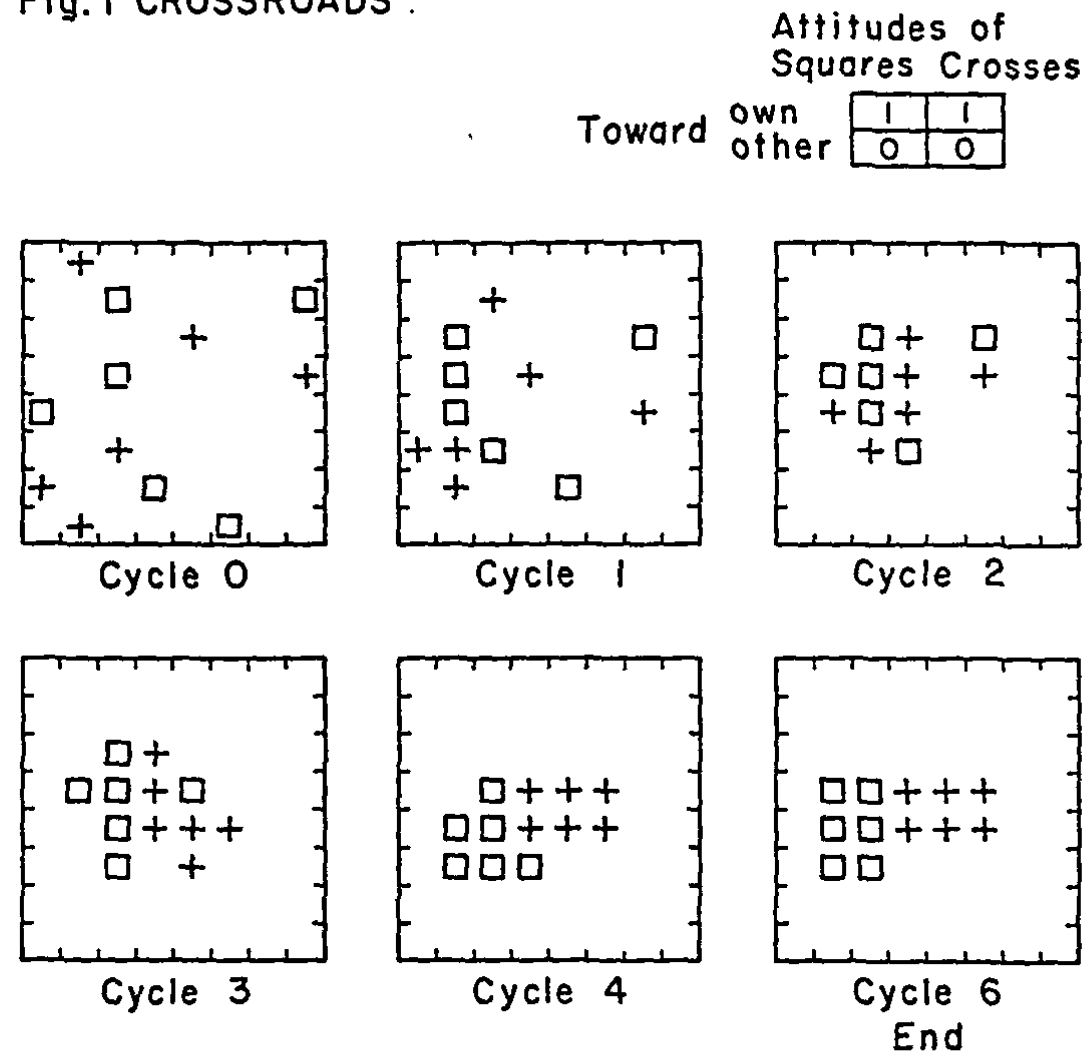


FIGURE 1 *Crossroads* (Squares: 1 to Own, 0 to Other; Crosses: 1 to Own, 0 to Other).

Fig. 2 MUTUAL SUSPICION

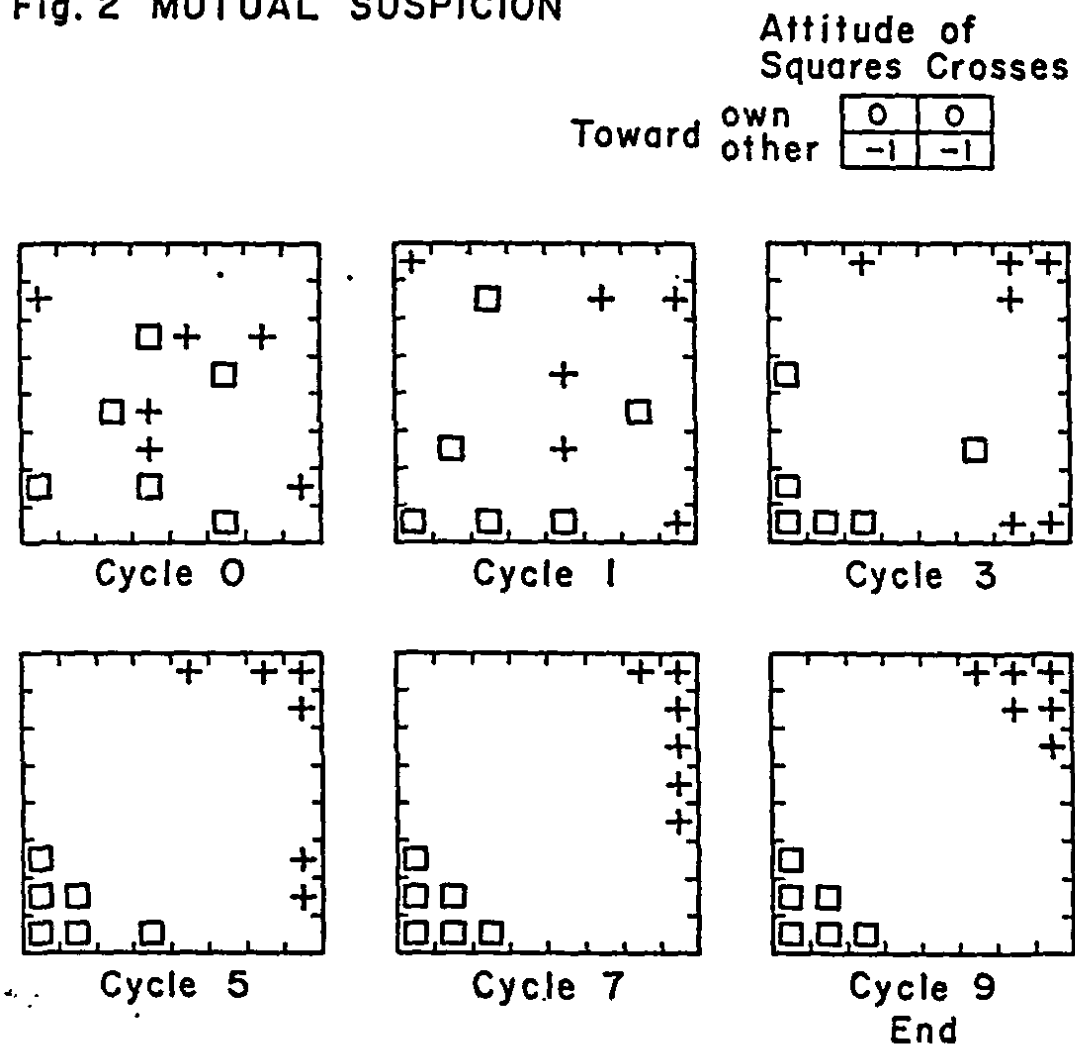


FIGURE 2 *Mutual Suspicion* (Squares: 0 to Own, -1 to Others; Crosses: 0 to Own, -1 to Others).

Fig. 3 SEGREGATION

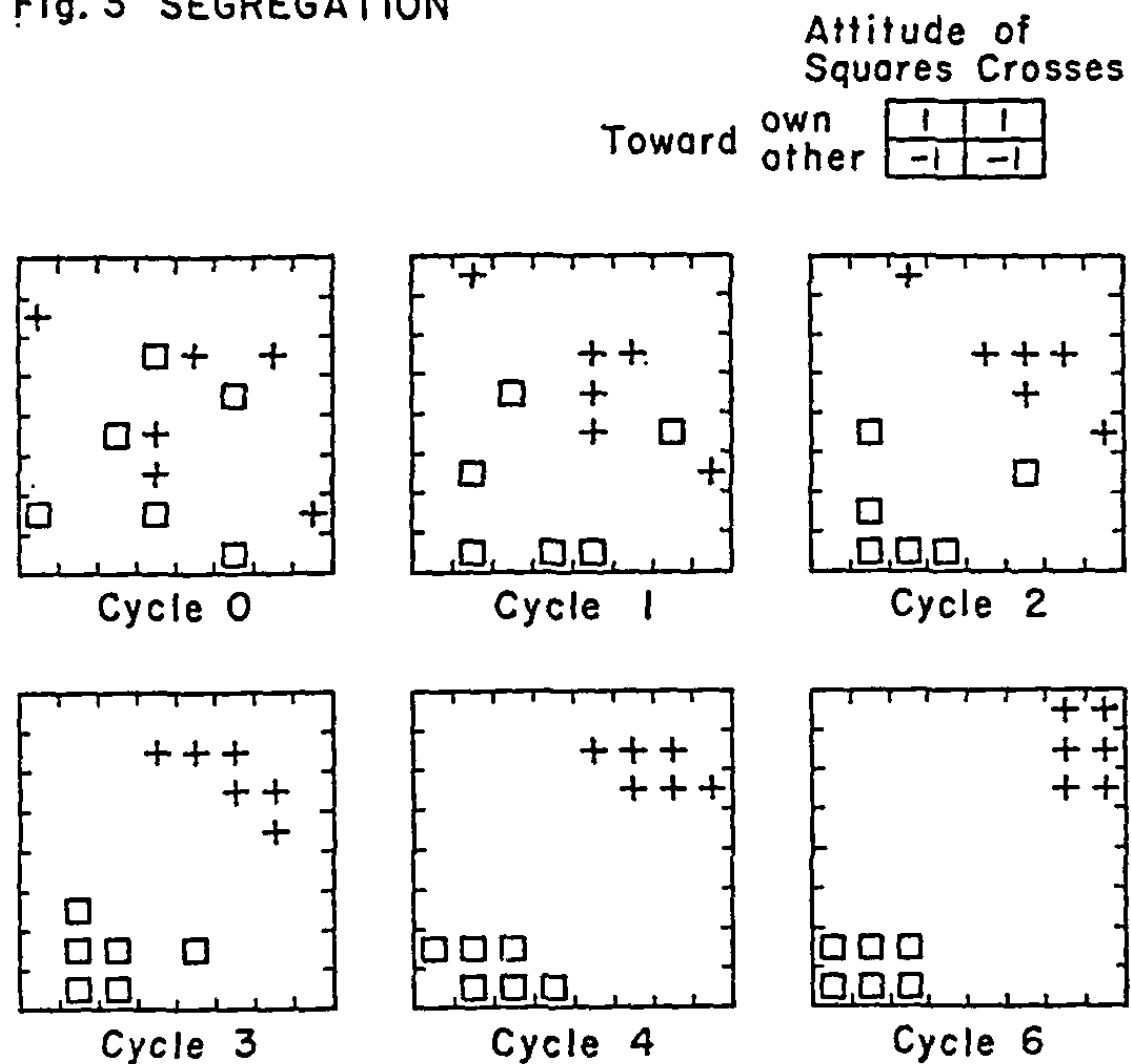
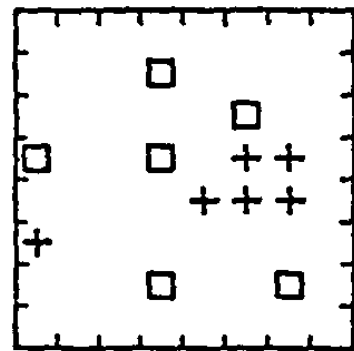


FIGURE 3 *Segregated Groups* (Squares: 1 to Own, -1 to Others, Crosses: 1 to Own, -1 to Others).

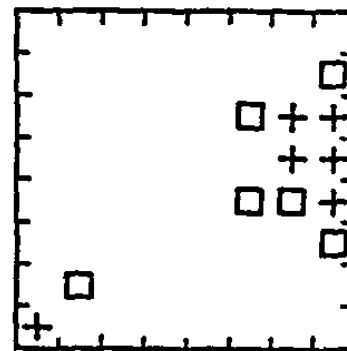
Fig.4 SOCIAL CLIMBERS

Attitude of
Squares Crosses
Toward
own other

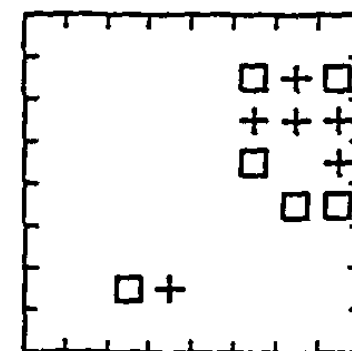
-1	1
1	-1



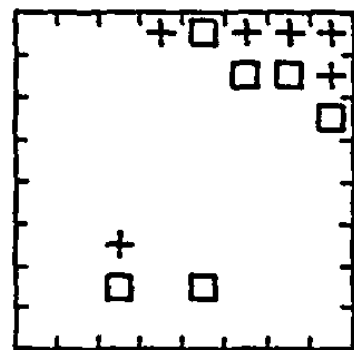
Cycle 0



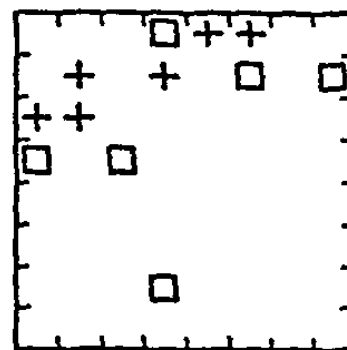
Cycle 3



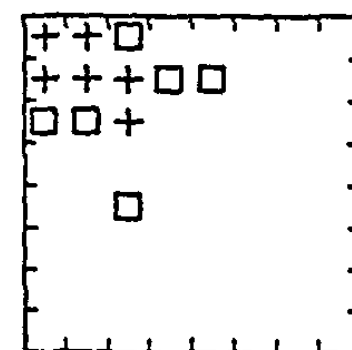
Cycle 6



Cycle 9



Cycle 12



Cycle 15

FIGURE 4 *Social Climber* (Squares: -1 to Own, 1 to Other; Crosses: 1 to Own, -1 to Other).

Fig. 5 SOCIAL WORKER

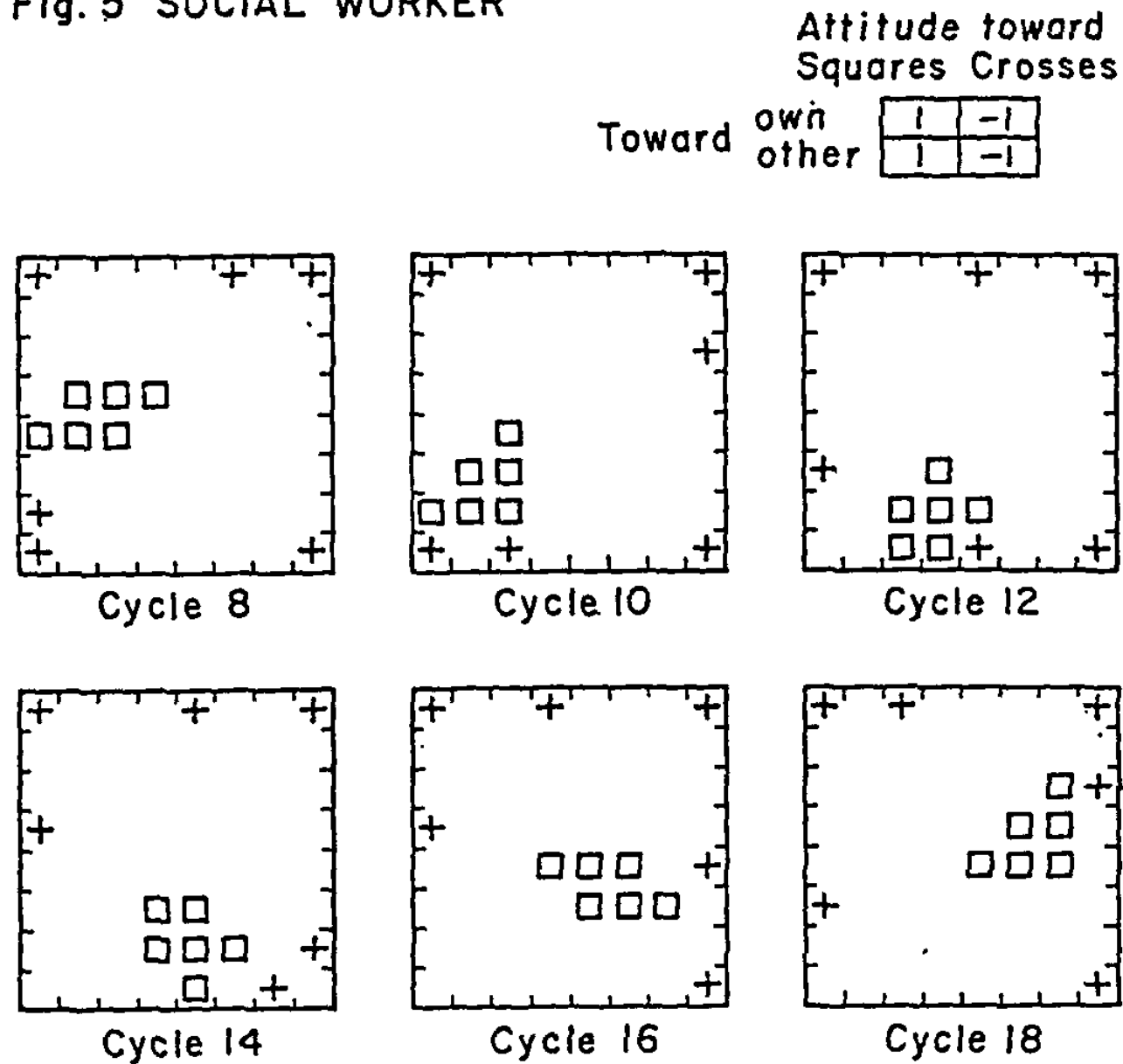


FIGURE 5 *Social Worker* (Squares: 1 to Own, 1 to Other; Crosses: -1 to Own, -1 to Other).

Fig. 6 BOY - GIRL

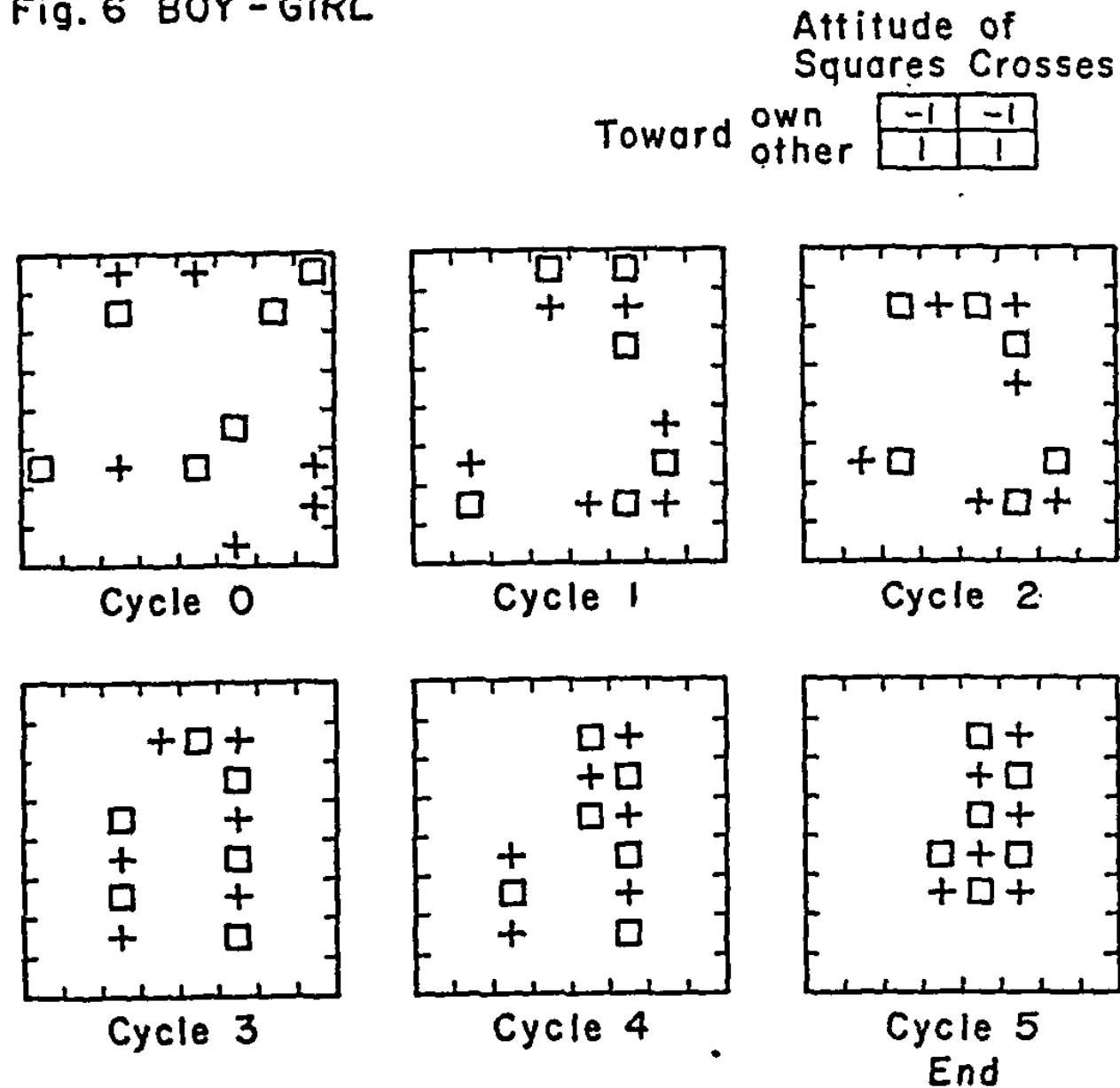


FIGURE 6 *Boy-Girl Situation* (Squares: -1 to Own, 1 to Other; Crosses: -1 to Own, 1 to Other).

The local field:

$$f_k = \sum_{j=1}^N \delta(x_k, x_j) v(r_{kj})$$

$$\delta(x_k, x_j) = \begin{cases} s_{\alpha\beta} & \text{for } x_k, x_j \neq 0 \\ 0 & \text{otherwise} \end{cases}$$

The Energy:

$$E[x] = -\frac{1}{2} \sum_k f_k = -\frac{1}{2} \sum_{k,j} \delta(x_k, x_j) v(r_{kj})$$

$$v(r_{kj}) = \frac{1}{r_{kj}^2}$$

E is decreasing when S is symmetric and (in general cases of v functions)

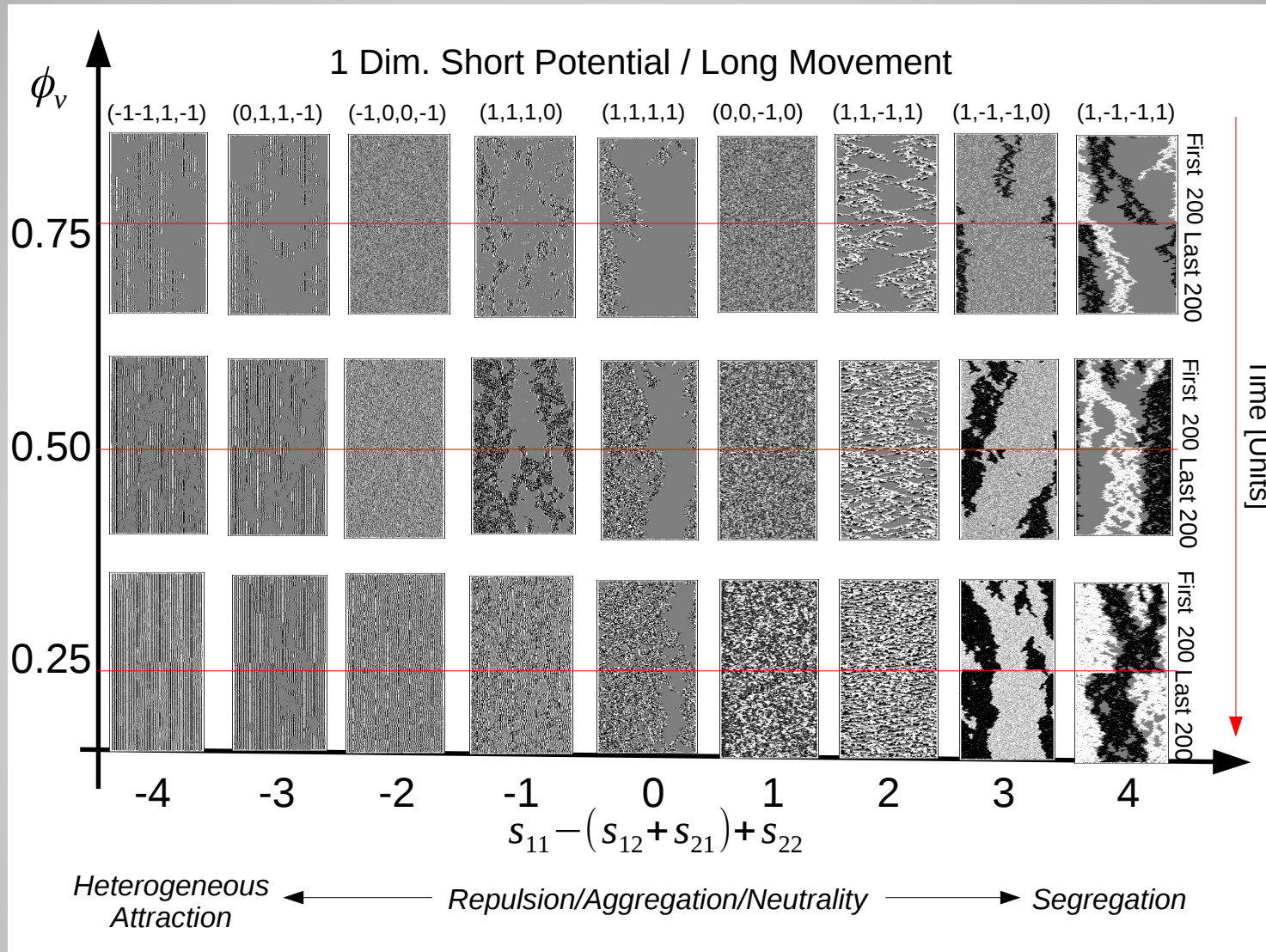


Figure 5: Phase diagram for different values of ϕ_v and χ considering Short influence potential/Long range movement in a one dimensional lattice. These attractors are the results of simulations considering 128 one dimensional lattice. The time goes from top to bottom; the red line divides between the first 200 evolution steps and the final 200 evolution steps. We consider periodic boundary conditions.

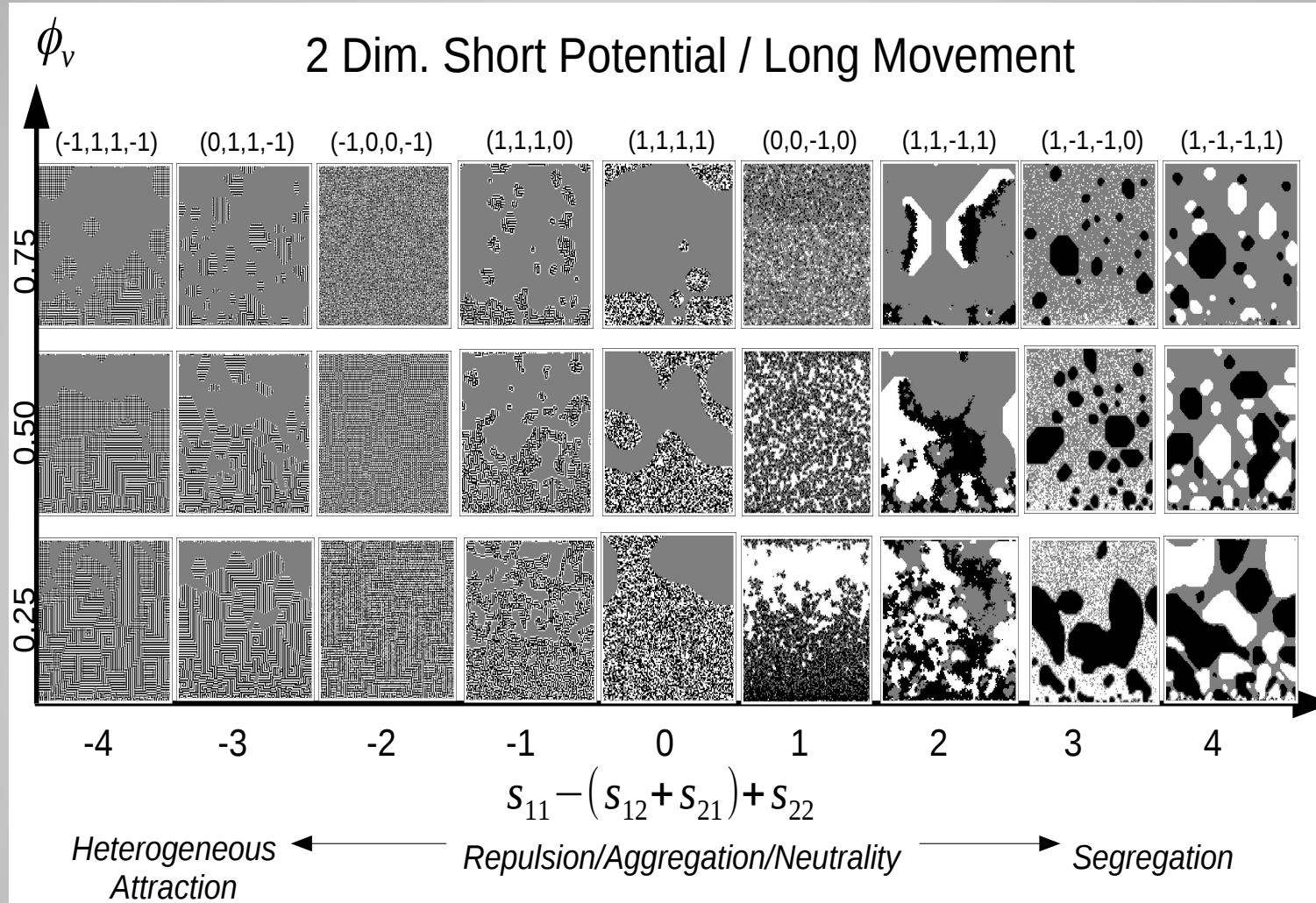
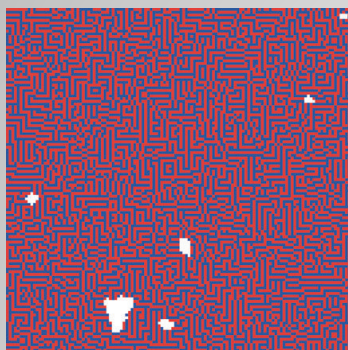
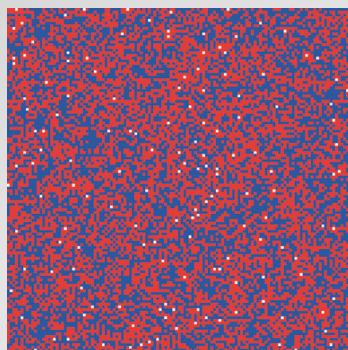


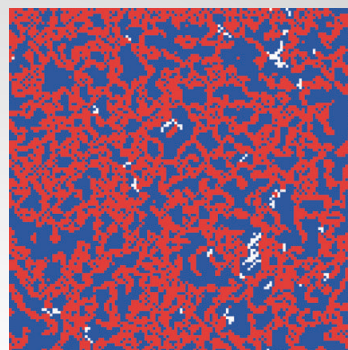
Figure 13: Different interaction types (attractors) in terms of the entries of the S -matrix in 128×128 two dimensional lattice considering Moore neighborhood and boundary periodic conditions.



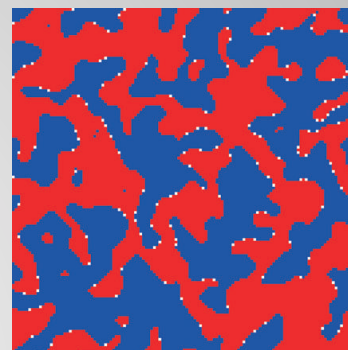
(I)



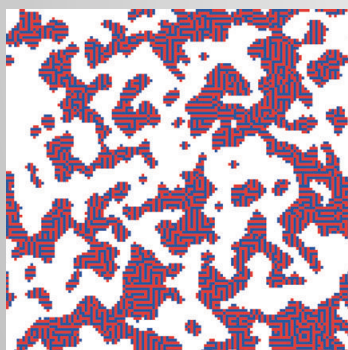
(I)



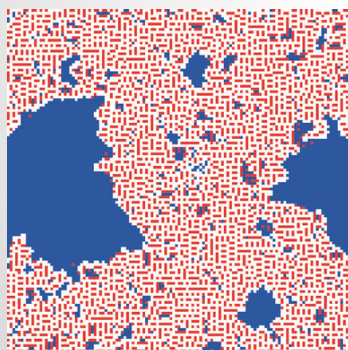
(I)



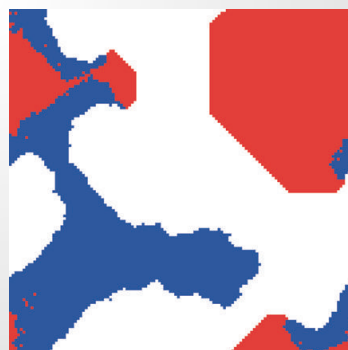
(I)



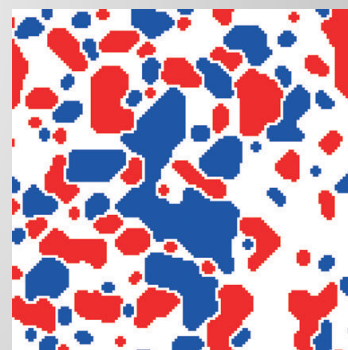
(I)



(I)



(I)



(I)

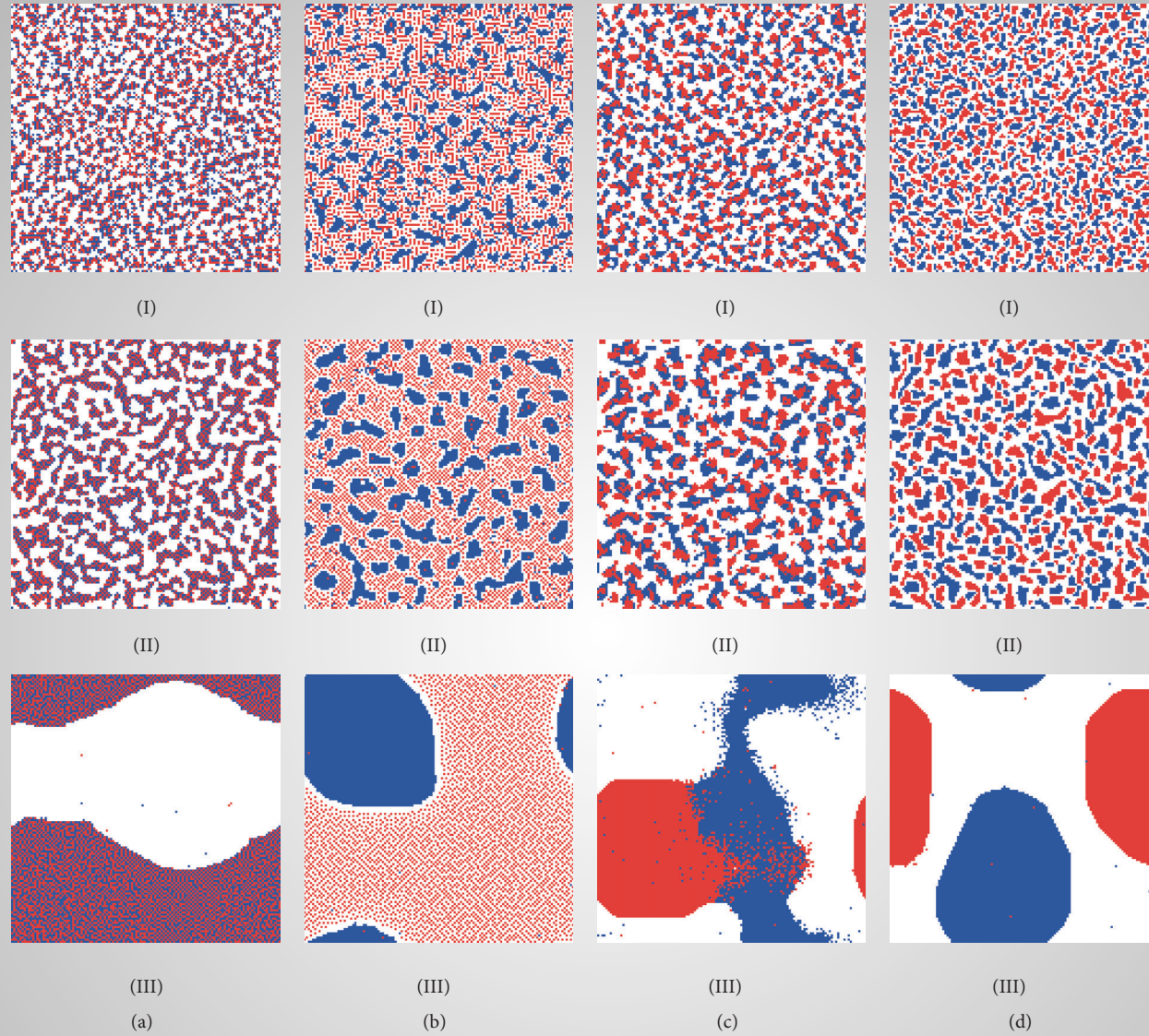


FIGURE 7: Snapshots for different interaction and movement (rest) rules for the same cases as in Figure 1. (a) $S = (0, 1, 1, 0)$, (b) $S = (1, 1, -1, -1)$, (c) $S = (1, 1, -1, 1)$, and (d) $S = (1, -1, -1, 1)$. The first line (I) corresponds to the case of short range interaction and short range movement. The second row (II) corresponds to long range interaction/short range movement, and, finally the third line (III) corresponds to the case of long range interaction and long range movement. Simulations were run in a $N = 128 \times 128$ lattice with $\phi_V = 0.5$ and for 2×10^5 steps for (I) and (II) and 5×10^4 steps for (III).

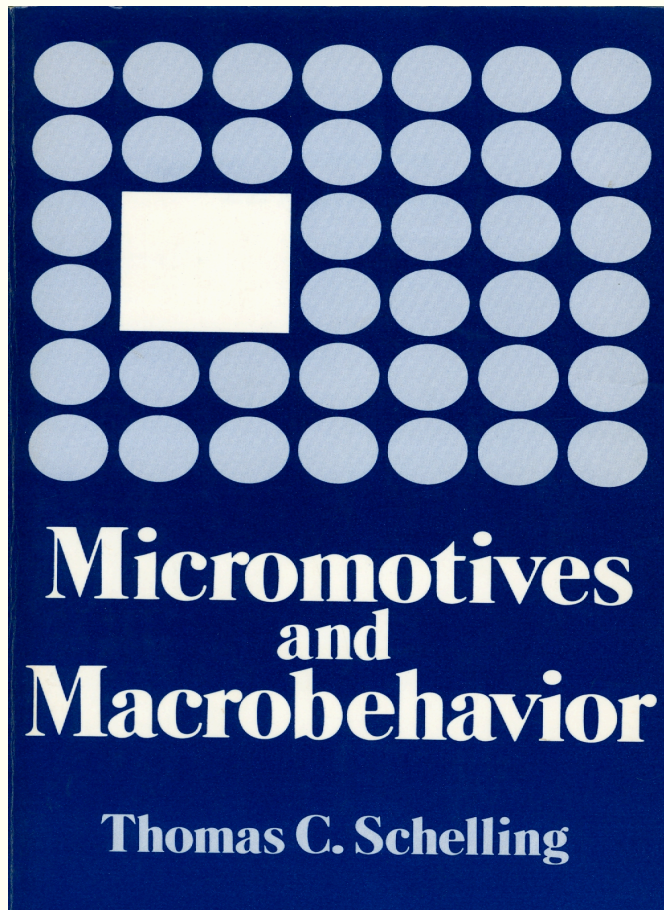
The Schelling Segregation model



(Nicolás Goles-Domic, Sergio Rica, E.G.)

PHYSICAL REVIEW E **83**, 056111 (2011)

And work in progress.



chapter 4:
Sorting and Mixing

DYNAMIC MODELS OF SEGREGATION†

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1971, Vol. 1, pp 143–186

The Model of Segregation by Shelling

Thomas C. Schelling (1969 - 1972)

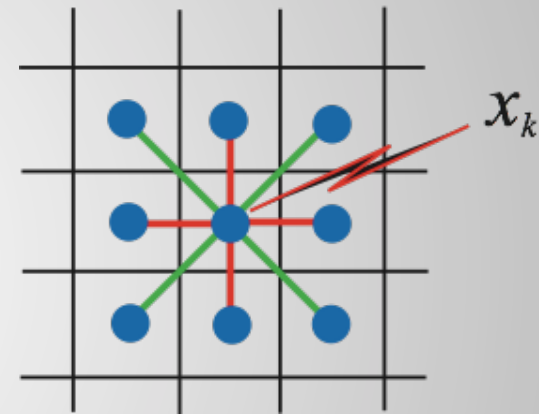
- Lattice one or two dimensional with periodic conditions

- State $x_k = \pm 1$

- Neighborhood Moore (green and red arrows) and von Neumann (red arrows)

- Tolerance threshold

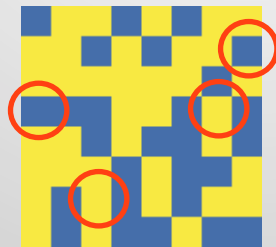
$$\theta \in \{1, \dots, |V|\}$$



Happiness threshold

An individual is unhappy if there are more than θ individuals on the other state in its neighborhood

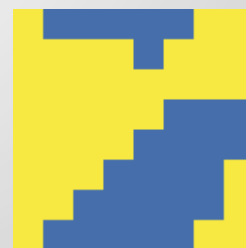
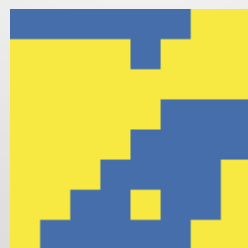
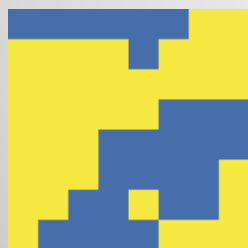
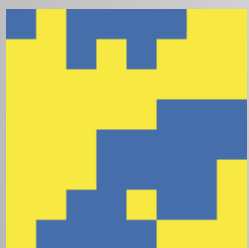
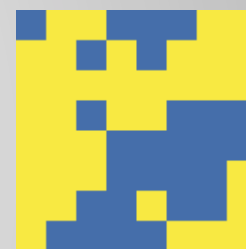
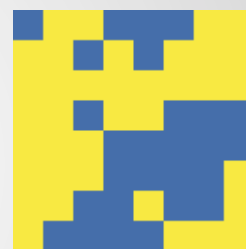
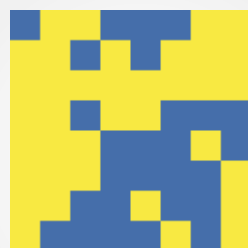
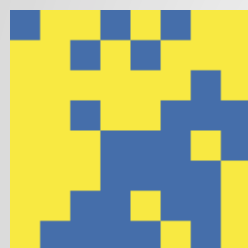
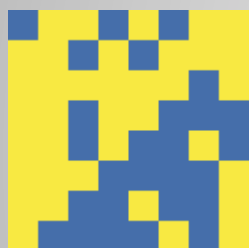
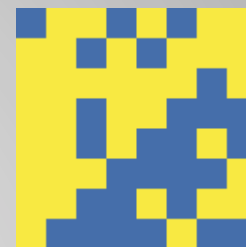
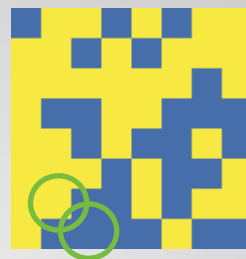
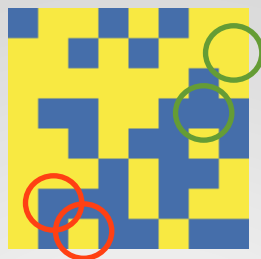
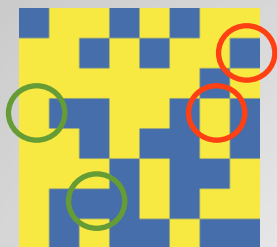
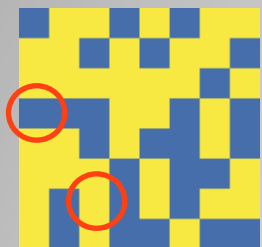
eg. For the Moore's neighborhood and $\theta = 5$ then :



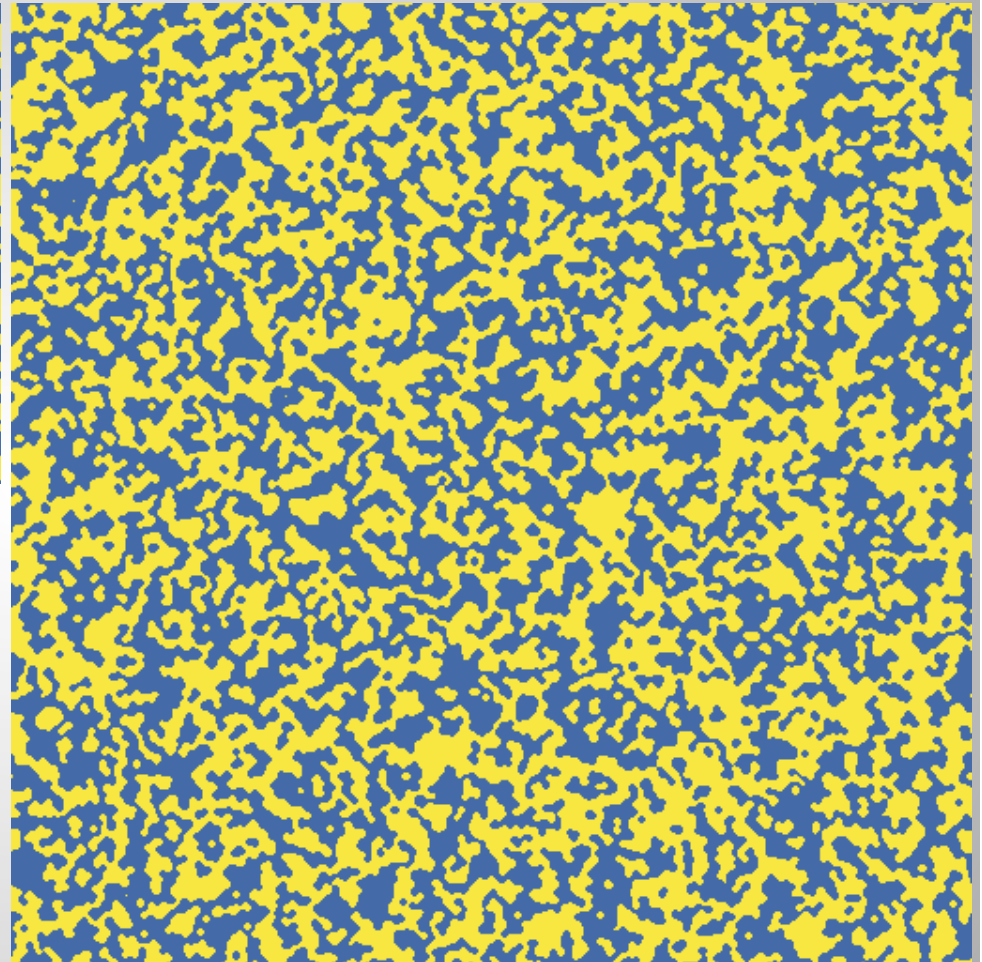
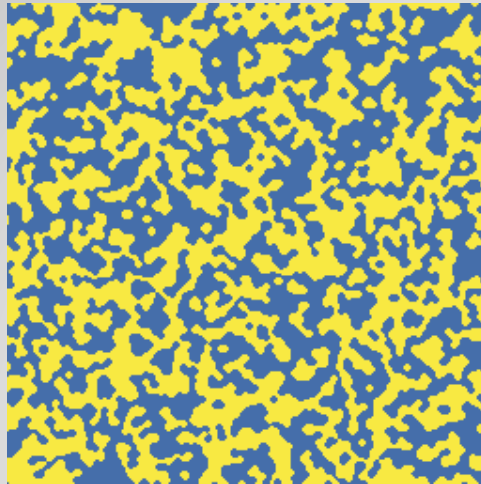
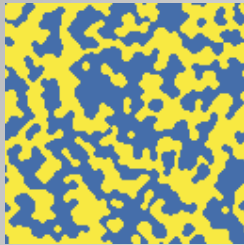
The update rule

At each step, one lists the unhappy individuals of both species, and then randomly (for instance) one exchanges two individuals of opposite value.

$$\theta = 5$$



Length scale for $\theta = 5$



32 x 32

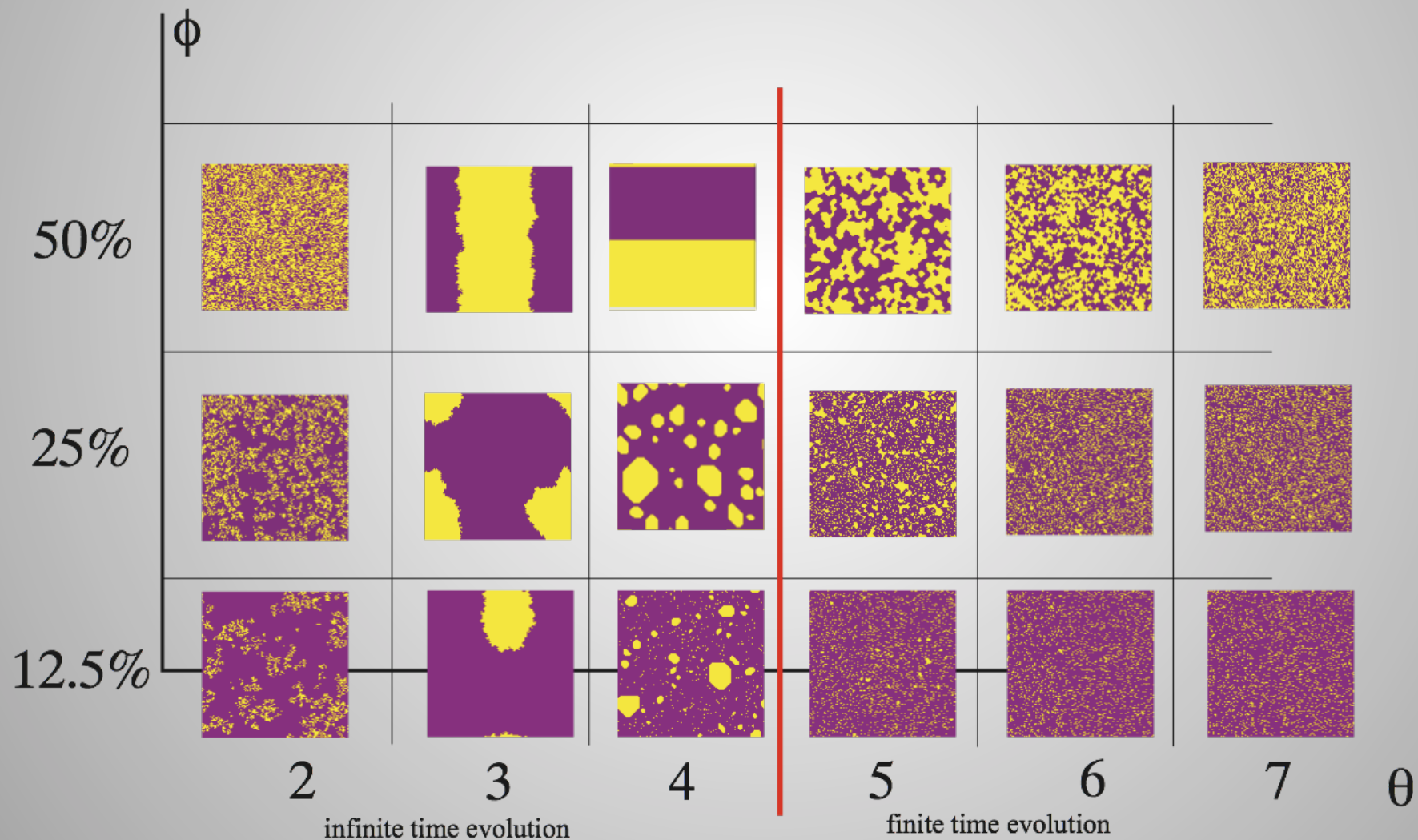
64 x 64

128 x 128

256 x 256

512 x 512

Phase diagram for Moore's neighborhood



Quantitative behavior

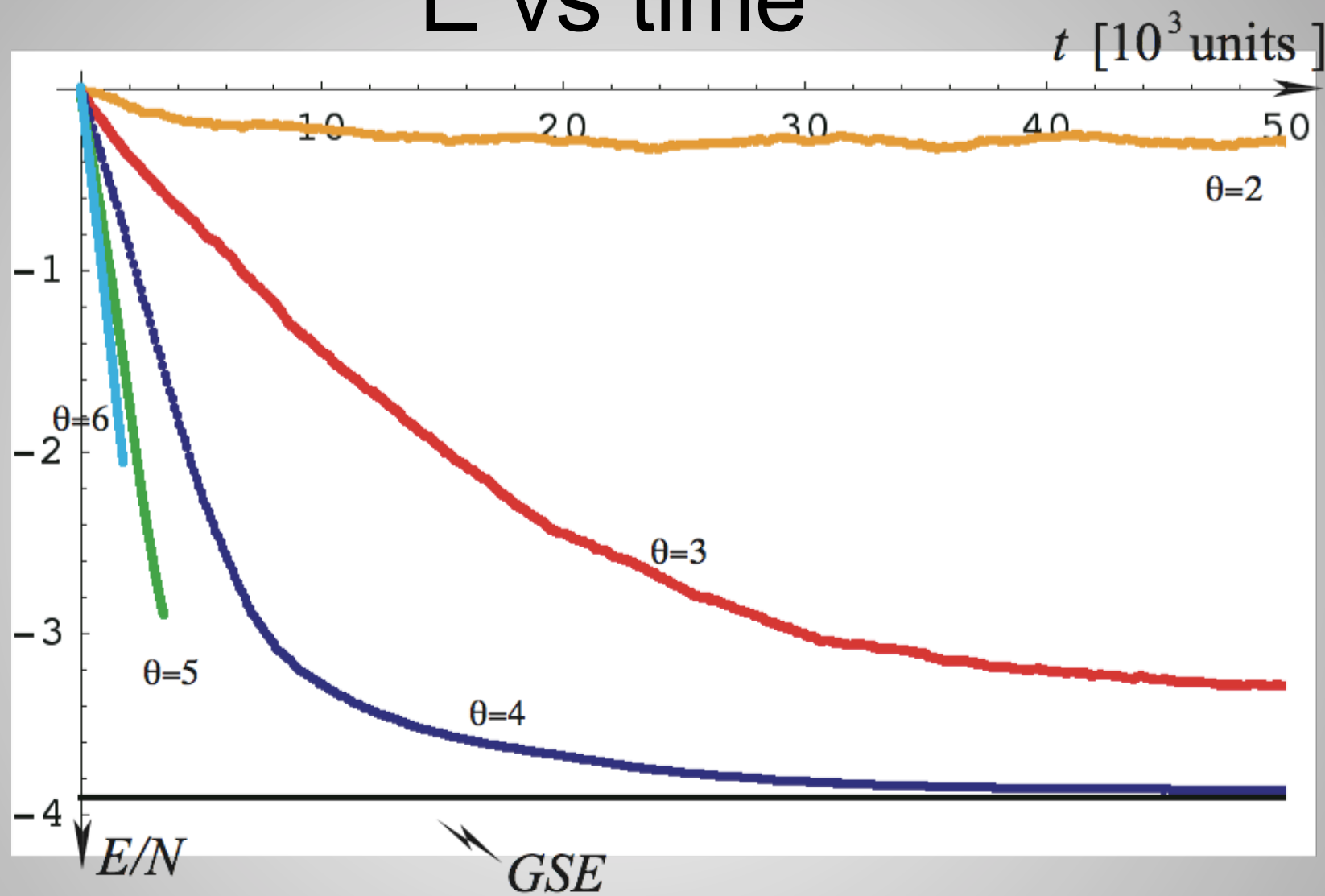
$\theta \geq 5$:the energy decreases

$$E[\{x\}] = -\frac{1}{2} \sum_{k=1}^N x_k \sum_{i \in V_k} x_i$$

In general, if V is the neighborhood, the energy decreases
If and only if

$$\theta > \frac{|V|}{2}$$

E vs time



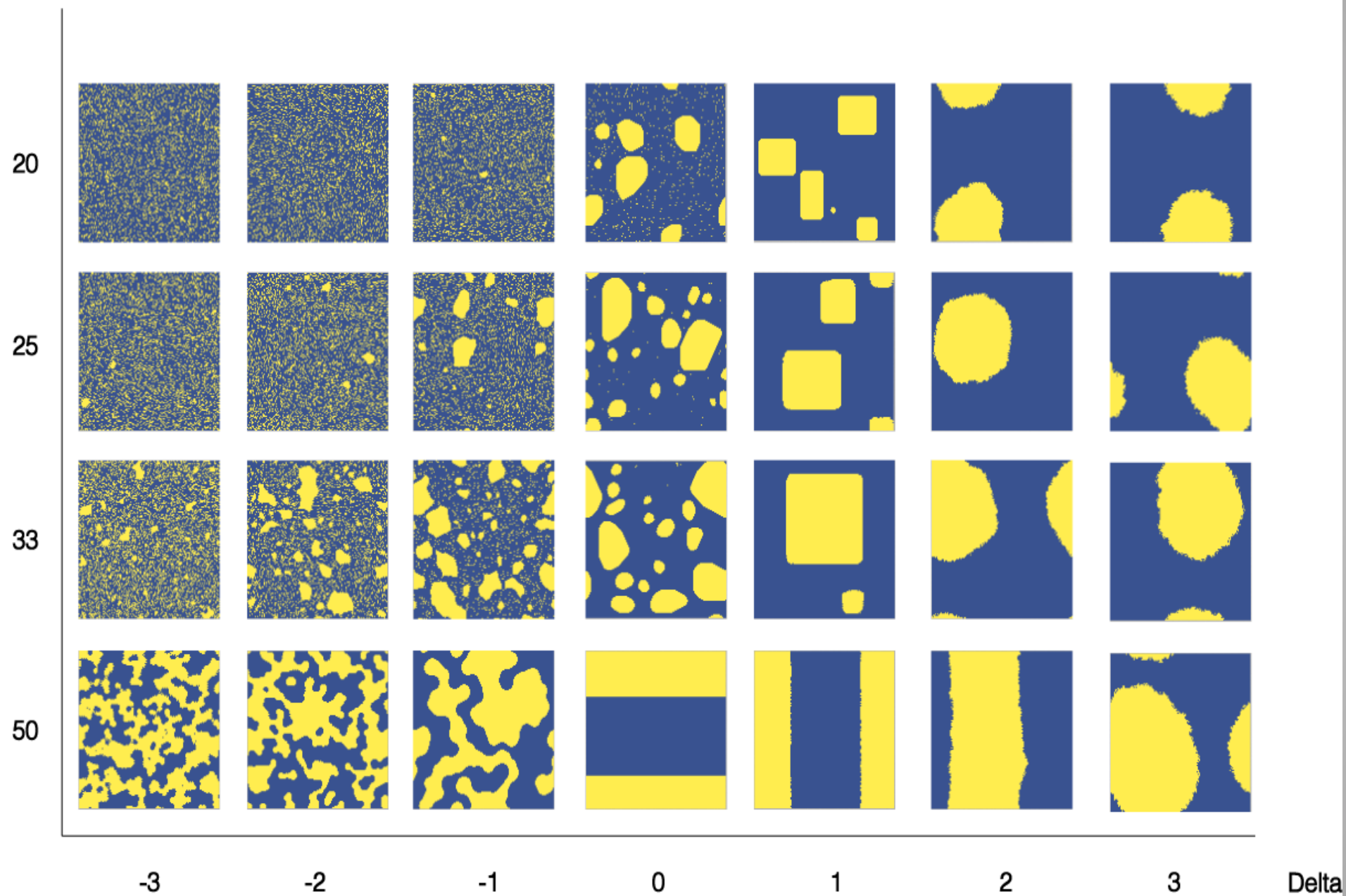
Geometrical interpretation

It is easy to see by a transformation of the energy that
Minimize it, is equivalent to minimize the perimeter of
The clusters so the dynamics try to do that !!

Others phase diagrams with circle-neighborhoods
with different radios (Nicolas Goules-Domic Simulations):

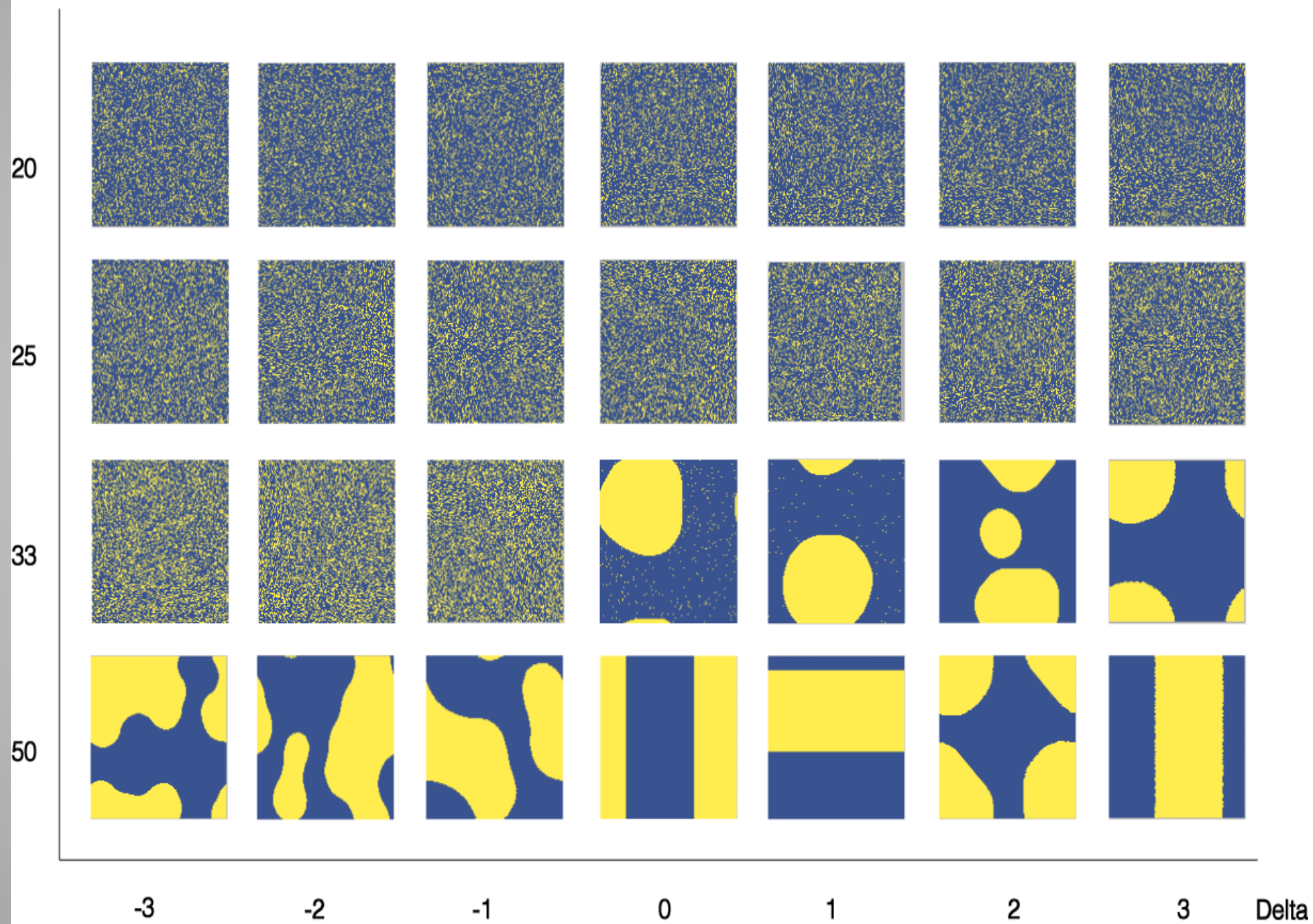
Fraction %

$r = 2$



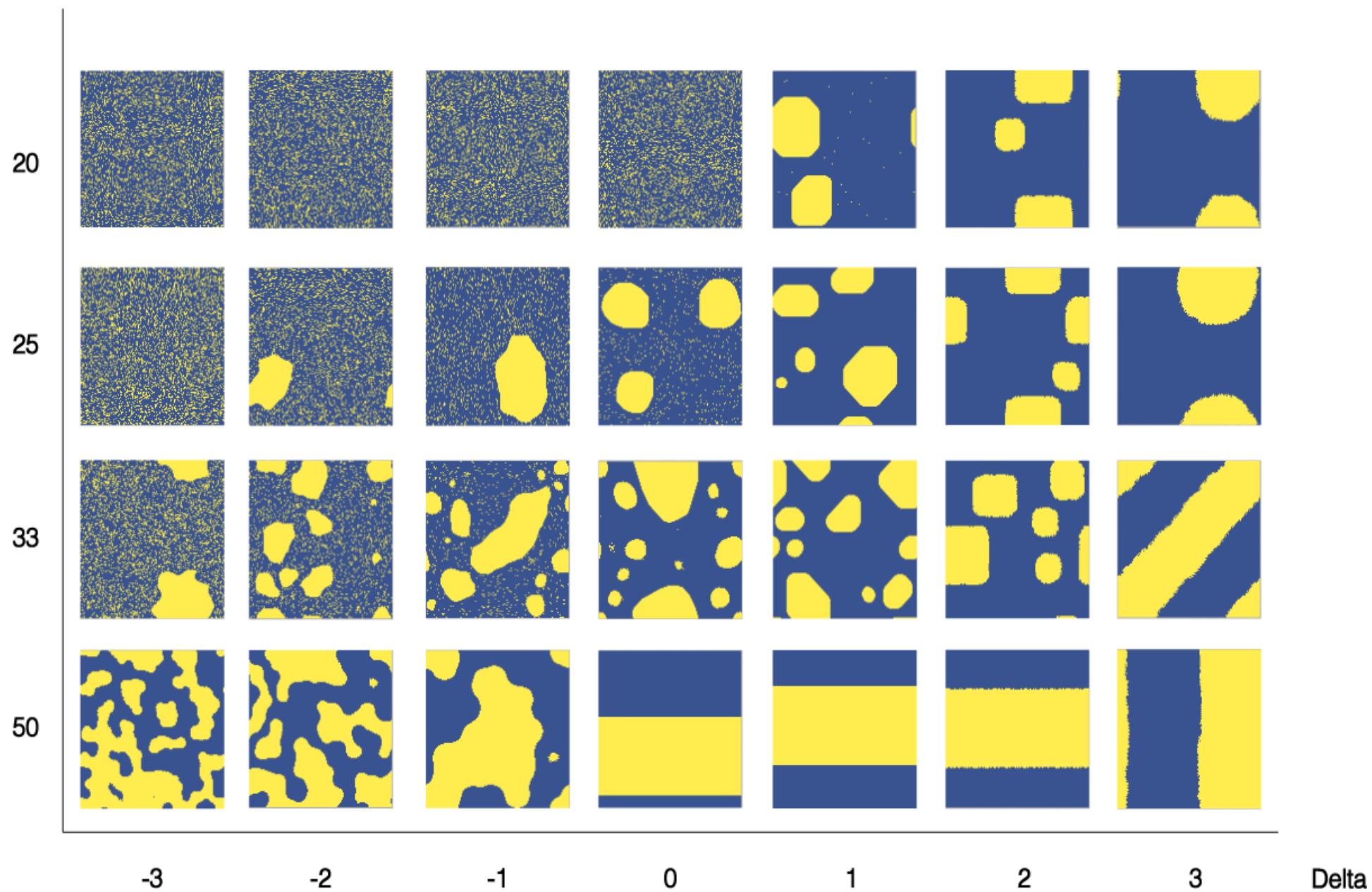
Fraction %

$r = 5$



Fraction %

$r = 3$



Regulatory Boolean networks

- Stuart. Kauffman, Metabolic stability and epigenesis in randomly connected nets, *J. Of Theor. Biol*, 22, 437-67, 1969.
- René Thomas, "Regulatory networks seen as asynchronous automata : a logical description.", *J. Theor. Biol.* **153** ,(1991) 1-23
- François Robert, Discrete Iterations, Springer Verlag, 1986).

The dynamics may change a lot for different updates.

Cycles may appear or disappear.

Given a regulation network what is the “right” way to update it?.

Conditions such that there exists only fixed points.

Condition for the robustness of the network (roughly speaking, same behavior for different updates).

Since there are an exponential number of updates
To study all them implies a huge amount of computation
So it is important to determine tools in order to diminish
the computing time

We will present here *dynamical equivalence classes*
and the notion of *alliances*

Previous notions where defined to study yeast's regulation networks

Below we will always consider threshold interactions

$$x'_i = 0 \Leftrightarrow \sum_{j=1}^n w_{ij} x_j - \theta_i \leq 0$$

1 otherwise

We consider threshold interactions

$$x'_i = 0 \Leftrightarrow \sum_{j=1}^n w_{ij} x_j - \theta_i \leq 0$$

1 otherwise

Equivalent classes: given a regulatory network (F,G) and the updates modes s_1 and s_2 we obtain two dynamics:

$$(F, s_1) \text{ and } (F, s_2)$$

They are equivalent if and only if its phase space is the same.

There are “good” algorithms to determine equivalent classes for reasonable size regulatory networks (say n no more than 15 and no to much interconnections).

Aracena, J., E.G, E., Moreira, A., & Salinas, L. (2009).

On the robustness of update schedules in Boolean networks. *Biosystems*, 97, 1–8.

Montalva, M. (2011). *Feedback set problems and dynamical behavior in regulatory networks*. PhD, Universidad de Concepción, Concepción, Chile.

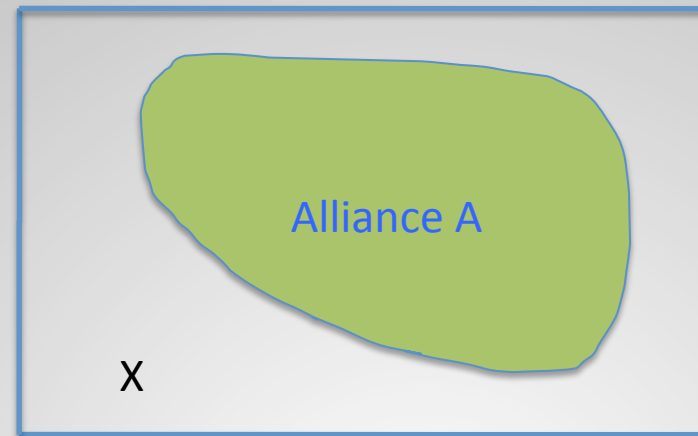
Alliances: Given a regulatory network (F,G)

We say that a subconfiguration $(a_{i_1}, \dots, a_{i_p}) \in \{0,1\}^p$ is an *alliance* if and only if

$$a_{i_k} = H\left(\sum_{j=1}^p w_{i_k i_j} a_{i_j} + \sum_{j \notin \{i_1, \dots, i_p\}} w_{i_k j} x_j - \theta_{i_k}\right) \quad k \in \{1, \dots, p\}$$
$$x \in \{0,1\}^{n-p}$$

An *alliance* are a kind of “local” fixed point but stronger....

It is invariant under updates changes



After update

EXAMPLE1

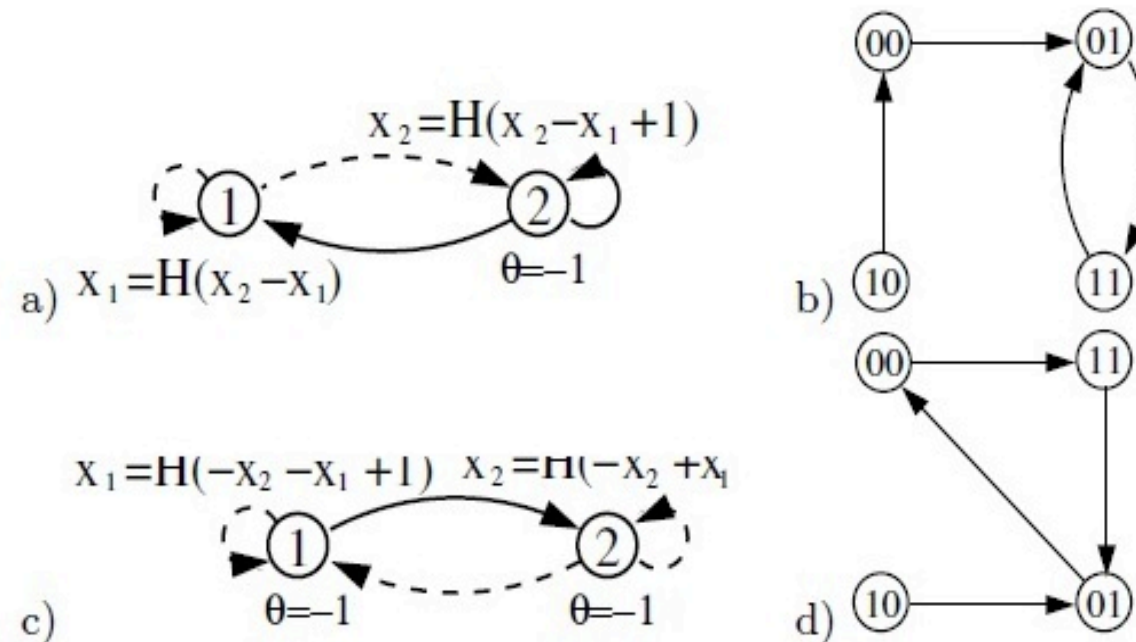


Fig. 1 In figures a) and c), the dotted lines represent negative interactions (weight = -1) while the others are positive interactions (weight = 1). a) A BN of 2 nodes with threshold Boolean functions defined as x_1 , x_2 , and thresholds $\theta = 0$ and $\theta = -1$ respectively. b) The dynamical behavior of a) for the parallel update schedule. Note that $x_2 = 1$ is an alliance although the dynamic has no fixed point. c) A BN as in a) but with both thresholds equal to -1. d) The dynamical behavior of c) for the parallel update schedule. Note in this case that the network has no alliance.

EXAMPLE 2: reduction of the network from an alliance

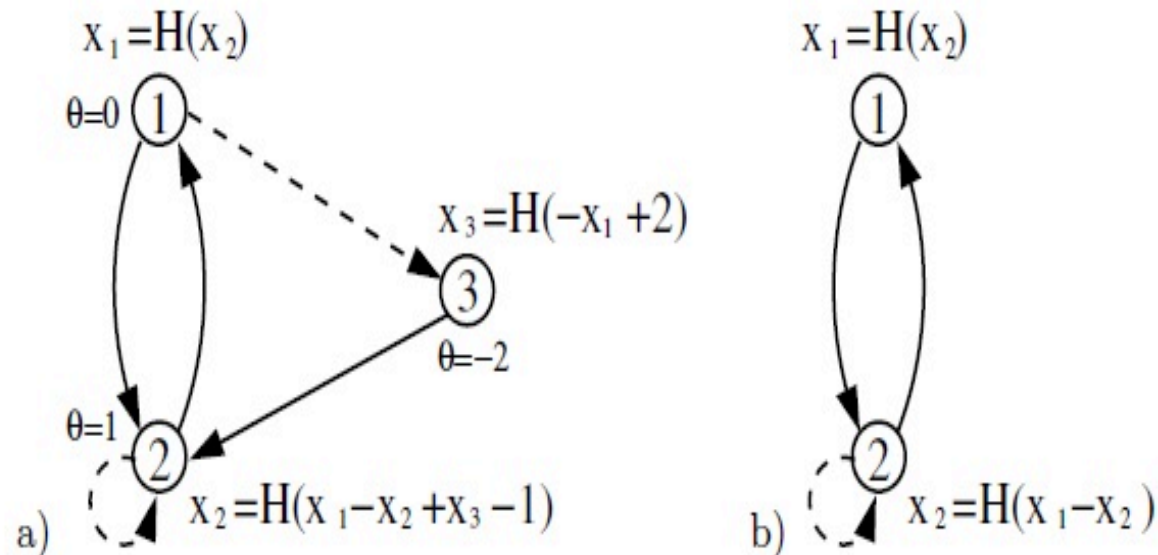
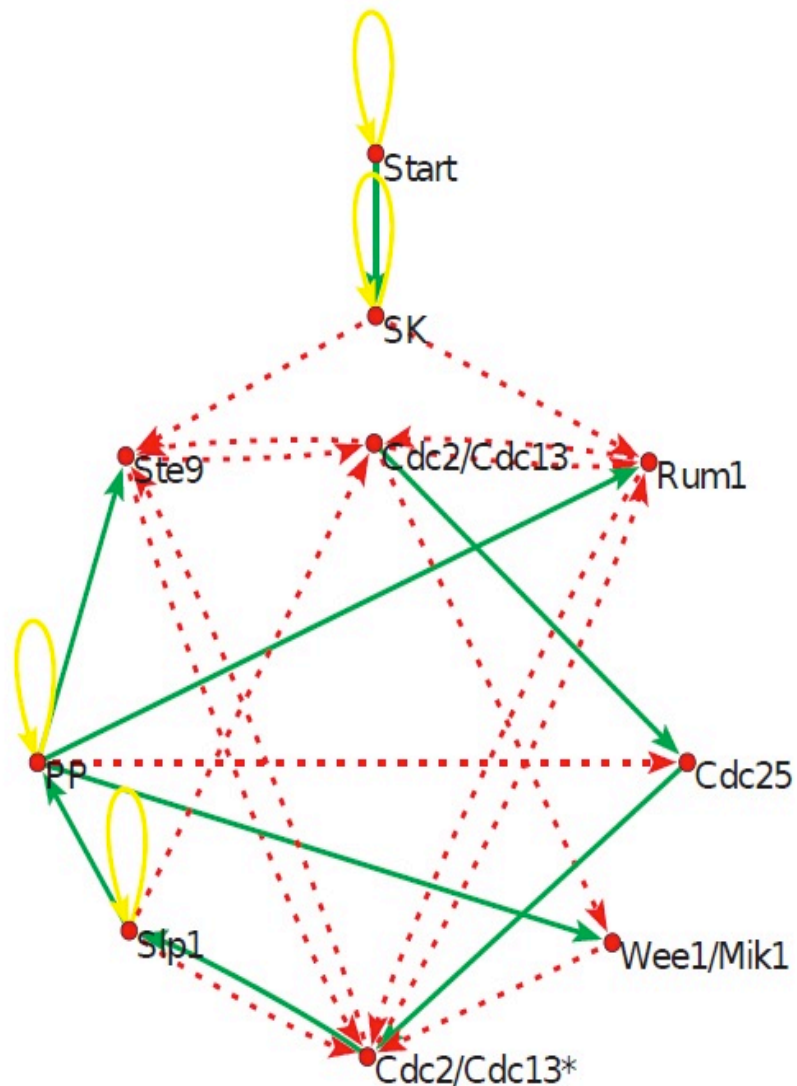


Fig. 16 a) A BN of 3 nodes with threshold Boolean functions defined as x_1 , x_2 , x_3 and thresholds $\theta = 0$, $\theta = 1$ and $\theta = -2$ respectively. Dotted lines represent negative interactions (weight = -1) while the others are positive interactions (weight = 1). b) The BN of a) is reduced after considering the alliance $x_3 = 1$. Note that, the effect of $x_3 = 1$ over x_2 is equivalent to write $x_2 = H(x_1 - x_2)$ while x_1 remains the same.



Fission yeast cell-cycle model (*Yeast1*)

Model proposed in Davidich,
Bornholdt (2008) **PLoS ONE**

Fig. 3 The fission yeast cell-cycle threshold Boolean network. Using the same configuration as [3], (color online) the green/solid edges represent positive weights (activations), the red/dashed edges represent negative weights (inhibitory). The yellow/solid loops represent self-degradation.

Threshold functions and interaction matrix for *Yeast1*

$$x'_i = H\left(\sum_{j=1}^n w_{ij}x_j - \theta_i\right) = \begin{cases} 0 & \text{if } \sum_{j=1}^n w_{ij}x_j - \theta_i < 0 \\ 1 & \text{if } \sum_{j=1}^n w_{ij}x_j - \theta_i > 0 \\ x_i & \text{if } \sum_{j=1}^n w_{ij}x_j - \theta_i = 0 \end{cases}$$

$$W = \begin{pmatrix} & \text{Start} & SK & Cdc2/Cdc13 & Ste9 & Rum1 & Slp1 & Cdc2/Cdc13^* & Wee1/Mik1 & Cdc25 & PP \\ \text{Start} & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ SK & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ Cdc2/Cdc13 & 0 & 0 & 0 & -1 & -1 & -1 & 0 & 0 & 0 & 0 \\ Ste9 & 0 & -1 & -1 & 0 & 0 & 0 & -1 & 0 & 0 & 1 \\ Rum1 & 0 & -1 & -1 & 0 & 0 & 0 & -1 & 0 & 0 & 1 \\ Slp1 & 0 & 0 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 \\ Cdc2/Cdc13^* & 0 & 0 & 0 & -1 & -1 & -1 & 0 & -1 & 1 & 0 \\ Wee1/Mik1 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ Cdc25 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ PP & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 \end{pmatrix} \Theta = \begin{pmatrix} 0 \\ 0 \\ -0.5 \\ 0 \\ 0 \\ 0 \\ 0.5 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

Fig. 2 Weight matrix and threshold vector for *Yeast1*

Fixed points and the limit cycle (synchronous update)

Table 1 Attractors of *Yeast1* under the parallel updating mode. There are two types of attractors, fixed points (FP) and limit cycles (LC).

Attractor	Type	Basin size	<i>Start</i>	<i>SK</i>	<i>Cdc2/Cdc13</i>	<i>Ste9</i>	<i>Rum1</i>	<i>Slp1</i>	<i>Cdc2/Cdc13*</i>	<i>Wee1/Mkl1</i>	<i>Cdc25</i>	<i>PP</i>
1	FP	762	0	0	0	1	1	0	0	1	0	0
2	LC	208	0	0	0	0	0	0	0	0	1	1
	LC	0	0	0	0	0	0	1	0	0	1	0
	LC	0	0	0	1	1	1	0	1	1	0	0
3	FP	18	0	0	0	0	1	0	0	1	0	0
4	FP	18	0	0	0	1	0	0	0	1	0	0
5	FP	2	0	0	0	1	0	0	0	0	0	0
6	FP	2	0	0	0	1	0	0	0	0	1	0
7	FP	2	0	0	0	1	0	0	0	1	1	0
8	FP	2	0	0	0	0	1	0	0	0	0	0
9	FP	2	0	0	0	0	1	0	0	0	1	0
10	FP	2	0	0	0	0	1	0	0	1	1	0
11	FP	2	0	0	0	1	1	0	0	0	0	0
12	FP	2	0	0	0	1	1	0	0	0	1	0
13	FP	2	0	0	0	1	1	0	0	1	1	0

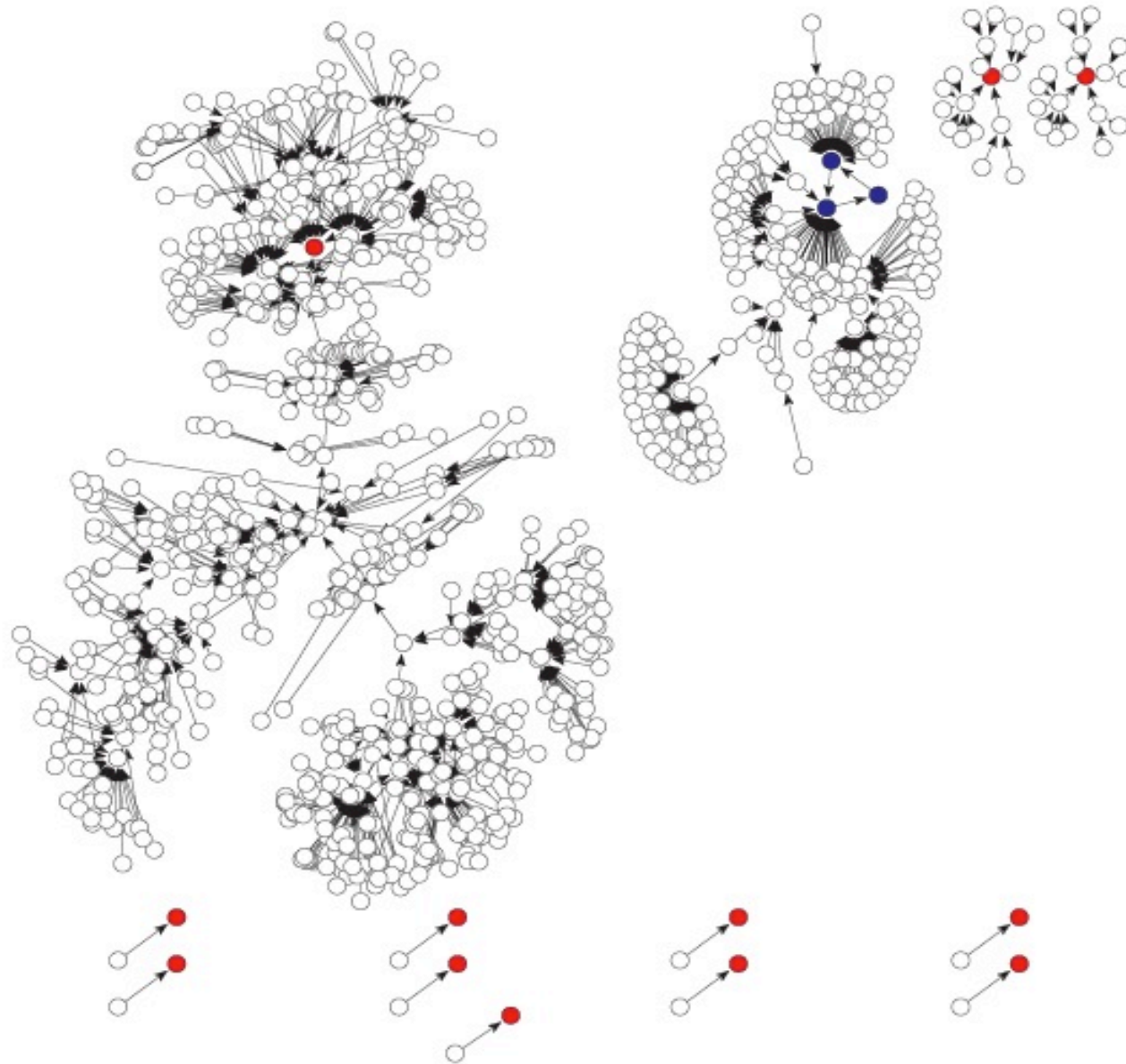
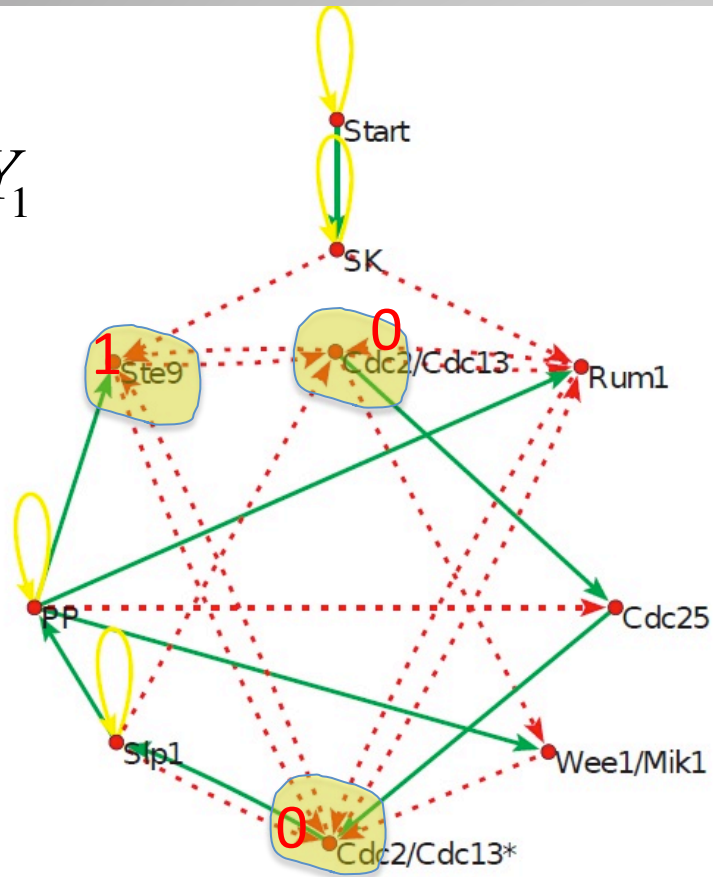
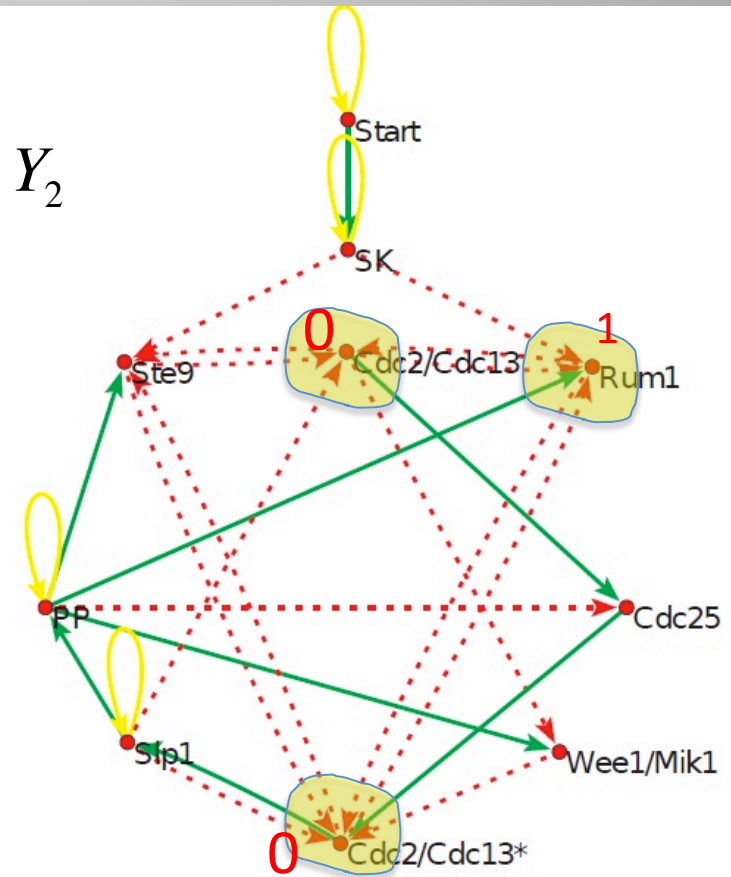


Fig. 7 State transition graph for *Yeast1* using the parallel updating scheme. (Color online)
The twelve red circles represent the fixed point states, the three blue circles represent the states that belong to the limit cycle.

Y_1

 Y_2


Alliances

$$Y_1 = (Cdc2/cdc13, Ste9, Cdc2/Cdc13^*) = (0, 1, 0)$$

$$Y_2 = (Cdc2/cdc13, Rum1, Cdc2/Cdc13^*) = (0, 1, 0)$$

For any initial vector such that it contains one of the two previous alliances then for any update mode the dynamics converges to fixed points

It remains to study what happens when in initial condition we do not have (as a sub-configuration) an *alliance*.

$$S_n = P_1(z) \cup P_2(z) \cup P_3(z) \cup P_4(z) \cup P_5(z) \cup P_6(z) \cup P_7(z) \cup P_8(z) \cup P_9(z)$$

$$z \in \{Ste9, Rum1\}$$

P_1	Cdc2/Cdc13	>	Z	<	Cdc2/Cdc13*
P_2	Cdc2/Cdc13	<	Z	>	Cdc2/Cdc13*
P_3	Cdc2/Cdc13	<	Z	<	Cdc2/Cdc13*
P_4	Cdc2/Cdc13	>	Z	>	Cdc2/Cdc13*
P_5	Cdc2/Cdc13	=	Z	<	Cdc2/Cdc13*
P_6	Cdc2/Cdc13	=	Z	>	Cdc2/Cdc13*
P_7	Cdc2/Cdc13	>	Z	=	Cdc2/Cdc13*
P_8	Cdc2/Cdc13	<	Z	=	Cdc2/Cdc13*
P_9	Cdc2/Cdc13	=	Z	=	Cdc2/Cdc13*

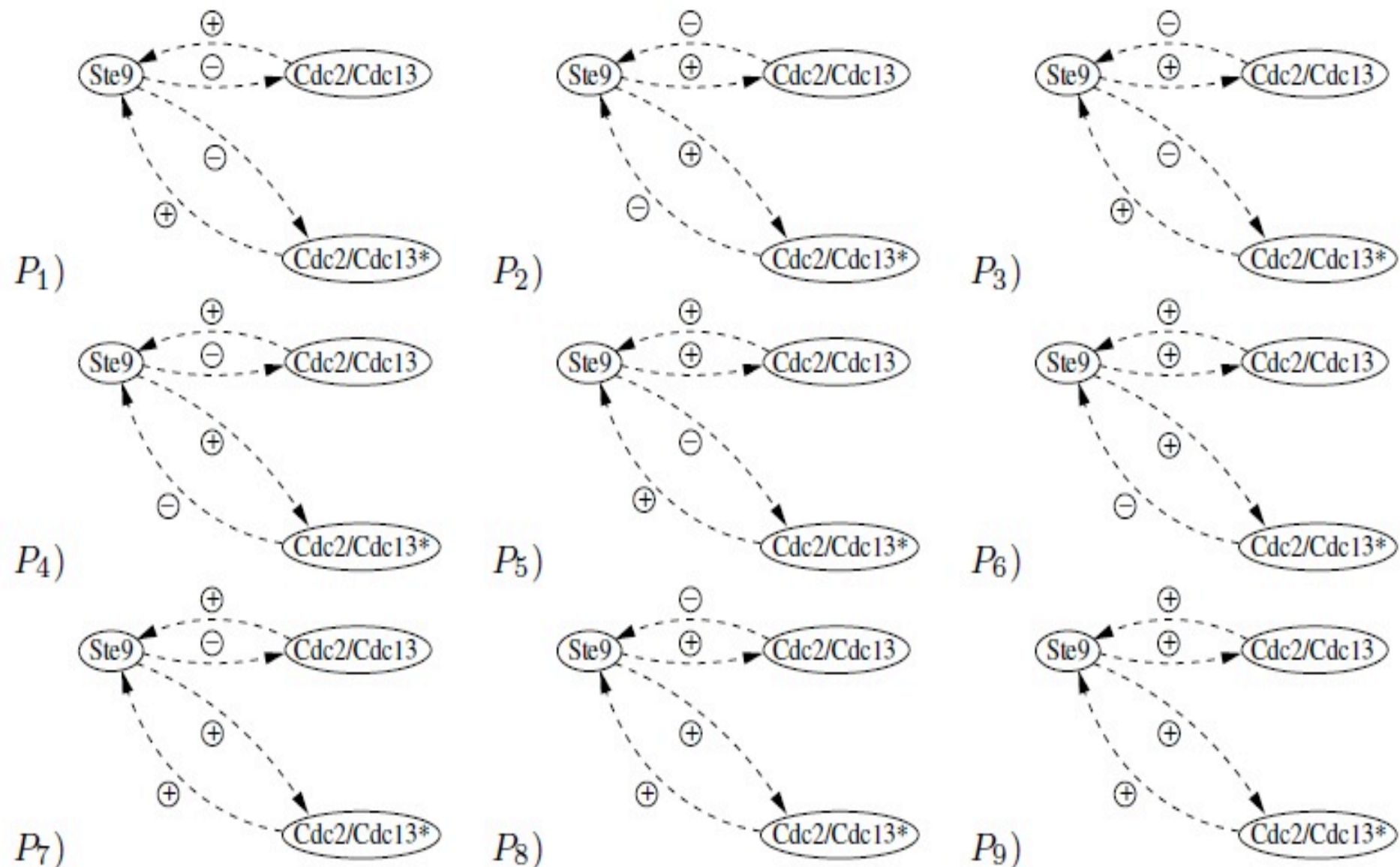


Fig. 5 The update subdigraphs associated with the partitions $P_1(Ste9), \dots, P_9(Ste9)$ respectively, where an edge (i, j) is labeled by $\oplus$ if and only if $s(i) \geq s(j)$, otherwise, the edge is labeled by $\ominus$ (see [17] for more details)

The total number of updates is 545835

By algorithms and the notion of alliances, we reduce to study only 15350 different equivalent classes

So there exists 5513 classes with a limit cycle (period between 2 and 5)

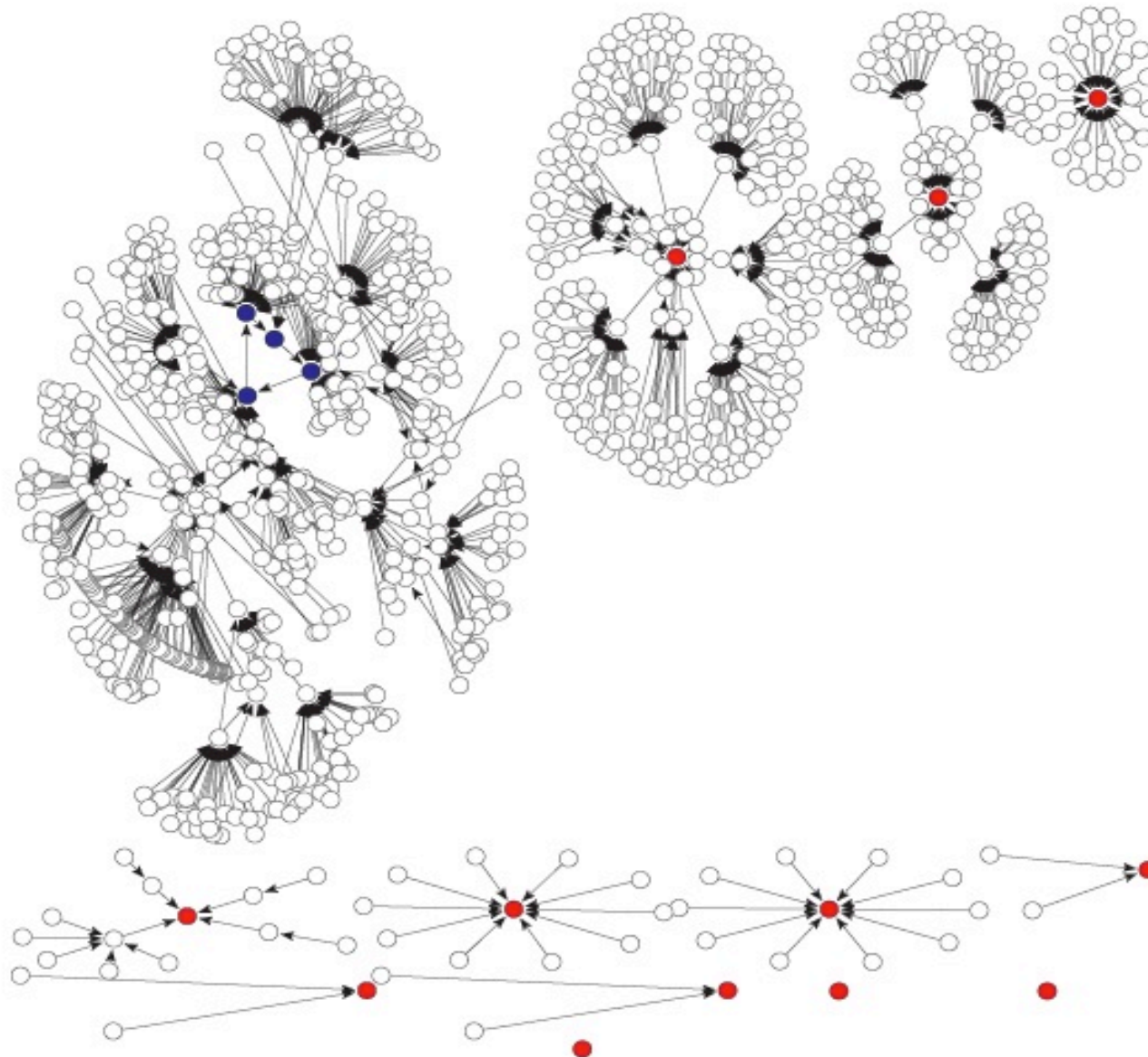


Fig. 8 State transition graph for *Yeast1* using the block-sequential updating mode: $s(Wee1/Mik1) = s(Cdc25) < s(Cdc2/Cdc13) = s(Cdc2/Cdc13^*) = s(Ste9) < s(Rum1) = s(Slp1) = s(PP) = s(Start) = s(SK)$. (Color online) The twelve red circles represent the fixed point states, the four blue circles represent the states that belong to the limit cycle.

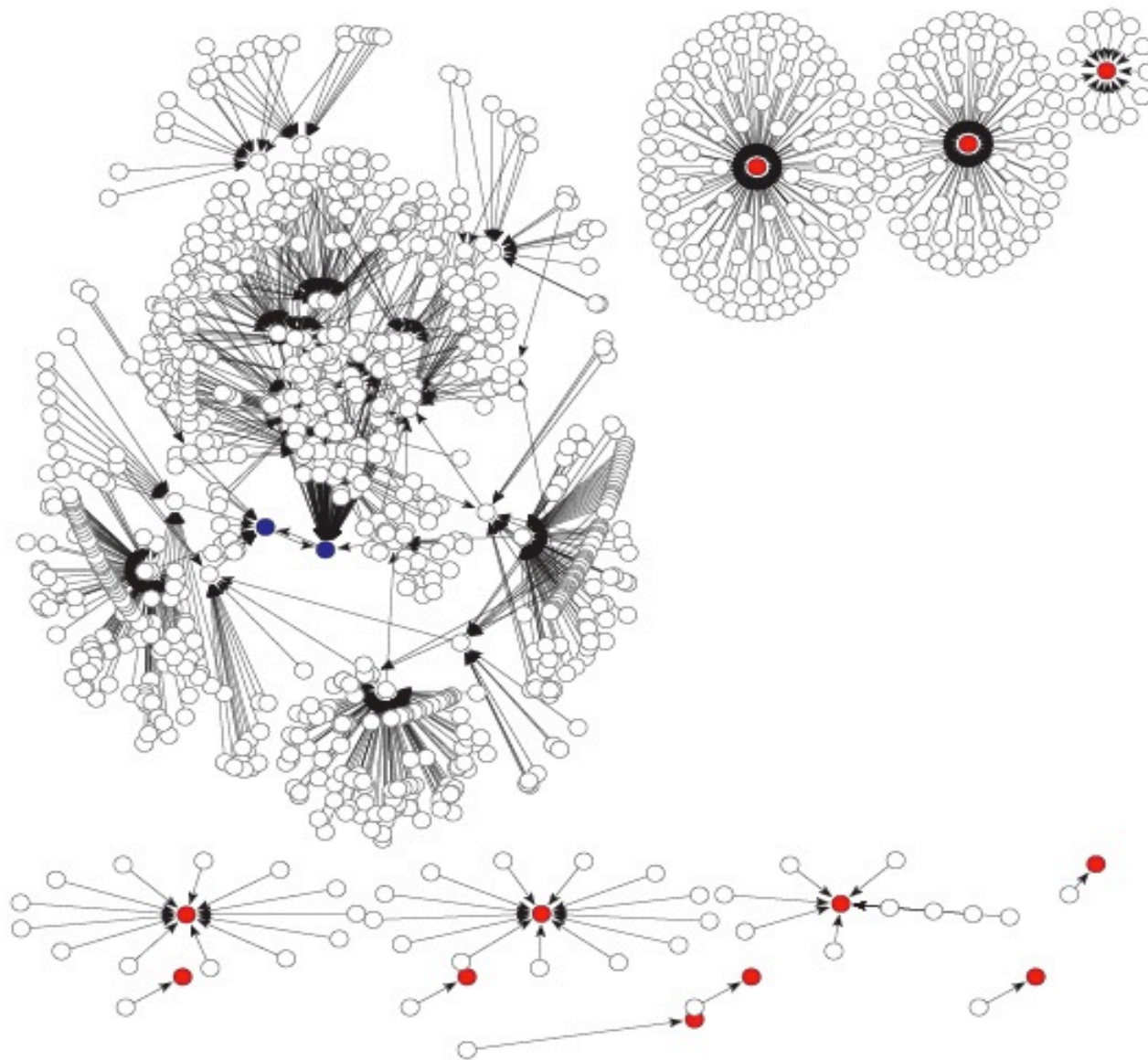


Fig. 9 State transition graph for *Yeast1* using the block-sequential updating mode: $s(Rum1) < s(Cdc2/Cdc13^*) < s(Slp1) < s(Cdc2/Cdc13) < s(Ste9) = s(Wee1/Mik1) = s(Cdc25) = s(PP) < s(Start) = s(SK)$. (Color online) The twelve red circles represent the fixed point states, the two blue circles represent the states that belong to the limit cycle.

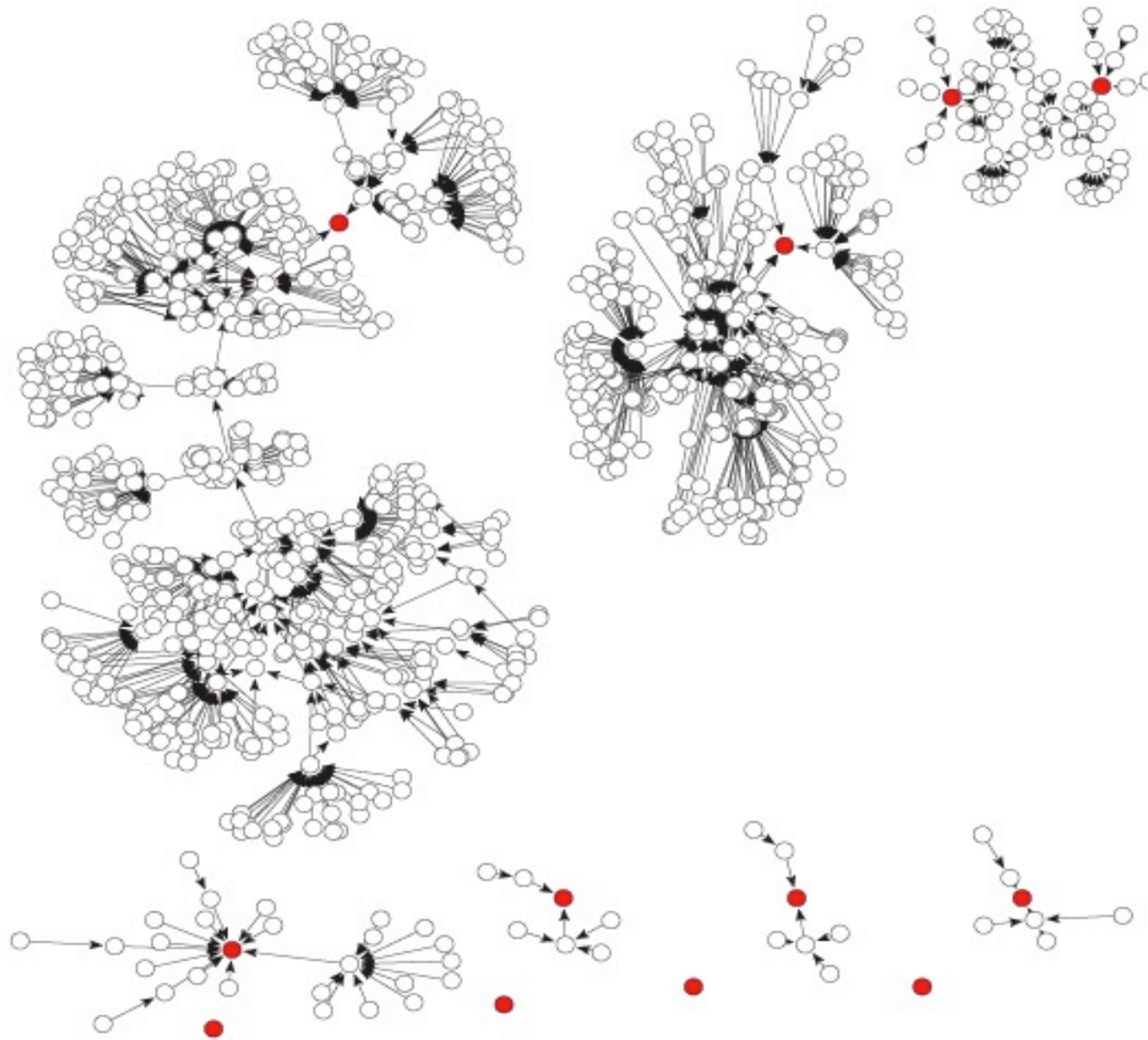
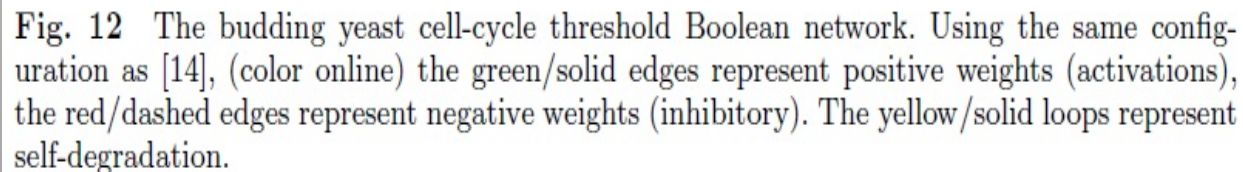


Fig. 10 State transition graph for *Yeast1* using the block-sequential updating mode: $s(Ste9) < s(PP) < s(Wee1) = s(Mik1) = s(Cdc25) < s(Start) = s(SK) = s(Cdc2/Cdc13) = s(Rum1) = s(Slp1) = s(Cdc2/Cdc13^*)$. (Color online) The twelve red circles represent the fixed point states, there are no limit cycles.

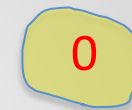
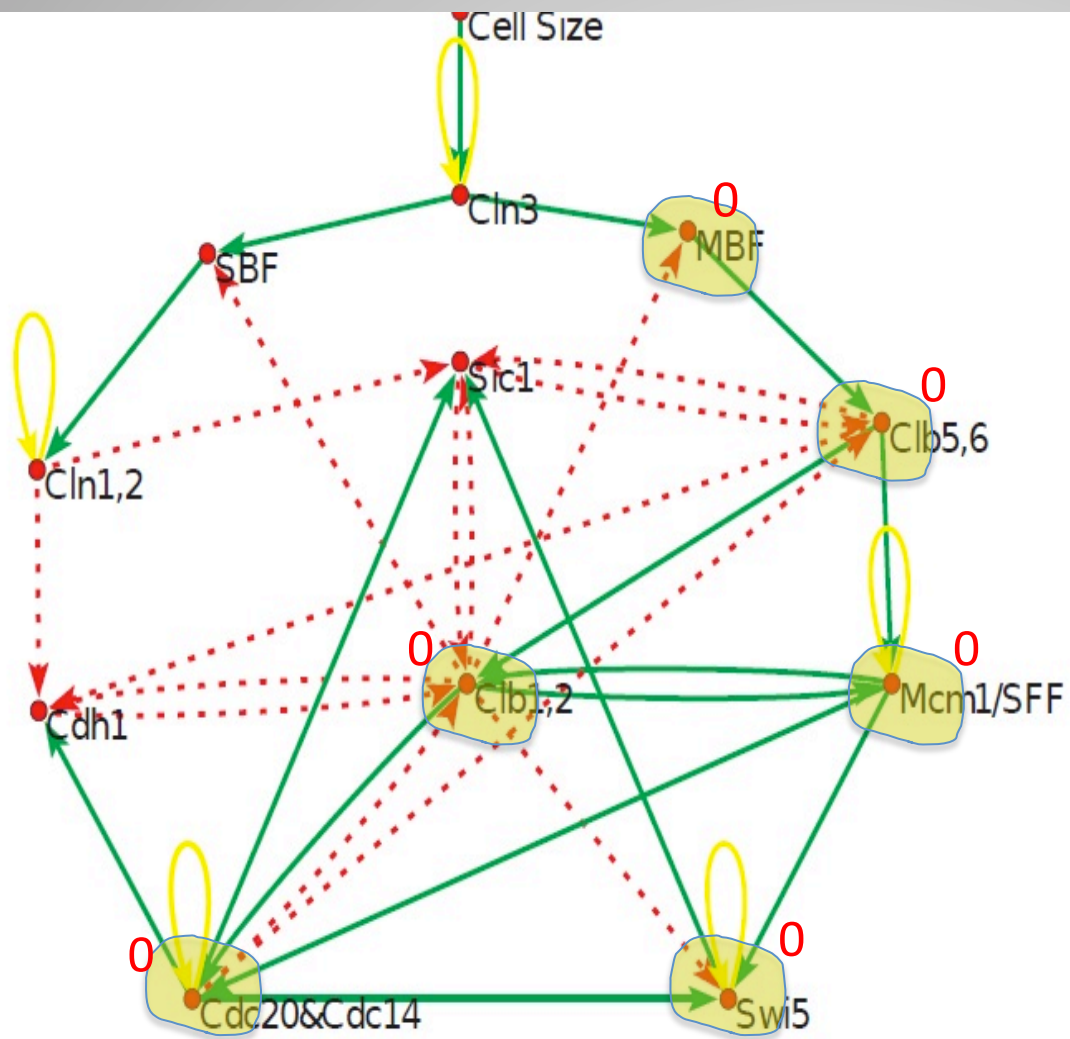
Li, Long, Lu, Tang,(2004) The yeast cell-cycle network is robustly designed, PNAS,101, 4781-4786



Matrix and transition vector of the yeast2 network

$$W = \begin{pmatrix} & Cln3 & MBF & SBF & Cln1,2 & Cdh1 & Swi5 & Cdc20 & Clb5,6 & Sic1 & Clb1,2 & Mcm1 \\ Cln3 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ MBF & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ SBF & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ Cln1,2 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ Cdh1 & 0 & 0 & 0 & -1 & 0 & 0 & 1 & -1 & 0 & -1 & 0 \\ Swi5 & 0 & 0 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & -1 & 1 \\ Cdc20 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 1 & 1 \\ Clb5,6 & 0 & 1 & 0 & 0 & 0 & 0 & -1 & 0 & -1 & 0 & 0 \\ Sic1 & 0 & 0 & 0 & -1 & 0 & 1 & 1 & -1 & 0 & -1 & 0 \\ Clb1,2 & 0 & 0 & 0 & 0 & -1 & 0 & -1 & 1 & -1 & 0 & 1 \\ Mcm1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & -1 \end{pmatrix} \quad \Theta = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

Fig. 11 Weight matrix and threshold vector for *Yeast2*

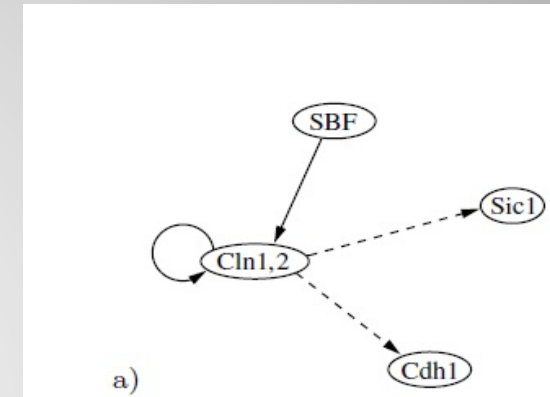


Alliance elements

For any update *yeast2* admits only fixed points

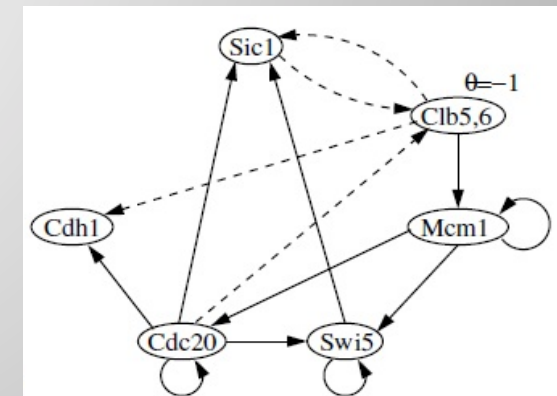
To prove that it's enough to study two cases: MBF= 0 or MBF=1

For MBF=0, any initial configuration converges to the alliance. After that, the sub-network to analyze is a tree, so for any initial vector and any update it converges to fixed points.



Tree for MBF=0

For MBF =1 by studying numerically the equivalent classes for a reduced network, we determine that every dynamics admits only fixed points.



Reduced network for MBF=1

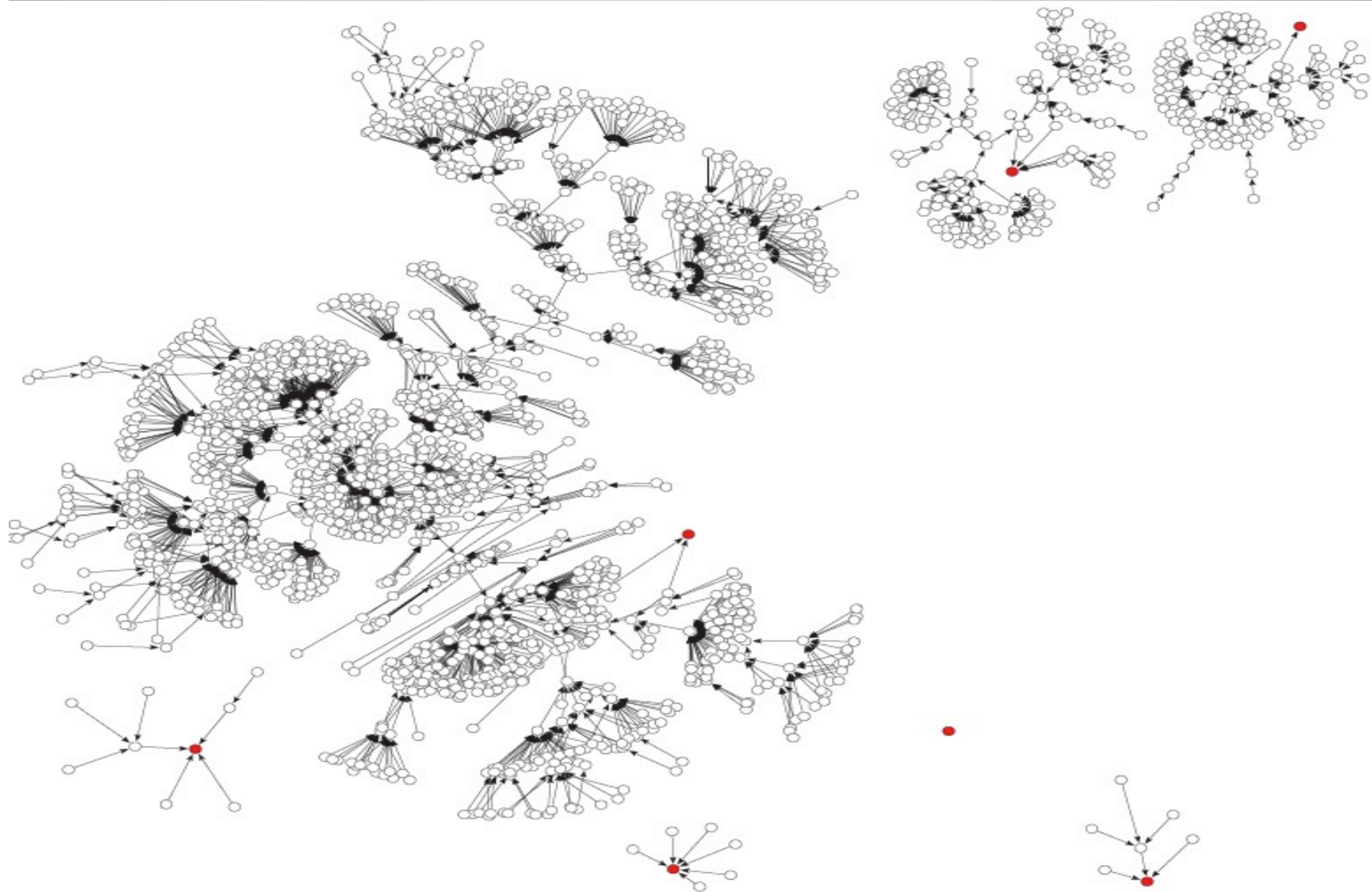


Fig. 14 State transition graph for *Yeast2* using the parallel updating scheme. (Color online)
The seven red circles represent the fixed point states, there are no limit cycles.

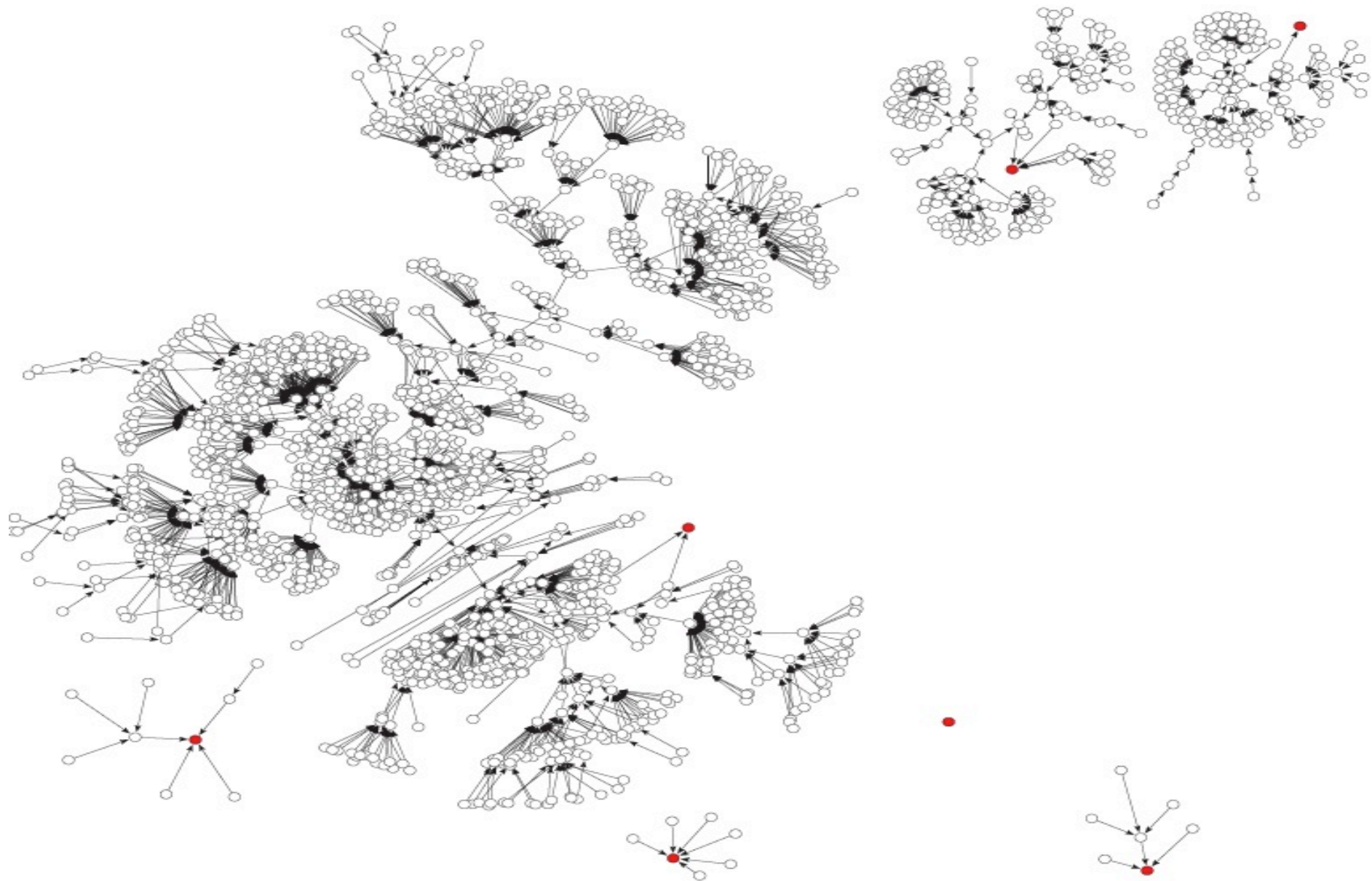


Fig. 14 State transition graph for *Yeast2* using the parallel updating scheme. (Color online)
The seven red circles represent the fixed point states, there are no limit cycles.

Gracias !!!

