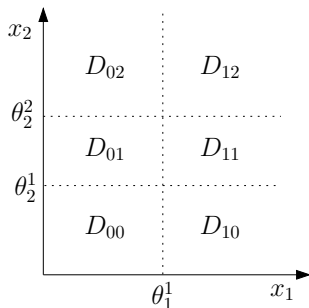
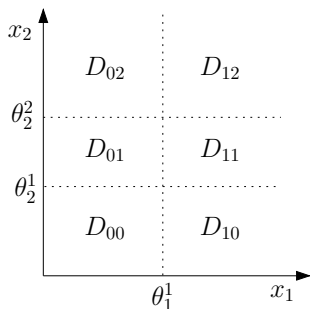


# From PLDE to FDS



- ▶ regular domain  $D_s$  is identified with qualitative state  $s = (s_1, \dots, s_n)$ , integer values describe position w.r.t. thresholds
- ▶ trajectories tend towards target value  $\Phi(D)$
- ▶ target value position in a regular domain can be described by corresponding state  $s^{\Phi(D)}$

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Describe the system dynamics by a function

$$f : \{s \mid D_s \text{ regular domain}\} \rightarrow \{s \mid D_s \text{ regular domain}\}, s \mapsto s^{\Phi(D)}$$

Consider “trajectories”  $(s, f(s), f(f(s)), \dots)$

# Discrete modeling

- ▶ system description by means of discrete functions
  - ▶ including structural information: network components and dependencies
  - ▶ capturing of interaction character and impact
- predicting/analyzing dynamics

**Hypothesis:** kinetic details of interactions less important than network organization

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## Ingredients

- ▶ system with  $n$  components  $\alpha_i$  interpreted as variables in  $X_i := \{0, \dots, p_i\}$  with  $p_i \in \mathbb{N}$
- ▶ state space  $X := X_1 \times \dots \times X_n$
- ▶  $n$  functions  $f_i : X \rightarrow X_i$  capture rules to calculate future value of  $\alpha_i$  from current value of its regulators
- ▶ system description: discrete function  $f = (f_1, \dots, f_n) : X \rightarrow X$

E.g. Boolean networks:  $p_i = 1$  for all  $i \in \{1, \dots, n\}$

# Dynamics

Consider  $f : X \rightarrow X$ ,  $X = \prod_{i=1}^n X_i$ ,  $X_i = \{0, 1, \dots, p_i\}$ ,  $p_i \in \mathbb{N}$ , (FDS)  
and dynamics  $(f^k(x))_{k \in \mathbb{N}}$ ,  $x \in M$ , with  $f^1 = f$ ,  $f^k = f \circ f^{k-1}$

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## State transition graph $S(f)$ of $f$

- ▶ vertex set  $X$  (state space, exponential in  $n$ )
- ▶ edge set  $\{(x, f(x)) \mid x \in X\}$  – **synchronous update**
- ▶ trajectories: infinite paths  $(x, f(x), f^2(x), \dots)$  in  $S(f)$

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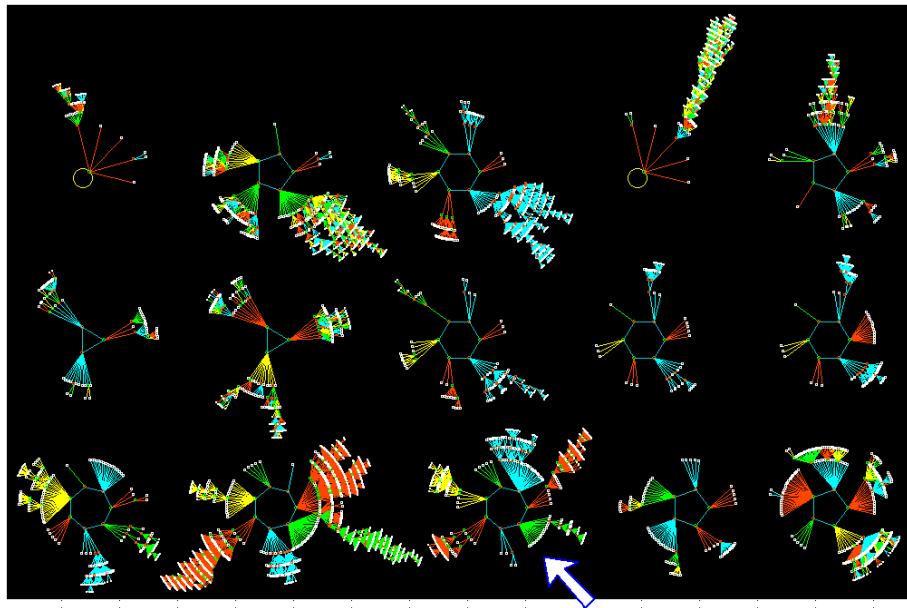
**Note** conceptual differences to ODE/PLDE description:

explicit description of trajectories, trajectories can merge

## Consequences of synchronous update and finite state space

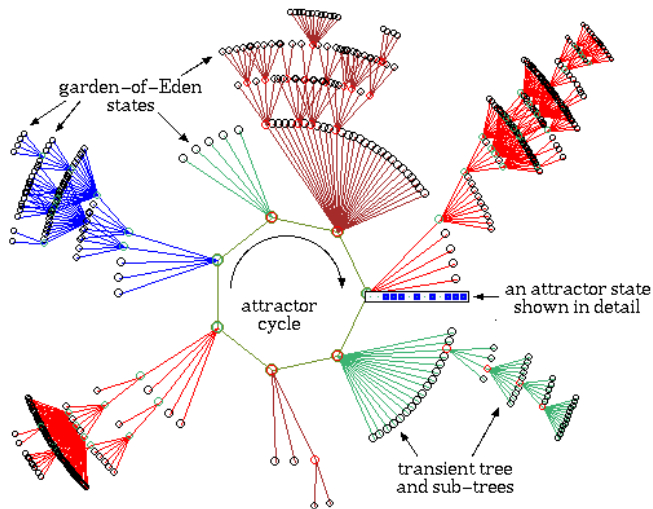
- ▶ each trajectory “ends” in a cycle
- attractor: terminal strongly connected components of  $S(f)$

# Finite dynamics (n=13)





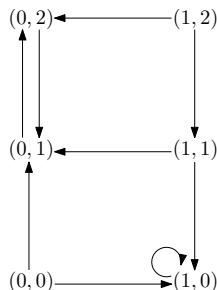
# Finite dynamics ( $n=13$ )



# Asynchronous update

## State transition graph

- ▶ vertex set  $X$
- ▶ edges  $x \rightarrow x'$  iff  $x' = f(x) = x$  or  $x'_i = x_i + \text{sgn}(f_i(x) - x_i)$  for some  $i \in \{1, \dots, n\}$  satisfying  $x_i \neq f_i(x)$  and  $x'_j = x_j$  for all  $j \neq i$   
**(asynchronous update)**
  - ▶ gradual activity level evolution
  - ▶ all time delays are distinct
  - **more realistic for modeling e.g. biological systems**
  - ⇒ non-deterministic representation of possible behaviors
- ▶ attractors and trajectories may differ from the synchronous case



**asynchronous dynamics is more complex and harder to analyze**

# Structure

Given  $f : X \rightarrow X$ ,  $X = \prod_{i=1}^n X_i$ ,  $X_i = \{0, 1, \dots, p_i\}$ ,  $p_i \in \mathbb{N}$  (FDS)

## Interaction graph $G(f)$

- ▶ vertices represent network components
- ▶ directed edges capture interactions, may be labeled
  - ▶ signs carry information on interaction character
  - ▶ thresholds specify conditions on edge activity
- labeled interaction graphs may be multigraphs (parallel edges)

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## Deriving $G(f)$ from $f$

- ▶  $\alpha_j \rightarrow \alpha_k$  iff  $f_k$  depends on the variable  $x_j$ , i.e.,  
there exists  $x \in X$  with  $f_k(x) \neq f_k(\tilde{x})$  where  $\tilde{x}_j \neq x_j$  and  $\tilde{x}_l = x_l$  for all  $l \neq j$
  - ▶ signs and labels can also be derived mathematically from  $f$
- ⇒  $G(f)$  represents functional network topology of  $f$

# Modeling

Modeling specific systems often starts with structural information:

- ▶ translate data on regulatory processes into directed, possibly labeled (multi)graphs

**Definition** An *interaction (multi-)graph*  $I$  is a finite (labeled) directed (multi)graph. (Vertices are understood as variables.)

**vertex:** component (genes, proteins, chemical complexes,...), set of components (similar function, identification {gene, RNA, protein},...), signal,...

**edge:** inhibiting/activating activity (TFs, enzymes,...), complex forming, information flow,...

**value:** activity status, concentration, configuration,...

- ▶ translate behavioral rules into discrete function  $f : X \rightarrow X$ 
  - ▶ for each component decide the impact of its predecessors in a given state on its value  $\rightarrow$  choice of parameters

**Consistency:**  $I = G(f)$

# Exploring the Structure

Consider interaction graph  $I = (V, E)$

Use graph theoretical characteristics and measures

- ▶ quantify organizational features of  $I$ 
  - ▶ importance of nodes
  - ▶ reachability among nodes
  - ▶ homogeneity/heterogeneity w.r.t. a given property
- ▶ relate to biological features
  - ▶ robustness, sensitivity, control,...
  - ▶ identify modules with characteristic function

# Degree distribution and clustering

- ▶ **degree** of a node: # of edges originating (**outdegree**) or ending (**indegree**) in the node
- ▶ **hubs**: highest degree nodes
- ▶ **degree distribution**  $P(k)$ : fraction of nodes with degree  $k$  (indegree/outdegree distribution)  
[cellular networks are often scale-free]
- ▶ **neighborhood** of a node  $v$ : set of nodes  $\neq v$  adjacent to  $v$  (in/out-neighborhood)
- ▶ **clique**: completely connected subgraph
- ▶ **clustering coefficient** of a node: ratio of # of edges in neighborhood and # of edges if neighborhood were a clique  
[large average clustering coefficients indicate redundancy, cohesiveness; observed in protein-protein interaction and metabolic networks]

# Paths and connectivity

- ▶ **distance** between two nodes: shortest path length connecting the nodes
- ▶ **small world**: average shortest path length of large networks stays small  
[facilitates rapid spread of information in response to input; signal transduction, protein interaction, metabolic networks]
- ▶ **path redundancy** [robustness]
- ▶ **betweenness centrality** of node  $v$ : ratio of # shortest paths from  $s$  to  $t$  through  $v$  and total # of shortest  $st$ -paths  
[importance of a node in flow from sources to sinks]
- ▶ **connectivity** of the network: existence of paths between every pair of nodes (distinguish directed/undirected graphs)
  - ▶ **strongly connected** directed graphs: all node pairs connected in both directions
  - ▶ **strongly connected components**: maximal subgraphs that are strongly connected  $\rightarrow$  acyclic scc-graph with initial and terminal components  
[modularity of signaling networks]