Modeling Cell-Cycle Regulation by Discrete Dynamical Systems

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- Introduction
- Genetic Regulatory Networks
- Probabilistic Genetic Networks
- **Cell-Cycle Control System Overview**
- Yeast Cell-Cycle Model
- Our Cell-Cycle Control Model
- Discussion



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MODELING is an important tool for BIOLOGICAL RESEARCH Challenge:

DESIGN A MODEL THAT MIMICS CELL-CYCLE CONTROL

Recently published model of the yeast cell-cycle (built from documented biological knowledge):

ROBUSTNESS PROBLEMS.

We created a model based on biological hypothesis.
Interactively, it was simulated and modified.
The designed model presents a Remarkable Robustness

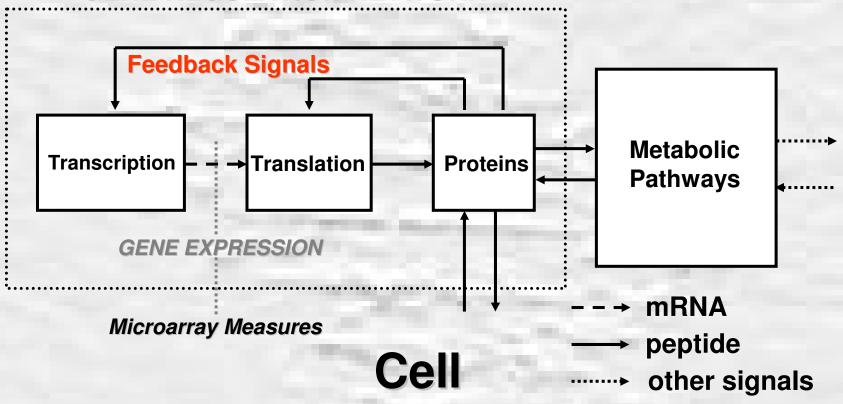
Our model possesses **MECHANISMS** ensuring **ROBUSTNESS**, that are not in the previous model and may exist in nature



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GENE REGULATION NETWORK





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GENE is a NON LINEAR STOCHASTIC GATE

Expression of a Gene depends on Activator and Inhibitory Signals

SYSTEM: built by compiling these gates



Expression of a gene at time t $x_i \in R$, $R = \{0, 1, 2\}$

State of the regulatory network
$$x(t) = \begin{bmatrix} x_1(t) \\ x_2(t) \\ \vdots \\ x_N(t) \end{bmatrix} \in R^N$$

Network Dynamics
$$x(t) = \phi \left[x(t-1), x(t-2), \dots, x(t-m) \right]$$



Transition Function

$$\phi \in R^{N \times m} \to R$$

$$\phi = \begin{bmatrix} \phi_1 \\ \phi_2 \\ \vdots \\ \phi_N \end{bmatrix}, \quad x_i(t) = \phi_i \left[x(t-1), x(t-2), \dots, x(t-m) \right]$$

Predictors
$$x_{j}(t-1), \dots, x_{j}(t-m) \longrightarrow x_{i}(t) \text{ Target}$$

$$x_{k}(t-1), \dots, x_{k}(t-m) \longrightarrow x_{i}(t) \text{ Target}$$



$$x_j(t-1), \ldots, x_j(t-m)$$
 $x_i(t)$
 $x_i(t)$
 $x_i(t)$
 $x_i(t)$
 $x_i(t)$
Stochastic Transition Function:

$$x_i(t) = \begin{cases} 0 & p(0|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m)) \\ 1 & p(1|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m)) \\ 2 & p(2|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m)) \end{cases}$$

$$\exists y, w, z \in \{0, 1, 2\}, \quad y \neq w \neq z :$$

$$p(y|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m)) \gg$$

$$p(w|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m)) +$$

$$p(z|x_j(t-1), \dots, x_j(t-m), x_k(t-1), \dots, x_k(t-m))$$



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CELL CYCLE:

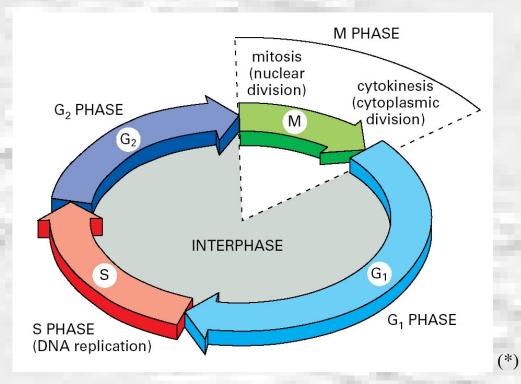
Orderly sequence of events for the the duplication and division of the cell in two daughter cells

(mechanism by which all living things reproduce)

The basic organization of the cycle and its control system are essentially the same in all eucaryotic cells



Phases of the Cell Cycle



Interphase: (the cell continuously **grows**)

- \blacksquare G_1 phase: gap between M and S phases
- S phase: DNA replication
- \blacksquare G_2 phase: gap between S and M phases

M phase:

- Mitosis: nuclear division
- **Cytokinesis:** cytoplamatic division



^{*} from: Molecular Biologyof the Cell - Alberts et al - Garland Science

The control system can arrest de cell-cycle at specific CHECKPOINTS, if some events have not been completed.

Checkpoints generally operate through

NEGATIVE INTRACELLULAR SIGNALS.



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Model Architecture and Dynamics

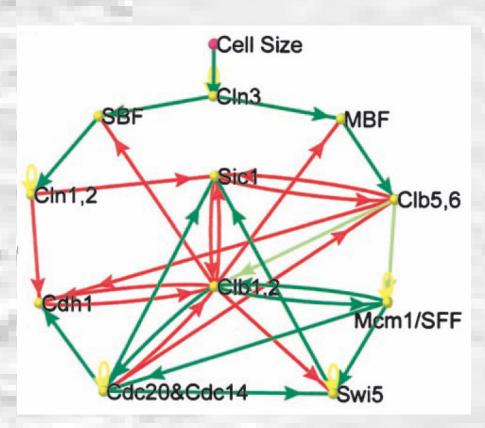
Each node *i* has a binary value $S_i = 1$ or $S_i = 0$

$$S_{i}(t+1) = \begin{cases} 1, & \sum_{j} a_{ij}S_{j}(t) > 0 \\ 0, & \sum_{j} a_{ij}S_{j}(t) < 0 \\ S_{i}(t), & \sum_{j} a_{ij}S_{j}(t) = 0 \end{cases}$$

Transition Function

$$a_{ij} = a_g$$
 green arrow from i to j
 $a_{ij} = a_r$ red arrow from i to j

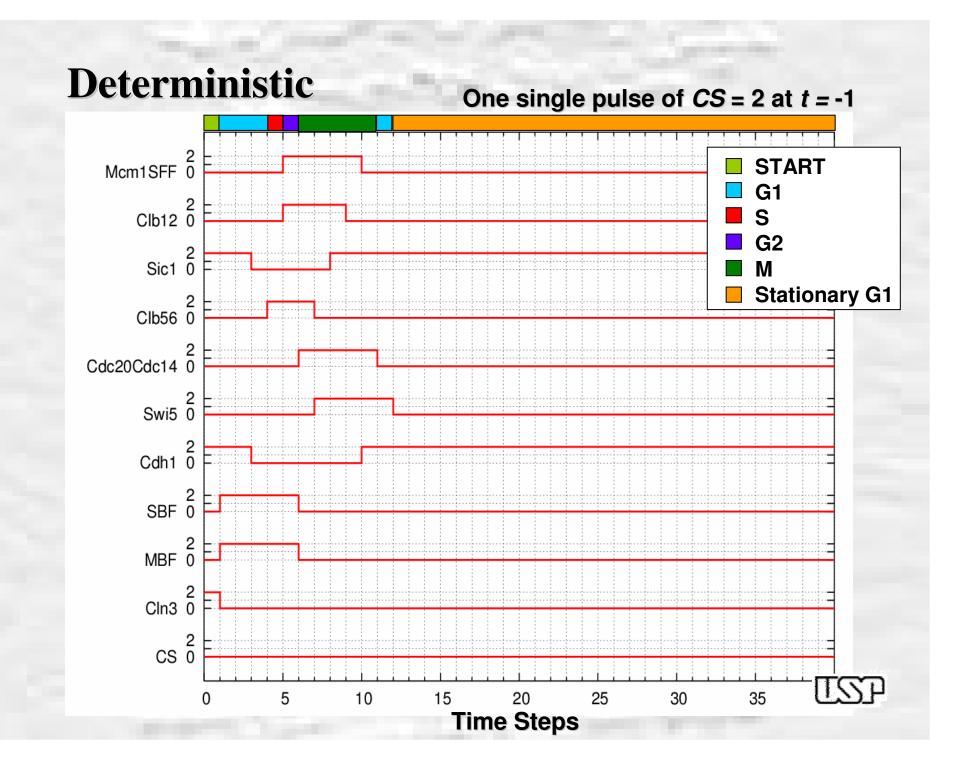
Self Degradation: (yellow loops) If a node *i* with a self yellow arrow has value $S_i(t) = 1$ and its total input from t + 1 to $t = t + t_d$ is zero then $S_i(t + t_d) = 0$

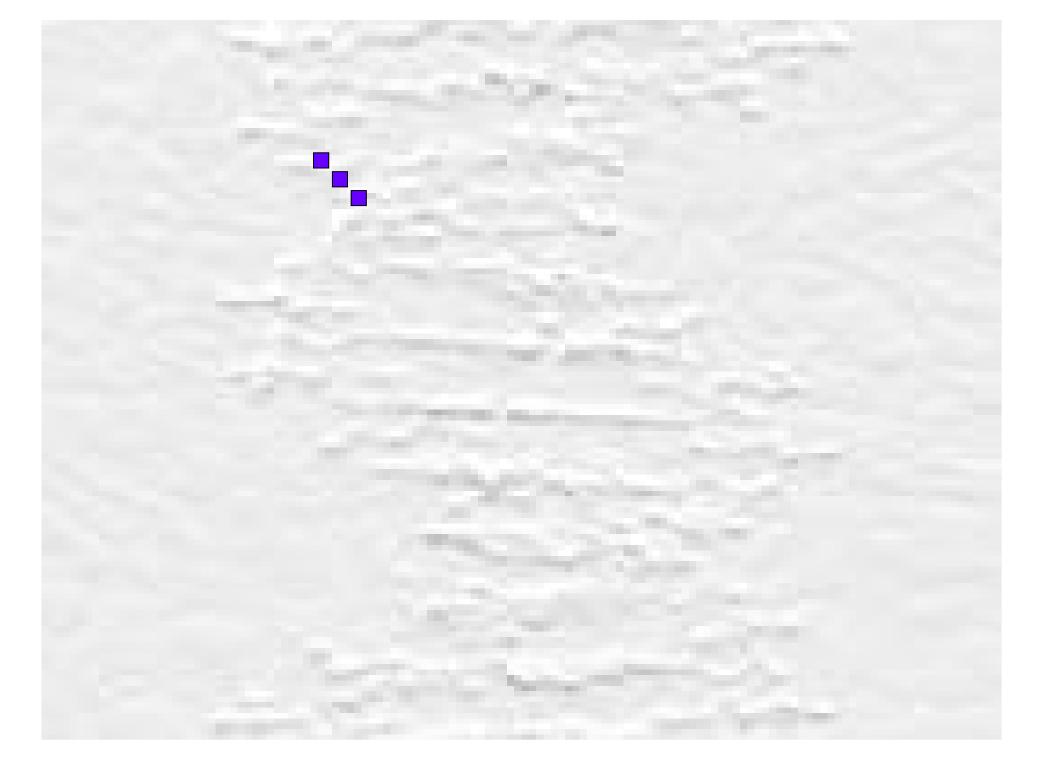


Simplified Cell-Cycle Network Fig. 1 (B)

Simulation parameters: $a_g = -a_r = 1$, $t_d = 1$







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$$1 \rightarrow 2$$

3 Levels (0, 1, 2)

n		0
U	7	U

$\sum a_{ij}S_j(0)$	$S_j(t+1)$		
$\sum_{j} \alpha_{ij} S_{j}(0)$	$S_j(t) = 0$	$S_j(t) = 1$	
<u> </u>	•	:	
3	1	1	
2	1	1	
1	1	1	
0	0	1	
-1	0	0	
-2	0	0	
-3	0	0	

$\sum a_{ij}S_{j}(0)$	$y_j(t+1)$			
$\sum_{j} a_{ij} S_{j}(0)$	$S_j(t) = 0$	$S_j(t) = 1$	$S_j(t) = 2$	
3	2	2	2	
2	2	2	2	
1	1	2	2	
0	0	1	2	
-1	0	0	1	
-2	0	0	0	
-3	0	0	0	
			:	

Stochastic Transition Function

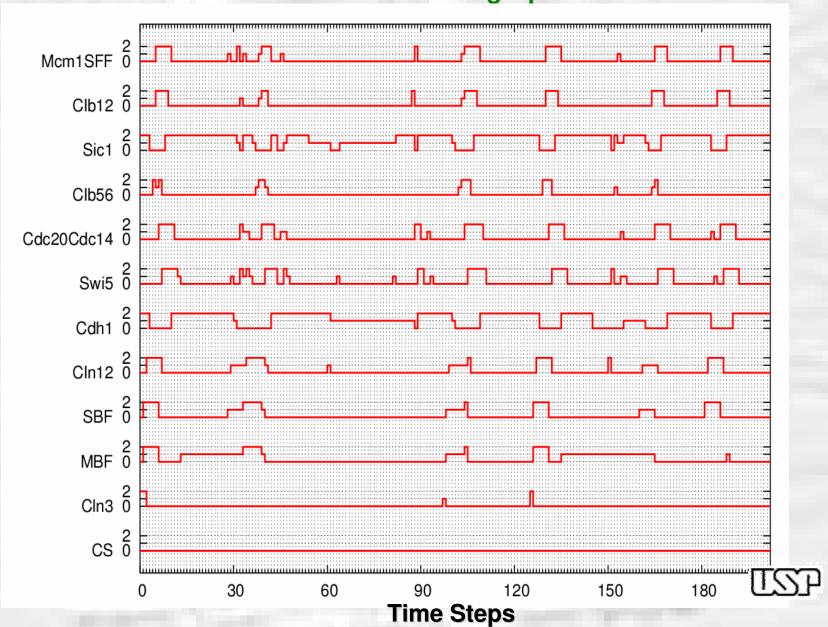
$\sum a_{ij} S_j(0)$	$y_j(t+1)$			
$\sum_{j} a_{ij} S_{j}(0)$	$S_j(t) = 0$	$S_j(t) = 1$	$S_j(t) = 2$	
· · · · · · · · · · · · · · · · · · ·	:		÷	
3	2	2	2	
2	2	2	2	
1	1	2	2	
0	0	1	2	
-1	0	0	1	
-2	0	0	0	
-3	0	0	0	

$$x_{i}(t+1) = \begin{cases} y_{i}(t+1) & \text{with } P = 0.99 \\ a & \text{with } P = 0.005 \\ b & \text{with } P = 0.005 \end{cases}$$

where
$$a, b \in \{0,1,2\} - \{y_i(t+1)\}$$



One single pulse of CS = 2 at t = -1



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Gene Model

Driving Function

Total input signal driving a generic variable

$$x_i(t) \in \{0, 1, 2\} \quad (1 \le i \le N)$$
 is

$$d_i(t-1) = \sum_{j=1}^{N} \sum_{k=1}^{m} a_{ji}^k x_j(t-k)$$

Driving function for x_i

m: memory of the system a_{ji}^k : weight for variable x_j at time t-k



Gene Model

Transition Function

Let
$$y_i(t) = \begin{cases} 2 & \text{if } d_i(t-1) \ge th2_{x_i} \\ 1 & \text{if } th1_{x_i} \le d_i(t-1) < th2_{x_i} \\ 0 & \text{if } d_i(t-1) < th1_{x_i}. \end{cases}$$

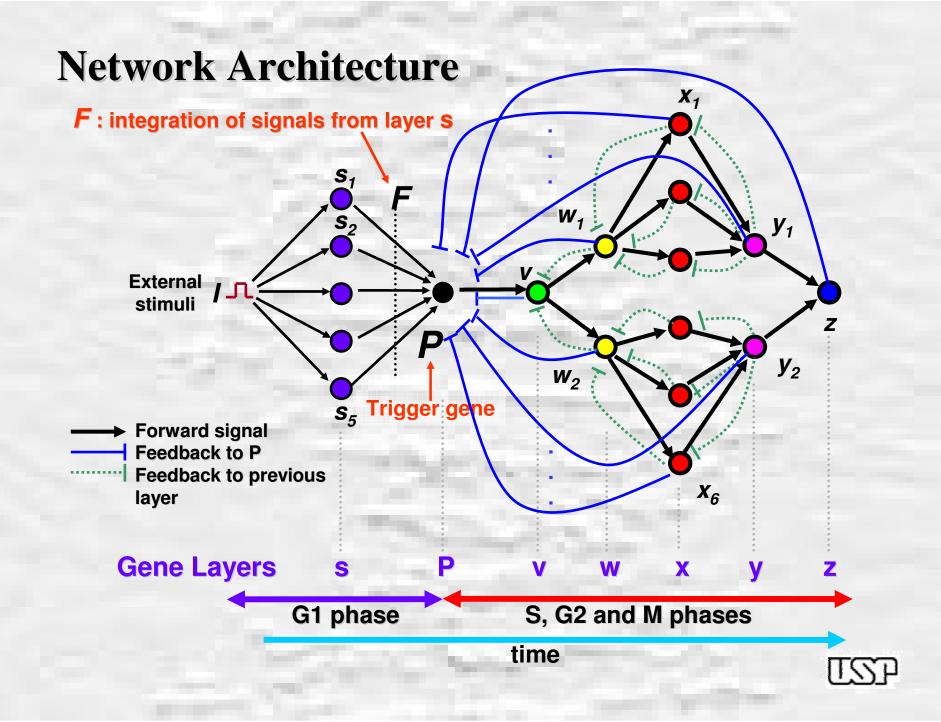
 $th1_{x_i}, th2_{x_i}$: threshold values for one and two.

Stochastic Transition Function

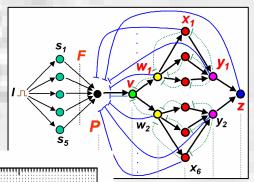
$$x_i(t) = \left\{ egin{array}{ll} y_i(t) & \mathrm{with} & P pprox 1 \ & a & \mathrm{with} & (1-P)/2 \ & b & \mathrm{with} & (1-P)/2. \end{array}
ight.$$

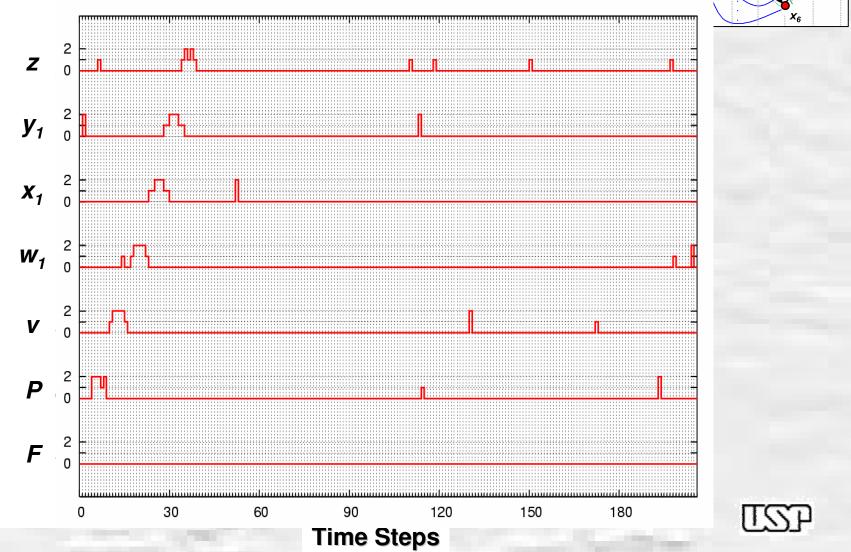
$$a, b \in \{0, 1, 2\} - \{y_i(t)\}$$

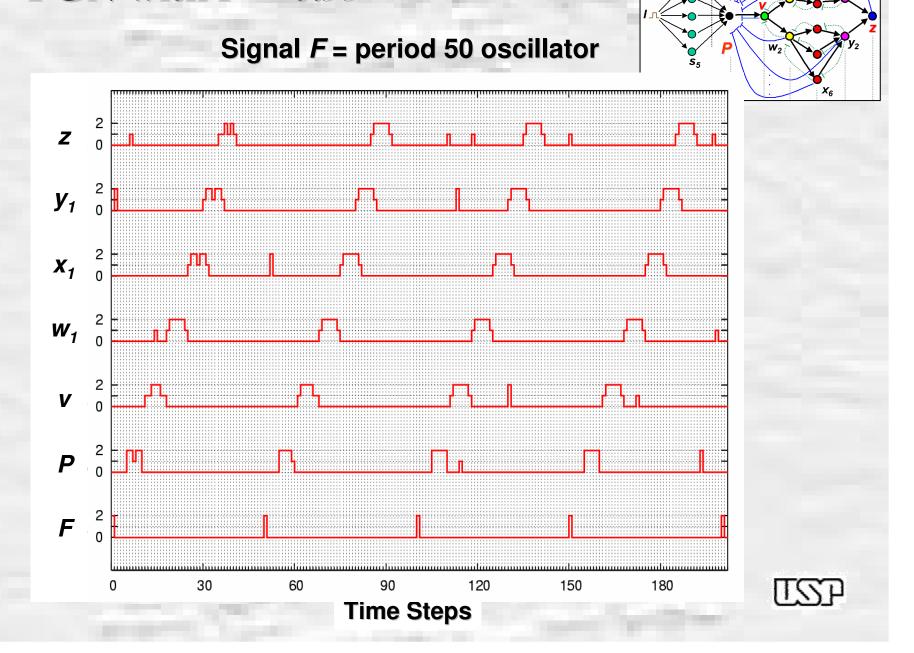


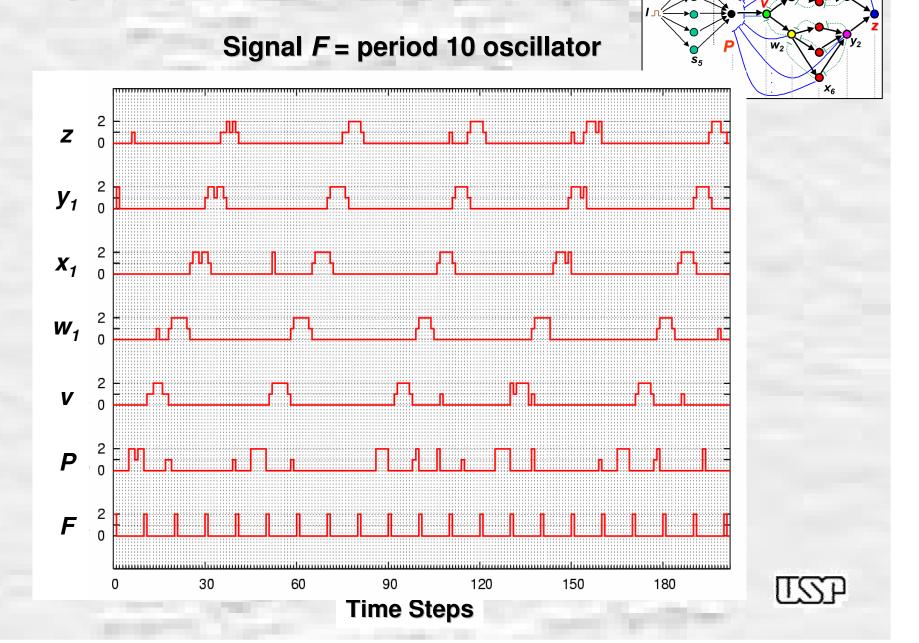


One single pulse of F = 2 at t = -1

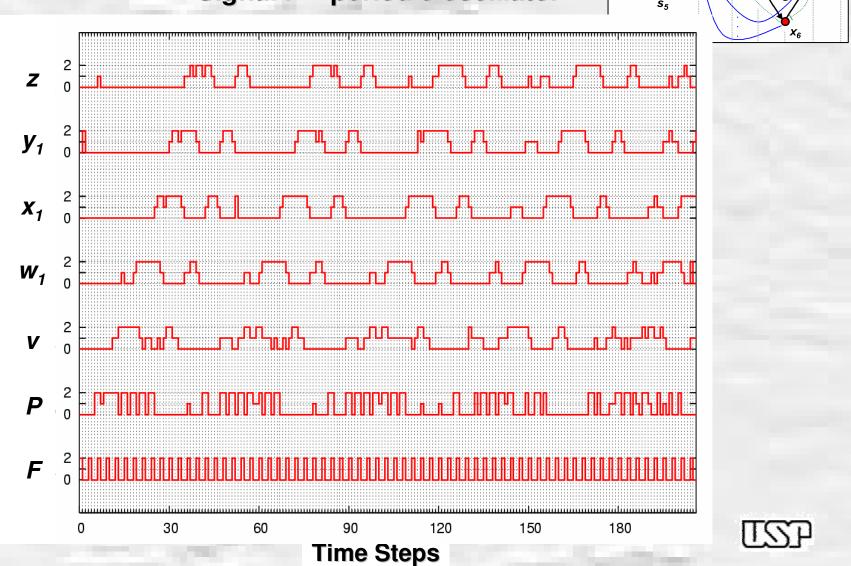








Signal F = period 3 oscillator



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Model Design

Hypothetical, based on observed behavior

X

Based on documented biological interactions

Similarities:

Checkpoint triggers cycle progression
Signal wave propagation
Stability in the presence of variable excitation (without noise)



New Characteristics

- •Hierarchical negative feed back structure
- Robustness in the presence of noise and variable excitation

Hierarchical NEGATIVE FEEDBACK LOOPS provide STABILITY and ROBUSTNESS



Thanks!

