

# Quantifying Flows in Time-Irreversible Markov Chains: Application to Gene Regulatory Network

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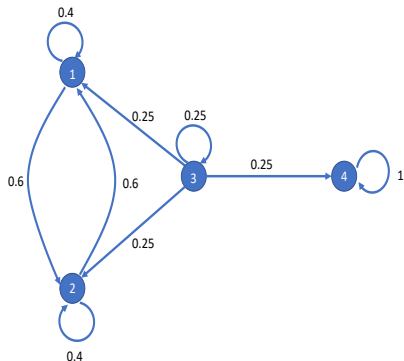
# Outline

- 1 Background
  - Markov Chains
  - Transition Path Theory
- 2 Methodology for Quantifying Transitions
- 3 Application to Gene Regulatory Networks
  - Exploring the Dynamical Network
  - Mutation Analysis
- 4 Conclusion

# Discrete-Time Markov Chains

A discrete-time Markov chain is defined by:

- A sequence of random variables  $(X_n)_{n \geq 0} \in$  a countable set  $S$  characterized by the Markov property,
- Transition matrix  $P$ ,
- Initial distribution  $\lambda$ .



## Time-Reversible VS Time-Irreversible

- A Markov chain with transition matrix  $P$  and stationary distribution  $\pi$  satisfying

$$\pi P = \pi, \quad \sum_{i \in S} \pi = 1$$

is called **time-reversible** if it satisfies the detailed balance condition, i.e

$$\pi_i P_{i,j} = \pi_j P_{j,i}$$

- A Markov chain is called **time-irreversible** if the detailed balance condition is not satisfied. Hence, the transition probabilities for the reversed process is given by

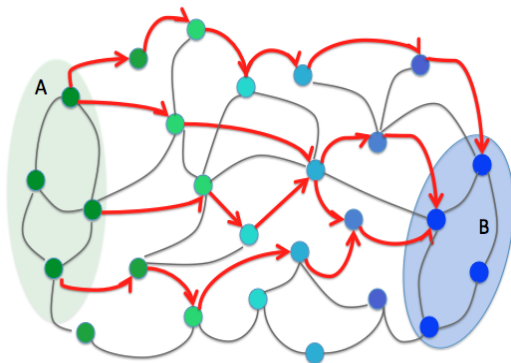
$$\hat{P}_{i,j} = \frac{\pi_j}{\pi_i} P_{j,i}$$

# Objective

- Time-irreversible Markov chains can arise in applications in
  - Economics
  - Physics
  - Social sciences
  - Biology
  - Etc.
- Our goal is to develop efficient computational tools for the study of transition process in large and complex Markov chains.

## Transition Path Theory: E & Vanden-Eijnden (2006)

Transition Path Theory (TPT) is a framework to analyze the statistical properties of reactive trajectories i.e. those going from  $A$  to  $B$  without returning to  $A$  in between.



## Key Concepts of Transition Path Theory

The forward committor function  $q^+ = (q_i^+)_{i \in S}$  is the probability that starting at a state  $i$ , the trajectory will reach set  $B$  prior to set  $A$  and satisfies:

$$\begin{cases} q_i^+ = \sum_{j \in S} P_{i,j} q_j^+, & i \in S \setminus (A \cup B) \\ q_i^+ = 0, & i \in A \\ q_i^+ = 1, & i \in B \end{cases} \quad (1)$$

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The backward committor  $q^- = (q_i^-)_{i \in S}$  is the probability that the process arriving at state  $i$  last came from  $A$  rather than  $B$  and satisfies:

$$\begin{cases} q_i^- = \sum_{j \in S} \hat{P}_{i,j} q_j^-, & i \in S \setminus (A \cup B) \\ q_i^- = 1, & i \in A \\ q_i^- = 0, & i \in B \end{cases} \quad (2)$$

with  $\hat{P}_{i,j}$  being the transition matrix for the time-reversed process



## Key Concepts of Transition Path Theory

The probability current of reactive trajectories is given by

$$f_{i,j} = \begin{cases} \pi_i q_i^- P_{i,j} q_j^+, & \text{if } i \neq j \\ 0, & \text{otherwise} \end{cases} \quad (3)$$

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The effective current

$$f_{i,j}^+ = \max\{f_{i,j} - f_{j,i}, 0\} \quad (4)$$

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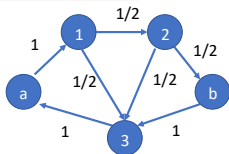
$$f_{i,j}^+ = \max\{f_{i,j} - f_{j,i}, 0\} \quad (4)$$

Transition rate

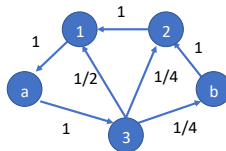
$$\nu_{AB} = \sum_{i \in A, j \in S} f_{ij} = \sum_{i \in S, j \in B} f_{ij} \quad (5)$$

# Illustrative example

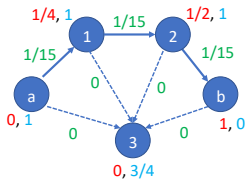
Original MC



Time-reversed MC

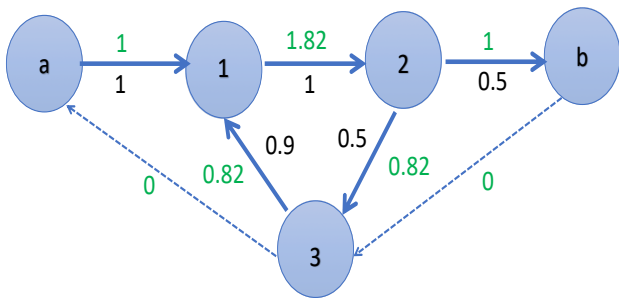


Forward committor, Backward committor and effective current



Transition rate:  
 $v_{ab}=1/15$

# Challenges with Time-Irreversible Markov Chains



Transition rate:

$$v_{ab}=1$$

**Figure:** A cyclic effective current (green). Transition probabilities (black).

## Cycle Removal Algorithm for Obtaining Acyclic Current

We develop an algorithm for generating a weighted directed acyclic graph  $G(S, \{F^+\})$

---

**Input:** Weighted directed graph  $G(S, \{f^+\})$

**Output:** Weighted directed acyclic graph  $G(S, \{F^+\})$

**The main body**

**while**  $flag == 0$  **do**

    Find cycle in  $G(S, \{f^+\})$  using DFS algorithm

**if** *cycle is found* **then**

        Find minimum current in the cycle  $f_{min}^+$

**for** each edge in the cycle

            subtract minimum current from edge

**end for**

**else**

        |  $flag == 1$

**end**

**end**

# Application to Gene Regulatory Network

# GRN for Budding Yeast Cell Cycle

Chen, Csikasz-Nagy, Gyorffy, Val, Novak, & Tyson (2000)

Li, Long, Lu, Ouyang, & Tang (2003)

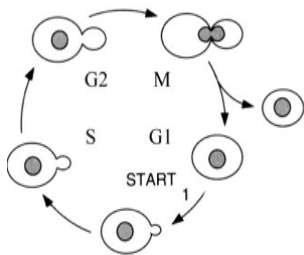


Figure: Budding Yeast Cell Cycle.

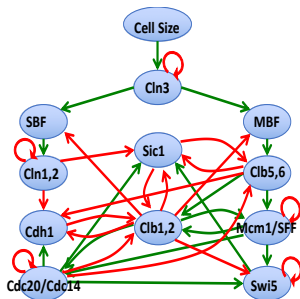
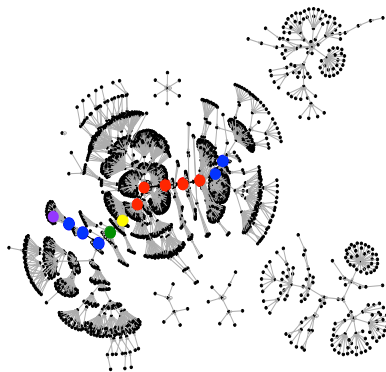


Figure: Gene-regulatory network of budding yeast.



# Deterministic Model



- $a_{ij} = 1$  for protein  $j$  activating protein  $i$ .
- $a_{ij} = -1$  for protein  $j$  repressing protein  $i$ .
- Each node  $i$  has only two states,  $S_i = 1$  and  $S_i = 0$ .

$$S_i(t+1) = \begin{cases} 1, & \sum_i a_{ij} S_j(t) > 0 \\ 0, & \sum_i a_{ij} S_j(t) < 0 \\ S_i(t), & \sum_i a_{ij} S_j(t) = 0 \end{cases}$$

Figure: Dynamical trajectories

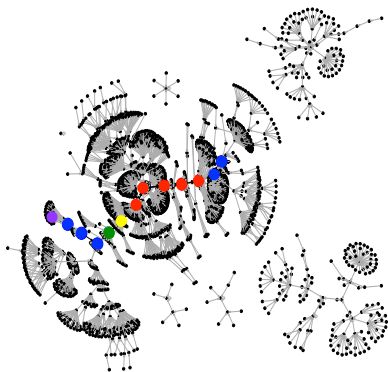


Figure: Dynamical trajectories

$i$	Cln3	SBF	MBF	Cln1,2	Sic1	Clb5,6	Cdh1	Clb1,2	Mcm1/SFF	Cdc20,14	Swi5	Phase
1	1	0	0	0	1	0	1	0	0	0	0	START
2	0	1	1	0	1	0	1	0	0	0	0	G1
3	0	1	1	1	1	0	1	0	0	0	0	G1
4	0	1	1	1	0	0	0	0	0	0	0	G1
5	0	1	1	1	0	1	0	0	0	0	0	S
6	0	1	1	1	0	1	0	1	1	0	0	G2
7	0	0	0	1	0	1	0	1	1	1	0	M
8	0	0	0	0	0	0	0	1	1	1	1	M
9	0	0	0	0	1	0	0	1	1	1	1	M
10	0	0	0	0	1	0	0	0	1	1	1	M
11	0	0	0	0	1	0	1	0	0	1	1	M
12	0	0	0	0	1	0	1	0	0	0	1	G1
13	0	0	0	0	1	0	1	0	0	0	0	G1*

Figure: Biological pathway of deterministic model

## Stochastic Model: Zhang, Qian, Ouyang, Deng, Li, &amp; Tang (2006)

let  $v = As$

$$\mathbb{P}\{s_1(t+1), \dots, s_{11}(t+1) | s_1(t), \dots, s_{11}(t)\} = \prod_{i=1}^{11} \mathbb{P}\{s_i(t+1) | s_1(t), \dots, s_{11}(t)\} \quad (6)$$

where if  $v_i \neq 0$

$$\mathbb{P}\{s_i(t+1) = 1 | s_1(t), \dots, s_{11}(t)\} = \frac{e^{\beta v_i}}{e^{\beta v_i} + e^{-\beta v_i}} \quad (7)$$

$$\mathbb{P}\{s_i(t+1) = 0 | s_1(t), \dots, s_{11}(t)\} = \frac{e^{-\beta v_i}}{e^{\beta v_i} + e^{-\beta v_i}} \quad (8)$$

if  $v_i = 0$

$$\mathbb{P}\{s_i(t+1) = s_i(t) | s_1(t), \dots, s_{11}(t)\} = \frac{1}{1 + e^{-\alpha}} \quad (9)$$

## Results of Cycle Removal Algorithm to GRN

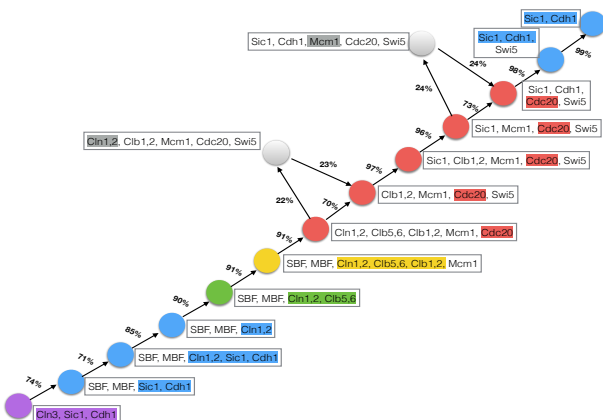
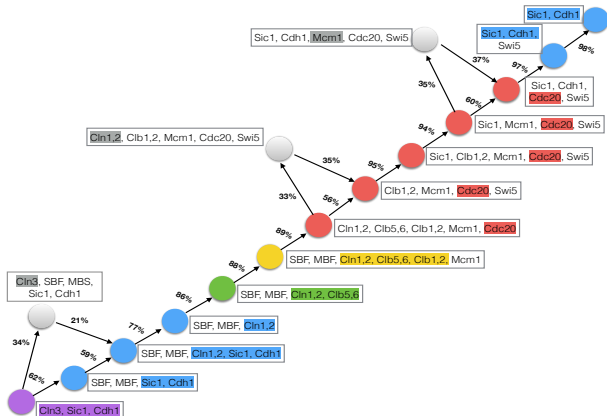


Figure: Acyclic current through cell cycle for  $\alpha = 5$ ,  $\beta = 6$ .

## Results of Cycle Removal Algorithm to Stochastic Model

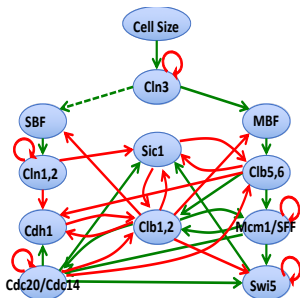
Figure: Acyclic current through cell cycle for  $\alpha = 5$ ,  $\beta = 3$ .

## Mutation Analysis (Cameron & Middlebrooks)

We use our cycle removal algorithm to identify essential edges in the GRN.

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We use our cycle removal algorithm to identify essential edges in the GRN.



- Recompute transition matrix
- Run cycle removal algorithm on  $G(S, \{f^+\})$  to obtain acyclic current
- Run DFS algorithm to obtain pathways

## Analysis of Deterministic Model

	Non-Essential Edges	Essential Edges
5	<p>No effect:</p> <p><i>Clb5,6</i> → <i>Sic1</i></p> <p><i>Clb5,6</i> → <i>Cdh1</i></p> <p><i>Cdh1</i> → <i>Clb1,2</i></p> <p><i>Clb1,2</i> → <i>Sic1</i></p> <p><i>Clb1,2</i> → <i>Cdc20/Cdc14</i></p>	<p><i>Cln3</i> → <i>Cln3</i></p> <p><i>Cln3</i> → <i>SBF</i></p> <p><i>Cln3</i> → <i>MBF</i></p> <p><i>SBF</i> → <i>Cln1,2</i></p> <p><i>MBF</i> → <i>Cln5,6</i></p> <p><i>Cln1,2</i> → <i>Cln1,2</i></p> <p><i>Cln1,2</i> → <i>Sic1</i></p> <p><i>Sic1</i> → <i>Clb1,2</i></p> <p><i>Clb1,2</i> → <i>SBF</i></p> <p><i>Clb1,2</i> → <i>MBF</i></p>
6	<p>Small effect:</p> <p><i>Clb5,6</i> → <i>Mcm1/SFF</i></p> <p><i>Clb1,2</i> → <i>Cdh1</i></p> <p><i>Clb1,2</i> → <i>Mcm1/SFF</i></p> <p><i>Clb1,2</i> → <i>Swi5</i></p> <p><i>Mcm1/SFF</i> → <i>Clb1,2</i></p> <p><i>Mcm1/SFF</i> → <i>Cdc20/Cdc14</i></p>	<p><i>Mcm1/SFF</i> → <i>Mcm1/SFF</i></p> <p><i>Mcm1/SFF</i> → <i>Swi5</i></p> <p><i>Cdc20/Cdc14</i> → <i>Sic1</i></p> <p><i>Cdc20/Cdc14</i> → <i>Clb5,6</i></p> <p><i>Cdc20/Cdc14</i> → <i>Cdh1</i></p> <p><i>Cdc20/Cdc14</i> → <i>Clb1,2</i></p> <p><i>Cdc20/Cdc14</i> → <i>Cdc20/Cdc14</i></p> <p><i>Cdc20/Cdc14</i> → <i>Swi5</i></p>
3	<p>Lost of G2 phase:</p> <p><i>Cln1,2</i> → <i>Cdh1</i></p> <p><i>Sic1</i> → <i>Clb5,6</i></p> <p><i>Clb5,6</i> → <i>Clb1,2</i></p>	<p><i>Swi5</i> → <i>Sic1</i></p> <p><i>Swi5</i> → <i>Swi5</i></p>
	Total: 14	Total: 20

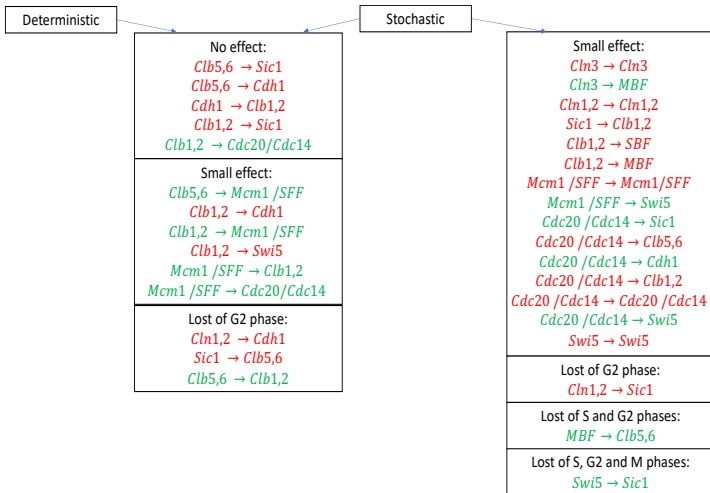


# Analysis of Stochastic Model

Non-Essential Edges		Essential Edges
5	No effect: <i>Clb5,6</i> → <i>Sic1</i> <i>Clb5,6</i> → <i>Cdh1</i> <i>Cdh1</i> → <i>Clb1,2</i> <i>Clb1,2</i> → <i>Sic1</i> <i>Clb1,2</i> → <i>Cdc20/Cdc14</i>	Lost of S and G2 phases: <i>MBF</i> → <i>Clb5,6</i>
	Lost of G2 phase: <i>Cln1,2</i> → <i>Cdh1</i> <i>Cln1,2</i> → <i>Sic1</i> <i>Sic1</i> → <i>Clb5,6</i> <i>Clb5,6</i> → <i>Clb1,2</i>	
4	Small effect: <i>Cln3</i> → <i>Cln3</i> <i>Cln3</i> → <i>MBF</i> <i>Cln1,2</i> → <i>Cln1,2</i> <i>Sic1</i> → <i>Clb1,2</i> <i>Clb1,2</i> → <i>SBF</i> <i>Clb1,2</i> → <i>MBF</i> <i>Clb5,6</i> → <i>Mcm1/SFF</i> <i>Clb1,2</i> → <i>Cdh1</i> <i>Clb1,2</i> → <i>Mcm1/SFF</i> <i>Clb1,2</i> → <i>Swi5</i> <i>Mcm1/SFF</i> → <i>Clb1,2</i> <i>Mcm1/SFF</i> → <i>Cdc20/Cdc14</i> <i>Mcm1/SFF</i> → <i>Mcm1/SFF</i> <i>Mcm1/SFF</i> → <i>Swi5</i> <i>Cdc20/Cdc14</i> → <i>Sic1</i> <i>Cdc20/Cdc14</i> → <i>Clb5,6</i> <i>Cdc20/Cdc14</i> → <i>Cdh1</i> <i>Cdc20/Cdc14</i> → <i>Clb1,2</i> <i>Cdc20/Cdc14</i> → <i>Cdc20/Cdc14</i> <i>Cdc20/Cdc14</i> → <i>Swi5</i> <i>Swi5</i> → <i>Swi5</i>	Lost of S, G2 and M phases: <i>Swi5</i> → <i>Sic1</i>
		No pathway found <i>Cln3</i> → <i>SBF</i> <i>SBF</i> → <i>Cln1,2</i>
	Total: 30	Total: 4

21

# Comparison of Results



## Conclusion

- We developed a methodology supported by theoretical results for quantifying transition processes in time-irreversible Markov chains.
- This technique is applied to the Budding yeast GRN.
- Stochastic GRN is much more robust to mutation analysis compared to deterministic GRN.

Future research:

- Develop strategy for selecting key subset of nodes to make applicable to larger and more complex networks.

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## Framework for Quantifying Transitions

### Cameron and Vanden-Eijnden (2013)

Two modified Markov jump processes were designed for the original time-reversible irreducible Markov chain.

- The stationary probability current coincided with the probability current of reactive trajectories.
- The stationary probability current was equal to the reactive current.

### Cameron and Middlebrooks

- Combined these two propositions to a generalized version for time-irreversible Markov chains.

## Theorem (Transition Path Process: Cameron & Middlebrooks)

Suppose we have defined a current  $e$  satisfying the following properties:

[1.] Non-negativity:  $e_{ij} \geq 0$

[2.] The conservation of current:  $\forall i \in S_R, \sum_{j \in S} (e_{ij} - e_{ji}) = 0$

[3.] Transition rate:  $\sum_{i \in A} \sum_{j \in S} e_{ij} = \sum_{i \in S} \sum_{j \in B} e_{ij} = \nu_{AB}$

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Let  $S_R = S \setminus (A \cup B)$  and  $R := \{i \in S_R \mid \exists j \in S : e_{ij} > 0\}$ . Consider the process on the state space  $\tilde{S} = R \cup \{s\}$  defined by the generator  $M$  given by

$$\begin{cases} M_{ij} = \frac{e_{ij}}{\mu_i}, & i, j \in R \\ M_{is} = \sum_{j \in B} \frac{e_{ij}}{\mu_i}, & i \in R \\ M_{sj} = \frac{1}{1-\rho_R} \sum_{i \in A} e_{ij}, & j \in R \end{cases} \quad (10)$$

where  $\rho_R = \sum_{i \in R} \mu_i$ .

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where  $\rho_R = \sum_{i \in R} \mu_i$ . Then the desired invariant probability distribution of the

transition path process is given by  $\tilde{\mu}_i = \begin{cases} \mu_i, & i \in R \\ 1 - \rho_R, & i = s \end{cases}$  and the stationary

current in the network with state space  $\tilde{S}$  and the generator matrix  $M$  coincides with the current  $e$  in the original network.



## Framework for Quantifying Transitions

### Outline of proof

#### Proof.

To show the stationary current in the network with state space  $\tilde{S}$  and the generator matrix  $M$  coincides with the current  $e$  in the original network we must show the following:

- The invariant distribution in the modified MJP is  $\tilde{\mu}$ , i.e show

$$\sum_{i \in RU\{s\}} \tilde{\mu}_i M_{ij} = 0.$$

- The stationary current in the MJP with generator matrix  $M$  coincides with stationary current  $E_{i,j} = e_{i,j} - e_{j,i}$ .

