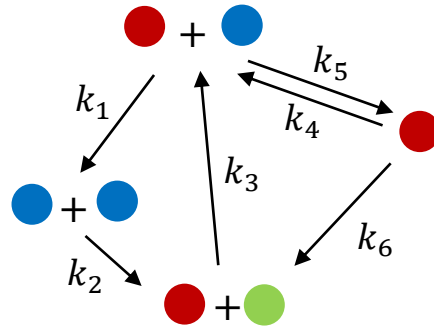


Studying infection disease models with chemical reaction network theory



Jinsu Kim

Department of Mathematics, POSTECH

June 13th, 2022

Preparing for the next pandemic, BIRS 2022

Network representation for biochemical systems

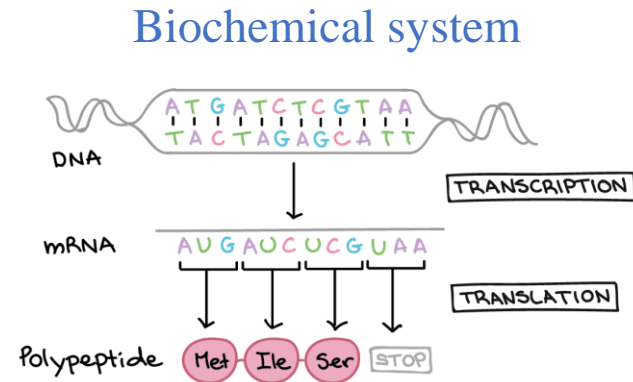
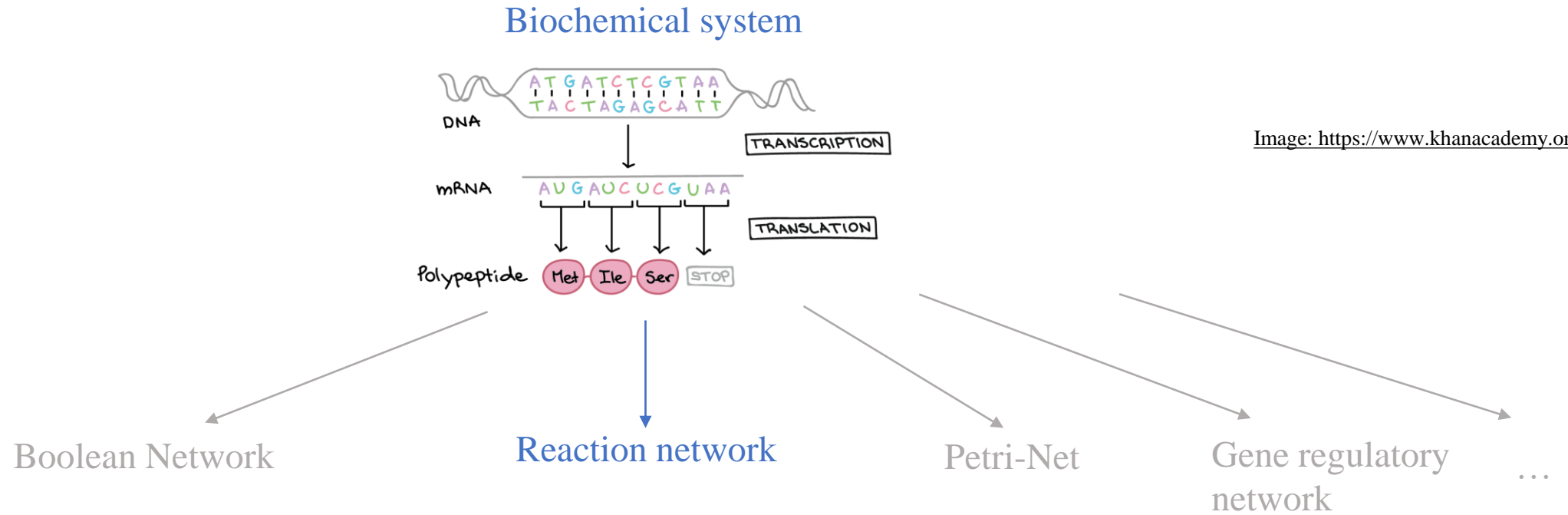
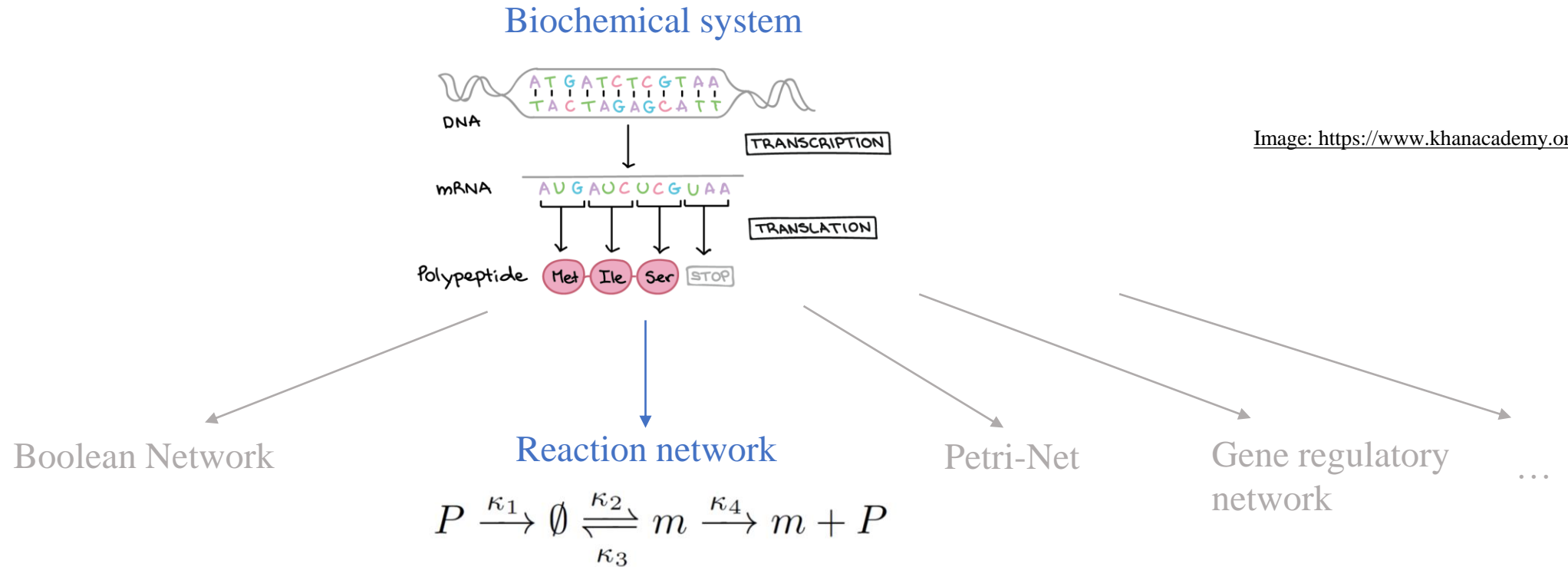


Image: <https://www.khanacademy.org>

Network representation for biochemical systems



Network representation for biochemical systems



Network representation for biochemical systems

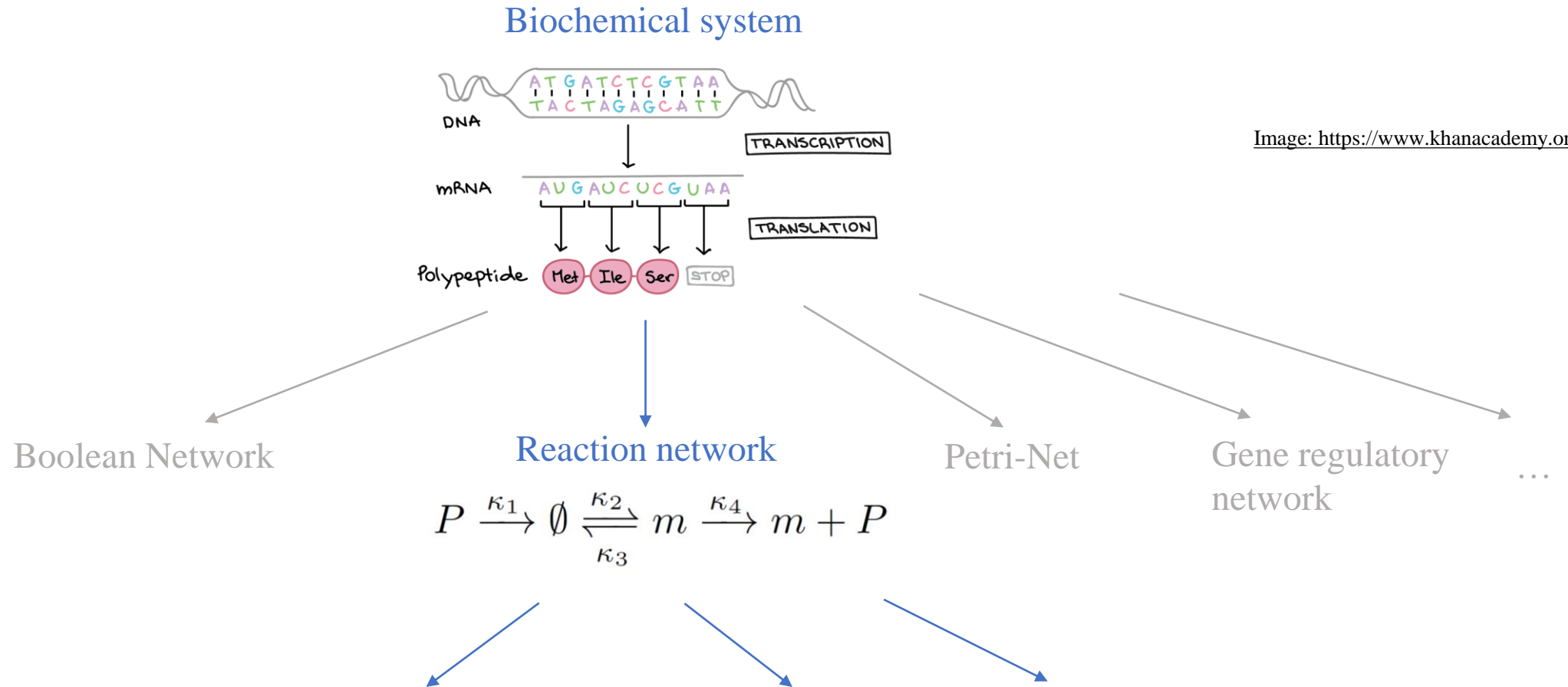
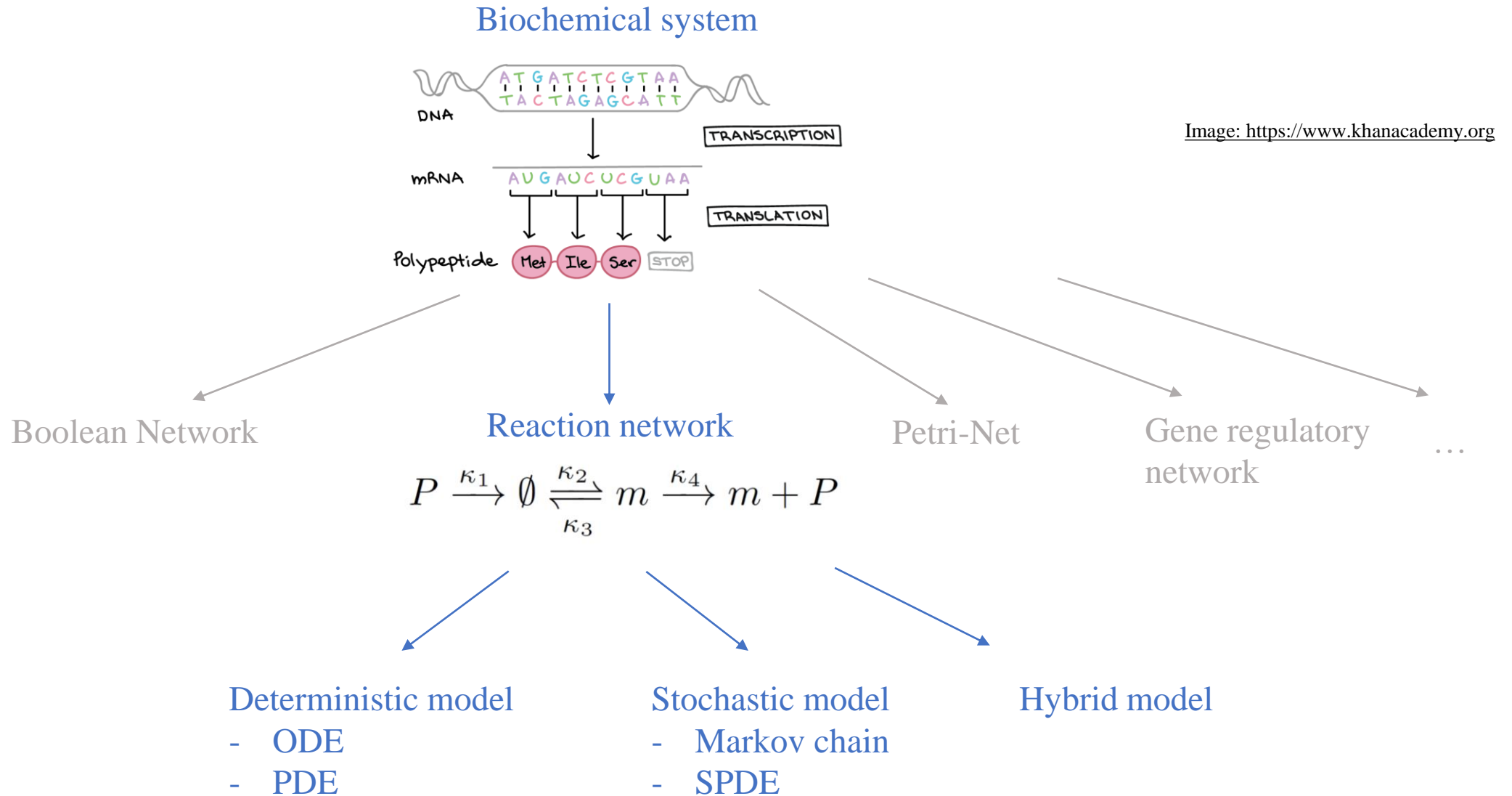
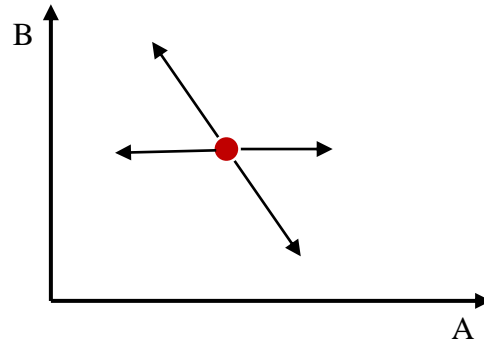
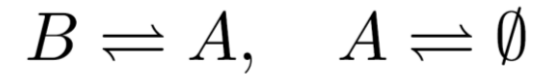


Image: <https://www.khanacademy.org>

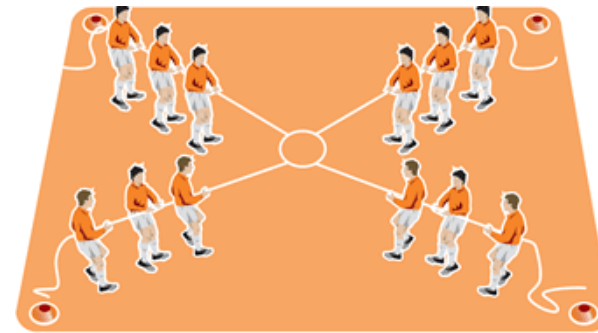
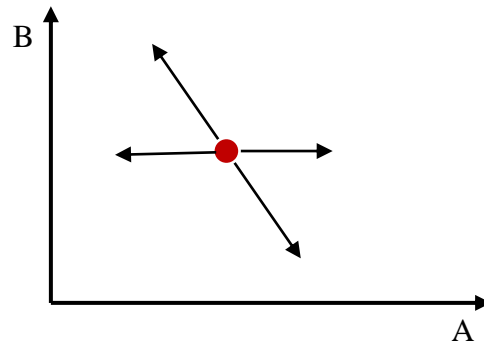
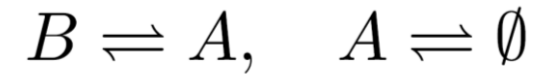
Network representation for biochemical systems



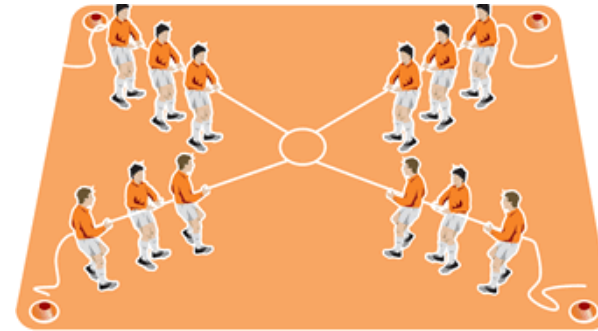
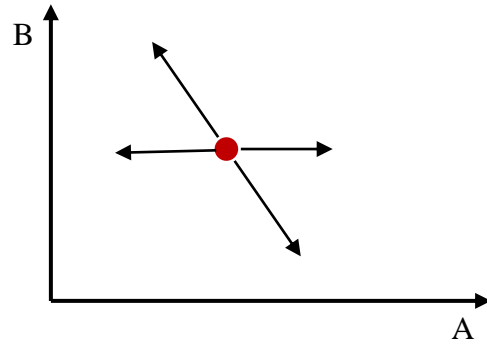
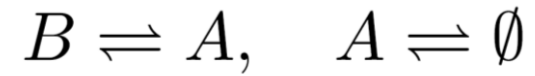
Deterministic modeling for reaction networks



Deterministic modeling for reaction networks

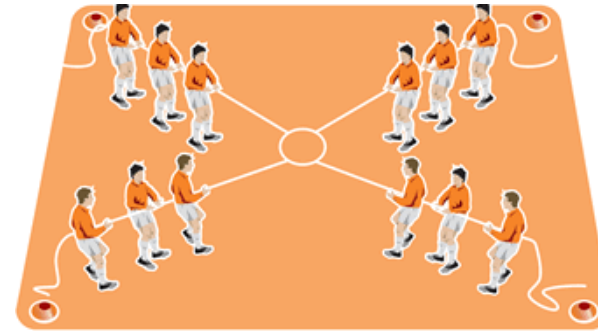
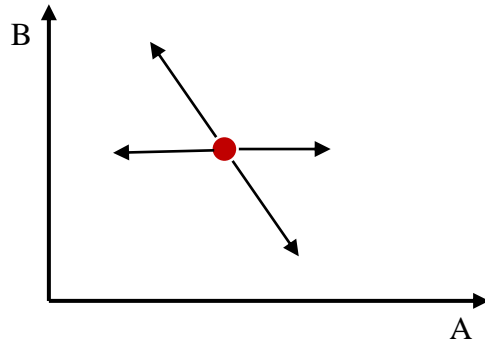
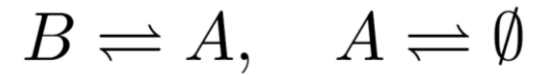


Deterministic modeling for reaction networks



$x(t) = (x_A(t), x_B(t))$: Concentration of A and B

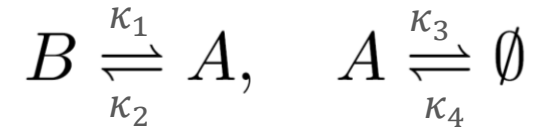
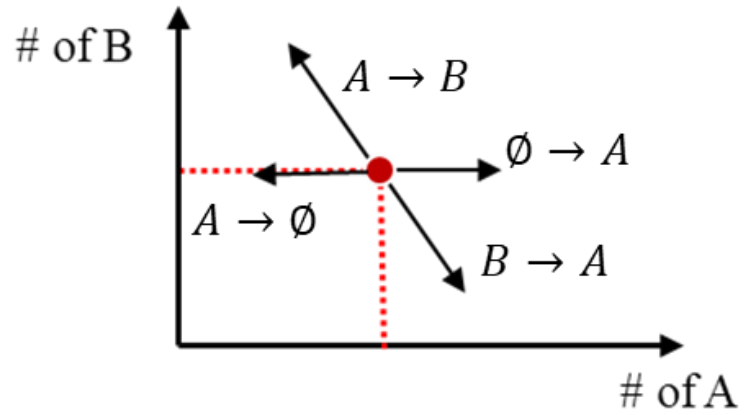
Deterministic modeling for reaction networks



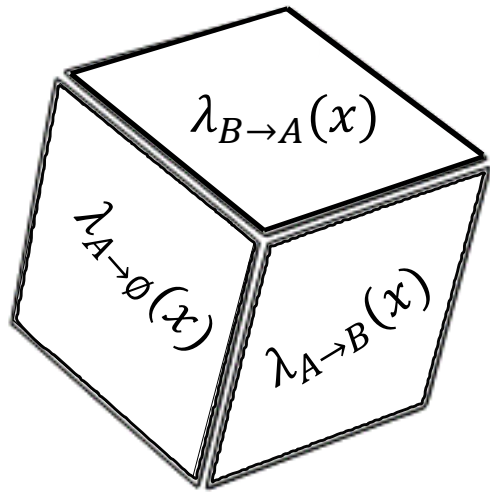
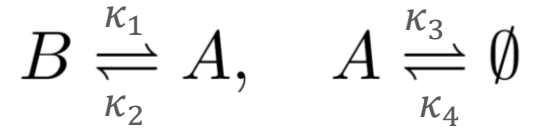
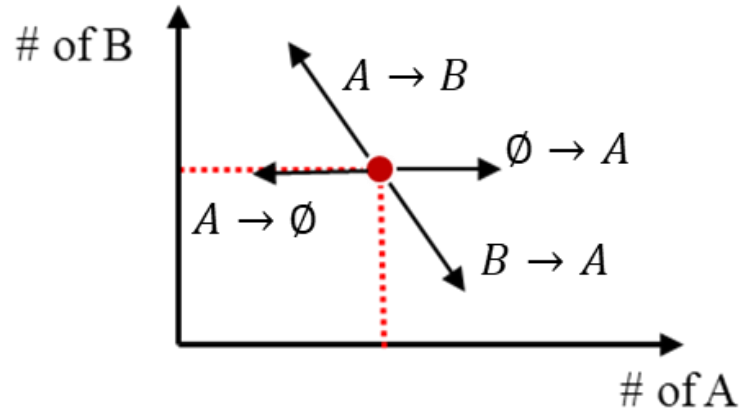
$x(t) = (x_A(t), x_B(t))$: Concentration of A and B

$$\dot{x}(t) = \sum_{y \rightarrow y'} \mathcal{K}_{y \rightarrow y'}(x(t))(y' - y).$$

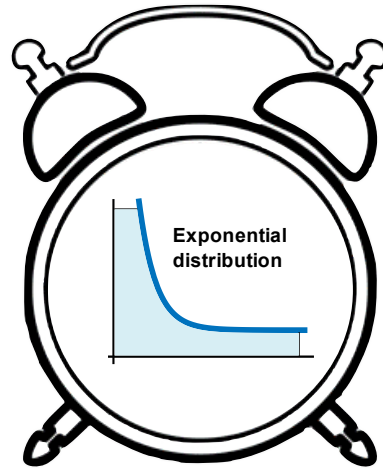
Stochastic modeling for reaction networks



Stochastic modeling for reaction networks

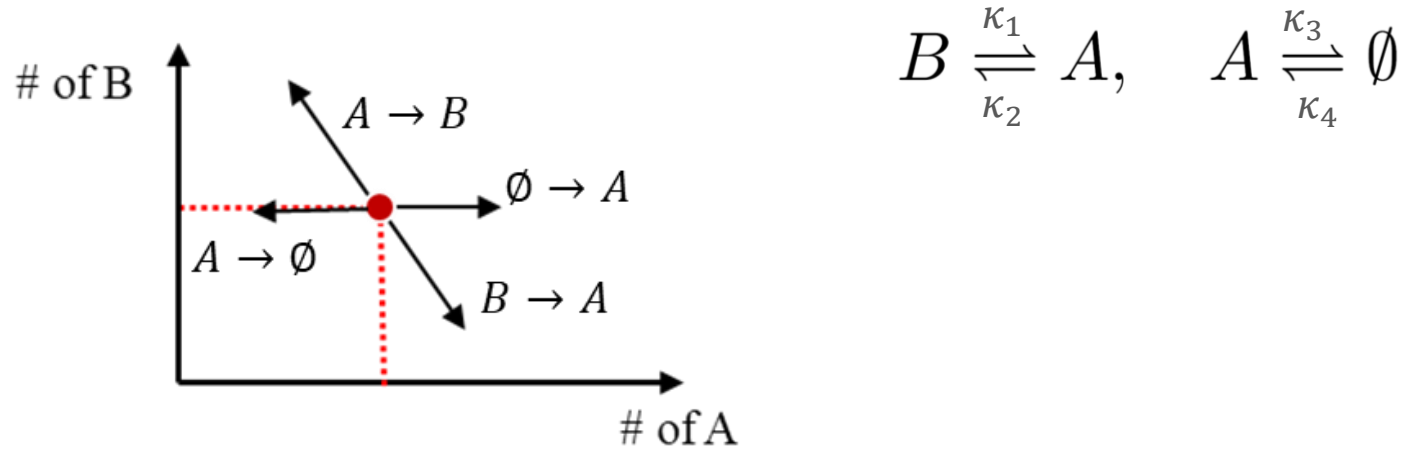


Where to go



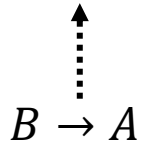
When to go

Stochastic modeling for reaction networks

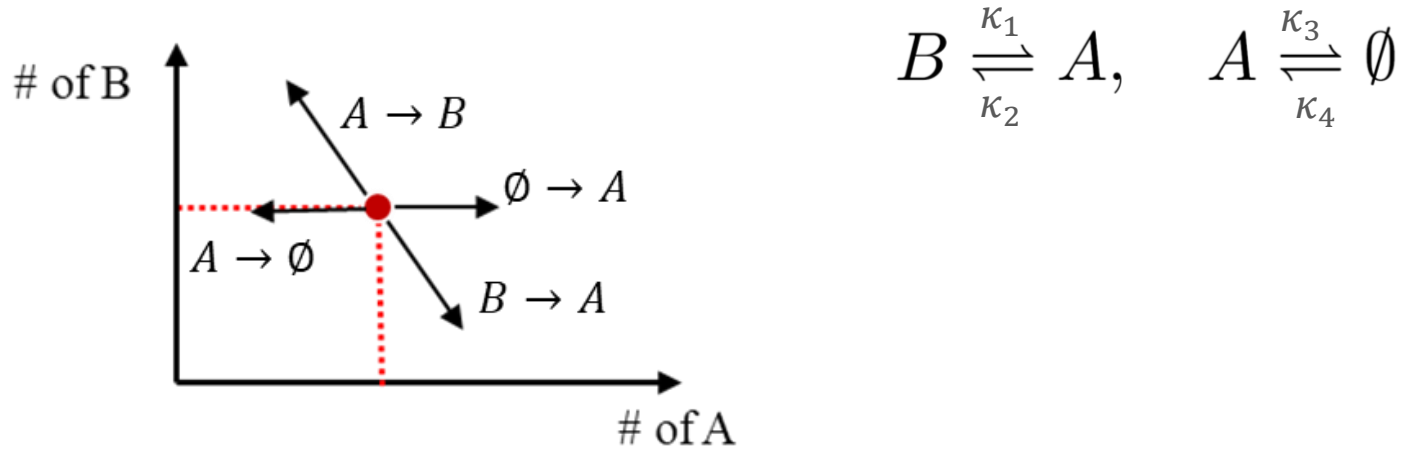


$X(t) = (X_A(t), X_B(t))$: Copy numbers of A and B , Continuous time Markov chain

$$P(X(t + \Delta t) = x + (1, -1)^\top | X(t) = x) = \lambda_{B \rightarrow A}(x) \Delta t + o(\Delta t)$$

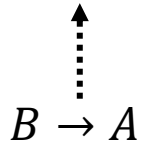


Stochastic modeling for reaction networks



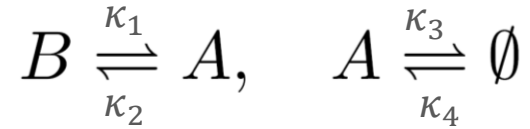
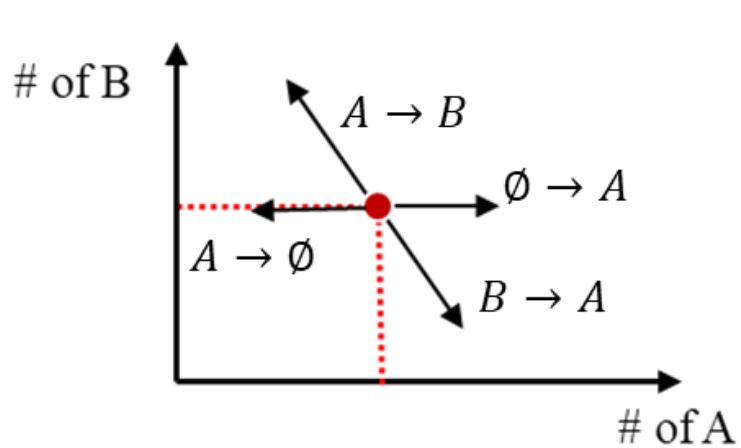
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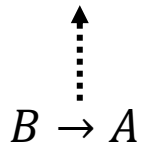
Reaction
Intensity

Stochastic modeling for reaction networks

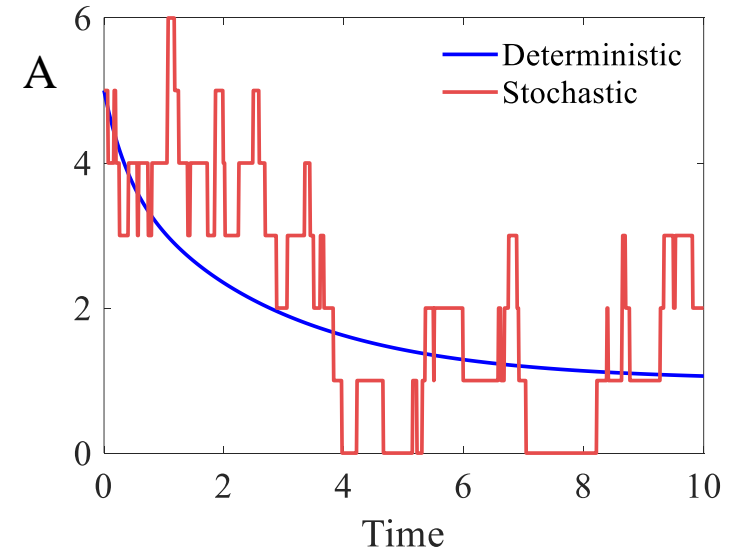


$X(t) = (X_A(t), X_B(t))$: Copy numbers of A and B , Continuous time Markov chain

$$P(X(t + \Delta t) = x + (1, -1)^T | X(t) = x) = \lambda_{B \rightarrow A}(x) \Delta t + o(\Delta t)$$

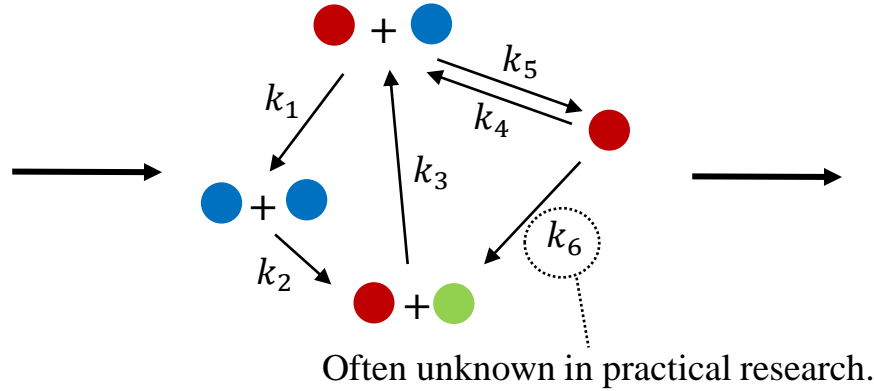


Reaction
Intensity



Network structural conditions \Rightarrow Dynamical Properties

Biological interaction systems

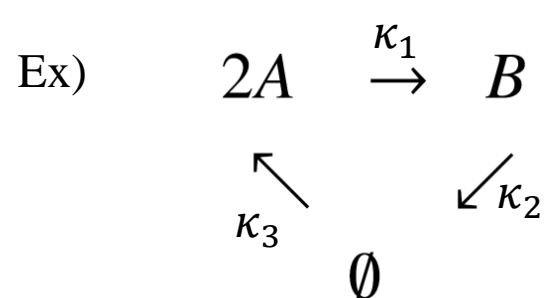


Derive **qualitative behaviors** of the associated dynamics by solely using **graph topological conditions**, regardless of the parameters κ'_i 's.

Theorem [Horn and Jackson(1972), Feinberg (1972)] :

If **# nodes - # connected components - dim{reaction vectors} = 0** and weakly reversible network

\Rightarrow The associated ODE under mass action admits a unique locally stable steady state on each compatibility class.



of complexes = 3

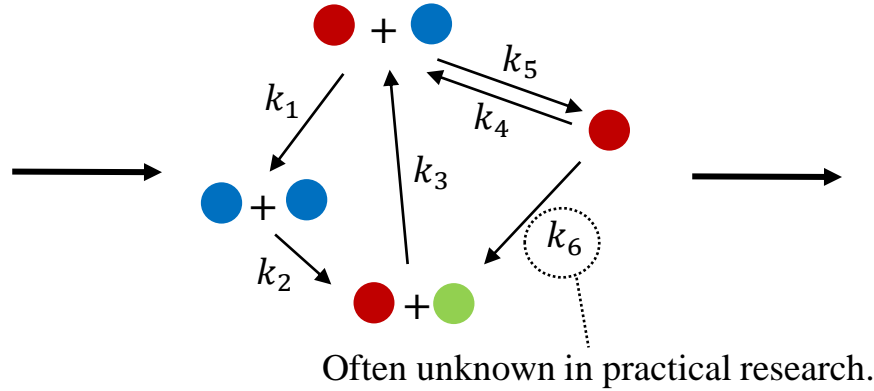
of connected component = 1

dim(reaction vectors) = dim{ (-2,1), (0,-1), (2,0) } = 2

$$3 - 2 - 1 = 0$$

Network structural conditions \Rightarrow Dynamical Properties

Biological interaction systems



Derive **qualitative behaviors** of the associated dynamics by solely using **graph topological conditions**, regardless of the parameters κ'_i 's.

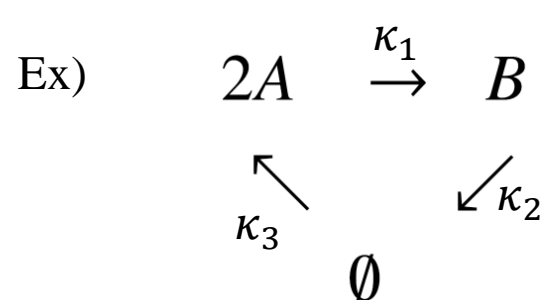
Theorem [Anderson, Craciun and Kurtz (2010)] :

If **# nodes - # connected components - dim{reaction vectors} = 0** and weakly reversible network

\Rightarrow For the associated Markov chain under mass action,

$$\lim_{t \rightarrow \infty} p(A, t) = \pi(A) \text{ for any } A \in \mathbb{Z}_{\geq 0}^d \text{ and } \pi \text{ is a product form of Poissons.}$$

Stationary distribution



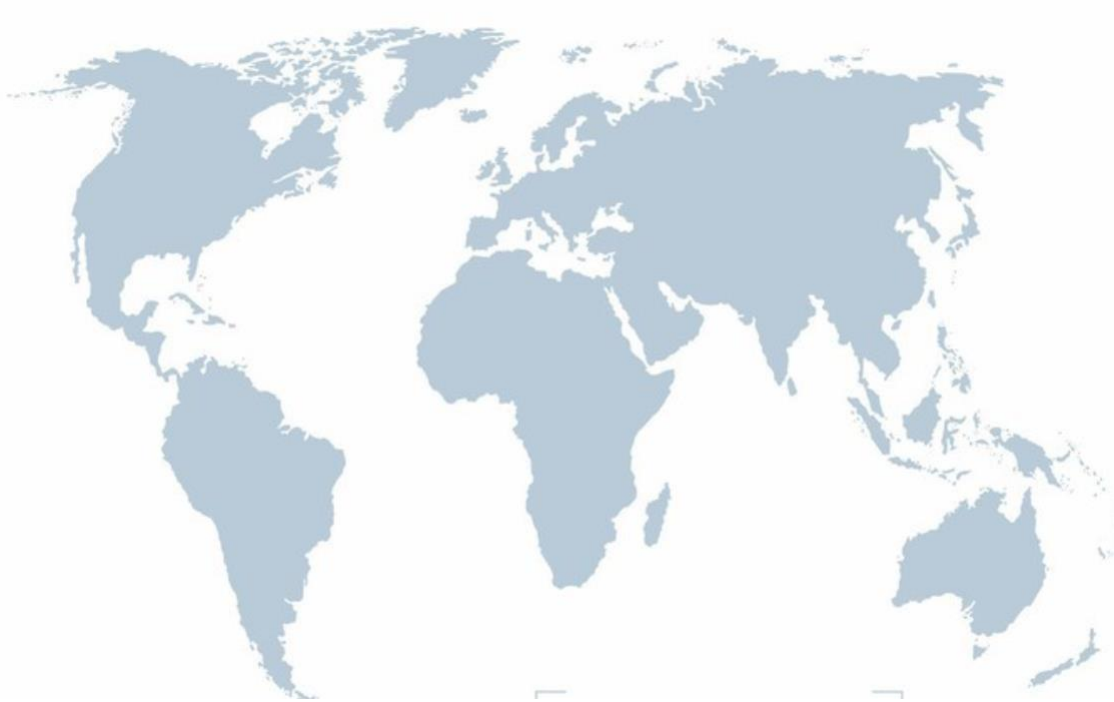
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dim(reaction vectors) = dim{ (-2,1), (0,-1), (2,0) } = 2

$$3 - 2 - 1 = 0$$

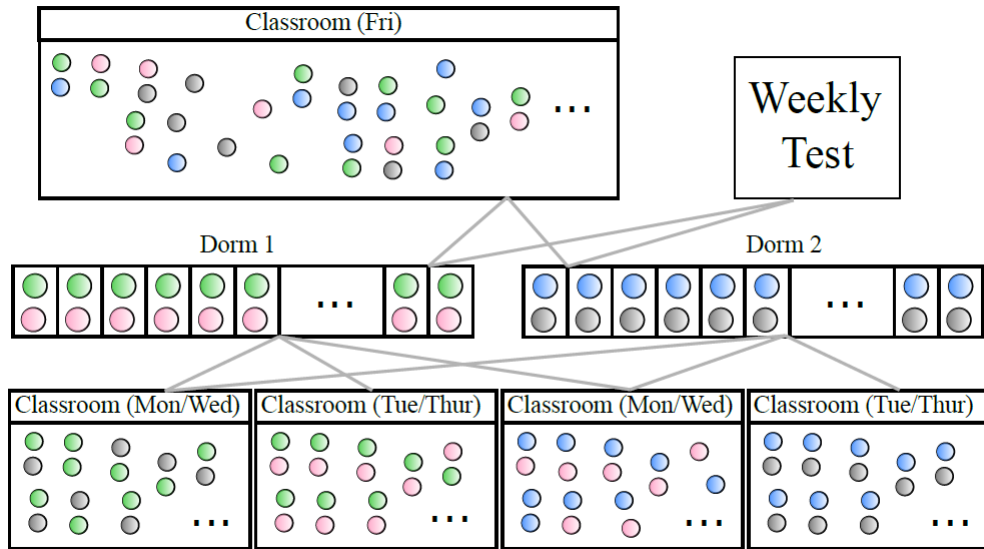
When the network structural conditions can be used for studying infection-disease models?



SIR
SEIR
SIRSS
...

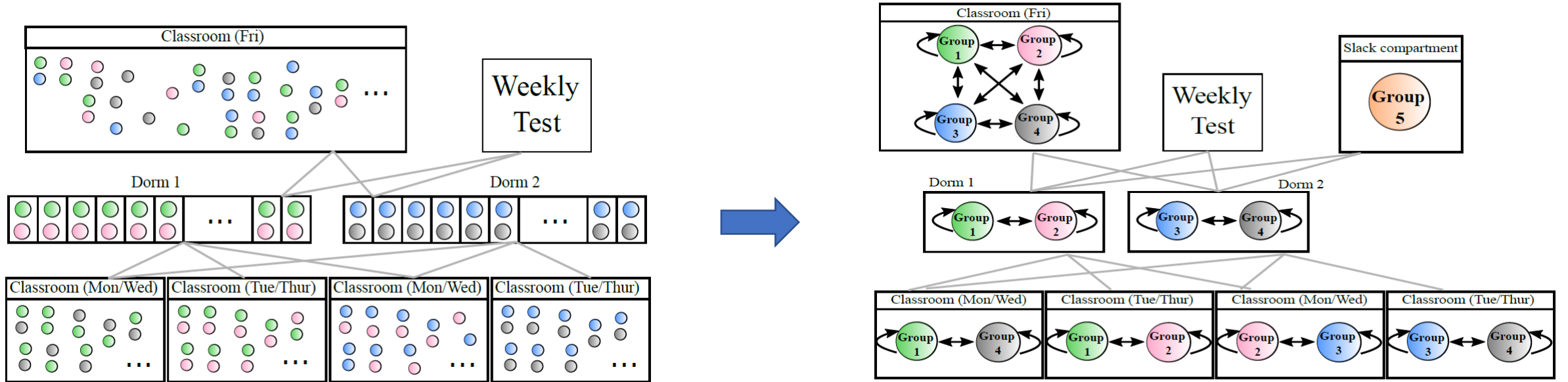
In macroscale, each model may have the same structure, but have different parameters.

Infection-disease models of small communities



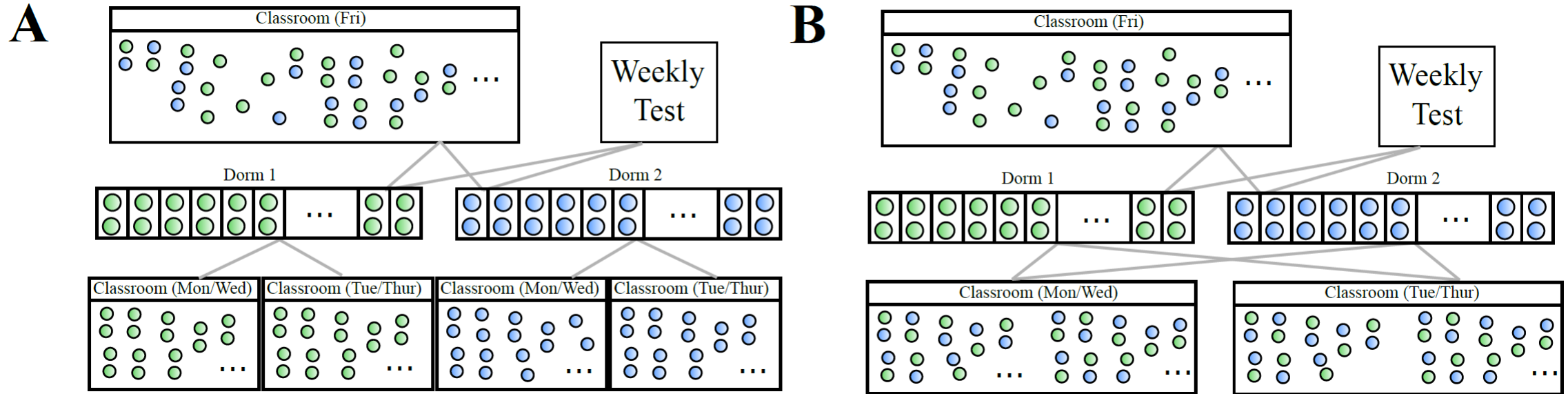
Joint work with German Enciso (UC Irvine) and Suzanne Sindi (UC Merced)

Infection-disease models of small communities



Joint work with German Enciso (UC Irvine) and Suzanne Sindi (UC Merced)

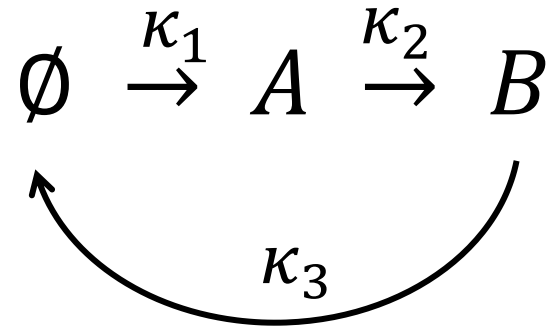
Infection-disease models of small communities



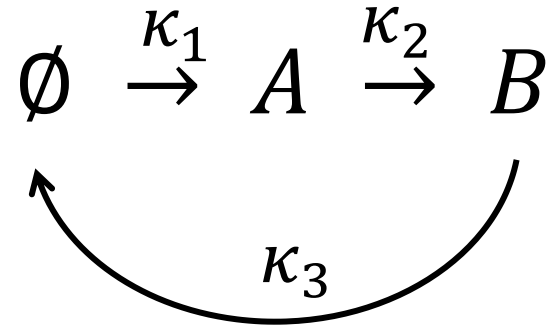
Joint work with German Enciso (UC Irvine) and Suzanne Sindi (UC Merced)

Structural reduction for steady states

Toy examples



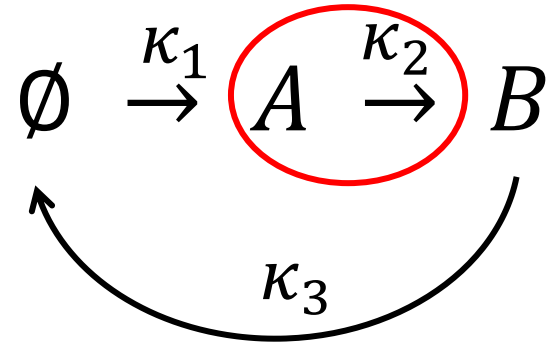
Toy examples



$$a^* = \frac{\kappa_1}{\kappa_2}, \quad b^* = \frac{\kappa_2 a^*}{\kappa_3} = \frac{\kappa_1}{\kappa_3}.$$

Structural reduction for steady states

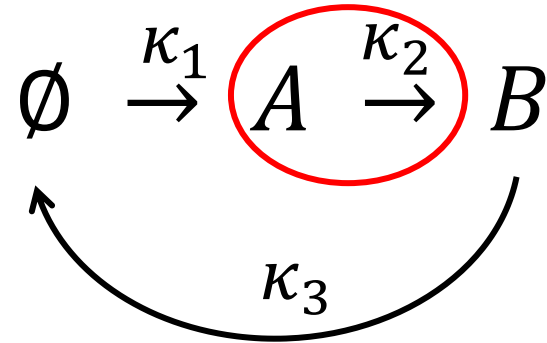
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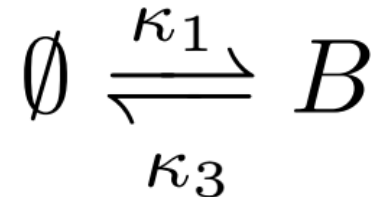
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Structural reduction for steady states

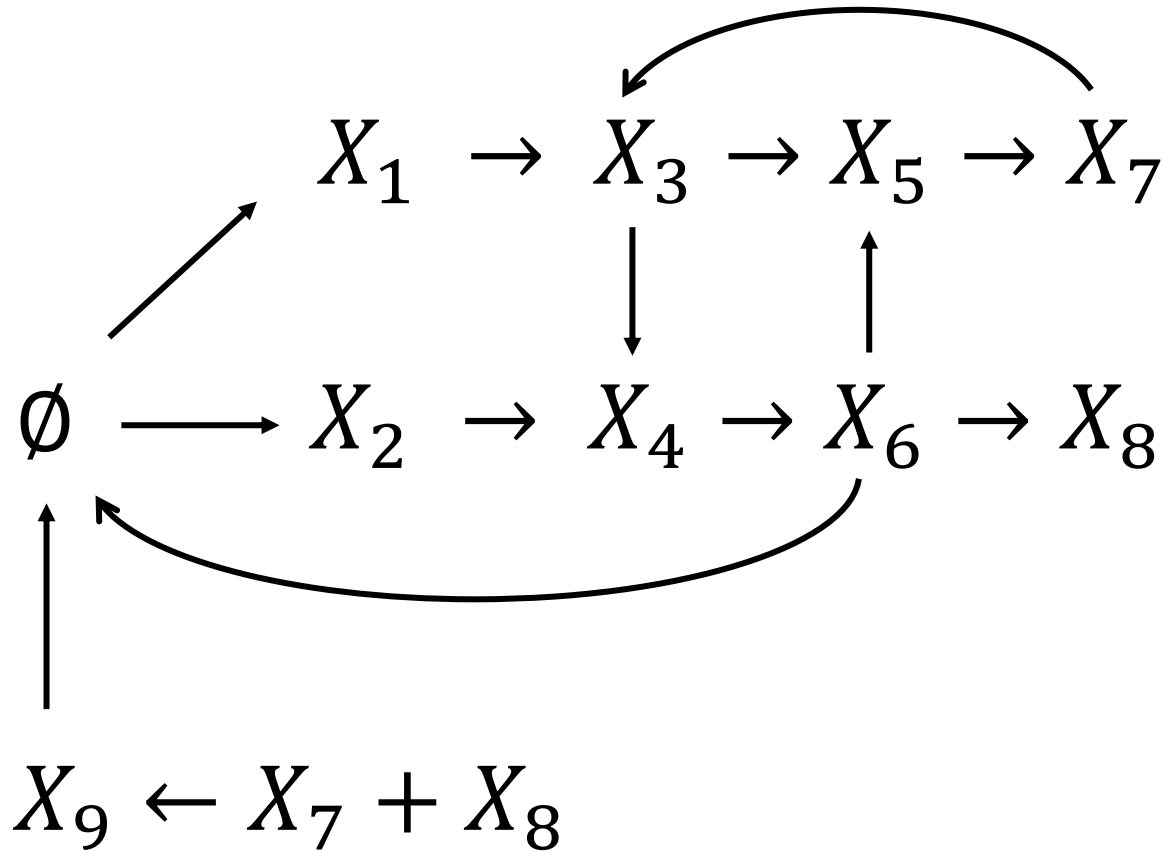
Toy examples



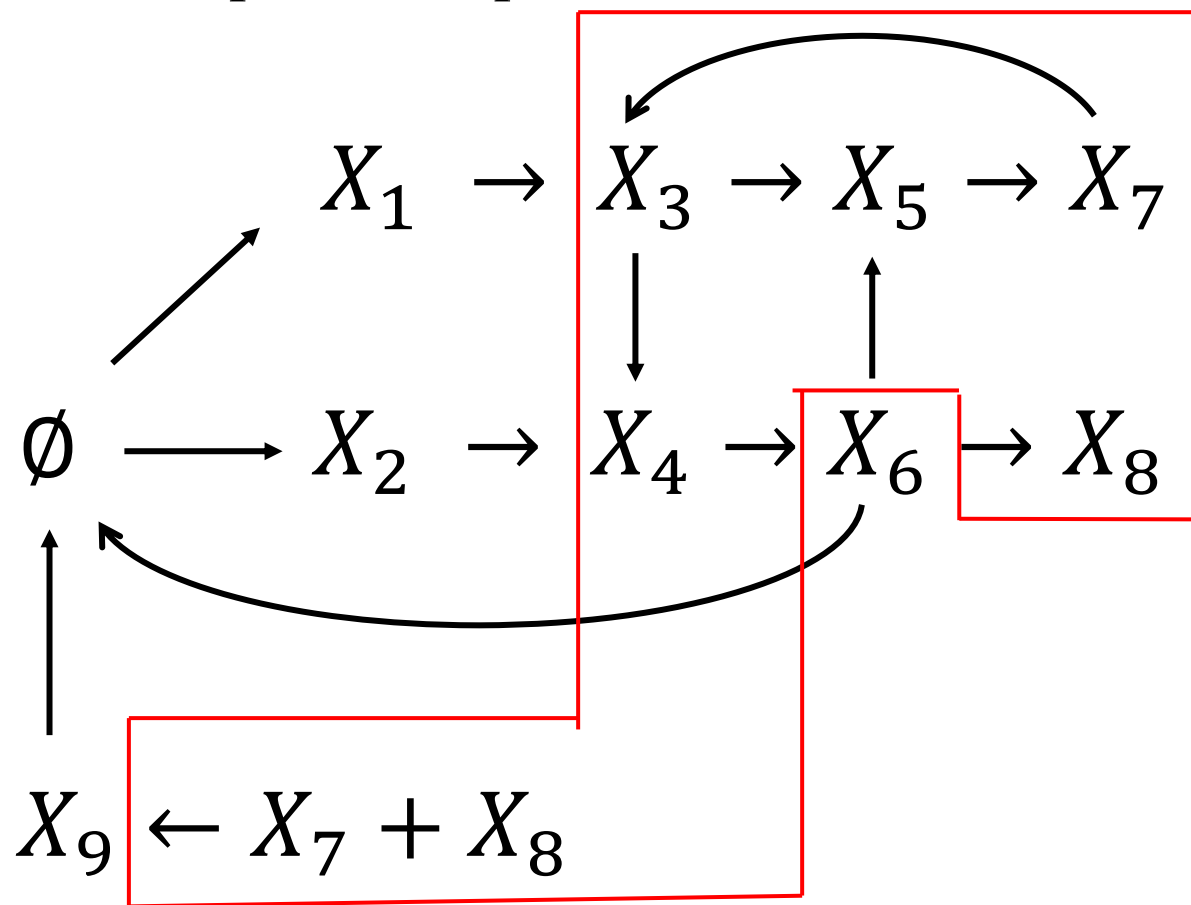
$$a^* = \frac{\kappa_1}{\kappa_2}, \quad b^* = \frac{\kappa_2 a^*}{\kappa_3} = \frac{\kappa_1}{\kappa_3}.$$



More complex example

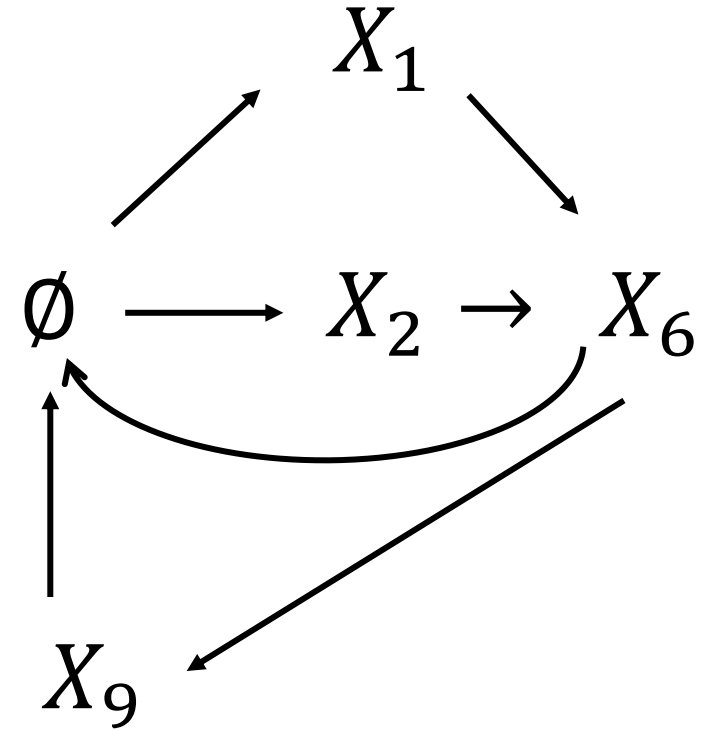
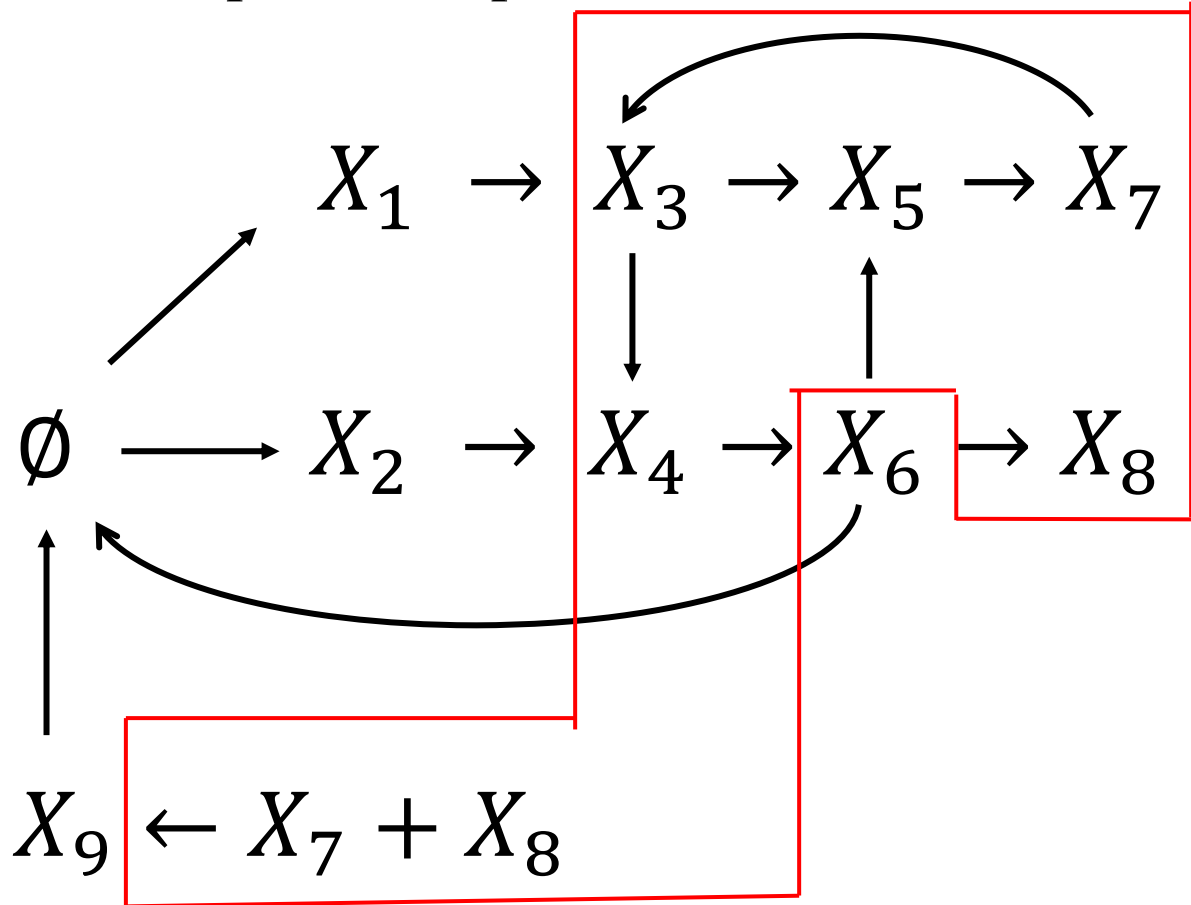


More complex example



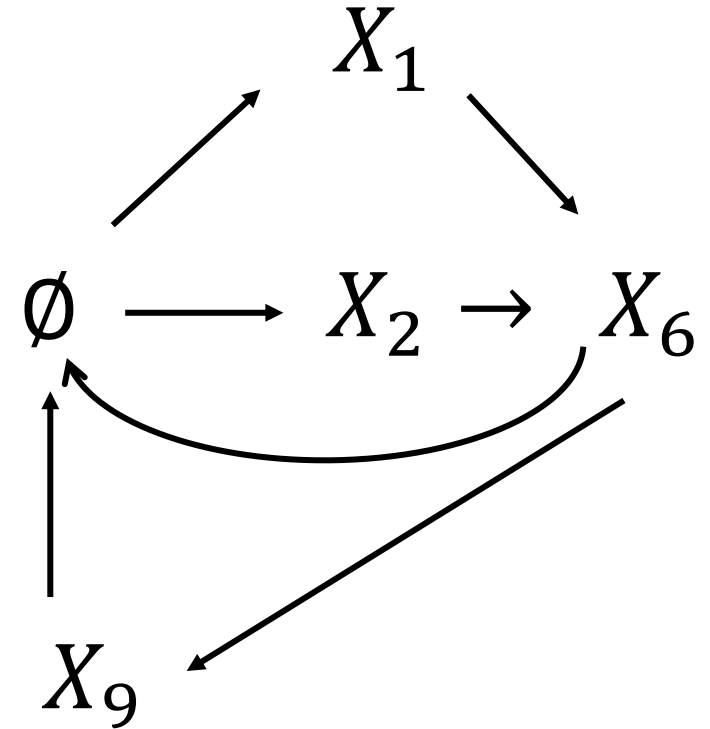
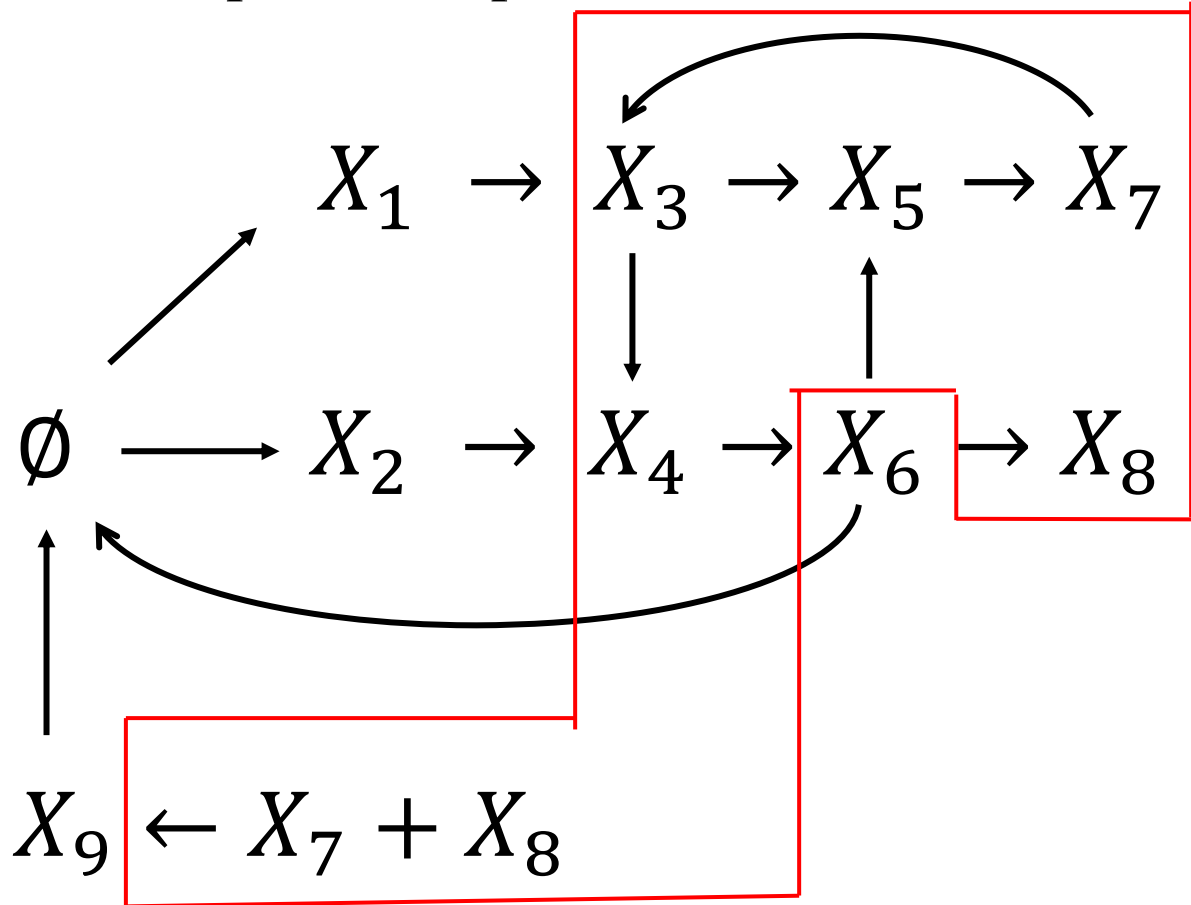
Structural reduction for steady states

More complex example



Structural reduction for steady states

More complex example



Relate the algebraic structure of the deterministic system to homology and cohomology.

Structural reduction for steady states

Extending to the stochastic model

