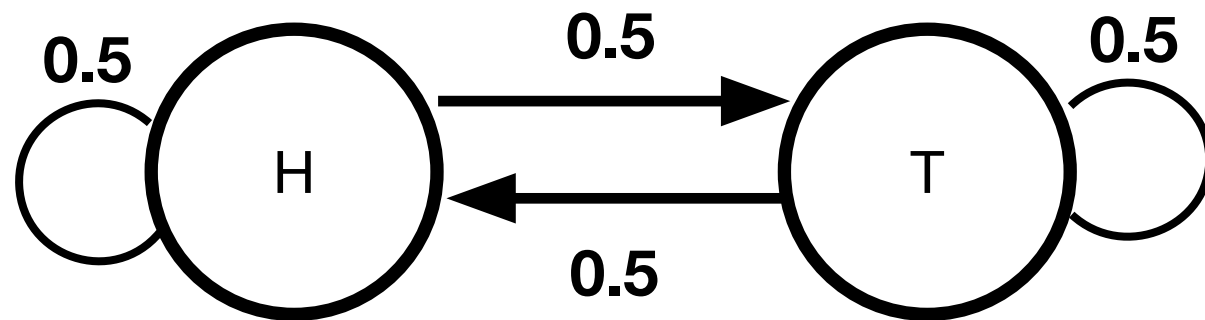


# Introduction to Markov State Models

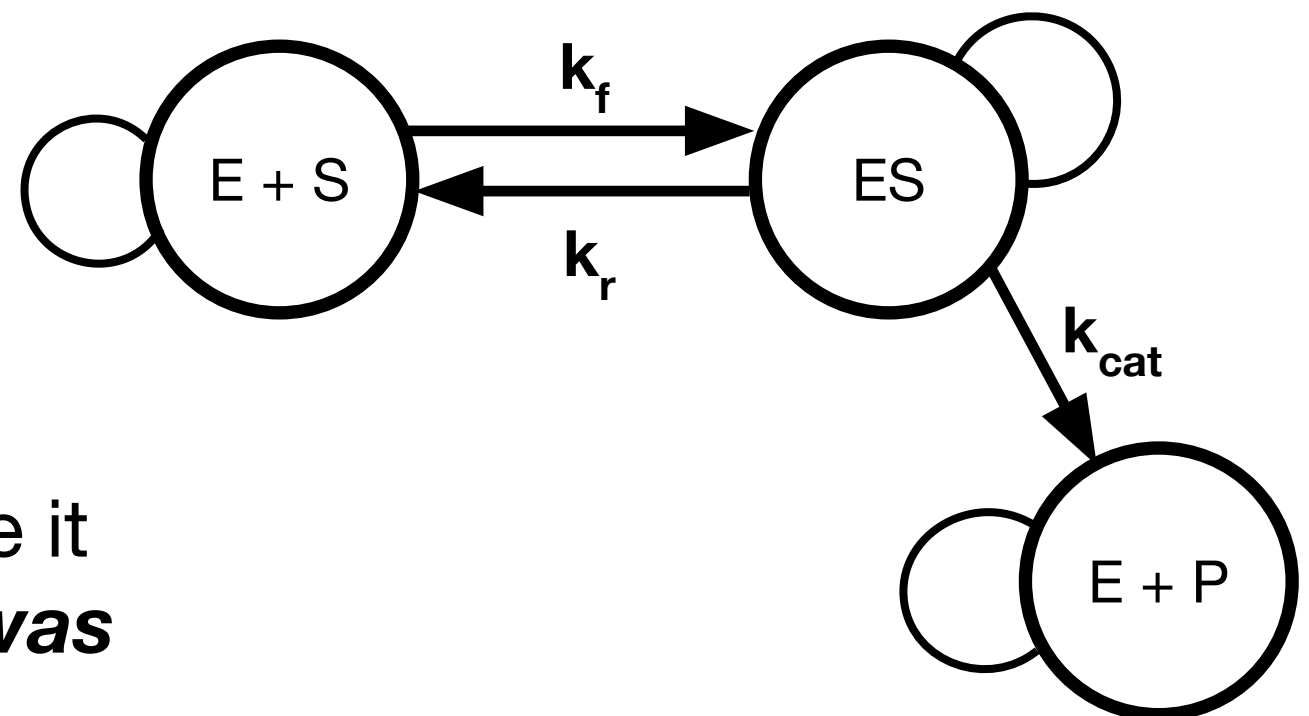
Drug Computing — Mobley Lab — UCI

# Markov processes describe the dynamics of systems that have no “long term memory”

Flipping a coin



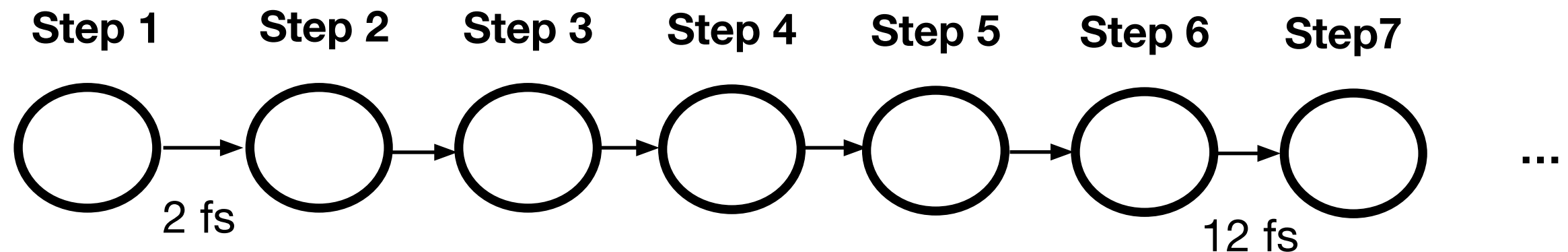
Michaelis-Menten Kinetics



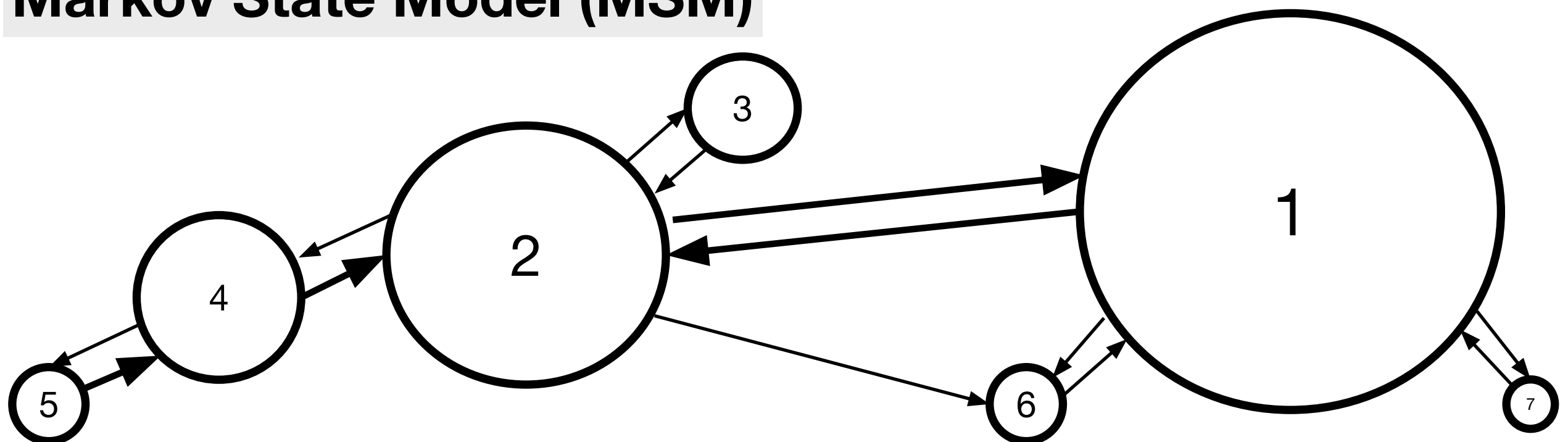
Where the system goes next is completely determined by where it ***currently*** is, and ***not where it was in the past***

# Markov State Models (MSMs) reveal kinetics of configurational transitions

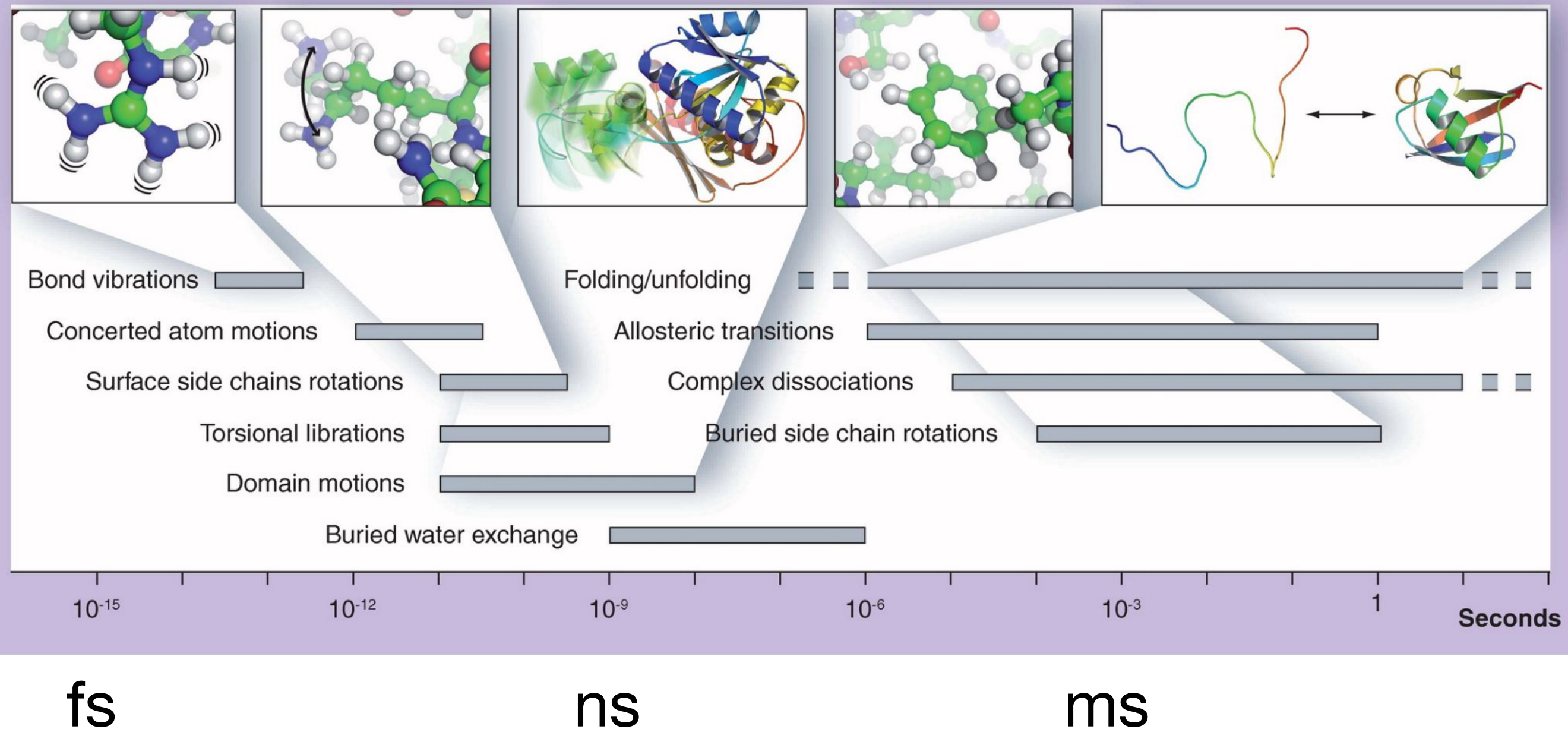
## Highly Disordered Trajectory



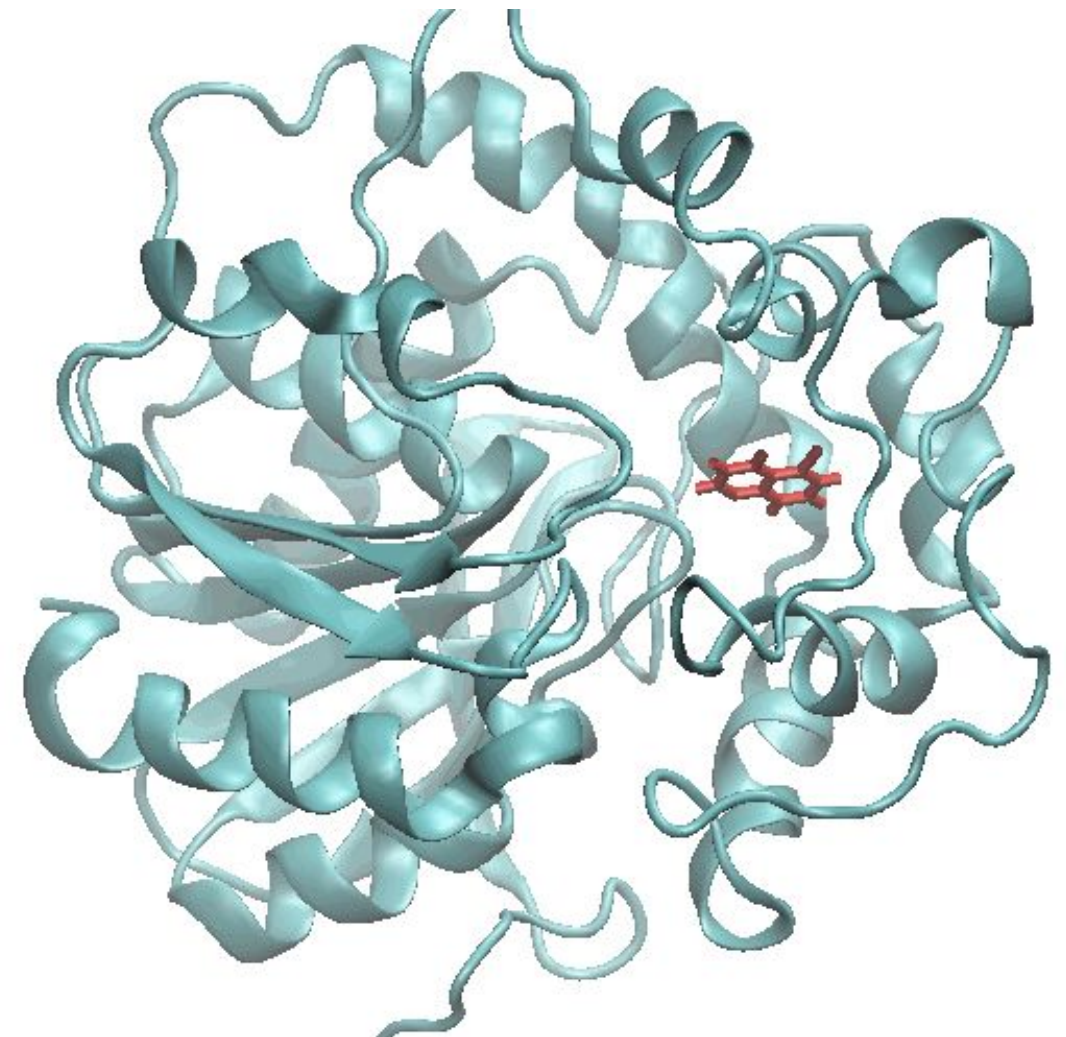
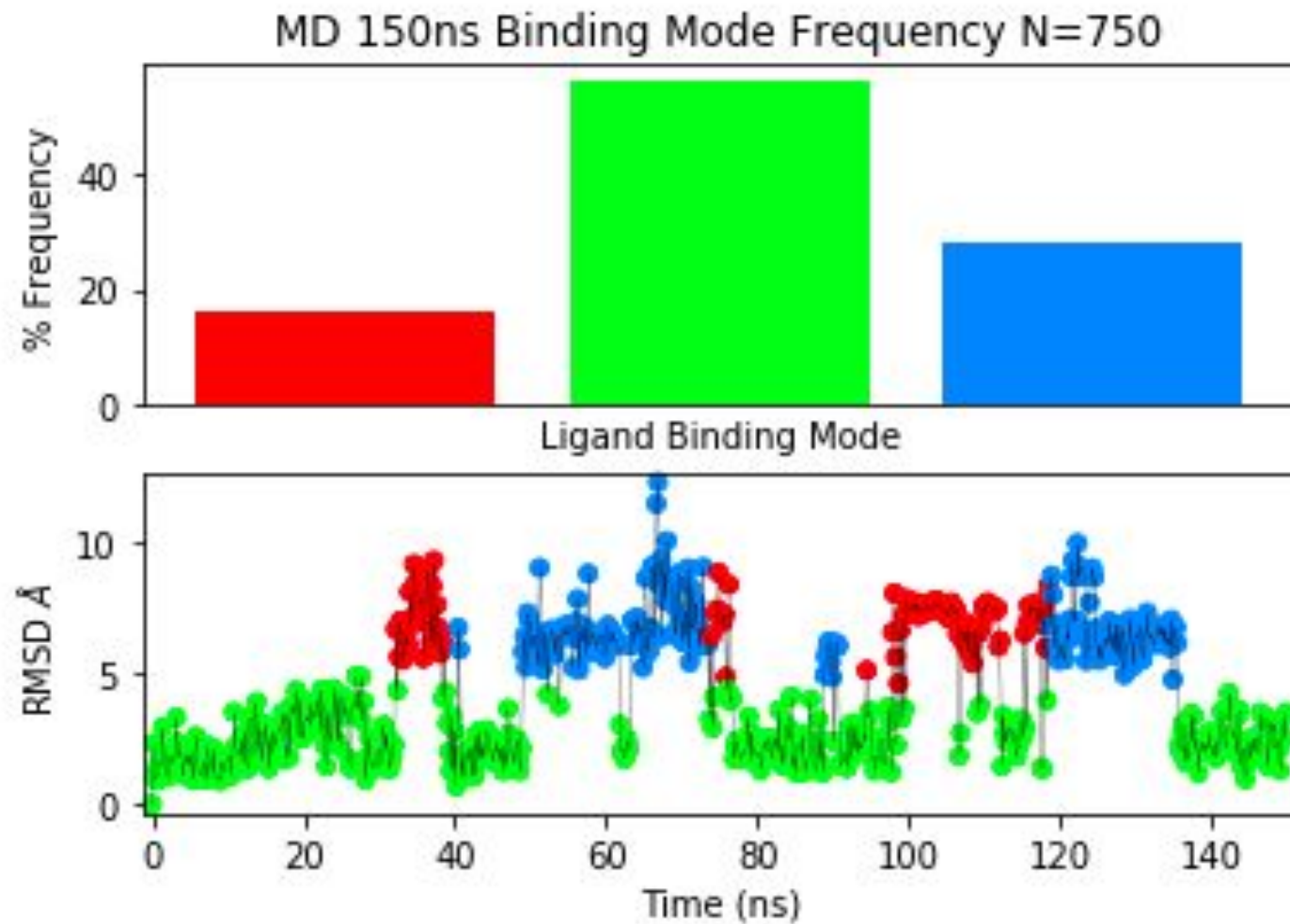
## Markov State Model (MSM)



# MSMs can be used to capture the macrostates of protein dynamics



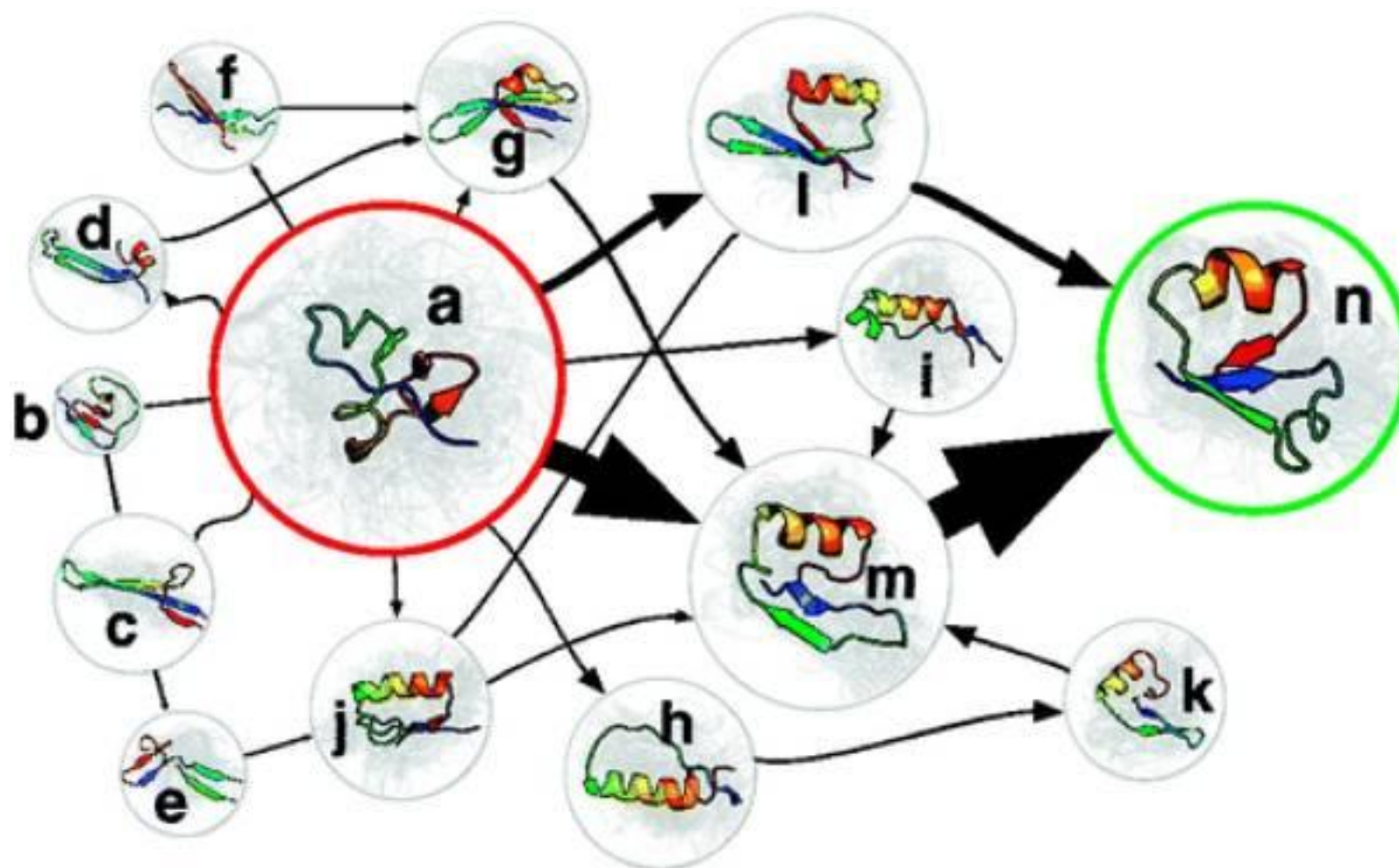
# Markov State Models (MSMs) reveal kinetics of configurational transitions





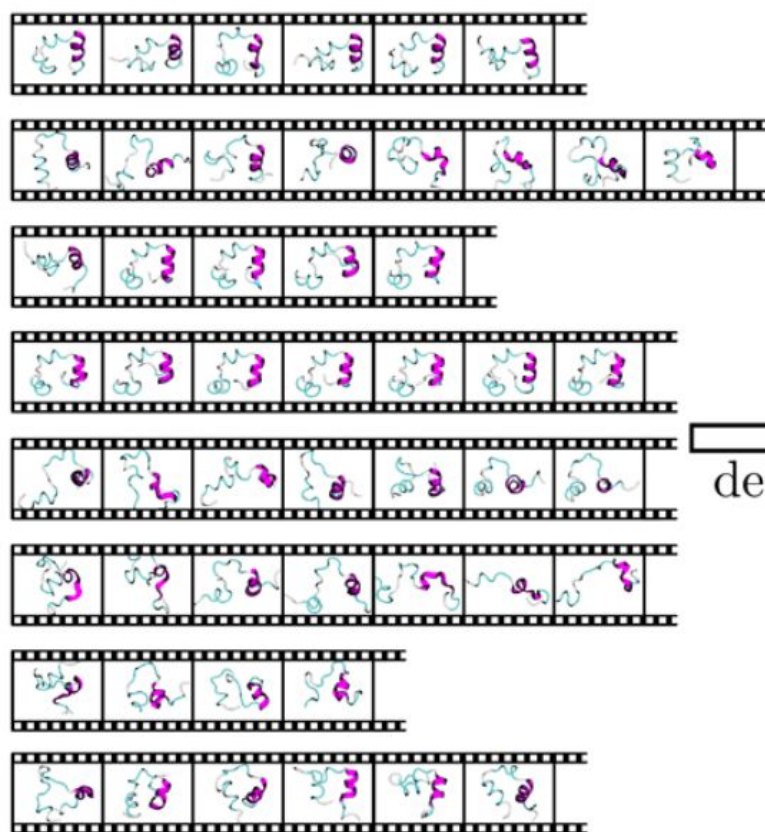
# Building a Markov State Model

Useful for combining many different simulations into a single model  
Example: building a (long timescale) kinetic protein folding pathway

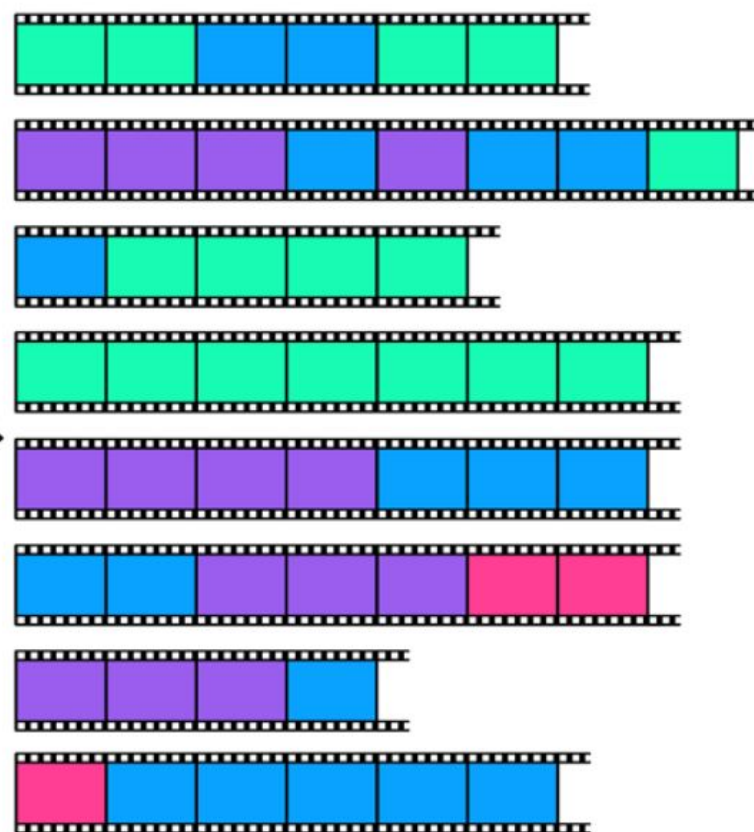


# MSMs can be built from many short simulations

(a) simulation data



(b) state assignments



(c) observed transition counts matrix









	Red	Blue	Green	Yellow
Red	11	1	0	0
Blue	3	9	2	0
Green	0	4	9	1
Yellow	0	1	0	1

(d) reversible transition probability matrix

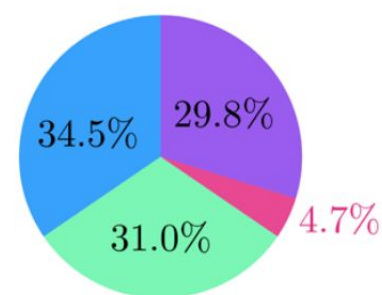
	Red	Blue	Green	Yellow
Red	0.85	0.15	0	0
Blue	0.14	0.62	0.21	0.03
Green	0	0.24	0.72	0.04
Yellow	0	0.25	0.25	0.5

# MSMs can describe the equilibrium process of the model









(c) observed transition counts matrix

				
	11	1	0	0
	3	9	2	0
	0	4	9	1
	0	1	0	1

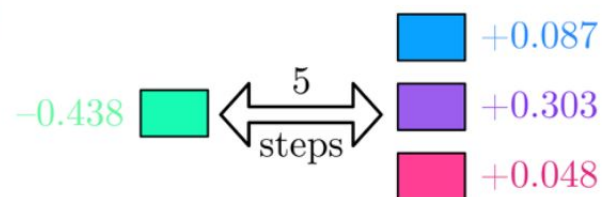
(e) adjusted populations



(d) reversible transition probability matrix

				
	0.85	0.15	0	0
	0.14	0.62	0.21	0.03
	0	0.24	0.72	0.04
	0	0.25	0.25	0.5

(f) slowest process eigenfluxes



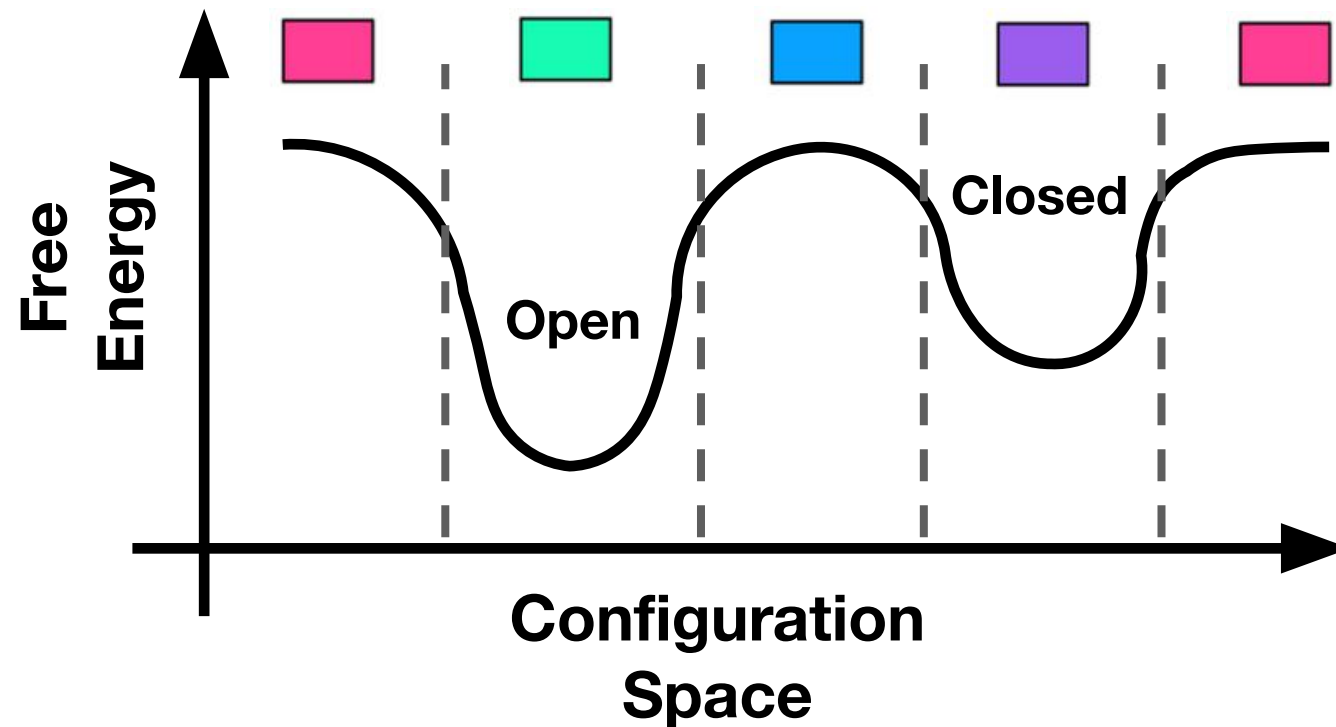
First eigenvector of the probability matrix describes the equilibrium populations

$$\pi^T = \pi^T \mathbf{T}(\tau)$$

Other eigenvectors (processes) show fluxes between states

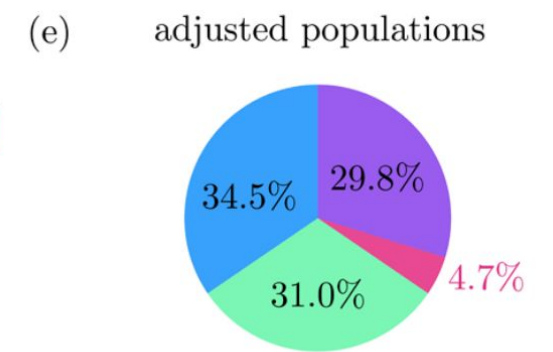


# Building a Markov State Model



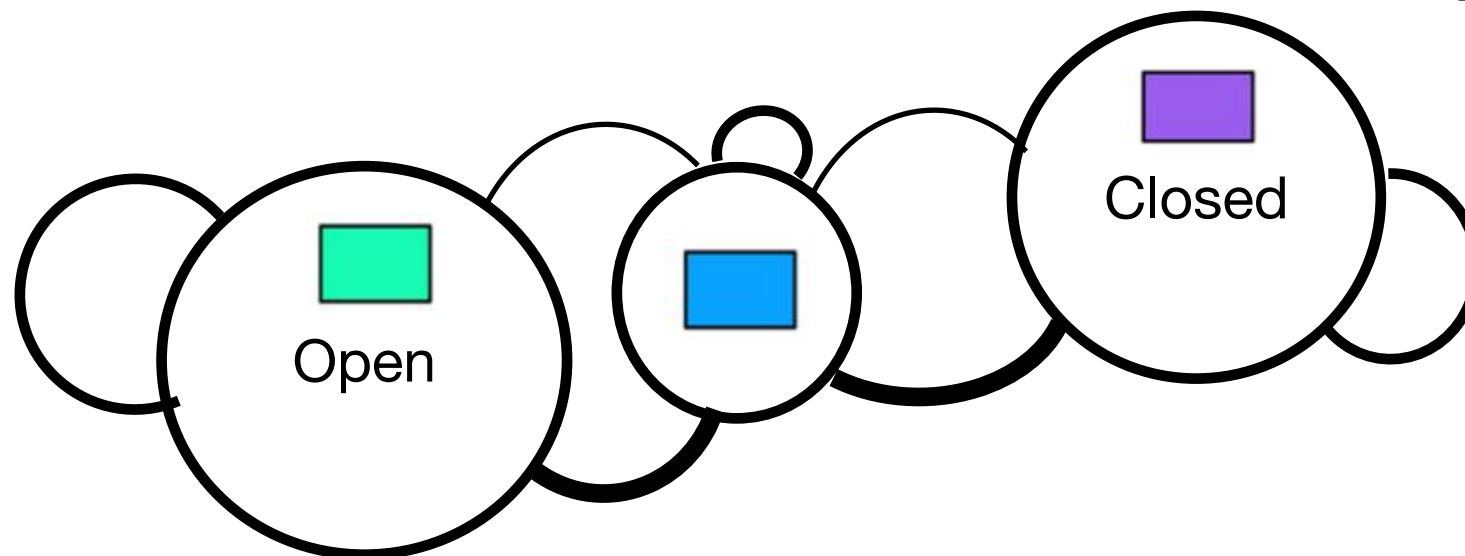
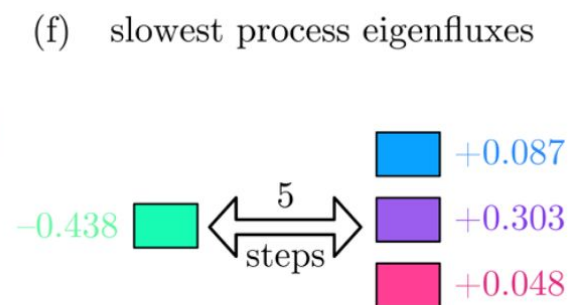
(c) observed transition counts matrix

	11	1	0	0
	3	9	2	0
	0	4	9	1
	0	1	0	1



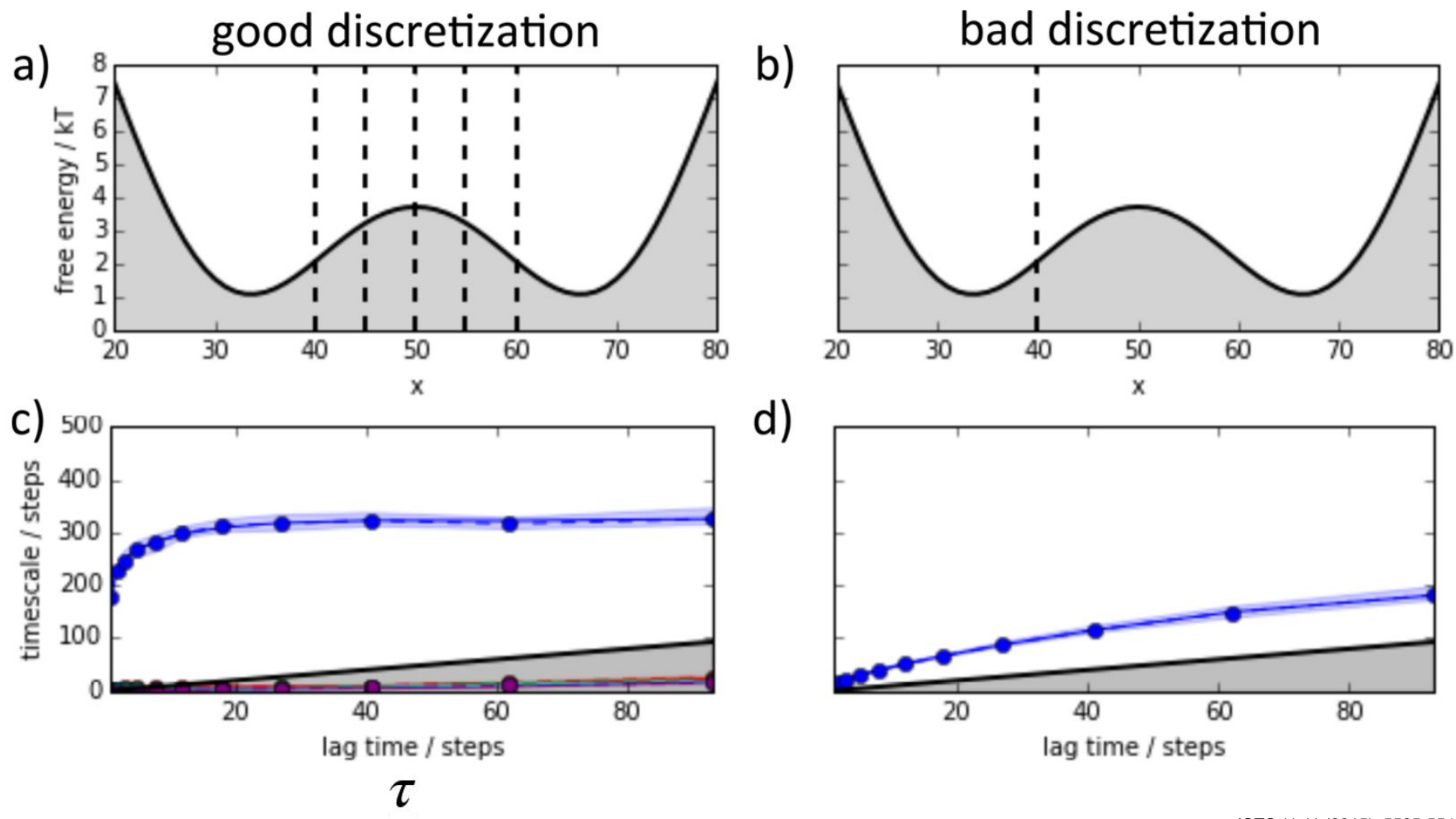
(d) reversible transition probability matrix

	0.85	0.15	0	0
	0.14	0.62	0.21	0.03
	0	0.24	0.72	0.04
	0	0.25	0.25	0.5



$$F_i = -k_B T \ln \frac{\pi_i}{\max_j \pi_j}$$

# Good clustering is necessary for maintaining Markovian properties

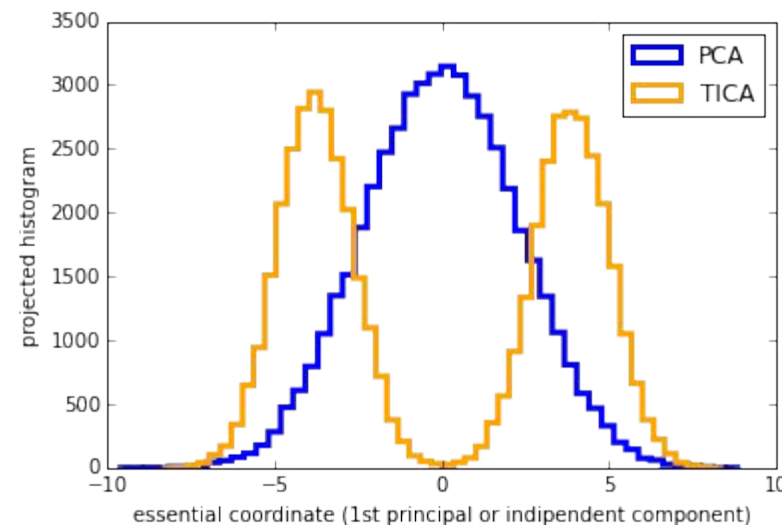


# Dimensionality Reduction: Principle Component Analysis (PCA) and Time-independent Component Analysis (TICA)

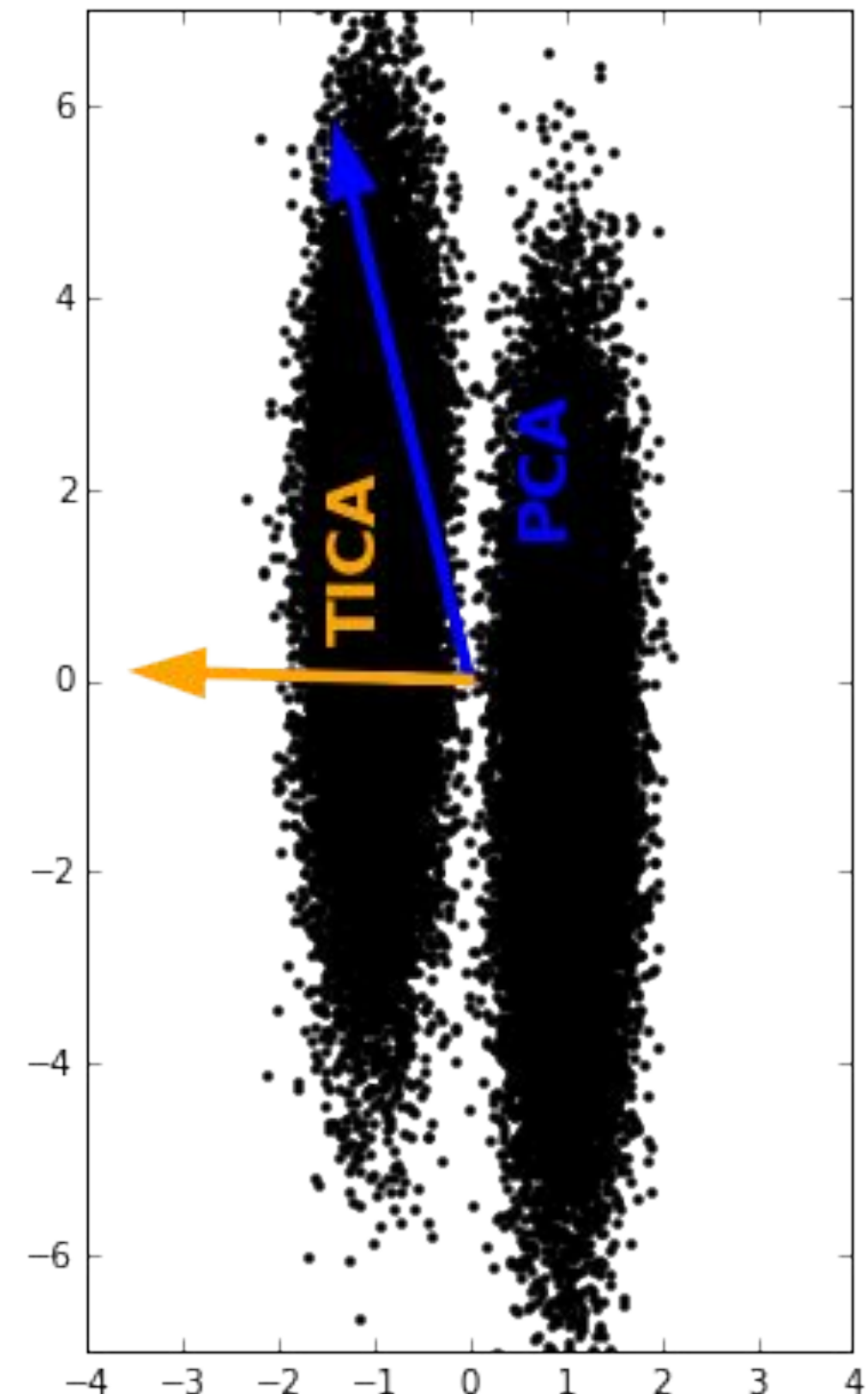
**PCA finds the direction of maximum variance in the data**

**TICA identifies the slowest reaction coordinates (maximum autocorrelation)**

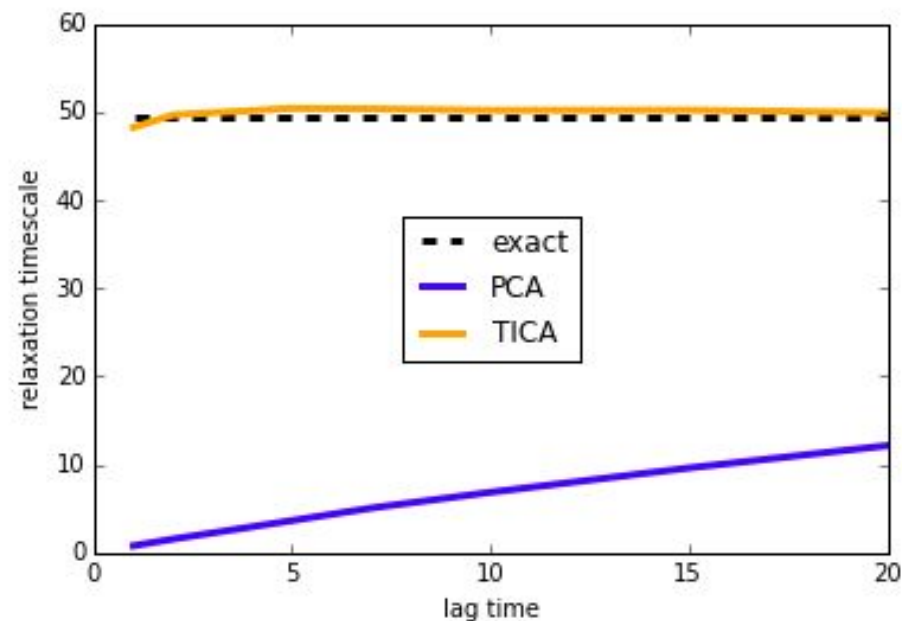
**Projection:**



[http://docs.markovmodel.org/lecture\\_tica.html](http://docs.markovmodel.org/lecture_tica.html)



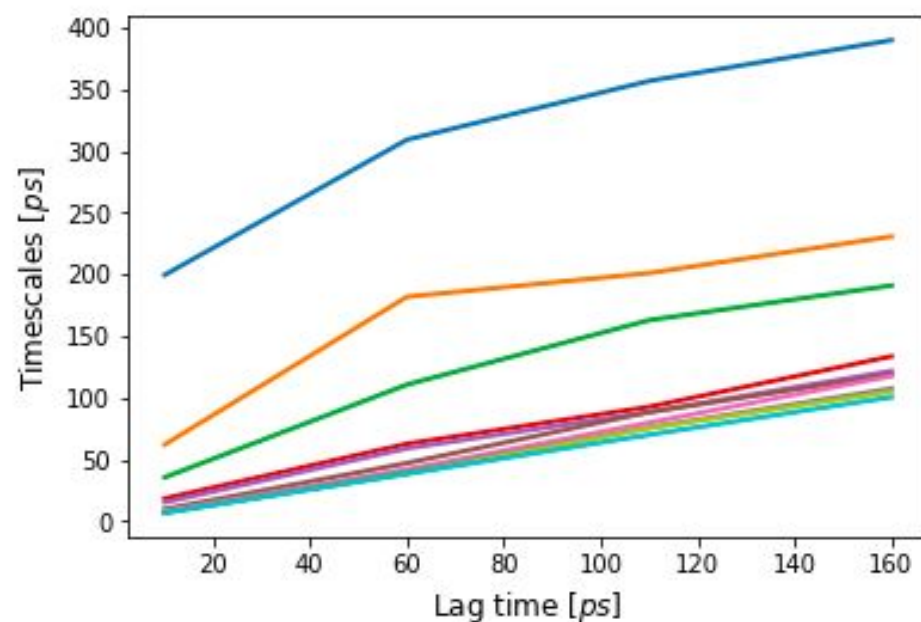
# Testing the dimensionality reduction: Implied Timescales



## Perfectly Markovian Process

$$t_i(k\tau_0) = t_i = -\frac{\tau_0}{\ln \lambda_i(\tau_0)}$$

[http://docs.markovmodel.org/lecture\\_implied\\_timescales.html](http://docs.markovmodel.org/lecture_implied_timescales.html)



## Imperfect Markov Model

$$t_i(k\tau_0) = -\frac{k\tau_0}{\ln \lambda_i(k\tau_0)}$$

**Choose a time scale at which the model appears to start behaving Markovian**

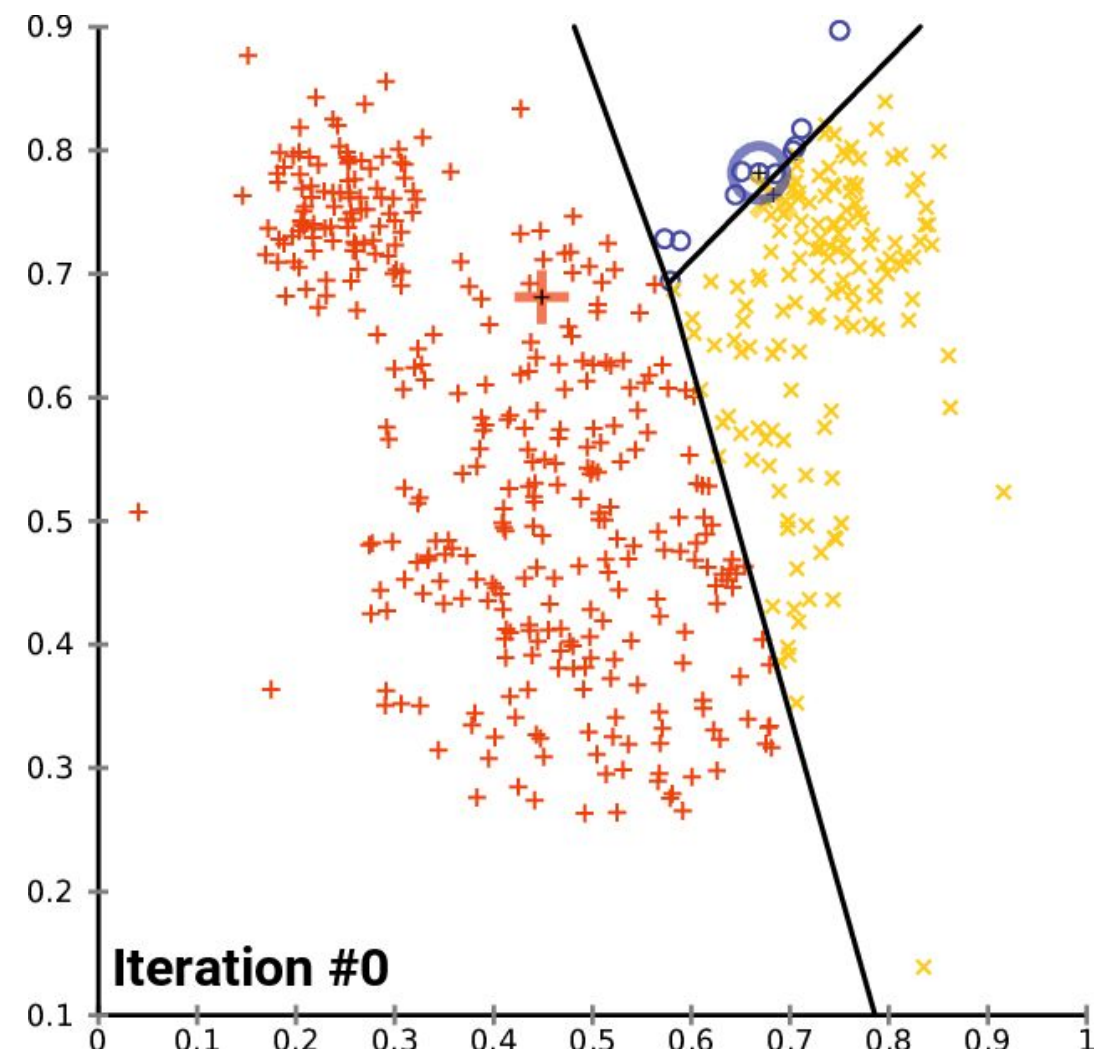
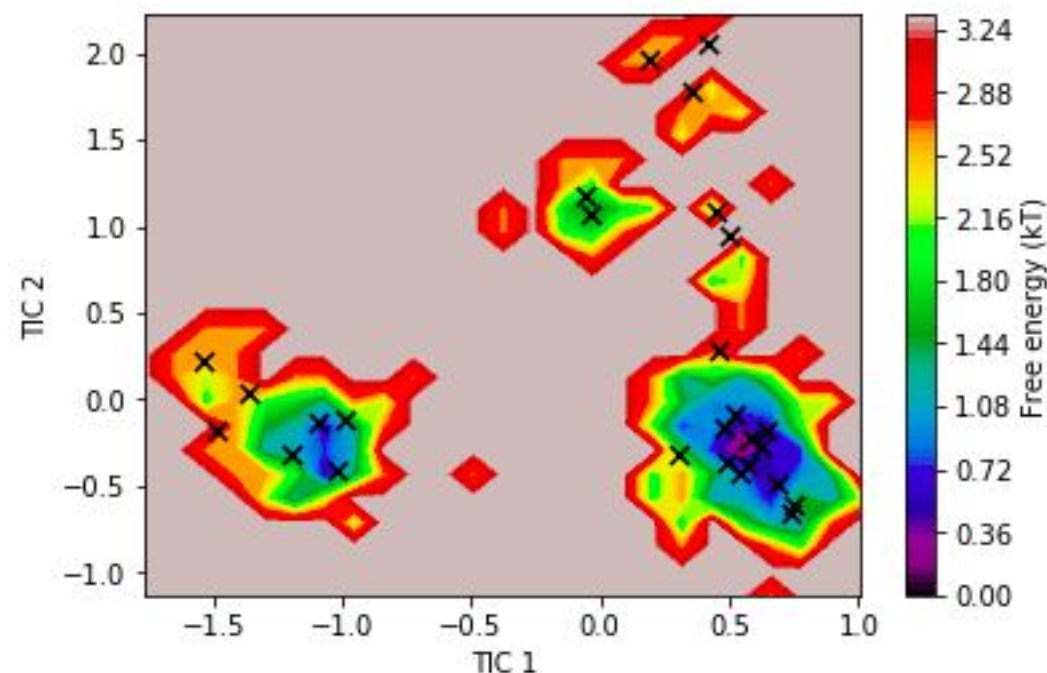


# Using the dimension reduction to identify macrostates of the system

## PCCA and K-means Clustering

### K-means Clustering:

- Identifies clusters based on distance in TICA space

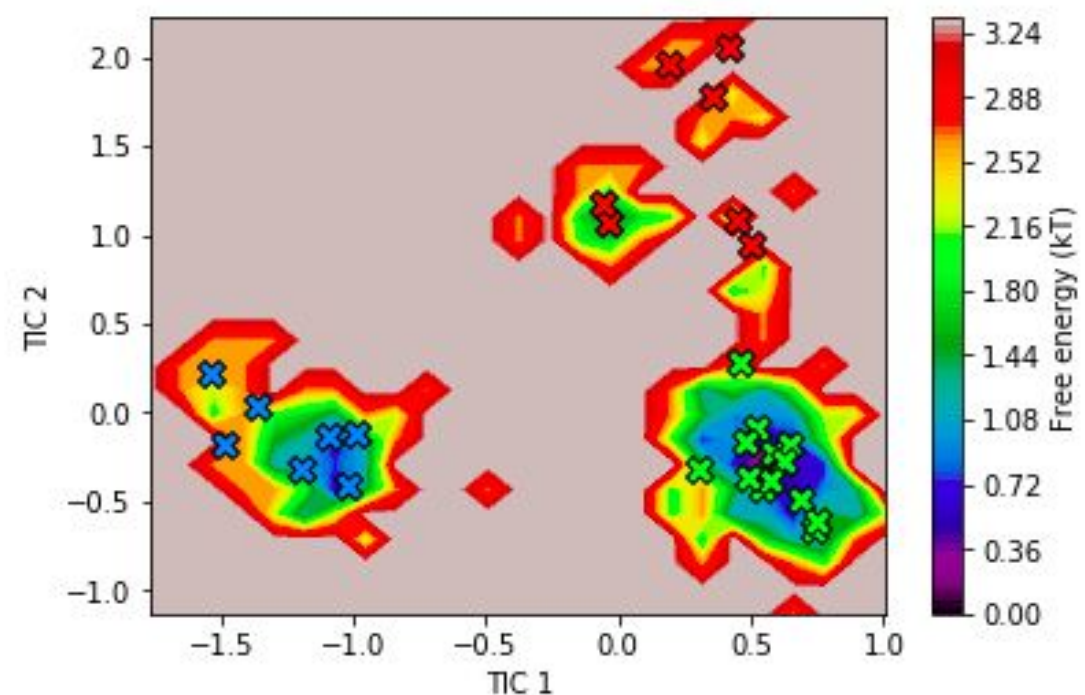
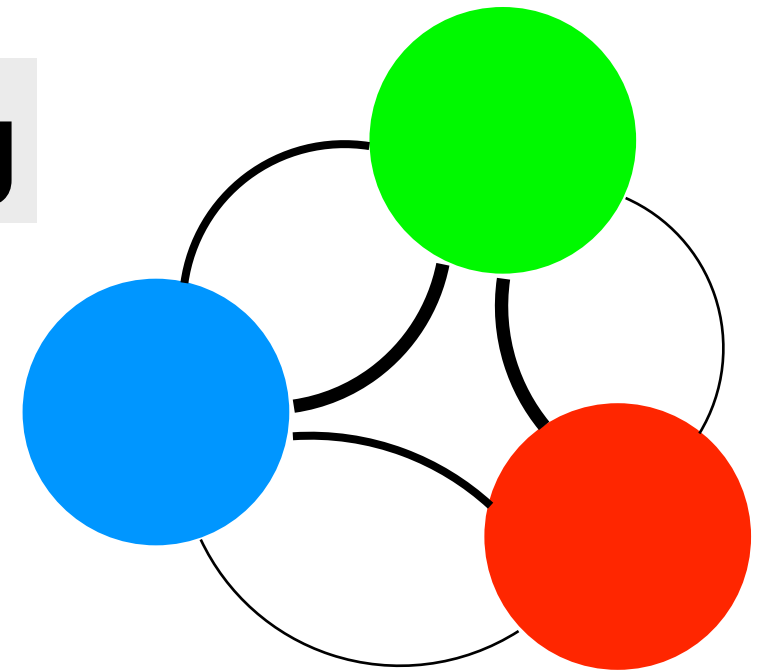


# Using the dimension reduction to identify macrostates of the system

## PCCA and K-means Clustering

### PCCA: Perron-Cluster Cluster Analysis

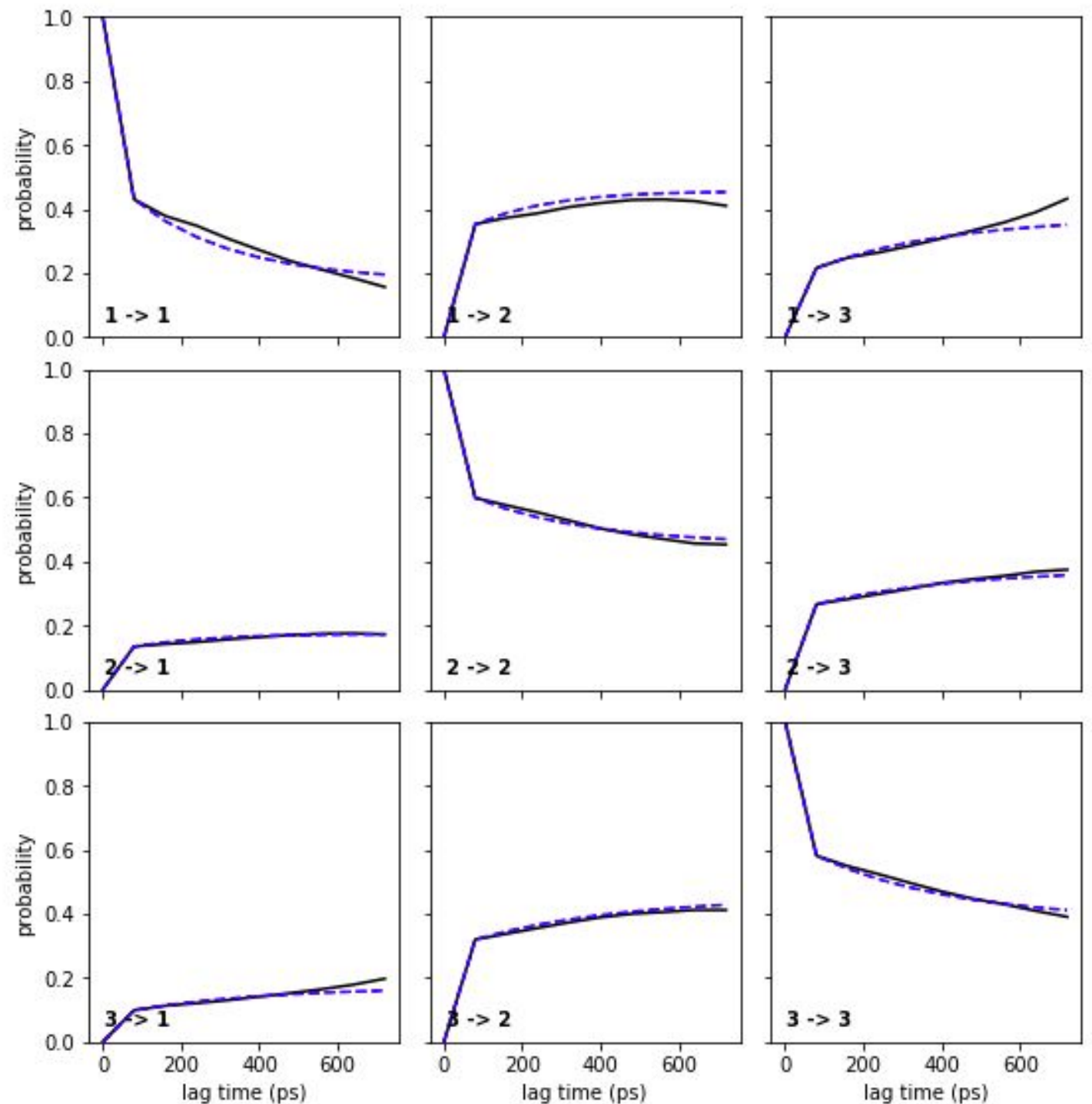
- Uses the eigenvector-eigenvalue decomposition to identify meta-stable states
- Splits the available conformational state space in order of longest relaxation time



# Testing the Markov Model: Chapman-Kolmogorov test

How well do the  
interconversions  
between the  
coarse-grained  
macro-states  
of the model  
compare to the  
real trajectory?

$$[\hat{\mathbf{T}}(\tau)]^k \approx \hat{\mathbf{T}}(k\tau)$$



# **Core concepts and procedure to use Markov models**

## **(1) Identify Configuration Microstates**

- Dimensionality Reduction**

  - TICA, PCA**

- Clustering**

  - K-means**

## **(2) Construct Transition Matrix Between States**

## **(3) Test for Self-Consistency**

## **(4) Calculate Kinetics + Free Energy Between State**