Markov-state modeling of biomolecular systems, II



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Thesis projects available

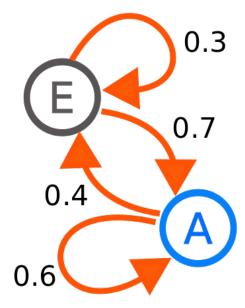
github.com/giorginolab/ Markov-Tutorial-UniPd-2022

University of Padova c/o Prof. Fuxreiter Mar 23, 2022

Discrete-time Markov chains



Andrei Markov 1856-1922



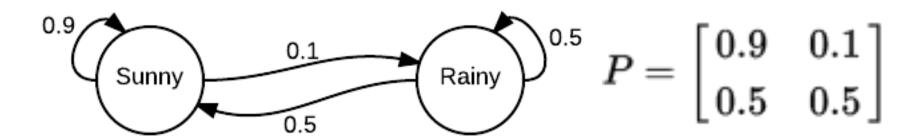
Discrete Time Markov Chains

- A random process.
- The system's state is a discrete variable.
- It undergoes transitions between states at uniformlyspaced (discrete) time

points.

Transition probabilities
 do not depend on the
 previous history of states
 (memorylessness).

First example



Assume a deterministic initial condition:

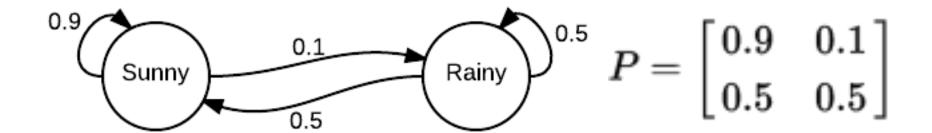
$$X_0$$
 = Sunny with certainty; *i.e.*,

$$p(Sunny | t=0)=I$$
 and $p(Rainy | t=0)=0$ *i.e.*

$$s_0 = [1, 0]$$

...now, what is s_1 ?

First example



What is s_1 ?

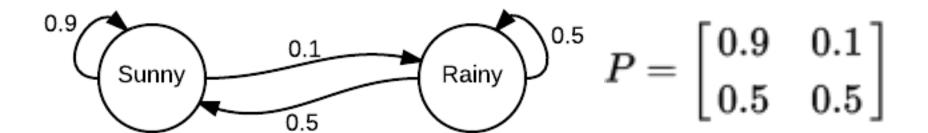
$$S_1 = \begin{cases} p(Sunny | t=I) = 0.9 \\ p(Rain | t=I) = 0.I \end{cases}$$

In matrix form...

$$\mathbf{s}_1 = \mathbf{s}_0 P$$

...now, what is s_2 ?

First example



What is s_2 ?

$$S_2 = \begin{cases} p(Sunny \mid t=2) = 0.9 \ p(Sunny \mid t=1) + 0.5 \ p(Rainy \mid t=1) = 0.86 \\ p(Rainy \mid t=2) = 0.1 \ p(Sunny \mid t=1) + 0.5 \ p(Rainy \mid t=1) = 0.14 \end{cases}$$

In matrix form...

$$\mathbf{s}_2 = \mathbf{s}_1 P$$

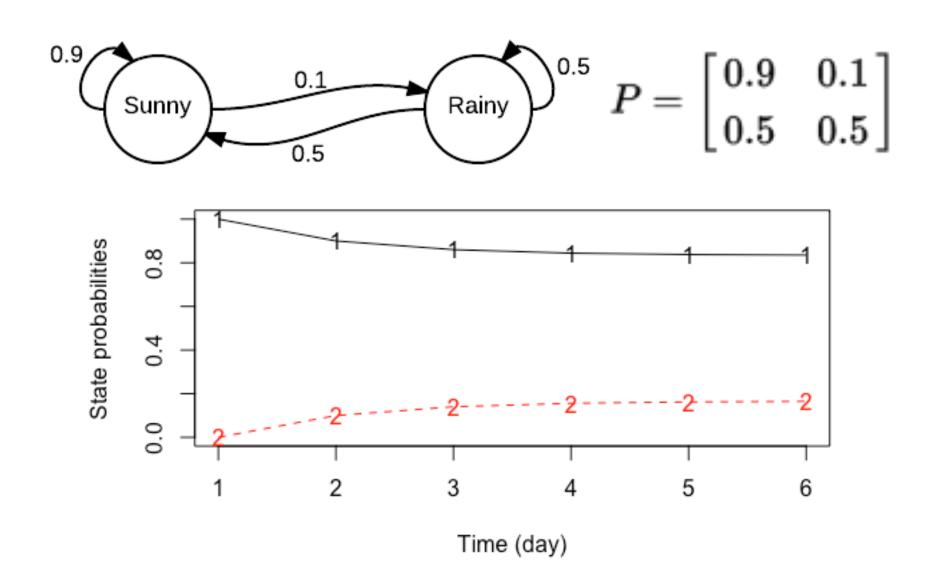
And in general...

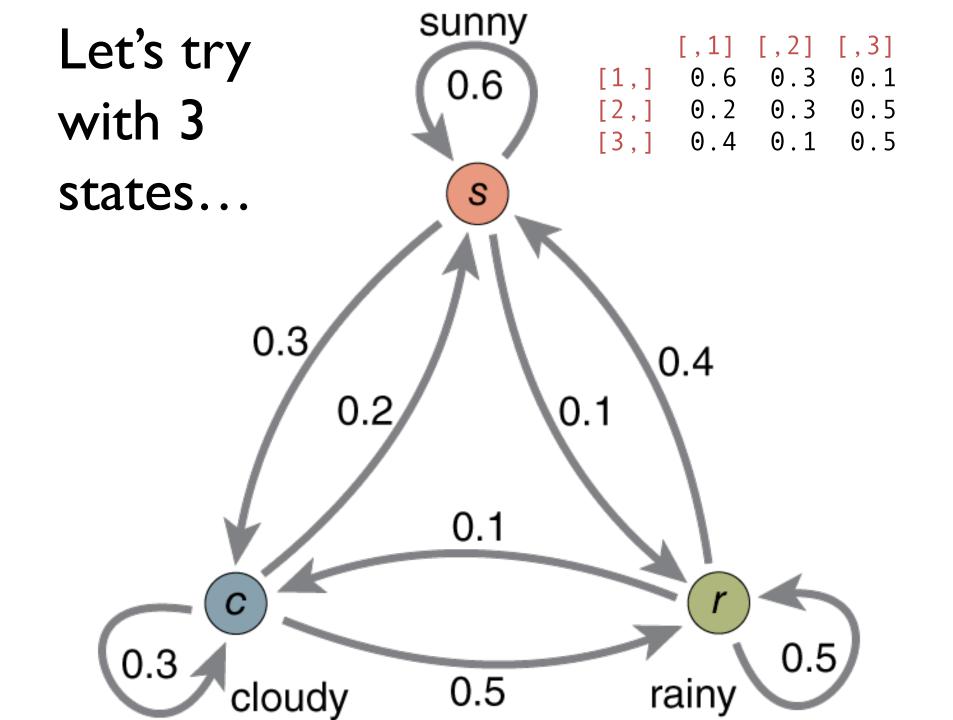
$$\mathbf{s}_{t+1} = \mathbf{s}_t P$$

Meaning...

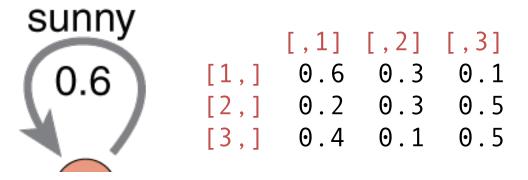
$$\mathbf{s}_t = \mathbf{s}_0 P^t$$

Let's do a numerical test...

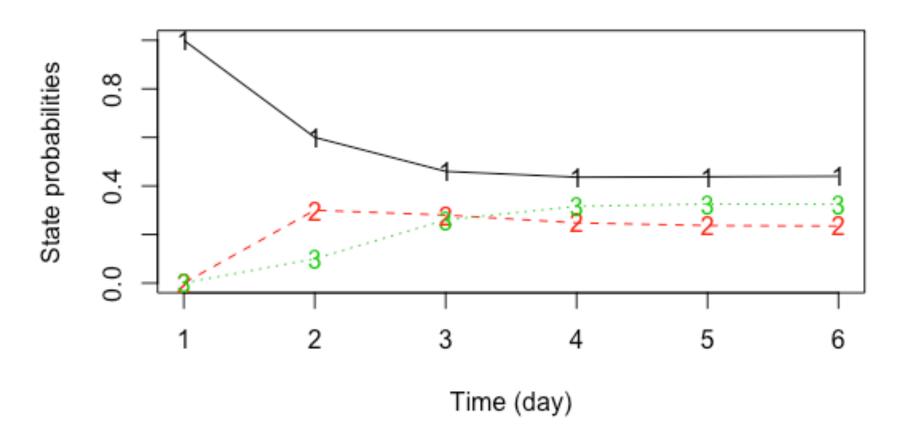




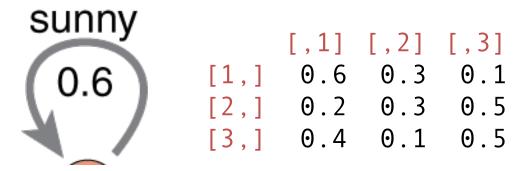
Starting from Sunny...



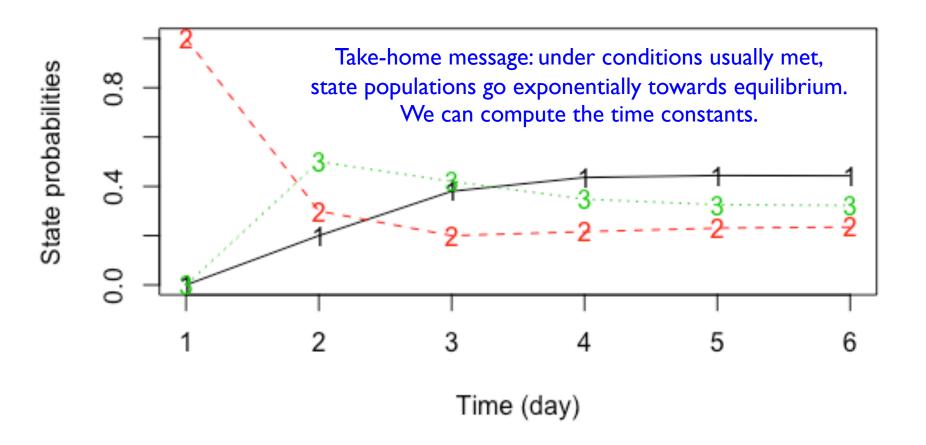
Initial state: s0 = [1,0,0]



Starting from Cloudy...



Initial state: s0 = [0,1,0]



Homogeneity

- If the transition probabilities do not change with time, we have an homogeneous Markov chain
- Example of non-homogeneous MC: weather transition probabilities Markovian, but dependent on the season.

Important quantities we can compute

- Stationary distribution (\rightarrow eq. probabilities)
- Relaxation times
- Mean-first passage times (→ kinetic rates)
- And others we won't discuss:
 - Committor probabilities
 - Fluxes

— ...

Learning matrices from trajectories (of discrete states)

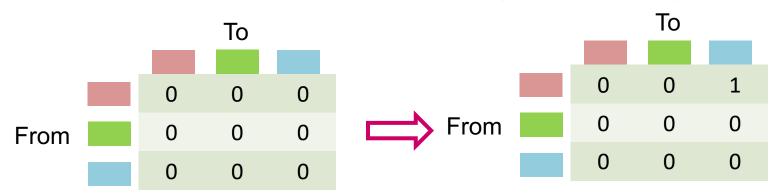
Total sampled time (e.g. 100 µs)

Define the discrete state of the system in discrete time (e.g. via reaction coordinates)



Lag time τ (here: 4 time units)

Compute the transition probability matrix sliding a window of lag time τ



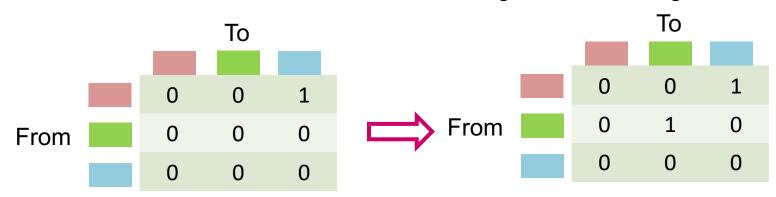
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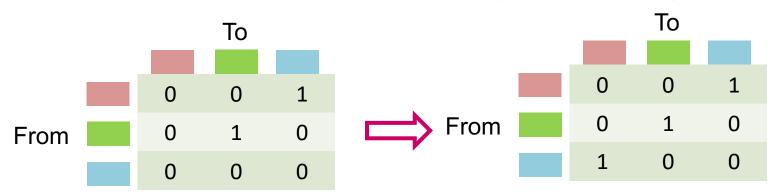
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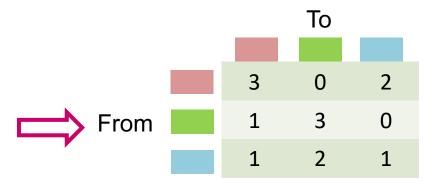
Total sampled time (e.g. 100 µs)

Define the discrete state of the system in discrete time (e.g. via reaction coordinates)



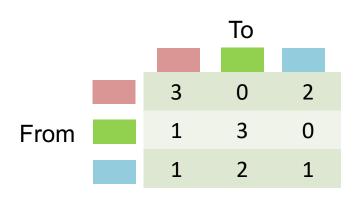
Lag time τ (here: 4 time units)

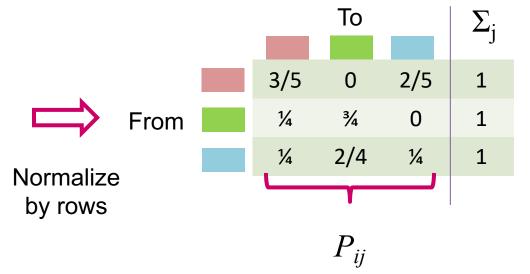
Compute the transition probability matrix sliding a window of lag time τ



Transition counts

Transition probabilities

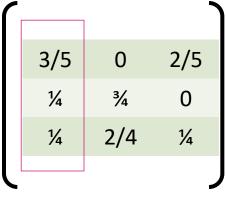






1 0 0

X



Evolved (after τ) state

$$S_i$$
 P_{ij} S

Probability vector

 S_i

1

Evolved state

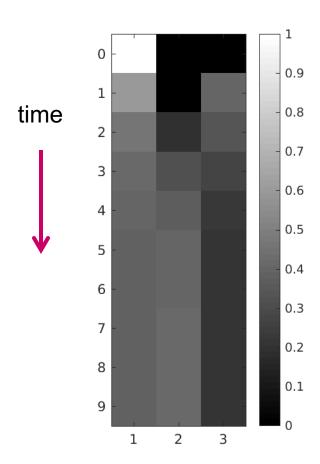
$$S_j$$

$$s' = sP$$

$$s'' = (sP)P = sP^{2}$$

$$s^{(n)} = sP^{n}$$

1	0	0
.60	0	.40
.46	.20	.34
.41	.32	.27
.39	.37	.23
.39	.40	.22
•••	•••	



Probability vector

1 0 0

 S_i

3/5 0 2/5 $\frac{3}{4}$ 0 $\frac{3}{4}$ 0 $\frac{2}{4}$ $\frac{1}{4}$ $\frac{2}{4}$ $\frac{1}{4}$

Χ

Evolved state (after tau)

 S_{j}

$$s' = sP$$

$$s'' = (sP)P = sP^{2}$$

$$s^{(n)} = sP^{n}$$

$$e^{\infty}$$
 — '

$$s^{\infty}P = s^{\infty}$$

Left eigenvector of P (eigenvalue 1)

Is the stationary state

- = equilibrium probabilities
- = the free energy surface

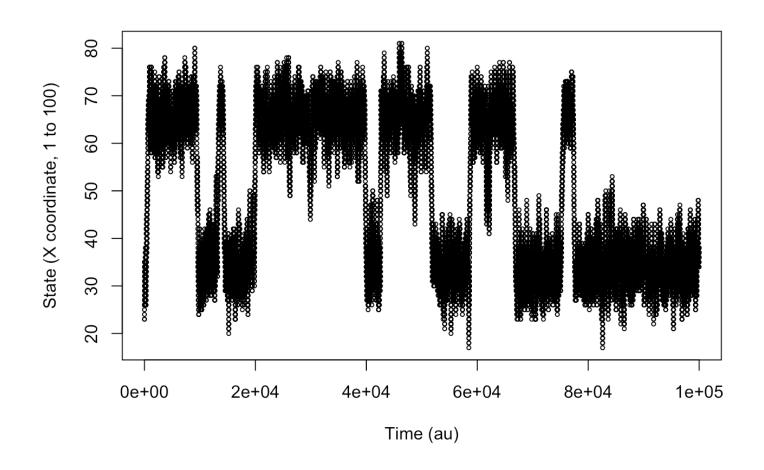
```
[a,b]=eig(P')
a(:,3)/sum(a(:,3))
= 0.385 0.410 0.205 = [5/13 16/39 8/39]
```

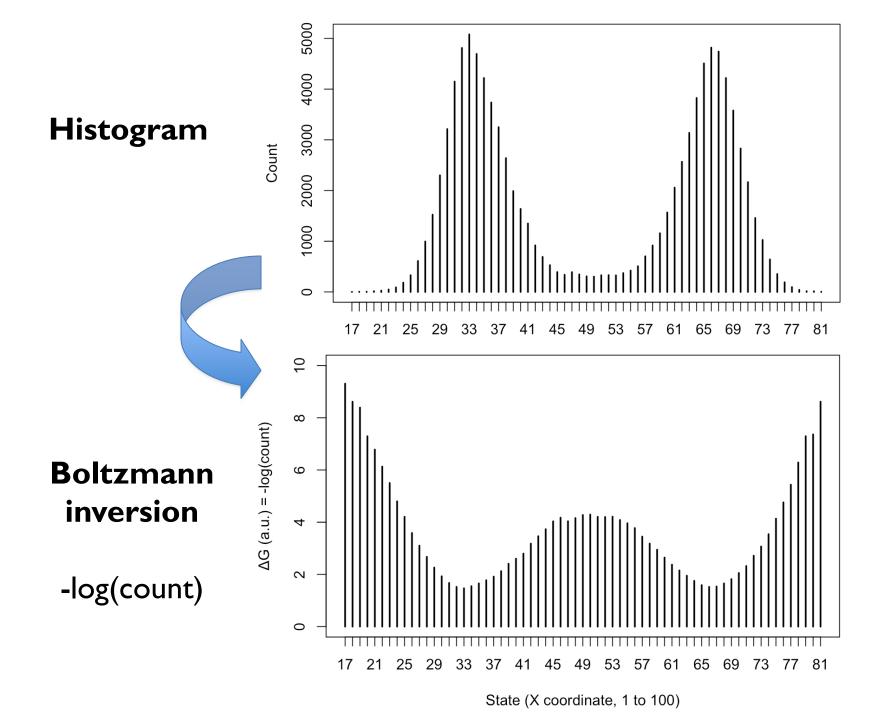
Markov modeling a ID trajectory

(Please find the extended version online, "Markov state models of a 1D trajectory", with R code at github.com/giorginolab/Markov-Tutorial-Data)

Start with a I-D trajectory

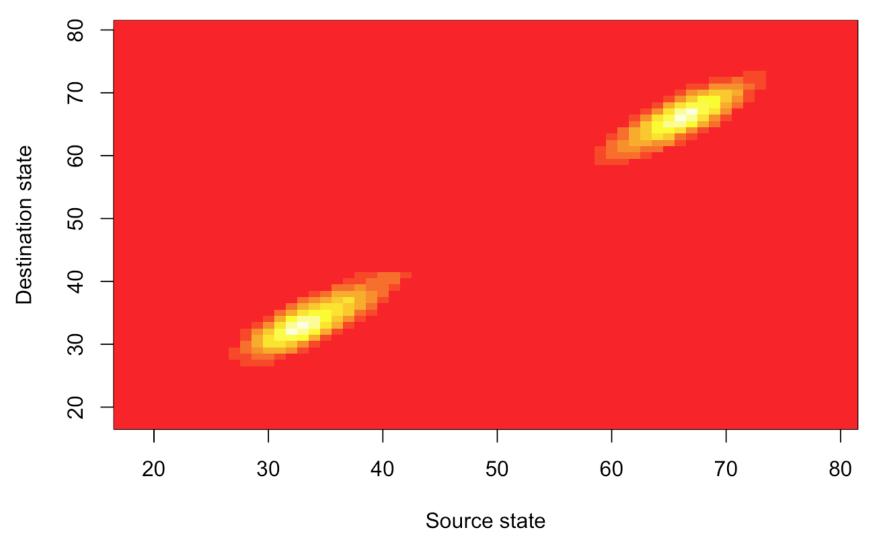
Already discretized in 100 bins





The transition *count* matrix*

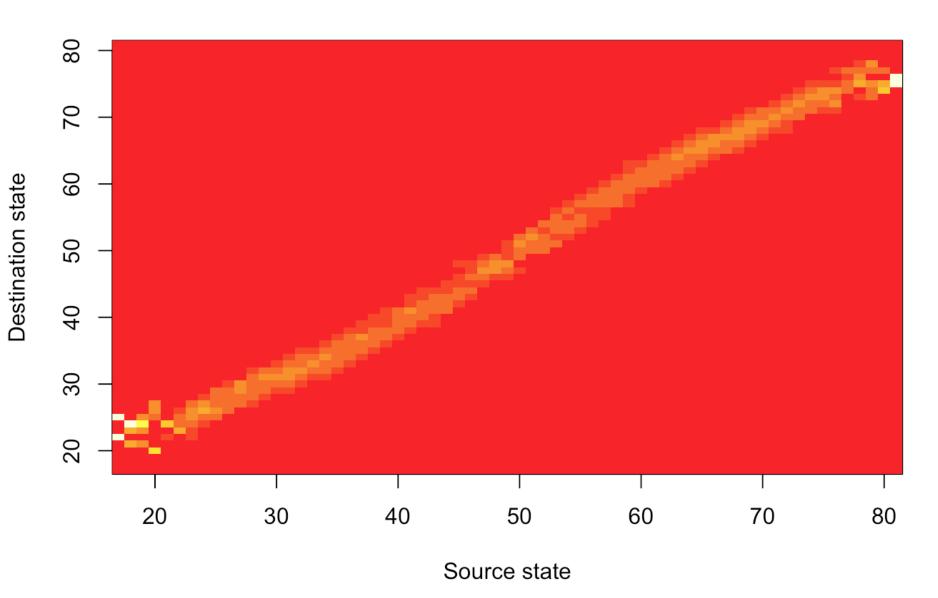
How many times we have seen state i going to j after τ =10 time units



^{*} shown as an image for compactness

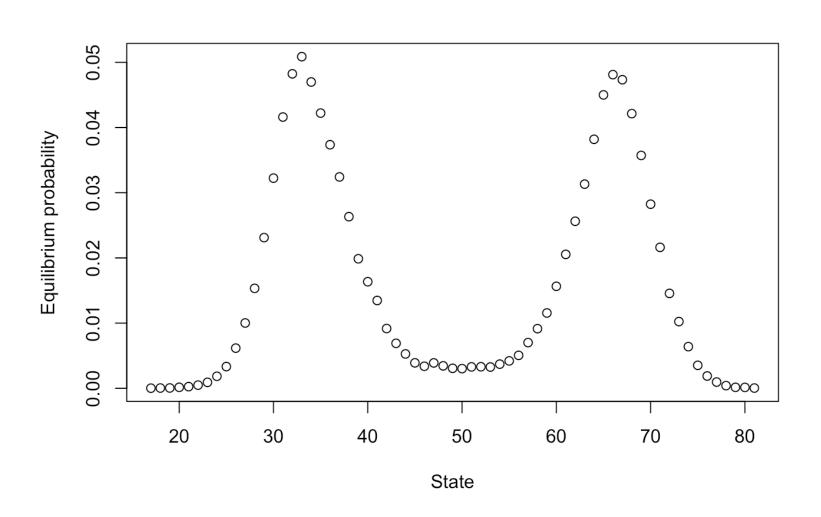
The transition probability matrix

Rows normalized to sum to I



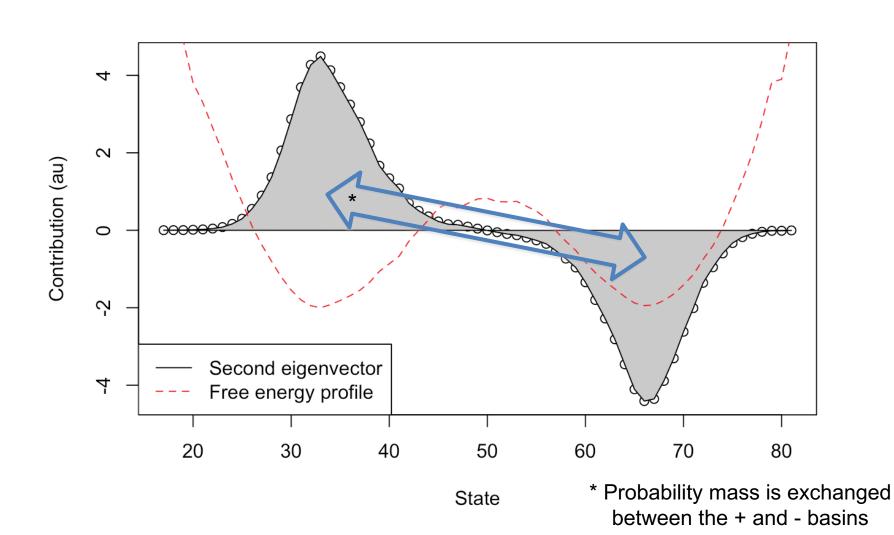
First eigenvector $(\mu_I = I)$

This is the stationary state (normalize so it sums to I)



Second eigenvector (μ_2 =0.997)

This is the slowest relaxation mode: ITS τ_2 = 3610 time units



Take-home message

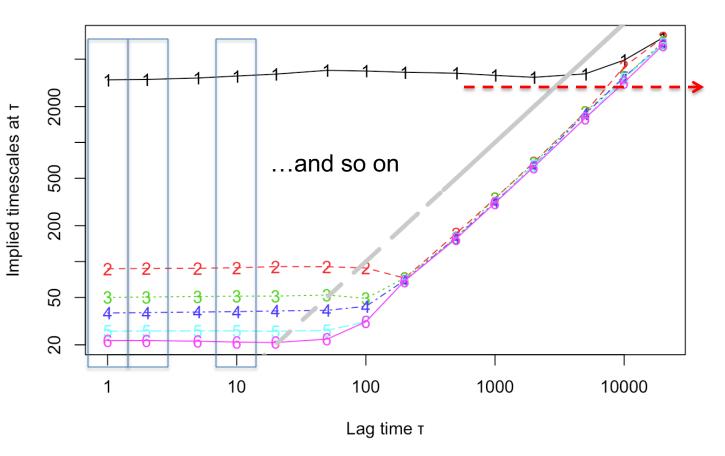
- Define states.
- Use trajectories to count transitions \rightarrow P_{ij}
- Eigenvalues: 1.0, μ₁, μ₂, ...
 - These are the time-scales (after -log)
- Eigenvectors: s_∞, s₁, s₂, ...
 - These are the equilibrium configuration, i.e. ΔG ; and faster "oscillations" (kinetics)

Markovianity

- The state transition probabilities only depend on the current state.
- Examples
 - Today's weather, not yesterday's
 - Where the ligand is, not how did it got there
- The property may be false at short timescales but true at longer ones (system's memory)
- It does depend on the chosen states

Implied timescales plot

Repeat the eigenvalues determination for several lags. Check convergence.



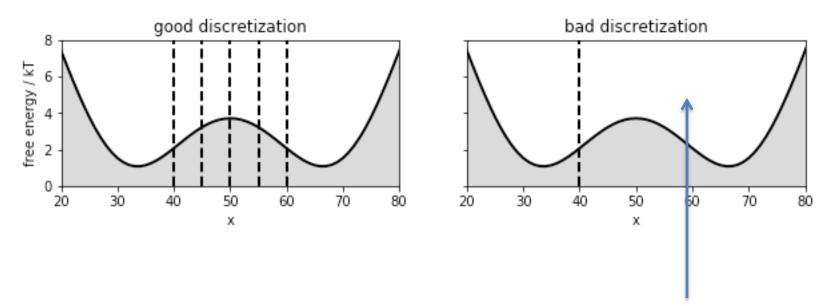
Here, convergence is achieved very early.

Reasons:

- (a) true two-state dynamics;
- (b) absence of orthogonal degrees of freedom;
- (c) fine space discretization

Macrostates

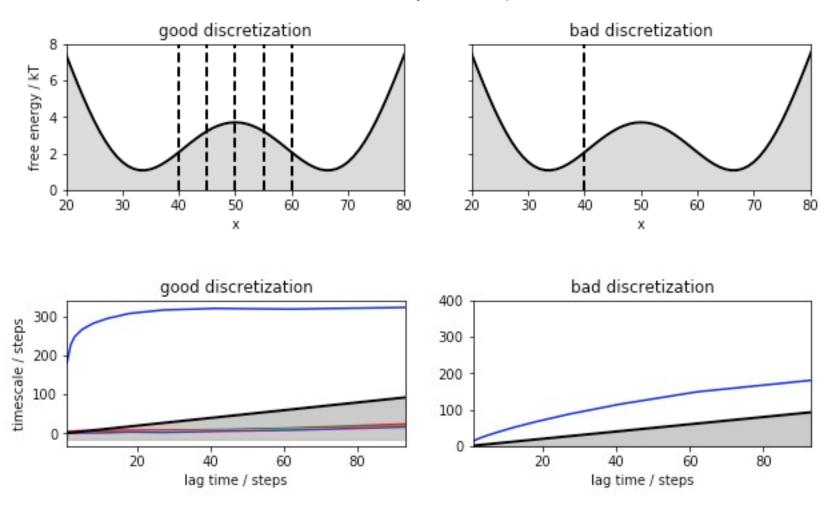
A bad choice of the discretization breaks the Markovianity assumption



In the "bad discretization" case, the barrier is embedded in one of the states. This generates a "long term memory" effect: the rightmost state could actually be short-lived (if we are on the left of the barrier) or long-lived (if we are on its right). These two cases are convoluted into the same, so that the present state information itself is not sufficient to predict the "future" of the system any more.

Macrostates

A bad choice of the discretization breaks the Markovianity assumption



End