

Lecture 17

Recall from last lecture...

- Integrals can be evaluated using Monte Carlo algorithms ...

$$\langle |m| \rangle = \frac{\sum_{S_1=\pm 1} \sum_{S_2=\pm 1} \dots \sum_{S_N=\pm 1} e^{-\beta E(S_1, S_2, \dots, S_N)}}{Q(\beta, h)} \left| \frac{1}{N} \sum_i S_i \right|$$

Sum/integrate out 1st spin

- Randomly pick ± 1 for each S_i (Uniformly)
- Compute a weighted average of the samples, giving each spin configuration a weight of:

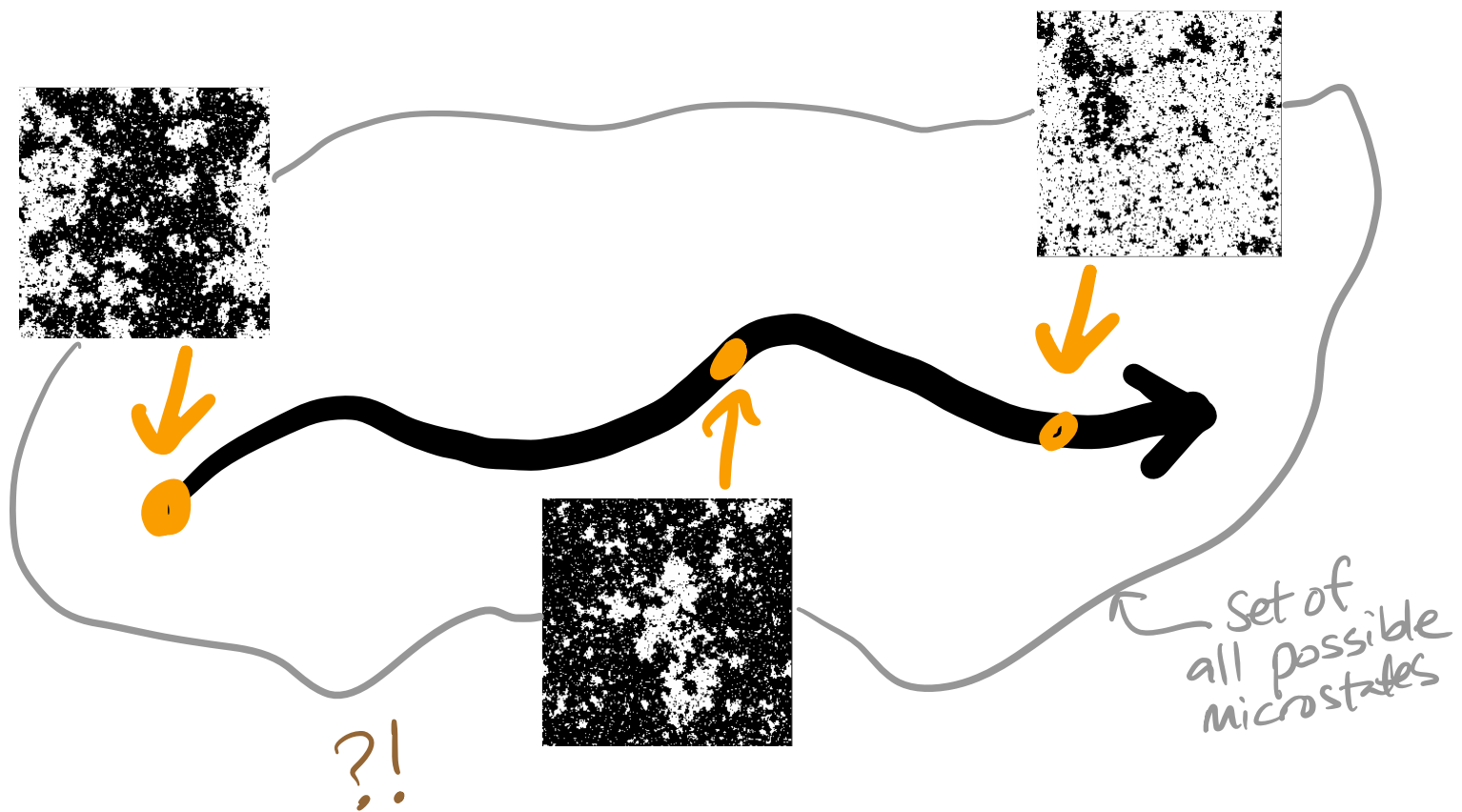
$$\frac{e^{-\beta E(S_1, S_2, \dots, S_N)} \left| \frac{1}{N} \sum_i S_i \right|}{Q(\beta, h)}$$

Unfortunately this scheme requires that we already know $Q(\beta, h)$ if we want to give the proper weight to each sample.

Viewed differently, we could think of drawing samples from the canonical (rather than uniform) distribution and giving them a simpler weight.

How should we sample spin configurations from the canonical ensemble?

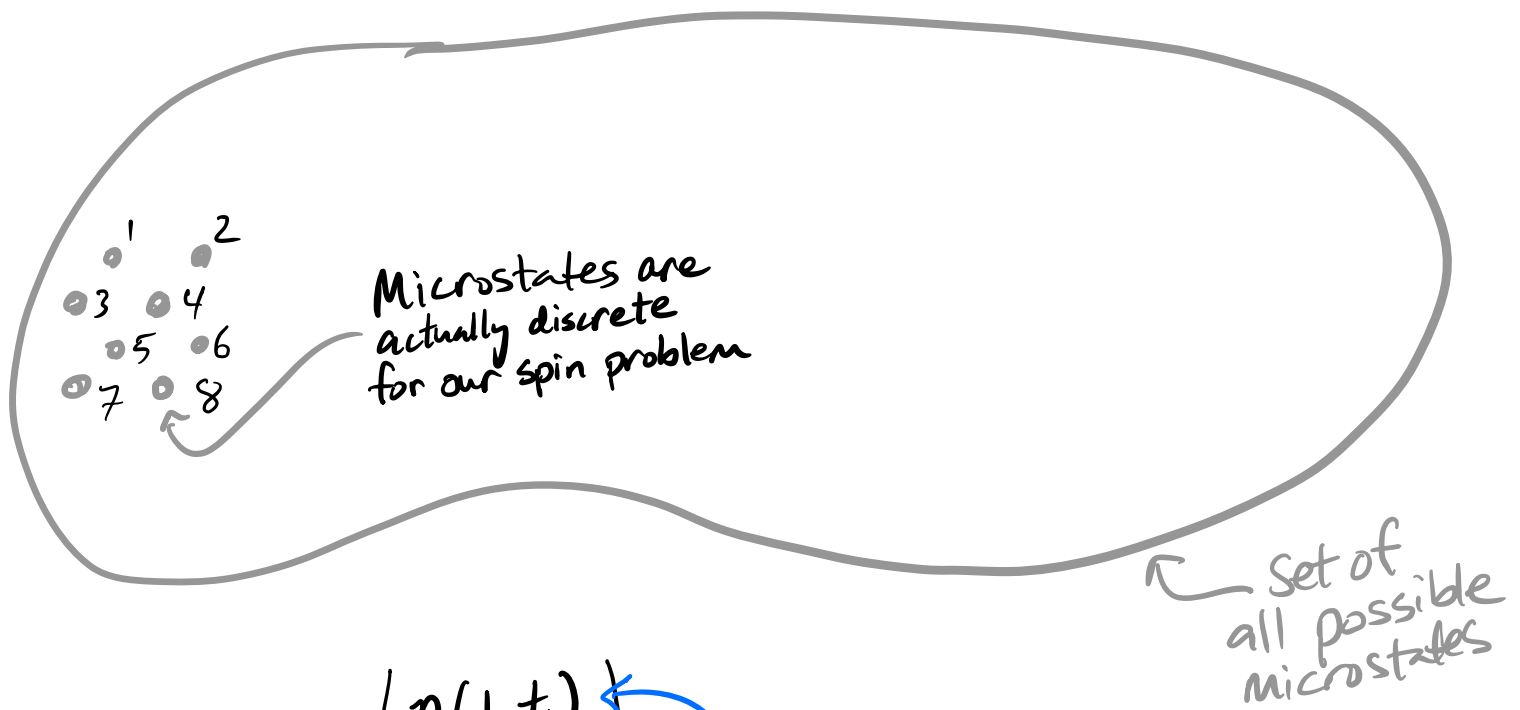
Use Dynamics!



We will make up a *dynamics* (a set of rules for how to transition from one configuration to another), constructed for the sole purpose of visiting the various microstates with probability $e^{-\beta E}/Q$

Even though the number of possible microstates is HUGE, I can still define a time-dependent vector which records the probability of each v at time t .

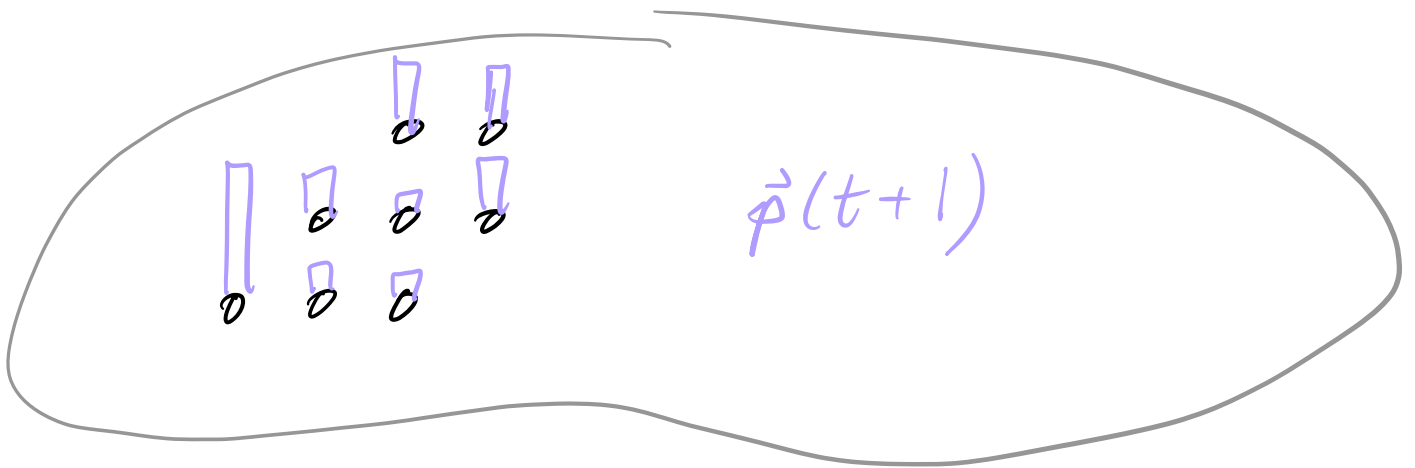
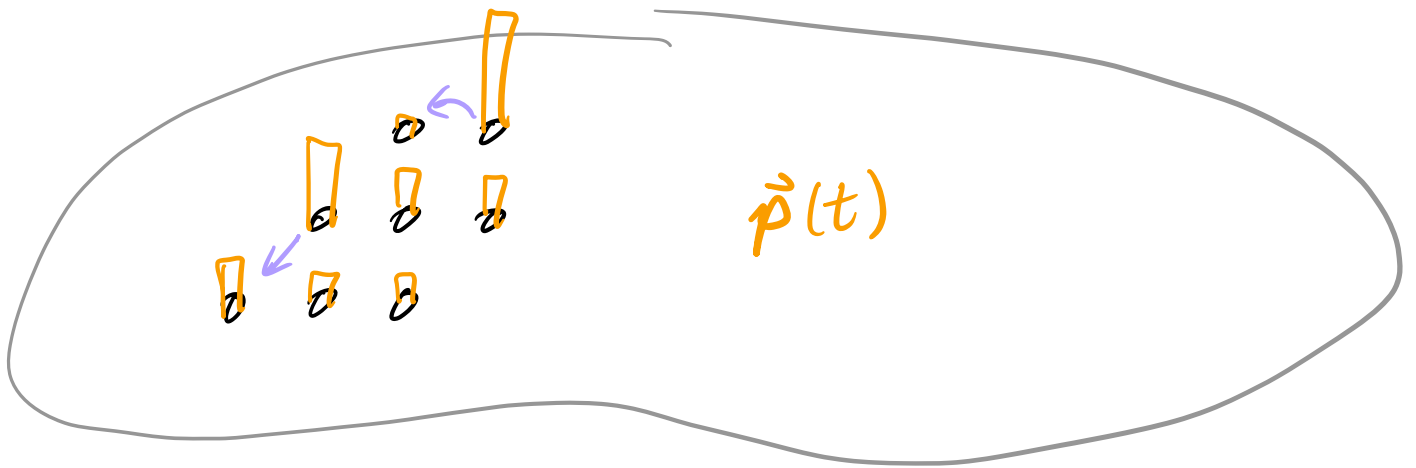
(I could never practically write down the whole vector)



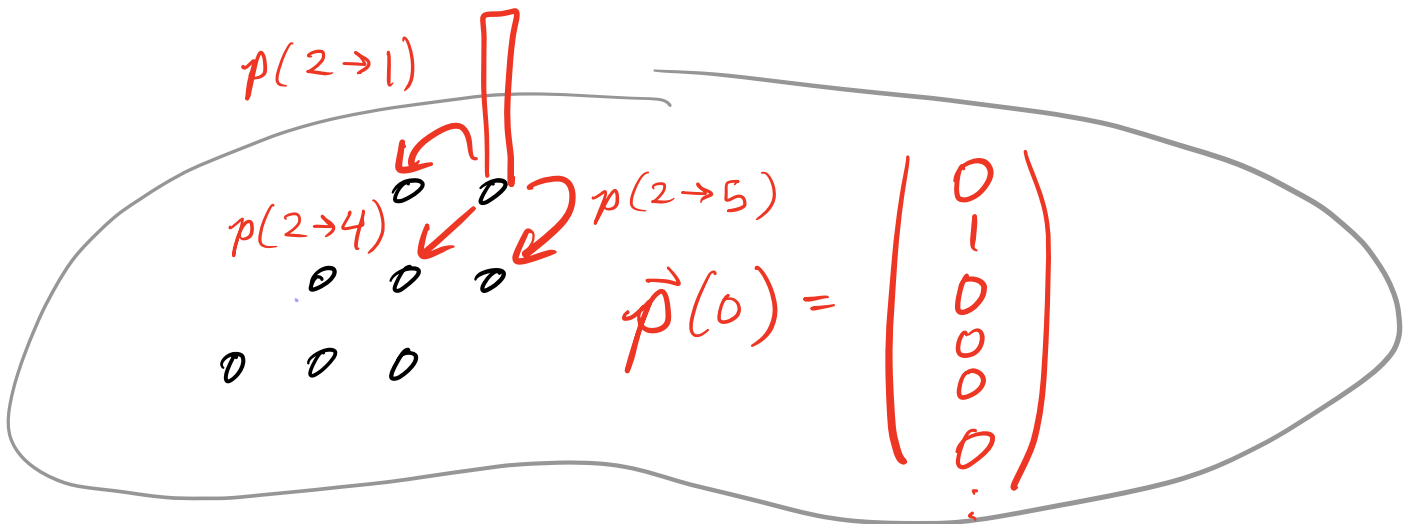
$$\vec{p}(t) = \begin{pmatrix} p(1,t) \\ p(2,t) \\ p(3,t) \\ \vdots \\ p(L^2,t) \end{pmatrix}$$

Probability of microstate #1 @ time t .

After one step of dynamics, what is $\vec{p}(t+1)$?



Easier to think through if we had started in a specific state.

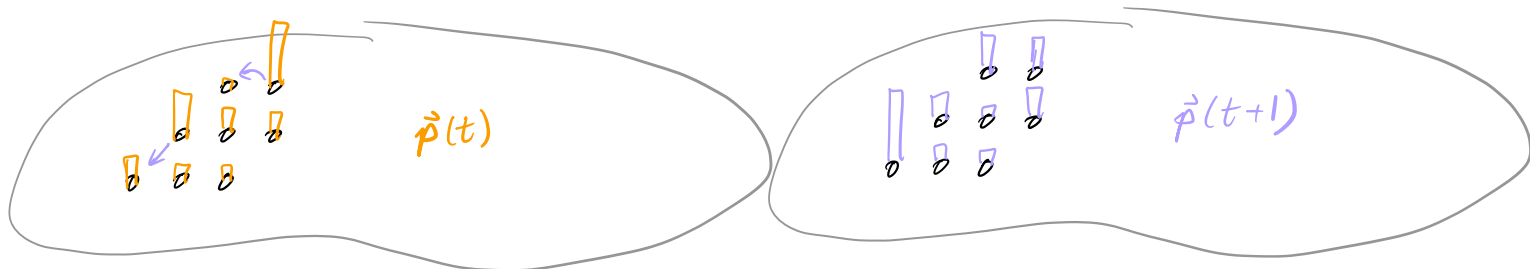


a coordinate vector with a 1 in the row corresponding to the initial microstate

$$\vec{p}(1) = \begin{pmatrix} p(2 \rightarrow 1) \\ p(2 \rightarrow 2) \\ p(2 \rightarrow 3) \\ \vdots \end{pmatrix}$$

Can you go from any state to any state?

[In principle yes, for our Ising MC, we will choose $p(i \rightarrow j) = 0$ unless i & j differ by a single spin flip.]



$$\vec{p}(t+1) = p(1,t) \begin{pmatrix} p(1 \rightarrow 1) \\ p(1 \rightarrow 2) \\ p(1 \rightarrow 3) \\ \vdots \end{pmatrix} + p(2,t) \begin{pmatrix} p(2 \rightarrow 1) \\ p(2 \rightarrow 2) \\ p(2 \rightarrow 3) \\ \vdots \end{pmatrix} + \dots$$

$$= \begin{pmatrix} p(1 \rightarrow 1) & p(2 \rightarrow 1) & \dots \\ p(1 \rightarrow 2) & p(2 \rightarrow 2) & \\ \vdots & & \ddots \end{pmatrix} \underline{\underline{\vec{p}(t)}}$$



Call this matrix of all transition probabilities the "transition matrix" T .

T defines the dynamics. It tells how probability evolves in time.

$$\vec{p}(t+1) = T \vec{p}(t)$$

$$\vec{p}(t+n) = T^n \vec{p}(t)$$

↑
n steps

Our goal was to design a dynamics such that

$$\lim_{t \rightarrow \infty} \vec{p}(t) = \frac{1}{Q} \begin{pmatrix} e^{-\beta E(v_1)} \\ e^{-\beta E(v_2)} \\ \vdots \end{pmatrix} \equiv \vec{\pi}$$

$\vec{\pi}$ is a stationary distribution (not a function of time).
Once you reach $\vec{\pi}$, more time steps don't change the probability distribution.

⇒ Our dynamics must satisfy

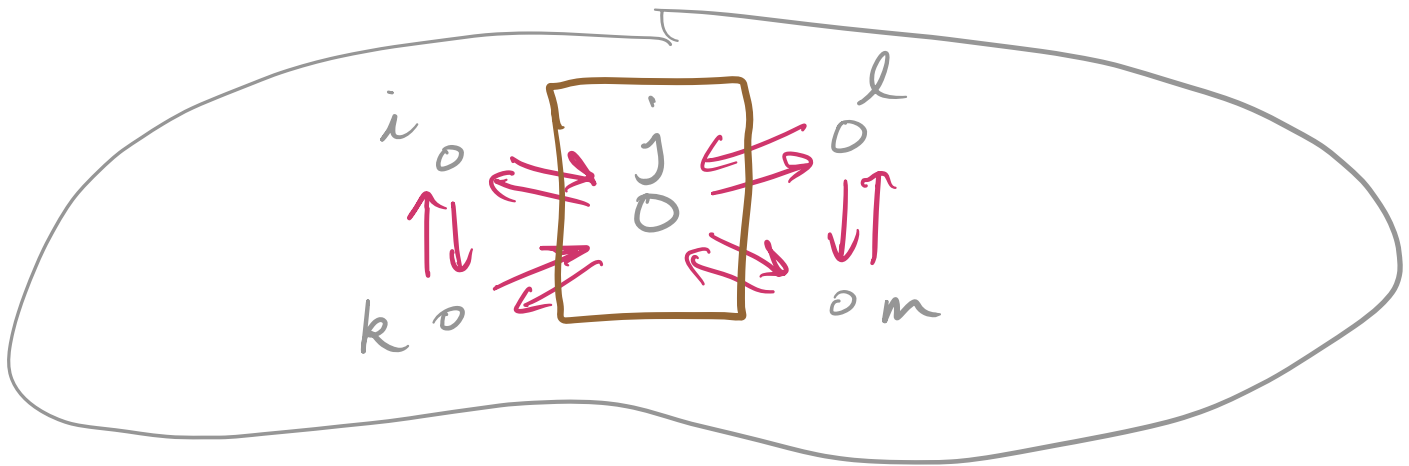
$$T \vec{\pi} = \vec{\pi}$$

Balance Condition

Result of another step of dynamics

Exactly the same distribution we started with

Why must T satisfy that balance condition?



The total probability of leaving site j :

$$\pi(j) (p(j \rightarrow l) + p(j \rightarrow m) + \dots)$$

out flows

must balance with the total probability entering j :

$$\pi(l) p(l \rightarrow j) + \pi(m) p(m \rightarrow j) + \dots$$

in flows

If the in-flows + out-flows did not balance then the probability of j would change from one time to the next.

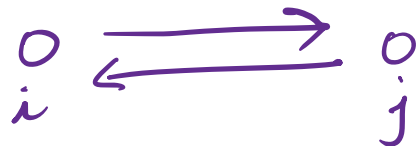
$$\vec{p}(0) = \vec{\pi} + \vec{\Delta} \quad \leftarrow \begin{array}{l} \text{deviation from} \\ \text{Steady state} \end{array}$$

$$\vec{p}(1) = T(\vec{\pi} + \vec{\Delta}) = \vec{\pi} + T\vec{\Delta}$$

$$\vec{p}(n) = T^n(\vec{\pi} + \vec{\Delta}) = \vec{\pi} + T^n\vec{\Delta}$$

One way (not the only way) to ensure balance is to require that every pair of states is balanced

Right flow = $\pi(i) p(i \rightarrow j)$ prob. site i is losing to go into j



Left flow = $\pi(j) p(j \rightarrow i)$

Forcing every pair to be balanced is called "detailed balance". It is a stronger condition that implies "global balance" ($T\vec{\pi} = \vec{\pi}$)

For every pair of configurations $i \leftrightarrow j$, we need a rule for picking $p(i \rightarrow j) + p(j \rightarrow i)$ such that...

$$\pi(i) p(i \rightarrow j) = \pi(j) p(j \rightarrow i)$$

$$\Rightarrow \frac{p(j \rightarrow i)}{p(i \rightarrow j)} = \frac{\pi(i)}{\pi(j)} = \frac{e^{-\beta E(i)} / \cancel{Q}}{e^{-\beta E(j)} / \cancel{Q}} = e^{-\beta [E(i) - E(j)]}$$

The partition function has dropped out!

An obvious choice...

$$p(j \rightarrow i) = e^{-\beta E(i)} + p(i \rightarrow j) = e^{-\beta E(j)} \quad (\times)$$

This would satisfy $\frac{p(j \rightarrow i)}{p(i \rightarrow j)} = e^{-\beta [E(i) - E(j)]}$

but there is a problem.

Problem? We require that

$$\sum_j p(i \rightarrow j) = 1 \quad (\text{Normalization})$$

Given you start in i , you must go to some new configuration

But, there is another way!

Conceptually, we split $p(i \rightarrow j)$ into two:

1. Propose a new j with some probability you pick

$p_{\text{gen}}(i \rightarrow j)$: generation probability

2. Decide to accept or reject that proposal with probability $p_{\text{acc}}(i \rightarrow j)$. If you reject, stay in i .

To transition from $i \rightarrow j$, you must both generate $i \rightarrow j$ and accept that $i \rightarrow j$, so

$$p(i \rightarrow j) = p_{\text{gen}}(i \rightarrow j) p_{\text{acc}}(i \rightarrow j)$$

$P_{\text{gen}}(i \rightarrow j)$ can be almost anything you want,
but then $P_{\text{acc}}(i \rightarrow j)$ must be constructed accordingly
so detailed balance will hold:

$$\pi(i) P_{\text{gen}}(i \rightarrow j) P_{\text{acc}}(i \rightarrow j) = \pi(j) P_{\text{gen}}(j \rightarrow i) P_{\text{acc}}(j \rightarrow i)$$

$$\Rightarrow \frac{P_{\text{acc}}(i \rightarrow j)}{P_{\text{acc}}(j \rightarrow i)} = \frac{\pi(j) P_{\text{gen}}(j \rightarrow i)}{\pi(i) P_{\text{gen}}(i \rightarrow j)}$$

There are many ways to choose such a P_{acc} .
The Metropolis and Glauber criteria are the most popular.

Metropolis:

$$P_{\text{acc}}(i \rightarrow j) = \min \left[1, \frac{\pi(j) P_{\text{gen}}(j \rightarrow i)}{\pi(i) P_{\text{gen}}(i \rightarrow j)} \right]$$

$$P_{\text{acc}}(j \rightarrow i) = \min \left[1, \frac{\pi(i) P_{\text{gen}}(i \rightarrow j)}{\pi(j) P_{\text{gen}}(j \rightarrow i)} \right]$$

To confirm that Metropolis satisfies detailed balance, it is useful to split into 3 cases.

$$\frac{\min\left[1, \frac{\pi(j) P_{gen}(j \rightarrow i)}{\pi(i) P_{gen}(i \rightarrow j)}\right]}{\min\left[1, \frac{\pi(i) P_{gen}(i \rightarrow j)}{\pi(j) P_{gen}(j \rightarrow i)}\right]} \stackrel{?}{=} \frac{\pi(j) P_{gen}(j \rightarrow i)}{\pi(i) P_{gen}(i \rightarrow j)}$$

$$\pi(i) P_{gen}(i \rightarrow j) P_{acc}(i \rightarrow j) \boxed{?} = \pi(j) P_{gen}(j \rightarrow i) P_{acc}(j \rightarrow i)$$

↑
Check this
for Metropolis



$$\pi(i) P_{gen}(i \rightarrow j) \min\left[1, \frac{\pi(j) P_{gen}(j \rightarrow i)}{\pi(i) P_{gen}(i \rightarrow j)}\right] =$$

$$\pi(j) P_{gen}(j \rightarrow i) \min\left[1, \frac{\pi(i) P_{gen}(i \rightarrow j)}{\pi(j) P_{gen}(j \rightarrow i)}\right]$$

Case 1: $\pi(i) P_{gen}(i \rightarrow j) < \pi(j) P_{gen}(j \rightarrow i)$

$$\pi(i) P_{gen}(i \rightarrow j) \cdot 1 = \cancel{\pi(j)} \cancel{P_{gen}(j \rightarrow i)} \frac{\pi(i) P_{gen}(i \rightarrow j)}{\cancel{\pi(j)} \cancel{P_{gen}(j \rightarrow i)}}$$

$$\text{Case 2: } \pi(i) p_{\text{gen}}(i \rightarrow j) > \pi(j) p_{\text{gen}}(j \rightarrow i) \checkmark$$

$$\text{Case 3: } \pi(i) p_{\text{gen}}(i \rightarrow j) = \pi(j) p_{\text{gen}}(j \rightarrow i) \checkmark$$