



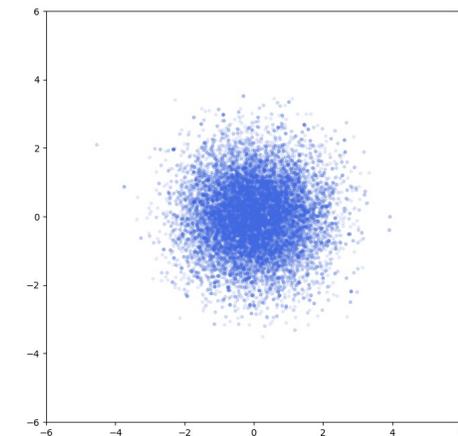
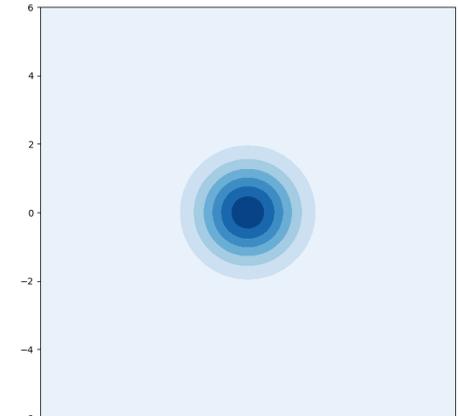
Fixed-distance Hamiltonian Monte Carlo

Hadi Mohasel Afshar, Sally Cripps

CSIRO's Data61 & The University of Sydney

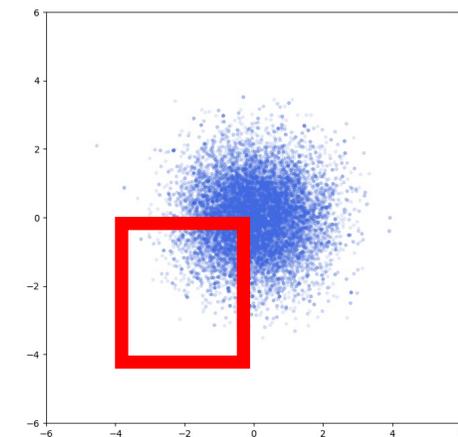
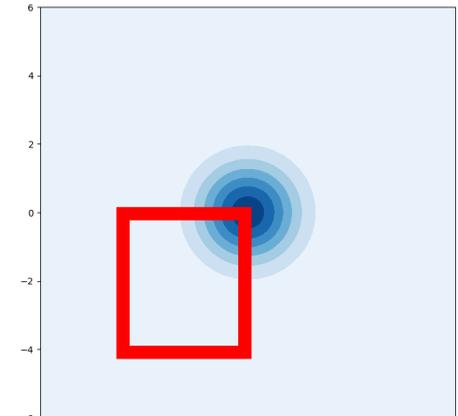
Markov Chain Monte Carlo (MCMC)

- MCMC are a class methods that approximate a probability distribution with a set of states a.k.a. samples.



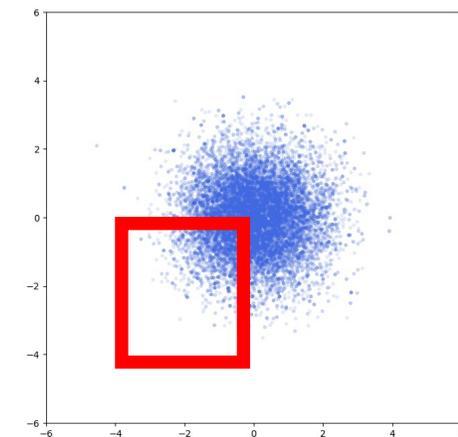
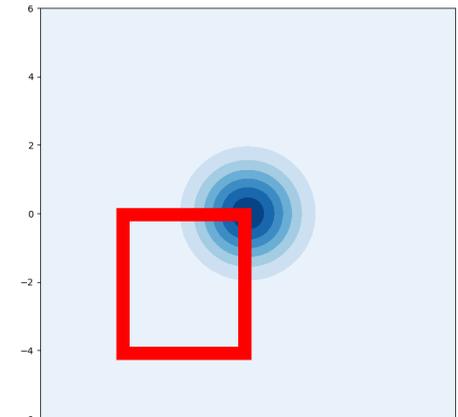
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- Sampling is unbiased if #draws from each region is proportional to the probability mass of that region.



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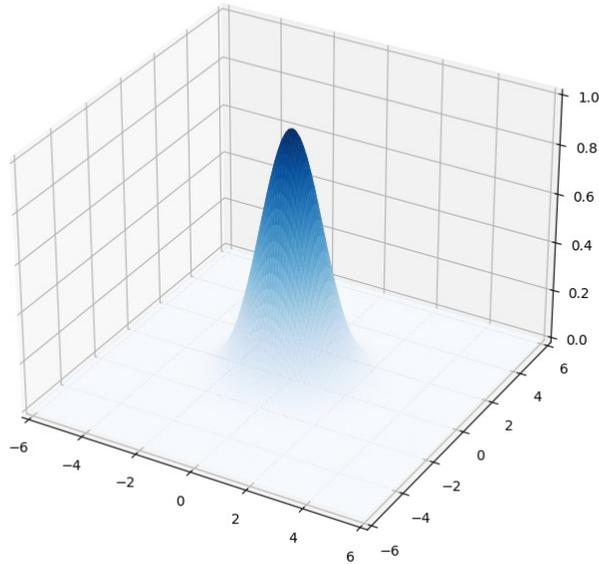
- MCMC are a class methods that approximate a probability distribution with a set of states a.k.a. samples.
- Sampling is unbiased if #draws from each region is proportional to the probability mass of that region.
- The state of the art MCMC methods (e.g. NUTS) are variations of the Hamiltonian Monte Carlo (HMC)



Hamiltonian Monte Carlo (HMC)

- In HMC, the potential energy is defined as the $-\log$ of PDF.

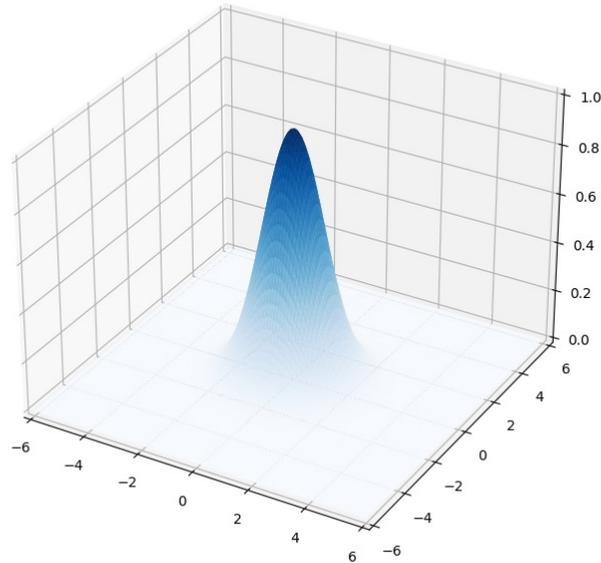
Target probability density: $\pi(\mathbf{q})$



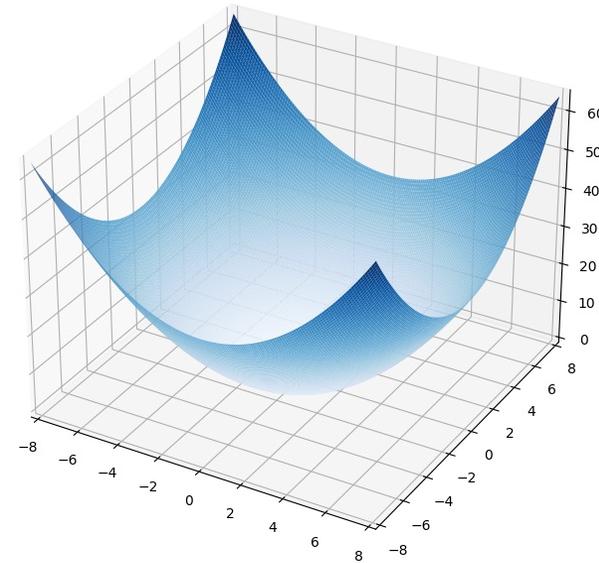
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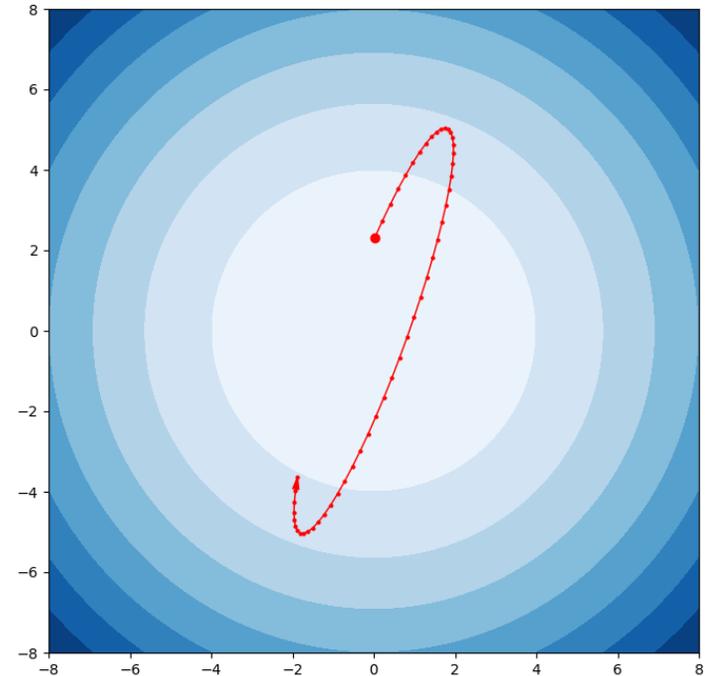


Potential energy: $U(\mathbf{q}) = -\log \pi(\mathbf{q})$



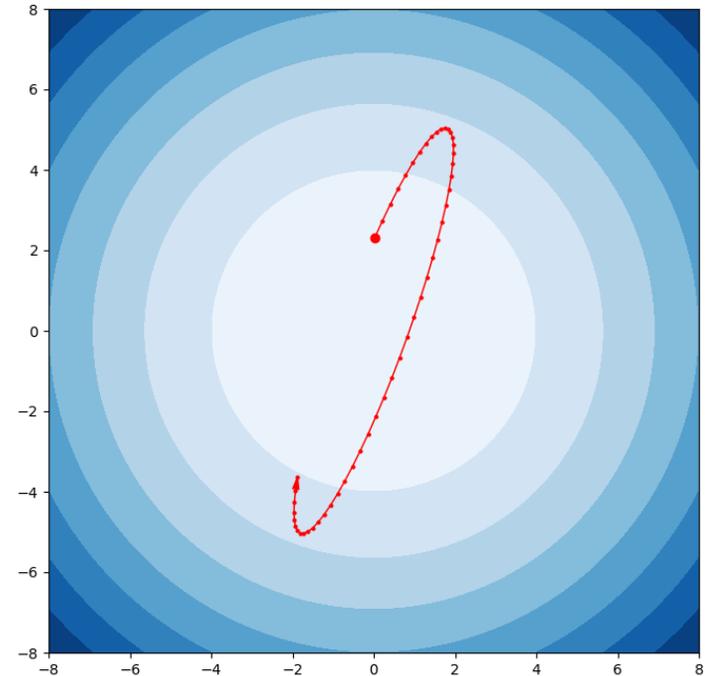
Hamiltonian Monte Carlo (HMC)

- In HMC, the potential energy is defined as the neg. log of the PDF.
- An auxiliary momentum $\mathbf{p} \sim N(0, I)$ is assigned to the current state. Then, it is evolved via the simulation of the equations of motion for a fixed time.

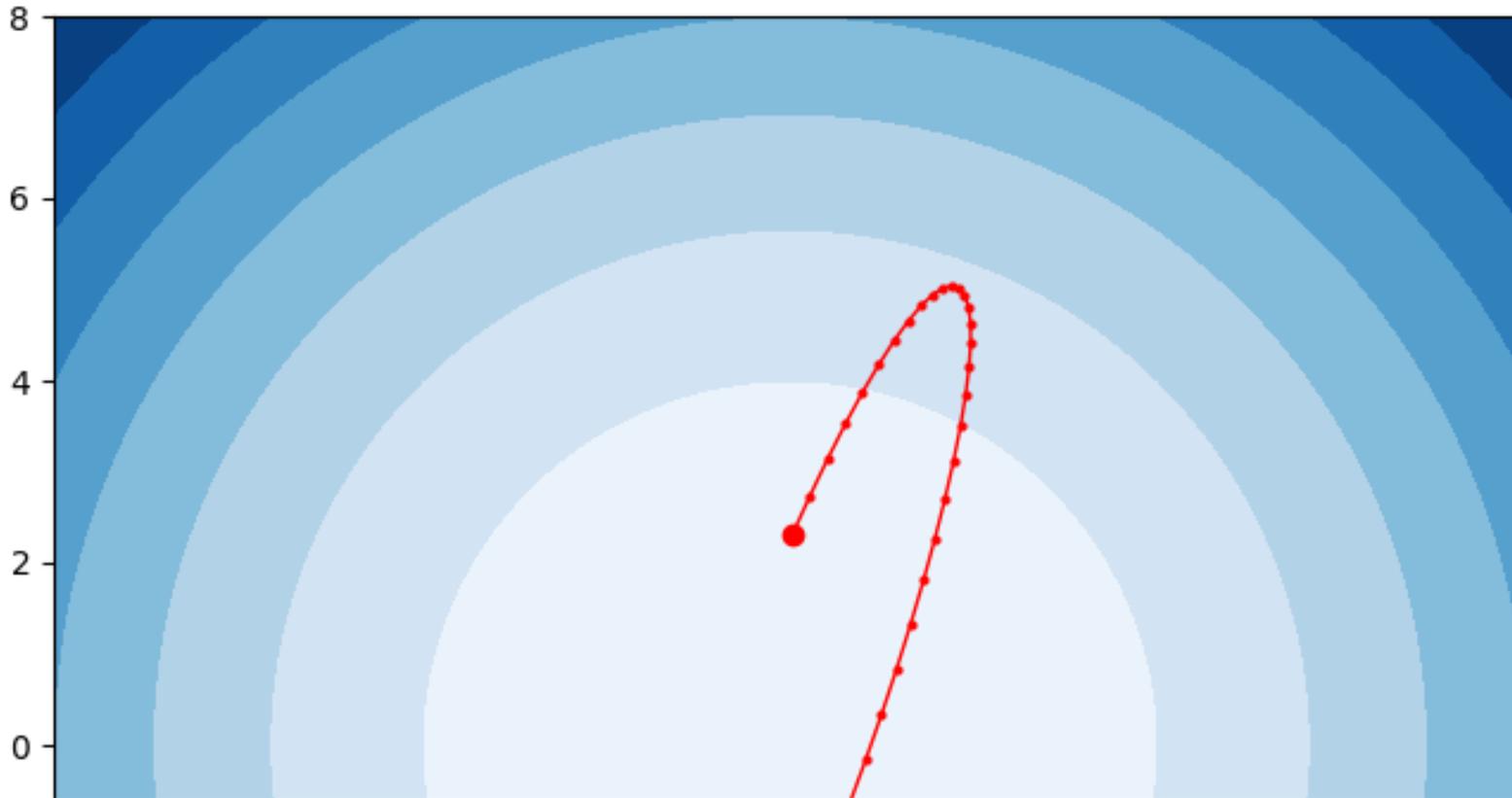


Hamiltonian Monte Carlo (HMC)

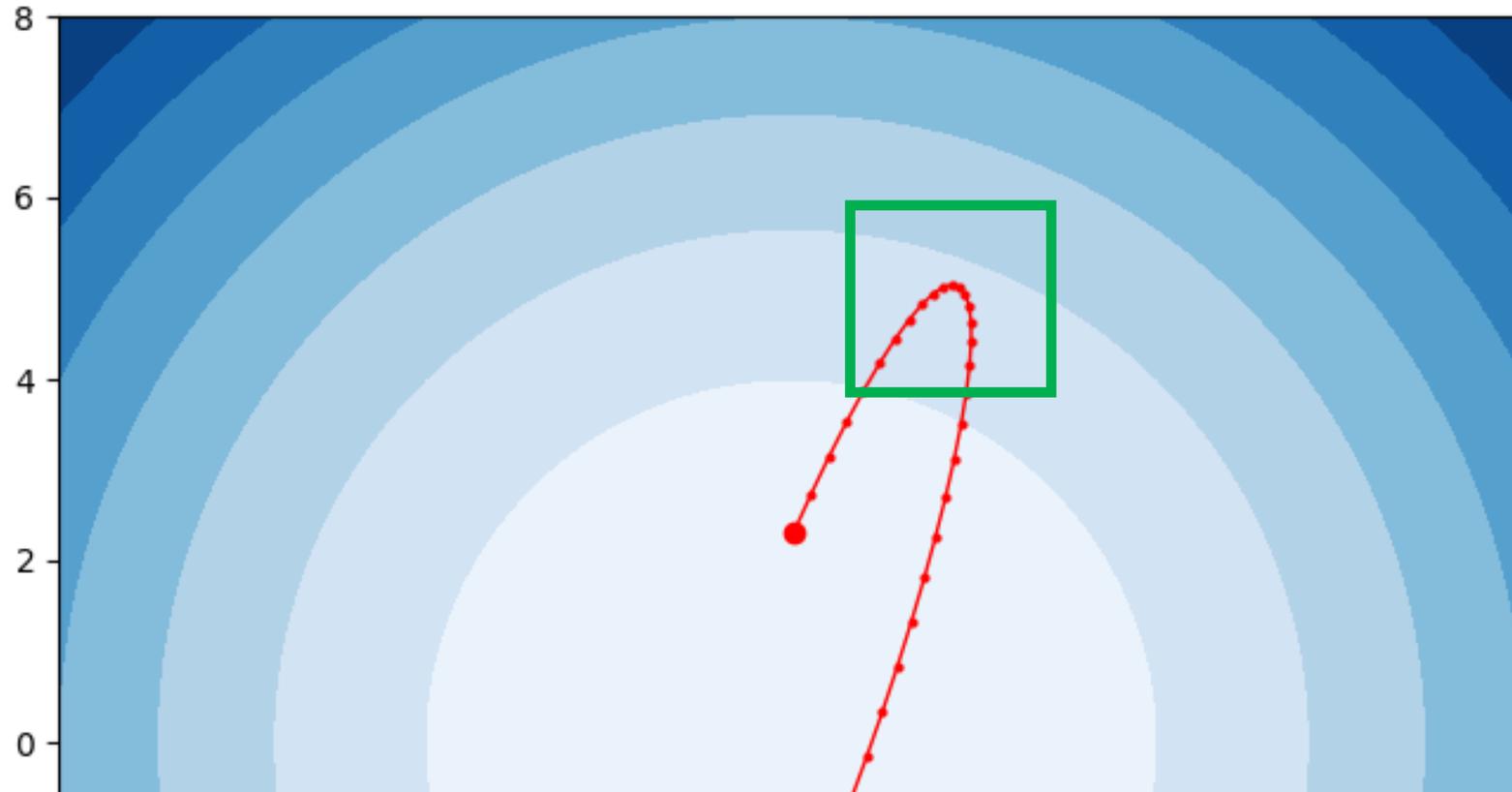
- In HMC, the potential energy is defined as the neg. log of PDF.
- An auxiliary momentum $\mathbf{p} \sim N(0, I)$ is assigned to the current state. Then, it is evolved via the simulation of the equations of motion for a fixed time.
- If the simulation is precise, the acceptance probability of the resulting proposal is high.



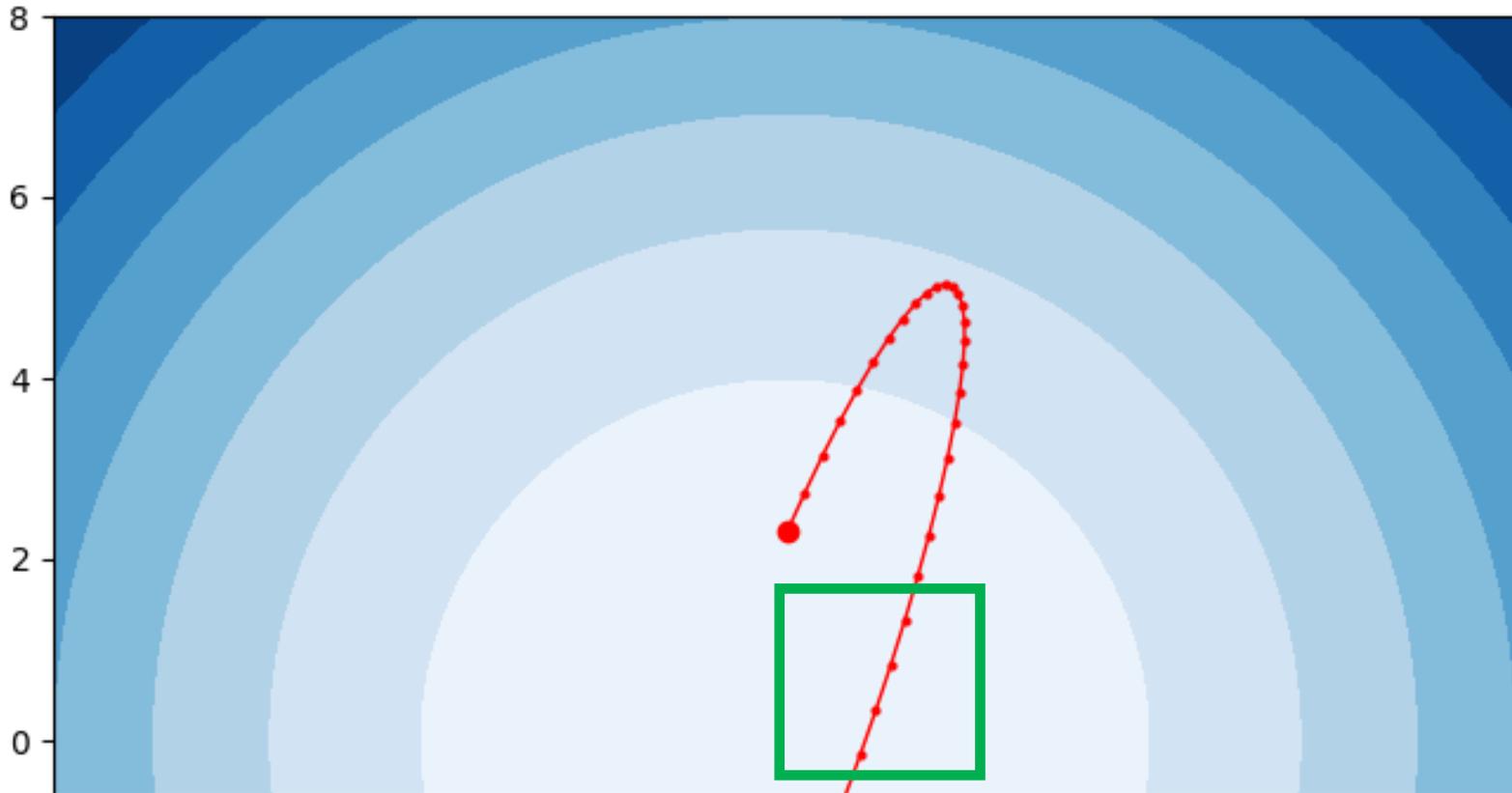
Note: In high potential (i.e. low probability) regions the velocity is low



More states are generated from these regions...

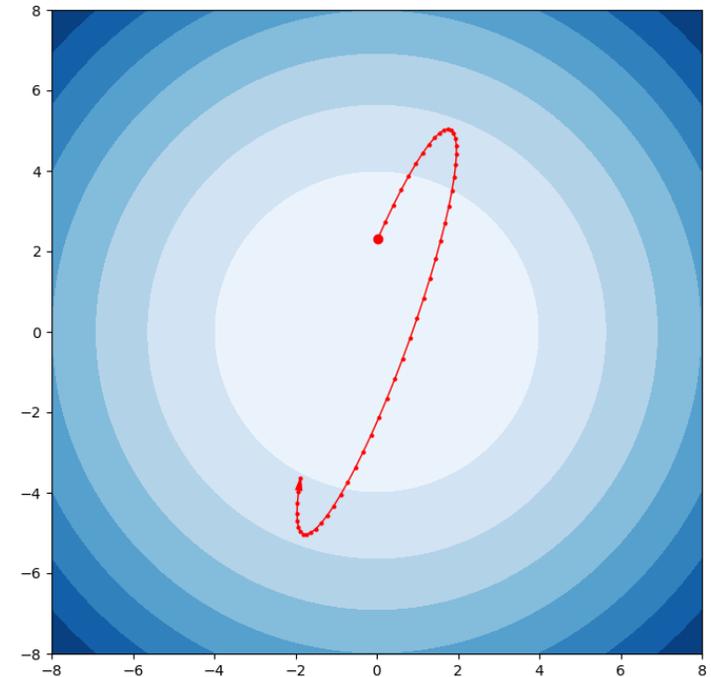


Conversely, less time is spent in the high-probability regions



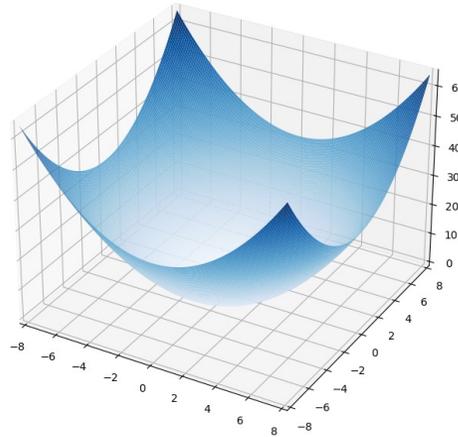
Evolution bias

- As such, there is bias towards proposing low-probability states which is counter-intuitive!



To verify ...

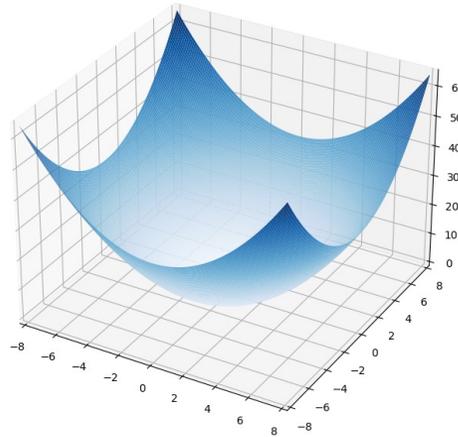
Consider a potential energy function:



To verify ...

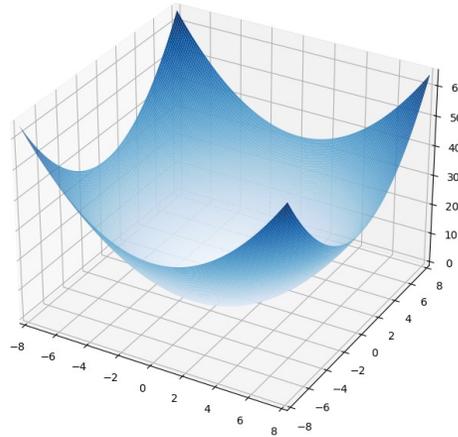
Consider a potential energy function:

We let the current state be on the unit circle



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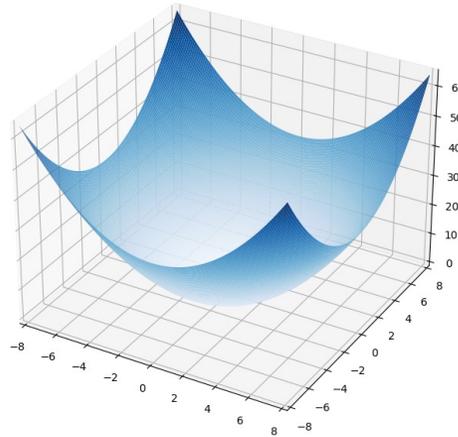


We let the current state be on the unit circle

We fix the momentum magnitude but randomly choose its direction

To verify ...

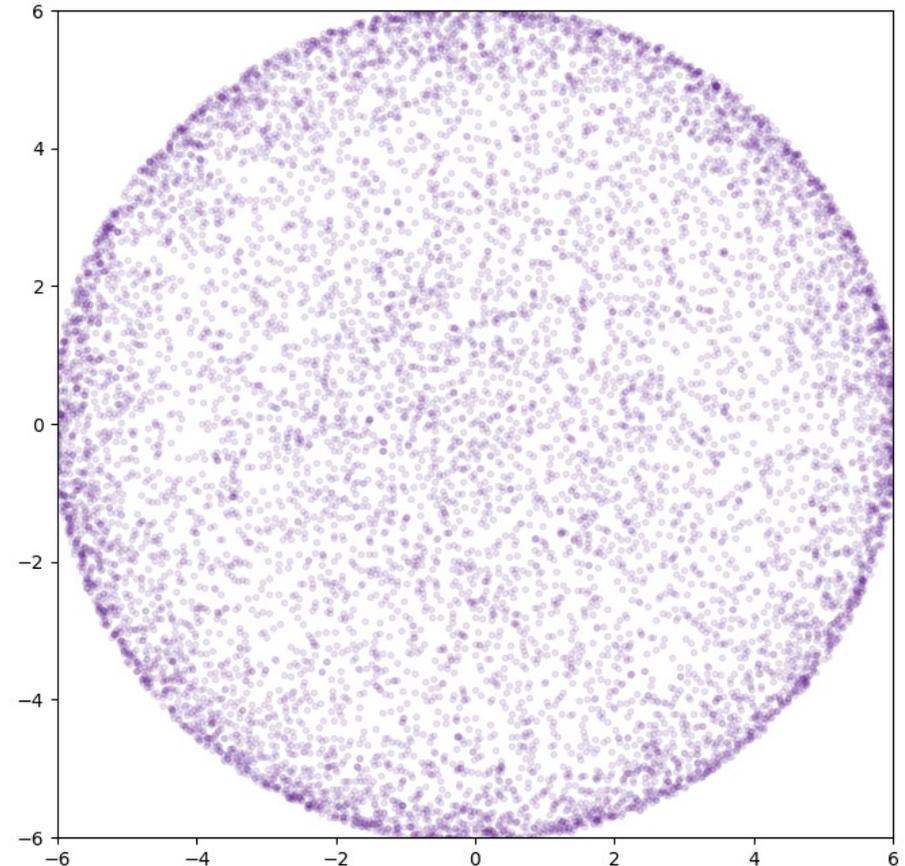
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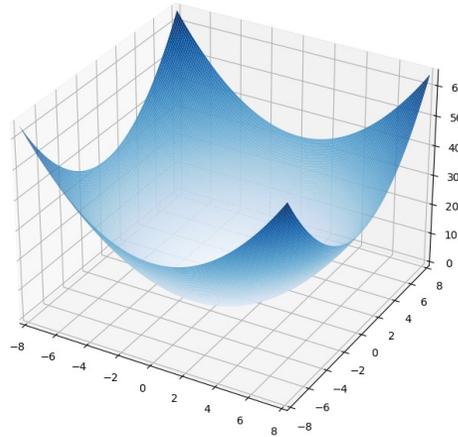
We fix the momentum magnitude but randomly choose its direction

... and plot the proposals:



To verify ...

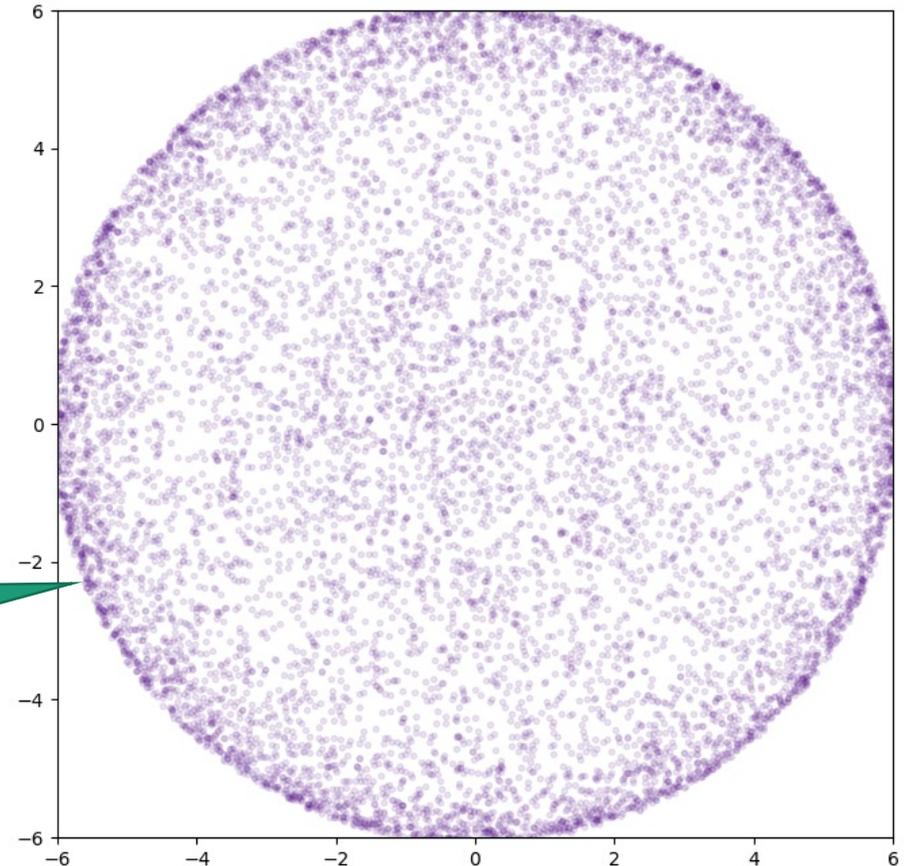
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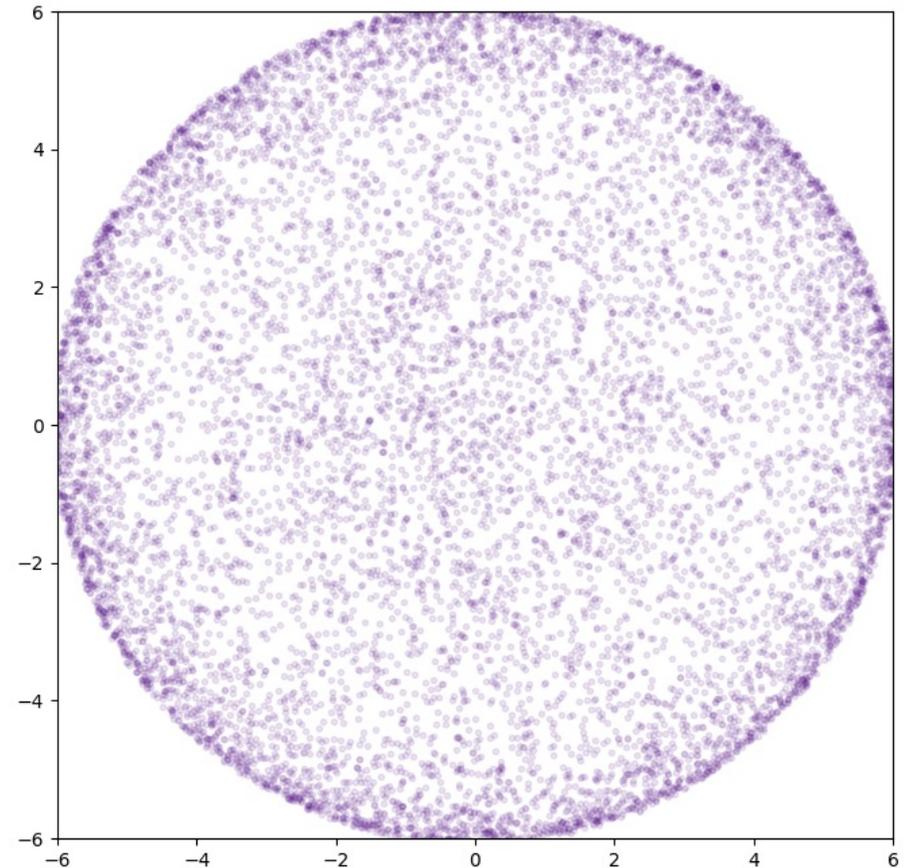
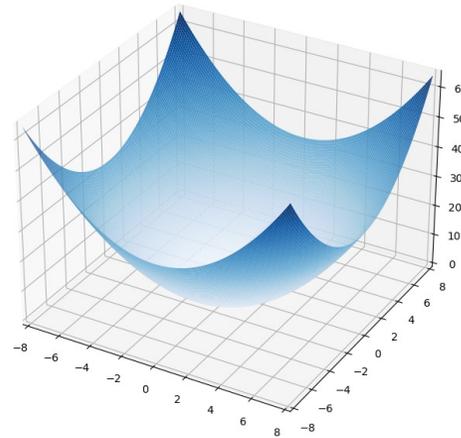
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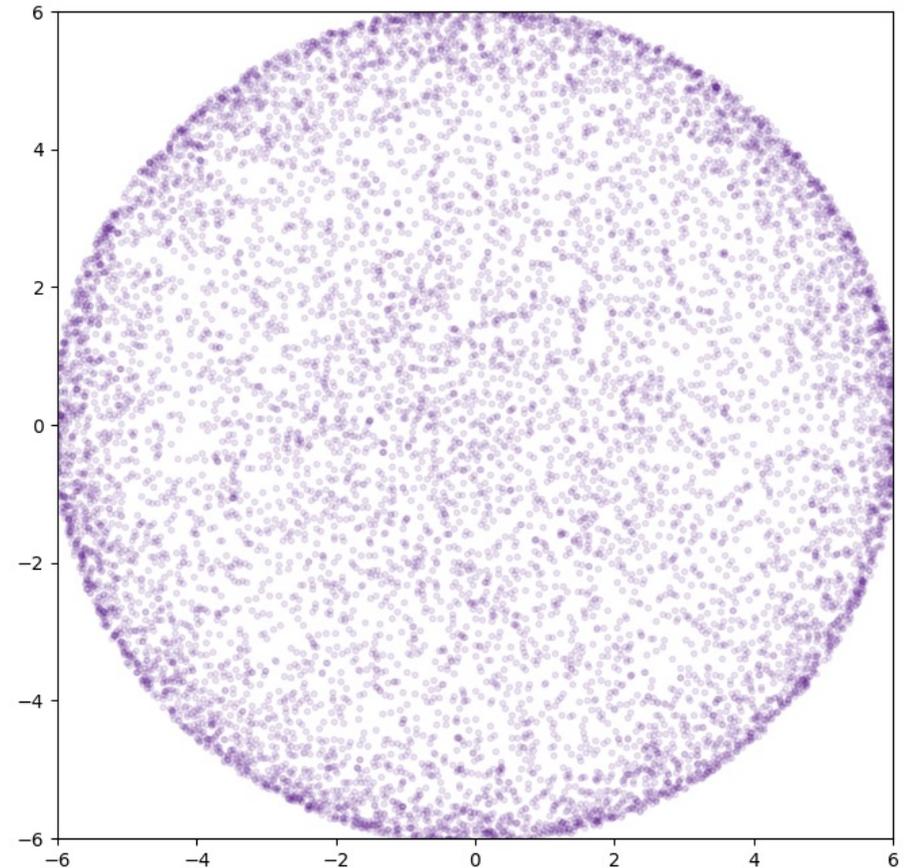
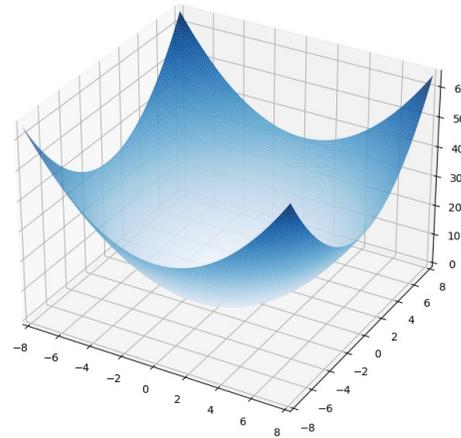
**Regions of low probability
are over-represented**



Then, what makes the total HMC sampling unbiased?

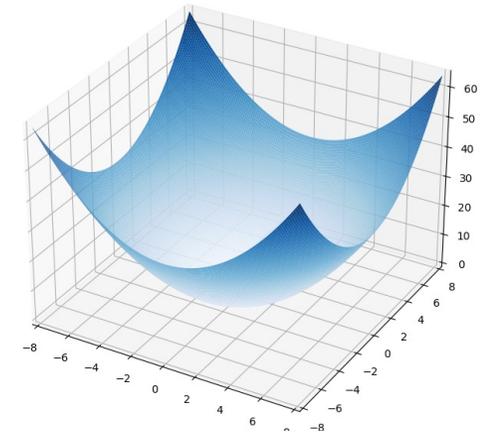
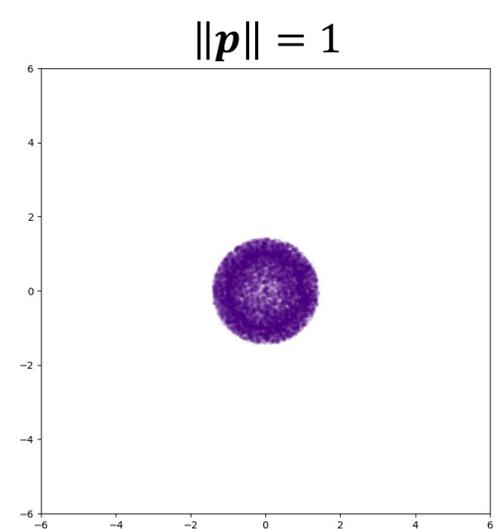
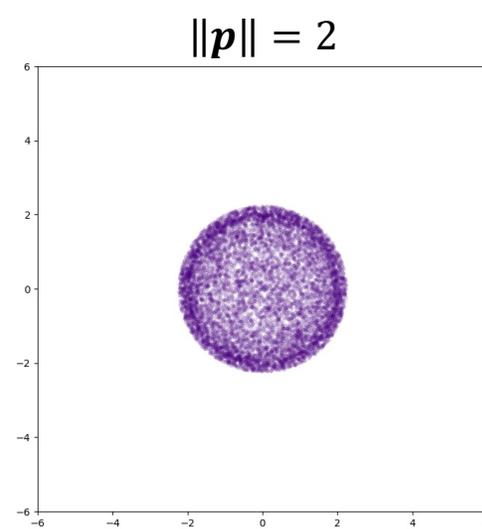
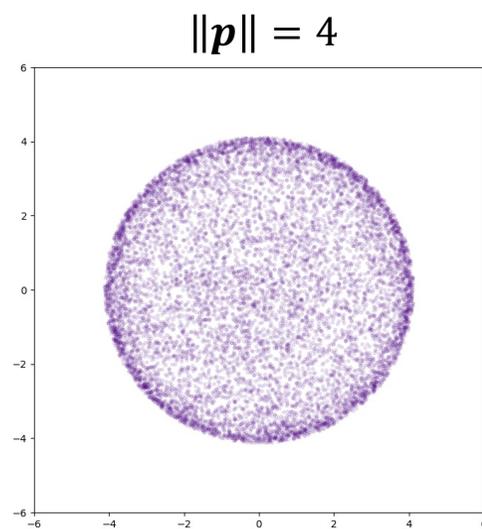
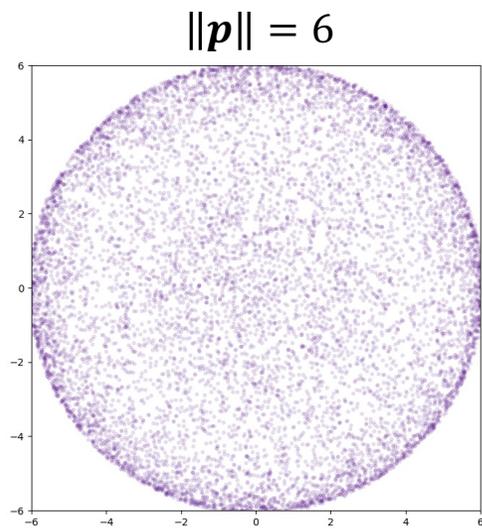


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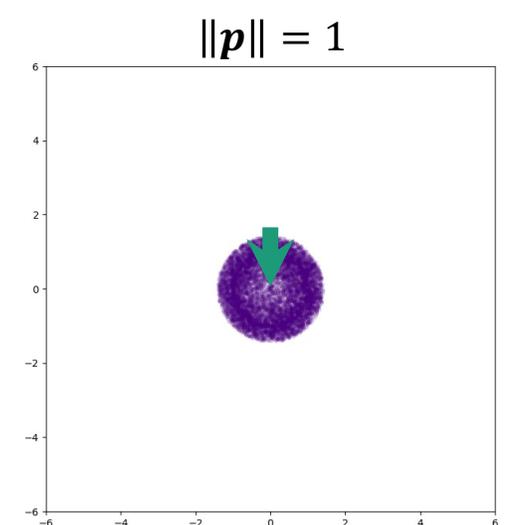
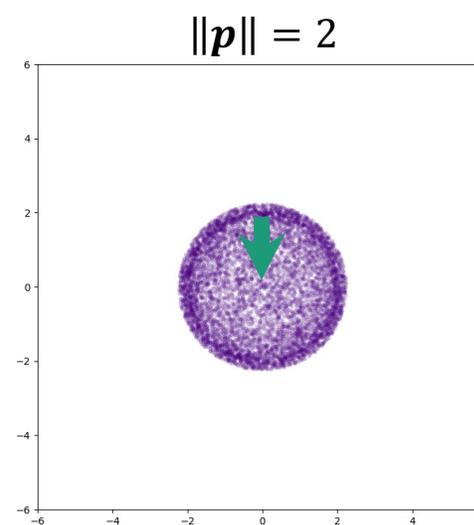
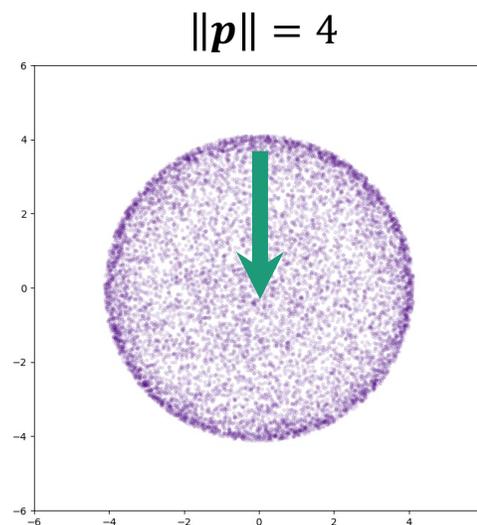
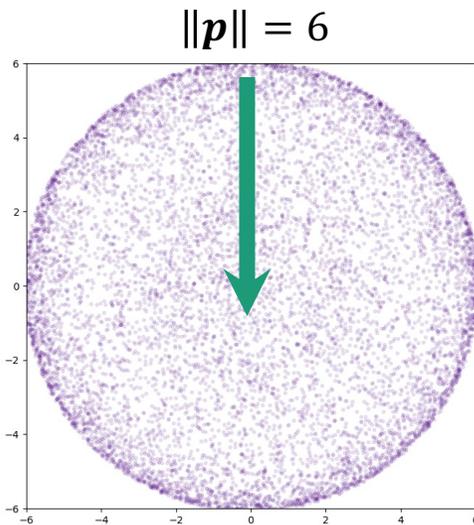
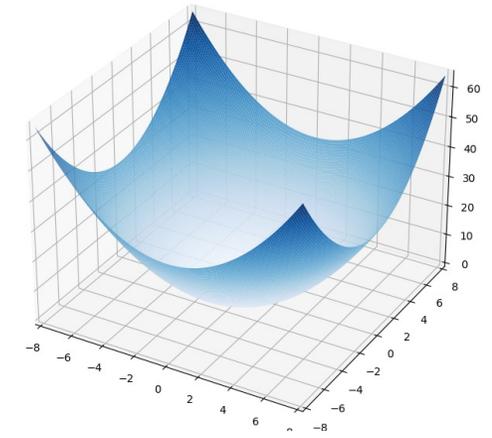
The momentum distribution...

Previous example with different momentum magnitudes...



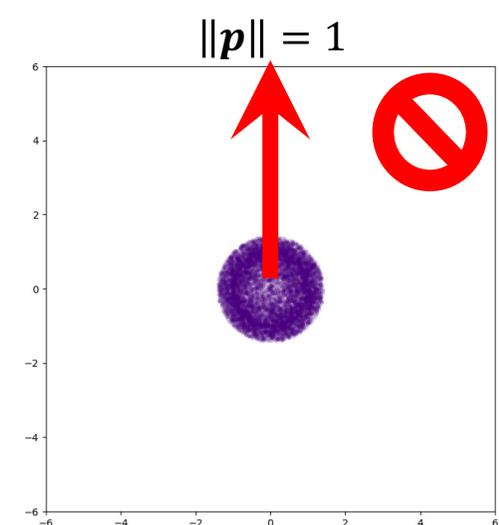
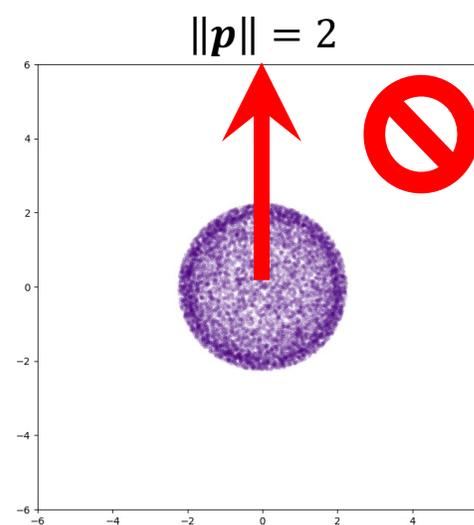
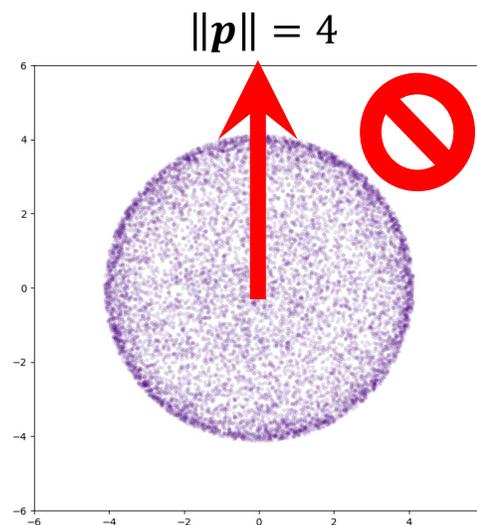
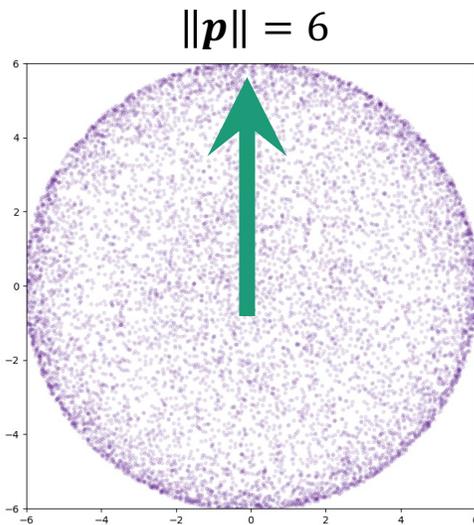
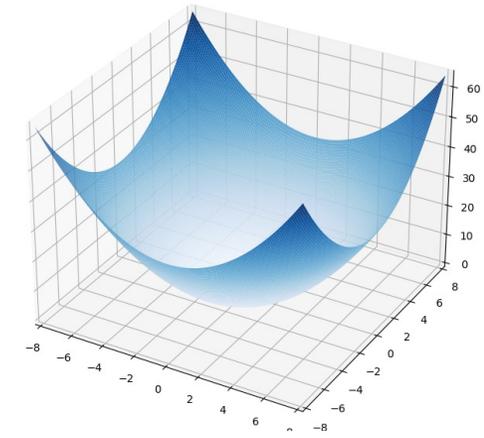
Previous example with different momentum magnitudes...

The transition from a low to high probability region is always possible



Previous example with different momentum magnitudes...

But if the momentum's magnitude is low, the transition from a high to low probability region may NOT be possible.



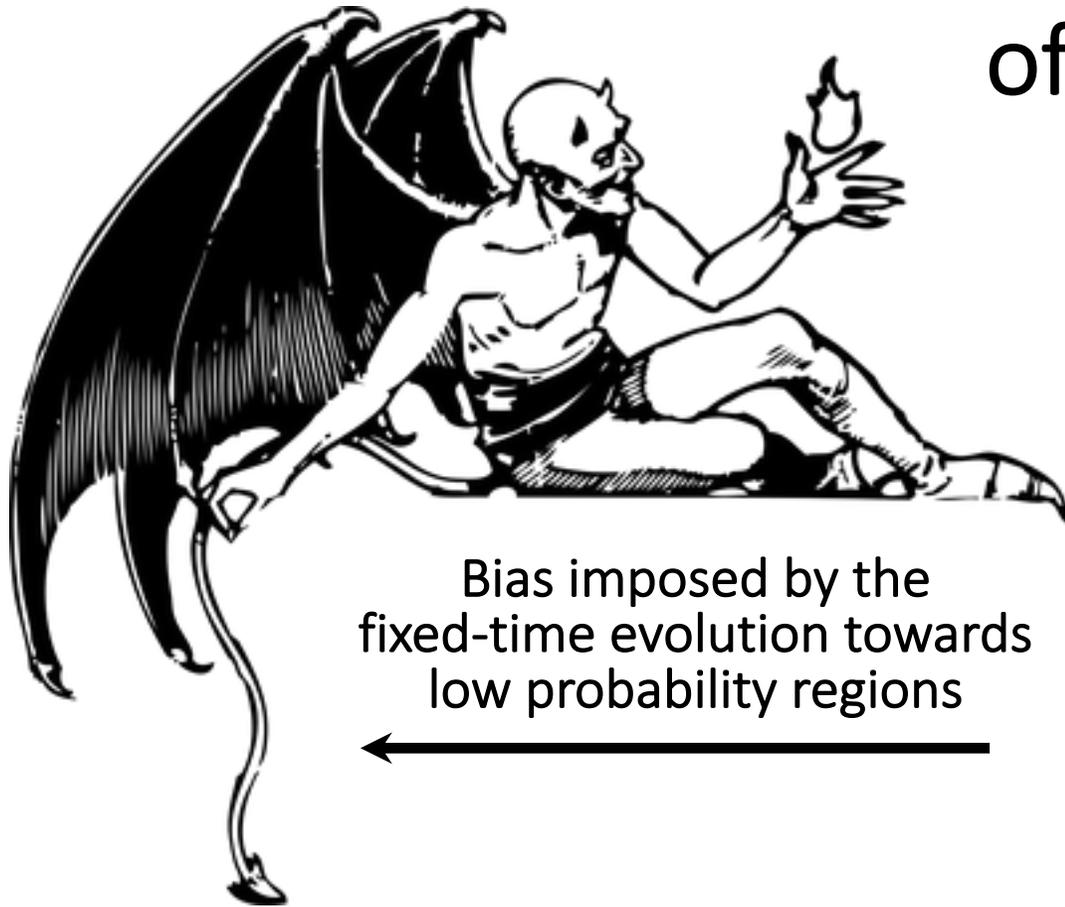
Two counter-balancing biases...

Convergence of HMC



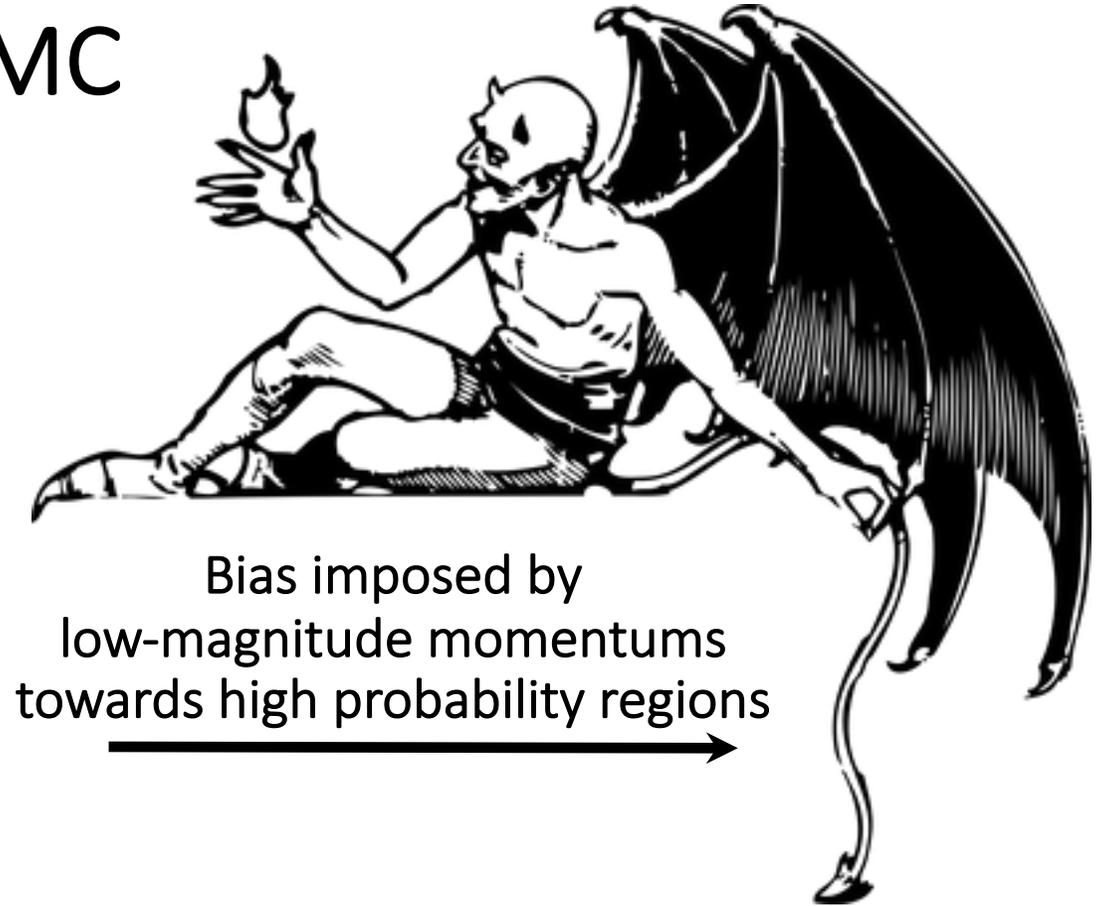
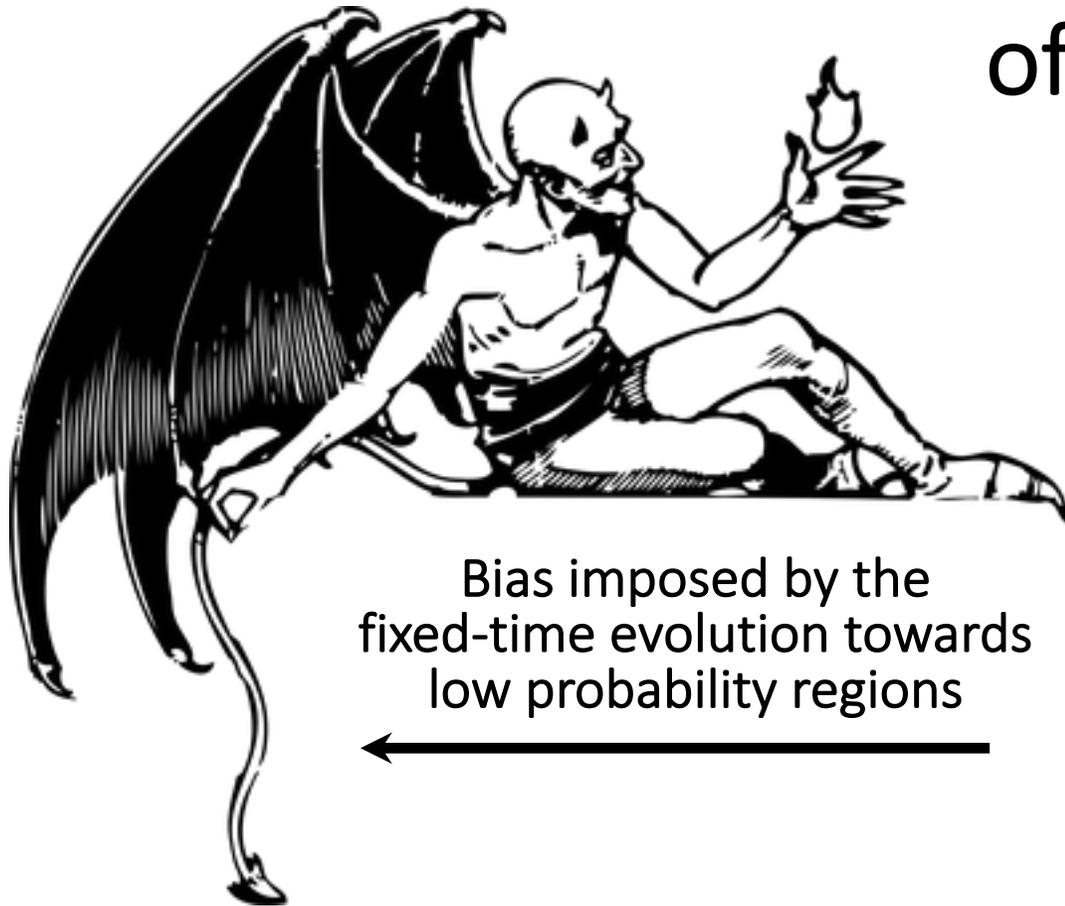
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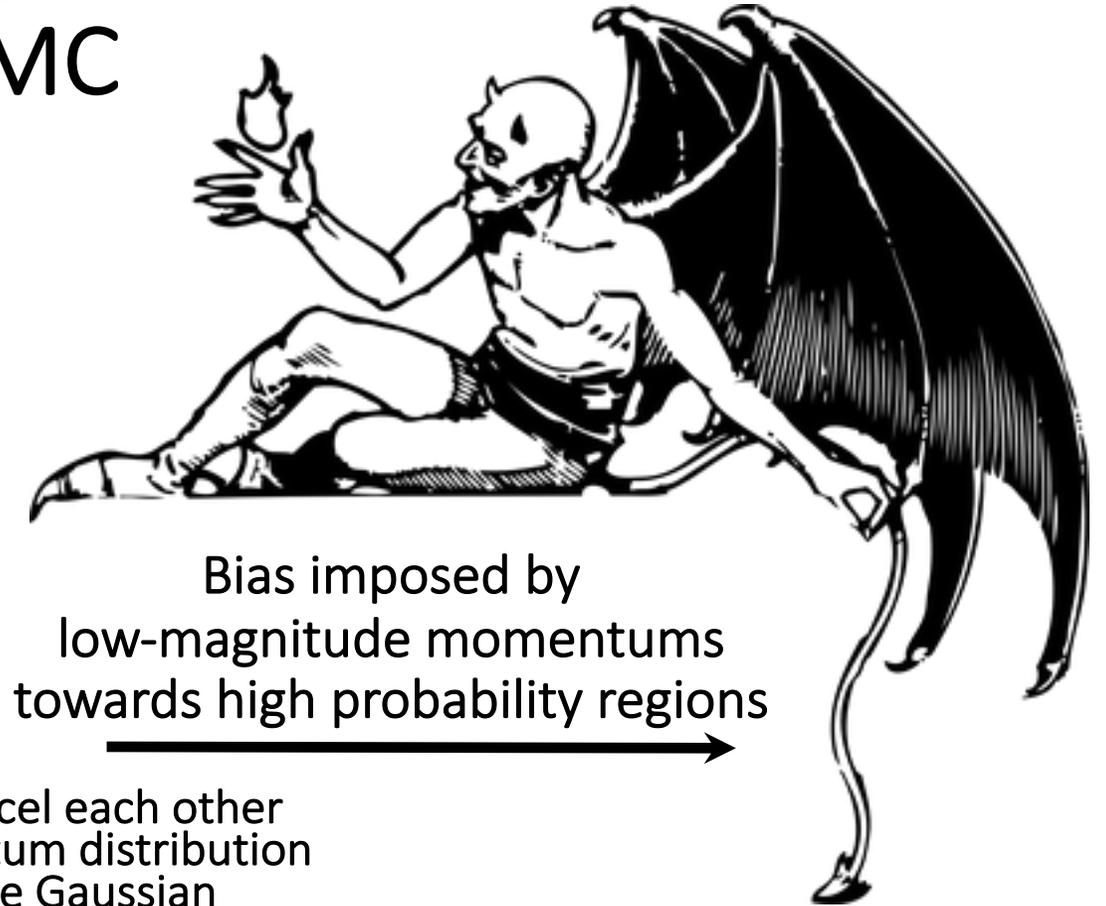
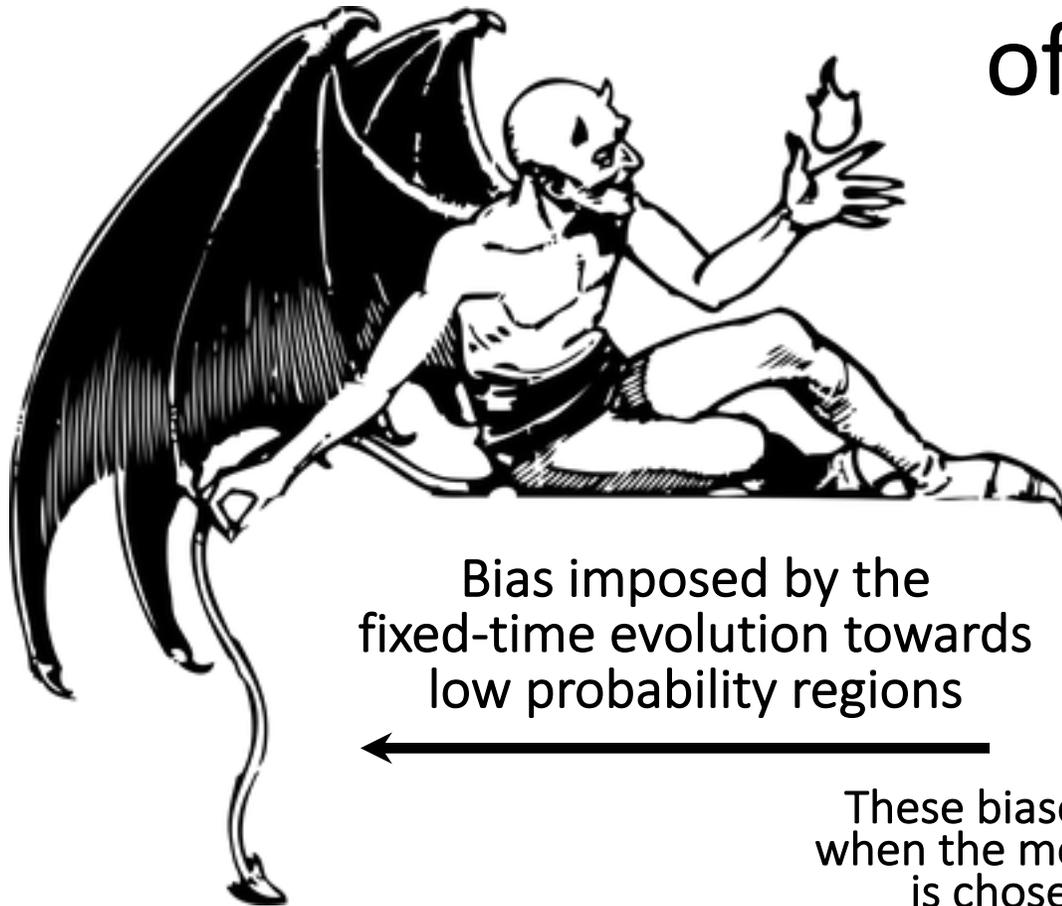
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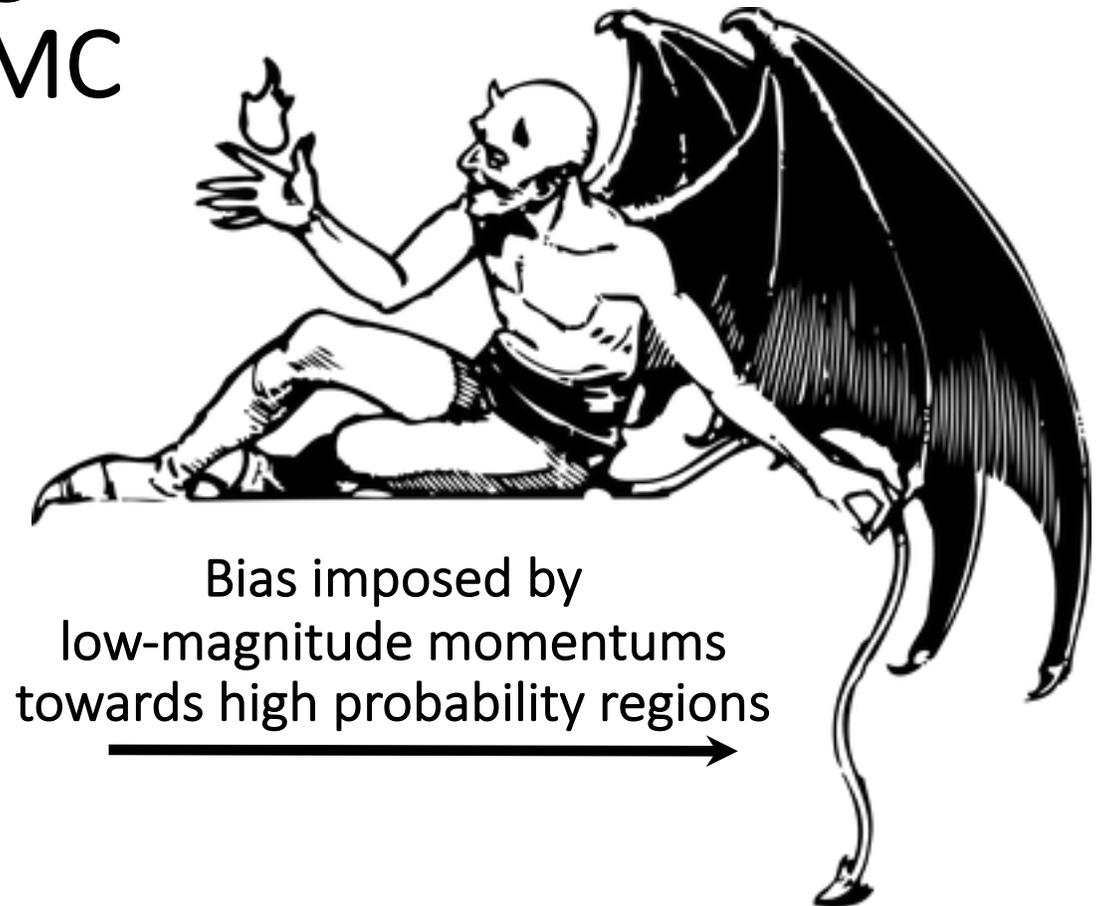


These biases cancel each other
when the momentum distribution
is chosen to be Gaussian

Resolving the first bias

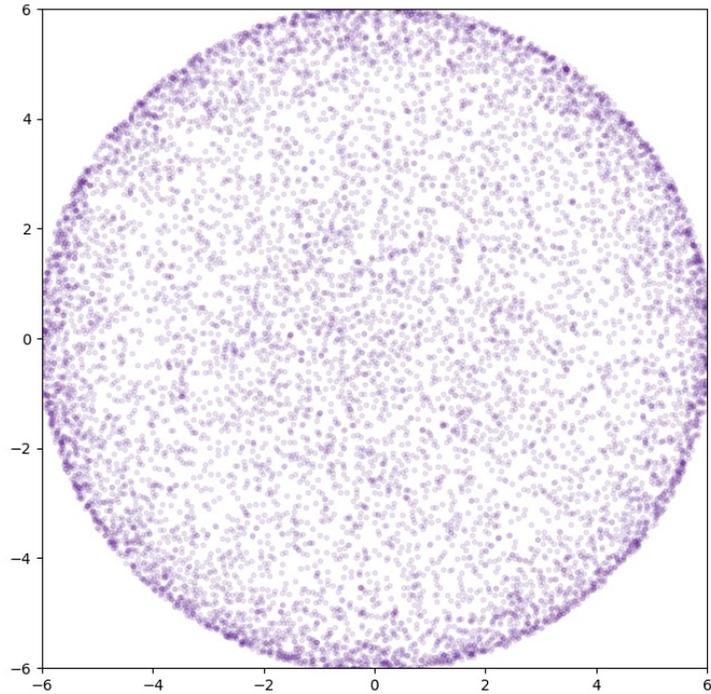
Convergence of HMC

Fixed distance
(rather than fixed-time)
evolution

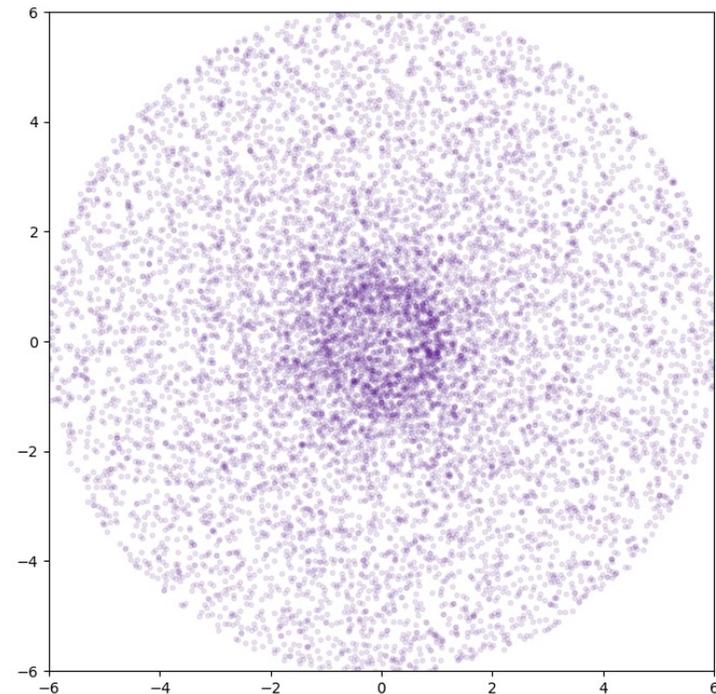


Bias imposed by
low-magnitude momentums
towards high probability regions

Fixed-distance simulation of the equations of motion

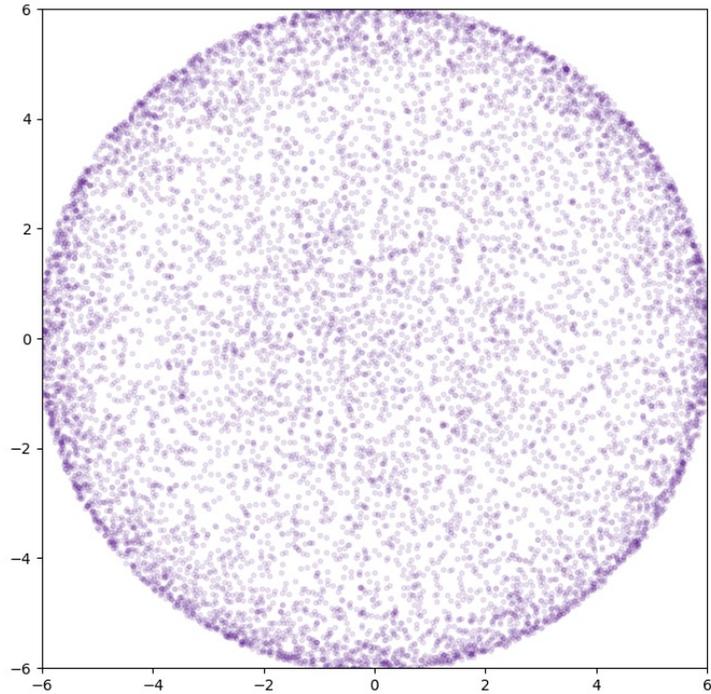


Fixed-time evolution

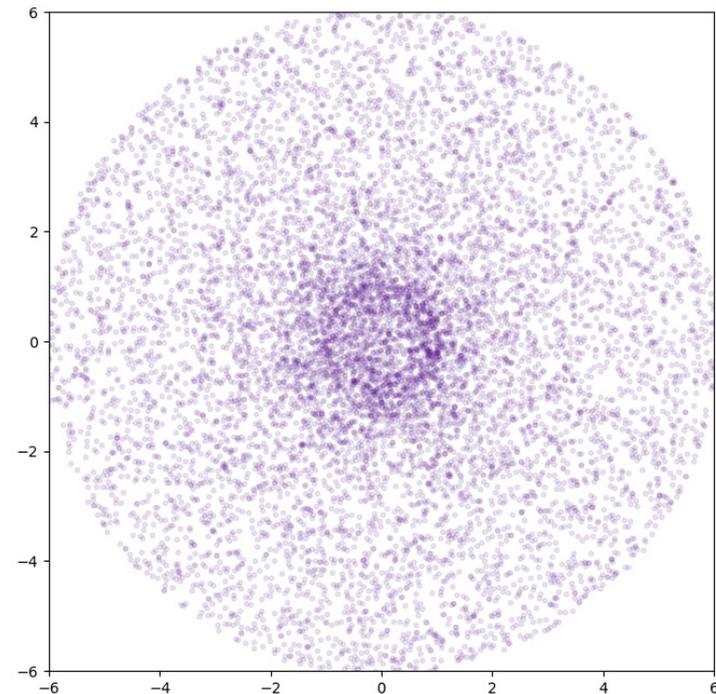


Fixed-distance evolution

Fixed-distance simulation of the equations of motion



Fixed-time evolution

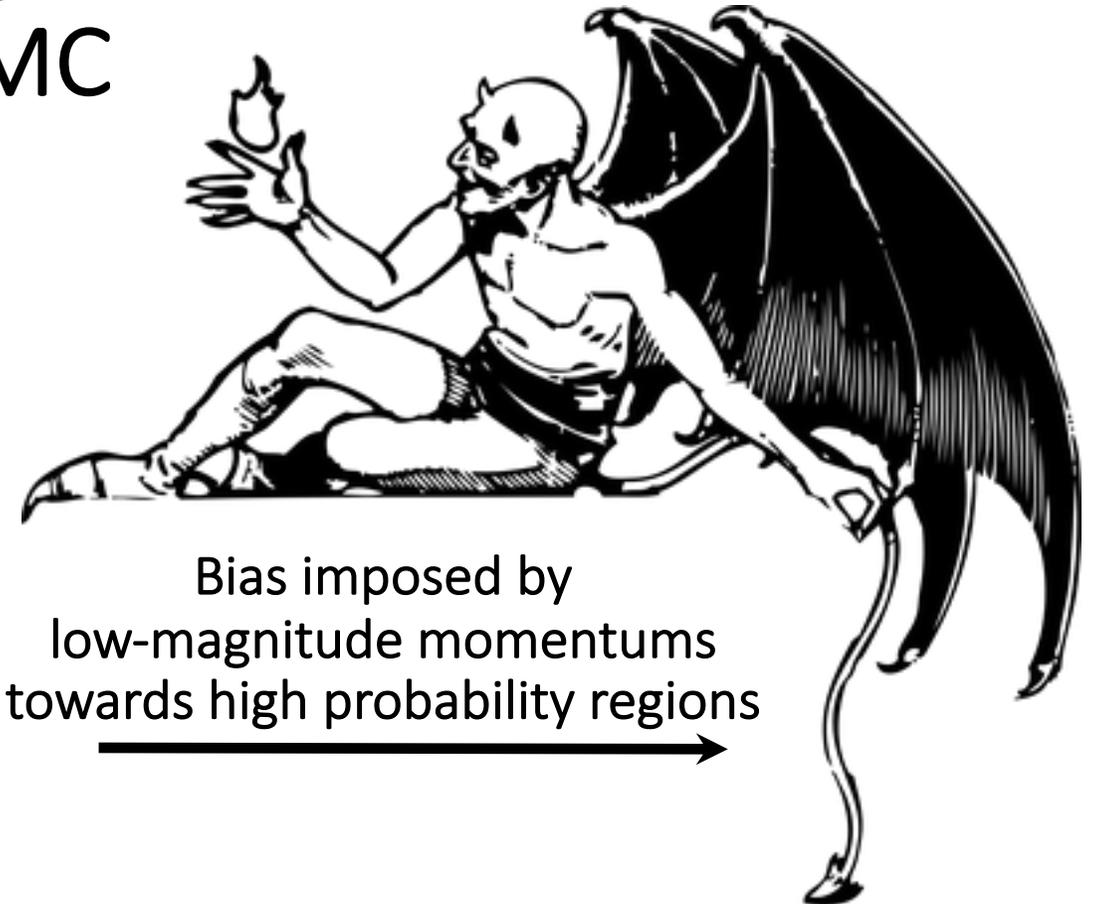


Fixed-distance evolution

Even though more time is spent in low-probability regions, more distance is not traversed there

To resolve the second bias...

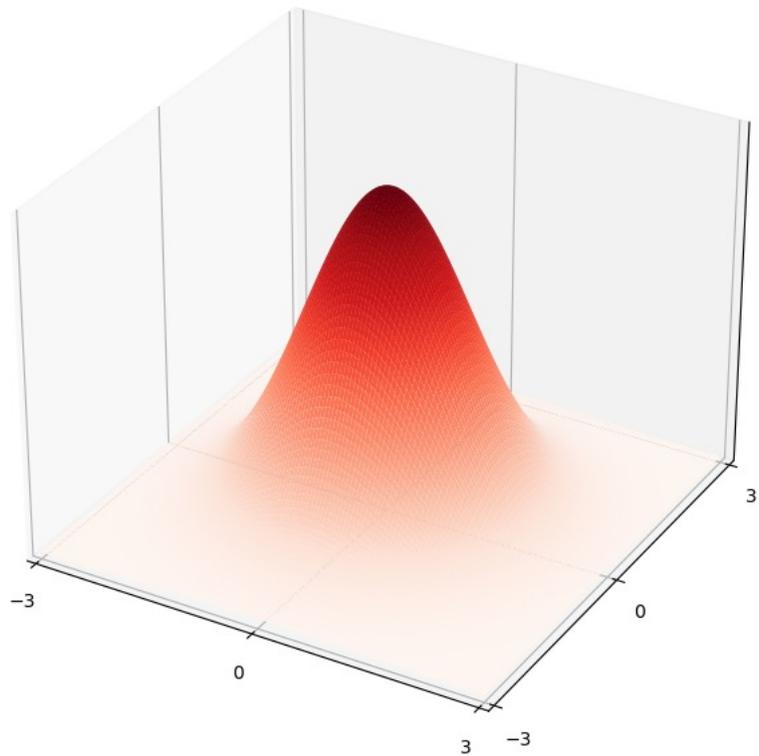
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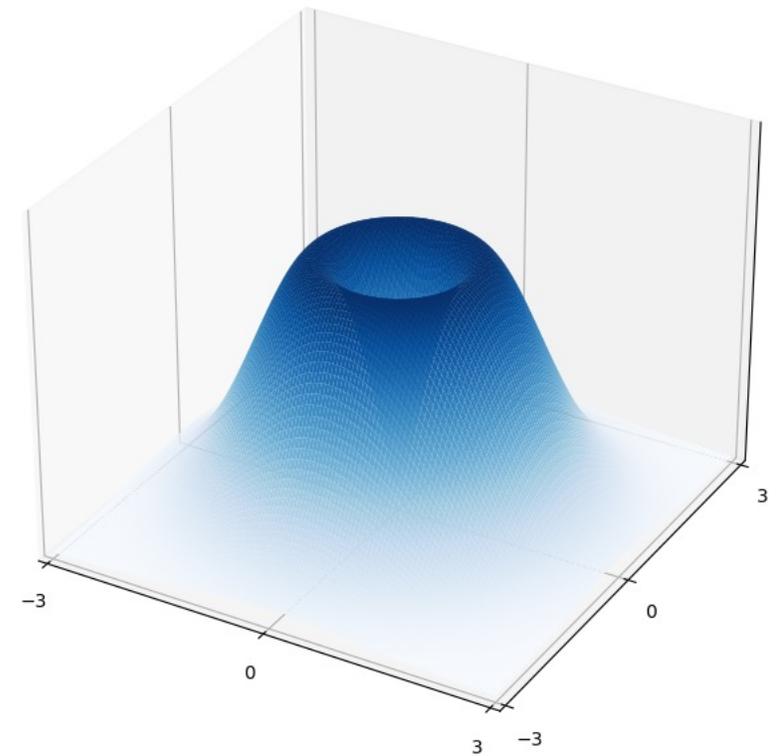
Bias imposed by
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We prove...



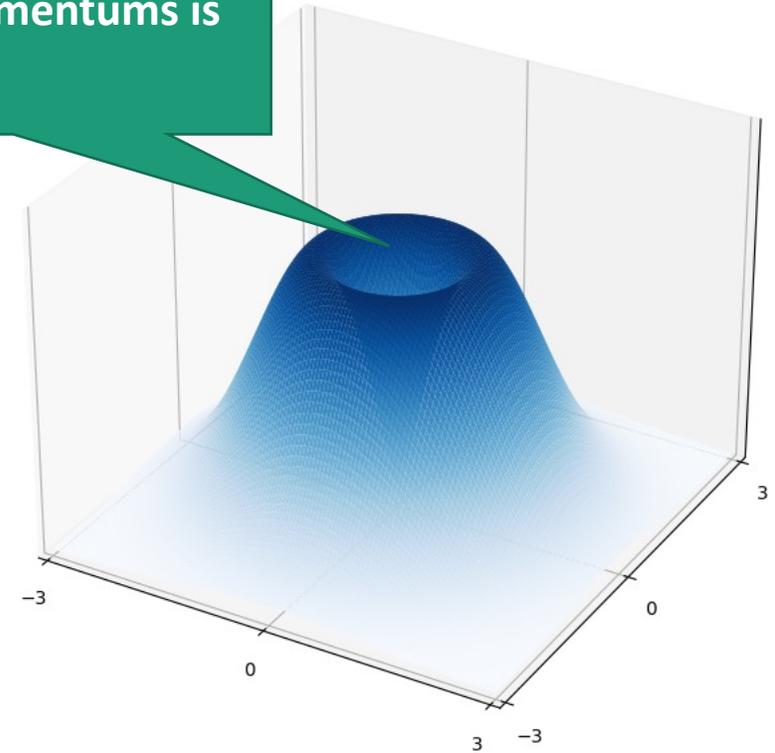
HMC's momentum distribution



FDHMC's momentum distribution

FDHMC's momentum distribution

Probability assigned to low-magnitude momentums is low

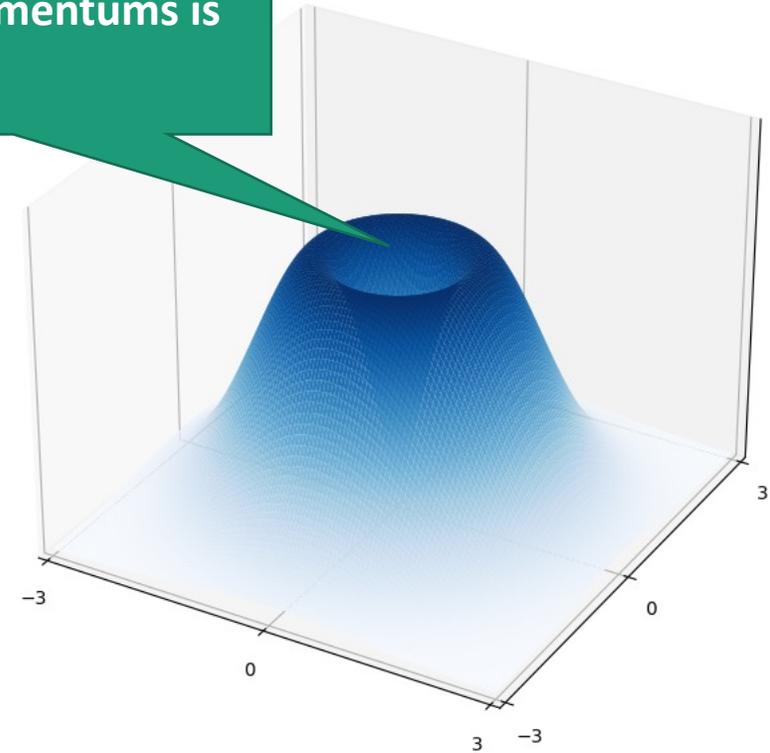


FDHMC's momentum distribution

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Probability assigned to low-magnitude momentums is low

The expected magnitude of FDHMC's momentum vector is higher



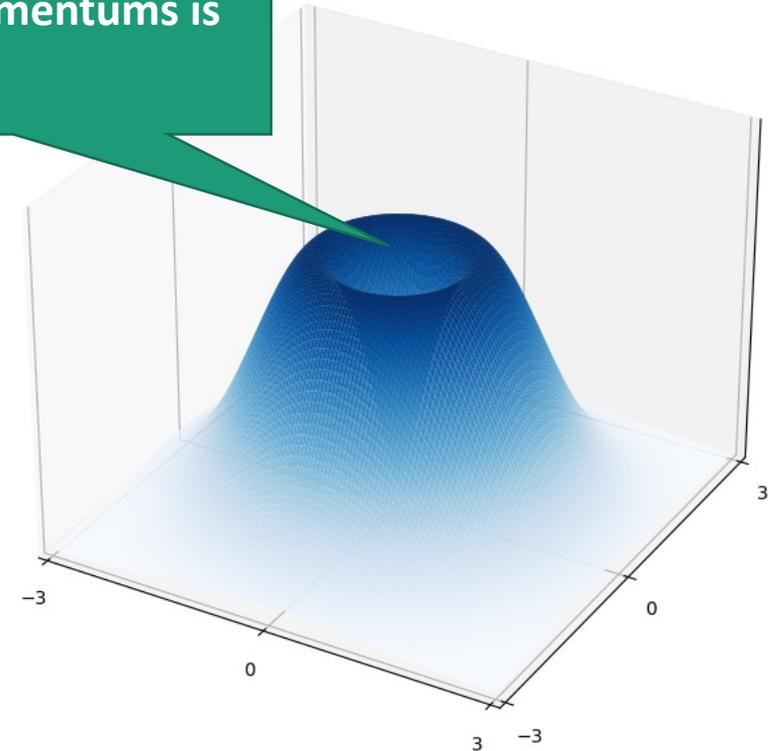
FDHMC's momentum distribution

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Probability assigned to low-magnitude momentums is low

The expected magnitude of FDHMC's momentum vector is higher.

This translates to higher ESS and better exploration of target probability modes.



FDHMC's momentum distribution

Conclusion

- With negligible computational overhead, we resolved two counter-balancing biases that exist in the core of HMC algorithms.

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- Our experiments show that the resulting FDHMC has a higher ESS/grad.