Computational Methods in Stochastics

Lecture VI

Hamiltonian Monte Carlo (Also called Hybrid Monte Carlo) HMC

The Basic HMC Scheme

Hamiltonian dynamics (from mechanics) is used in combination with Metropolis sampling to construct a MCMC method. (Note that the <u>method</u> runs as a Markov chain, the simulated <u>system</u> is not necessarily one.)

The motivation for HMC is to sample the state space more efficiently, so that larger movements from the current state could be made in one step than what is possible in Metropolis-Hastings (M-H) sampling. This comes at the price of increased computation per time step. Despite this, HMC typically samples states much faster than M-H.

When reading this,

- 1. first have a look at this <u>site</u>.
- 2. Refer to it when reading.
- 3. After having stumbled this through, (I suggest you) play around with the graphical models on the site.

The Basic HMC Scheme

Hamiltonian function H(q, p) is determined in terms of the probability distribution we want to sample from.

The **"position" variables** *q* are the ones we are interested in.

The **"momentum" variables** p are auxiliary that we need in order to move within the distribution and so to do the sampling. These momentum (p) – or velocity (v = p/m) – variables provide the more efficient sampling.

Simple updates of these variables alternate with Metropolis updates.

Gain: Proposed states can be distant from the current states and still have a high probability of acceptance.

Hamiltonian (function) gives the total - here constant - energy of a (deterministic) dynamical system.

 $H(q,p) = U(q) + K(p) = E_{tot},$

where U(q) is the potential energy and K(p) is the kinetic energy.

The dynamical system is completely described when we know how *q* and *p* change over time *t*. This is stated by <u>equations of</u> <u>motion</u>, here **Hamilton's equations**

$$\frac{dq_i}{dt} = \frac{\partial H}{\partial p_i}, \qquad i = 1, ..., d ; (d \text{ is dimension})$$
$$\frac{dp_i}{dt} = -\frac{\partial H}{\partial q_i}.$$

Combining vectors q and p into the vector z = (q, p) we get

$$\frac{dz}{dt} = J\nabla H(z),$$

where the gradient $\nabla H = [\nabla H]_k = \partial H / \partial z_k$, and

$$J = \begin{bmatrix} 0_{d \times d} & I_{d \times d} \\ -I_{d \times d} & 0_{d \times d} \end{bmatrix}.$$

Potential and Kinetic Energy

In *d* dimensions, the kinetic energy is

$$K(p)=\frac{p^TM^{-1}p}{2}.$$

M is a symmetric, positive-definite mass matrix. It is often diagonal and a scalar multiple of the identity matrix; this latter part means that all "particles" have the same mass *m*.

Note that p = Mv, where $v = \dot{q}$, so

$$K(v)=\frac{v^T M v}{2}.$$

This form of K(p) corresponds to $-\log(p_P(p)) + \text{Const.}$ Here, $p_P(p) = N(0, \Sigma = M)$ (zero-mean Gaussian with covariance matrix M).

$$p_P(p) = \frac{1}{Z} \exp\left(\frac{-K(p)}{T}\right) = \frac{1}{Z} \exp\left(-\frac{p^T M^{-1} p}{2}\right).$$
 (T = 1)

With these forms, Hamilton's equations become

$$\frac{dq_i}{dt} = [M^{-1}p]_i, \quad \text{(Velocity.)}$$
$$\frac{dp_i}{dt} = -\frac{\partial U}{\partial q_i}. \quad \text{(Force.)}$$

Example: One-dimensional harmonic oscillator

$$H(q,p) = U(q) + K(p), \quad U(q) = \frac{q^2}{2}, K(p) = \frac{p^2}{2m} = \frac{p^2}{2}.$$

Here, we choose m = 1.

So, distributions for both q and p are N(0, 1). Here, Boltzmann factor "transforms" potentials to distributions.

The dynamics:

$$\frac{dq_i}{dt} = p,$$
$$\frac{dp_i}{dt} = -q.$$

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(Hamilton's equations)

Solution (*a* and *r* are constants determined by initial conditions): $q(t) = r \cos(a + t), \quad p(t) = -r \sin(a + t)$

Properties of Hamiltonian dynamics

Reversibility (for deterministic dynamics – no stochastics)

The **mapping** from the state at time t, (q(t), p(t)), to the state at time t + s, (q(t + s), p(t + s)), **is one-to-one** and so has an inverse, which is obtained by negating the time derivatives in Hamilton's equations.

Conservation of the Hamiltonian (= Constant Energy)

The dynamics keeps the Hamiltonian invariant.

$$\frac{dH}{dt} = \sum_{i=1}^{d} \left[\frac{\partial H}{\partial q_i} \frac{dq_i}{dt} + \frac{\partial H}{\partial p_i} \frac{dp_i}{dt} \right] = \sum_{i=1}^{d} \left[\frac{\partial H}{\partial q_i} \frac{\partial H}{\partial p_i} - \frac{\partial H}{\partial p_i} \frac{\partial H}{\partial q_i} \right] = 0$$

 $\frac{dH}{dt} = 0$: *H* is a constant of motion.

Volume Preservation

Any **phase-space volume** evolving in time may change its shape but the volume **does not change**

$$\nabla \cdot \left(\frac{d\boldsymbol{q}}{dt}, \frac{d\boldsymbol{p}}{dt}\right) = \sum_{i=1}^{d} \left[\frac{\partial}{\partial q_i} \frac{dq_i}{dt} + \frac{\partial}{\partial p_i} \frac{dp_i}{dt}\right] = \sum_{i=1}^{d} \left[\frac{\partial}{\partial q_i} \frac{\partial H}{\partial p_i} - \frac{\partial}{\partial p_i} \frac{\partial H}{\partial q_i}\right] =$$
$$= \sum_{i=1}^{d} \left[\frac{\partial^2 H}{\partial q_i \partial p_i} - \frac{\partial^2 H}{\partial p_i \partial q_i}\right] = 0.$$

(A vector field with zero divergence preserves volume.)

In the present context this means that **probability measure** is invariant in time. (My wording, so subject to misinterpretations [©])

Symplectictness

The **volume preservation** is the most important consequence of this more universal property. Hamiltonian dynamics is symplectic. In dynamics symplectictness and volume preservation are often treated as synonyms. Symplectictness can be defined via the Jacobian of the transformation defining the propagation in time (dynamics).

In Hamiltonian dynamics the **symplectic form** is defined as $\omega = dq \wedge dp$. Hamiltonian flow keeps $\int_{S} \omega$ invariant. (See e.g. **differentiable manifolds**, if you are interested.)

(\land is the exterior (vector) product (\times).)

Discretization of Hamilton's Equations

Euler's Method

$$p_{i}(t+\varepsilon) = p_{i}(t) + \varepsilon \frac{dp_{i}}{dt}(t) = p_{i}(t) - \varepsilon \frac{\partial U}{\partial q_{i}}(q(t)),$$

$$q_{i}(t+\varepsilon) = q_{i}(t) + \varepsilon \frac{dq_{i}}{dt}(t) = q_{i}(t) + \varepsilon \frac{\partial K}{\partial p_{i}}(p(t))$$
We use $K(p) = \sum_{i=1}^{d} \frac{p_{i}^{2}}{2m_{i}} \Rightarrow q_{i}(t+\varepsilon) = q_{i}(t) + \varepsilon \frac{p_{i}(t)}{m_{i}}.$
(ε is the step size)

The following examples of numerical integration are for the 1-D harmonic oscillator \rightarrow

Discretization of Hamilton's Equations

(a) Euler's Method, stepsize 0.3

Euler's Method



Integrating in time using Euler involves **numerical error**; try to minimise it \rightarrow

A Modified Euler's Method

$$p_{i}(t + \varepsilon) = p_{i}(t) - \varepsilon \frac{\partial U}{\partial q_{i}}(q(t)),$$

$$q_{i}(t + \varepsilon) = q_{i}(t) + \varepsilon \frac{p_{i}(t + \varepsilon)}{m_{i}}. \quad \leftarrow \text{Here's the difference.}$$

The computed trajectory deviates less from the exact trajectory.

A Modified Euler's Method

(b) Modified Euler's Method, stepsize 0.3



We can do still better \rightarrow

The Leapfrog Method

Propagate p_i in half steps.

$$p_i(t + \varepsilon/2) = p_i(t) - (\varepsilon/2) \frac{\partial U}{\partial q_i}(q(t)),$$
$$q_i(t + \varepsilon) = q_i(t) + \varepsilon \frac{p_i(t + \varepsilon/2)}{m_i}.$$

$$p_i(t+\varepsilon) = p_i(t+\varepsilon/2) - (\varepsilon/2)\frac{\partial U}{\partial q_i}(q(t+\varepsilon)).$$

The Leapfrog Method

Even with increased time step the computation is stable.

(c) Leapfrog Method, stepsize 0.3

(d) Leapfrog Method, stepsize 1.2



The requirement: Translate **the density function** for the distribution to be sampled from **to a potential energy function** and introduce momentum variables to go with the original variables of interest, now seen as position variables.

The task: Simulate a Markov chain in which each iteration resamples the momentum and then performs a **Metropolis update with a proposal found by using Hamiltonian dynamics**.

How do we map the probability distribution to a potential energy function?

Probability and the Hamiltonian: Canonical Distributions

From statistical physics we know that in a canonical system (temperature and volume are constant) **the probability density function for the state** x, whose energy is E(x), is the **canonical distribution (Gibbs ensemble)**. The probability

$$p_X(x) = \frac{1}{Z} \exp\left(\frac{-E(x)}{kT}\right)$$

Here, *T* is the temperature and *k* is the Boltzmann constant, which we just set to 1, since absolute energy values are of no consequence in what we do.

$$\Rightarrow p_X(x) = \frac{1}{Z} \exp\left(\frac{-E(x)}{T}\right)$$

Z is the **partition function**. It is the sum over *all* states in the system. It corresponds to the normalisation constant in the distributions we encounter in statistics/stochastics. Typically incalculable.

In our liberal spirit we also set T = 1 and write

 $E(x) = -\log P(x) - \log Z$ and choose for Z a convenient value.

Since the Hamiltonian H(q,p) = U(q) + K(p) is an energy function for the *joint state* of position q and momentum p, it defines the *joint distribution*

$$p_{q,p}(q,p) = \frac{1}{Z} \exp\left(\frac{-U(q)}{T}\right) \exp\left(\frac{-K(p)}{T}\right)$$

q represent the variables of interest and *p* provide the dynamics. $H(q,p) = E_{total} = const. \Rightarrow p_{q,p}(q,p) = const.$ when computation is exact.

In *Bayesian statistics*, the distribution of interest is the posterior distribution for the model. **The posterior distribution** can be expressed as a canonical distribution (T = 1) using a potential energy function defined as:

 $U(q) = -\log[\pi(q)L(q|D)],$

where $\pi(q)$ is the prior density and L(q|D) is the likelihood function given data D. (log = ln.)

So, to **construct the potential function** to go with the distribution, use $\pi(q)L(q|D) = \exp[-U(q)]$.

Betancourt writes the (joint) canonical density as $\pi(q,p) = e^{-H(q,p)}$.

 $\Leftrightarrow H(q,p) = -\log \pi(q,p) = -\log[\pi(p|q)\pi(q)].$

Accordingly, the decomposition of the Hamiltonian and the joint density correspond as

$$H(q,p) = -\log[\pi(p|q)] - \log[\pi(q)]$$

$$\equiv K(q,p) + V(q).$$

[Note that there's a (notational) difference here compared to Hamiltonian on the previous slide: $V(q) = -\log[\pi(q)]$ instead of $V(q) = -\log[\pi(q)L(q|D)]$; "target distribution" instead of "posterior distribution".]

Note that since only the gradient $\nabla V(\boldsymbol{q})$ is used in HMC, <u>possible prefactors are of no concern</u>. This is the reason for the sloppy definitions of the distributions in this context, which, of course, nobody cares to mention.

For example, take the target distribution $\pi(q) = Ae^{-Bq^2}$. We can write this as $\pi(q) = \exp[-Bq^2 + \ln A]$. Then $V(q) = -\ln \pi(q) = Bq^2 - \ln A$ $\Rightarrow \frac{dV(q)}{dq} = 2Bq$.

The prefactor *A* does not show in $\nabla V(q)$ and so has no effect on the HMC implementation. Also, energies in HMC are scaled anyway, so the minimal form suffices. In HMC, the potential can be thus used in the minimal form $V(q) = Bq^2$.

In general, for any
$$\pi(q) = Cf(q)$$
:
 $\Rightarrow V(q) = -\ln \pi(q) = -\ln[f(q)] - \ln C \Rightarrow \frac{dV(q)}{dq} = \frac{-df(q)/dq}{f(q)}$

The **minimal form** that can be used in HMC is

$$V(q) = -\ln[f(q)].$$

The Hamiltonian Monte Carlo Algorithm

HMC can be used to sample only from continuous **distributions** on \mathbb{R}^d for which

- the density function can be evaluated (up to an unknown normalising constant)
- the partial derivative of the density function (or the gradient of *U*(*q*)) can be computed: the derivatives must exist except for on a set of points with probability zero, where some arbitrary value can be returned

HMC samples from the canonical distribution $p_{q,p}(q,p)$. *q* has the distribution of interest, as specified by U(q). The distribution of *p* can be chosen freely via K(p). **Common practise is to use quadratic** K(p); **consequently** *p* has a zero**mean multivariate Gaussian distribution**.

 p_i defined as independent with component *i* having **variance** m_i (and setting T = 1):

$$K(p) = \sum_{i=1}^d \frac{p_i^2}{2m_i}$$

The Two Steps of the HMC Algorithm

The First Step

Draw new values for p_i , independently of the current values of q_i . For $K(p) = \sum_{i=1}^d \frac{p_i^2}{2m_i}$ the *d* variables $p_i \sim N(0, \sigma_i^2)$. This step leaves $p_{q,p}(q, p)$ invariant.



The Second Step

<u>Propose a new state by performing a Metropolis update with</u> <u>Hamiltonian dynamics:</u>

Start with the current state (q, p).

Simulate Hamiltonian dynamics for *L* steps using the leapfrog method (or some other reversible volume-preserving method) with a step size ε . (When L = 1, HMC is also called L(angevin)MC.)

At the end of *L* steps, negate $p_i (p_i \rightarrow -p_i)$. Now you have **the proposed state** (q^*, p^*) .

Accept this proposed state (as the next state of the Markov chain) with probability (Metropolis) Boltzmann

 $P = \min[1, \exp(-H(q^*, p^*) + H(p, q))] \leftarrow \exp(-\Delta E) \\ = \min[1, \exp(-U(q^*) + U(q) - K(p^*) + K(p))].$

If the proposed state is rejected, the next state is the current state. Be sure to count the occurrences of these states also, when computing expectations etc.

"The negation of the momentum is done to ensure that the Metropolis proposal is symmetric." (Neal) In fact, there is a more fundamental reason to momentum reversal (Betancourt): "If only states going forward can be proposed, i.e. $p^* > p$, the Metropolis-Hastings acceptance probability becomes ill-posed." (See Betancourt p. 39).

(Hmm... but $K(p) \propto p^2$, so "cut the smalltalk", as Bogie would say.)

Return to The First Step.



Viewing HMC as sampling from the joint distribution of q and p, the Metropolis step using a proposal found by Hamiltonian dynamics – i.e. the second step - leaves the probability density for (q, p) unchanged; in fact *almost* unchanged due to truncation in the used numerical method and finite numerical precision.

Movement to (q, p) points with a different probability density is accomplished only by the first step, the replacement of p by a new value. This replacement can change the probability density for (q, p) by a large amount.

To rephrase, a value for q with a very different probability density and, equivalently, a very different potential energy U(q) can be produced by Hamiltonian dynamics. Still, resampling of p is necessary for obtaining the proper distribution for q, since without resampling the Hamiltonian H(q,p) = U(q) + K(p) would be (nearly) constant and U(q)could never exceed the initial value of H(q,p).

First Step:

Random lift from the target parameter space onto phase space.



Second Step:

Deterministic Hamiltonian trajectory through phase space and a projection down to the target parameter space.



FIG 22. (a) Each Hamiltonian Markov transition lifts the initial state onto a random level set of the Hamiltonian, which can then be explored with a Hamiltonian trajectory before projecting back down to the target parameter space. (b) If we consider the projection and random lift steps as a single momentum resampling step, then the Hamiltonian Markov chain alternates between deterministic trajectories along these level sets (dark red) and a random walk across the level sets (light red).

Note: Energy level trajectories of this form are for the harmonic oscillator (see page 8).

Proof of the Invariance of the Canonical Distribution

Mentally partition the (q, p) space into regions A_k , each of the same small volume V. Define O as the operation of L leapfrog steps plus a negation of the momenta such that $O: A_k \rightarrow B_k$. $(B_k$ is the image of A_k .)

Leapfrog steps are reversible, so B_k also partition the (q, p) space. Since leapfrog steps and negation preserve volume, each B_k has volume V.

Detailed balance holds if $\forall i, j, P(A_i)T(B_j|A_i) = P(B_j)T(A_i|B_j)$.

Here, *P* is probability under the canonical distribution, and T(X|Y) is the conditional probability of proposing and then accepting a move to region *X* if the current state is in region *Y*.

When $i \neq j$, $T(A_i|B_j) = T(B_j|A_i) = 0$ and detailed balance holds.

When i = j:

In the limit as regions A_k and B_k become smaller, the Hamiltonian H_X within each region X becomes effectively constant. \rightarrow The canonical probability density and the transition probabilities become effectively constant within each region. \rightarrow The detailed balance condition when i = j reads:

$$\frac{V}{Z}\exp(-H_{A_k})\min[1,\exp(-H_{B_k}+H_{A_k})] = \frac{V}{Z}\exp(-H_{B_k})\min[1,\exp(-H_{A_k}+H_{B_k})]$$

This is seen to be true, so **detailed balance holds**.

We know from the stuff before that **if the detailed balance holds, the Markov chain renders the distribution invariant**.

So, the HMC algorithm leaves the canonical distribution invariant.

Ergodicity

Typically HMC is ergodic \rightarrow **all states can be reached**, i.e. no traps. This may be compromised by periodic trajectories in the Leapfrog, when $L\varepsilon \approx 2\pi$.

Benefits of HMC

Consider sampling from a distribution for two variables that is bivariate Gaussian, with means of zero, and correlation 0.95. Regard these as "position" variables.

Introduce two corresponding "momentum" variables, defined to have a Gaussian distribution with means of zero, standard deviations of one, and zero correlation.

The Hamiltonian will then be

 $H(q, p) = q^T \Sigma^{-1} q/2 + p^T p/2$, with covariance $\Sigma = \begin{bmatrix} 1 & 0.95 \\ 0.95 & 1 \end{bmatrix}$.

(In multiple dimensions the inverse Σ^{-1} is computed by e.g. Gauss-Jordan.)

Trajectories of a simulation based on this Hamiltonian. L = 25, $\varepsilon = 0.25$. The initial state



q moves from lower left to upper right corner and reverses – nothing like a random walk; efficient sampling. This comes from the projection of *p* in diagonal direction changing slowly (gradient in this direction is small) \rightarrow <u>the direction of *p* stays the same for many leapfrog steps</u>.

Smaller-scale oscillations result from high correlation between the variables. These oscillations set an upper limit to the step size.

The value of the Hamiltonian (the rightmost figure) varies **only** because of numerical inaccuracy. If the trajectory was simulated correctly, it would stay constant. For this example, at a critical step size $\varepsilon = 0.45$ the trajectory becomes unstable \rightarrow the value of the Hamiltonian grows without bound

Note that Neal (p. 16) gives the acceptance probability for the end point values of the Hamiltonian. This is the acceptance probability, if this difference due to numerical error is involved in the stage where new states are proposed.

But since the energy stays constant over the L steps, the proposals in HMC would be always accepted, if there were no numerical errors! This is not mentioned anywhere, but check if you can find something that would prove this not to be true.

The above then means that the only role that the Metropolis acceptance has in HMC is to reject proposals if the numerical errors get too large. Else, 100 % of the proposals are accepted, which, of course, means that HMC is extremely effective.

So, all the talk about Metropolis, but no mention about its redundancy! Another place for Bogey to step in...



Comparing *q*'s of 2d random-walk and HMC. Correlation is 0.98.

RW of 20 iterations with 20 updates or leapfrog steps per iteration Metropolis and HMC of 20 leapfrog steps per trajectory.



Two hundred iterations, starting with the 20 iterations shown above.



MCMC from Hamiltonian Dynamics Another way of visualising the motivation for/benefit of HMC. (Betancourt; also refer back to Lecture 5, pp. 28-29.) In high dimensions the random-walk Metropolis proposal density (green) is strongly biased towards the outside of the typical set. (a) Large proposal variances \rightarrow proposals will stray too far from the typical set and be rejected. (b) Smaller proposal variances \rightarrow proposals stay within the typical set and are accepted, but stay close to the initial point.



Both (a) and (b) result in slow exploration of the typical set.

HMC incorporates coherent Markov transitions that remain within the typical set: it explores it faster than random-walk Metropolis.



MCMC from Hamiltonian Dynamics HMC, like RW Metropolis sampling, also involves a random-walk part. This comes in the momentum resampling. The variance of this part is given by the mass m_i in the kinetic energy; this gives σ^2 in $N(\mu, \sigma^2)$ for the

auxiliary momentum variables p_i . And this should be chosen judiciously:



FIG 23. The momentum resampling in a Hamiltonian Markov transition randomly changes the energy, inducing a random walk between level sets. (a) When the energy transition distribution, $\pi(E \mid q)$ is narrow relative to the marginal energy distribution, $\pi(E)$, this random walk will explore the marginal energy distribution only very slowly, requiring many expensive transitions to survey all of the relevant energies. (b) On the other hand, when the two distributions are well-matched the random walk will explore the marginal energy distribution extremely efficiently.

Btw: Other forms than $K(p) = \sum_{i=1}^{d} \frac{p_i^2}{2m_i}$ for the kinetic energy have been tried with no success.

MCMC from Hamiltonian Dynamics *The benefit of HMC stated naively.* <u>RW MCMC</u>: The variance in the position after *n* iterations of RW MCMC is proportional to $n. \rightarrow$ The standard deviation of the amount moved (the distance) in *q*-space $\propto \sqrt{n}$. <u>HMC</u>: The distance moved after *n* will tend to be proportional to *n*.

The advantage of HMC compared to movement by a random walk will be a factor roughly equal to the ratio of the standard deviations in the least confined direction and most confined direction.

There are ways to enhance HMC like using multiple step sizes.

Note: The following pseudocode is for **the first** iteration. In the following iterations you always start with q^* from the previous iteration, i.e. $q_0 = q^*$ and then you update q^* .

Pseudo algorithm for *a single iteration* of HMC in 1d (<u>R.M. Neal</u>, p 14):

- Initiate $q. q^* = q_0$. \leftarrow This is done only for the first iteration. 1.
- Sample $p_0 \sim N(0,1) \leftarrow$ New momentum (p^* from 7. is not used). 2.
- 3. Make a half step for momentum
- $p^* \coloneqq p_0 (\varepsilon/2) \cdot dU(q^*)/dq$ Note: This Alternate full steps for position and momentum step inside 4. for (i := 1, L)the loop

Make a full step for the position

$$q^*\coloneqq q^*+arepsilon\cdot p^*$$

Make a full step for the momentum, except at the end half-steps. If $i \neq L$, $p^* \coloneqq p^* - \varepsilon \cdot dU(q^*)/dq$

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- Make a half step for momentum at the end 5. $p^* \coloneqq p^* - (\varepsilon/2) \cdot dU(q^*)/dq$
- Negate momentum at the end of trajectory 6. $p^* \coloneqq -p^*$
- Evaluate potential and kinetic energies at start and end of trajectory 7. $U_0 = U(q_0); K_0 = p_0^2/2; U^* = U(q^*); K^* = (p^*)^2/2$
- 8. Accept or reject the proposed state

 $q^* = q^*$, if $u < \exp(U_0 - U^* + K_0 - K^*)$; $q^* = q_0$, if $u \ge \exp(U_0 - U^* + K_0 - K^*)$ THE FORM ON THE NEXT PAGE ENABLES CONSTRAINTS $(u \sim U(0,1))$

Pseudo algorithm for *a single iteration* of HMC in 1d (<u>R.M. Neal</u>, p 14):

- 1. Initiate $q, q^* = q_0$. \leftarrow This is done only for the first iteration.
- 2. Sample $p_0 \sim N(0,1)$. $p^* := p_0$
- 3. Alternate full steps for position and momentum for (i := 1, L)

Make a half step for momentum

 $p^* \coloneqq p^* - (\varepsilon/2) \cdot dU(q^*)/dq$ Make a full step for the position $q^* \coloneqq q^* + \varepsilon \cdot p^*$ Make a half step for momentum

Here you impose constraints (see the page after the next)

Make a half step for momentum

$$p^* \coloneqq p^* - (\varepsilon/2) \cdot dU(q^*)/dq$$

- 4. Negate momentum at the end of trajectory $p^* \coloneqq -p^*$
- 5. Evaluate potential and kinetic energies at start and end of trajectory $U_0 = U(q_0)$; $K_0 = p_0^2/2$; $U^* = U(q^*)$; $K^* = (p^*)^2/2$
- 6. Accept or reject the proposed state $q^* = q^*$, if $u < \exp(U_0 U^* + K_0 K^*)$; $q^* = q_0$, if $u \ge \exp(U_0 U^* + K_0 K^*)$ $(u \sim U(0,1))$

Implementing constraints in HMC (R.M. Neal, pp 36, 37)

Many distributions have a limited support, that is, the support $\neq (-\infty, \infty)$.

In such cases we need to impose constraints on *q*.

In order for the constraint to have minimal effect on the distribution it has to be imposed at every HMC step. Imposing after *L* steps would lead to regions near the constraint (boundary) where the target distribution does not hold.

In Hamiltonian dynamics constraints are elastic collisions of the imaginary particle with boundaries: positions are "mirrored" with respect to boundaries.

Implementing constraints in HMC (R.M. Neal, pp 36, 37)

For each variable, $i = 1, \ldots, d$:

- 1) Let $p'_i = p_i(t + \varepsilon/2)$
- 2) Let $q_i' = q_i(t) + \varepsilon p_i'/m_i$
- If q_i is constrained, repeat the following until q'_i satisfies all constraints:

a) If q_i has an upper constraint, and q'_i > u_i Let q'_i = u_i - (q'_i - u_i) and p'_i = -p'_i
b) If q_i has a lower constraint, and q'_i < l_i Let q'_i = l_i + (l_i - q'_i) and p'_i = -p'_i After this the momentum is 4) Let q_i(t + ε) = q'_i and p_i(t + ε/2) = p'_i propagated: p_i(t + ε) = p'_i - ^ε ^{∂U}/_{2 ∂q_i}(q(t + ε)) (See next p.)

Figure 8: Modification to the leapfrog update of q (equation (2.29)) to handle constraints of the form $q_i \leq u_i$ or $q_i \leq l_i$.

The Leapfrog Method with Constraints

$$p_{i}(t + \varepsilon/2) = p_{i}(t) - (\varepsilon/2) \frac{\partial U}{\partial q_{i}}(q(t))$$

$$q_{i}(t + \varepsilon) = q_{i}(t) + \varepsilon \frac{p_{i}(t + \varepsilon/2)}{m_{i}}$$
Upper constraint $q_{i}(t + \varepsilon) \le u_{i}$:
If $q_{i}(t + \varepsilon) > u_{i}$:
$$q_{i}(t + \varepsilon) = u_{i} - (q_{i}(t + \varepsilon) - u_{i}), p_{i}(t + \varepsilon/2) = -p_{i}(t + \varepsilon/2)$$

Lower constraint $q_i(t + \varepsilon) \ge l_i$: If $q_i(t + \varepsilon) < l_i$: $q_i(t + \varepsilon) = l_i + (l_i - q_i(t + \varepsilon)), p_i(t + \varepsilon/2) = -p_i(t + \varepsilon/2)$ $p_i(t + \varepsilon) = p_i(t + \varepsilon/2) - (\varepsilon/2) \frac{\partial U}{\partial q_i} (q(t + \varepsilon))$.

The Final Familiar View

MCMC takes states towards the energy minimum, that is, towards maximum probability density.

y = f(x) is proportional to the potential energy at x



The motivation is not just to get there and stay there, but to sample significant regions (those around equilibria, typical set) for distributions.

- And then there's the dynamical (non-equilibrium) aspect, which is a different ball game altogether.

CS-E5755 - Nonlinear Dynamics and Chaos, January – mid-April 2025

Something different if you should be curious...



Machine learning inference is increasingly being used with nonlinear dynamics.

CS-E5755 Nonlinear Dynamics & Chaos

Spring 2025 (the third and part of the Fourth period) 5 cr

Course book: Steven Strogatz: Nonlinear Dynamics and Chaos

Nonlinear dynamics is relevant in the fields of population and social dynamics, mathematical biology, physics, electrical engineering, and many more. The course covers the fundamental concepts and tools for solving systems involving nonlinear dynamics and provides the basis for understanding chaotic dynamics.



CS-E5795 - Computational Methods in Stochastics THE END (of lectures...)



(but the peer review battle will rage on) Thanks for the company!