

NUTS - No U-Turn Sampler

- (Brief) review of HMC

Physical particle simulation (potential + kinetic energy)

- Benefits

- Reduce auto-correlation a.k.a. get good samples from the target distr. faster

- Reject far fewer samples, since energy is conserved

Good, right?

Not so fast!!

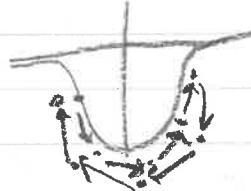
- Requirements:

- Differentiable log prob (for gradients)

- Hyper-parameters: $E + L$

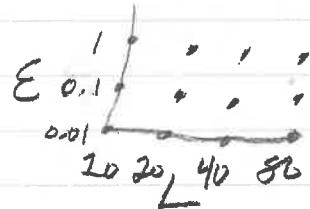
- Must be chosen

- Bad values result in updates near our starting position!



So... How do we pick good values?

- Naive/standard/fallback method: grid search



- Offline, i.e., must rerun HMC for each pair and compare results. Computationally expensive

- What we want: online method, i.e., the parameters are tweaked as the algo. runs. No need to run multiple times - the algo figures it out for us!

- Application: inference engines like BlaGSS, JAGS, STAN

• Heuristics for "good" values of ϵ, L

Sec. 3.2 • E : as ϵ approaches 0, we approach the true Hamiltonian, and reduce the error between initial energy + target energy to 0.

• Recall: error between these two values affects acceptance ratio, so there is a correspondence between $E \rightarrow h_\epsilon$, h_ϵ is avg. acceptance rate for ϵ .

• Pick a target acceptance rate, \bar{h} , and use the heuristic $\delta-h_\epsilon$ to increase or decrease ϵ

• Use "dual averaging method" to deal w/ the two modes of MCMC:

• Converging to target distr.

• Already at target distr.

L:

• Idea: Want to get as far away from current sample, θ , as possible

• If we start turning back, i.e., make a U-turn, don't take anymore steps!

$$(\hat{\theta} - \theta) \cdot \hat{r} < 0$$

Naive method to optimize L (bottom of p. 1597)

- Just sample r , then continue until a U-turn happens
- Why not? Not time reversible, so not a valid MCMC algo.
- Maybe worth spending some time to unpack this. I don't quite understand this, since it seems similar enough to HMC.

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NUTS - No U-Turn Sampler

So, we want to tune L , and we need to do it s.t. we still have a valid MCMC algo.

NuTS - no U-turn sampler:

- New Variables:

- u - "slice," I call it "error threshold"
- B - set of all leapfrog states visited during the physics simulation

- $C \subseteq B$, the set of valid moves from $\theta \rightarrow \theta'$

- Algorithm: (p. 1599)

- $r \sim N(0, I)$ (as in HMC)

- $u \sim \text{Uniform}(0, \exp\{\mathcal{L}(\theta^t) - \frac{1}{2} r \cdot r^T\})$

- B : (Key: simulate backwards in time as well as forward.)

- for $j \leftarrow 0 \dots \infty$

- Sample direction, $v_j \sim \text{Uniform}(-1, 1)$

- Simulate for 2^j steps from the corresponding endpoint already in B (front or back) using $v_j E$ as step size

- (Note: conceptually a tree, fig. 1)): Add these to B .

- Until a stop criteria is met

- one of the newly-added intermediate states either
 - had error above the threshold

$$\mathcal{L}(\theta) - \frac{1}{2} r \cdot r - \log(u) < \Delta_{\max} \quad (\text{p. 160}, \text{eqn. 3})$$

- ⑥ Made a U-turn

- ⑦ The two end-points make a U-turn, but no intermediate states make a U-turn

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- Deterministic, given B

- Prunes the possible new states to ensure good "next" states + a valid MCMC method

- Conditions at the bottom of p. 1599



- Show fig. 2
- Sample $\theta^{\text{int}} \sim T(\theta^t, r, L)$. T can be uniform
or more complicated to "weight" states that are further away
- Optimizations This is where the "tree" property comes in handy
- Experiments & results
 - How should we design the experiments
 - What metrics are we interested in?
 - Comparison w/ HMC w/ various hand-picked L .
 - Computational efficiency. How many accepted samples per grad.
 - Are we getting "good" samples in the first place? calc?