

# Computational Statistics II

Unit B.2: MALA algorithm & Hamiltonian Monte Carlo

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# Unit B.2

## Main concepts

- The MALA algorithm
- Optimal scaling and pre-conditioning
- Hamiltonian Monte Carlo
- Associated **R** code: [https://tommasorigon.github.io/CompStat/exe/un\\_B2.html](https://tommasorigon.github.io/CompStat/exe/un_B2.html)

## Main references

- Girolami, M. and Calderhead, B. (2011). Riemann manifold Langevin and Hamiltonian Monte Carlo methods. *JRSS-B*, **73**(2), 123–214.
- Neal, R. M. (2011). MCMC using Hamiltonian dynamics. CRC press.
- Roberts, G. O. and Rosenthal, J. S. (2001). Optimal scaling for various Metropolis-Hastings algorithms. *Statistical Science*, **16**(4), 351–367.

# Limitations of the MH algorithm

- The random walk Metropolis algorithm is very popular and appealing among practitioners because it is **general** and **easy to implement**.
- In addition, the RWM is quite **robust** to the choice of the tuning (scaling) parameters.
- Unfortunately, this seductive simplicity leads to performance that scales poorly with **increasing dimension** and **increasing complexity** of the target density.
- Even when the proposal is optimally chosen, the RWM relies on **local moves** that leads to slow mixing, especially in high dimensions.
- The proposal distribution of a RWM is indeed **randomly exploring** the interesting parts of the posterior density, without taking into account its structure.

# Gradient-based methods

- Intuitively, we are seeking for better proposal distributions that incorporate the **structure** of the target density and therefore will lead to **faster mixing**.
- Let  $\pi(\boldsymbol{\theta} \mid \mathbf{X})$  be a **continuous** and **differentiable** posterior density in  $\mathbb{R}^p$ .
- The key quantity we will exploit is the **gradient** of the logarithm of the target density, written

$$\nabla_{\boldsymbol{\theta}} \log \pi(\boldsymbol{\theta} \mid \mathbf{X}) = \nabla_{\boldsymbol{\theta}} \log \pi(\mathbf{X} \mid \boldsymbol{\theta}) + \nabla_{\boldsymbol{\theta}} \log \pi(\boldsymbol{\theta}).$$

- The gradient of the target density is often available in **closed form** and it does not require the knowledge of the normalizing constant.
- The gradient informs about the **direction** and the **rate of increase** of a given function.
- For instance, for a given value  $\boldsymbol{\theta}^{(r)}$  and  $\epsilon > 0$ , the update

$$\boldsymbol{\theta}^{(r+1)} \longleftarrow \boldsymbol{\theta}^{(r)} + \epsilon \nabla_{\boldsymbol{\theta}} \log \pi(\boldsymbol{\theta}^{(r)} \mid \mathbf{X}),$$

leads to an increase of  $\pi(\boldsymbol{\theta} \mid \mathbf{X})$ , for  $\epsilon$  small enough. This corresponds to the well-known **gradient ascent** method.

# Langevin diffusions

- Incorporating the gradient in the MCMC procedure is an intuitive and appealing idea: this will push the Markov chain towards values having **higher density**.
- Besides this intuition, there is a strong theoretical justification for gradient adjusted MH proposals, based on **Langevin diffusions**.
- Let  $\mathbf{B}^{(t)}$  be a  $p$ -dimensional standard Brownian motion.
- We consider a continuous-time stochastic process  $\theta^{(t)}$  satisfying the following stochastic differential equation

$$d\theta^{(t)} = \frac{1}{2} \nabla_{\theta} \log \pi(\theta^{(t)} | \mathbf{X}) dt + d\mathbf{B}^{(t)}.$$

- **Key result.** The stationary distribution of the above Langevin diffusion is the posterior density  $\pi(\theta | \mathbf{X})$ .

# The MALA algorithm

- In practice, we need to consider **discrete approximations** of the Langevin diffusion, for example using the so-called **Euler method**.
- This leads to the following discrete-time stochastic process

$$\boldsymbol{\theta}^{(r+1)} = \boldsymbol{\theta}^{(r)} + \frac{\epsilon^2}{2} \nabla_{\boldsymbol{\theta}} \log \pi(\boldsymbol{\theta}^{(r)} | \mathbf{X}) + \epsilon \mathbf{z}^{(r)},$$

for any chosen discretization step  $\epsilon > 0$ , and with iid  $\mathbf{z}^{(r)} \sim \mathcal{N}_p(0, I_p)$ .

- This discrete approximation is no longer guaranteed to converge to  $\pi(\boldsymbol{\theta} | \mathbf{X})$ .
- There is a delicate trade-off between the accuracy of this approximation ( $\epsilon \rightarrow 0$ ) and the sampling efficiency, increasing as  $\epsilon$  grows.
- This issue is solved by treating the above distribution as **proposal density** of a Metropolis-Hastings algorithm.

# The MALA algorithm

- The Metropolis adjusted Langevin algorithm (MALA) therefore can be seen as a specific MH algorithm with proposal distribution

$$(\theta^* | \theta) \sim N_p \left( \theta + \frac{s_p^2}{2} \nabla_{\theta} \log \pi(\theta | \mathbf{X}), s_p^2 I_p \right),$$

where  $s_p^2 > 0$  is some **tuning parameter** that must be carefully chosen.

- **Remark.** This proposal distribution is not symmetric as in the RWM case, therefore the acceptance probability takes into account also the proposal densities, namely

$$\alpha = \min \left\{ 1, \frac{\pi(\theta^* | \mathbf{X})}{\pi(\theta | \mathbf{X})} \frac{q(\theta | \theta^*)}{q(\theta^* | \theta)} \right\}.$$

- There is strong theoretical and empirical evidence showing that the price paid for computing the gradient is compensated by a much faster mixing in several problems.

# Asymptotics and optimal scaling

- As for the RWM, some insights about the **optimal choice** of  $s_p^2$  can be gained by looking at the **asymptotic behaviour** of the MALA, for large values of  $p$ .
- Let us assume again that the posterior distribution has the following form

$$\pi(\boldsymbol{\theta} \mid \mathbf{X}) = \prod_{j=1}^p f(\theta_j), \quad \text{var}(\boldsymbol{\theta} \mid \mathbf{X}) = \sigma^2 I_p$$

namely the components of  $\boldsymbol{\theta}$  are iid from some density  $f$ , satisfying the same **smoothness conditions** mentioned in **Unit B.1** and described in Roberts et al. (1997).

- It turns out that in order to get sensible asymptotic results, in this case we need to set

$$s_p^2 = \ell^2 / p^{1/3},$$

as opposed to the  $p^{-1}$  term we have in the RWM case.



# Diffusion processes

- As for the RWM case, let us define a **speeded-up** continuous-time stochastic process,

$$Z^{(t)} = \theta_1^{(\lfloor tp^{1/3} \rfloor)},$$

parametrized to make jumps every  $p^{-1/3}$  units.

## Theorem (Roberts and Rosenthal, 1997)

The continuous time stochastic process  $Z$  weakly converges to

$$Z \xrightarrow{d} W, \quad p \rightarrow \infty,$$

where  $W$  is a diffusion process satisfying the stochastic differential equation

$$dW^{(t)} = h(\ell)^{1/2} dB^{(t)} + \frac{h(\ell) \nabla \log f(W^{(t)})}{2} dt,$$

where the **speed of the diffusion** is

$$h(\ell) = \ell^2 2\Phi(-\mathcal{J}\ell^3),$$

for some constant  $\mathcal{J}$  that only depends on  $f$ .

# Speed of diffusion $h(\ell)$

- As in the RMW, the speed of diffusion  $h(\ell)$  is strictly related to the asymptotic variance. Hence, we will look for the **optimal**  $\ell$  that maximizes the diffusion  $h(\ell)$ .
- Let  $\tau_g(\ell)$  be the integrated autocorrelation of the MALA. Then for large  $p$  it holds that

$$\tau_g(\ell)^{-1} \approx h(\ell) e_g p^{-1/3},$$

where  $e_g > 0$  is some constant depending only on  $g(\cdot)$ .

- **Remark.** These findings imply that the MALA algorithm has complexity  $\mathcal{O}(p^{1/3})$ , which is considerably more efficient than the  $\mathcal{O}(p)$  complexity of the RWM.
- In practice, these theoretical results suggest that the MALA algorithm should have better performance especially in high-dimensional problems (large  $p$ ).

# Speed of diffusion and acceptance rate

- Let us recall that the acceptance rate of a MH algorithm is informally defined as

$$A_p(\ell) = \lim_{R \rightarrow \infty} \frac{\text{"# of accepted moves"}}{R}.$$

- Then, it can be shown that in the MALA case we have

$$\lim_{p \rightarrow \infty} A_p(\ell) = A(\ell) = 2\Phi(-\mathcal{J}\ell^3),$$

implying, as in the RWM case, that **speed of diffusion** relates to the **acceptance rate**.

- In practice, the optimal value  $\ell_{\text{opt}}$  maximizing  $h(\ell)$  does not require to calculate  $\mathcal{J}$ .

- Indeed, the asymptotic acceptance rate evaluated at the optimum is such that

$$A(\ell_{\text{opt}}) \approx 0.574,$$

so  $\ell$  can be chosen by trial and error or by means of adaptive methods.

- **Remark.** This means that the optimally scaled MALA has faster mixing than the RWM.

# Getting practical

- Let us consider again the **logistic regression** problem under iid Gaussian priors and variance 100, using the Pima indian dataset.
- In this example, we **do not standardize the predictors**, to make the problem more challenging.
- Recall that the **gradient** of the log-posterior in this case is easily obtained as follows

$$\nabla_{\theta} \log \pi(\theta \mid \mathbf{X}) = \nabla_{\theta} \log \pi(\mathbf{X} \mid \theta) + \nabla_{\theta} \log \pi(\theta) = \mathbf{X}^T(\mathbf{y} - \boldsymbol{\pi}) - \beta/100,$$

where each entry of  $\boldsymbol{\pi}$  is  $[1 + \exp\{-(x_{i1}\beta_1 + \dots + x_{ip}\beta_p)\}]^{-1}$ , for  $i = 1, \dots, n$ .

- The mathematical simplicity of the gradient follows from the fact that the logistic regression belong to an **exponential family**.

# MALA algorithm in practice

- After some trial and error, we set  $s_p = 0.0017$ , to get the optimal acceptance rate.
- However, the results are a **complete disaster**. The chain does not reach convergence and the samples are garbage.

---

```
# Scaling parameter (after few trials)
s <- 0.0017

# Running the MCMC (R = 30000, burn_in = 5000)
fit_MCMC <- as.mcmc(MALA(R = R, burn_in = burn_in, y, X, s, S = diag(ncol(X))))

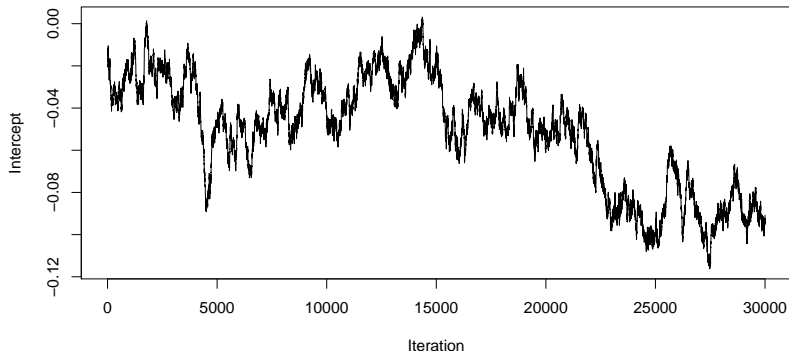
summary(effectiveSize(fit_MCMC)) # Effective sample size (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#  2.900   9.358  27.201  44.321  46.238 166.223

summary(R / effectiveSize(fit_MCMC)) # Integrated autocorrelation time (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 180.5   728.7 1208.5 2671.3 3283.2 10343.4

summary(1 - rejectionRate(fit_MCMC)) # Acceptance rate (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 0.5638 0.5638 0.5638 0.5638 0.5638 0.5638
```

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# MALA algorithm in practice



- The true posterior density places mass in values in the interval  $(-12, -7)$ . The sampled values are not even close to that region  $\implies$  the results are garbage.

# What went wrong?

- These performance issues are not specific of MALA. Indeed, a vanilla RWM with isotropic covariance matrix  $\mathbf{S} = s^2 \mathbf{I}_p$  would also perform quite badly.
- In both cases, the theory assumes a posterior distribution with iid components. Broadly speaking, we need the posterior variances of each components  $\theta_1, \dots, \theta_p$  to be similar.
- If we **standardize the predictors**, the results improve remarkably. However, this is a workaround that can not be applied in general models.
- In the RWM case we solved this issue by considering a covariance matrix  $\mathbf{S}$  depending on the posterior covariance matrix  $\Sigma$ .
- The very same strategy can be applied to the MALA algorithm, as well as in more elaborate contexts such as Hamiltonian Monte Carlo.

# Rotating the diffusion

- Let  $\Sigma$  be the posterior covariance and let  $\Sigma = \mathbf{A}\mathbf{A}^\top$  be its **Cholesky decomposition**.
- Let us consider a rotation of the parameters  $\tilde{\theta} = \mathbf{A}^{-1}\theta$  (reparametrization), implying that the new set of parameters are such that

$$\text{var}(\tilde{\theta} \mid \mathbf{X}) = \mathbf{A}^{-1}(\mathbf{A}\mathbf{A}^\top)(\mathbf{A}^{-1})^\top = \mathbf{I}_p,$$

i.e. they are **orthogonal**. If the posterior of  $\theta$  is Gaussian, they are also independent.

- Therefore, the MALA based on the rotated Langevin diffusion is

$$d\tilde{\theta}^{(t)} = \frac{1}{2} \nabla_{\tilde{\theta}} \log \pi(\tilde{\theta}^{(t)} \mid \mathbf{X}) dt + d\mathbf{B}^{(t)}.$$

- This leads to a MALA proposal distribution targeting the posterior law of  $\tilde{\theta}$ , namely

$$(\tilde{\theta}^* \mid \tilde{\theta}) \sim N_p \left( \tilde{\theta} + \frac{s_p^2}{2} \nabla_{\tilde{\theta}} \log \pi(\tilde{\theta} \mid \mathbf{X}), s_p^2 \mathbf{I}_p \right),$$

which is expected to perform well due to the orthogonality of  $\tilde{\theta}$ .



# Rotating the diffusion

- By pre-multiplying by  $\mathbf{A}$  the diffusion for  $\tilde{\theta}^{(t)}$ , one obtain that

$$d\theta^{(t)} = \frac{1}{2} \Sigma \nabla_{\theta} \log \pi(\theta^{(t)} | \mathbf{X}) dt + \mathbf{A} dB^{(t)},$$

which by construction targets the posterior law of  $\theta$ .

- This leads to a **pre-conditioned** MALA, targeting the posterior law of  $\theta$ , namely

$$(\theta^* | \theta) \sim N_p \left( \theta + \frac{s_p^2}{2} \Sigma \nabla_{\theta} \log \pi(\theta | \mathbf{X}), s_p^2 \Sigma \right),$$

with  $s_p^2 = \ell^2 / p^{1/3}$ .

- In other words, this simple modification of the original MALA proposal is **equivalent** to running the MALA algorithm on the orthogonal parametrization.
- Obviously  $\Sigma$  is unknown, but a fast approximations and/or adaptive strategies can be used, following the guidelines outlined in **unit B.1**.

# Pre-conditioned MALA algorithm

- After some trial and error, we set  $s_p = 1.68$ , to get the optimal acceptance rate.
- The pre-conditioned MALA, based on the Laplace approximation, leads to a very high effective sample size.

---

```
# Covariance matrix is selected via Laplace approximation
fit_logit <- glm(y ~ X - 1, family = binomial(link = "logit"))
S <- vcov(fit_logit)
s_p <- 1.68 # After some trial and error

# Running the MCMC (R = 30000, burn_in = 5000)
fit_MCMC <- as.mcmc(MALA(R = R, burn_in = burn_in, y, X, s_p, S))

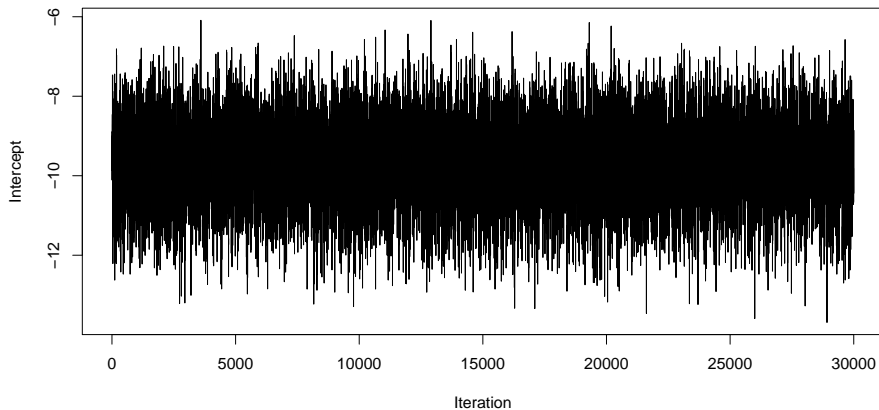
summary(effectiveSize(fit_MCMC)) # Effective sample size (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#   8583   8762   9196   9063   9312   9409

summary(R / effectiveSize(fit_MCMC)) # Integrated autocorrelation time (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#   3.189   3.222   3.263   3.314   3.424   3.495

summary(1 - rejectionRate(fit_MCMC)) # Acceptance rate (beta)
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 0.5686 0.5686 0.5686 0.5686 0.5686 0.5686
```

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# Pre-conditioned MALA algorithm in practice



# General comments

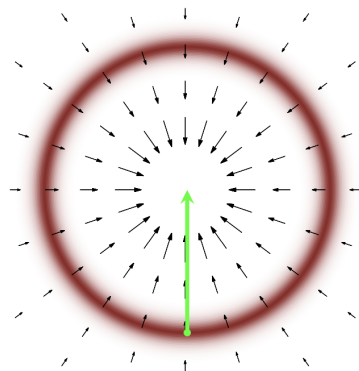
- The take-home message is that pre-conditioning is crucial for both the RWM and the MALA in order to get practically useful samples.
- In high-dimensional problems, when obtaining an estimate for  $\Sigma$  could be problematic, it is recommended to use at least a diagonal matrix specification.
- Gradient-based methods such as MALA are more fragile than RWM, meaning that misscalibrations for the proposal of density leads to drastic performance drop.
- These issues motivated recent works on **robust** gradient-based proposals aimed at correcting this behaviour.

## Main reference

Livingstone, S. and G. Zanella (2020). The Barker proposal: combining robustness and efficiency in gradient-based MCMC. arXiv:1908.11812.

# Hamiltonian Monte Carlo

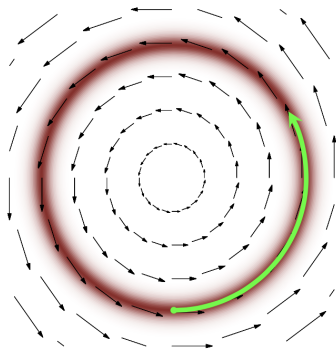
- In complicated inferential problems, pushing the Markov chain **towards the mode**, as in the MALA, may lead to an inefficient exploration of the parameter space.



MALA dynamics. Picture ~~stolen~~ taken from Betancourt (2017).

# Hamiltonian Monte Carlo

- Ideally, we would like the Markov Chain to explore the values of a given **level set**, following the complex dynamics that are implied by the **gradient information**.



Hamiltonian dynamics. Picture ~~stolen~~ taken from Betancourt (2017).

# Hamiltonian Monte Carlo

- Hamiltonian Monte Carlo (HMC) is essentially a Metropolis-Hastings algorithm with a “smart” proposal distribution based on the **gradient**.
- HMC performs several steps in the parameter space before accepting / rejecting the move, therefore favoring leading to jumps and better mixing.
- The proposed value is far from the previous one, but it remains on a similar level set. This is in contrast with RWM, in which big jumps often leads to values with low density.
- HMC, also known as Hybrid Monte Carlo, has been known for some time in physics, but it seems to have be considered only recently in statistics.

## Main reference

Neal, R. M. (2011). MCMC using Hamiltonian dynamics. CRC press.

# HMC: basic quantities

- Recall that  $\theta \subseteq \mathbb{R}^p$  is the parameter of interests. We aim at sampling from the posterior distribution  $\pi(\theta \mid \mathbf{X})$ .
- In HMC we rely on an **auxiliary** set of parameters  $\psi \subseteq \mathbb{R}^p$  independent on  $\theta$ , so that the joint density of  $(\theta, \psi)$  is given by

$$\pi(\theta, \psi \mid \mathbf{X}) = \pi(\theta \mid \mathbf{X}) \pi(\psi).$$

- We let  $\psi \sim N_p(0, \mathbf{M})$  be multivariate Gaussian with zero mean and covariance  $\mathbf{M}$ .
- The term  $\mathcal{H}(\theta, \psi) = -\log \pi(\theta, \psi \mid \mathbf{X})$  is called the **Hamiltonian**, which equals

$$\mathcal{H}(\theta, \psi) = -\log \pi(\theta \mid \mathbf{X}) + \frac{1}{2} \psi^\top \mathbf{M}^{-1} \psi,$$

up to an irrelevant additive constant not depending on  $(\theta, \psi)$ .

- In HMC we will sample values from the joint distribution  $\pi(\theta, \psi \mid \mathbf{X})$  and then we will discard the samples for  $\psi$ .



# Hamiltonian dynamics

- The gradient of  $\mathcal{H}(\theta, \psi)$  with respect to  $(\theta, \psi)$  admits a physical interpretation as the **time evolution**, with respect to a **fictitious time**  $t$ , of an Hamiltonian dynamic system.
- Let us assume that  $(\theta(t), \psi(t))$  is a deterministic evolution flowing according to the following set of **differential equations**

$$\begin{aligned}\frac{d\theta(t)}{dt} &= \frac{\partial \mathcal{H}(\theta, \psi)}{\partial \psi} = \mathbf{M}^{-1} \psi(t), \\ \frac{d\psi(t)}{dt} &= -\frac{\partial \mathcal{H}(\theta, \psi)}{\partial \theta} = \nabla_{\theta} \log \pi(\theta(t) \mid \mathbf{X}).\end{aligned}$$

- By assuming that  $\mathcal{H}(\theta, \psi)$  does not depend on time  $t$ , for any  $t, s \in \mathbb{R}$  we have that

$$(\theta(t+s), \psi(t+s)) = \mathcal{T}_s\{\theta(t), \psi(t)\},$$

for some mapping  $\mathcal{T}_s$  depending only on  $s$ .

# Properties of Hamiltonian dynamics

- These differential equations preserve the value of the Hamiltonian, namely

$$\mathcal{H}\{\boldsymbol{\theta}(t), \boldsymbol{\psi}(t)\} = \mathcal{H}\{\boldsymbol{\theta}(t+s), \boldsymbol{\psi}(t+s)\},$$

- Hence, they also preserve the value of the **joint density**

$$\pi(\boldsymbol{\theta}(t) \mid \mathbf{X}) \pi(\boldsymbol{\psi}(t)) = \pi(\boldsymbol{\theta}(t+s) \mid \mathbf{X}) \pi(\boldsymbol{\psi}(t+s)).$$

- **Remark.** Any move according to Hamiltonian dynamics preserve the **level set**.
- The mapping  $\mathcal{T}_s$  is also **time-reversible**, which is crucial for showing that MCMC updates that use the dynamics leave the desired distribution invariant.
- Moreover, the mapping **preserves the volume**, a property which significantly simplifies the computations of the MCMC algorithm.

# A Gaussian example

- Let us assume that  $(\theta, \psi) \sim N_2(0, I_2)$ , so that the Hamiltonian is equal to

$$\mathcal{H}\{\theta(t), \psi(t)\} = \frac{\theta(t)^2}{2} + \frac{\psi(t)^2}{2}.$$

- In this special case, the **differential equations** simplify as follows

$$\begin{aligned}\frac{d\theta(t)}{dt} &= \frac{\partial \mathcal{H}(\theta, \psi)}{\partial \psi} = \psi(t), \\ \frac{d\psi(t)}{dt} &= -\frac{\partial \mathcal{H}(\theta, \psi)}{\partial \theta} = -\theta(t).\end{aligned}$$

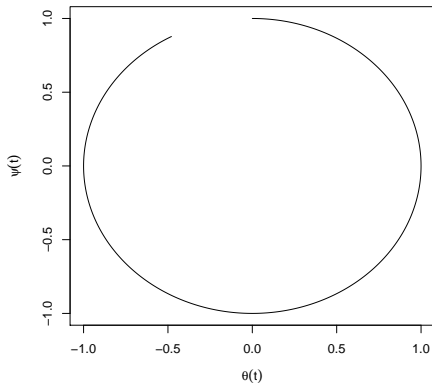
- It is easy to show that the solution are in the following form

$$\theta(t) = \rho \cos(\alpha + t), \quad \psi(t) = -\rho \sin(\alpha + t),$$

for some constants  $\rho$  and  $\alpha$ .

- Hence, the mapping  $\mathcal{T}_s$  is a rotation by  $s$  radians clockwise around the origin.

# A Gaussian example



- Trajectory of the dynamics with  $\rho = 1$ ,  $\alpha = -\pi/2$  and for values of  $t \in [0, 2\pi - 1/2]$ .

# The ideal HMC algorithm

- If the solution of the Hamiltonian dynamics were available in **closed form**, the HMC would proceed as follows.
- Recall that we aim at sampling values from the joint distribution  $\pi(\boldsymbol{\theta}, \boldsymbol{\psi} \mid \mathbf{X})$  using a algorithm. Let  $\boldsymbol{\theta}^{(r)}$  be the current value of the chain.
- At each step of the chain, draw a new value  $\boldsymbol{\psi}$  sampling from a multivariate Gaussian distribution  $N_p(0, \mathbf{M})$ ; this identifies a **new level set**.
- Obtain the proposed values  $(\boldsymbol{\theta}^*, \boldsymbol{\psi}^*)$  remaining on the given level set, by applying the mapping

$$(\boldsymbol{\theta}^*, \boldsymbol{\psi}^*) = \mathcal{T}_s\{\boldsymbol{\theta}^{(r)}, \boldsymbol{\psi}\},$$

for a certain value of time  $s$ , which is basically a tuning parameter.

- Thanks the properties of Hamiltonian dynamics, the acceptance probability is always 1, therefore the next value of the chain coincides with the proposal  $\boldsymbol{\theta}^{(r+1)} \leftarrow \boldsymbol{\theta}^*$ .

# Approximating Hamiltonian dynamics

- Unfortunately, most of the times the Hamiltonian differential equations do not admit a closed-form solution, thus **approximations** are required.
- To maintain the main properties of the ideal  $\text{HMC}$ , we look for discretized Hamiltonian dynamics **preserving the volume** and also being **time-reversible**.
- Among several methods that aims at solving this issue, we focus on the **leapfrog** method which unfortunately does not keep the Hamiltonian exactly constant over time.
- The leapfrog method is essentially a variation and more reliable version of the natural Euler's discretization method.
- **Remark.** The leapfrog method retains most of the properties of the ideal  $\text{HMC}$ , thus making it extremely appealing for sampling purposes.

# The leapfrog method

- We aim at approximating the mapping  $\mathcal{T}_\epsilon$  for some small  $\epsilon > 0$ .
- For any given time  $t$  and set of values  $\theta(t), \psi(t)$ , a small step ahead in time of size  $\epsilon$  in the Hamiltonian dynamics can be obtained using the leapfrog method.
- We make a first update on the **auxiliary variables** of size  $\epsilon/2$ , namely we get

$$\psi(t + \epsilon/2) = \psi(t) + \frac{\epsilon}{2} \nabla_{\theta} \log \pi(\theta(t) \mid \mathbf{X}).$$

- Secondly, we make a full step for the **variables of interest**, namely

$$\theta(t + \epsilon) = \theta(t) + \epsilon \mathbf{M}^{-1} \psi(t + \epsilon/2).$$

- Finally, we update again the **auxiliary variable** of size  $\epsilon/2$ , so that

$$\psi(t + \epsilon) = \psi(t + \epsilon/2) + \epsilon \nabla_{\theta} \log \pi(\theta(t + \epsilon/2) \mid \mathbf{X}).$$

# A single HMC step

- A single step of HMC proceeds as follows. Let  $\theta^{(r)}$  be the current value of the chain.
- Draw a new value  $\psi$  sampling from a multivariate Gaussian distribution  $N_p(0, \mathbf{M})$ .
- Obtain the proposed values  $(\theta^*, \psi^*)$  by applying  $L$  times the **leapfrog method** with step-size  $\epsilon$  and starting time  $t = 0$ , thus aiming at approximating the ideal dynamics

$$(\theta^*, \psi^*) \approx \mathcal{T}_s\{\theta^{(r)}, \psi\},$$

for a certain time value  $s = L \epsilon$ .

- Due to the symmetricity of the proposal, **accept or reject** the proposed value with a probability depending only on the Hamiltonian, namely

$$\min[1, \exp\{-\mathcal{H}(\theta^*, \psi^*) + \mathcal{H}(\theta^{(r)}, \psi^{(r)})\}],$$

which is usually very close to 1 as the Hamiltonian is kept **approximately constant** by the leapfrog method.



# Connection with the MALA algorithm

- There is a **strong connection** between MALA and HMC, even though these methods rely on very different notions.
- Indeed, it can be shown HMC using a single  $L = 1$  leapfrog step coincides with the pre-conditioned MALA algorithm.

- More precisely, at each step we propose from

$$(\theta^* | \theta) \sim N_p \left( \theta + \frac{\epsilon^2}{2} \mathbf{M}^{-1} \nabla_{\theta} \log \pi(\theta | \mathbf{X}), \epsilon^2 \mathbf{M}^{-1} \right),$$

and the acceptance probability coincides with that of MALA.

- This connections highlights that the covariance matrix of the Gaussian auxiliary variables is of great **practical importance**.
- In practice, it is advised to set  $\mathbf{M} = \Sigma^{-1}$ , where  $\Sigma$  represents an estimate for the posterior covariance; see Neal (2010) for further details and a **deeper perspective**.

# How to choose $\epsilon$ and $L$ ?

- Beside the covariance matrix  $\mathbf{M}$ , there are other 2 tuning parameters that must be chosen: the stepsize  $\epsilon$  and number of leapfrog steps  $L$ .
- The **trajectory length**  $\epsilon L$  is often set equal to some constant, say  $\epsilon L = 1$  or selected by trial and error.
- Small values for the **step-size**  $\epsilon$  increase the goodness of the leapfrog approximation but require larger values for  $L$  and leads to a higher computational costs.
- Large values for the **step-size**  $\epsilon$  could lead to catastrophic results, as the approximated trajectory could diverge from the ideal dynamics.
- The NO-U-TURN algorithm implemented in **Stan** automatically selects  $L$  so that the trajectory completes a “loop”.
- However, the NO-U-TURN requires a somewhat complex procedure that preserve the reversibility of the chain.

# HMC algorithm in practice

- After some trial and error, we set  $\epsilon = 0.1$  and  $L = 10$ .
- We again relied on the Laplace approximation for  $\hat{\Sigma} = \mathbf{M}^{-1}$ , which leads to an extremely high effective sample size.

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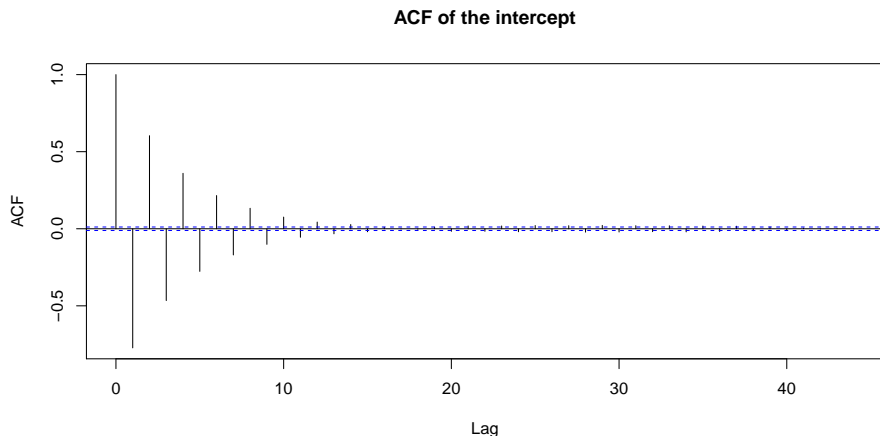
```
epsilon <- 0.25 # Stepsize - After some trial ad error
L <- 10 # Number of leapfrog steps

# Covariance matrix is selected via laplace approximation
fit_logit <- glm(y ~ X - 1, family = binomial(link = "logit"))
S <- vcov(fit_logit)
# Running the MCMC
fit_MCMC <- as.mcmc(HMC(R = R, burn_in = burn_in, y, X, epsilon, S, L))

# Running the MCMC (R = 30000, burn_in = 5000)
summary(effectiveSize(fit_MCMC)) # Effective sample size
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 215765 222946 226610 225565 228360 233334
summary(R / effectiveSize(fit_MCMC)) # Integrated autocorrelation time
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 0.1286 0.1314 0.1324 0.1331 0.1346 0.1390
summary(1 - rejectionRate(fit_MCMC)) # Acceptance rate
#   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
# 0.9892 0.9892 0.9892 0.9892 0.9892 0.9892
```

---

# HMC algorithm in practice



- The ACF has an alternate sign behaviour, implying that the integrated autocorrelation  $\tau_g < 1$  is smaller than 1, leading to an efficiency which is higher than iid sampling.

# Summary of the results

- The following table compare the **average** results. Here ESS represents the estimated and average **effective sample size**.
- A suitably tuned HMC can be extremely effective and it is the clear winner in this case.
- The implementation could be even improved by writing it in **Rcpp**!
- Refer to the link: [https://tommasorigon.github.io/CompStat/exe/un\\_B2.html](https://tommasorigon.github.io/CompStat/exe/un_B2.html)

	Seconds	ESS	ESS / Sec.	Acceptance rate
MH Laplace in <b>Rcpp</b>	0.61	1165.76	1897.52	0.27
MALA	3.43	44.32	12.91	0.56
Pre-conditioned MALA	3.85	9063.32	2351.34	0.57
HMC	15.32	225565.17	14724.08	0.99
<b>Stan</b>	78.85	29864.59	378.77	1