Hybrid Monte Carlo

- In conventional Monte-Carlo (MC) calculations of condensed matter systems, such as an N-particle system with a Hamiltonian $\mathcal{H} = \mathcal{U}$, only local moves (displacement of a single particle) are made.
- Updating more than one particle typically results in a prohibitively low average acceptance probability $\langle P_A \rangle$.
- This implies large relaxation times and high autocorrelations especially for macromolecular systems.
- In a Molecular Dynamics (MD) simulation, with $\mathcal{H} = \mathcal{T} + \mathcal{U}$, on the other hand, global moves are made.
- The MD scheme, however, is prone to errors and instabilities due to the finite step size in time.

- In order to introduce temperature in the microcanonical context, isokinetic MD schemes are often used.
- However, they do not yield the canonical probability distribution, unlike Monte-Carlo calculations.
- The Hybrid Monte-Carlo (HMC) method combines the advantages of Molecular Dynamics and Monte-Carlo methods: it allows for global moves (which essentially consist in integrating the system through *phase* space); HMC is an exact method, i.e., the ensemble averages do not depend on the step size chosen; algorithms derived from the method do not suffer from numerical instabilities due to finite step size as MD algorithms do; and temperature is incorporated in the correct

statistical mechanical sense.

- In the HMC scheme global moves can be made while keeping the average acceptance probability $\langle P_A \rangle$ high.
- One global move in *configuration* space consists in integrating the system through *phase* space for a fixed time t using some discretization scheme (δt denotes the step size)

$$\begin{aligned} g^{\delta t}: \quad \mathbb{R}^{6N} &\longrightarrow \mathbb{R}^{6N} \\ (x,p) &\longrightarrow g^{\delta t}(x,p) =: (x',p') \end{aligned}$$

of Hamilton's equations

$$\begin{aligned} \frac{dx}{dt} &= \frac{\partial \mathcal{H}}{\partial p} \\ \frac{dp}{dt} &= -\frac{\partial \mathcal{H}}{\partial x}. \end{aligned} \tag{1}$$

- Since the system is moved deterministically through phase space, the conditional probability of suggesting configuration x' starting at x is given by

$$p_C(x \to x')dx' = p_C(p)dp. \tag{2}$$

- The initial momenta are drawn from a Gaussian distribution at inverse temperature β:

$$p_C(p) \propto e^{-\beta \sum_{j=1}^{N} \frac{p_j^2}{2m}}. \tag{3}$$

- Thus

$$P_A((x,p) \to g^{\delta t}(x,p)) = \min\{1, e^{-\beta \delta \mathcal{H}}\}, \tag{4}$$

where

$$\delta \mathcal{H} = \mathcal{H}(g^{\delta t}(x,p)) - \mathcal{H}(x,p)$$

is the discretization error associated with $g^{\delta t}$. Using the algebraic identity

$$e^{-\mathcal{H}(x,p)} \min\{1, e^{-\delta \mathcal{H}}\} = e^{-\mathcal{H}(g^{\delta t}(x,p))} \min\{e^{\delta \mathcal{H}}, 1\} \tag{5}$$

- it can be shown that for a discretization scheme which is *time-reversible*

$$g^{-\delta t} \circ g^{\delta t} = id \tag{6}$$

and *area-preserving*

$$\det \frac{\partial g^{\delta t}(x,p)}{\partial (x,p)} = 1, \tag{7}$$

detailed balance is satisfied:

$$\begin{aligned} p(x)p_M(x \to x')dxdp &= p(x)p_C(p)P_A((x,p) \to g^{\delta t}(x,p))dxdp \\ &= p(x')p_C(p')P_A(g^{\delta t}(x,p) \to (x,p))dxdp \end{aligned}$$

$$
\begin{aligned}
&= p(x')p_C(p')P_A((x',p') \to g^{-\delta t}(x',p'))dxd \\
&= p(x')p_C(p')P_A((x',p') \to g^{-\delta t}(x',p'))dx'd \\
&= p(x')p_M(x' \to x)dx'dp'.
\end{aligned}
$$

- Thus, provided the discretization scheme used is *time-reversible* and *area-preserving*, the HMC algorithm generates a Markov chain with the stationary probability distribution $p(x)$.
- The probability distribution is entirely determined by the detailed balance condition.
- Therefore neither $p(x)$ nor any ensemble averages depend on the step size δt chosen.

- However, the average acceptance probability $\langle P_A \rangle$, because of (4), depends on the average discretization error $\langle \delta \mathcal{H} \rangle$ and hence does depend on δt.
- It can be shown that for $(\varrho, T) \neq (\varrho_c, T_c)$

$$\langle P_A \rangle = \mathrm{erfc}(\frac{1}{2}\sqrt{\beta \langle \delta \mathcal{H} \rangle})$$

  is a good approximation for sufficiently large systems ($N \rightarrow \infty$) and small step sizes ($\delta t \rightarrow 0$).
- From normalization and the area-preserving property one has

$$\langle e^{-\beta \delta \mathcal{H}} \rangle = 1. \tag{8}$$

- Equation (8) can be expanded into cumulants

$$\langle \delta\mathcal{H} \rangle = \frac{\beta}{2} \langle (\delta\mathcal{H} - \langle \delta\mathcal{H} \rangle)^2 \rangle + \cdots \quad .$$

- In order to obtain a nonzero average acceptance probability $\langle P_A \rangle$ in the limit $N \rightarrow \infty$ one has to let $\delta t \rightarrow 0$, keeping $\langle (\delta\mathcal{H} - \langle \delta\mathcal{H} \rangle)^2 \rangle$ fixed.
- In this limit higher-order cumulants will vanish. The resulting distribution of the discretization error will thus be gaussian with mean and width related through

$$\langle \delta\mathcal{H} \rangle = \frac{\beta}{2} \langle (\delta\mathcal{H} - \langle \delta\mathcal{H} \rangle)^2 \rangle. \qquad (9)$$

- From (4) and (9) one has in this case

$$\begin{aligned}\langle P_A\rangle &= \frac{1}{\sqrt{2\pi\langle(\delta\mathcal{H}-\langle\delta\mathcal{H}\rangle)^2\rangle}}\int_{-\infty}^{\infty} dt\,\min\{1,e^{-\beta t}\}e^{-\frac{(t-\langle\delta\mathcal{H}\rangle)^2}{2\langle(\delta\mathcal{H}-\langle\delta\mathcal{H}\rangle)^2\rangle}} \\ &= \operatorname{erfc}(\frac{1}{2}\sqrt{\beta\langle\delta\mathcal{H}\rangle}). \qquad (10)\end{aligned}$$

- The square root in (10) is always well defined since (8) implies

$$\langle\delta\mathcal{H}\rangle \geq 0.$$

- Equality holds in the limit $\delta t \to 0$, where energy is conserved exactly and $\langle P_A\rangle = 1$.
- Increasing the step size will result in a lower average acceptance probability $\langle P_A\rangle$. Varying δt, the average

acceptance probability $\langle P_A \rangle$ can thus be adjusted to minimize autocorrelations.

- The momenta do not necessarily have to be drawn from the Gaussian distribution.
- A particularly simple and computationally efficient alternative to would be a uniform momentum distribution.
- This choice, however, did not prove successful, since a cut-off has to be introduced for computational reasons. This cut-off must be taken into account in P_A, leading to a very low average acceptance probability $\langle P_A \rangle$.

- It is clear that instead of choosing a discretization scheme of Hamilton's equations (1) any time-reversible and area-preserving discrete mapping can be used to propagate the system through phase space.