SUPPLMENTARY INFORMATION:

On the Use of Accelerated Molecular Dynamics to Enhance Configurational Sampling in Ab Initio Simulations.

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1) Derivation of the formula for the forces :

With the bias potential defined as:

$$\Delta V(r) = \frac{\left(E_b - V(r)\right)^2}{E_b - V(r) + \alpha}$$

The A-AIMD forces are:

$$F_{aMD} = -\frac{\partial (V(r) + \Delta V(r))}{\partial r} = \frac{\partial V(r)}{\partial r} - \frac{\partial\left[\left(E_b - V(r)\right)^2 / \left(E_b - V(r) + \alpha\right)\right]}{\partial r}$$

The quotient rule is used to compute the derivatives:

$$F_{aMD} = -\frac{\partial V(r)}{\partial r} - \frac{\left(E_b - V(r) + \alpha\right)\left(-2E_b \frac{\partial V(r)}{\partial r} + 2V(r)\frac{\partial V(r)}{\partial r}\right) - \left(E_b - V(r)\right)^2\left(-\frac{\partial V(r)}{\partial r}\right)}{\left(E_b - V(r) + \alpha\right)^2}$$

This expression can be simplified by recognizing that $-\delta V(r)/\delta r = F_{MD}$:

$$F_{aMD} = F_{MD}\left(1 - \left[\frac{\left(E_b - V(r) + \alpha\right)\left(2E_b - 2V(r)\right) - \left(E_b - V(r)\right)^2}{\left(E_b - V(r) + \alpha\right)^2}\right]\right)$$

Which can be further simplified as:

$$F_{aMD} = F_{MD}\left(1 - \left[\frac{\left(E_b + V(r)\right) + 2\alpha\left(E_b - V(r)\right)}{\left(E_b - V(r) + \alpha\right)^2}\right]\right)$$

and rewritten (Eq. 3) as:

$$F_{aMD} = F_{MD}\cdot\left(1 + \left[\left(E_b - V(r)\right)^2 / \left(E_b - V(r) + \alpha\right)^2 - 2\left(E_b - V(r)\right) / \left(E_b - V(r) + \alpha\right)\right]\right)$$

2) Geometrical criteria used to analyze the cyclohexane trajectories:

The 6 dihedral angles of the ring (τ_i, i=1,6) have been used to define the different ring structures (Table SI1), [see also, Berces, Whitfield et al. (2001) 57(3): 477-491]. The 5 most common structures (chair, boat, twist-boat, half-chair, envelope) belong to the (D_{3d},C_{2v},D_2,C_2,C_s) symmetry groups. A deviation of 10 degrees for each dihedral angle was deemed acceptable as long as all the 6 angles constraints are satisfied.

Table SI1. Geometric criteria used to analyze the trajectories: [C = chair, B = boat, S = skew (or twist-boat), H = half-chair (or sofa), E = envelope].

	τ_1	τ_2	τ_3	τ_4	τ_5	τ_6
$^{1}C_{4}$	60	-60	60	-60	60	-60
$^{4}C_{1}$	-60	60	-60	60	-60	60
$B_{2,5}$	0	60	-60	0	60	-60
$^{3,6}B$	60	0	-60	60	0	-60
$B_{1,4}$	-60	0	60	-60	60	0
$^{2,5}B$	-60	60	0	-60	60	0
$^{1}S_{5}$	30	30	-60	30	30	-60
$^{6}S_{2}$	60	-30	-30	60	-30	-30
$^{3}S_{1}$	30	-60	30	30	-60	30
$^{5}S_{1}$	-30	-30	60	-30	-30	60
$^{2}S_{6}$	-60	30	30	-60	30	30
$^{1}S_{3}$	-30	60	-30	-30	60	-30
$^{1}H_{2}$	45	-15	0	-15	45	-60
$^{3}H_{2}$	60	-45	15	0	15	-45
$^{3}H_{4}$	45	-60	45	-15	0	-15
$^{5}H_{4}$	15	-45	60	-45	15	0
$^{5}H_{6}$	0	-15	45	-60	45	-15
$^{1}H_{6}$	15	0	15	-45	60	-45
$^{4}H_{5}$	-15	45	-60	45	-15	0
$^{6}H_{5}$	0	15	-45	60	-45	15
$^{6}H_{1}$	-15	0	-15	45	-60	45
$^{2}H_{1}$	-45	15	0	15	-45	60
$^{2}H_{3}$	-60	45	-15	0	-15	45
$^{4}H_{3}$	-45	60	-45	15	0	15
^{1}E	30	0	0	-30	60	-60

$\mathbf{E}_2$	60	-30	0	0	30	-60
$^{3}\mathbf{E}$	60	-60	30	0	0	-30
$\mathbf{E}_4$	30	-60	60	-30	0	0
$^{5}\mathbf{E}$	0	-30	60	-60	30	0
$\mathbf{E}_6$	0	0	30	-60	60	-30
$^{4}\mathbf{E}$	-30	60	-60	30	0	0
$\mathbf{E}_5$	0	30	-60	60	-30	0
$^{6}\mathbf{E}$	0	0	-30	60	-60	30
$\mathbf{E}_1$	-30	0	0	30	-60	60
$^{2}\mathbf{E}$	-60	30	0	0	-30	60
$\mathbf{E}_3$	-60	60	-30	0	0	30

3) Constrained MD calculations:

For cyclohexane, the constrained MD method (Ciccotti, Ferrario et al. 1989) was used in order to compute the free energy of the twist-boat form, relative to the chair form. The reaction coordinate used was a single C-C-C-C dihedral angle (τ_1). 21 simulations were performed with different values of the angle, between -60 deg, and 60 deg. The mean force converged after 2 ps, and the resulting free energy profile has an associated error of ~ 0.3 kcal/mol.

In an ab initio MD implementation, the mean force is equal to the corresponding Lagrange multiplier $\lambda(c)$ with an additional compensating term that arises from constraining the reaction coordinate. We did not take the latter explicitly into account because the correction was smaller than the statistical errors in our calculations. It is in general not significant for dihedral angles [e.g., see: W. K. den Otter and W. J. Briels J. Chem. Phys. 109, 7737 (1998); K. Doclo and U. Rothlisberger, J. Phys. Chem A, 104 (27), 6464(2000)].

For Na-Cl in solution, both ions were fixed, and the Lagrange multiplier $\lambda(c)$ was calculated on the original potential surface V(r). For a simple distance constraint, the compensating term is zero, because the Fixman determinant is indepent of the constraint.