

Amber free energy tools: Interoperable software for free energy simulations using generalized quantum mechanical/molecular mechanical and machine learning potentials

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ABSTRACT: We report the development and testing of new integrated cyberinfrastructure for performing free energy simulations with generalized hybrid quantum mechanical/molecular mechanical (QM/MM) and machine learning potentials (MLPs) in Amber. The Sander molecular dynamics program has been extended to leverage fast, density-functional tight-binding models implemented in the DFTB+ and xTB packages, and an interface to the DeePMD-kit software enables use of machine-learning potentials (MLPs). The software is integrated through application program interfaces that circumvent the need to perform “system calls” and enables the incorporation of long-range Ewald electrostatics into the external software’s self-consistent field procedure. The infrastructure provides access to QM/MM models that may serve as the foundation for QM/MM- Δ MLP potentials which supplement the semiempirical QM/MM model with a MLP correction trained to reproduce *ab initio* QM/MM energies and forces. Efficient optimization of minimum free energy pathways is enabled through a new surface-accelerated finite-temperature string method implemented in the FE-ToolKit package. Furthermore, we interfaced Sander with the i-PI software by implementing the socket communication protocol used in the i-PI client-server model. The new interface with i-PI allows for the treatment of nuclear quantum effects with semiempirical QM/MM- Δ MLP models. The modular interoperable software is demonstrated on proton transfer reactions in guanine-thymine mispairs in DNA. The current work represents a considerable advance in the development of modular software for performing free energy simulations of chemical reactions that are important in a wide range of applications.

Introduction

Free energy simulations are used to study a wide range of reactive chemical processes in the condensed phase.^{1,2} Calculation of multi-dimensional free energy surfaces^{3,4} (FES) and minimum free energy paths⁵⁻⁹ (MFEP) can be used to predict mechanism. The insight gained by these predictions can aid in the interpretation of experimental data, guide new experiments, and ultimately inform the design of new technology. *Ab initio* quantum mechanical models can provide high accuracy in these simulations; however, their computational cost can severely limit the size of the quantum system and/or the degree of sampling that can be realized. This limitation is further amplified if path integral molecular dynamics (PIMD)¹⁰⁻¹⁵ is required to introduce nuclear quantum effects, as these simulations are even more computationally intensive.

An attractive alternative to *ab initio* QM/MM simulation is the design quantum mechanical force fields^{2,16,17} and machine learning models.¹⁸⁻²³ Of particular relevance to the current work is the development of QM/MM- Δ MLP models, whereby the energies and forces of a fast, approximate QM model are corrected with a machine-learning potential.^{20,24-30} These models have the potential to offer the computational efficiency needed to address complex chemical mechanisms that require sampling of high-dimensional free energy surfaces, while providing accuracy comparable to high level QM methods. A barrier to progress in the development and validation of such methods is their availability in flexible software packages that enable a wide range of applications in the condensed phase.

The purpose of the present work is to report the development and testing of interoperable simulation software in Amber for performing free energy simulations (including PIMD) with QM/MM- Δ MLP models. A list of software components is itemized in Table 1 and Figure 1 illustrates their interoperation. Specifically, we have extended the QM/MM capabilities of the Sander molecular dynamics program by introducing interfaces to the DFTB+⁴² and xTB³⁸⁻⁴¹ semiempirical QM packages. This enables access to a wide range of powerful new density-functional tight-binding models with enabled dispersion and hydrogen bond-

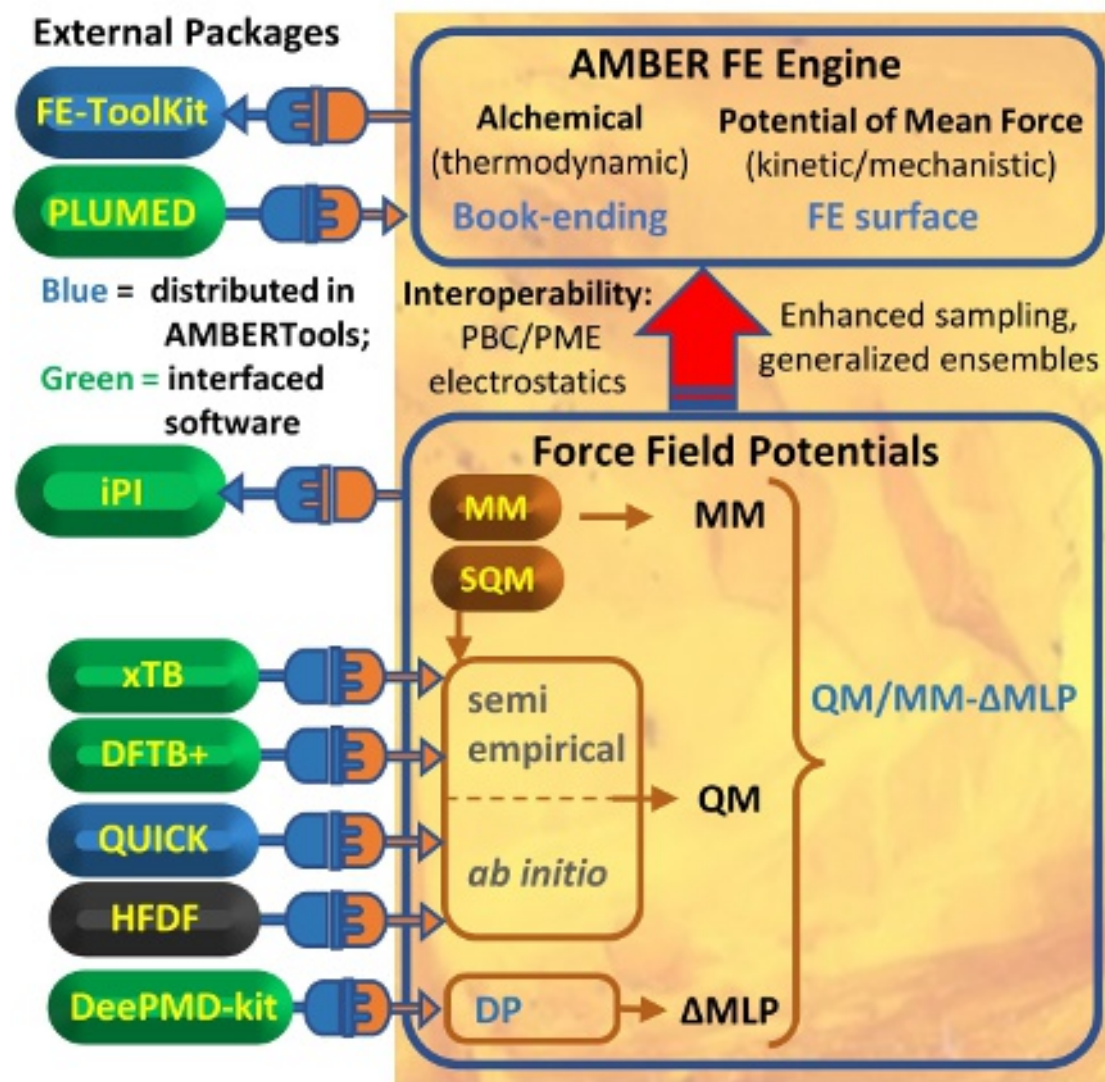


Figure 1: Interoperable software in Amber for conducting free energy simulations in the condensed phase with QM/MM- Δ MLP models. Amber-colored rectangle indicates Sander program with general internal components encircled by blue. Arrows indicate calling sequence. Green ovals are external software packages not distributed with Amber/AmberTools, whereas blue ovals indicate new cyberinfrastructure distributed with Amber. The program names and functionality are described in Table 1.

Table 1: Summary of program acronyms and functionality.

Program	Function
Sander	A molecular dynamics program with support for QM/MM potentials. ³¹
QUICK	A GPU-accelerated <i>ab initio</i> QM program. ^{32–36}
HFDF	An <i>ab initio</i> QM program optimized for large memory CPU machines. ³⁷
xTB	A semiempirical tight-binding program that implements the GFN1-xTB and GFN2-xTB models. ^{38–41}
DFTB+	A self-consistent charge density functional tight binding program that implements the DFTB2 and DFTB3 methods and various dispersion models. ⁴²
DeePMD-kit	A machine learning library for performing deep potential training and inference based on the TensorFlow platform. ^{43–45}
i-PI	A program for performing path integral molecular dynamics. ⁴⁶
PLUMED	A library that implements enhanced-sampling algorithms, collective variable definitions, and biasing potentials to calculate free energy surfaces. ^{47,48}
WESTPA	An interoperable, scalable software package for weighted ensemble simulation and analysis. ^{49,50}
FE-ToolKit	A collection of programs used to analyze alchemical free energy simulations and umbrella window sampling. ⁵¹

ing corrections for use in condensed phase QM/MM simulations with rigorous long-ranged electrostatics under periodic boundary conditions.^{37,52–54} Furthermore, we incorporated the DeePMD-kit software^{43–45} into Sander³¹ to evaluate new machine-learning potentials. Path integral molecular dynamics (PIMD) have been enabled through a new interface with the i-PI software.⁴⁶ Finally, a recently developed surface-accelerated finite-temperature string method⁹ has been incorporated into the FE-ToolKit software⁵¹ (distributed within Amber-Tools³¹) to locate minimum free energy paths.

The Methods section describes the interfaces between Sander, the DFTB+ and xTB semiempirical packages, the DeePMD-kit software, and i-PI. The nature of the QM/MM interactions and the incorporation of Ewald electrostatics within the self-consistent field (SCF) procedures are discussed. We demonstrate the features of the software framework through an example application that examines guanine-thymine mispair tautomerization reactions in B-DNA. These mispairs are enabled by formation of rare tautomer forms, and have been implicated in the formation of mutations in DNA replication and translation.^{55,56} The

Results and Discussion section begins with a validation of the implementation by demonstrating QM/MM and QM/MM- Δ MLP energy conservation in simulations performed in the microcanonical ensemble. We then compare free energy profiles generated from *ab initio*, semiempirical, and Δ MLP-corrected semiempirical methods obtained from QM/MM umbrella sampling. Finally, we perform QM/MM umbrella sampling with PIMD to explore how nuclear quantum effects alter the profiles.

Methods

The QM/MM- Δ MLP force fields are supplement the QM/MM energy with a nonelectrostatic correction, $E_{\text{ML}}(\{\mathbf{r}\})$, where $\{\mathbf{r}\}$ is the $3N$ array of atomic positions.

$$E_{\text{QM/MM-}\Delta\text{MLP}} = E_{\text{MM}}(\{\mathbf{r}\}) + E_{\text{QM}}(\{\mathbf{r}\}; \mathbf{P}) + E_{\text{QM/MM}}(\{\mathbf{r}\}; \mathbf{P}) + E_{\text{ML}}(\{\mathbf{r}\}) \quad (1)$$

E_{MM} and E_{QM} are the MM and QM contributions to the energy, and $E_{\text{QM/MM}}$ is their interaction. E_{ML} is the machine learning correction (referred to as a machine learning potential correction, Δ MLP). E_{QM} and $E_{\text{QM/MM}}$ depend on the single particle density matrix, $\mathbf{P}$. In the present work, we incorporated the DFTB+ and xTB packages into Sander for calculating E_{QM} , and the interface to DeePMD-kit is used to evaluate E_{ML} . The details of the implementation, and a description of the QM/MM interactions are discussed below.

Sander interface with DFTB+ and xTB

The DFTB+ and xTB source codes^{57,58} are not distributed with AmberTools, but they can be downloaded and compiled as standalone applications and/or software libraries to be used in other applications. In our implementation, we directly link the DFTB+ and xTB libraries with the Sander executable during compilation. Unlike many of the other QM/MM interfaces supported by Sander, this strategy circumvents the cost associated with writing an input file for the external QM program, executing the external program via a system call, and

reading the external program's output file at each molecular dynamics step. Instead, Sander directly interacts with DFTB+ and xTB via function calls. Furthermore, this allows us to incorporate variational long-range Ewald electrostatics into their SCF procedures.^{37,52–54} Detailed instructions for configuring Sander with DFTB+ and xTB support are provided in the AmberTools 2024 user manual.

The QM/MM interaction is performed with electrostatic embedding.

$$E_{\text{QM/MM}} = E_{\text{QM/MM,LJ}} + \sum'_{b \in \text{MM}} \int \int \frac{q_{\text{QM}}(\mathbf{r}') q_b(\mathbf{r} - \mathbf{r}_b)}{|\mathbf{r} - \mathbf{r}'|} d^3r d^3r' + \sum_{a \in \text{QM}} q_a \left(\Delta\phi_{\text{MM}}(\mathbf{r}_a) + \frac{1}{2} \Delta\phi_{\text{QM}}(\mathbf{r}_a) \right) \quad (2)$$

$E_{\text{QM/MM,LJ}}$ is the Lennard-Jones interaction between the QM and MM atoms. The second term is the electrostatic interaction between the QM charge density (determined from the density matrix), $q_{\text{QM}}(\mathbf{r})$, and the field of nearby MM charges $q_b(\mathbf{r} - \mathbf{r}_b)$. The primed summation denotes that only those MM atoms within a cutoff of the QM region are included. The last term accounts for the long-range electrostatic interactions. The QM charge density is modeled by Mulliken charges, q_a , $\Delta\phi_{\text{MM}}(\mathbf{r}_a)$ is the electrostatic potential caused by all MM atoms outside of the cutoff, and $\Delta\phi_{\text{QM}}(\mathbf{r}_a)$ the interaction between the QM region and its periodic images.

$$\Delta\phi_{\text{MM}}(\mathbf{r}_a) = \text{Re} \sum_{\mathbf{k} \neq 0} \frac{4\pi}{k^2 V} e^{i\mathbf{k}^T \cdot \mathbf{r}_a - \frac{k^2}{4\beta^2}} \sum_{b \in \text{MM}} q_b e^{-i\mathbf{k}^T \cdot \mathbf{r}_b} - \sum'_{b \in \text{MM}} \frac{q_b \text{erf}(\beta r_{ab})}{r_{ab}} - \frac{\pi Q_{\text{MM}}}{\beta^2 V} \quad (3)$$

$$\Delta\phi_{\text{QM}}(\mathbf{r}_a) = \text{Re} \sum_{\mathbf{k} \neq 0} \frac{4\pi}{k^2 V} e^{i\mathbf{k}^T \cdot \mathbf{r}_a - \frac{k^2}{4\beta^2}} \sum_{b \in \text{QM}} q_b e^{-i\mathbf{k}^T \cdot \mathbf{r}_b} - \sum_{b \in \text{QM}} \frac{q_b \text{erf}(\beta r_{ab})}{r_{ab}} - \frac{\pi Q_{\text{QM}}}{\beta^2 V} \quad (4)$$

The first term in eqs. 3 and 4 is the reciprocal space potential of the MM and QM charge densities, respectively. V is the volume of the unit cell, β is the Ewald coefficient, $\mathbf{k}$ is the angular wave number of the plane wave, and Q_{MM} and Q_{QM} are the net charge of the MM and QM regions. The second term in eqs. 3 and 4 is a real-space correction that removes the potential caused by the nearby Ewald Gaussian functions. The third term in eqs. 3 and 4 is a neutralizing uniform background correction for charged systems. The MM energy, $E_{\text{MM}}(\{\mathbf{r}\})$ contains an analogous background correction $-\pi Q_{\text{MM}}^2/(2\beta^2V)$, such that the net correction for the entire system is $-\pi(Q_{\text{MM}} + Q_{\text{QM}})^2/(2\beta^2V)$.

The Sander program is responsible for calculating E_{MM} , $E_{\text{MM,LJ}}$, $\Delta\phi_{\text{MM}}$, and $\Delta\phi_{\text{QM}}$. The DFTB+ and xTB libraries are responsible for calculating E_{QM} , q_a , and the second term in eq. 2. A similar separation of responsibilities occurs when calculating atomic forces. At each step of dynamics, Sander evaluates $\Delta\phi_{\text{MM}}$ with the particle mesh Ewald (PME) method,^{59,60} and it precomputes the exponentials appearing in eq. 4. The MM atoms are imaged around the QM region, and a list of MM atoms within a cutoff of any QM atom is generated. A SCF calculation is requested by providing the current set of QM atomic coordinates, and the locations, charges, and “hardness” values of the nearby MM atoms. The xTB software uses the hardness values to represent the nearby embedding charges as diffuse monopoles. For example, in GFN2-xTB, the second term in eq. 2 is given by eq. 5, where s indexes the atomic orbital shells, and q_s is a shell-resolved partial charge.

$$\sum'_{b \in \text{MM}} \int \int \frac{q_{\text{QM}}(\mathbf{r}') q_b(\mathbf{r} - \mathbf{r}_b)}{|\mathbf{r} - \mathbf{r}'|} d^3r d^3r' \approx \sum'_{b \in \text{MM}} \sum_{a \in \text{QM}} \sum_{s \in a} \frac{q_s q_b}{\sqrt{r_{ab}^2 + \left[\frac{\eta_s + \eta_b}{2}\right]^{-2}}} \quad (5)$$

In the present work, we assign all MM atoms the hardness of hydrogen. The Sander interface with DFTB+ currently treats the MM atoms as point charges; however, this can be generalized in a similar fashion in the future.

The interfaces to both QM packages take advantage of object oriented features of the Fortran 2008 programming language to communicate the variational contribution of the

long-range electrostatics within the SCF procedure. The DFTB+ interface with Sander is contained in the file `dftbplus_module.F90` located in the Sander source directory of the AmberTools 2024 package. The interface creates a child class that inherits from the `TQDepExtPotGen` data structure provided by the DFTB+ software.⁵⁷ This class was specifically designed by the DFTB+ developers to include charge-dependent external potential corrections. The xTB interface with Sander is similarly contained in the file `xtb_module.F90` within the Sander source directory. The xTB interface inherits from the `TSolvation` structure defined within the xTB software.⁵⁸ xTB normally uses this class to interact the QM region with an implicit solvent model. In both interfaces, the child class redefines the parent class methods to evaluate the last term in eq. 2 and the “shift” in the atom potentials: $\Delta\phi_{\text{MM}}(\mathbf{r}_a) + \Delta\phi_{\text{QM}}(\mathbf{r}_a)$.

One enables QM/MM calculations by setting `ifqnt=1` in the Sander input file, which will cause the options in the `&qmmm` Fortran namelist to be read. Setting the option `qm_theory='DFTBPLUS'` or `qm_theory='XTB'` will read the interface-specific options in the `&dftbplus` or `&xtb` namelists, respectively. Additional details are described in the upcoming AmberTools 2024 documentation, due to be released in the spring of 2024.

Sander interface with DeePMD-kit

The design of the DeePMD-kit interface^{43–45} with the Sander program³¹ is heavily influenced by the development of QM/MM- Δ MLP potentials.^{20,21,61–64} In the Sander input file, the user makes a selection of atoms to be corrected with a MLP. In the context of evaluating a QM/MM- Δ MLP, the MLP selection is the set of atoms in the QM region. One must also provide the name of the file containing the DeePMD-kit neural network definition and parameters. The Deep-Potential Range-Corrected model (DPRc)²⁰ corrects the interactions between the QM atoms and the interactions between the QM and nearby MM atoms in a manner that conserves energy. That is to say, the MLP correction to the QM/MM interactions smoothly approaches zero as the MM atom reaches a specified cutoff distance. When

using a DPRc model, the Sander input file must also specify the MLP cutoff for the QM/MM interactions. Previous parametrizations of DPRc-based MLP models have used a 6 Å cutoff, which is also used in the present work. At each step of dynamics, Sander will request the MLP energy and forces from DeePMD-kit by providing the position and “type” of each QM and (optionally) nearby MM atoms. A QM atom type is its 2-character element symbol, whereas the MM atom type – from the perspective of DeePMD-kit – is the element symbol prefixed with the letter “m”. This strategy allows the neural network to correct a QM/QM interaction differently than a QM/MM interaction.

The DPRc energy is the sum of atomic contributions, E_i ,

$$E_{\text{DPRc}} = \sum_{i=1}^N E_i(\mathbf{r}_i, \{\mathbf{r}_j\}_{j \in n(i)}) \quad (6)$$

where N is the number of atoms, $\mathbf{r}_i$ is the location of atom i , and $n(i)$ denotes the set of neighboring atoms (i.e., atoms within the DPRc cutoff radius). The expressions for the E_i values from the neural network can be found elsewhere.^{20,21} The atomic decomposition of DPRc model is readily amenable to parallel calculation. The DPRc contribution to the energy is activated by setting the `idprc=1` option within the Sander input `&dprc` Fortran namelist.

As written, the DPRc application programming interface is specific to DeePMD-kit because it instantiates software objects defined within the DeePMD-kit library. Many emerging MLPs, such as *allegro*⁶⁵ and *mace*,⁶⁶ are based on the PyTorch framework.⁶⁷ We are currently developing a generic Sander/PyTorch QM/MM-ΔMLP interface to evaluate these models.

Sander interface with i-PI

The i-PI software⁴⁶ is a standalone molecular dynamics program that supports state-of-the-art path integral sampling,⁶⁸ including the PIGLET thermostat, which has been shown to

dramatically reduce the expense of computing the quantum kinetic energy.^{69,70} The path integral dynamics is performed with a ring polymer Hamiltonian, consisting of several replicas (beads) that are harmonically restrained in series. At each time step, the potential energy of each bead must be computed; however, these calculations are independent and can be performed in parallel. The i-PI software defines a client-server communication protocol to evaluate the potential energy with external driver programs. We have implemented the “internet socket” variation of the protocol, where multiple instances of Sander can be launched on different computers. When launching a Sander instance, one must provide the hostname (internet protocol address) and port number used for interprocess communication. These quantities are specified as command-line arguments `-host` and `-port`, respectively. Furthermore, the Sander input file must set the option `imin=7`, which causes the program to wait for communication from the server process.

Free energy profiles of tautomer reactions from classical molecular dynamics

We prepared a B-form DNA system (PDB ID: 113D)⁷¹ to demonstrate the functionality of the new software infrastructure. The B-DNA crystal structure⁷¹ has drawn interest due to the presence of two G-T wobble pair mismatches^{55,72,73} which could give rise to errors in replication^{74,75} and translation.⁷⁶ This subsequently led to computational investigation of G-T tautomerization reactions with QM/MM.⁵⁶

In the present work, we explore tautomerization reactions involving residues G4 and T21. The B-DNA system consists of 762 solute atoms solvated by 5151 waters in a truncated octahedron with 59.3 Å real-space lattice vectors lengths. A total of 13 Cl[−] and 35 Na⁺ ions were added to neutralize the charge and achieve a 0.14 M ion concentration. The system was prepared using an elaborate 15-step procedure described in Ref. 77 using a MM potential. The preparation procedure involves geometry optimization, heating, solvent annealing, and equilibration of the system density while restraining solute heavy atoms.

Over the course of the equilibration procedure, the solute restraints are gradually reduced. In total, this procedure involved 6.2 ns and 2.6 ns of simulation in the *NVT* and *NPT* ensembles, respectively, using a 1 fs time step. The system was then equilibrated for an additional 100 ns in the *NPT* ensemble. The temperature was maintained at 298 K with a Langevin thermostat⁷⁸ (5.0 ps⁻¹ collision frequency) and the density was equilibrated at 1 atm using the Berendsen isotropic barostat. The MM potential modeled the DNA with the OL15 force field,⁷⁹ and the solvent environment was modeled with SPC/Fw waters⁸⁰ and the Li *et al.* ion parameters.⁸¹ Electrostatics were calculated with the particle mesh Ewald method^{59,60} using 10 Å real-space cutoffs, a 1 Å reciprocal space grid spacing, and tinfoil boundary conditions.

Free energy profiles of the tautomeric reactions depicted in Figure 3 were calculated from QM/MM umbrella sampling using a variety of *ab initio* and semiempirical methods. The reactions are decomposed into 3 steps connecting 3 tautomeric forms. The “wGT” state corresponds to the G-T wobble base pair in which the T21:N3 position is protonated. The “GT*” state is a tautomer in which the T21:H3 proton is covalent bonded to the T21:O4 position. Similarly, the “G*T” state is a tautomer in which the H3 proton is bound to the G4:O6. The 3 steps involve the proton displacement between these states: wGT→GT*, GT*→G*T, G*T→wGT. The QM/MM methods compared in this work are: PBE0/6-31G*, GFN2-xTB,⁴¹ DFTB3-D3 DFTB3-D4(2b), DFTB3-D4(3b), and AM1/d.⁸²⁻⁸⁴ The DFTB3-D3 model applies Grimme’s D3 dispersion correction^{85,86} to the DFTB3/3ob Hamiltonian.^{87,88} Similarly, the DFTB3-D4(2b) and DFTB3-D4(3b) models supplement the DFTB/3ob method with the D4 dispersion model.⁸⁹ The DFTB3-D4(3b) method includes a 3-body contribution to the dispersion, whereas DFTB3-D4(2b) is limited to 2-body contributions. Furthermore, we parametrized a reaction-specific DPRc correction for the AM1/d model (described in the next section), which will be denoted AM1/d+ML. The QM region consists of 51 atoms (the nucleobase and sugar of G4 and T21), and it has a net neutral charge. The minimum free energy path of each step was independently optimized

for every QM/MM model. The optimizations were performed with the surface-accelerated finite temperature string method⁹ in the space of 5 reaction coordinates. The reaction coordinates are distance differences meant to represent the transfer of H3 proton and the relative displacement of the hydrogen bond pattern: $\xi_1 = R_{\text{N3-H3}} - R_{\text{O6-H3}}$, $\xi_2 = R_{\text{O6-H3}} - R_{\text{O4-H3}}$, $\xi_3 = R_{\text{N1-H1}} - R_{\text{N3-H1}}$, $\xi_4 = R_{\text{N1-O2}} - R_{\text{N2-O2}}$, $\xi_5 = R_{\text{N2-O2}} - R_{\text{N1-N3}}$. All umbrella sampling described in this work used $200 \text{ kcal mol}^{-1} \text{ \AA}^{-2}$ force constants for each reaction coordinate. The string method began from an initial guess that linearly interpolated the reaction coordinates between the step's reactant and product states. Each string was sampled with 32 umbrella windows. The initial configurations of each window were sequentially prepared, starting from the reactant state. The QM/MM structure of each window was optimized for 1000 steps of conjugate gradient minimization. The temperature was gradually raised from 0 K to 298 K over the course of 40 ps, and an additional 10 ps of QM/MM umbrella sampling was performed in the *NVT* ensemble. 50 iterations of the string method were performed with 4 ps/window/iteration of sampling and a 1 fs time step. Production sampling of the final path was performed for 25 ps, and each production simulation was repeated 4 times with different thermostat random number seeds. The reaction coordinate values were recorded every 10 fs, and the aggregate sampling from all 3 reaction steps were analyzed with the multistate Bennett's acceptance ratio (MBAR) method⁹⁰ implemented in the ndfes software^{4,51} to produce 5-dimensional free energy surfaces. The profiles presented in the manuscript are the free energies along the minimum free energy path. The PBE0/6-31G* simulations is very expensive in relation to the other models. In this case, only 10 iterations of the string method were performed, starting from the optimized AM1/d path. Each string was sampled for 2 ps/window/iteration, and 4 sets of production simulations were run for 10 ps/window/trial with a 1 fs time step. The *ab initio* QM/MM electrostatics were calculated with the ambient-potential composite Ewald method³⁷ using a 10 Å real-space cutoff, 1 Å reciprocal space grid spacing, and tinfoil boundary conditions.

Free energy profiles of tautomer reactions from path integral molecular dynamics

We recalculated the free energy profiles from path integral molecular dynamics (PIMD) umbrella sampling performed with the new interface to the i-PI software.⁶⁸ The profiles generated from classical and path integral dynamics are compared to explore how nuclear quantum effects change the free energy predictions. The PIMD dynamical motion was propagated with 6 beads (replicas) at a 0.25 fs timestep at 298 K using the PIGLET quantum thermostat;^{69,91} therefore, up to 6 Sander instances can be launched. The parameters for the PIGLET thermostat were taken from the GLE4MD website.^{92,93} The parameters were chosen to reproduce the quantum fluctuations at 298 K and span a range of frequencies up to 4142 cm⁻¹. Each step's path was sampled with 32 umbrella windows using 200 kcal mol⁻¹ Å⁻² force constants. The PIMD restraint potentials were applied to the centroid positions (the bead-averaged positions) by making use of the i-PI interface to PLUMED.^{47,48} PIMD umbrella sampling was performed at 32 windows positioned along the path previously optimized from the classical sampling. Each window was sampled for 2.5 ps, and repeated 4 times with different thermostat random number seeds. The reaction coordinate values were calculated from the centroid positions, and the free energy surface was generated from MBAR analysis of the aggregate sampling obtained from the 3 reaction steps.

QM/MM-ΔMLP model training

We demonstrate the new interface between Sander and DeePMD-kit by parametrizing a DPRc correction for the AM1/d-PhoT Hamiltonian. The architecture of the DPRc neural network was previously described in Ref. 94, and we have summarized the model in the Supporting Information for completeness. The AM1/d+ML neural network parameters were optimized with the DP-GEN software⁹⁵ to reproduce PBE0/6-31G* QM/MM energies and forces in the B-DNA system. The DPRc MLP corrects the interactions between the

QM atoms, and the QM/MM interactions within a 6 Å cutoff. Four sets of neural network parameters were trained against 93617 samples extracted from the AM1/d-PhoT string calculations using the Adam stochastic optimizer with different random number seeds.⁹⁶ The parameter sets were then updated through 7 iterations of active learning. An active learning iteration consists of 3 steps: exploration, labeling, and retraining. The exploration step uses the current set of neural network parameters to perform QM/MM+ΔMLP umbrella sampling. For each saved sample, the energy and forces produced by the 4 parameter sets are compared; if the models disagree, then the sample is categorized as a “candidate”. The “labeled” samples are a random selection of (up to) 2000 samples drawn from the pool of candidates. The energy and forces of labeled samples are recalculated with PBE0/6-31G* QM/MM and included as additional reference data within the next round of training. The active learning procedure terminates when 10 % (or fewer) of the samples are selected for labeling.

Each active learning iteration sampled 1920 umbrella windows for 2 ps and saved 50 samples/simulation. These simulations correspond to the first 20 and 40 iterations of the finite temperature string method applied to the wGT→GT* and GT*→G*T reaction steps, respectively. A sample was made a candidate if the standard deviation in the MLP energy corrections was larger than 10^{-4} eV/atom or the standard deviation in the force correction exceeds 0.08 eV/Å for any atom. The active learning procedure terminated after 7 iterations, requiring a total of 9293 *ab initio* QM/MM evaluations. Neural network parameters were produced from 4 million steps of Adam stochastic optimization with a learning rate that exponentially decays from 10^{-3} to 5×10^{-8} .⁹⁶ As previously described, production sampling of the B-DNA tautomeric reactions were simulated 4 times with different random number seeds. The AM1/d+ML production sampling was repeated with each of the 4 neural network parameter sets (1 trial/parameter set), and the results were averaged.

Results and Discussion

Validation tests: Force evaluation and energy conservation in NVE simulations

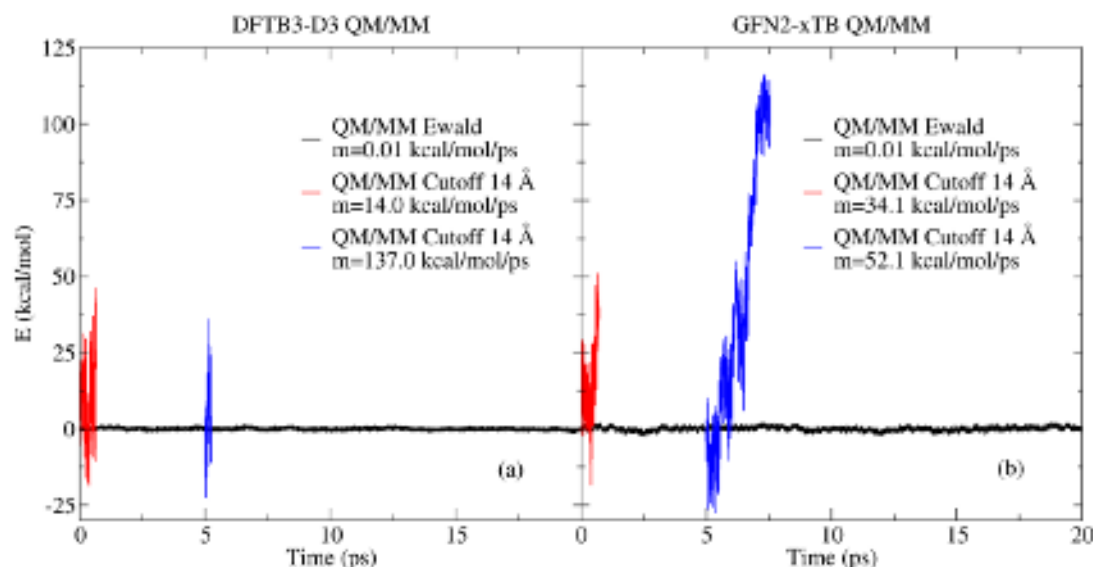


Figure 2: QM/MM energy conservation of B-DNA in the microcanonical ensemble. (a) DFTB3-D3 performed with Sander/DFTB+. (b) GFN2-xTB performed with Sander/xTB. All methods compute the MM/MM electrostatics with particle mesh Ewald. The QM/MM Ewald method similarly models the QM/QM and QM/MM electrostatics with Ewald. The QM/MM Cutoff 14 Å method truncates the QM/MM interactions beyond 14 Å, and long-range QM/QM interactions are ignored. The QM/MM Cutoff 14 Å simulations were repeated at different starting configurations taken from the QM/MM Ewald trajectory. The “m” values are the slope of the energy obtained from linear regression.

In this section, we validate the Sander interface with DFTB+ and xTB software by performing DFTB3-D3 and GFN2-xTB QM/MM simulations of the B-DNA system in the microcanonical ensemble and monitor the total energy. Energy conservation is achieved when the potential energy is smooth and the analytic atomic forces are numerically consistent with the potential energy gradients.

Figure 2 plots the total energy of the B-DNA reactant state as a function of time. The lines labeled “QM/MM Ewald” were simulated with Ewald electrostatics using 10 Å real-

space cutoffs, whereas “QM/MM Cutoff 14 Å” truncates the QM/MM electrostatics at 14 Å (and it does not model the long-range QM/MM electrostatics). We ran the simulations with truncated electrostatics twice, starting from the GFN2-xTB (Ewald) or DFTB3-D3 (Ewald) configurations at times 0 ps and 5 ps. The “m” values are slopes of the energy from linear regression. Each simulation was performed for 20 ps using a 1 fs time step.

The QM/MM Ewald interface described in the methods section assumes that the short-range QM/MM electrostatic interactions (the second term in eq. 2) behave like point monopoles at the real-space cutoff; the Ewald correction models the electrostatics outside of the cutoff from a point charge approximation. The short-range electrostatics (eq. 5) adopt the Mataga–Nihshimoto–Ohno–Klopman^{97–99} damped Coulomb interaction model. This model mimics a point charge interaction at large distances.

Figure 2 suggests that the slight discrepancy between eq. 5 and point charge electrostatics is negligible when using a 10 Å real-space cutoff for both GFN2-xTB and DFTB3-D3. The energy conservation of GFN2-xTB is almost identical to DFTB3-D3 in DFBT+. Both models exhibit negligible energy drift over 20 ps (slopes 0.01 kcal/mol/ps). However, when the GFN2-xTB and DFTB3-D3 QM/MM electrostatics are truncated at 14 Å, large deviations in the total energy are encountered, and the self-consistent field procedure often fails to converge within a few picoseconds of simulation. Similar behavior has been illustrated elsewhere in validation tests that compare the stability of QM/MM simulations with and without long-ranged electrostatic interactions.³⁷

Free energy surfaces for guanine-thymine mispair tautomerization reactions

In this section, we examine free energy profiles of guanine-thymine mispair tautomerization reactions using a wide range of *ab initio* and semiempirical/DFTB QM/MM and QM/MM- Δ MLP models. Free energy surfaces (FESs) and minimum free energy paths (MFEPs) were

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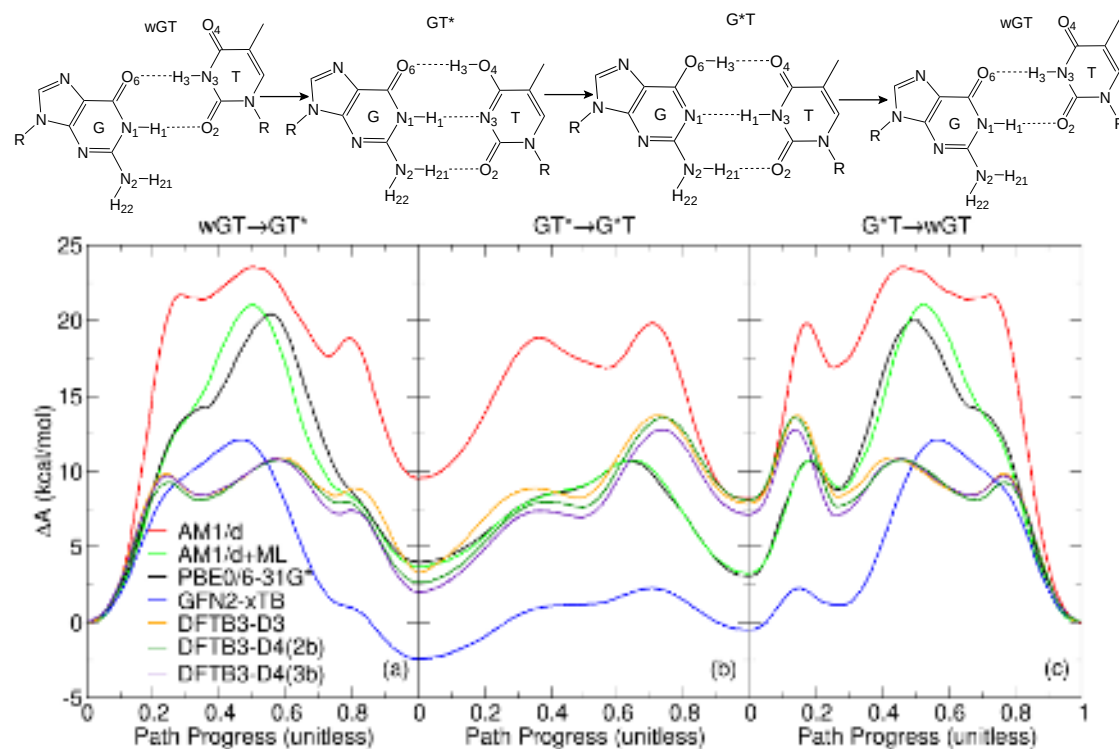


Figure 3: Helmholtz free energy profiles for guanine-thymine mispair tautomerization reactions using different *ab initio* and semiempirical/DFTB QM/MM and QM/MM- Δ MLP models performed in the canonical ensemble. (a) wGT $\rightarrow$ GT*; (b) GT* $\rightarrow$ G*T; (c) G*T $\rightarrow$ wGT. “wGT” indicates a G-T wobble pair, and G* and T* are non-standard tautomer states of G and T, respectively, as indicated in the figure and described in the text.

determined using the surface-accelerated string method⁹ with 5 different reaction coordinates as described in the Methods section. Figure 3 compares the 1D free energy profiles for the MFEPs for the following QM/MM models: PBE0/6-31G*, AM1/d, GFN2-xTB, DFTB3-D3, DFTB3-D4(2b), and DFTB3-D4(3b). PBE0/6-31G* is an *ab initio* QM/MM model, and it is approximately 500 times slower than the other semiempirical/DFTB QM/MM models for these systems. Several QM/MM models based on DFTB3 are available through the interface with DFTB+, and in particular the use of different dispersion models are examined. The notation “D3” and “D4” refers to the dispersion correction, (2b) and (3b) mean 2-body and 3-body interaction, respectively, as described in the Methods section. In addition, the GFN2-xTB model is examined through an interface with the xTB package. The AM1/d model is an NDDO-based semiempirical Hamiltonian available within the SQM module of Sander. AM1/d also serves as the base QM model upon which the QM/MM-ΔMLP was developed (AM1/d+ML) through an interface with DeePMD-kit.^{43–45} Neural network parameters were trained to reproduce PBE0/6-31G* QM/MM energies and forces. In this way, functionality for a wide range of QM/MM models is demonstrated, and their results compared.

The reaction itself is decomposed and presented in three steps that form a closed thermodynamic cycle as illustrated at the top of Figure 3. In the first step a G-T wobble pair (wGT) undergoes a coupled proton transfer/hydrogen bond register shift to a G-T* basepair where T* represents the thymine enol tautomer. In the second step of the reaction, the GT* undergoes a second proton transfer/hydrogen bond register shift to form a (G*)-T basepair where G* is the guanine enol tautomer. The third step of the reaction involves a coupled proton transfer/hydrogen bond register shift to return to the original GT wobble basepair.

It is immediately evident from Figure 3 that there are large variations in the free energy profiles for the various QM/MM models. Most notably, none of the semiempirical/DFTB-based QM/MM models closely reproduce the *ab initio* PBE0/6-31G* profile. The AM1/d model systematically overestimates the profile with respect to the wGT state, whereas the DFTB models underestimate the profiles with respect to the wGT state. The GFN2-xTB

model, in this example, further predicts that the tautomer basepairs (GT* and G*T) are more favorable than the GT wobble (wGT) where the nucleobases are in their most stable tautomer keto forms.

Table 2 (top) lists values of key stationary points along the free energy profiles calculated with classical molecular dynamics shown in Figure 3 and compares them to experimentally-derived reference values. Overall, the *ab initio* PBE0/6-31G* QM/MM model does the best job at reproducing the experimentally derived values. The differences in ΔA are less than 1 kcal/mol, and the differences in $\Delta A^\ddagger$ are less than 3.5 kcal/mol. It should be noted that the comparison with experiment here is only approximate in the sense that the $\Delta A^\ddagger$ is only crudely approximated from the experimental rates using transition state theory with unit transmission coefficient. Taking the PBE0/6-31G* values as a high-level theoretical reference, it is clear that the other QM/MM models differ considerably. For example, the difference between PBE0/6-31G* and semiempirical/DFTB model wGT→GT* $\Delta A^\ddagger$ values range from -6.4 to 5.6 kcal/mol. Only the machine-learning potential corrected model AM1/d+ML gives results that are close to the *ab initio* values. The ΔA and $\Delta A^\ddagger$ values agree with PBE0/6-31G* to within 0.5 and 0.8 kcal/mol, respectively. The AM1/d+ML QM/MM model is thus by far the closest agreement with the *ab initio* QM/MM model, despite the uncorrected AM1/d model having very large differences (maximum differences for ΔA and $\Delta A^\ddagger$ of 5.6 and 3.5 kcal/mol for ΔA and $\Delta A^\ddagger$, respectively).

The main point of this section is to demonstrate that: 1. *ab initio* QM/MM simulations provide reasonable agreement with experimental results such that they can provide, at very high computational cost, a valuable molecular-level interpretation and can potentially be used for prediction; 2. existing semiempirical/DFTB models may not be able to accurately describe a chemical process that was outside the scope of their development; and 3. machine-learning potential corrections can provide an avenue toward improving efficient semiempirical/DFTB QM/MM models for specific applications. The software infrastructure reported here enables new types of QM/MM- Δ MLP models to be developed and applied in

Amber to efficiently compute free energy surfaces and minimum free energy paths.

Nuclear quantum effects on guanine-thymine mispair tautomerization reactions

Table 2: Tautomer free energies and forward reaction barriers (kcal/mol) determined from classical and path integral molecular dynamics umbrella sampling.^a

Method	wGT→GT*		GT*→G*T		G*T→wGT	
	ΔA	$\Delta A^\ddagger$	ΔA	$\Delta A^\ddagger$	ΔA	$\Delta A^\ddagger$
Expt.	4.43	16.88	-0.62	9.21	-3.82	...
Classical MD						
PBE0/6-31G*	3.97(0.04)	20.41(0.05)	-0.91(0.03)	6.72(0.05)	-3.06(0.04)	17.02(0.05)
AM1/d	9.54(0.04)	23.51(0.06)	-1.36(0.03)	10.26(0.03)	-8.16(0.04)	15.36(0.04)
AM1/d+ML	3.67(0.07)	21.01(0.07)	-0.43(0.07)	7.06(0.07)	-3.24(0.07)	17.78(0.07)
GFN2-xTB	-2.44(0.06)	12.09(0.05)	1.94(0.08)	4.68(0.06)	0.50(0.06)	12.59(0.07)
DFTB3-D3	3.27(0.07)	10.91(0.08)	4.58(0.08)	10.41(0.08)	-7.85(0.09)	5.83(0.09)
DFTB3-D4(3b)	2.01(0.10)	10.81(0.09)	5.13(0.12)	10.75(0.09)	-7.14(0.12)	5.59(0.11)
DFTB3-D4(2b)	2.63(0.07)	10.75(0.07)	5.46(0.07)	10.91(0.06)	-8.09(0.07)	5.43(0.06)
PIMD						
AM1/d	7.98(0.07)	21.87(0.08)	-1.46(0.08)	6.90(0.06)	-6.51(0.09)	15.41(0.08)
AM1/d+ML	3.48(0.03)	20.65(0.04)	0.26(0.03)	4.21(0.08)	-3.75(0.04)	16.88(0.04)
GFN2-xTB	-3.10(0.06)	10.93(0.06)	1.70(0.05)	2.47(0.06)	1.34(0.06)	12.26(0.05)
DFTB3-D3	1.68(0.09)	10.59(0.08)	4.41(0.09)	7.96(0.08)	-6.03(0.09)	4.57(0.08)
DFTB3-D4(3b)	-0.57(0.08)	9.99(0.10)	5.12(0.07)	8.12(0.07)	-4.55(0.07)	5.44(0.09)
DFTB3-D4(2b)	2.17(0.07)	9.78(0.08)	4.20(0.08)	7.04(0.07)	-6.37(0.08)	3.40(0.08)

^a Each free energy profile was computed 4 times from independent sets of simulations. The tabulated values are the mean of the 4 trials. The numbers in parenthesis are the standard error of the mean. Experimental reference values were derived from rates measured in ref. 55, and free energy values approximated from transition state theory assuming a unit transmission coefficient.

In this section, we demonstrate the new interface with the i-PI software by calculating free energy profiles from PIMD simulation, as described in the Methods section. These calculations are considerably more computationally intensive (by roughly an order of magnitude, or more depending on the number of replicas used in the ring polymer Hamiltonian). Nonetheless, inclusion of nuclear quantum effects is important, especially for modeling chemical reactions that involve proton transfer events such as those presented here. Other recent

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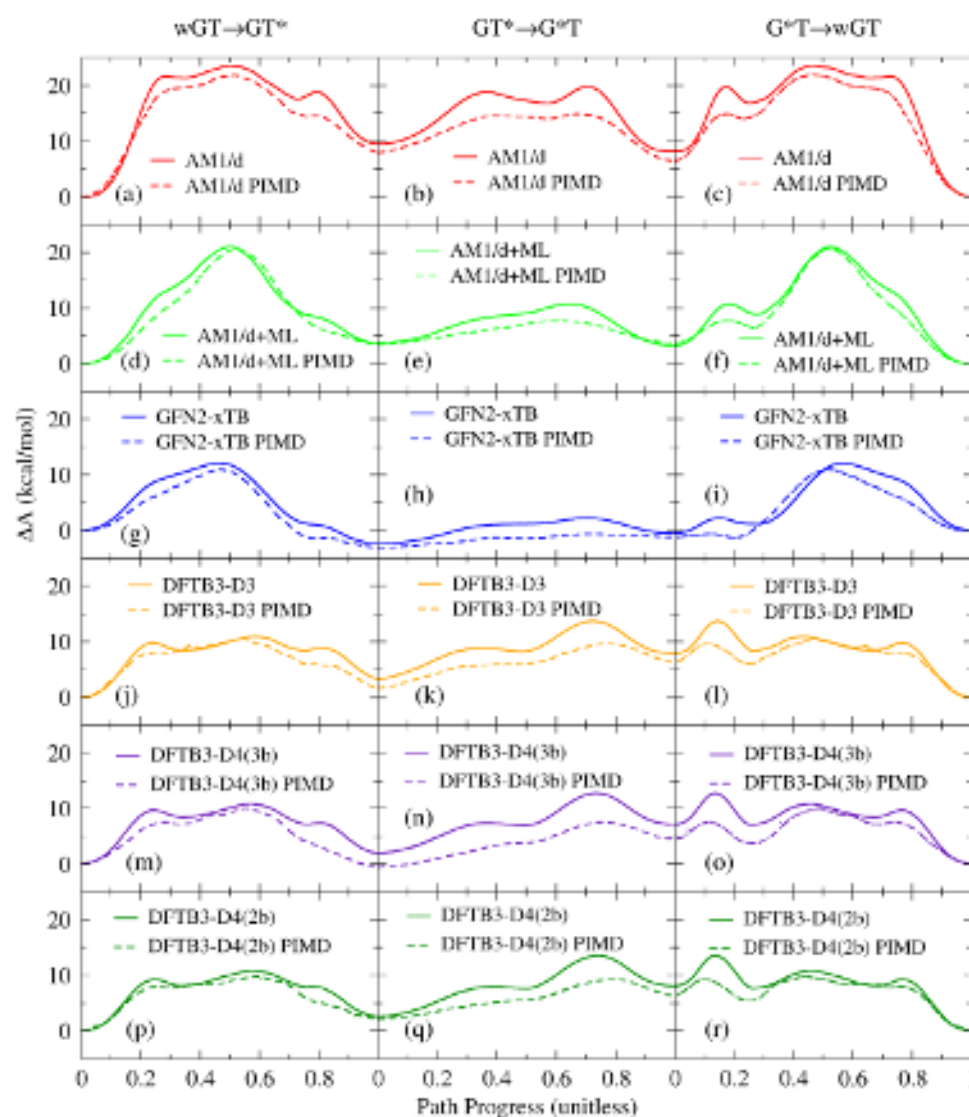


Figure 4: Classical and path-integral molecular dynamics free energy profiles for guanine-thymine mispair tautomerization reactions using different semiempirical/DFTB QM/MM and QM/MM- Δ MLP models described in the text: (a) $wGT \rightarrow GT^*$ (a,d,g,j,m,p); (b) $GT^* \rightarrow G^*T$ (b,e,h,k,n,q); (c) $G^*T \rightarrow wGT$ (c,f,i,l,o,r). Here “wGT” indicates a G-T wobble pair, and G^* and T^* are non-standard tautomer states of G and T, respectively. Profiles from classical and PIMD are shown as solid and dashed lines, respectively. Color schemes for different models are the same as for those shown in Figure 3.

works have addressed the issue of computational cost in PIMD simulations using fast density-functional tight-binding models¹⁰⁰ or machine learning potentials¹⁰ optimized to high-level reference data.

Figure 4 compares the classical (solid lines) and path-integral molecular dynamics (dashed lines) free energy profiles for different semiempirical/DFTB QM/MM and QM/MM- Δ MLP models. Table 2 (bottom) lists values of key stationary points along the free energy profiles calculated with PIMD shown in Figure 4 and compares them to corresponding classical and experimentally-derived reference values. Table S2 summarizes differences between classical and PIMD free energy values. Overall, the inclusion of nuclear quantum effects generally lowers the free energy barrier ($\Delta A^\ddagger$) for proton transfer steps, in some cases exceeding 3 kcal/mol, whereas the effect on ΔA is variable (ranging up to roughly ± 2.5 kcal/mol). The PIMD free energy profiles were calculated from the ring polymer centroid positions. These profiles generally have lower barriers than those produced from classical molecular dynamics. The apparent smoothing of the profile is due to the delocalization of the nuclear wave packet, which can partially be attributed to tunneling effects.^{101–103} The current demonstration examines differences between independently-calculated free energy profiles; however, other applications of i-PI can directly evaluate equilibrium and kinetic isotope effects from umbrella sampling using thermodynamic perturbation and frequency factors.^{21,104}

The main point of this section is to demonstrate that inclusion of nuclear quantum effects can have important quantitative effects on the free energy profiles and $\Delta A^\ddagger$ values for the tautomerization reactions considered here. These calculations are made practical in Amber with fast semiempirical/DFTB QM/MM and QM/MM- Δ MLP models, and enabled by the interface with i-PI.⁴⁶

Performance

We measured the performance of the B-DNA microcanonical QM/MM simulations shown in Fig. 2 on a single Intel Xeon E5-2630 v3 CPU core clocked at 2.40 GHz. Table 3 expresses

the performance as the number of classical molecular dynamics time steps per day. For example, 1,000 steps/day would correspond to 1 ps/day of sampling using a 1 fs time step. More efficient sampling with a longer integration time step may be obtained by using the “middle” thermostat scheme described in Refs. 105 and 106 in conjunction with hydrogen mass repartitioning.¹⁰⁷ The “QM/MM Ewald” timings use 10 Å real-space cutoffs, whereas the “QM/MM Cutoff” timings truncate the QM/MM interactions at 14 Å. The subheadings “Linked” and “File-based” refer to the communication between Sander and the QM program: Linked means there is direct communication via function calls, whereas File-based relies on disk input/output and system calls.

Table 3: Classical molecular dynamics performance using Sander with several QM/MM potentials. The values are time steps/day.

Potential	QM/MM Ewald	QM/MM Cutoff	QM/MM Cutoff
	Linked	Linked	File-based
DFTB3-D3	163,000	99,000	80,000
GFN2-xTB	133,000	88,000	80,000
AM1/d	133,000	86,000	...
AM1/d+ML	66,000	51,000	...
PBE0/6-31G*	200	...	...

Table 3 suggests that linking the semiempirical programs into the Sander executable increases the performance by 10%-to-20% over file-based communication. Direct linkage further improves the performance by enabling the use of the QM/MM Ewald method, which achieves stable dynamics with smaller real-space cutoffs. The single core performance of AM1/d, GFN2-xTB, and DFTB3-D3 are very similar. The inclusion of the DPRc Δ MLP halves the AM1/d performance; however, previous examination of DPRc timings found that it decreases the performance by only 10% when the Δ MLP is evaluated on an Nvidia V100 GPU. The AM1/d+ML performance on a single CPU core is 300 times faster than PBE0/6-31G* QM/MM evaluation using the HFDF *ab initio* program.

The high cost of *ab initio* QM/MM evaluation often prevents its use within PIMD simulations. To illustrate the cost of PIMD simulations, we measured the performance of the

Table 4: AM1/d QM/MM path integral molecular dynamics performance using i-PI and multiple Sander instances. N is the number of Sander instances. The path integral dynamics is propagated with 6 beads.

N	steps/day
1	17,000
2	27,000
3	37,000
4	37,000
5	37,000
6	60,000

wGT reactant state discussed in the previous section. The PIMD simulations were run with 6 beads; therefore, a pool of up to 6 Sander instances can be launched. Table 4 reports the simulation performance as the number of PIMD time steps evaluated per day. The total number of CPU cores is $N + 1$, where N is the number of Sander instances; the additional core is reserved for the i-PI dynamics program. At each time step, 6 potential energy evaluations are required for the corresponding set of 6 beads; therefore, running 4 or 5 Sander instances does not improve the 3-instance performance because they are not divisors of the number of beads. When 6 instances are used, the performance is about half of what is obtained during classical dynamics due to the communication between i-PI and the Sander instances.

Conclusion

We reported new integrated software infrastructure for conducting free energy simulations in the condensed phase under periodic boundary conditions with long-ranged PME/Ewald electrostatics using a wide range of fast QM/MM potentials made available through interfaces with DFTB+ and xTB. Further, integration with DeePMD-kit enables new QM/MM- Δ MLP models to be developed and efficiently applied. Nuclear quantum effects (beyond the harmonic approximation) can be treated using free energy surface sampling with path integral molecular dynamics. The software infrastructure reported here extends the capabilities of Amber for developing new QM/MM- Δ MLP models and using them to compute free en-

ergy surfaces and related properties for a wide range of applications. Near-future directions for development will involve expanding the scope of interoperability to include interfaces with enhanced sampling software, and in particular with WESTPA,^{49,50} a scalable software package for high-performance weighted ensemble simulation and analysis.

Supporting Information

A description of the DPRc neural network and tables of tautomeric reaction free energy differences.

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Data Availability

Example Sander input files and the trained DPRc neural network parameter sets for the B-DNA system can be downloaded from https://gitlab.com/RutgersLBSR/LBSR_SuppInfo. We are preparing tutorials describing how to use the new software infrastructure and making them available at <https://gitlab.com/RutgersLBSR/AmberTutorials>.

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