An analytical derivation of MC-SCF vibrational wave functions for the quantum dynamical simulation of multiple proton transfer reactions: Initial application to protonated water chains

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This paper presents an analytical derivation of a multiconfigurational self-consistent-field (MC-SCF) solution of the time-independent Schrödinger equation for nuclear motion (i.e., vibrational modes). This variational MC-SCF method is designed for the mixed quantum/classical molecular dynamics simulation of multiple proton transfer reactions, where the transferring protons are treated quantum mechanically while the remaining degrees of freedom are treated classically. This paper presents a proof that the Hellmann–Feynman forces on the classical degrees of freedom are identical to the exact forces (i.e., the Pulay corrections vanish) when this MC-SCF method is used with an appropriate choice of basis functions. This new MC-SCF method is applied to multiple proton transfer in a protonated chain of three hydrogen-bonded water molecules. The ground state and the first three excited state energies and the ground state forces agree well with full configuration interaction calculations. Sample trajectories are obtained using adiabatic molecular dynamics methods, and nonadiabatic effects are found to be insignificant for these sample trajectories. The accuracy of the excited states will enable this MC-SCF method to be used in conjunction with nonadiabatic molecular dynamics methods. This application differs from previous work in that it is a real-time quantum dynamical nonequilibrium simulation of multiple proton transfer in a chain of water molecules. © 1997 American Institute of Physics.

I. INTRODUCTION

Multiple proton transfer reactions play a critical role in many important chemical and biological processes. For example, a wide range of enzyme reactions, including those involving serine proteases,1,2 alcohol dehydrogenases,3 and carbonic anhydrases,4 require multiple proton transfer reactions. Moreover, in the proton pumping mechanisms of photosynthetic reaction centers,5,6 protons are transported across a membrane through a series of proton transfer steps involving the side chains of amino acid residues in the protein and water molecules. These proton pumps establish electrochemical potential gradients across biological membranes, which are essential for energy conversion in biological systems. The initial application in this paper focuses on proton transport along chains of hydrogen-bonded water molecules, which is thought to play an important role in the fast translocation of protons over large distances in these proton pumps.9 The new simulation methods developed in this paper will be applicable to a wide range of other multiple proton transfer reactions.

The computer simulation of proton transfer reactions in the condensed phase is particularly challenging because the light mass of the hydrogen atom being transferred gives rise to significant quantum mechanical effects such as hydrogen tunneling.10 Classical molecular dynamics simulations, in which all of the nuclei move classically, are incapable of describing the quantum mechanical behavior of the hydrogen atom. Moreover, an exact quantum mechanical treatment of all of the nuclei is computationally infeasible for systems involving more than a few atoms. As a result, a number of mixed quantum/classical molecular dynamics methods, in which a few nuclei are treated quantum mechanically and the remaining nuclei are treated classically, have been developed and applied to proton transfer reactions in solution.11–36 Most of these methods have been applied to single proton transfer reactions, where only one hydrogen atom is treated quantum mechanically, and are not easily extendable to processes involving coupled multiple proton transfer steps, where many hydrogen atoms must be treated quantum mechanically. The extension to coupled multiple proton transfer reactions is challenging because the correlation among the quantum mechanical protons must be included in a computationally tractable way. Methods based on the Feynman path integral formalism28–36 have been utilized to treat multiple hydrogen atoms quantum mechanically, but typically these methods employ a transition state theory approximation rather than directly predict real-time dynamical properties. (One notable exception is the recently developed centroid molecular dynamics method,36,37 which is a dynamical method based on the path centroid variable in Feynman path integration.)

One method that has been applied to the quantum dynamical simulation of multiple nuclei or vibrational modes
is the time-dependent self-consistent-field (TDSCF) method.\textsuperscript{38–43} In TDSCF, an $N$-particle wave function is approximated as a product of $N$ single-particle wave functions. In this way, the $N$-particle time-dependent Schrödinger equation can be separated into $N$ coupled single-particle equations of motion, which leads to substantial computational savings. Each quantum particle moves in a time-dependent mean potential that is obtained by averaging over the motion of all of the other quantum particles in the system. Typically the single-particle equations of motion and the mean potentials in which the quantum particles move must be solved self-consistently. In the application of TDSCF to mixed quantum/classical systems (often called the Q/C TDSCF method\textsuperscript{25,41–43}) the classical particles move in a time-dependent mean potential obtained by averaging over the motion of all of the quantum particles in the system. TDSCF has been extended to incorporate correlation among the quantum particles\textsuperscript{44–59} using, for example, multiconfigurational TDSCF methods,\textsuperscript{45–55} but not in the context of mixed quantum/classical simulations.

One limitation of TDSCF is that it cannot properly describe branching processes (i.e. processes involving multiple pathways).\textsuperscript{44,45} The accurate description of branching processes is critical in proton transfer reactions because typically there are two distinct states of very different character (i.e. one ionic and one covalent), and the system must experience different forces from each of these two distinct states. One dynamical method that can accurately describe branching processes is the “molecular dynamics with quantum transitions” (MDQT) method. In the formulation of MDQT, for a single proton transfer reaction,\textsuperscript{26} only the hydrogen atom being transferred is treated quantum mechanically and the remaining degrees of freedom in the system are treated classically. At each time step of the molecular dynamics simulation (i.e. for each new classical configuration) the adiabatic proton quantum states are calculated by solving the time-independent Schrödinger equation. The proton remains in a single adiabatic quantum state except for the possibility of instantaneous switches from one state to another. The algorithm used to determine when such a switch occurs ensures that for a large ensemble of trajectories, the fraction in any state at any time is the quantum probability as determined by integration of the time-dependent Schrödinger equation. Since a large number of trajectories are calculated, where each trajectory follows a single path, MDQT can accurately describe branching processes. Note that in the adiabatic limit, MDQT is equivalent to the standard adiabatic molecular dynamics method,\textsuperscript{16–18,22} where the system remains in a single adiabatic state. One advantage of MDQT is that it is valid in the adiabatic and nonadiabatic limits and in the intermediate regime.

The extension of both MDQT and the adiabatic method to processes involving multiple proton transfer reactions requires the accurate incorporation of the correlation among the quantum particles. In other words, the adiabatic states, which are solutions to the time-independent Schrödinger equation, must include the significant correlation. A single configuration (Hartree product) wave function does not include the significant correlation among the quantum protons for coupled multiple proton transfer reactions. This correlation can be incorporated in a number of ways, including configuration interaction methods (where the wave function is approximated as a linear combination of configurations comprised of fixed one-particle orbitals), multiconfigurational self-consistent-field (MC-SCF) methods (where both the coefficients of the configurations and the one-particle orbital coefficients are optimized), and perturbation methods. These methods are analogous to their electronic counterparts, except that electronic configurations are represented as Slater determinants rather than as Hartree products. Previously configuration interaction methods\textsuperscript{60,61} have been used to include correlation in solutions of the time-independent Schrödinger equation for vibrational modes. This paper presents the first rigorous MC-SCF method for solution of the time-independent Schrödinger equation for vibrational modes.

In a previous paper one of us\textsuperscript{62} presented the multiconfigurational MDQT (MC-MDQT) method, which combines an MC-SCF method with MDQT to allow the quantum mechanical treatment of multiple hydrogen atoms. The adiabatic states are expanded in a basis set of single configurations that are products of one-particle states calculated using effective one-particle Hamiltonians derived from the occupied adiabatic state. This method was successfully applied to several simple model systems. The advantage of this previous method is that it provides a clear physical picture of the reaction dynamics while also incorporating the significant correlation between the quantum particles. Each proton can be viewed as moving in a potential determined by both the occupied adiabatic state and the classical configuration. The one-particle adiabatic states can be calculated for each proton, and except for during branching processes each proton can be viewed as occupying a single one-particle adiabatic state. The multiconfigurational mixing that occurs during branching processes is required to move from one single configurational adiabatic state to another. One disadvantage of this previous method is that it is not variational. Another disadvantage is that the Hellmann–Feynman forces,

\[
F^\mu = -\langle \Phi_k(r;R) | \partial H(r;R) / \partial R_\mu | \Phi_k(r;R) \rangle, \tag{1}
\]

are not rigorously equal to the “exact” forces defined as

\[
F^\mu = -\frac{\partial}{\partial R_\mu} \langle \Phi_k(r;R) | H(r;R) | \Phi_k(r;R) \rangle. \tag{2}
\]

Here $\Phi_k(r;R)$ is the occupied multiconfigurational adiabatic state and $\mu$ indicates the $x$, $y$, or $z$ component of a particular classical coordinate.

Although the Hellmann–Feynman force is identical to the exact force for the exact wave function, it has been shown to differ from the exact force for some types of approximate electronic wave functions.\textsuperscript{63,64} As a result, Pulay derived the so-called Pulay corrections to the Hellmann–Feynman force for electronic wave functions.\textsuperscript{63,64} The analogous correction terms for proton (or vibrational) wave functions are numerically difficult to calculate with the approximate MC-SCF method presented in Ref. 62.
In this paper we present an analytical derivation of a variational MC-SCF method for vibrational modes. We also prove that the Hellmann–Feynman force in Eq. 1 is rigorously identical to the exact force in Eq. 2 (i.e. all Pulay corrections vanish) with an appropriate choice of basis set. We apply this new MC-SCF method in conjunction with an adiabatic mixed quantum/classical molecular dynamics method to multiple proton transfer in a protonated linear chain of three hydrogen-bonded water molecules. We determine that nonadiabatic effects are insignificant for the trajectories studied in this paper. Only the two hydrogen-bonding hydrogen atoms are treated quantum mechanically. We utilize the PM6 dissociable polarizable potential surface developed by Stillinger and co-workers.65–67 We test the new variational MC-SCF method by comparing our results to a complete configuration interaction calculation.

Recently numerous simulations of proton transfer in water have been performed.34–36,68–71 In particular, Pomes and Roux used Feynman path integral methods to study the equilibrium properties of protonated chains of water molecules,34,35 and Lobaugh and Voth used the centroid molecular dynamics method to study the dynamics of a single proton transfer reaction in water.36 The work presented in this paper differs from previous work in that we perform quantum dynamical nonequilibrium simulations of multiple proton transfer reactions in chains of water molecules. Note that only the transferring hydrogen atoms are treated quantum mechanically due to computational limitations arising from the need to calculate multidimensional integrals for the many-body polarization terms in the PM6 potential. Moreover, in this paper we employ the adiabatic molecular dynamics method, in which the system remains in the ground proton quantum state. However, we integrate the time-dependent Schrödinger equation to monitor the quantum amplitudes for the sample trajectories and determine that nonadiabatic effects are insignificant (i.e. the probability of remaining in the ground proton quantum state is larger than 99.9%). Thus for these trajectories identical results should be obtained using a nonadiabatic molecular dynamics method such as MDQT. We are currently simulating water chains with a combination of this MC-SCF method and the MDQT method.

An outline of this paper is as follows. In Section II we present the derivation of this new MC-SCF method and the proof that the Hellmann–Feynman force is exact for an appropriate choice of basis set. Section III describes the results of the initial application of this method to multiple proton transfer in a protonated chain of three hydrogen-bonded water molecules. Section IV summarizes our results.

II. THEORY

A. MC-SCF

Our general system consists of \( N \) quantum particles (or vibrational modes) with the Hamiltonian

\[
H = \sum_i t_i + V(\mathbf{r}),
\]

where \( t_i \) is the kinetic energy operator for particle \( i \), \( \mathbf{r} \) is a vector representing the coordinates of the quantum particles (or vibrational modes), and \( V(\mathbf{r}) \) is the potential energy of the system. We approximate the wave function for this system by a normalized linear combination of single configurations:

\[
\Phi(\mathbf{r}) = \sum_j c_j(\mathbf{r}) \phi_j(\mathbf{r}),
\]

where \( c_j(\mathbf{r}) \) are products of the orthonormal one-particle states \( \phi_j(\mathbf{r}) \) that only the transferring hydrogen atoms are treated quantum mechanically. However, we integrate the time-dependent Schrödinger equation to monitor the quantum amplitudes for the sample trajectories and determine that nonadiabatic effects are insignificant for the trajectories studied in this paper. Only the two hydrogen-bonding hydrogen atoms are treated quantum mechanically. We utilize the PM6 dissociable polarizable potential surface developed by Stillinger and co-workers.65–67 We test the new variational MC-SCF method by comparing our results to a complete configuration interaction calculation.
and
\[
\frac{\partial}{\partial d'_j} \left[ E - \eta \left( \sum_{j} d_j - 1 \right) \right] = 0
\]  
(10)

and
\[
\frac{\partial}{\partial c^{(k)}_{ij}} \left[ E - \sum_{ij} \epsilon_{ij}^{(k)} \left( \sum_{\alpha \beta} c^{(k)}_{\alpha \beta} S^{(k)}_{\alpha \beta} - \delta_{ij} \right) \right] = 0,
\]  
(11)

where \( \eta \) and the \( \epsilon^{(k)}_{ij} \)s are Lagrange multipliers.

If we express the energy as
\[
E = \sum_{ij} d_i d_j \langle \xi_i | H | \xi_j \rangle,
\]  
(12)

Eq. 10 can be simplified to the standard eigenvalue equation
\[
\mathbf{H} d = \eta d,
\]  
(13)

where the matrix \( \mathbf{H} \) has matrix elements \( H_{ij} = \langle \xi_i | H | \xi_j \rangle \) and the vector \( d \) has elements \( d_j \). As in standard electronic structure theory, the coefficients \( d_j \) can be calculated by diagonalizing the \( \mathbf{H} \) matrix. Note that for the general Hamiltonian expressed in Eq. 3,
\[
H_{ij} = \langle \xi_i | V(r) | \xi_j \rangle + \sum_{p} \left( \prod_{i \neq p} \delta_{ij - j_i} \right) \langle \phi_{ip}^{(p)} | t_p | \phi_{ip}^{(p)} \rangle.
\]  
(14)

For convenience we adopt the notation of Ref. 47 for the simplification of Eq. 11. Thus we define \( J^{(k)} = \{ (j_1 \ldots j_{k+1} k_{k+2} \ldots j_N) \} \), which is \( J \) without the index for particle \( k \). Note that there are \( M_k = \prod_{j \neq k} M_j \) values of \( J^{(k)} \). We also define
\[
e^{(k)}(r) = \phi_{j_1}^{(1)} \ldots \phi_{j_{k-1}}^{(k-1)} \phi_{j_k}^{(k+1)} \ldots \phi_{j_N}^{(N)},
\]  
(15)

which is the configuration \( \xi_J \) without the basis function \( \phi_{j_k}^{(k)} \), and
\[
D^{(k)}(J) = \phi_{j_1}^{(1)} \cdots \phi_{j_{k-1}}^{(k-1)} \phi_{j_k}^{(k+1)} \cdots \phi_{j_N}^{(N)},
\]  
(16)

which is the coefficient \( d_j \) with \( J \) equal to \( J^{(k)} \) with the addition of \( j_k = \) (analogous to a single excitation coefficient in electronic structure theory). Note that for convenience we omit the superscript \( k \) on the index \( J \) when \( J \) is the subscript of a quantity including the superscript \( k \) (e.g. \( \xi_J^{(k)} \)). Using this notation, the total energy can be expressed as
\[
E = \sum_{p \neq k} \left( \sum_{i \neq p} \left( \delta_{j_i - j_p} \right) \right) \langle \phi_{ip}^{(p)} | t_p | \phi_{ip}^{(p)} \rangle + \sum_{i \neq k} \delta_{j_i - j_k} t_k,
\]  
(17)

where
\[
H_{ij}^{(k)} = \langle \xi_J^{(k)} | H | \xi_J^{(k)} \rangle
\]  
(18)

for the general Hamiltonian in Eq. 3. Substituting this energy into Eq. 11 and simplifying gives the matrix equation
\[
\begin{pmatrix}
\bar{H}_{11}^{(k)} & \bar{H}_{12}^{(k)} & \cdots & \bar{H}_{1m_k}^{(k)} \\
\bar{H}_{21}^{(k)} & \bar{H}_{22}^{(k)} & \cdots & \bar{H}_{2m_k}^{(k)} \\
\vdots & \vdots & \ddots & \vdots \\
\bar{H}_{m_k1}^{(k)} & \bar{H}_{m_k2}^{(k)} & \cdots & \bar{H}_{m_km_k}^{(k)}
\end{pmatrix}
\begin{pmatrix}
c_1^{(k)} \\
c_2^{(k)} \\
\vdots \\
c_{m_k}^{(k)}
\end{pmatrix}
= S^{(k)}
\begin{pmatrix}
\epsilon_1^{(k)} \\
\epsilon_2^{(k)} \\
\vdots \\
\epsilon_{m_k}^{(k)}
\end{pmatrix},
\]  
(19)

where each element \( c^{(k)}_n \) is a \( k \)-dimensional vector with elements \( c^{(k)}_{i \alpha} \), the overlap matrix \( S^{(k)} \) is a \( k \times k \) matrix with elements \( S^{(k)}_{\alpha \beta} \), and each element \( \bar{H}_{ij}^{(k)} \) is a \( k \times k \) matrix with elements
\[
\bar{H}_{ij}^{(k)} = \sum_{p \neq k} \left( \delta_{j_i - j_p} \right) \langle \phi_{ip}^{(p)} | t_p | \phi_{ip}^{(p)} \rangle + \sum_{i \neq k} \delta_{j_i - j_k} t_k,
\]  
(20)

This matrix equation can be solved in a variety of ways. As described by Hinze,\textsuperscript{72} a sufficient and necessary condition for the solution of Eq. 19 is a symmetric \( \epsilon^{(k)} \) matrix:
\[
\epsilon_{ij}^{(k)} = \epsilon_{ij}.
\]  
(21)

The elements of the \( \epsilon^{(k)} \) matrix can be calculated as follows:
\[
\epsilon_{ij}^{(k)} = \sum_{i \neq j} \langle \bar{c}_j^{(k)} | \bar{H}_{ij}^{(k)} | \bar{c}_i^{(k)} \rangle.
\]  
(22)

Numerically, the \( \epsilon^{(k)} \) matrix can be symmetrized by an iterative procedure, where each iteration involves the successive Jacobi rotation of pairs of states \( \bar{c}_i^{(k)} \) and \( \bar{c}_j^{(k)} \).\textsuperscript{72,73}

The calculation of the coefficients \( c_{i \alpha}^{(k)} \) also requires an iterative procedure, where each iteration involves cycling through all quantum particles \( k \). For each particle \( k \) the \( \epsilon^{(k)} \) matrix is symmetrized by the above procedure and the Hamiltonian matrices \( \bar{H}_{ij}^{(k)} \) are recalculated using the new coefficients \( c_{i \alpha}^{(k)} \). This iterative procedure is continued until all of the \( \epsilon^{(k)} \) matrices are symmetric to within a specified tolerance.

Moreover, the calculation of the coefficients \( d_j \) and \( c_{i \alpha}^{(k)} \) also requires an iterative procedure, where first the coefficients \( c_{i \alpha}^{(k)} \) are calculated by solving Eq. 19 and then the coefficients \( d_j \) are calculated by solving Eq. 13 as described above. This iterative procedure is continued until self-consistency. A schematic picture of the entire iterative procedure is depicted in Figure 1.

Excited proton quantum states have been shown to play a significant role in some proton transfer reactions.\textsuperscript{26} The MC-SCF methods described in this section can be used to calculate excited states as well as ground states. In this case the coefficients \( d_j \) in Eq. 4 become \( d_{j K} \), where \( K \) indicates a particular multiconfigurational adiabatic state, and the vector \( d \) in Eq. 13 becomes a matrix with elements \( d_{j K} \). These excited states are important when the MC-SCF method is
combined with the surface hopping MDQT method for nonadiabatic dynamical simulations of multiple proton transfer reactions.

**B. Hellmann-Feynman theorem**

As mentioned above, the aim of this paper is to develop a rigorous MC-SCF method for mixed quantum/classical molecular dynamics methods, where a small number of degrees of freedom are treated quantum mechanically (with coordinates \( \mathbf{r} \)), while the remaining degrees of freedom are treated classically (with coordinates \( \mathbf{R} \)). In this case the Hamiltonian depends on both quantum and classical degrees of freedom (i.e. \( H(\mathbf{r};\mathbf{R}) \)), and the coefficients depend on the classical degrees of freedom (i.e. \( d_j(\mathbf{R}) \) and \( c_{ia}^{(k)}(\mathbf{R}) \)). In addition, each basis function \( N_{ia}^{(k)} \) depends on a set of parameters \( P_{ia}^{(k)} \) (including, for example, the center and the width), which may depend explicitly on the classical degrees of freedom.

In order to calculate the forces on the classical degrees of freedom the following quantities must be calculated for each component \( R_{\mu} \), where \( \mu \) indicates both a classical particle and a component (i.e. \( x, y, \) or \( z \)):

\[
F_{R_{\mu}} = -\frac{\partial E(\mathbf{R})}{\partial R_{\mu}}
\]

\[
= -\frac{\partial}{\partial R_{\mu}} \langle \Phi(d_j,c_{ia}^{(k)},P_{ia}^{(k)})|H(\mathbf{r};\mathbf{R})|\Phi(d_j,c_{ia}^{(k)},P_{ia}^{(k)}) \rangle.
\]

(23)

Often the Hellmann-Feynman force
is used to approximate the exact force in Eq. 23. Although the Hellmann–Feynman force is identical to the exact force for exact wave functions, it has been shown to differ significantly from the exact force for some types of approximate wave functions. As a result, substantial effort has been directed toward calculating the Pulay corrections to the Hellmann–Feynman forces in the context of electronic wave functions. In this section we show that the Hellmann–Feynman force is rigorously identical to the exact force for mixed quantum/classical molecular dynamics simulations using the MC-SCF formulation derived in this paper with an appropriate choice of basis functions.

The expression in Eq. 23 can be divided into four terms, corresponding to the dependence of the Hamiltonian on $d_j$, $c_{ia}^{(k)}$, and $p_{av}^{(k)}$. Thus, the total derivative of $E$ can be written as

$$
\frac{dE}{dR_\mu} = \langle \Phi | \frac{\partial H}{\partial R_\mu} | \Phi \rangle + \sum_j \frac{\partial E}{\partial d_j} \frac{\partial d_j}{dR_\mu} + \sum_{k} \sum_{i} \sum_{\alpha} \frac{\partial E}{\partial c_{ia}^{(k)}} \frac{\partial c_{ia}^{(k)}}{dR_\mu} + \sum_{k} \sum_{i} \sum_{\alpha} \frac{\partial E}{\partial p_{av}^{(k)}} \frac{\partial p_{av}^{(k)}}{dR_\mu}.
$$

(25)

The first term $\langle \Phi | \frac{\partial H}{\partial R_\mu} | \Phi \rangle$ is just the negative of the Hellmann–Feynman force. The second term is

$$
\sum_j \frac{\partial E}{\partial d_j} \frac{\partial d_j}{dR_\mu} = 2 \eta \sum_j d_j \frac{\partial d_j}{dR_\mu} = \eta \frac{d}{dR_\mu} \sum_j d_j = 0.
$$

(26)

The first equality arises from Eq. 10, and the second equality arises from the normality constraint Eq. 9. Thus, the second term vanishes.

The third term is

$$
\sum_{k} \sum_{i} \sum_{\alpha} \frac{\partial E}{\partial c_{ia}^{(k)}} \frac{\partial c_{ia}^{(k)}}{dR_\mu} = \sum_{k} \sum_{ij} \sum_{\alpha} \frac{\partial E}{\partial c_{ia}^{(k)}} \frac{\partial c_{ia}^{(k)}}{dR_\mu} = \sum_{k} \sum_{ij} \sum_{\alpha} \frac{\partial E}{\partial c_{ia}^{(k)}} \frac{\partial c_{ia}^{(k)}}{dR_\mu}.
$$

(27)

The first equality arises from Eq. 11, and the second equality arises from differentiation of the orthonormality condition in Eq. 8 with respect to $R_\mu$. As discussed below, for simulation of proton transfer reactions the basis functions can be chosen such that $\partial d_j^{(k)}/\partial R_\mu = 0$, in which case this third term also vanishes.

The fourth term can be problematic in electronic MC-SCF calculations. As discussed below, however, for proton transfer reactions the basis functions can be chosen to be independent of the classical coordinates (i.e. $\partial p_{av}^{(k)}/\partial R_\mu = 0$ for all $\alpha$, $\nu$, and $k$). In this case the fourth term vanishes.

In order to illustrate the conditions under which the third and fourth terms vanish, we will consider the case in which each proton is confined to one-dimensional motion. The extension to three-dimensional motion is conceptually straightforward. The first condition is that the center of basis function $\chi_a^{(k)}$ is indicated by $r_{ca}^{(k)}$, which is a constant scalar quantity equal to the distance of the center of the basis function $\chi_a^{(k)}$ relative to a specified origin $O^{(k)}(R)$ in a direction $\hat{e}^{(k)}(R)$. The origin and axis direction are the same for all basis functions for a given particle $k$, and the proton coordinate $r_k$ is also a scalar quantity indicating the distance relative to the same origin $O^{(k)}(R)$ in the same direction $\hat{e}^{(k)}(R)$. The second condition is that the basis functions depend only on $r_k-r_{ca}^{(k)}$ and other constant parameters (such as the width) that are independent of the classical coordinates. If these two conditions are satisfied then the basis functions and their overlaps do not depend on the classical coordinates (i.e. $\partial p_{av}^{(k)}/\partial R_\mu = 0$ and $\partial d_j^{(k)}/\partial R_\mu = 0$), so the third and fourth terms vanish. Note that these are sufficient but not necessary conditions for the third and fourth terms to vanish.

These conditions are easily satisfied for the typical situation in which each proton is confined to the region between a different pair of nuclei $N1$ and $N2$ (which are oxygen nuclei for the case of a chain of water molecules). For one-dimensional motion, the proton can be confined to move along the $N1-N2$ bond axis. In this case, the basis function centers can be chosen to lie along this bond axis at a constant distance from an origin also defined to be along this bond axis. The proton coordinate and basis function centers are measured relative to the same origin along this bond axis. This situation is illustrated schematically in Figure 2, which depicts the nuclei $N1$ and $N2$, the origin $O$ (chosen to be the midpoint of the $N1-N2$ bond), and two possible basis function centers $r_{ca}$ and $r_{c\beta}$. (Note that $r_{ca}$ and $r_{c\beta}$ are constant distances from the origin $O$ along the $N1-N2$ axis.) Even as the nuclei $N1$ and $N2$ move in three-dimensional space and the distance between them changes, the overlap between basis functions centered at $r_{ca}$ and $r_{c\beta}$ will remain constant because the distance between these basis functions remains constant. Thus, the third and fourth terms vanish, and the Hellmann–Feynman forces are rigorously identical to the exact forces. Note that since $r_{ca}$ and $r_{c\beta}$ remain fixed relative to the origin along the bond axis, they cannot respond to changes in the shape of the potential curve (e.g. movement of the minima in a double well potential) and hence are not the optimal basis functions for all classical configurations. Thus several sets of basis functions must be centered at various positions along the $N1-N2$ axis to span the entire region between $N1$ and $N2$. These basis functions must be
tested to ensure an accurate description of the wave function for all physically attainable classical configurations. For our simulations of chains of water molecules, we found that including three sets of basis functions centered at three different positions was adequate.

Note that the potential \( V(r;R) \) typically depends explicitly on the three-dimensional coordinates \( R_{ij} \) of the protons, so it can also be written as \( V(R_{ij}, R) \). Using the above formalism, the three-dimensional coordinates of the protons are

\[
R_{ij}^{(k)}(R) = O^{(k)}(R) + r_i \epsilon^{(k)}(R).
\]

Thus, the Hellmann-Feynman force can be expressed as

\[
F_{RF}^{(k)}(R) = -\left( \Phi \frac{\partial V(R_{ij}, R)}{\partial R_{ij}} + \sum_k \nabla R_{ij}^{(k)} V(R_{ij}, R) \right)
\]

\[
= \frac{\partial R_{ij}^{(k)}}{\partial R_{ij}} \frac{\partial V(R_{ij}, R)}{\partial R_{ij}} \Phi.
\]

C. Comparison to previous approximate MC-SCF method

Reference 62 presents an approximate MC-SCF method in which the one-particle states are calculated by solving the eigenvalue equation

\[
h_{ij}^{(k)} \phi_j^{(k)}(r_k) = \epsilon_j^{(k)} \phi_j^{(k)}(r_k),
\]

where

\[
h_{ij}^{(k)} = I_j + \sum_{j=1}^Q d_{ij} R^{(k)} \left( \prod_{i \neq k} \phi_j^{(i)}(r_i) \right) V(r;R) \left( \prod_{i \neq k} \phi_j^{(i)}(r_i) \right).
\]

Here \( K \) indicates the occupied multiconfigurational adiabatic state as determined using MDQT. For the purposes of this paper we will indicate this previous approximate MC-SCF method as MC-SCF* to distinguish it from the current variational MC-SCF method. One advantage of the MC-SCF* method is that it provides a clear physical picture of the reaction dynamics. Each proton can be viewed as moving in a potential determined by both the occupied adiabatic state and the classical configuration. The one-particle adiabatic states can be calculated for each proton, and except for during branching processes each proton can be viewed as occupying a single one-particle adiabatic state. The multiconfigurational mixing that occurs during branching processes is required to move from one single configurational adiabatic state to another. The MC-SCF* method has been shown to incorporate the significant correlation for a series of simple model systems.62

The disadvantages of the MC-SCF* method are that it is not variational and the Hellmann-Feynman forces on the classical particles are not rigorously exact. We have also found that although the MC-SCF method is a bit more complicated to program, for the systems studied to date the MC-SCF method is slightly computationally faster than the MC-SCF* method.

III. NUMERICAL METHODS AND RESULTS

A. System and potential model

Multiple proton transfer in chains of water molecules is a biologically important process in which both quantum dynamical effects and correlation between quantum particles are expected to be important. Recently Pomès and Roux simulated small chains of water molecules using equilibrium Feynman path integral methods. The advantage of our MC-SCF method over such methods is that we can also study dynamical properties of multiple proton transfer reactions. In this paper we apply the MC-SCF method described above to a protonated linear chain of three hydrogen-bonded water molecules.

In order to model the interactions in the system we use the PM6 dissociable polarization model for water developed by Stillinger and co-workers.65–67 The basic elements of this model are \( \mathrm{H}^+ \) and \( \mathrm{O}^{2-} \) atoms, which allows the full dissociation of water into ionic fragments. The oxygen atoms are polarizable, so the interaction potential consists of both pairwise additive terms and many-body polarization terms due to the induced dipole moments. The PM6 model was parametrized to reproduce the structures and energies of small cat-ionic and anionic water clusters. In addition, the PM6 model has been shown to provide a qualitatively reasonable description of proton transfer in \( \mathrm{H}_2\mathrm{O}_2^+ \).35 At the minimum energy structure the potential for the proton is a single well, but as the donor–acceptor distance increases the potential evolves into a double well, and the barrier height increases with donor–acceptor distance. However, as shown in Ref. 35, the dependence of the barrier height on the donor-acceptor distance obtained from the PM6 model differs significantly from the dependence obtained from \( \text{ab initio} \) calculations at the Hartree-Fock 4-31G level. In order to achieve a more quantitatively accurate potential surface, methods such as density functional theory68,74 could be implemented. Unfortunately, these more sophisticated methods are currently computationally prohibitive for our quantum dynamical simulations. The PM6 model is suitable for our purposes, however, because it is dissociable, predicts qualitatively accurate barrier heights for proton transfer in small water clusters, and is computationally fast enough for our quantum dynamical simulations.

B. Simulation details

For the simulation of water molecules within the mixed quantum-classical simulation framework, a classical description for the oxygen atoms is expected to suffice, while the hydrogen atoms are expected to require a quantum mechanical description. Unfortunately, the quantum mechanical treatment of all seven hydrogen atoms in our system using MC-SCF is computationally impractical. Note that the main computational limitation is the calculation of the matrix elements, which involves multidimensional integrals due to the many-body terms in the PM6 model for water, and not from the MC-SCF procedure. With our current methodology we could treat up to four nuclei quantum mechanically, and if
we obtain a potential including only three- and four-body terms we could treat more nuclei quantum mechanically. Therefore we apply the quantum mechanical treatment to only those hydrogen atoms that are hydrogen bonded in an equilibrated classical chain of water molecules. The other protons are treated classically, resulting in a total of two “quantum” protons for the system under study. An example of a starting configuration of the system is shown in Figure 3, where the protons that are treated quantum mechanically are labeled $H_A$ and $H_B$, respectively. To avoid coupling between the motion of the “quantum” protons and the OH-bond vibrational modes of the “classical” protons we constrain the latter at a fixed OH-bond length of 0.9584 Å (the equilibrium value). Moreover, the quantum protons are restricted to one-dimensional motion on the axis spanned by the two neighboring oxygen atoms, i.e. in Figure 3 protons $H_A$ and $H_B$ are restricted to move on the O1-O2 axis and O2-O3 axis, respectively. These constraints prohibit reorientations of the water molecules, which would change the identity of the hydrogen-bonding protons. (Note that the distances between oxygen atoms are not constrained.) In order to keep the chain approximately linear it is placed in a channel, i.e. harmonic restraints pull the oxygen atoms back to the central axis of the channel when their position is too far off-center, as described in Ref. 35. We used the same channel radius of 0.75 Å and force constant of 10 kcal/(mol Å) as in Ref. 35. The channel is aligned along the $x$ axis.

The basis functions $\chi_\alpha^{(k)}$ in the expansion of the one-particle wave functions are of the form of the solutions for a quantum mechanical simple harmonic oscillator:

$$\chi_\alpha^{(k)}(r) = 2^{-\mu/2} \pi^{1/4}(\mu !)^{-1/2} \gamma^{1/2} H_{\mu} \left[ \gamma(r-r_c) \right] \times \exp[ -\gamma^2 (r-r_c)^2/2 ],$$

where $\mu$ is an integer, $H_{\mu}(x)$ is a Hermite polynomial, and the index $\alpha$ on the basis function represents a pair of values for $\mu$ and $r_c$. For each quantum proton we use 21 basis functions consisting of 3 sets of 7 basis functions (where $\mu = 0 \ldots 6$ for each set) centered at $r_{ca}^{(k)} = 0$ (chosen to be the midpoint between the two oxygen atoms) and $r_{ca}^{(k)} = \pm 0.5$ Å. In an equilibrated chain of water molecules the O-O distance is $\sim 3$ Å, in which case the centers at $r_{ca}^{(k)} = \pm 0.5$ Å correspond roughly to the minima of the double well potential.

The center at the origin is included to accurately describe the proton wave functions for a single well potential. All basis functions have the same characteristic frequency of $\omega = 2000$ cm$^{-1}$, which corresponds to $\gamma = 7.732$ Å$^{-1}$ in Eq. 33. These basis functions were tested to ensure that they adequately span the region between the two oxygen atoms. The wave functions are represented on one-dimensional grids along the O-O axes. These grids span 3 Å and are centered around the origin $r^{(k)} = 0$ for each quantum proton. We use 51 grid points per one-dimensional grid. We performed two types of MC-SCF simulations. In the first type, only the two lowest energy adiabatic eigenstates for each quantum proton are included, i.e. $m_k = 2$ for each proton and the number of included configurations is $Q = 4$. In the second type, the three lowest energy adiabatic eigenstates for each quantum proton are included, i.e. $m_k = 3$ for each proton and the number of included configurations is $Q = 9$. The convergence of the simulation results with respect to all above stated parameter values was tested, and we verified that use of these values captures the essential physics.

In the complete configuration interaction description for our system, $m_k = 21$ for each quantum proton, and the one-particle states $\phi^{(k)}(r_c)$ are the pure basis functions $\chi_\alpha^{(k)}(r_c)$. In this case there are $Q = 21^2$ configurations for our system. (Note that the complete configuration interaction description becomes computationally impractical for more than two quantum protons.) As mentioned above, in our simulations $m_k = 2$ or 3 for each quantum proton, so the number of configurations is $Q = 4$ or 9 for our system. This reduction of the number of configurations could lead to qualitatively incorrect results if a nonphysical starting guess for the wave function is chosen. By comparison to the complete configuration interaction description, we determined that an excellent starting guess for the wave function can be obtained using the effective Hamiltonians derived in Ref. 62. Thus, for each classical molecular dynamics time step we initialize the one-particle expansion coefficients $c_{ia}^{(k)}$ using the effective Hamiltonian in Eq. 32 and then initialize the configuration interaction coefficients $d_{ij}$ using these one-particle wave functions. After this initialization the MC-SCF procedure described in Sec. II A is performed to ensure that the Hellmann–Feynman forces are correct. We have found that this procedure is more accurate than using the coefficients from the previous time step as an initial guess.

The classical equations of motion are integrated using the RATTLE method for constrained molecular dynamics, which is based on the velocity Verlet algorithm, using a time step of 0.0625 fs. These initial simulations are adiabatic, where the system remains in the ground adiabatic multiconfigurational state. However, we integrate the time-dependent Schrödinger equation to obtain the occupation probability of the multiconfigurational adiabatic states at each time step in order to gain insight into the importance of nonadiabatic effects. For these trajectories we found that nonadiabatic effects are insignificant (i.e. the probability of remaining in the ground proton quantum state is larger than 99.9%). Thus for this system we should obtain identical results using a method such as MDQT to incorporate nonadiabatic effects. We integrated about 10 trajectories with different starting conditions. These trajectories ranged from 62.5 fs to 1 ps in length. In
the remainder of this section we will discuss the performance of the MC-SCF method using one trajectory as an example. We emphasize that the initial simulation presented in this paper is useful only as a numerical test of the new MC-SCF method. In order to elucidate the physical process of multiple proton transfer in chains of water, we are currently simulating a large number of trajectories with different starting conditions. For the sample trajectory we generated the starting conditions by classically equilibrating the chain while constraining proton $H_A$ to be on the left end of the chain, as depicted in Fig. 3. In the equilibrium configuration for this chain, both protons $H_A$ and $H_B$ are bonded to the middle O2 oxygen atom. Thus Fig. 3 represents a nonequilibrium starting configuration for the mixed quantum/classical molecular dynamics simulations. These starting conditions are intended to mimic the situation in a transmembrane protein, where a proton is transferred from an amino acid to one end of a water chain.

In the first stage of the classical equilibration, the sample trajectory is equilibrated classically for 100 ps as an $H_2O^+$ molecule and 2 water molecules constraining all bond lengths within the individual molecules. For this first stage of the equilibration the temperature is controlled by simple velocity rescaling to maintain a temperature of 300 K. In the second stage of classical equilibration, the two protons that will be designated “quantum” protons for the mixed quantum/classical simulations are constrained on the O-O axes without constraining bonds involving these specific hydrogen atoms but still constraining all other bond lengths within the individual molecules. (Note that the “quantum” protons are chosen to be the hydrogen-bonding protons.) The purpose of this second stage of equilibration is to decrease the nonequilibrium effects caused by the sudden change in the OHO angle from 175 to 180 degrees in the classically equilibrated chain for a shorter period of time (10 ps) to avoid possible “classical” transfer of the protons. For the second stage of the equilibration and the mixed quantum/classical simulations the temperature control is switched off and evolution continues in a microcanonical ensemble.

The MC-SCF simulations are more than one order of magnitude faster than the complete configuration interaction simulations. (However, note that no attempts were made to optimize the complete configuration interaction simulations.) For MC-SCF the integration of a thousand time steps typically takes 1.5 hrs on an IBM RISC/6000-390, and the total energy is well conserved (better than 1 part in $10^{-6}$) in our constant NVE simulations.

C. Results

Figure 4 shows some snapshots of the time evolution of the configurations in our sample trajectory. The quantum protons are obviously wave functions rather than particles, but for illustrative purposes we depict them as particles centered at the expectation values of their coordinates. Also OH-bonds are drawn when the OH-distance is in the range of an OH-bond in water. As explained in the previous paragraph, we start the trajectory with an equilibrated $H_2O^+$ at the left end of the chain, as depicted in Fig. 3. Due to the importance of quantum effects the quantum proton $H_A$ transfers almost instantaneously from the O1 to the O2 atom, as shown in Fig. 4(a). The second quantum proton $H_B$ then gets pushed off O2 so that its bond breaks, as depicted in Fig. 4(b). At this time the $H_A$–O2 bond breaks and both $H_A$ and $H_B$ are free and located approximately midway on their respective O-O axes, as can be seen in Fig. 4(c). Subsequently, first $H_A$ and then $H_B$ bond again to O2, as shown in Fig. 4(d), after which the simulation is terminated. These snapshots indicate that the motion between the two quantum protons is correlated.

Figures 5 and 6 depict the ground state and first few excited state energies and the ground state Hellmann-Feynman forces as a function of time for both the MC-SCF method and the complete configuration interaction method in our sample trajectory. These figures were obtained by integrating the trajectory using the MC-SCF forces and at intervals calculating the complete configuration interaction wave function, energy, and forces for the generated configurations. The $x$-component of the force on the middle oxygen O2 [shown in Fig. 6(b)] is most illustrative of the dynamical processes occurring during this trajectory. In this case the peaks correspond to the formation or breaking of an OH bond, and the big peak corresponds to the situation when both protons are free. Figures 5 and 6 illustrate that the MC-SCF and complete configuration interaction ground state energies and forces are virtually indistinguishable. Thus, these figures show that the small number of configurations ($Q=4$) in the MC-SCF method captures the essential physical elements of the complete configuration interaction method ($Q=21^2$) for the ground state. Figure 5(a) indicates that the first two excited states are described qualitatively well with $Q=4$ configurations, but the third excited state, which is not shown, is not described adequately. The inclusion of more configurations in the MC-SCF calculations [i.e. $Q=9$ in Fig. 5(b)] leads to a noticeable improvement in the first two excited states and to an accurate description of the third excited state. We did not calculate higher excited states.

We verified the accuracy of the Hellmann-Feynman forces by comparing them to numerical forces obtained by a two point numerical differentiation of the energy. We found that the numerical forces are indistinguishable from the Hellmann-Feynman forces for the MC-SCF method on the scale of Fig. 6.

We also performed a single configurational calculation with the identical starting conditions as those in the sample trajectory described above. We found that the ground state energy and forces for this single configurational calculation are similar (but not identical) to those for the MC-SCF method. This comparison indicates that for this sample trajectory the ground state wave function is predominantly single configurational. However, as shown in Fig. 5, a multiconfigurational wave function is required for the accurate description of the excited states. We would expect the mul-
A configurational description of the ground state wave function to be more critical for trajectories in which two complete proton transfer reactions occur (i.e. the translocation of the proton from one end of the chain to the other). We are currently developing the methodology to induce this process by applying an electric field along the chain. We are also combining the MC-SCF method with the MDQT method to study nonadiabatic effects for these types of systems. As mentioned above, we have found that nonadiabatic effects are not significant for the sample trajectory discussed in this paper because the average occupation probability of the ground state is always above 0.999.

Furthermore, we also performed an MC-SCF* calculation with the identical starting conditions as those in the sample trajectory described above. The ground state energy and forces for the MC-SCF* method are indistinguishable from those for the MC-SCF method on the scale of Fig. 6. This remarkable agreement may be due to the predominantly single-configurational nature of the ground state wave function. Surprisingly, the MC-SCF method is ≈1.4 times faster than the MC-SCF* method for these simulations. Although the symmetrization of the \( \hat{e}^{(1)} \)-matrices is an iterative process, it is computationally fast because we include a limited number of one-particle states and use effective Hamiltonians to generate a good starting guess. Moreover, the convergence of the coefficients \( c^{(i)}_{\alpha} \) and \( d_j \) in the MC-SCF method requires about five times fewer iterations than in the MC-SCF* method, resulting in an increase in the overall speed of the calculations.

IV. SUMMARY AND CONCLUSIONS

This paper presents an analytical derivation of an MC-SCF solution to the time-independent Schrödinger equation for nuclear motion (i.e. vibrational modes). This variational MC-SCF method is designed for mixed quantum/classical molecular dynamics simulations of multiple proton transfer reactions, where the transferring protons are treated quantum mechanically while the remaining degrees of freedom are treated classically. This paper presents a proof that the Hellmann-Feynman forces on the classical degrees of freedom are identical to the exact forces (i.e. the Pulay corrections vanish) when this MC-SCF method is used with an appropriate choice of basis functions.

We applied this new MC-SCF method in conjunction with an adiabatic mixed quantum/classical molecular dynamics method to multiple proton transfer in a protonated chain of three hydrogen-bonded water molecules. In order to test the accuracy of this method, we compared the energies and forces obtained from the MC-SCF method to those obtained from a complete configuration interaction calculation. The remarkable agreement between the two methods indicates that the MC-SCF provides an accurate description of the ground and excited state wave functions. Furthermore, we found that the MC-SCF method was more than an order of magnitude faster than the complete configuration interaction method. We also verified the accuracy of the Hellmann-Feynman forces by comparing them to numerically derived forces. In addition, we integrated the time-dependent Schrödinger equation to monitor the quantum amplitudes and
found that nonadiabatic effects were negligible for the sample trajectories. However, the accuracy of the excited states enables us to use this MC-SCF method in conjunction with nonadiabatic molecular dynamics methods such as MDQT when nonadiabatic effects are significant. Thus, we have shown that this new MC-SCF method is computationally practical and numerically accurate for the simulation of multiple proton transfer reactions.

These simulation methods could be improved in several different ways. One improvement would be to obtain a more quantitatively accurate potential surface that is computationally practical for these quantum dynamical simulations. Another improvement would be to include the quantum mechanical motion of the hydrogen atoms that are not hydrogen-bonding. Unfortunately this is computationally impractical with the current methodology. In addition, the chain of water could be embedded in a transmembrane protein such as bacteriorhodopsin, which is expected to significantly affect the proton transfer dynamics. With our current methodology we could simulate a chain of four water molecules, where only the three hydrogen-bonding protons are treated quantum mechanically. Thus we could study the chain of four water molecules postulated to be present in the bacteriorhodopsin proton channel. Note that re-orientations of the water molecules will change the identity of the hydrogen-bonding protons. Since we quantize only the hydrogen-bonding protons and constrain them to remain along the axis between two specified oxygen atoms, we are not allowing these types of re-orientations to occur. The application of this method to the bacteriorhodopsin proton channel will assume that once an excess proton arrives at one end of the chain, the proton transport shuttle occurs much faster than these re-orientations. These are all areas for future investigation.

This paper presents an initial quantum dynamical non-equilibrium simulation of multiple proton transfer in a chain of water molecules. We are currently investigating the effects of an external electric field and different chain lengths on the proton transfer dynamics. We are combining this MC-
SCF method with the MDQT surface hopping method to study the significance of nonadiabatic effects for these types of systems. These methods will help us to elucidate the fundamental dynamical principles of multiple proton transfer reactions in chains of water molecules.

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