

Chapter 6

Extending surface hopping

FOB-SH is a variant of Tully’s original fewest switches surface hopping¹⁰⁵. It has been used to simulate electron-nuclear dynamics in large systems of organic molecules and has been well tested against experimental studies and benchmarked against higher order studies^{14,69–76}. However, the code does not currently account for any electrostatic interactions. This presents a problem when looking at many systems; such as those with large amounts of disorder or those with polarisable molecules.

The standard Coulomb sum of partial charges is only conditionally convergent and extremely slow to calculate. The standard method for calculating electrostatic interactions is by decomposing interactions into long-range and short-range interactions (with corrections such as removing bonded terms etc..). This is normally carried out with an Ewald sum¹⁰⁶ where a short-range interactions are calculated in real-space and long-range interactions are calculated in reciprocal-space. This results in 2 summations that are now unconditionally, quickly convergent. Further extensions to the standard Ewald technique provide an additional decrease in computational time by interpolating particles onto a grid and using fast fourier transforms to calculate the sums. In Wolf, 99¹⁰⁷, a technique for removing the (expensive) reciprocal-space term from the sum altogether was proposed by ensuring charge neutrality within a cutoff sphere from each atom. This idea was developed to improve energy conservation and to remove discontinuities within the forces and energies^{108,109}. In this work I will investigate the applicability of both the standard Ewald technique and a development of the Wolf method (named DSF¹⁰⁹) to calculate

the electrostatic interactions within FOB-SH.

6.1 Implementation details

6.1.1 Addition Subtraction Method

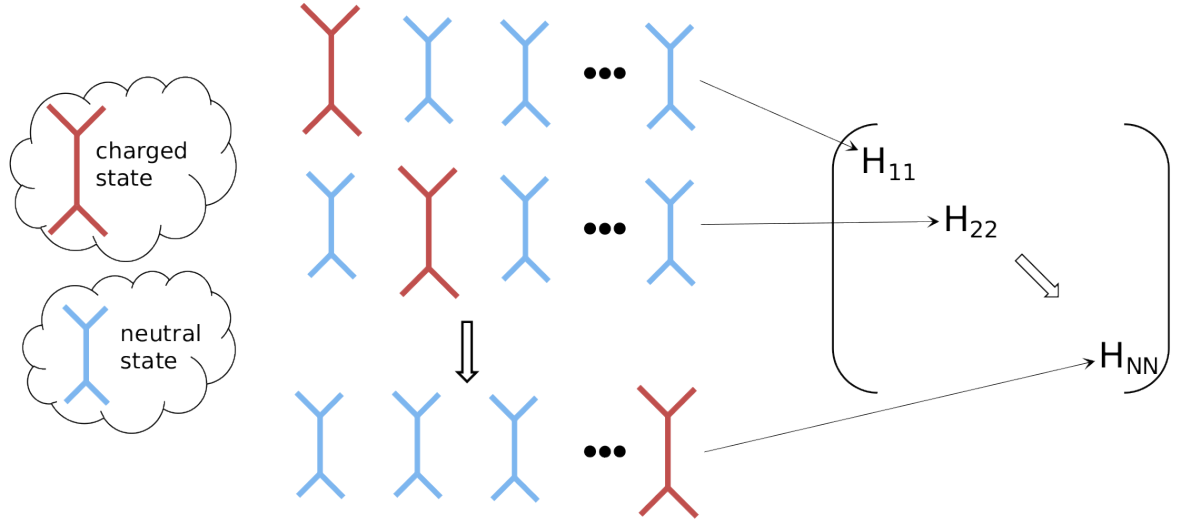


Figure 6.1: A demonstration of the procedure to calculate diagonal elements of the Hamiltonian (site-energies). Red (blue) shapes represent a molecule in its charged (neutral) state. A horizontal line of these shapes represent the full system with all molecules; where a single molecule is in its charged state. The arrow denotes which matrix element this saved as.

In FOB-SH, nuclear dynamics are determined by the Hamiltonian. The Hamiltonian is constructed such that the diagonal elements (site-energies) come from a classical forcefield and the off-diagonal elements (electron couplings) are proportional to the overlap of the diabatic wavefunctions. Each site-energy, $H_{\gamma\gamma}$, is defined as the potential energy of the system where the excess charge is localised on the molecule γ . For the avoidance of doubt, I will denote the molecule with the excess charge localised on it as the ‘charged’ molecule and other molecules as ‘neutral’. The presence of the excess charge on molecule γ results in different input parameters (such as the charge distribution or the length of bonds) than the other neutral molecules. This results in the calculation of site-energies and forces having to be repeated N_{mol} times for each permutation of the charged molecule. This is

summarised in figure 6.1.

To determine whether it is feasible to repeat the calculation of the electrostatic interactions N_{mol} times a quick timing run was carried out. This simulated 250 pentacene molecules (9,000 atoms) and the time was measured to calculate the electrostatic interactions with the 3 methods already implemented within CP2K: Smooth Particle Mesh Ewald (SPME), Particle Mesh Ewald (PME) and standard Ewald. The measured time of a simulation without any electrostatics was then subtracted from each of these simulations to isolate the time spent on just the electrostatics. The results are given in figure 6.2.

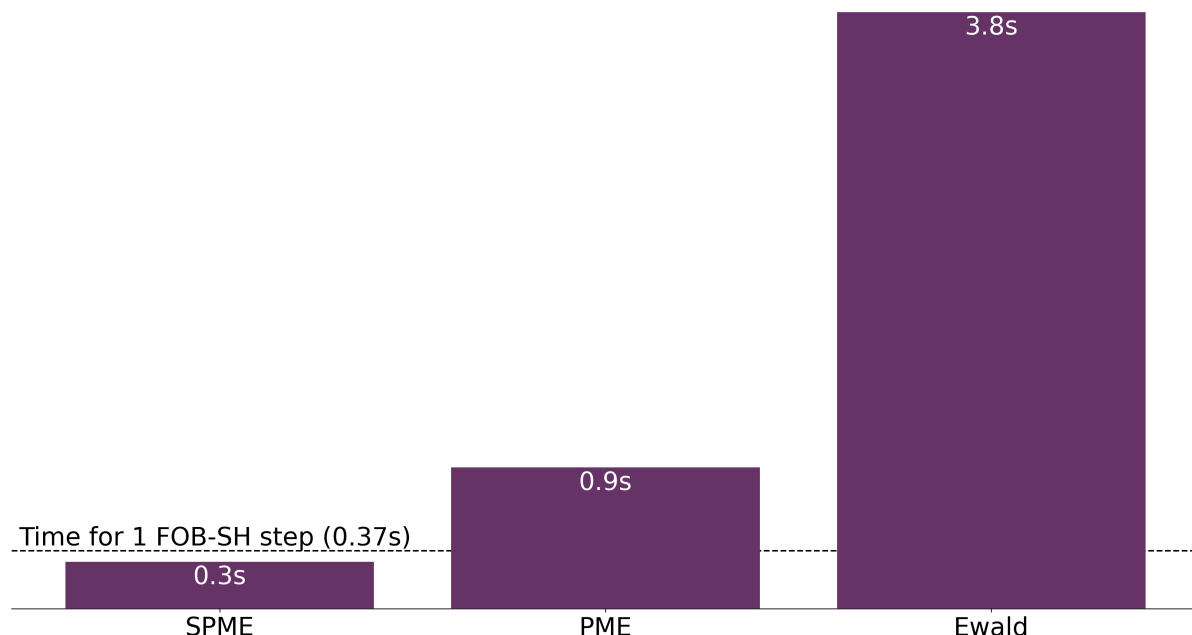


Figure 6.2: The time taken to calculate just the electrostatic interactions within CP2K for a 9,000 atom system using various methods. PME is particle mesh Ewald, SPME is smooth-PME, Ewald is the standard ewald method. The dashed line shows the time taken for a single FOB-SH step.

We can see that even a single calculation of the electrostatic interactions with the fastest method available within CP2K will take a comparable time to the rest of the surface hopping code. It is clear then that a more efficient method must be used to calculate the electrostatics in a more efficient way.

Within the current FOB-SH implementation the forces and energies consist of intra-

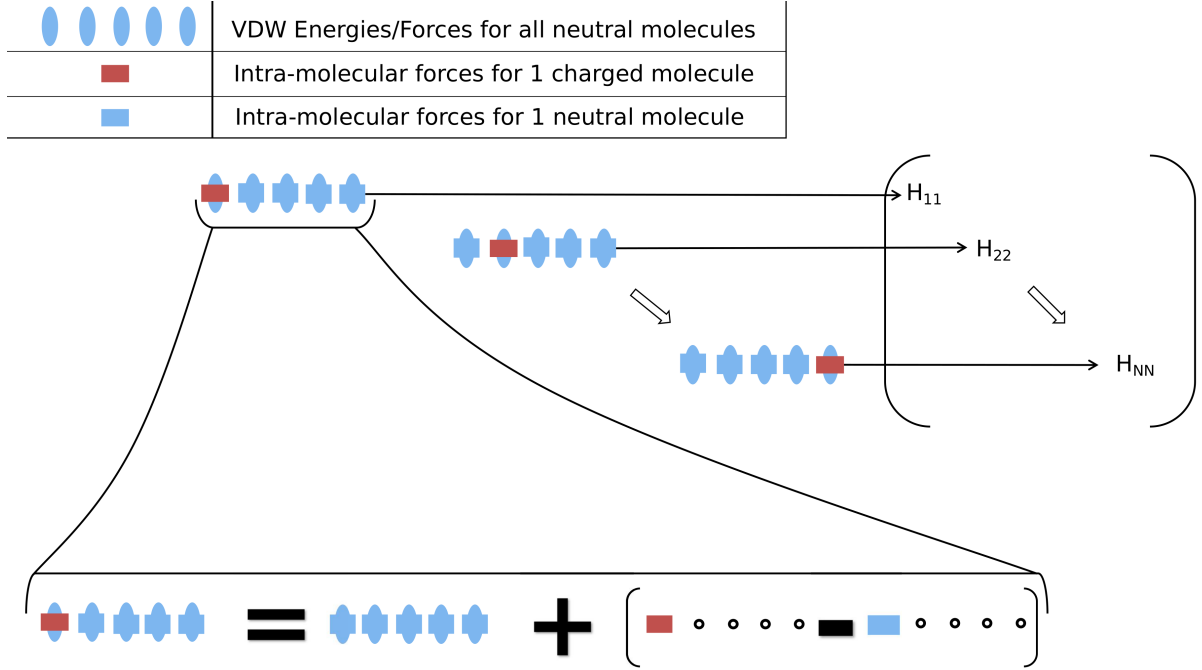


Figure 6.3: A depiction of the decomposition of the forces and energies within FOB-SH. First the all neutral VDW forces/energies are computed (blue ovals). Second the intra-molecular forces for each charged (neutral) molecule, represented by a red (blue) rectangle. The site-energy/force is then computed as a summation of all molecules in their neutral state with a molecule in its neutral state subtracted and the same molecule in its charged state added.

molecular components (bonds, bends, torsions etc...) and inter-molecular components (Van der Waals forces provided by a Leonard-Jones potential). The same repetition of the calculation of forces and energies would, at first glance, be required for the correct calculation of these terms. However, an addition-subtraction scheme is used to reduce the calculation time from $O(N_{mol}, N_{atom}^2)$ to $O(N_{atom}^2)$. This is summarised in figure 6.3 and relies on the fact that the intra-molecular forces and energies can be decomposed into independent molecular contributions. In order to calculate the force on each atom and site-energy with molecule γ in its charged state the code first calculates the force/energy with all molecules in their neutral state and then adds the contribution of molecule γ in its charged state and subtracts the contribution of molecule γ in its neutral state. We do not make the same adjustment for the VDW forces as the correction is negligible. This results in just 2 calculations of all forces and total energies rather than $O(N_{mol})$ calculations. Seeing as the electrostatics are normally one of the most expensive parts of

a classical force-field it is particularly important that these are treated efficiently.

The addition subtraction scheme applied to the electrostatic interactions cannot be the same as the one used for the intra-molecular interactions as separate molecules are not independent and energies and forces cannot be decomposed into molecular contributions for each different site-energy. However, a similar trick can be used to reduce the cost of the Ewald sum. In the following work, the recalculation method references the method of looping over all molecules and recalculating energies and forces without optimisations. The addition-subtraction scheme is explained in the proceeding chapters.

6.1.2 Ewald Equations and the additional subtraction scheme

The standard Ewald summation for evaluating electrostatic energies in molecular dynamics simulation are given below:

$$\begin{aligned}
 E_{coul}(\mathbf{r}^N) = & \frac{1}{2} \frac{1}{4\pi\epsilon_0} \sum_{\mathbf{n}} \sum_j^{N_{at}} \sum_i^{N_{at}} q_i q_j \frac{\text{erfc}(\alpha \cdot |\mathbf{r}_{ij} + \mathbf{n}|)}{|\mathbf{r}_{ij} + \mathbf{n}|} \Theta(r_{cut} - |\mathbf{r}_{ij} + \mathbf{n}|) \\
 & + \frac{1}{2\pi V} \frac{1}{4\pi\epsilon_0} \sum_{\mathbf{k} \neq 0} \frac{1}{|\mathbf{k}|^2} e^{-\frac{\pi^2 |\mathbf{k}|^2}{\alpha^2}} \left| \sum_j^{N_{at}} q_j e^{2\pi i \mathbf{k} \cdot \mathbf{R}_j} \right|^2 \\
 & - \frac{\alpha}{\sqrt{\pi}} \frac{1}{4\pi\epsilon_0} \sum_j q_j^2 \\
 & - \frac{1}{2} \frac{1}{4\pi\epsilon_0} \sum_j \sum_i^{N_{at}} q_i q_j \frac{\text{erfc}(\alpha \cdot |\mathbf{r}_{ij}|)}{|\mathbf{r}_{ij}|} \Theta(r_{cut} - |\mathbf{r}_{ij}|)
 \end{aligned} \tag{6.1}$$

In equation (6.1), the first term is the real-space sum. This sums over all periodic images (\mathbf{n}) and pairs of atoms i, j within a cutoff imposed by the Heaviside step function $\Theta(r_{cut} - |\mathbf{r}_{ij} + \mathbf{n}|)$. The distance between atoms is given by $\mathbf{r}_{ij} = \mathbf{r}_i - \mathbf{r}_j$, the charge on atom i is given by q_i and alpha is a convergence parameter. The factor $\frac{1}{2}$ accounts for any double counting of atoms. The second term is the most expensive part of this calculation and sums over reciprocal-space vectors \mathbf{k} and atoms, j . \mathbf{R}_j represents the position vector of atom j . The third term is the constant self-energy term and the fourth corrects for bonded (intra-molecular) interactions. The bonded interactions may be ignored in the real-space sum, this correction removes their effect from the reciprocal-space sum. As these 4 summations

are independent we can look at each one separately when implementing the addition-subtraction scheme, starting with the simplest -the self-energy term. Note in this section I will only discuss the energies, the forces are very similar and their equations are given in appendix ??.

6.1.3 Self-energy addition subtraction scheme

For each site-energy, γ , we must recalculate the full forces and energies with the excess charge located on molecule γ . This is demonstrated in equation (6.2). Note that for brevity I have replaced the factor $\frac{1}{4\pi\epsilon_0}$ with η .

$$E_{self}^{\gamma} = \frac{\alpha}{\sqrt{\pi}} \eta \left[\sum_{j \notin \gamma} (q_j^n)^2 + \sum_{j \in \gamma} (q_j^c)^2 \right] \quad (6.2)$$

In the above equation the Ewald self-energy correction contribution for site-energy γ is simply a sum of squared charges of molecules in their neutral state, for atoms belonging to molecules that aren't γ plus the sum of squared charges of atoms within γ . The molecule γ will have a different values due to the presence of the excess charge carrier. This is represented by the superscript n and c where q_j^n represents the charge on atom j where the force-field for the molecule it belongs to has been parameterised in it's neutral state (i.e. without an excess charge carrier). q_j^c represents the charge on atom j , where the force-field for the molecule the atom belongs to has been parameterised with an excess charge carrier localised on it (in its charged state).

For a single molecule system this value is the same for all γ and no optimisations are required, except to calculate this value once and use it for each γ . However, for a more complex system the addition subtraction scheme used is given in equation (6.3).

$$E_{self}^{\gamma} = \underbrace{\eta \frac{\alpha}{\sqrt{\pi}} \sum_j^{N_{at}} (q_j^n)^2}_{\text{Calculated Once}} + \underbrace{\frac{\alpha}{\sqrt{\pi}} \eta \sum_{j \in \gamma} [(q_j^c)^2 - (q_j^n)^2]}_{\text{Calculated for each } \gamma} \quad (6.3)$$

In equation (6.3) we have removed the γ index from the most expensive part of the sum; this means we can calculate it once and store it. In the second term we only sum

over atoms in charged molecule γ and remove the contribution from molecule γ in its neutral state and add the contribution from molecule γ in its charged state. Seeing as the correction part of equation (6.3) is the only part repeated from each γ this reduces the cost of this calculation from $O(N_{mol}, N_{atom})$ to just $O(N_{atom})$. The same idea is used for the remaining terms in the Ewald sum.

6.1.4 Real-space addition subtraction

The real-space term is more complicated than the self-energy term, though the idea is the same. That is, the fully neutral contribution is calculated and for individual sites/molecules a correction is applied. This is shown in equation (6.4)

$$\begin{aligned}
 E_{real}^{\gamma} = & \frac{\eta}{2} \sum_{\mathbf{n}} \sum_j^{N_{at}} \sum_i^{N_{at}} q_i^n q_j^n R^{dir}(\mathbf{r}_{ij} + \mathbf{n}) \\
 & + \frac{\eta}{2} \sum_{j \in \gamma, i \in \gamma} (q_j^c q_i^c - q_j^n q_i^n) R^{dir}(\mathbf{r}_{ij} + \mathbf{n}) \\
 & + \frac{\eta}{2} \sum_{j \in \gamma, i \notin \gamma} (q_j^c - q_j^n) q_i^n R^{dir}(\mathbf{r}_{ij} + \mathbf{n})
 \end{aligned} \tag{6.4}$$

In equation (6.4) the most expensive summation ($O(N_{atom}^2)$) is the first term. Fortunately, we can once again calculate this once and use the same value for each site-energy. This first term calculates all interactions between atoms belonging to molecules in their neutral state (neutral-neutral interactions). The next two terms show the addition-subtraction correction. The second term shows a sum over all pairs of atoms in the charged molecule, γ . In this term we subtract any neutral-neutral interactions and replace them with any charged-charged interactions. This scales as $O(N_{atom} \text{ per mol})$ and is repeated N_{mol} times so the full correction scales as $O(N_{atom})$. The third term replaces any interactions of atoms on the charged molecule with its environment (neutral molecules), hence it removes neutral-neutral interactions and replaces them with charged-neutral interactions. This scales as $O(N_{atom} \text{ per mol}, N_{atom})$ and is repeated N_{mol} times, resulting in an ultimate scaling of $O(N_{atom}^2)$. Therefore, this optimisation scales in the same manner as a single calculation of the Ewald interactions and any additional overheads will be minimal. For the avoidance of doubt, in equation (6.4) I have replaced the complementary error function and Heaviside step function in equation (6.1) with the term $R^{dir}(\mathbf{r}_{ij} + \mathbf{n})$.

6.1.5 Bonded corrections addition subtraction

The bonded correction terms remove electrostatic contributions to energies (and forces) for atoms that are bonded. This is because interactions are already accounted for by the intra-molecular force-field (bonds, bends, torsions etc...). These interactions occur within molecules and their contribution can be decomposed into molecular contributions. These interactions can therefore be handled in the same way as the intra-molecular addition-subtraction scheme as discussed in section 6.1.1.

6.1.6 Reciprocal-space addition subtraction

The reciprocal energies can be optimised using the addition-subtraction technique. However, the forces cannot. This is a big problem for any implementation of Ewald electrostatics within surface hopping as the electrostatic part of the Ewald sum is by far the most expensive. In fact in the same 250 molecule system as in figure 6.2 the reciprocal-space component took 88% of the calculation time. In larger systems this increases. Repeating this calculation N_{mol} times would be far too slow and would limit the surface hopping code to small systems of tens of molecules. However, the damped shifted forces technique (DSF)¹⁰⁹ can be used to approximate the electrostatic interactions without the reciprocal force term. For completeness I have included the addition-subtraction scheme for the reciprocal-space energies below in equation (6.5) and for the forces in appendix ??.

$$E_{recip}^{\gamma} = \frac{1}{2\pi V} \sum_{\mathbf{k} \neq 0} \frac{1}{|\mathbf{k}|^2} e^{\frac{\pi^2 |\mathbf{k}|^2}{\eta^2}} \left| \sum_j^{N_{at}} q_j^n e^{2\pi \mathbf{k} \cdot \mathbf{R}_j} + \sum_{j \in \gamma}^{N_{at}} (q_j^c - q_j^n) e^{2\pi \mathbf{k} \cdot \mathbf{R}_j} \right|^2 \quad (6.5)$$

Once again in equation (6.5) the summation over all atoms can be calculated once and reused for each site-energy γ . This calculates all neutral-neutral interactions. The additional sum over atoms belonging to molecule γ is then repeated N_{mol} times for each site-energy γ .

6.2 Timing the electrostatics implementation

In figure 6.4 we can see the time taken for a single step of a surface hopping simulation for various lengths of a 1D Ethylene chain. We see as the chain size increases it becomes more important that electrostatic interactions are efficiently handled. For the 800

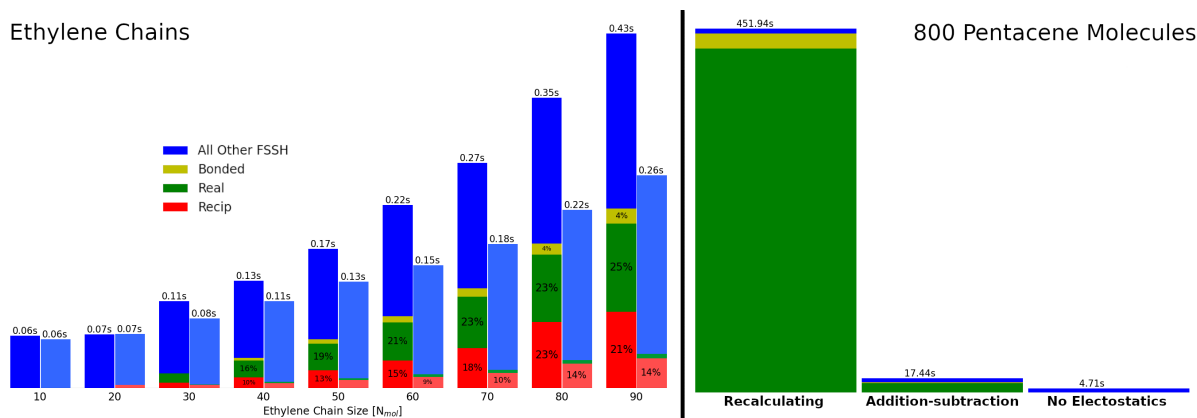


Figure 6.4: Time taken to run surface hopping and electrostatics for various lengths of 1D Ethylene chain (left) and 800 molecule pentacene plane (right). Darker colors show data from the recalculation method for the electrostatics and less saturated colors to the right show data from the addition subtraction scheme. Green bars show the time taken to calculate real-space interactions, red is reciprocal, yellow is the bonded corrections and blue shows all other parts of the surface hopping code. In the right pane reciprocal interactions are omitted as they took too long to run.

molecule pentacene plane, the reciprocal calculations were taking far too long and had to be turned off to measure the time taken for the other components. We see also that even with the addition-subtraction scheme the full reciprocal-space calculations don't see a very significant speedup. This is because the calculation of the forces are still repeated N_{mol} times as they cannot be optimised in the same way. A small speedup is seen due to the addition-subtraction scheme being used with the reciprocal-space energies. However, we see that the addition-subtraction scheme offers a major speedup for all other components. It is also vital that the results outputted are correct. I have tested both the recalculation method and the addition-subtraction method against standard CP2K calculations to ensure the implementation is correct.

6.2.1 Testing the electrostatics implementation

To test the recalculation of site-energies and forces within CP2K a 10 molecule Ethylene chain was used. In order to calculate the site-energies and forces with standard MD in CP2K, 10 different simulations were carried out. In each one of these simulations a different molecule was chosen to have charged geometry and the rest were chosen to have neutral geometry in the input files. A single step of MD was then carried out and forces and energies were outputted. These forces and energies were subsequently compared

to the forces and energies outputted by the recalculation method and the results are shown in figure 6.5. We see in figure 6.5 that the values of energy and forces as calculated

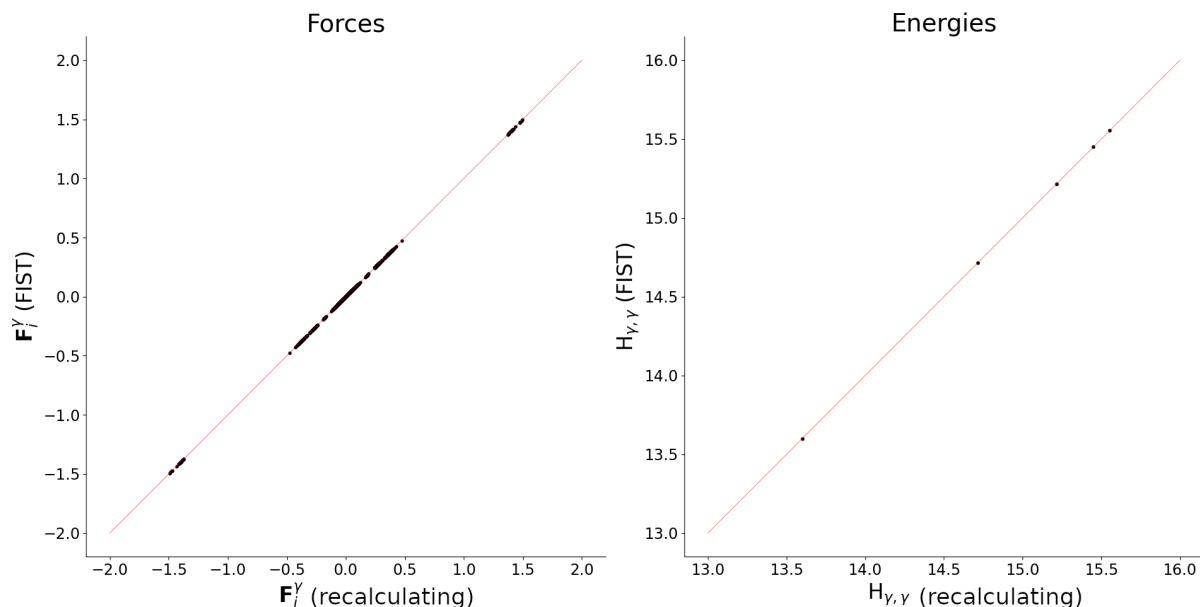


Figure 6.5: A comparison of forces and energies calculated with the recalculation method and the forces and energies calculated through multiple CP2K calculations.

with CP2K's standard MD package (FIST) and my implementation of a simple loop carrying out the same thing in the code are exactly the same. In fact the maximum absolute difference between results was 5×10^{-13} i.e. numerical error. This confirms the implementation of the recalculation scheme. The reason only 5 values for the site-energies can be seen is some points are extremely close and it is hard to see differences in them. This shows the recalculation method can now be used to benchmark the addition-subtraction scheme.

Appendix A

Tully Model Paramters

A.1 Model 1 -Single Avoided Crossing

Hamiltonian Paramters:

$$H_{11}(\mathbf{R}) = A \tanh(B\mathbf{R})$$

$$H_{12}(\mathbf{R}) = Ce^{-D\mathbf{R}^2}$$

$$H_{21}(\mathbf{R}) = H_{12}(\mathbf{R})$$

$$H_{22}(\mathbf{R}) = -H_{11}(\mathbf{R})$$

Where A = 0.03, B = 0.4, C = 0.005 and D = 0.3

Quantity	Value	Unit
Initial Position	-20	a.u.
Initial Velocities	15.0, 25.0	a.u.
Initial Adiab Pop	ground state	-
Simulation Time	6000, 4000	a.u.
$\sigma_v^{(I)}$	0.5	a.u.
M (σ constant)	40	-
$\Delta t_{\text{nuclear}}$	0.1	fs
$\Delta t_{\text{electronic}}$	0.01	fs
$\frac{\delta \mathbf{R}_{lk,v}^{(I)}}{\delta t}$ threshold	0.15	a.u.
N_{rep}	200	-

A.2 Model 2 -Dual Avoided Crossing

	Quantity	Value	Unit
Hamiltonian Paramters:	Initial Position	-8	a.u.
	Initial Velocities	16.0, 30.0	a.u.
$H_{11}(\mathbf{R}) = 0$	Initial Adiab Pop	ground state	-
$H_{12}(\mathbf{R}) = Ce^{-D\mathbf{R}^2}$	Simulation Time	2500, 1500	a.u.
$H_{21}(\mathbf{R}) = H_{12}(\mathbf{R})$	$\sigma_v^{(I)}$	0.5	a.u.
$H_{22}(\mathbf{R}) = -Ae^{-B\mathbf{R}^2} + E$	M (σ constant)	40	-
	$\Delta t_{\text{nuclear}}$	0.1	fs
Where A = 0.1, B = 0.28, C = 0.015, D =	$\Delta t_{\text{electronic}}$	0.01	fs
0.06 and E = 0.05	$\frac{\delta \mathbf{R}_{lk,v}^{(I)}}{\delta t}$ threshold	0.15	a.u.
	N_{rep}	200	-

A.3 Model 3 -Extended Coupling

	Quantity	Value	Unit
Hamiltonian Paramters:	Initial Position	-15	a.u.
	Initial Velocities	10, 30	a.u.
$H_{11}(\mathbf{R}) = A$	Initial Adiab Pop	ground state	-
$H_{12}(\mathbf{R}) = \begin{cases} Be^{C\mathbf{R}}, & R \leq 0 \\ B(2 - e^{-C\mathbf{R}}), & R > 0 \end{cases}$	Simulation Time	5000, 1500	a.u.
$H_{21}(\mathbf{R}) = H_{12}(\mathbf{R})$	$\sigma_v^{(I)}$	0.5	a.u.
$H_{22}(\mathbf{R}) = -H_{11}(\mathbf{R})$	M (σ constant)	40	-
	$\Delta t_{\text{nuclear}}$	0.1	fs
	$\Delta t_{\text{electronic}}$	0.01	fs
Where A = 6×10^{-4} , B = 0.1 and C = 0.9	$\frac{\delta \mathbf{R}_{lk,v}^{(I)}}{\delta t}$ threshold	0.15	a.u.
	N_{rep}	200	-

A.4 Model 4 -Dual Arch

Hamiltonian Paramters:

$$H_{11}(\mathbf{R}) = A$$

$$H_{12}(\mathbf{R}) = \begin{cases} B \left[-e^{C(\mathbf{R}-D)} + e^{C(\mathbf{R}+D)} \right] & R \leq -D \\ B \left[e^{-C(\mathbf{R}-D)} - e^{-C(\mathbf{R}+D)} \right] & R \geq D \\ B \left[2 - e^{C(\mathbf{R}-D)} - e^{-C(\mathbf{R}+D)} \right] & -D < R < D \end{cases}$$

$$H_{21}(\mathbf{R}) = H_{12}(\mathbf{R})$$

$$H_{22}(\mathbf{R}) = -H_{11}(\mathbf{R})$$

Where $A = 6 \times 10^{-4}$, $B = 0.1$, $C = 0.9$ and

$$D = 4$$

Quantity	Value	Unit
Initial Position	-20	a.u.
Initial Velocities	10, 40	a.u.
Initial Adiab Pop	ground state	-
Simulation Time	6000, 2000	a.u.
$\sigma_v^{(I)}$	0.5	a.u.
M (σ constant)	40	-
$\Delta t_{\text{nuclear}}$	0.1	fs
$\Delta t_{\text{electronic}}$	0.01	fs
$\frac{\delta \mathbf{R}_{lk,v}^{(I)}}{\delta t}$ threshold	0.15	a.u.
N_{rep}	200	-

Appendix B

Wigner Distribution Derivation

The nuclear wavepacket (at time 0) is given by:

$$\chi(R) = \frac{1}{(\pi\mu^2)^{\frac{1}{4}}} e^{-\frac{(R-R_0)^2}{2\mu^2} + ik_0(R-R_0)} \quad (\text{B.1})$$

The Wigner quassprobability function for momentum and position (p, R) is given by:

$$W(p, R) = \frac{1}{\pi\hbar} \int_{-\infty}^{\infty} \chi^*(R+y) \chi(R-y) e^{\frac{2ipy}{\hbar}} dy \quad (\text{B.2})$$

However, both Ehrenfest and CTMQC require atomic positions as input so we must extract the position and velocity probability densities from this. We get these from the marginal integrals of the Wigner distribution i.e.

$$|f(R)|^2 = \int_{-\infty}^{\infty} W(R, p) dp \quad (\text{B.3})$$

$$|f(p)|^2 = \int_{-\infty}^{\infty} W(R, p) dR \quad (\text{B.4})$$

In order to calculate these marignal integrals we must first crunch through the maths of equation (B.2). Substituting eq (B.1) into (B.2):

$$W(p, R) = \frac{1}{\pi\hbar} \int_{-\infty}^{\infty} \frac{1}{\mu\sqrt{\pi}} e^{-\frac{(R+y-R_0)^2}{2\mu^2} - 2ik_0y - \frac{(R-y-R_0)^2}{2\mu^2}} e^{\frac{2ipy}{\hbar}} dy \quad (\text{B.5})$$

Simplifying the 2 quadratic equations (equation (B.5)) we get:

$$W(p, R) = \frac{1}{\pi\hbar} \int_{-\infty}^{\infty} \frac{1}{\mu\sqrt{\pi}} e^{-\mu^{-2}(y^2 - 2ik_0 y \mu^2 + (R - R_0)^2)} e^{\frac{2ipy}{\hbar}} dy \quad (\text{B.6})$$

We can now take the expressions not dependant on y outside of the integral and combine the exponents.

$$W(p, R) = \frac{1}{\pi\sqrt{\pi}\mu\hbar} e^{-\frac{(R-R_0)^2}{\mu^2}} \int_{-\infty}^{\infty} e^{-\frac{y^2 + 2iy\mu^2(\frac{p}{\hbar} - k_0)}{\mu^2}} dy \quad (\text{B.7})$$

Integrating we get:

$$\int e^{-\frac{y^2 + 2iy\mu^2(\frac{p}{\hbar} - k_0)}{\mu^2}} dy = \frac{\sqrt{\pi}\mu}{2} e^{-\frac{\mu^2}{\hbar^2}(p - \hbar k_0)^2} \text{erf} \left[\frac{y}{\mu} + i \left(\frac{p\mu}{\hbar} - \mu k_0 \right) \right] \quad (\text{B.8})$$

Applying limits we get:

$$\int_{-\infty}^{\infty} e^{-\frac{y^2 + 2iy\mu^2(\frac{p}{\hbar} - k_0)}{\mu^2}} dy = \sqrt{\pi}\mu e^{-\frac{\mu^2}{\hbar^2}(p - \hbar k_0)^2} \quad (\text{B.9})$$

Substituting this back into the Wigner distribution (equation (B.2)) we finally get:

$$W(p, R) = \frac{1}{\pi\hbar} e^{-\frac{(R-R_0)^2}{\mu^2}} e^{-\frac{(p - \hbar k_0)^2}{\hbar^2/\mu^2}} \quad (\text{B.10})$$

Taking the maringal integrals we get the position and velocity probability distributions:

$$|f(R)|^2 = \frac{2}{\mu\sqrt{\pi}} e^{-\frac{(R-R_0)^2}{\mu^2}} \quad (\text{B.11})$$

$$|f(p)|^2 = \frac{2}{\frac{\hbar}{\mu}\sqrt{\pi}} e^{-\frac{\mu^2}{\hbar^2}(p - \hbar k_0)^2} \quad (\text{B.12})$$

The above distributions are randomly sampled to get initial atomic velocities and positions for each simulation.

Appendix C

$\mathbf{R}_{lk,v}$ Alternatives

C.1 $\mathbf{R}_{lk,v}$ Extrapolation

C.2 Alternative Quantum Momentum Intercept

In Agostini, 16² another quantum momentum intercept term is discussed. This term is not used because, as previously discussed in section 1.4, it leads to unphysical transfer of population between adiabatic states when the nonadiabatic coupling elements are 0. However, it can be used in these Tully Models as an effective fix to the discontinuities caused by the $\mathbf{R}_{lk,v}$ term.

The other quantum momentum intercept, $\mathbf{R}_{0,v}^{(I)}$, comes directly from the construction of the nuclear density using a linear combination of a product of gaussians (see equation (1.12) in the introduction). It is defined as in equation (C.1) below:

$$\mathbf{R}_{0,v}^{(I)} = \sum_J^{N_{lr}} \left[\frac{\hbar \prod_{v'} g_{\sigma_{v'}^{(J)}(t)} \left(\mathbf{R}_{v'}^{(I)}(t) - \mathbf{R}_{v'}^{(J)}(t) \right)}{2 \sigma_v^{(J)}(t)^2 \sum_K^{N_{lr}} \prod_{v'} g_{\sigma_{v'}^{(K)}(t)} \left(\mathbf{R}_{v'}^{(I)}(t) - \mathbf{R}_{v'}^{(K)}(t) \right)} \mathbf{R}_v^{(I)} \right] \quad (\text{C.1})$$

However, as switching to this intercept directly may cause discontinuities in itself a smoothing parameter is applied to ease the switch. This is given in equation (C.2) below:

$$[1 - A(t)] R_{good}(t) + A(t) R_{bad}(t) = R_{effective}(t) \quad (\text{C.2})$$

R_{good} refers to the intercept that should be switched to (e.g. for the detection of a spike in the $R_{lk,v}^{(I)}$ we switch to the intercept in equation (C.1)). $R_{lk,v}^{(I)}$ refers to the intercept that is being switched from (e.g. when it is detected that the divergence of $R_{lk,v}^{(I)}$ has finished then we switch from the alternative intercept back to $R_{lk,v}^{(I)}$). $A(t)$ is a smoothing parameter and is given in equation (C.3) below:

$$A(t) = \frac{D_v^{(I)}}{2} \left[\tanh \left(t - \frac{t_{final} + t_{init}}{0.6Ndt} \right) + 1 \right] \quad (C.3)$$

Where $D_v^{(I)}$ is the distance between the 2 intercepts (e.g. $D_v^{(I)} = R_{lk,v}^{(I)} - R_{0,v}^{(I)}$), N is the number of steps to take before settling solely on one intercept, t_{init} is the time of detection of the divergence, t_{final} is the time at which the code settles on 1 intercept and dt is the timestep taken.

A cartoon of this process is given in figure C.1

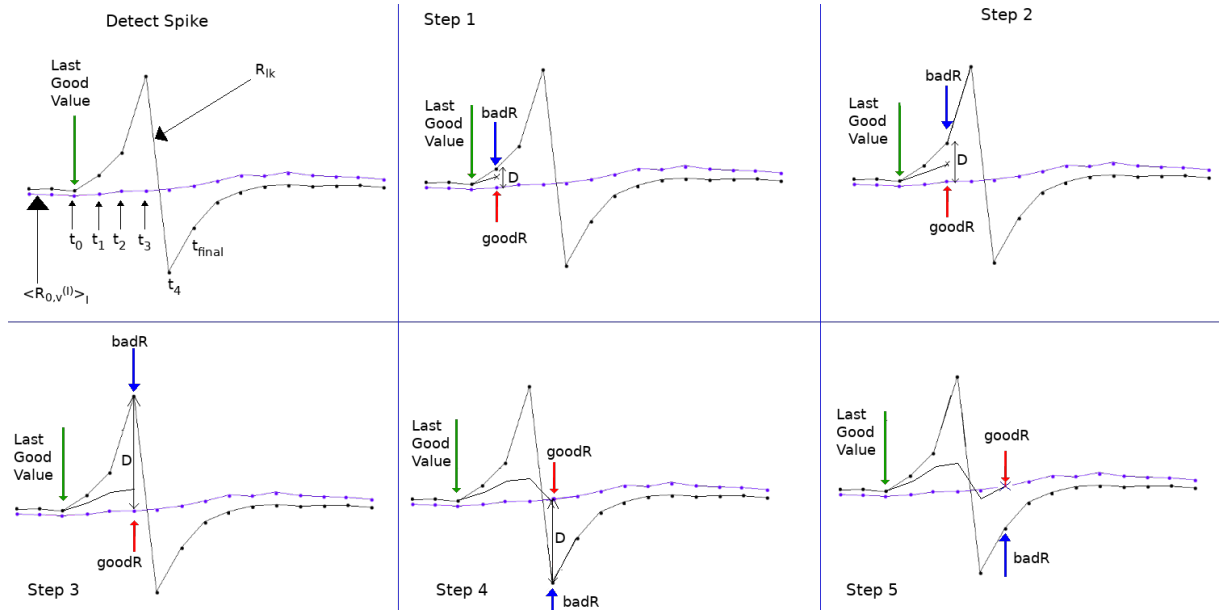


Figure C.1: A crude demonstration of the principle behind the smoothing procedure in switching between intercepts. The black line shows an intercept begin to diverge and the alternative intercept is shown in purple. As the step is incremented the amount of the alternative intercept that makes up the effective intercept is increased until only 1 intercept is used.

Appendix D

Rabi Oscillation

The time dependant Schrödinger equation is given below:

$$\hbar \frac{\delta}{\delta t} \Phi(\mathbf{R}(t), t) = \hat{H}(\mathbf{R}(t), t) \Phi(\mathbf{R}(t), t) \quad (\text{D.1})$$

If we hold the nuclear coordinates in place (e.g. remove time-dependence from nuclear coordinates) we get an ordinary differential equation as shown below:

$$\hbar \frac{d}{dt} \Phi(\mathbf{R}, t) = \hat{H}(\mathbf{R}, t) \Phi(\mathbf{R}, t) \quad (\text{D.2})$$

This has the following general solution. This can be solved with a Taylor series expansion.

$$\Phi(\mathbf{R}, t) = e^{\frac{i}{\hbar} \hat{H} t} \Phi(\mathbf{R}, 0)$$

Figure

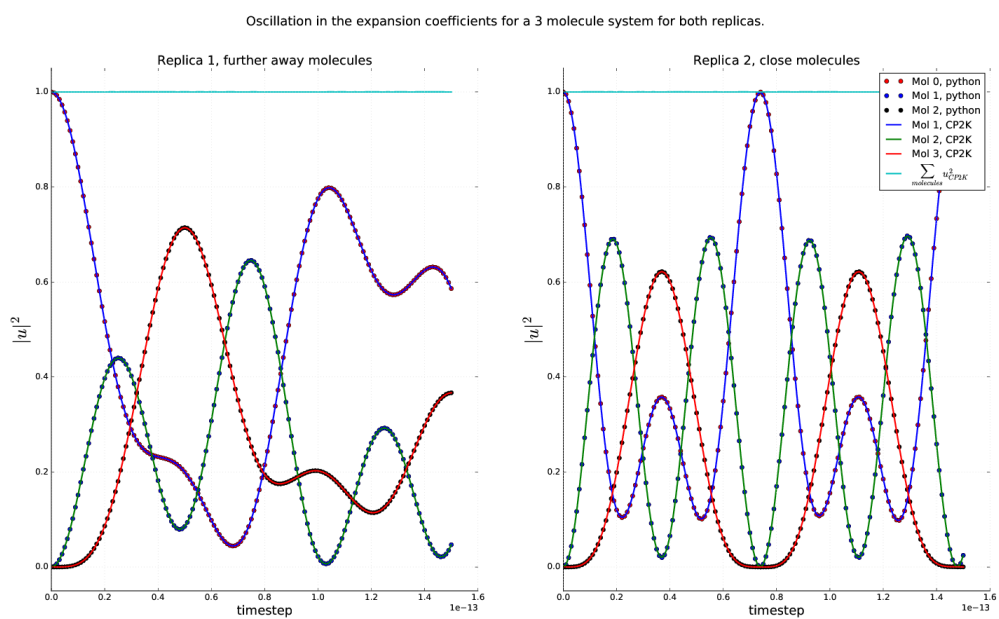


Figure D.1: Rabi oscillation occurring within a Ethylene trimer system. Dotted lines were calculated using equation (D.2), solid lines were calculated using the RK4 propagator within the CTMQC section of the CP2K code. The norm is shown on the top as a cyan line and the x axis shows the timestep in seconds.

Appendix E

Norm Conservation in CTMQC and Ehrenfest

A statement of the conservation of the norm, for a single trajectory, is given below in equation (E.1)

$$\frac{d}{dt} \sum_l |C_l(t)|^2 = \sum_l C_l^*(t) \frac{dC_l(t)}{dt} + \frac{dC_l^*(t)}{dt} C_l(t) = 2\mathbb{R} \left[\sum_l C_l(t)^* \frac{dC_l(t)}{dt} \right] \quad (\text{E.1})$$

Substituting the equation for the evolution of the adiabatic coefficients (and removing the purely imaginary term) into (??) we get equation (E.3)

$$\frac{d}{dt} \sum_l |C_l(t)|^2 = 2 \sum_l \mathbb{R} \left[\cancel{\frac{-i}{\hbar} \varepsilon_{BO}^l C_l(t)^* C_l(t)} - \sum_k \left[C_l(t)^* C_k(t) d_{lk}^{ad} - (A_l - B_l) C_l(t)^* C_l(t) \right] \right] \quad (\text{E.2})$$

$$= -2 \sum_l \mathbb{R} \left[\sum_k \left[C_l(t)^* C_k(t) d_{lk}^{ad} - (A_l - B_l) C_l(t)^* C_l(t) \right] \right] \quad (\text{E.3})$$

Where:

$$A_l = \sum_{v=1}^{N_n} \sum_k \frac{\mathcal{Q}_{lk,v}(t)}{\hbar M_v} \cdot \mathbf{f}_{k,v}(t) |C_k(t)|^2 \quad (\text{E.4})$$

$$B_l = \sum_{v=1}^{N_n} \sum_k \frac{\mathcal{Q}_{lk,v}(t)}{\hbar M_v} \cdot \mathbf{f}_{l,v}(t) |C_k(t)|^2 \quad (\text{E.5})$$

The NACE term evaluates to 0 due to the anti-symmetry of the NACE giving us equation (E.7).

So far, we have proved that the norm should be conserved here for all terms apart from the quantum momentum terms i.e. Ehrenfest.

$$\frac{d}{dt} \sum_l \left| C_l^{QM}(t) \right|^2 = 2 \sum_l \Re [(A_l - B_l) C_l(t)^* C_l(t)] \quad (\text{E.6})$$

$$= 2 \left[\sum_l A_l |C_l(t)|^2 - \sum_l B_l |C_l(t)|^2 \right] \quad (\text{E.7})$$

However, $\sum_l A_l |C_l|^2 \equiv \sum_l B_l |C_l|^2$, therefore there is no change in the population and the norm should be conserved.

Appendix F

Dynamic σ Calculation

The algorithm for dynamically updating the σ parameter outlined in Gossel, 18³ is provided below.

1. Set an initial width parameter ($\sigma_{\mathbf{v}}^{(I)}(t - dt)$) and a constant we will name D .
2. Calculate a cutoff distance via: $r_{cut}(t) = D\sigma_{\mathbf{v}}^{(I)}(t - dt)$.
3. For each atom index, \mathbf{v} , and replica, I , gather replicas within a cutoff distance of the current replica. Set the number of replicas within the cutoff distance to N .
4. Calculate the distance between atoms on different replicas.
5. Find the standard deviation of these distances and set the width of the gaussian, centered on atom \mathbf{v} and replica I , to this standard deviation.
6. If the standard deviation is smaller than $\frac{D}{N} \min_I \left[\sigma_{\mathbf{v}}^{(I)}(t - dt) \right]$ then set $\sigma_{\mathbf{v}}^{(I)}(t) = \frac{D}{N} \min_I \left[\sigma_{\mathbf{v}}^{(I)}(t - dt) \right]$.

Appendix G

Basis Transformation

We can expand the Schrödinger equation in terms of a diabatic basis, ϕ rather than an adiabatic one, ψ . These 2 expansions are given in equations (G.1) and (G.2).

$$|\Psi\rangle = \sum_n C_n |\psi_n\rangle \quad (\text{G.1})$$

$$|\Psi\rangle = \sum_l u_l |\phi_l\rangle \quad (\text{G.2})$$

It follows from this we can define a transformation matrix, U_{ln} to transform between the adiabatic and diabatic bases. This is shown in equation (G.3) where the $\overset{\leftrightarrow}{I}$ symbol represents the identity matrix. This identity only holds in the orthogonal diabatic basis ϕ and wouldn't hold for non-orthogonal bases.

$$|\psi_n\rangle = \overset{\leftrightarrow}{I} |\psi_n\rangle = \sum_l |\phi_l\rangle \langle \phi_l | \psi_n \rangle = \sum_l |\phi_l\rangle U_{ln} \quad (\text{G.3})$$

A similar relation between expansion coefficients exists

$$\sum_n C_n |\psi_n\rangle = \sum_l u_l |\phi_l\rangle \quad (\text{G.4})$$

$$\sum_n C_n \langle \psi_m | \psi_n \rangle = \sum_l u_l \langle \psi_m | \phi_l \rangle \quad (\text{G.5})$$

$$C_m = \sum_l u_l U_{lm}^* \quad (\text{G.6})$$

Finally an important property of the transformation matrix is given in equation (G.7).

$$\sum_m U_{im} U_{lm}^* = \sum_m \langle \phi_i | \psi_m \rangle \langle \psi_m | \phi_l \rangle = \langle \phi_i | \phi_l \rangle = \delta_{il} \quad (\text{G.7})$$

Equations (G.3), (G.6) and (G.7) will be used below to transform the propagation equations from the adiabatic basis to the diabatic one.

G.1 Forces

The equation for the propagation of the forces in the adiabatic basis is:

$$\begin{aligned} \mathbf{F}_v^{(I)} = & - \sum_n |C_n^{(I)}|^2 \nabla_v E_n^{(I)} - \sum_{n,m} C_m^{*(I)} C_n^{(I)} (E_n^{(I)} - E_m^{(I)}) \mathbf{d}_{v,mn}^{ad,(I)} \\ & - \sum_{m,n} |C_m^{(I)}|^2 \left(\sum_{v'} \frac{2}{\hbar M_{v'}} \mathcal{Q}_{v',mn}^{(I)} \cdot \mathbf{f}_{m,v'}^{(I)} \right) [\mathbf{f}_{n,v}^{(I)} - \mathbf{f}_{m,v}^{(I)}] |C_n^{(I)}|^2 \end{aligned} \quad (\text{G.8})$$

The quantum momentum part of the equation cannot be easily transformed so this will focus on the Ehrenfest part:

$$\mathbf{F}_{eh,v}^{(I)} = - \sum_n |C_n^{(I)}|^2 \nabla_v E_n^{(I)} - \sum_{n,m} C_m^{*(I)} C_n^{(I)} (E_n^{(I)} - E_m^{(I)}) \mathbf{d}_{v,mn}^{ad,(I)} \quad (\text{G.9})$$

Using equation (10) in Carof, 17⁶⁸ and the Hellman-Feynman theorem we can rewrite equation (G.9) as equation (G.10):

$$\mathbf{F}_{eh,v}^{(I)} = \sum_{m,n} C_m^{*(I)} C_n^{(I)} \langle \psi_m | \nabla_v H | \psi_n \rangle \quad (\text{G.10})$$

We can substitute the coefficients and basis functions for those in equations (G.3) and (G.6). This carried out in equation (G.15). However, I have removed the trajectory and

atom index from the terms to make the notation clearer.

$$F_{eh,v} = \sum_{m,n} C_m^* C_n \langle \psi_m | \nabla H | \psi_n \rangle \quad (G.11)$$

$$= \sum_{m,n} \sum_i u_i^* U_{im} \sum_j u_j U_{jn}^* \sum_l U_{lm}^* \sum_k U_{kn} \langle \phi_l | \nabla H | \phi_k \rangle \quad (G.12)$$

$$= \sum_{m,n} \sum_{i,j,k,l} u_i^* u_j U_{im} U_{lm}^* U_{jn}^* U_{kn} \langle \phi_l | \nabla H | \phi_k \rangle \quad (G.13)$$

$$= \sum_{i,j,k,l} u_i^* u_j \delta_{il} \delta_{jk} \langle \phi_l | \nabla H | \phi_k \rangle \quad (G.14)$$

$$= \sum_{i,j} u_i^* u_j \langle \phi_i | \nabla H | \phi_j \rangle \quad (G.15)$$

However, in the code the expectation value of the gradient of the Hamiltonian ($\langle \phi_i | \nabla H | \phi_j \rangle$) isn't very easily calculable. However, the gradient of the Hamiltonian matrix elements ($\nabla \langle \phi_i | H | \phi_j \rangle$) is easily calculable via the overlap term, $\nabla H = C \nabla S_{ij}$. Therefore, using chain rule we can re-write equation (G.15) as:

$$F_{eh,v} = \sum_{i,j} u_i^* u_j \langle \phi_i | \nabla H | \phi_j \rangle \quad (G.16)$$

$$= \sum_{i,j} u_i^* u_j \left(\nabla \langle \phi_i | H | \phi_j \rangle - \langle \nabla \phi_i | H | \phi_j \rangle - \langle \phi_i | H | \nabla \phi_j \rangle \right) \quad (G.17)$$

$$= \sum_{i,j} u_i^* u_j \left(\nabla \langle \phi_i | H | \phi_j \rangle - \sum_l \langle \nabla \phi_i | \phi_l \rangle \langle \phi_l | H | \phi_j \rangle - \sum_l \langle \phi_i | H | \phi_l \rangle \langle \phi_l | \nabla \phi_j \rangle \right) \quad (G.18)$$

$$= \sum_{i,j} u_i^* u_j \left(\nabla \langle \phi_i | H | \phi_j \rangle + \sum_l \mathbf{d}_{il} \langle \phi_l | H | \phi_j \rangle - \sum_l \mathbf{d}_{lj} \langle \phi_i | H | \phi_l \rangle \right) \quad (G.19)$$

Giving the final equation for the transformed forces as:

$$\mathbf{F}_{eh,v}^{(I)} = \sum_{i,j} \mathbf{u}_i^{*(I)} \mathbf{u}_j^{(I)} \left(\nabla_v H_{ij}^{(I)} + \sum_l \mathbf{d}_{lk,v}^{(I)} H_{lj}^{(I)} - \sum_l \mathbf{d}_{lj,v}^{(I)} H_{il}^{(I)} \right) \quad (G.20)$$

Appendix H

Adiabatic State Initialisation

By diagonalising the Hamiltonian we get the adiabatic energies (eigenvalues) for each state and transformation matrix (eigenvectors) to calculate diabatic states \mathbb{U} . We can calculate diabatic coefficients corresponding to each adiabatic state via equation (H.1) below.

$$\mathbb{U}\mathbf{C}_n = \mathbf{u}_n \quad (\text{H.1})$$

Where \mathbb{U} is the transformation matrix of size $(N_{\text{mol}}, N_{\text{mol}})$, \mathbf{C} is a complex vector of size N_{mol} containing coefficients for adiabatic state n and \mathbf{u} is a complex vector of size N_{mol} containing coefficients for diabatic state n .

Seeing as we would like to find the diabatic population corresponding to each adiabatic state we localise coefficients on each pure adiabatic state and carry out the transformation e.g: $C_i = (1+0i, 0+0i, 0+0i, \dots)$ when we want to find the diabatic coefficient corresponding to state 1 and $C_i = (0+0i, 1+0i, 0+0i, \dots)$ when we want to find the diabatic coefficient corresponding to state 2 etc.. Therefore, the column, n , of the transformation matrix, \mathbb{U} , gives the diabatic coefficients corresponding to adiabatic state, n , as shown below in equation (H.2)

$$U_{in} = u_i \quad (\text{H.2})$$

Where n is the adiabatic state index and i is the diabatic (molecular) state index.

Once we have the diabatic state corresponding to each adiabatic state, and the en-

ergy of that adiabatic state, we can find which state best fulfills the requirements of being close to the center of the system and being within $3KT$ of the ground state. In order to do this, we can loop over each adiabatic state in increasing order of energy. The center of the system is calculated and the population weighted average center of mass, \mathbf{R}_n of the diabatic coefficients corresponding to adiabatic state n is calculated as in equation (H.3).

$$\mathbf{R}_n = \sum_i |u_i|^2 \mathbf{R}_{COM,i} \quad (\text{H.3})$$

The Euclidean distance between the center of the system and $\mathbf{R}_{COM,i}$ is calculated and if this distance is below some threshold value then we initialise the surface hopping trajectory on that adiabatic state. If we do not find any states within $3KT$ of the ground state and within an acceptable radius of the center we start again this time increasing the maximum allowed distance from the center. If this maximum allowed distance is increased such that we reach another threshold distance the energy threshold is increased this time until a state is found that is close enough to the center. In this way we find an adiabatic state, which when transformed, gives a diabatic population close to center of the system and near the ground state energy.

Appendix I

Analytic Overlap Method

Appendix J

Colophon

This is a description of the tools you used to make your thesis. It helps people make future documents, reminds you, and looks good.

(example) This document was set in the Times Roman typeface using L^AT_EX (specifically LuaTeX) and BibT_EX, composed with Vim Used Archer, Kathleen etc...

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