# Excited State QMMM using NWChem

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Cyber Training Workshop 2023

Introduction

Photochemical reactions fall under the field of green chemistry since light is used as a renewable source of energy and occurs under mild conditions[1]. Light-promoted denitrogenation is one of the cleanest reactions, as its byproduct is nitrogen gas. The photo denitrogenation of diazabicyclo[2.1.1]hep-2-ene (DBH) has been utilized for over six decades[2] to synthesize retained and inverted bicyclo[2.1.0]pentane (housane) (Scheme 1). Housane is a highly strained compound used as a building block in stereoselective synthesis, including the synthesis of natural products with biological activity, such as (±)-vibralactone[3], an antibiotic and potentially an anti-obesity drug. Quantum mechanical calculations have provided a qualitative rationale for the mechanism of this reaction. In the past, I have performed non-adiabatic molecular dynamics (NAMD) with multiconfigurational methods on the gas phase to quantify the origin of stereoselectivity. Several studies have investigated the solvent effect on stereoselectivity. In this workshop, I will explore the effects of methanol solvent through a combined quantum mechanical/molecular mechanics (QM/MM) module in NWChem[4] to conduct dynamics. DBH will be treated quantum mechanically (QM) with time-dependent density functional theory (TD-DFT) and methanol molecules will be treated with classical molecular mechanics (MM).

Scheme 1 – Stereoselectivity in the Direct Photolysis of 2,3-Diazabicyclo[2.2.1]hept-2-ene
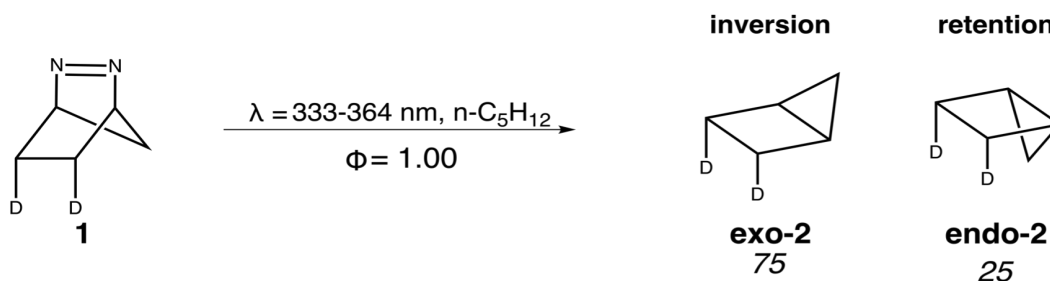
Methods

Generation of required files

To run QMMM dynamics, a preparation run is needed to generate the required files. These include the restart file (.rst), which describes the atom positions of the system; the topology file (.top), which contains all static information about the molecular system and described the connectivity of

the molecular system with the assigned force field, and the sequence file (.seq), which has a list of atoms with their force field, partial charges, and bonded interactions. First, I created a PDB file containing DBH coordinates formatted for use in the NWChem preparation module. Next, I copied the restart and segment files for methanol from the NWChem source directory. I then specified a 5.3 Å3 box with periodic boundary conditions in the preparation input and submitted the job. An initial preparation run was performed to generate a temporary fragment file for DBH. In this file, the force-field atom type for the AMBER force field (GAFF)[5] was manually specified. Finally, the preparation input was submitted again, and the necessary files for the methanol-solvated DBH system in a periodic box were generated.

<u>Optimization of the system</u>
For all atoms the 6-311G** basis set[6, 7,] and PBE0 hybrid exchange-correlation functional[8] for the QM region. The shake bond constraint was applied to the methanol, so their bond length and angle during the optimization. The optimization will cycle through the optimization of the QM region and the optimization of the solvent MM region.

<u>Equilibrating the regions and QMMM Simulation</u>
First, the MM region was equilibrated for 200 ps with a 0.002 timestep through an MD simulation where the solvent molecules were allowed to move and the DBH was held fixed at the center of the box. The temperature was kept fixed at 298.15 by using Berendsen's thermostat[9]. Then, the QM solute region and MM solvent region were equilibrated together for 0.05 ps with a 0.0005 timestep. Then the DBH was centered in the box of methanol molecules and the QMMM dynamics were submitted. The dynamics were submitted for ground state with DFT on the QM region as training and for the first excited state with TD-DFT.

Results
Since the procedure was performed for the ground and first excited state, it was obtained an optimized and equilibrated methanol-solvated DBH for both states. Figure 1 shows the structure of the chromophore and important geometrical parameters.
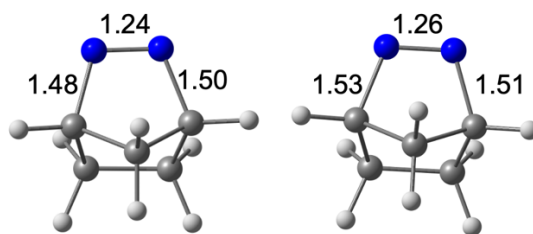

Figure 1 – Bond length in angstroms for the ground state structure (left) and first excited state structure (right).

From experimental studies, it was determined that the dominant electronic transition is $n \rightarrow \pi^*$ for DBH, and the geometrical changes between the ground state and excited state geometry are consistent with an increased population of the π^*_{NN} orbital since the bond between the nitrogen

increases from 1.24 to 1.26 Å. Also, the σ_{CN} distances change; one σ_{CN} bond length increases from 1.48 to 1.53 Å, and the other σ_{CN} bond length shortens from 1.50 to 1.51 Å. This suggests a possible asynchronous breakage of the σ_{CN} bond.

**Table 1** – Vertical Excitation Energies (eV)

State	Energy (eV)	Wavelength (nm)	Oscillator strength
S_1	3.51	353	0.0004
S_2	6.14	202	0.0002
S_3	6.91	179	0.0057
S_4	6.98	178	0.0290
S_5	7.10	175	0.0067
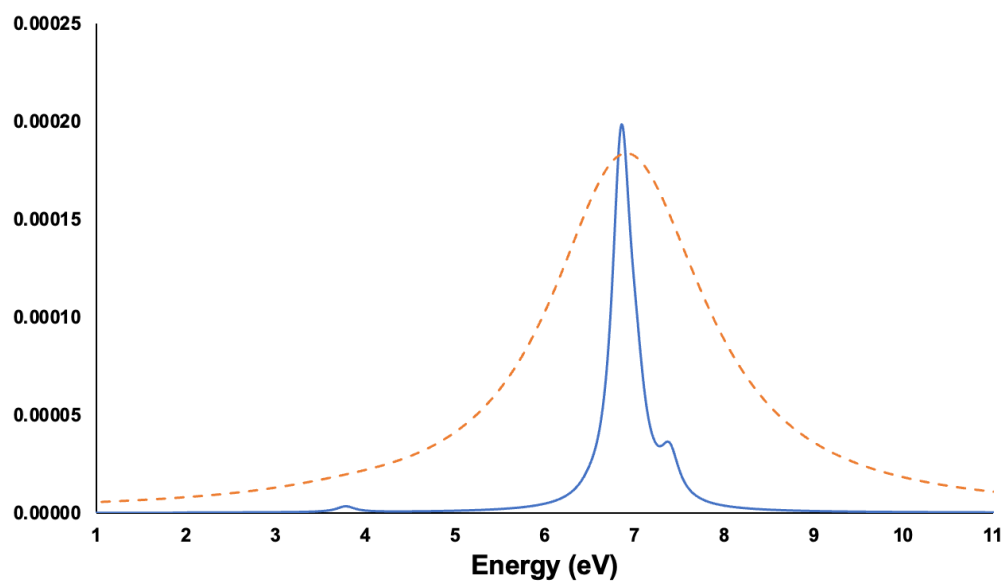
Figure 2 – UV Visible spectrum with 0.25 broadening in blue and 2.00 in orange

Table 1 shows the vertical excitations energies. The vertical excitation energy from S_0 to S_1 agrees with the experimental absorbance of $\lambda_{max} = 338$ nm (3.67 eV). Based on these energies only the S_1 state is accessible with the range of irradiation wavelengths of the experimentally used light source (333-364 nm). The QMMM dynamics were performed from the S_1 excited state. On figure 2, it is possible to see the effects of broadening the spectrum.
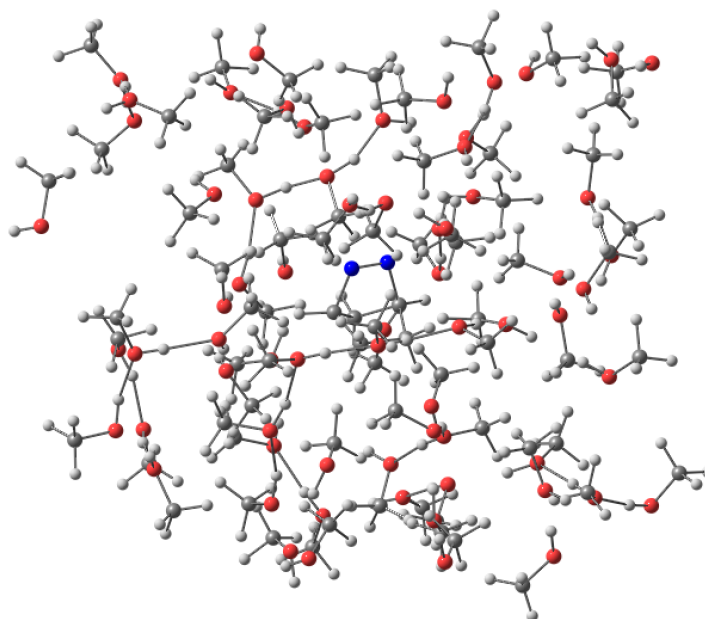
Figure 3 – Methanol solvated DBH

Conclusion

The QMMM with TD-DFT method proves to be significantly more costly compared to QMMM with DFT. Although the dynamics with TDDFT are still ongoing, no instances of bond breaking, or formation have been observed within the first 177fs. This project has served as an invaluable training experience for acquiring the skills to execute QMMM using NWChem. Moving forward, I intend to expand the scope of the project by incorporating diverse derivatives and solvents.

References

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