

# Tully Models revisited: The molecule is the limit?

Lea M. Ibele

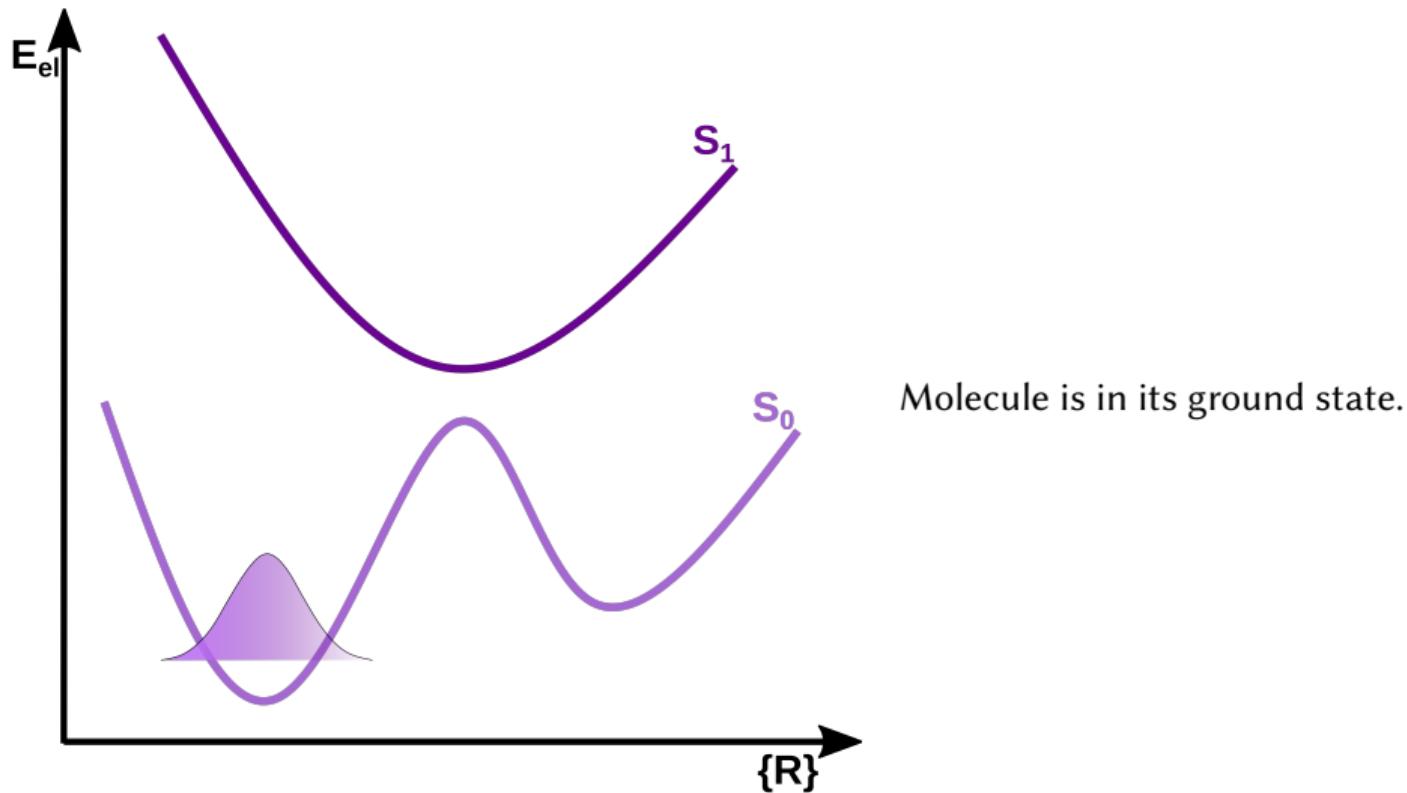
VISTA

October 22, 2020

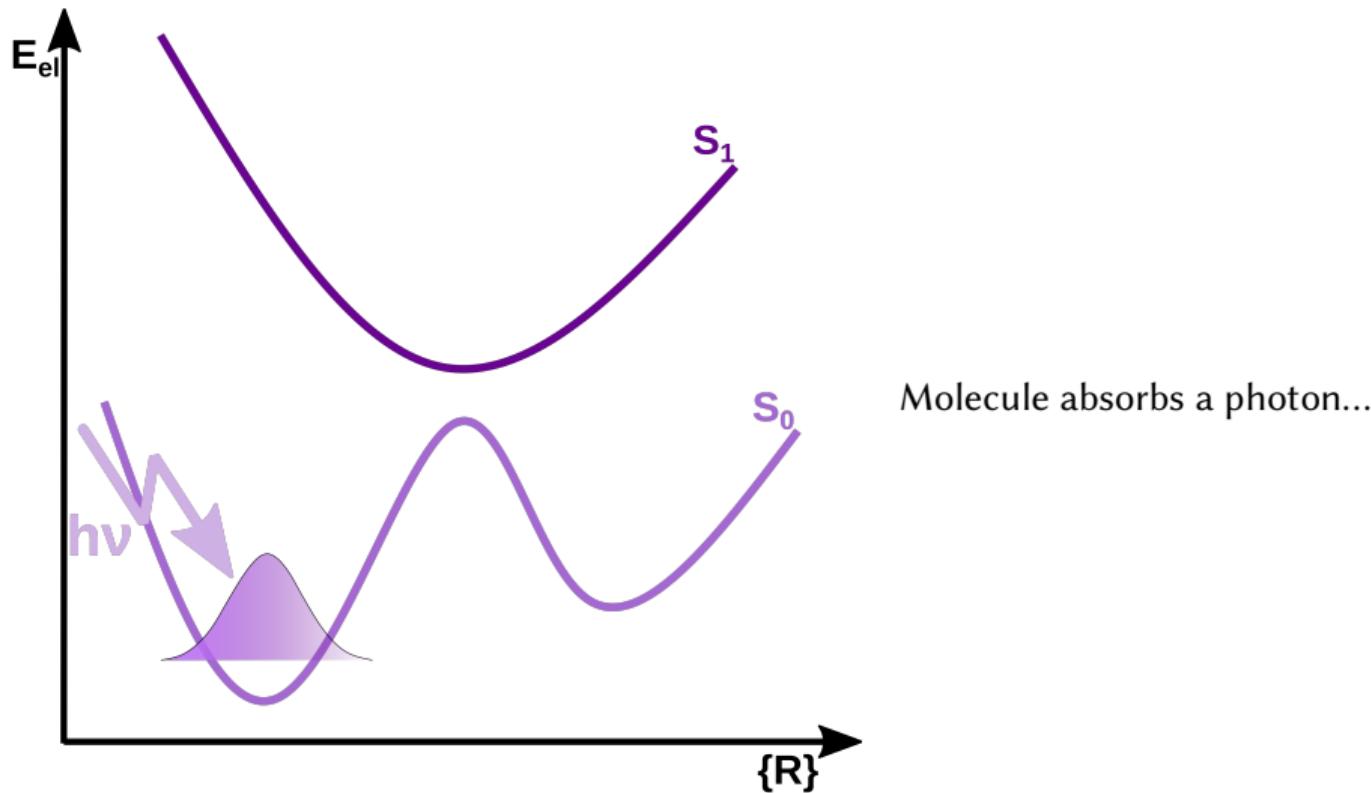


Engineering and Physical Sciences  
Research Council

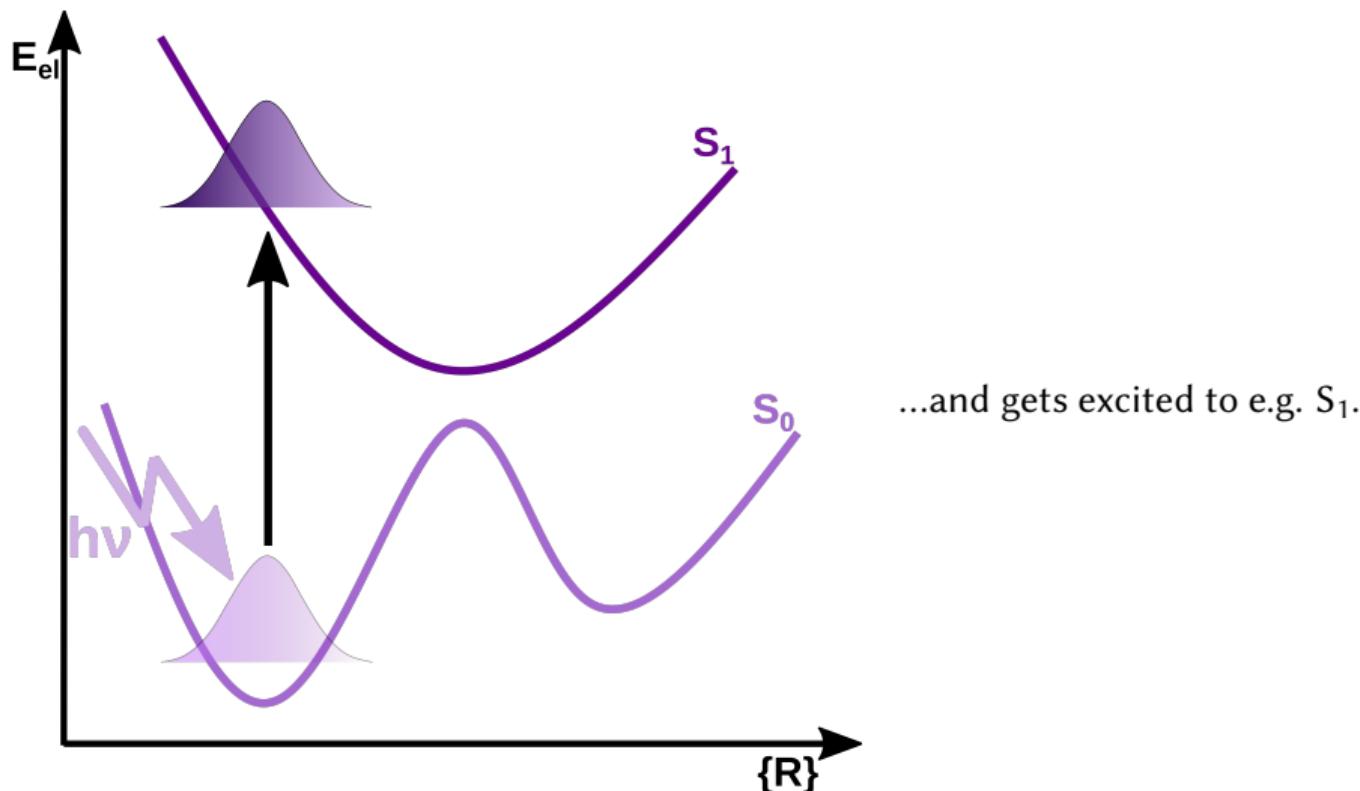
# In Silico Photochemistry



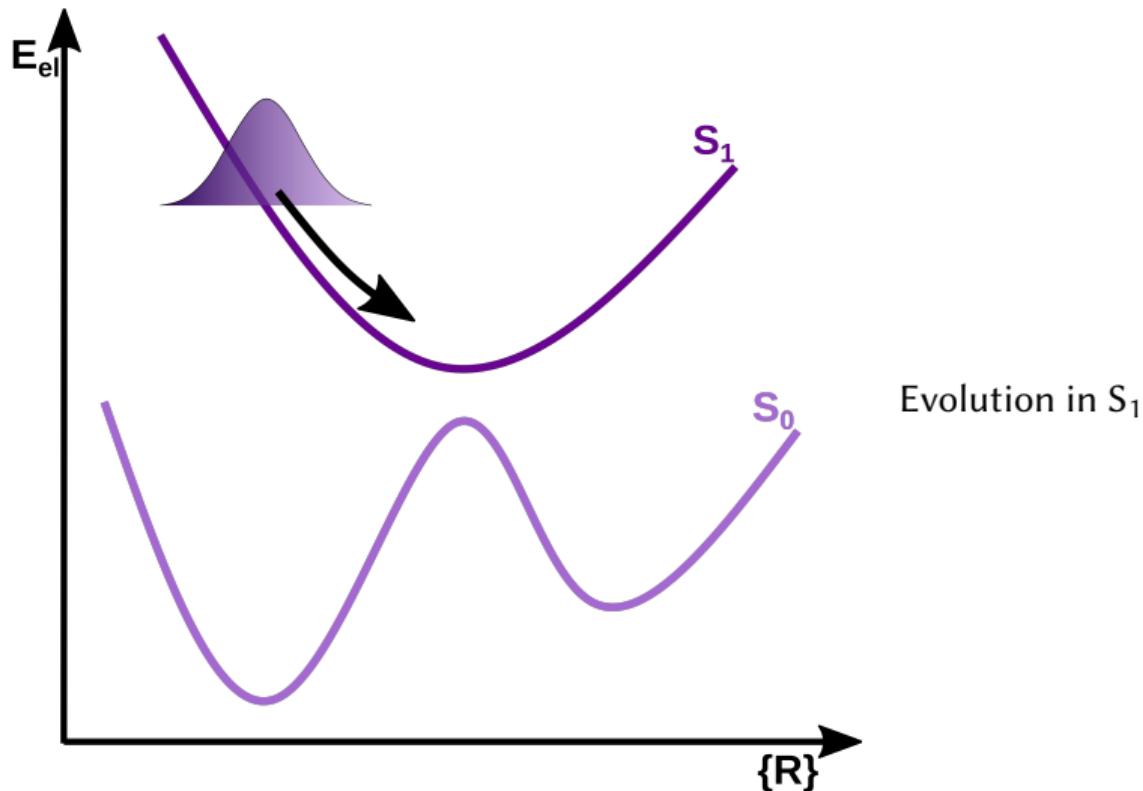
# In Silico Photochemistry



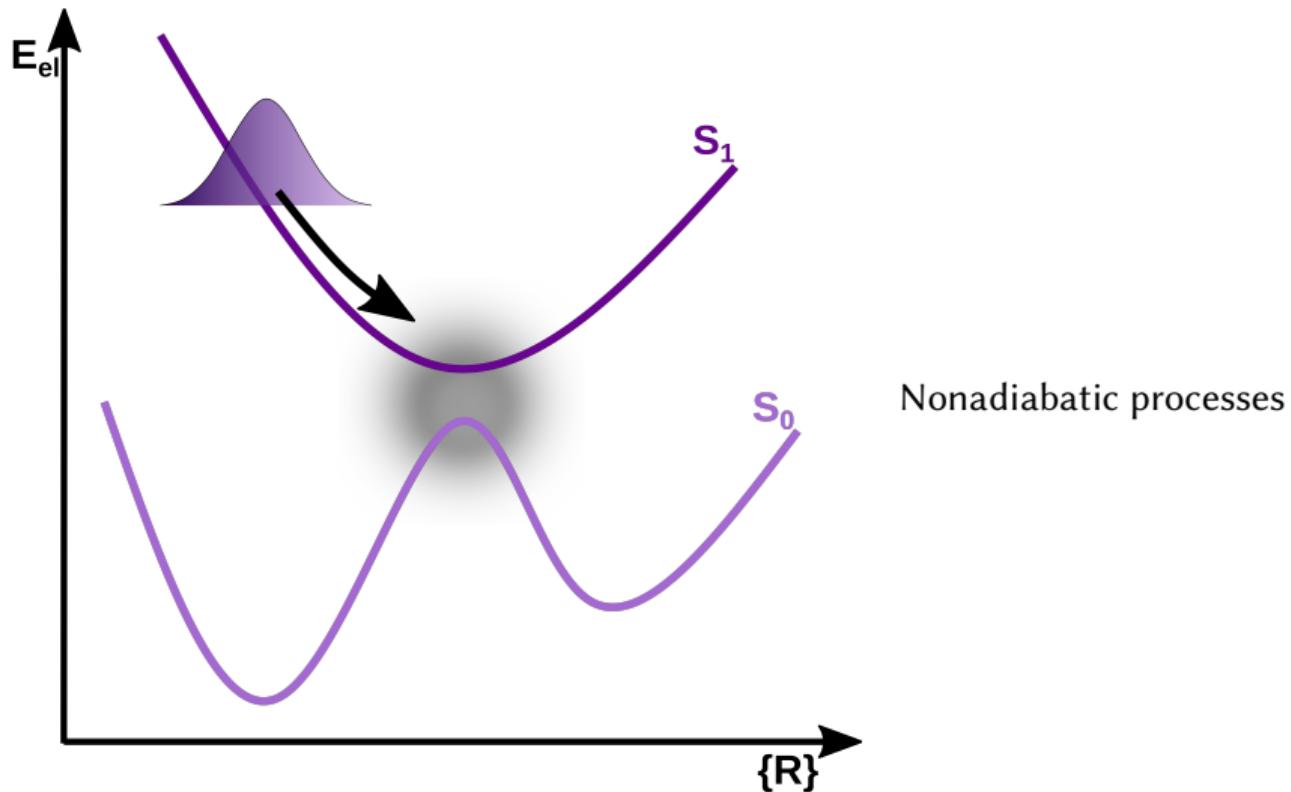
# In Silico Photochemistry



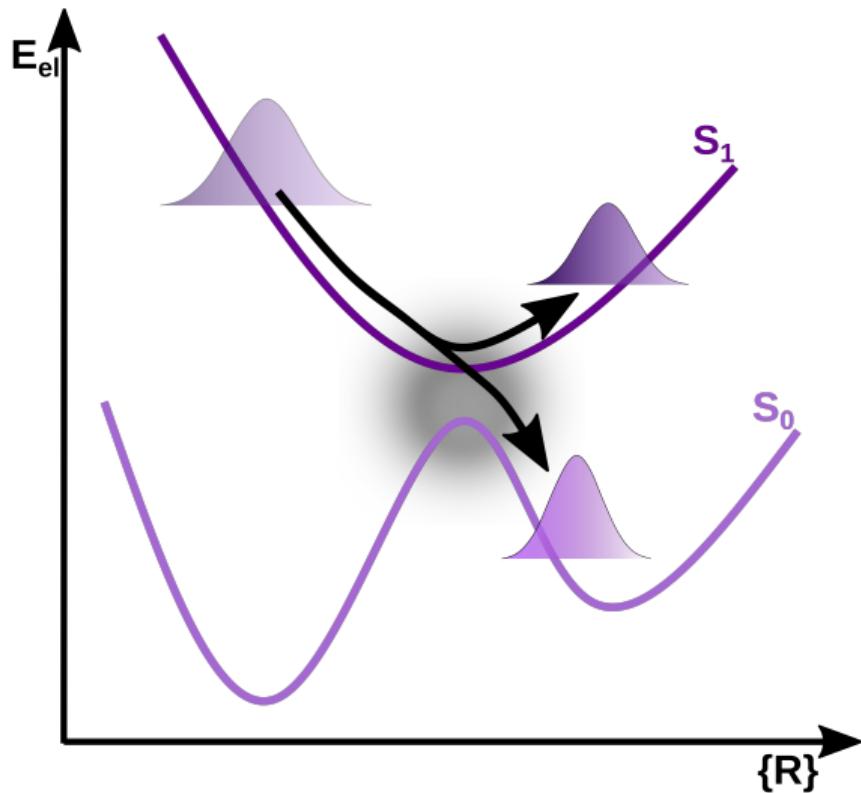
# In Silico Photochemistry



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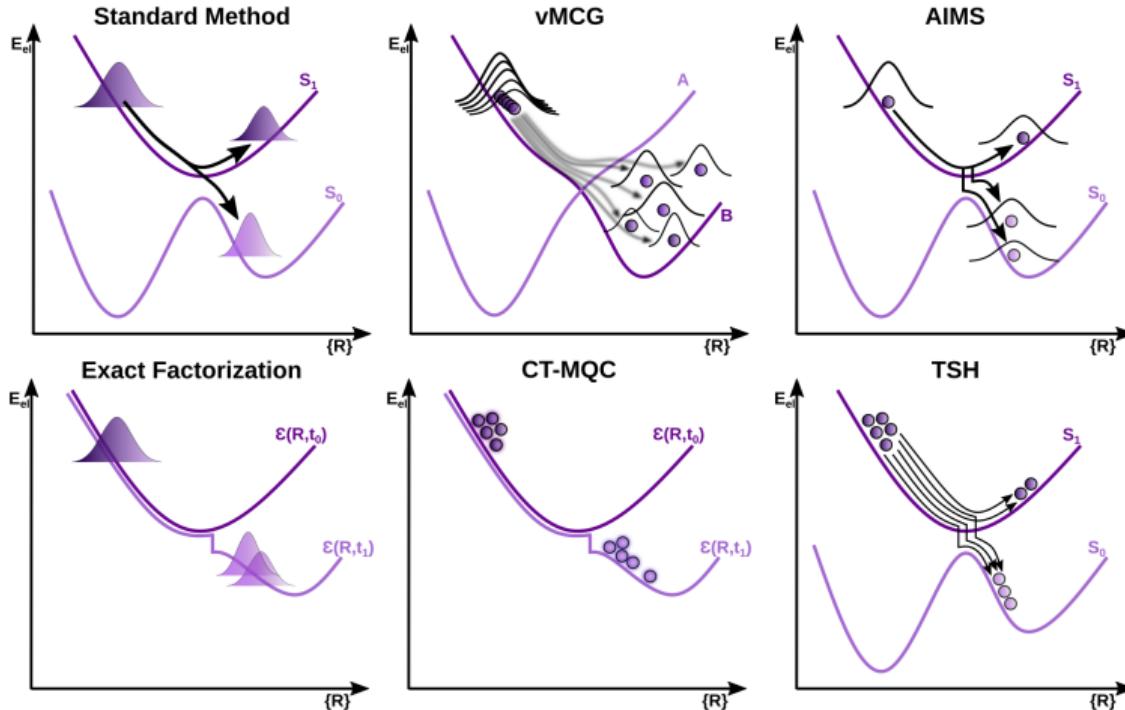


Splitting of wavepacket.

*Challenge for computational chemistry:*

- ▶ Electrons and nuclei coupled!
- ▶ Accurate electronic structure, valid at all times
- ▶ Nuclear dynamics

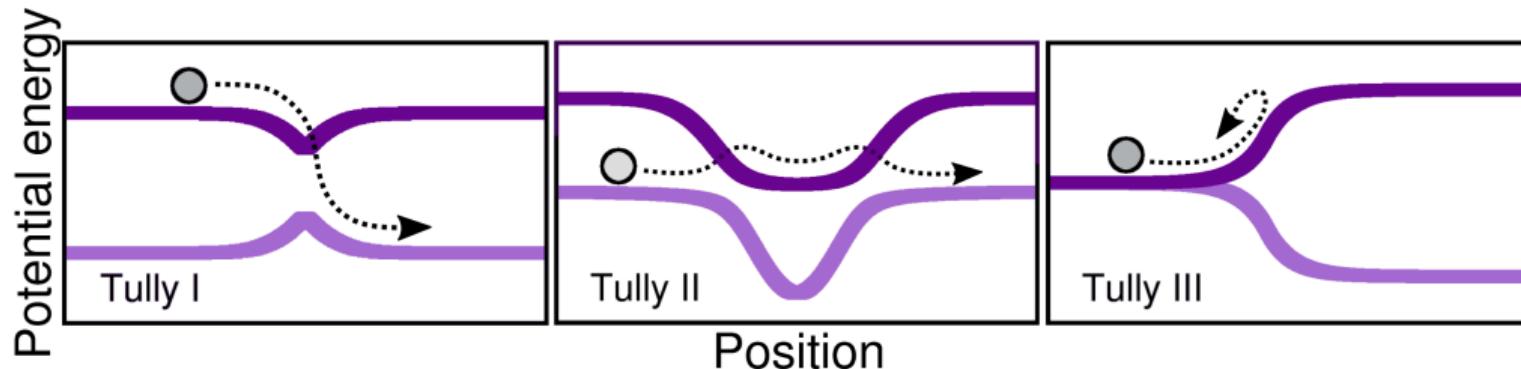
# Nonadiabatic Dynamics Approaches



Countless different methods to describe photodynamics:

- ▶ different representation of nuclear wavefunction
- ▶ different level of approximations
- ▶ quantum or classical nuclei
- ▶ accounting for quantum effects
- ▶ *Any new method needs to be duly tested to understand its limitations*

# Tully Models: A 1D Testbed

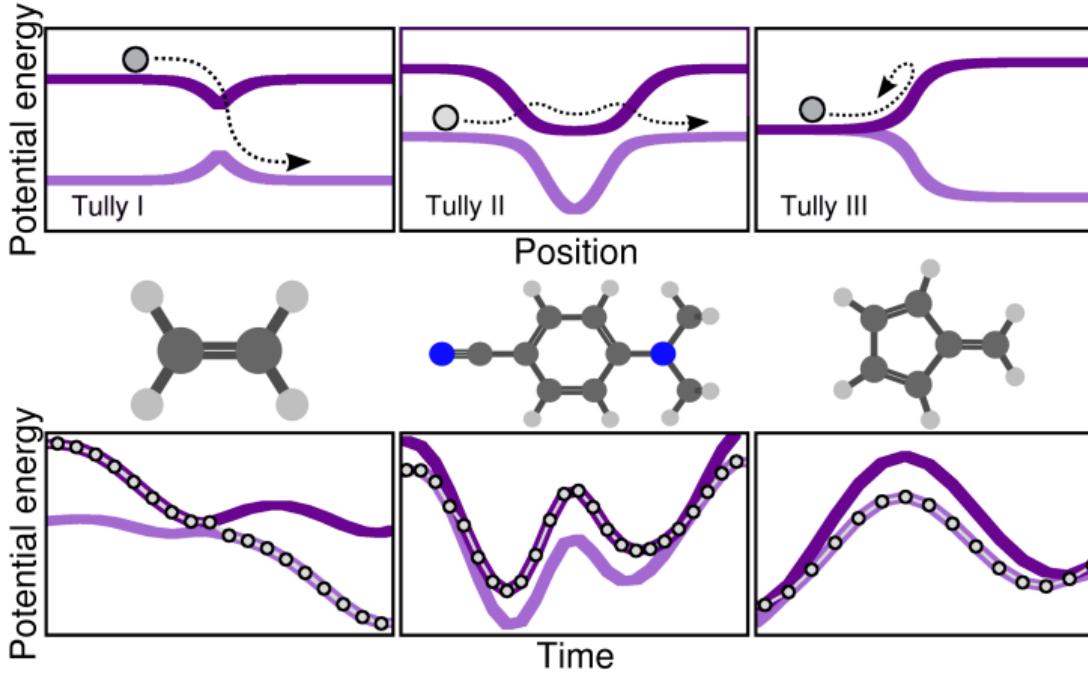


Used to test e.g.: full multiple spawning, semiclassical initial value representation, symmetrical quasi-classical windowing combined with Meyer-Miller mapping Hamiltonian, surface hopping Herman-Kluk semiclassical initial value representation method, semiclassical Monte-Carlo, dephasing representation of quantum fidelity, counter-propagating wave methods trajectories, Ehrenfest-Plus, coupled-trajectory mixed quantum/classical dynamics, quantum trajectory mean-field approach, iterative linearized approach to nonadiabatic dynamics, mean-field dynamics with stochastic decoherence, nonadiabatic Bohmian dynamics, mean-field molecular dynamics with surface hopping, non-Hermitian surface hopping, multi-state trajectory approach to nonadiabatic dynamics, partial linearized density matrix dynamics, ring polymer surface hopping, quantum trajectory surface hopping, consensus surface hopping, quasiclassical mapping Hamiltonian methods...

# Test Set for Molecular Simulations

As we want to ultimately simulate dynamics of molecular in their full dimensionality:

## Molecular Tully Models

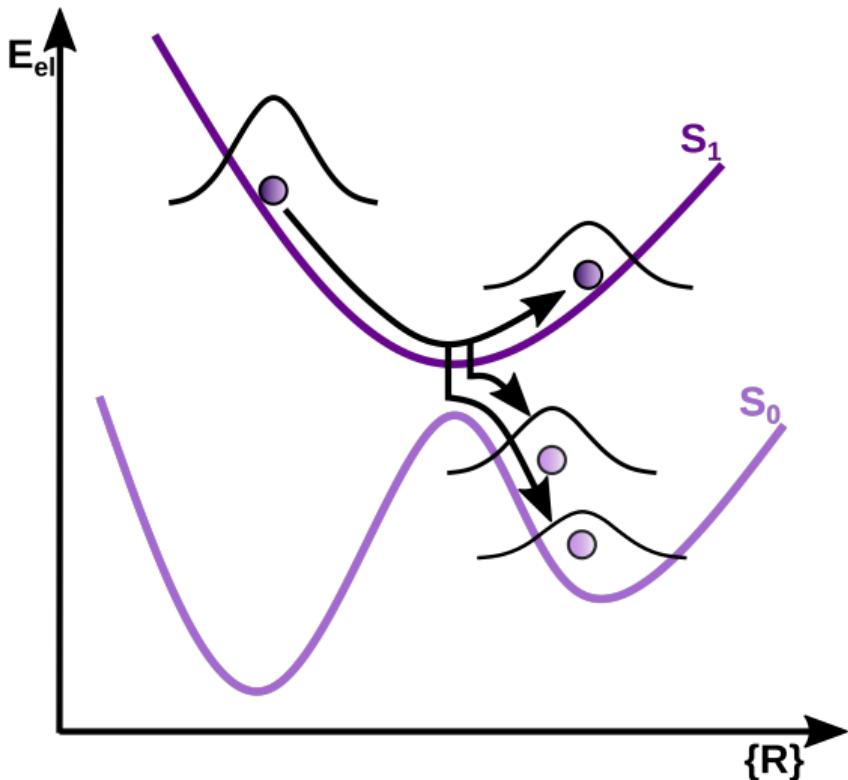


Highlighted challenges with *Ab Initio Multiple Spawning* and (*decoherence corrected*) *Trajectory Surface Hopping*

All initial conditions are available at  
[DOI:10.15128/r1qj72p715m](https://doi.org/10.15128/r1qj72p715m)

We want to provide a testset of real, full-dimensional, molecular systems for nonadiabatic dynamics!

# Ab Initio Multiple Spawning

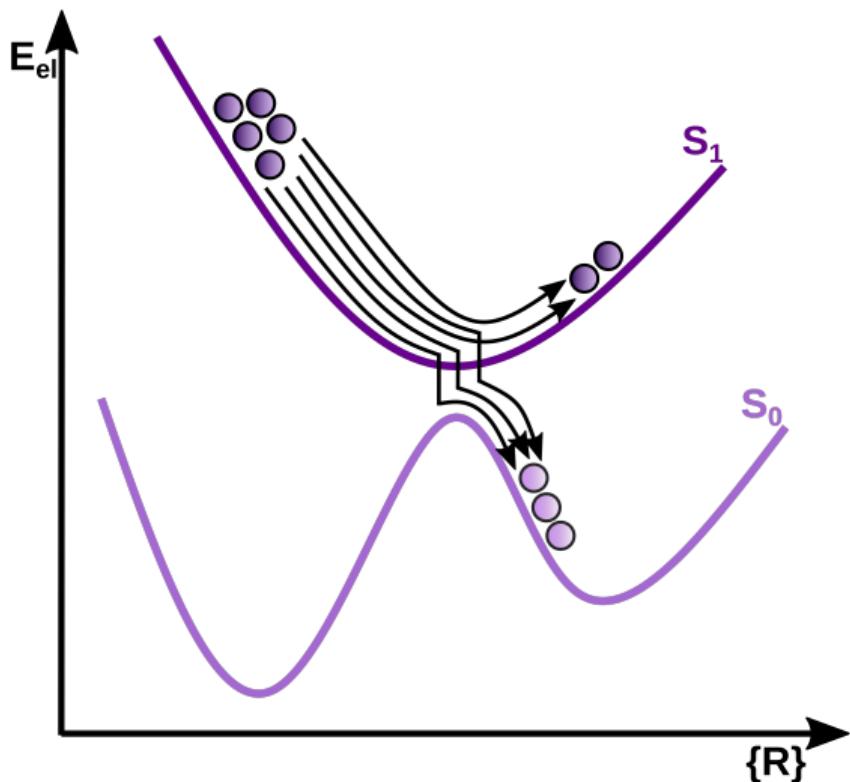


- ▶ Nuclear wavefunction expressed in basis of *Gaussian trajectory basis functions (TBFs)*
- ▶ TBFs propagated classically, but are fully coupled
- ▶ Spawning allows to adapt the size of the basis in regions of high nonadiabaticity
- ▶ Full Multiple Spawning (FMS) *in principle* exact
- ▶ Ab Initio Multiple Spawning (AIMS) for molecules approximates couplings:
  - ▶ Saddle Point Approximation of order zero (SPA0)
  - ▶ Independent First Generation Approximation (IFGA)

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Martínez et al., *J. Phys. Chem.* (1996), 100, 7884-7895;  
Martínez et al., *Adv. Chem. Phys.* (2002), 121, 439-513

# Trajectory Surface Hopping

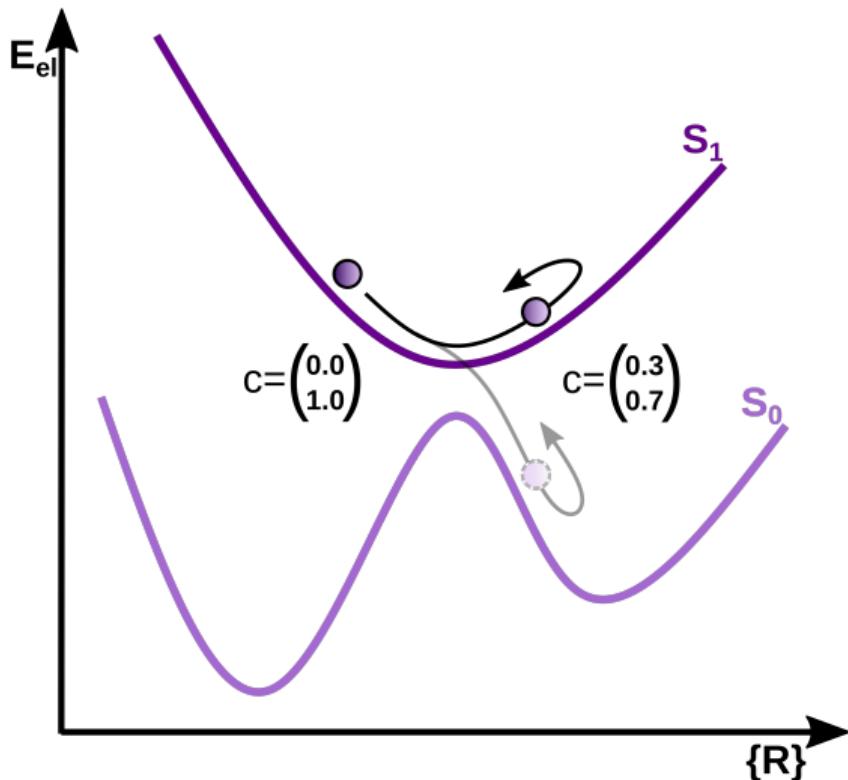


- ▶ Applying an *Independent Trajectory Approximation (ITA)*
- ▶ Swarm of totally independent classical trajectories
- ▶ Associated amplitudes mimic a wavepacket
- ▶ Nonadiabatic effects:  
Hops between surfaces allow change of electronic states

Tully, *J. Chem. Phys.* (1990), 93, 1061-1071;

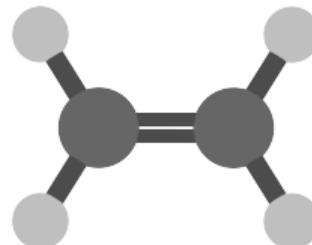
Hammes-Schiffer and Tully, *J. Chem. Phys.* (1994), 101, 4657-4667

# Trajectory Surface Hopping

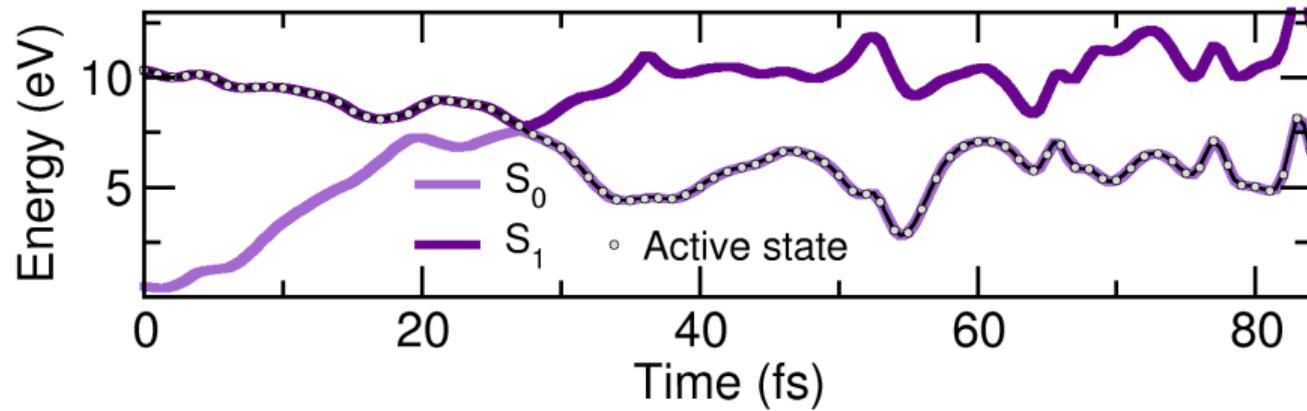
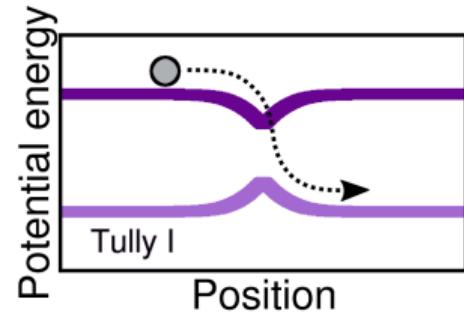


- ▶ *TSH is overcoherent*
- ▶ All electronic population follows force of active state
- ▶ A variety of *ad hoc* corrections (dTSH), see e.g.:
  - ▶ Zhu et al., *J. Chem. Phys.* (**2004**) 121, 7658
  - ▶ Jasper and Truhlar, *J. Chem. Phys.* (**2007**), 127, 194306
  - ▶ Granucci and Persico, *J. Chem. Phys.* (**2007**), 126, 134114
  - ▶ Granucci et al., *J. Chem. Phys.* (**2010**), 133, 134111
  - ▶ Shenvi et al., *J. Chem. Phys.* (**2011**), 134, 144102
  - ▶ Jain et al., *J. Chem. Theory Comput.* (**2016**), 12, 11, 5256
  - ▶ Ha et al., *J. Phys. Chem. Lett.* (**2018**), 9, 1097
  - ▶ ...

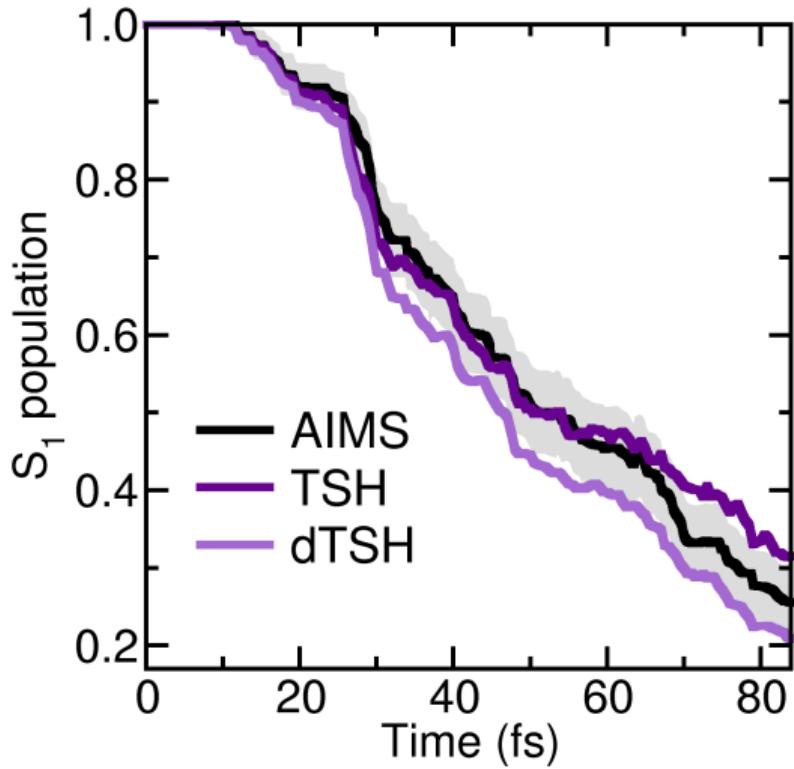
# Molecular Tully I: Ethylene



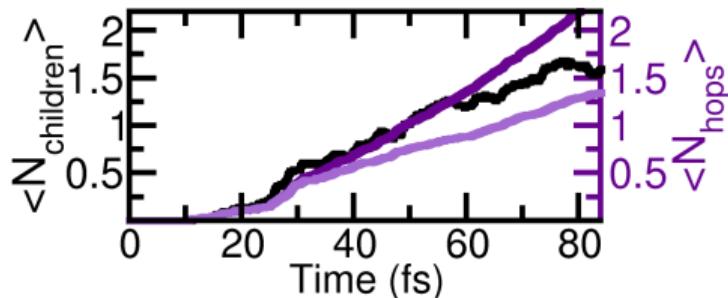
**Single avoided crossing**  
SA(3)-CASSCF(2/2)/6-31G\* (MOLPRO)  
66 Initial Conditions  
(d)TSH repeated with 10 random numbers  
with SHARC  
AIMS with FMS90 in Molpro



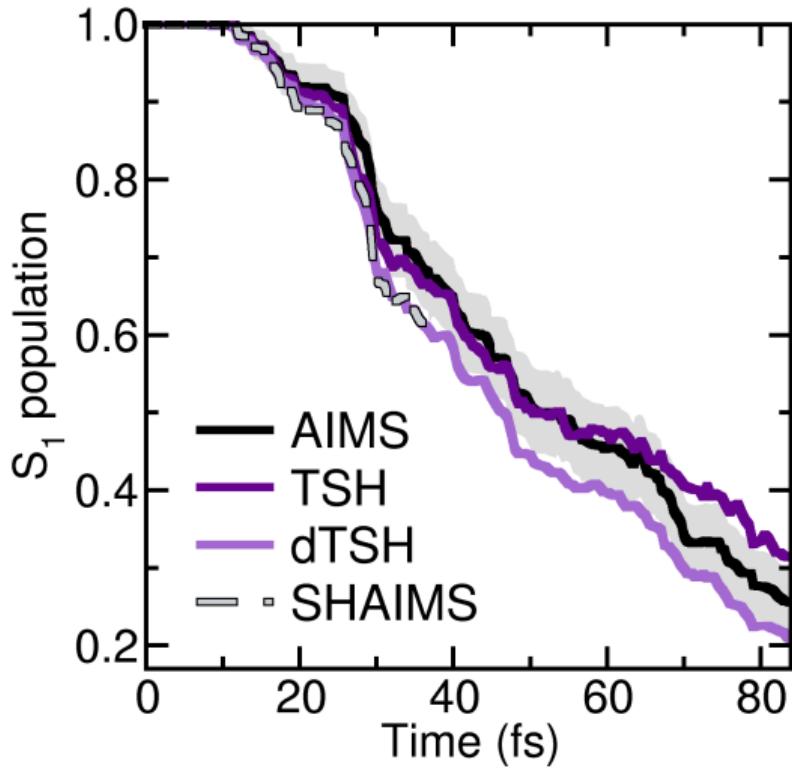
# Molecular Tully I: Ethylene



**AIMS:** rapid decay, on average below 2 spawns  
**TSH:** similar decay, number of hops rises above two  
**dTSH:** significantly slower decay than AIMS  
In TSH larger number of back hops – slower deactivation artifact of overcoherence



# Molecular Tully I: Ethylene

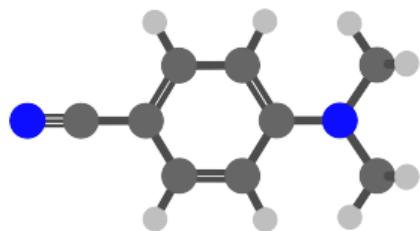


**Surface Hopping approach to AIMS:**  
Approximates AIMS equations of motion to resemble TSH:

- ▶ remove all intrastate couplings
- ▶ force overlap=1 between TBFs on different states
- ▶ place the TBFs on the same position
- ▶ only consider the NACV of parent TBF

Reproduces dTSH perfectly – differences due to ITA inherent to TSH

# Molecular Tully II: DMABN



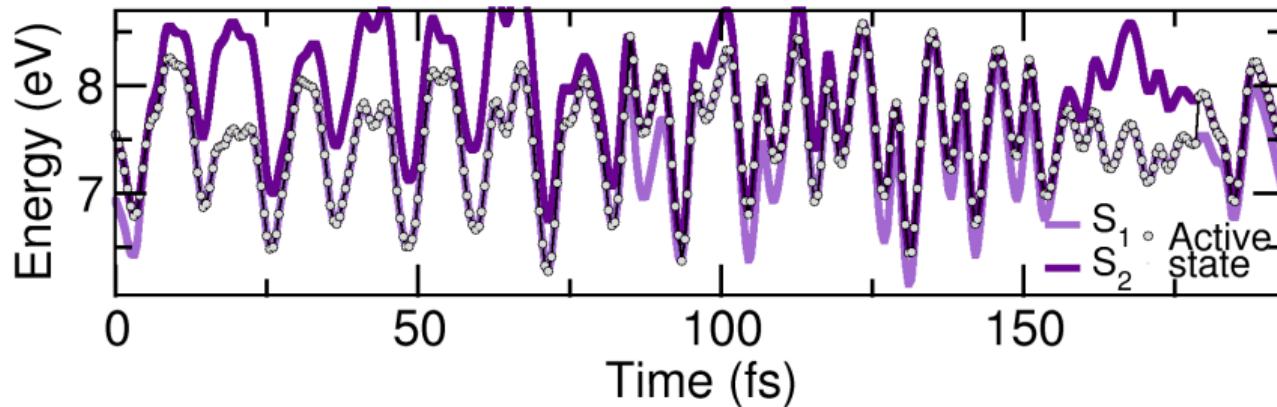
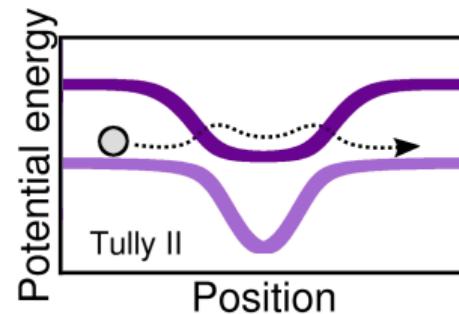
Dual avoided crossing

TDA-LC-PBA/6-31G

21 Initial Conditions

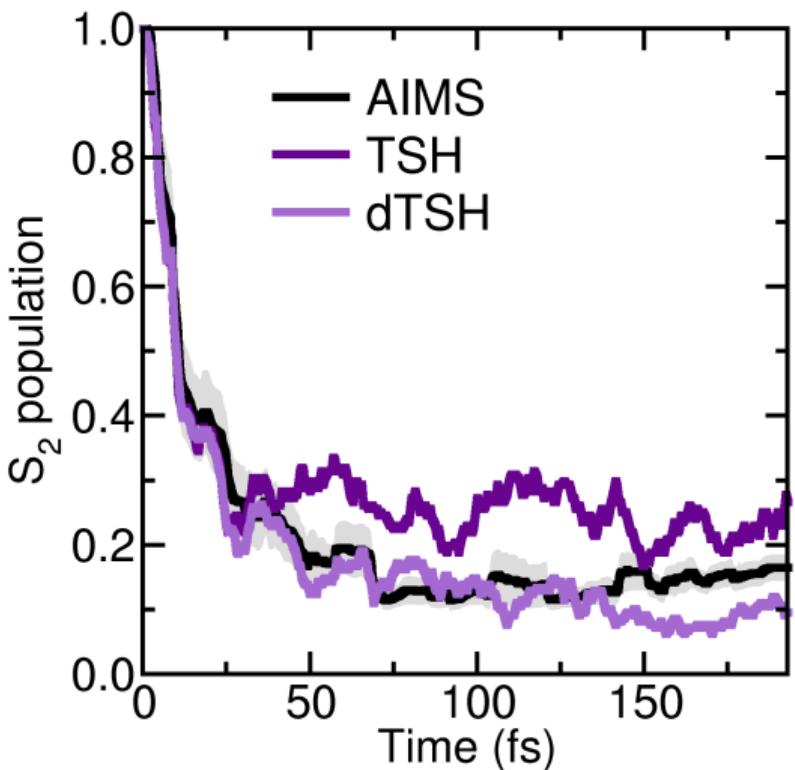
(d)TSH repeated with 10 random numbers  
with Gaussian09/SHARC

AIMS with FMS90 in TeraChem from <sup>a</sup>



<sup>a</sup>Curchod et al., *J. Phys. Chem. A* (2017), 121, 1, 265-276

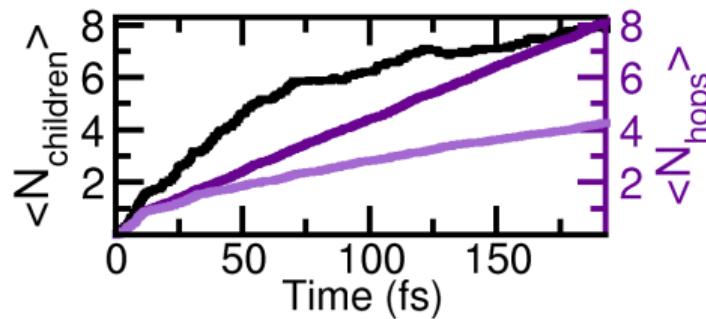
# Molecular Tully II: DMABN



**AIMS:**<sup>a</sup> rapid decay, after 50 fs oscillations in the population, large number of spawns

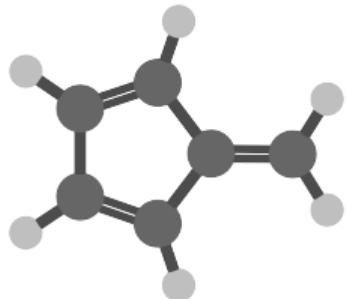
**TSH:** similar initial decay, deviations after 25 fs, total comparable number of hops

**dTSH:** great agreement with AIMS, much smaller number of hops



<sup>a</sup>Curchod et al., *J. Phys. Chem. A* (2017), 121, 1, 265-276

# Molecular Tully III: Fulvene

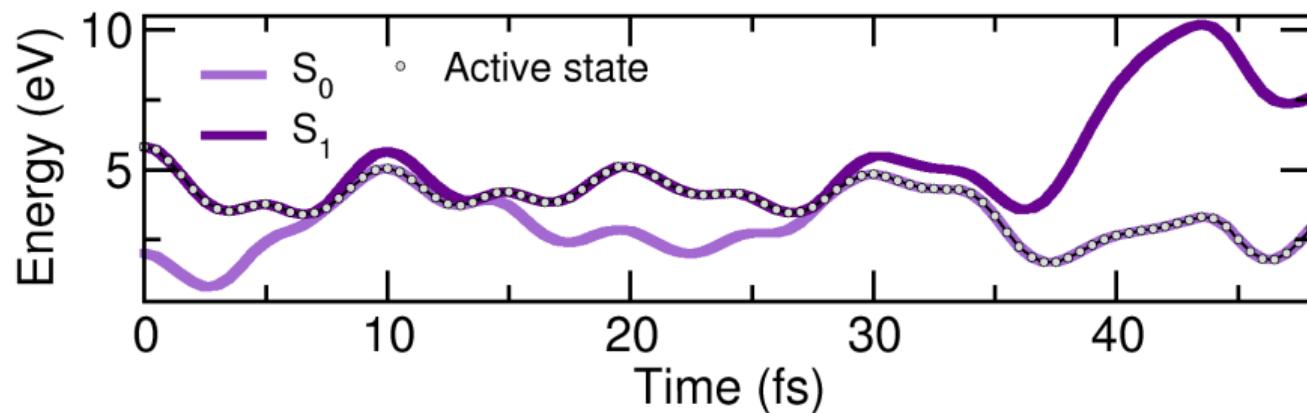
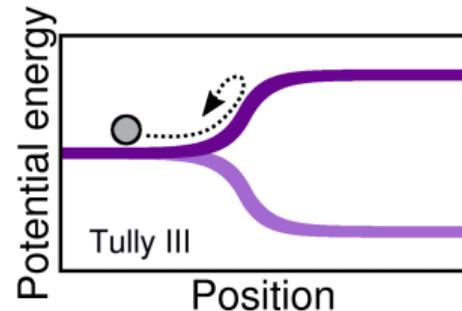


Extended coupling with reflection

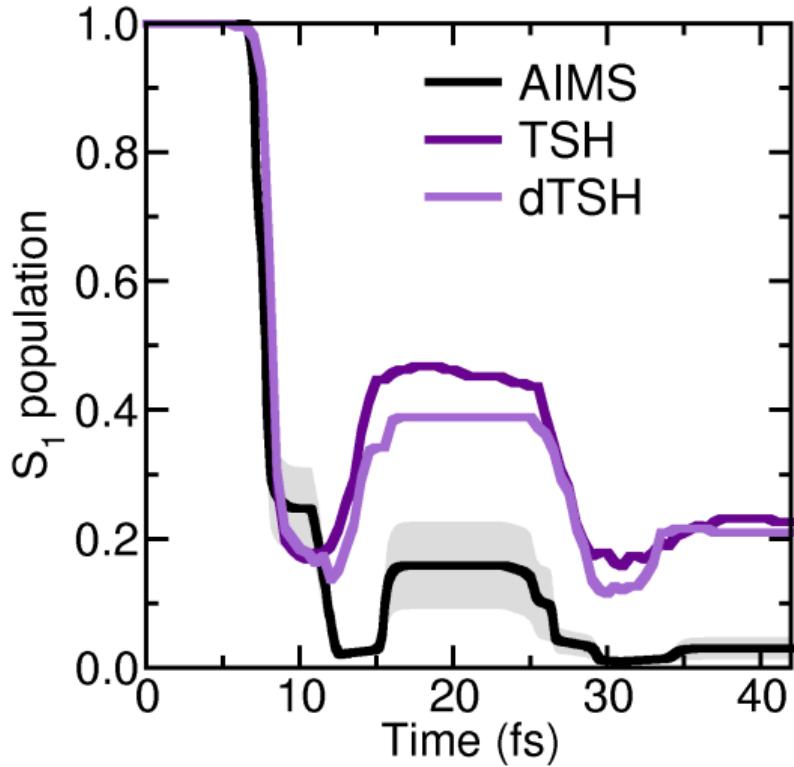
SA(3)-CASSCF(6/6)/6-31G\* (MOLPRO)

18 Initial Conditions (momenta set to zero)  
(d)TSH repeated with 10 random numbers  
with SHARC

AIMS with FMS90 in Molpro



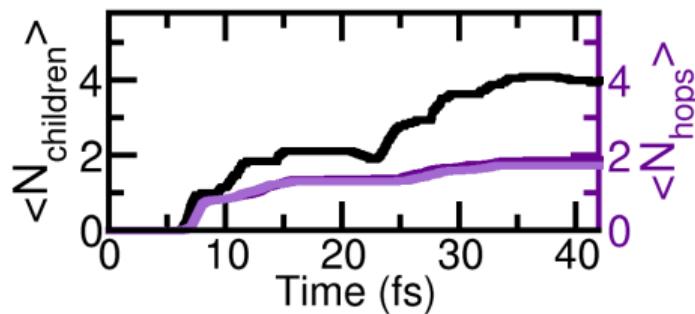
# Molecular Tully III: Fulvene



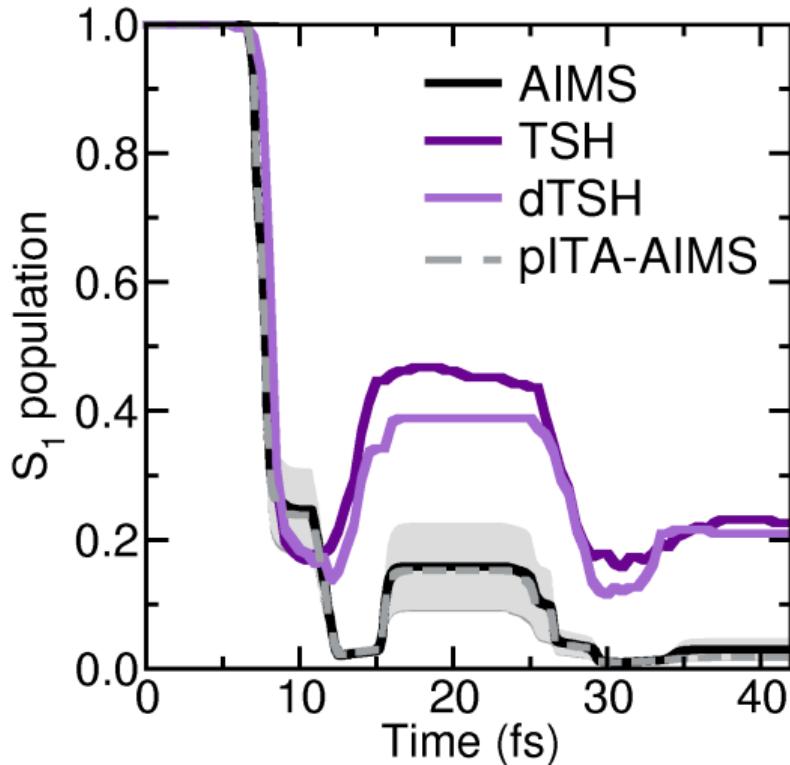
**AIMS:** almost complete initial decay, ~18% of reflection

**TSH:** less decay, stronger reflection (~48%)

**dTSH:** similar to TSH



# Molecular Tully III: Fulvene

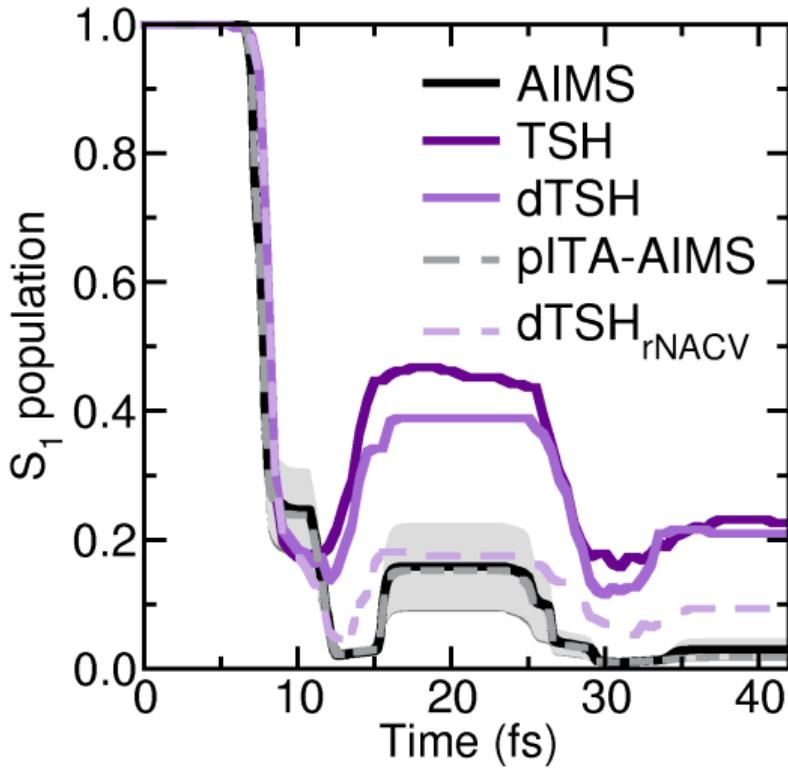


**pseudo Independent Trajectory Approximation in AIMS:**

removes all direct intrastate couplings between TBFs in AIMS

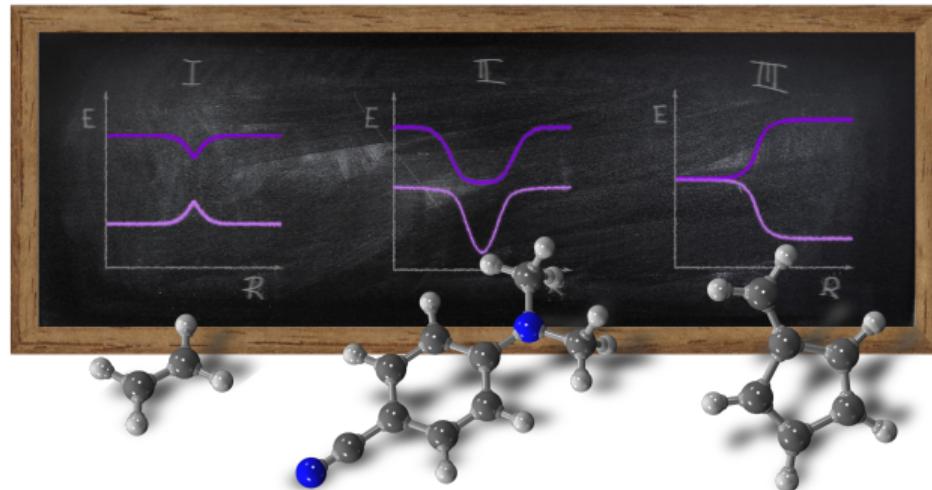
→ close agreement with AIMS – interstate couplings stronger effect

# Molecular Tully III: Fulvene



In TSH different scheme for the rescaling of the velocity after hops:  
Often default: isotropically along the velocity vector  
Alternatively parallel to the NACV – strong influence on the result.  
(Similar different rescalings after spawns in AIMS have no influence)

# Summary



Test your new nonadiabatic methods on a testset of real, full dimensional molecules!  
All initial conditions are available at [DOI:10.15128/r1qj72p715m](https://doi.org/10.15128/r1qj72p715m)



# Acknowledgements

