

Nonadiabatic molecular dynamics simulations with Libra

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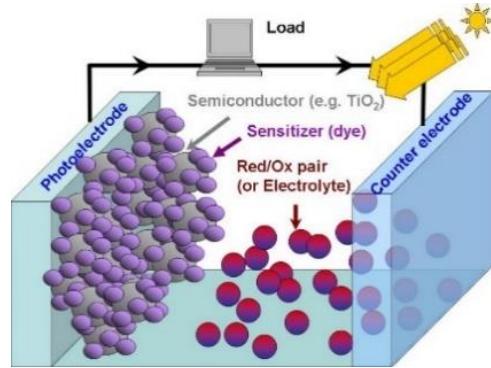
Akimov Research Group

Libra summer workshop 2024



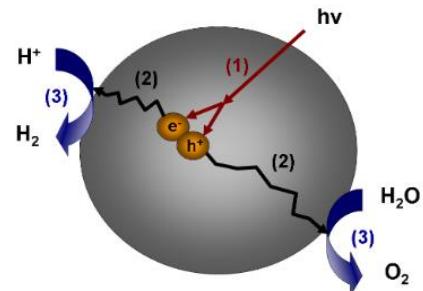
Motivation

- Solar energy materials

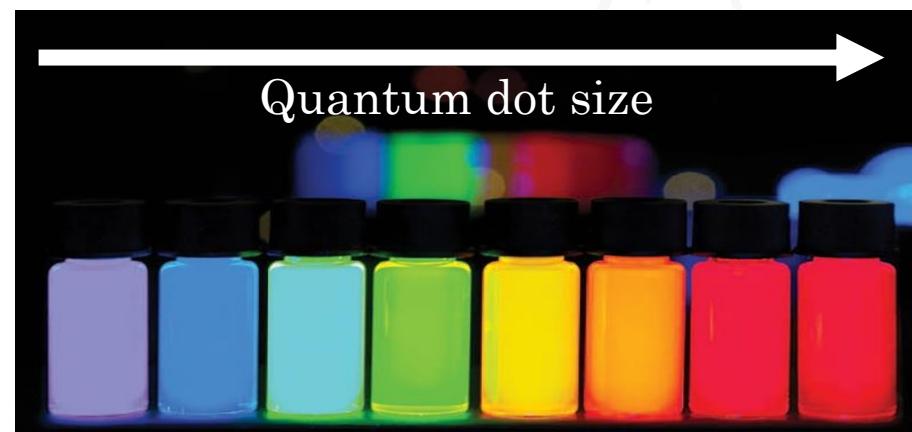


- Photocatalysis

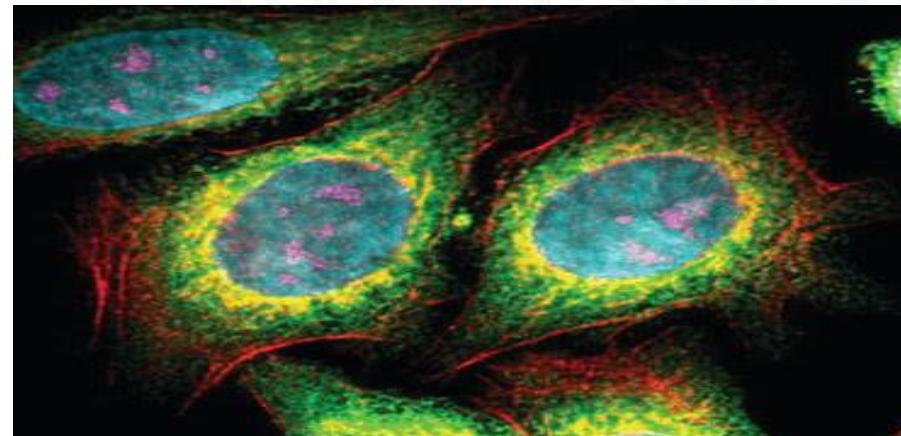
Artificial leaf



- Light-emitting diodes



- Bio-imaging



Nonadiabatic dynamics

- The total wavefunction:

$$\Psi(\mathbf{r}, \mathbf{R}(t)) = \sum_i c_i(t) \psi_i(r, R(t))$$

$$H_{el}(r, R) \psi_i(r, R) = E_i \psi_i$$

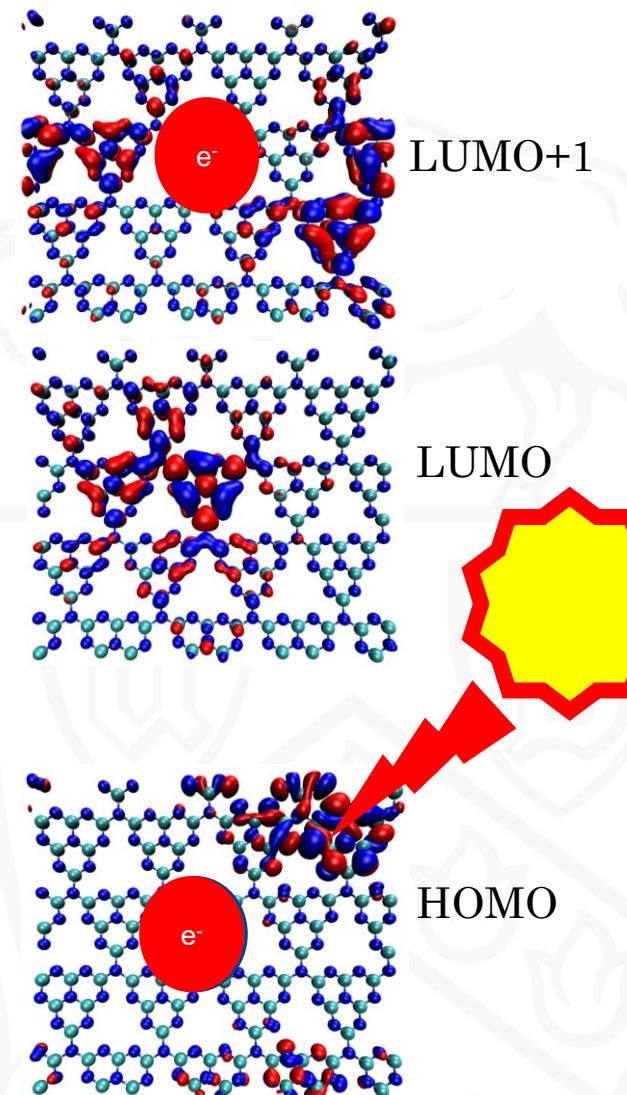
- The evolution of the electronic amplitudes:

$$i\hbar \frac{\partial c_i(t)}{\partial t} = \sum_j \left(E_i(t) \delta_{i,j} - i\hbar d_{ij}(t) \right) c_j(t)$$

$$d_{ij}(t) = \langle \psi_i | \frac{\partial}{\partial t} \psi_j \rangle$$

- Hammes-Schiffer and Tully method:

$$d_{ij}\left(t + \frac{\Delta t}{2}\right) \approx \frac{\langle \psi_i(t) | \psi_j(t + \Delta t) \rangle - \langle \psi_i(t + \Delta t) | \psi_j(t) \rangle}{2\Delta t}$$

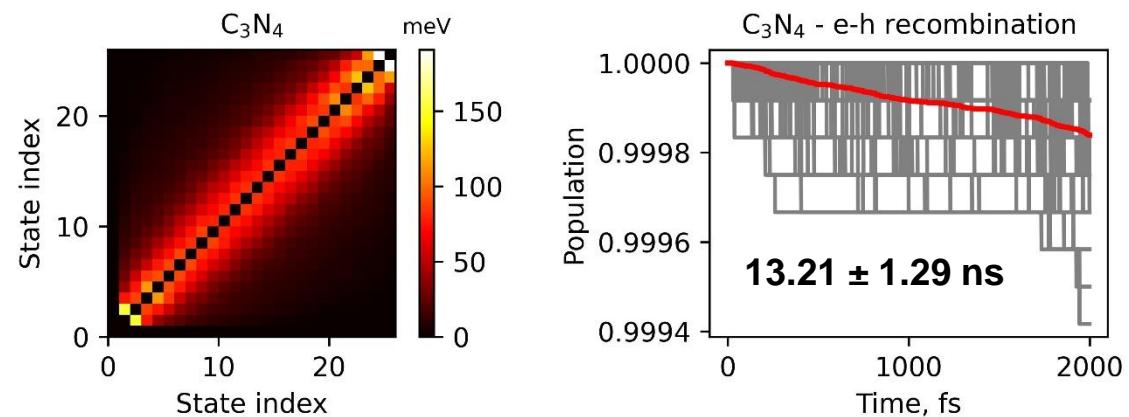


Trajectory surface hopping

- A stochastic method used for evolution of the simplified time-dependent Schrodinger equation
- A trajectory can stochastically hop from state i to state j with the hopping probability:

$$P_{i \rightarrow j}(t, t + \Delta t) = \max \left(0, \frac{\Delta t}{c_i c_i^*} \text{Im} (c_i c_j^* d_{ji} - c_j c_i^* d_{ij}) \right)$$

- Nonradiative electron-hole recombination, hot-electron, and hot-hole relaxation.

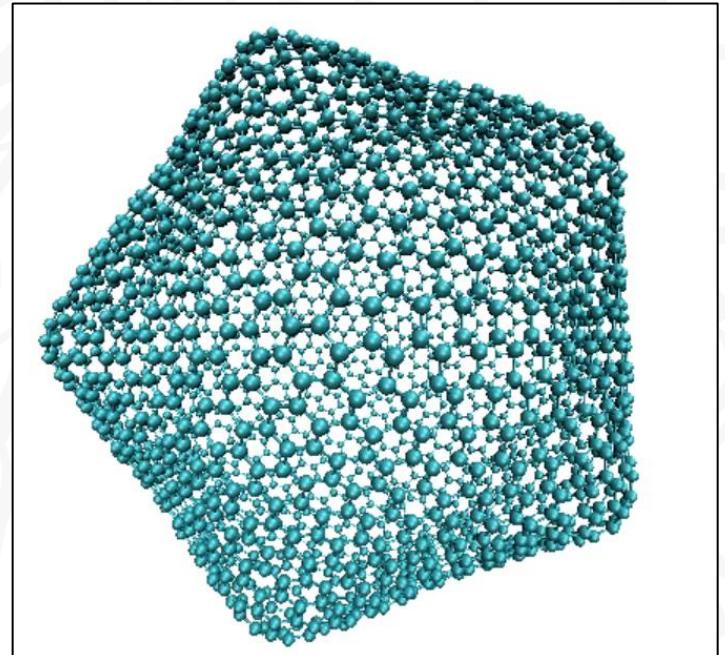


Challenges

- NA-MD simulations are limited to small-medium sized structures
- High computational cost of the simulation of excited states dynamics in nanoscale systems
- Different approximations are made
 - Pure functionals, tight-binding family of approaches, etc
 - Single-particle description of excited states
 - Neglect of back reaction approximation
 - etc

Goal

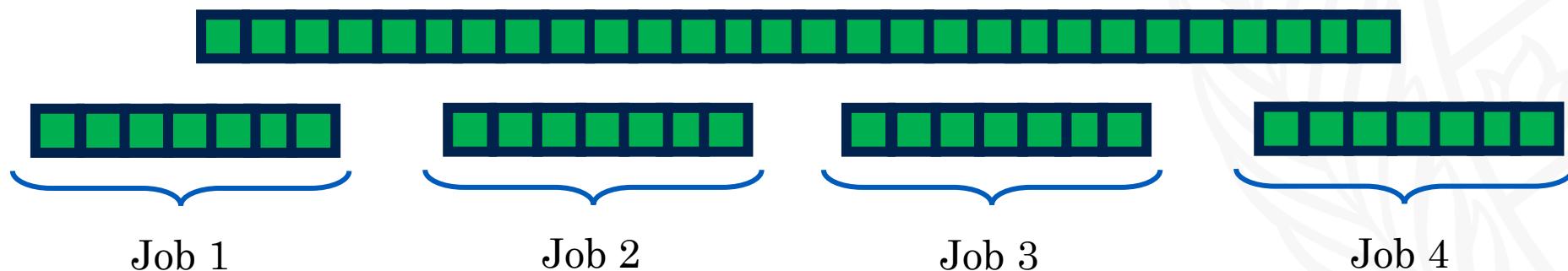
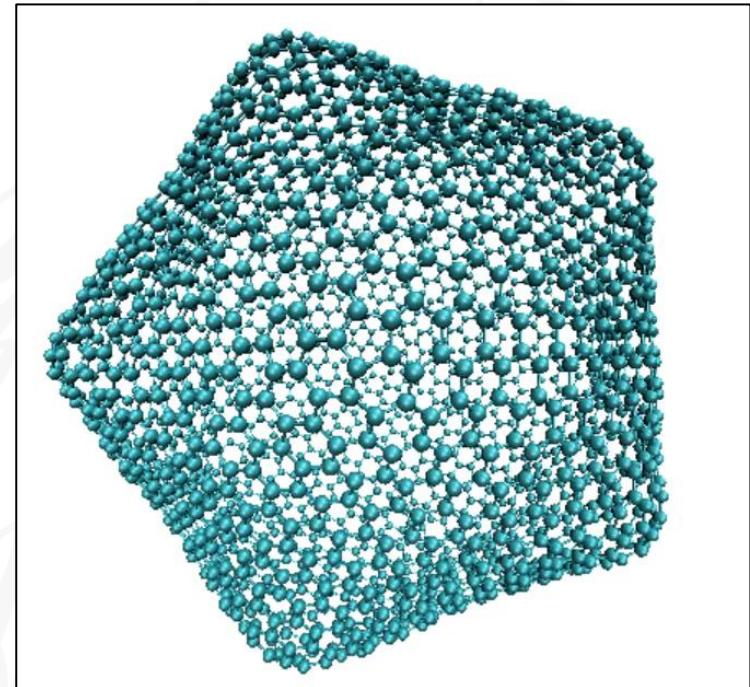
- To perform NA-MD calculations for large nanomaterials and periodic solids
- Can we speed up the calculations using machine-learning techniques?



Part I: Nonadiabatic molecular dynamics in large scale nanomaterials and periodic solids

Nonadiabatic dynamics in nanoscale systems

- Step 1:
 - Generate Pre-computed molecular dynamics trajectory: DFT, DFTB, xTB, or force fields for very large systems e.g. proteins
- Step 2:
 - Generate Kohn-Sham molecular orbitals, their overlap, time-overlap, nonadiabatic couplings
 - TD-DFT states and their configuration
- Step 3:
 - Build and computing the excited states properties
- Step 4:
 - Doing the dynamics with trajectory surface hopping



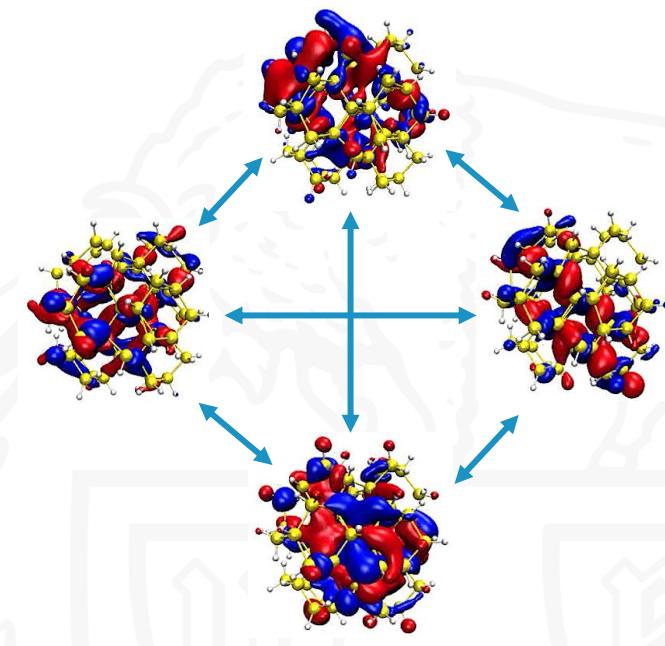
Time-overlap integration

- Grid-based approach using *.cube* files
 - Easy to implement
 - Most codes can output these file
 - Not suitable for large structures with large number of states
- Double-molecule approach
 - Easy to use and can be used in different codes
 - Very time-consuming for large structures
 - Not suitable for periodic structures
- Analytical approach
 - Suitable for large systems and large number of states
 - Recurrence relations for computing integrals: Libint2 package

$$S_{ij} = \int_{-\infty}^{\infty} \psi_i^* \psi_j d\nu$$

$$S^{MO} = c^T S^{AO} c$$

$$S^{AO} = \begin{bmatrix} \langle \psi_1 | \psi_1 \rangle & \cdots & \langle \psi_1 | \psi_n \rangle \\ \vdots & \ddots & \vdots \\ \langle \psi_n | \psi_1 \rangle & \cdots & \langle \psi_n | \psi_n \rangle \end{bmatrix}$$

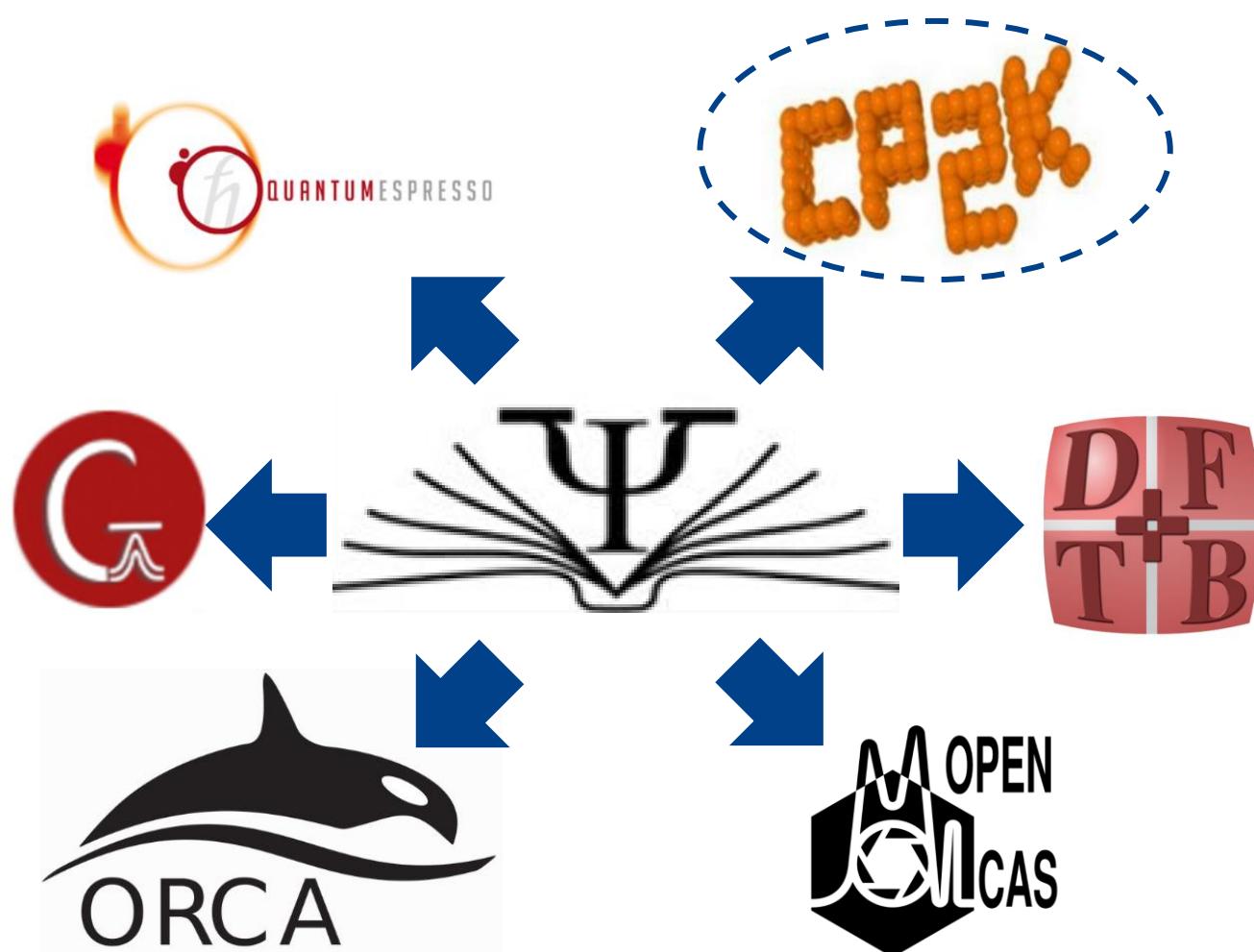


Smith, Shakiba, Akimov, J. Chem. Theory Comp. 2021, 17, 678–693

Libint, Version 2.6.0 Edward F. Valeev, <http://libint.valeev.net>.

Shakiba, Stippell, Li, Akimov, J. Chem. Theory Comp. 2022, 18, 5157-5180

Implementation



```

import os
from libra_py import CP2K_methods
from libra_py.workflows.nbra import step2

# Setup the parameters
params = {'istep': 1, 'fstep': 2000, 'nprocs': 9, 'mpi_executable': 'srun',
          'lowest_orbital': 512-20, 'highest_orbital': 512+21,
          'res_dir': os.getcwd() + '/results', 'isUKS': False,
          'is_periodic': True, 'periodicity_type': 'XY',
          'is_spherical': True, 'isxTB': True, 'remove_molden': True,
          'cp2k_exe': 'cp2k.psmp', 'cp2k_ot_input_template': 'es_ot.inp',
          'cp2k_diag_input_template': 'es_diag.inp',
          'trajectory_xyz_filename': 'C3N4-2x2-pos.xyz',
          'cube_visualization': True, 'vmd_input_template': 'vmd.tcl',
          'vmd_exe': 'vmd', 'states_to_plot': [512, 513],
          'plot_phase_corrected': True, 'remove_cube': True}

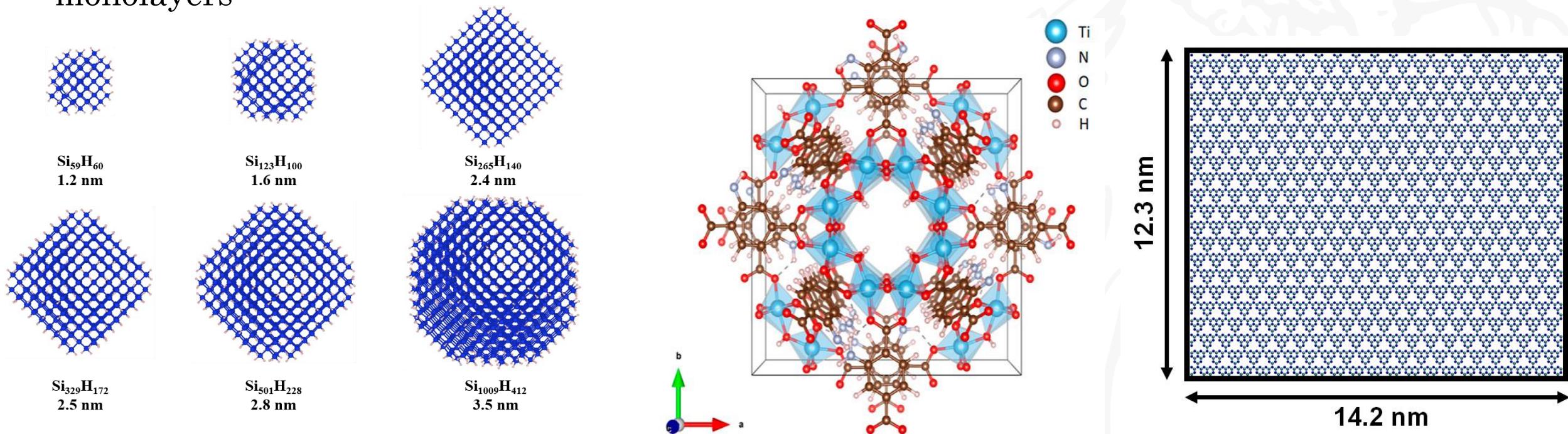
if params['is_periodic']:
    params['A_cell_vector'] = [28.483, 0.000, 0.000]
    params['B_cell_vector'] = [0.000, 24.669, 0.000]
    params['C_cell_vector'] = [0.000, 0.000, 15.000]
    # Set the origin and generate the translational vectors
    origin = [0,0,0]
    # Number of periodic images per each X, -X, Y, -Y, Z, and -Z directions
    num_periodic_images = [1,1,1]
    params['translational_vectors'] =
        CP2K_methods.generate_translational_vectors(origin, num_periodic_images,
                                                      params['periodicity_type'])

# Run the calculations
step2.run_cp2k_libint_step2(params)

```

Applications

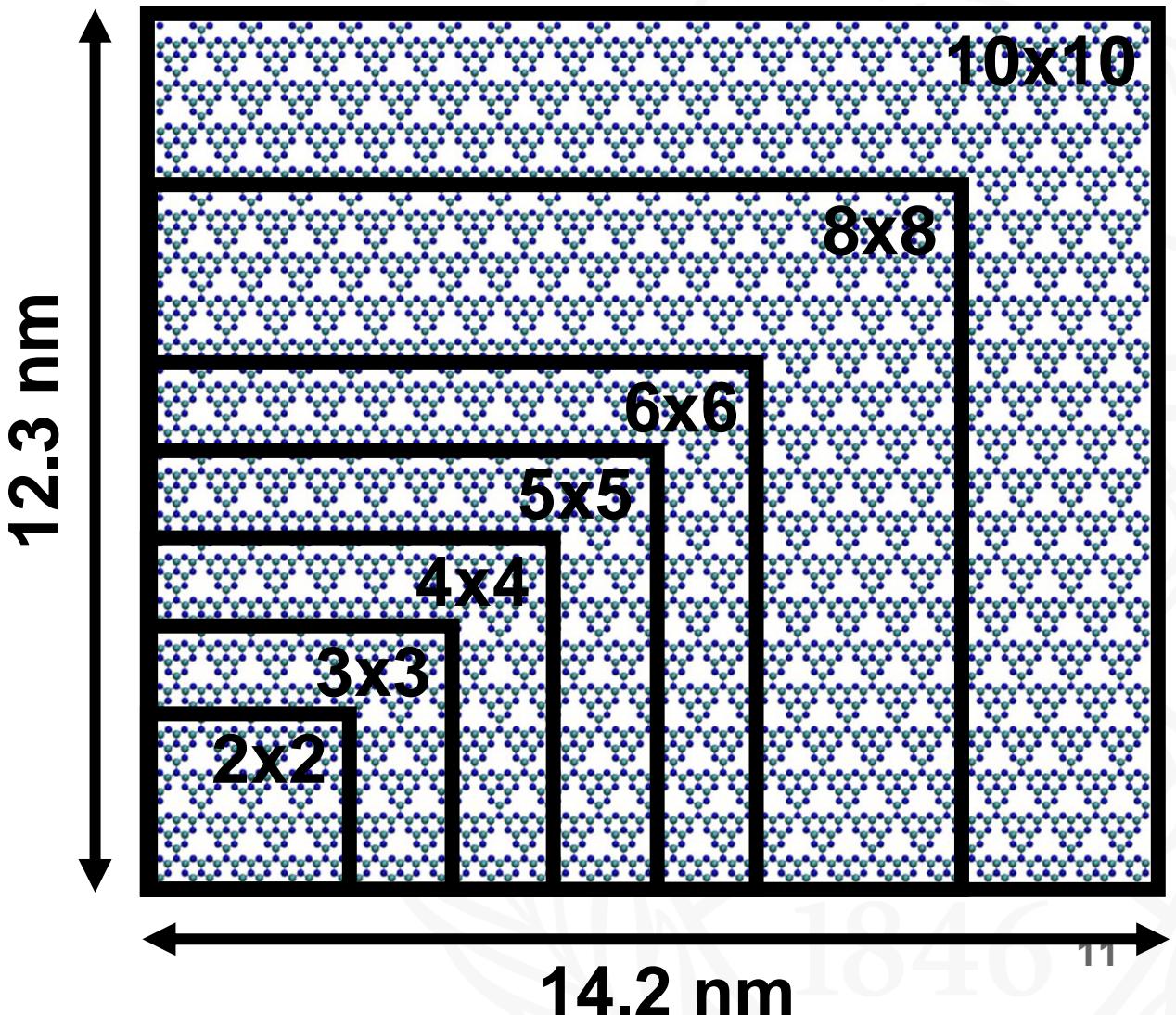
- Hot-electron cooling dynamics in silicon nanocrystals (Si NCs)
- Electron-hole recombination dynamics in metal organic frameworks and carbon nitride monolayers



Charge carrier concentration in C_3N_4 monolayers

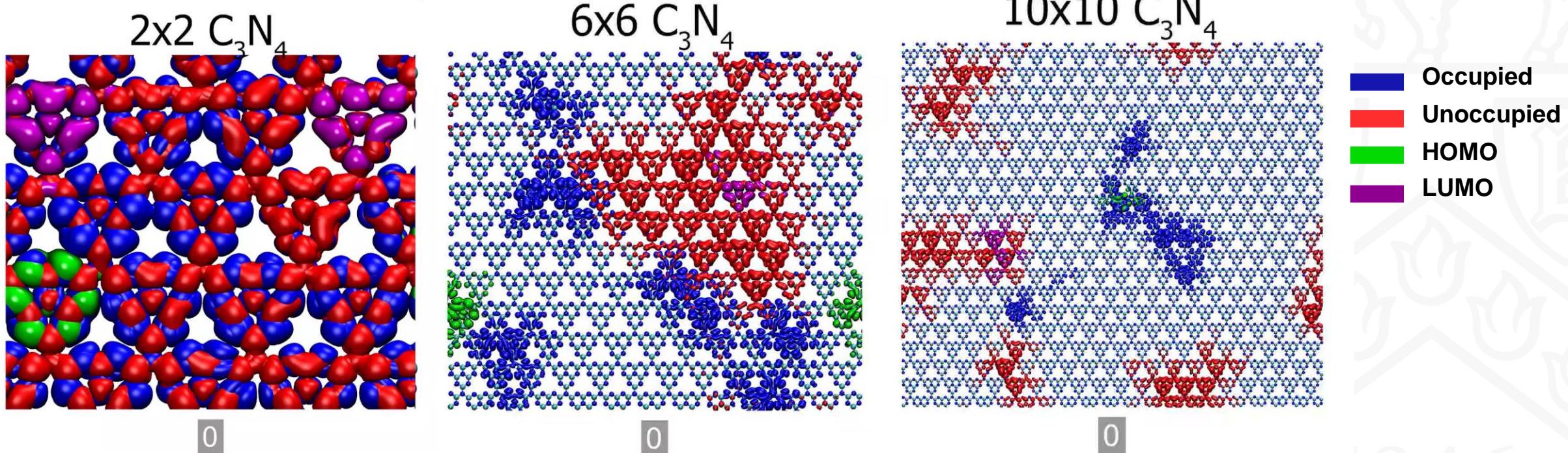
- Intrinsic charge carrier concentration in monolayers are in the range of $\sim 10^{10}\text{-}10^{12} \text{ cm}^{-2}$ in experimental studies
- Theoretical studies overestimate this value due to simulation of excited states in small cell size

224 # Atoms 5600
512 # Orbitals 12800

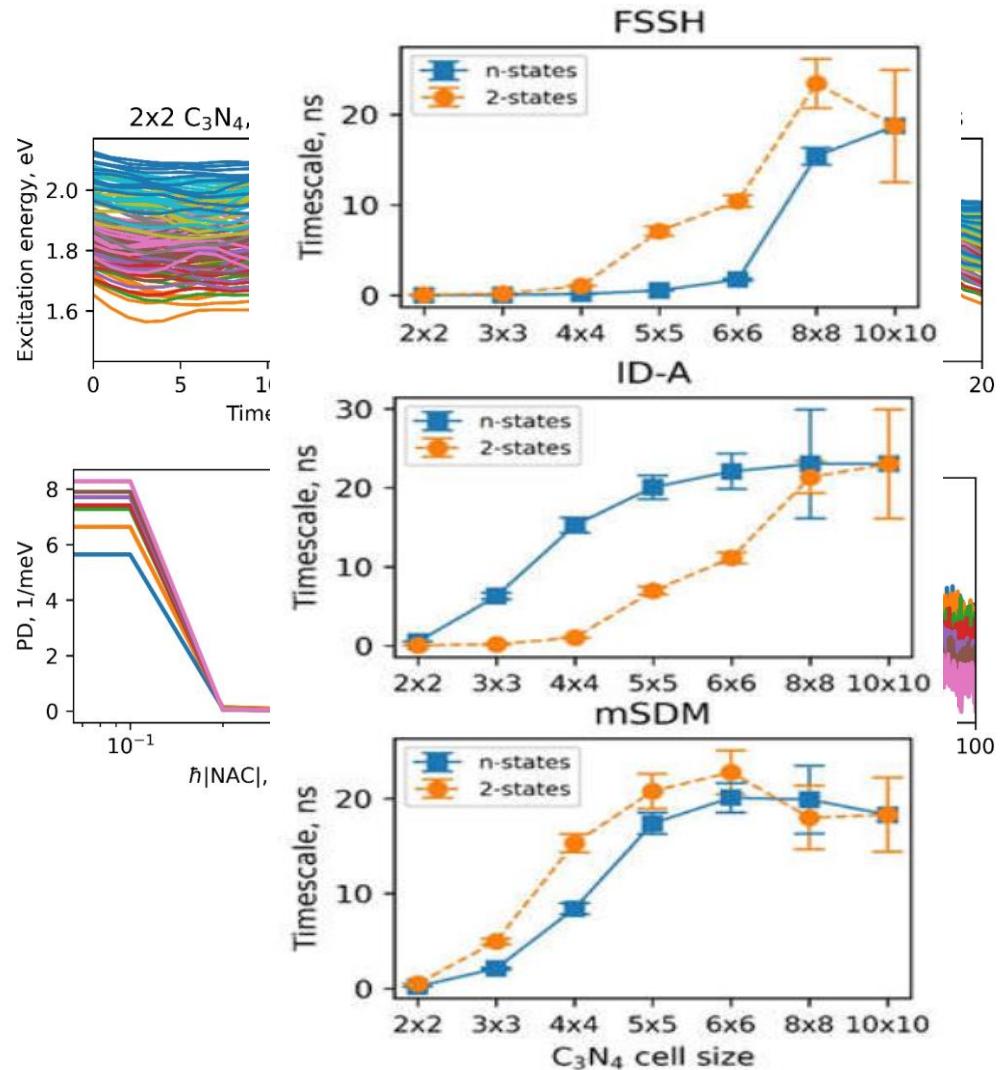


Molecular orbitals in C_3N_4 monolayers

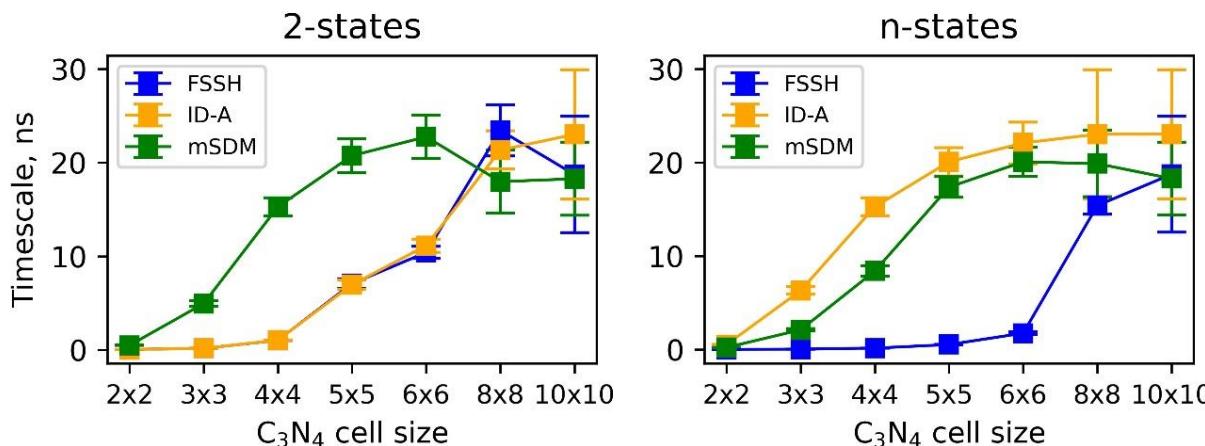
- Occupied orbitals are more localized on several melem (triangular repeated motif of 3 fused rings) units
- Unoccupied orbitals are delocalized over multiple connected melem units which is better observed in larger supercells



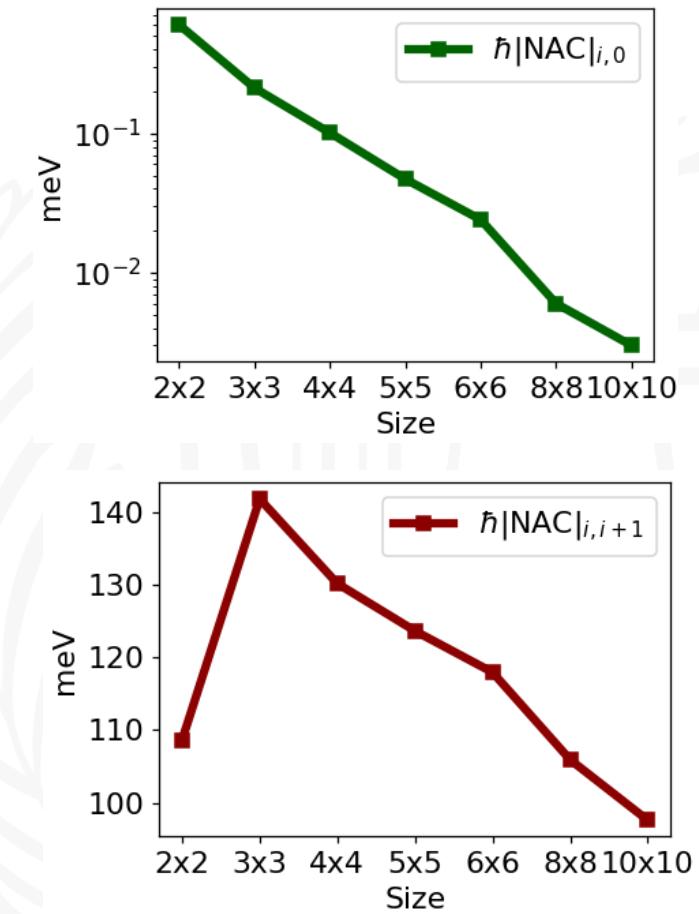
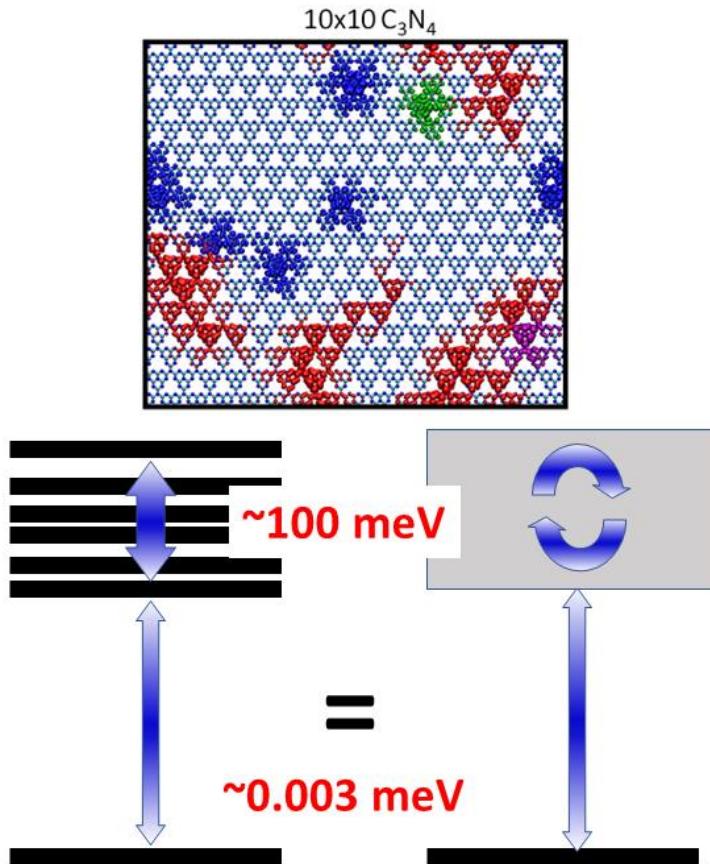
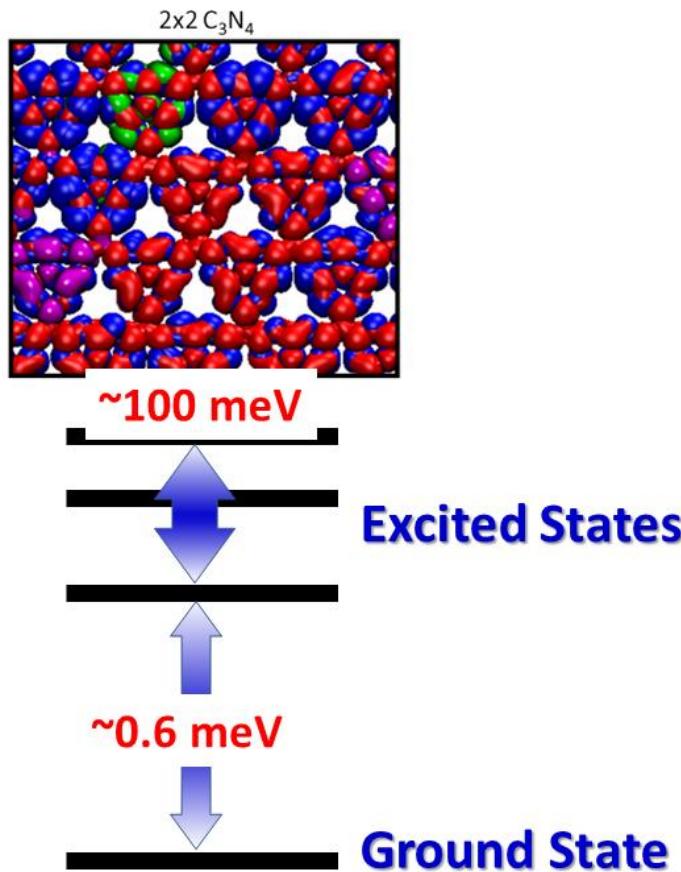
e-h recombination dynamics in C_3N_4 monolayers



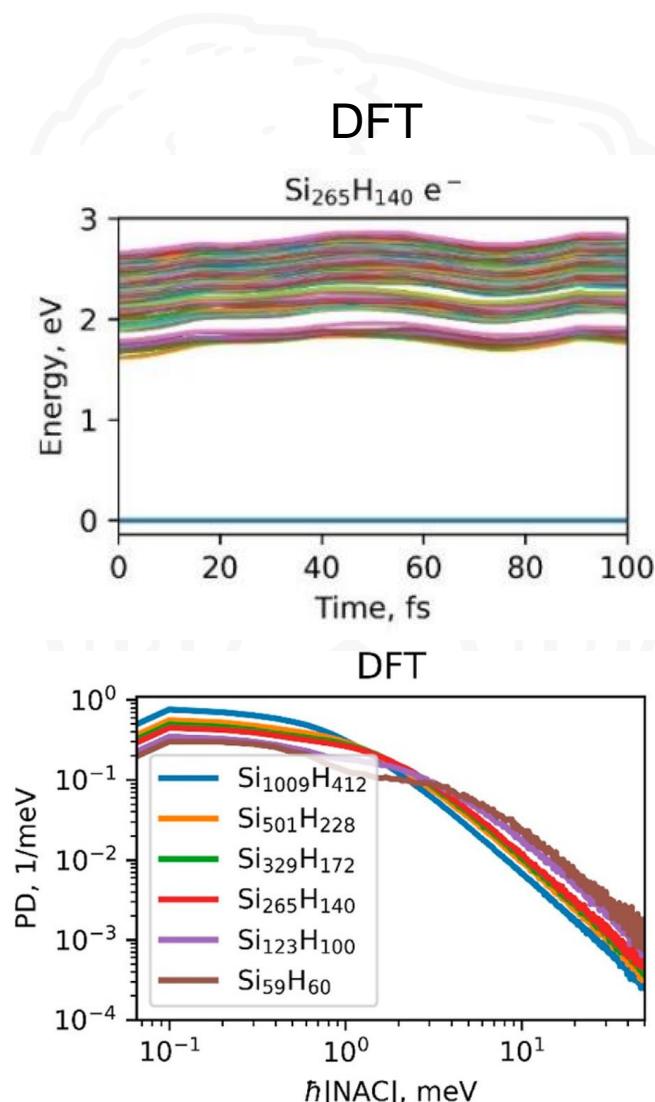
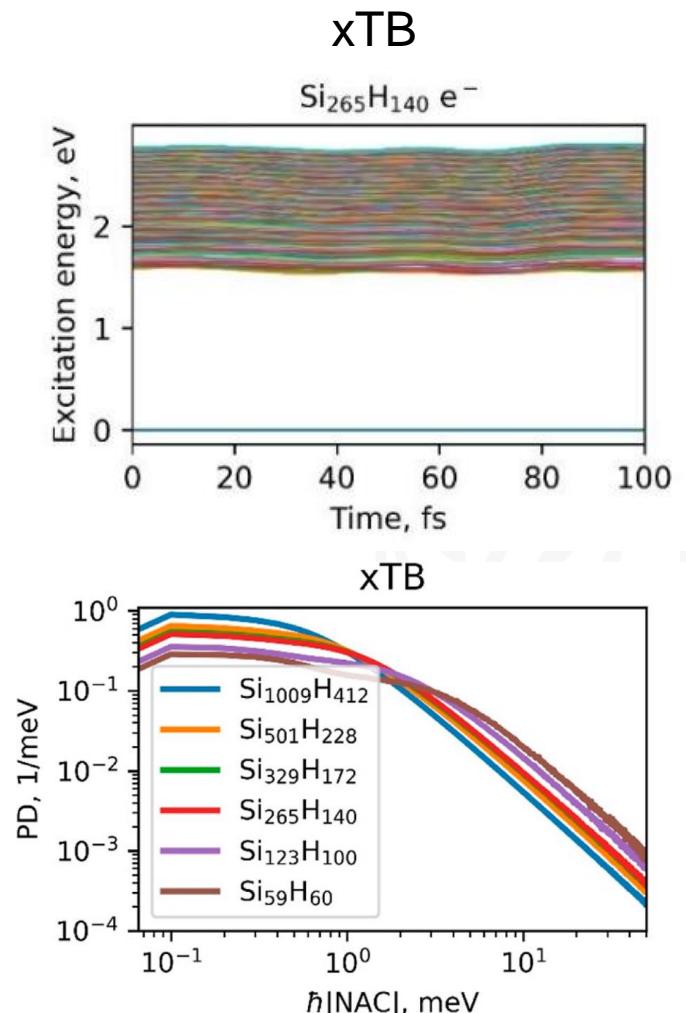
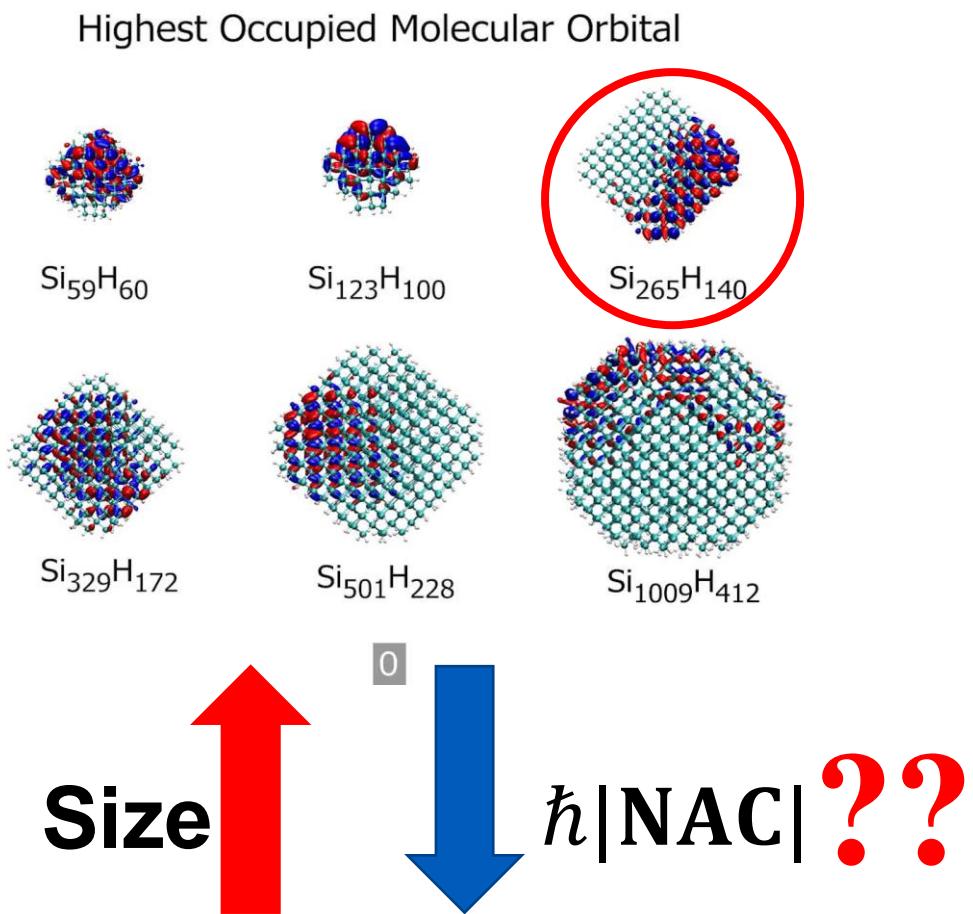
- 100 single-particle excitation states are built including all excitations from the first 10 occupied to the first 10 unoccupied molecular orbitals
- NAC values decrease by increasing supercell size
 - Small time-overlaps between molecular orbitals in large supercells
- Recombination dynamics becomes size-independent for all methods for very large supercell sizes



e-h recombination dynamics in C_3N_4 monolayers



Hot-electron cooling dynamics in Si NCs

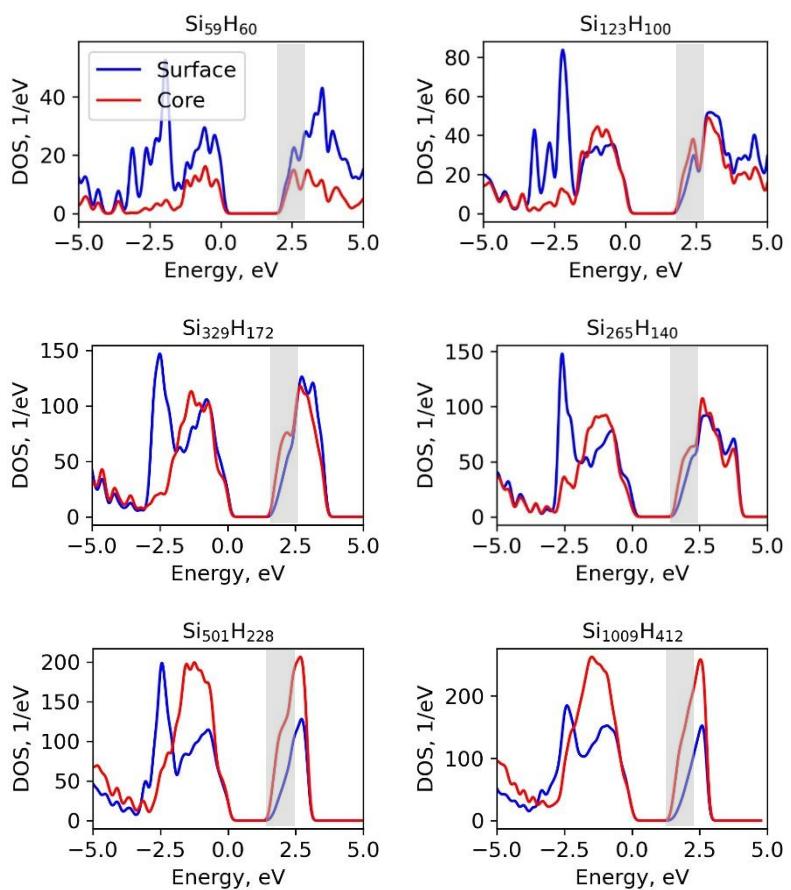
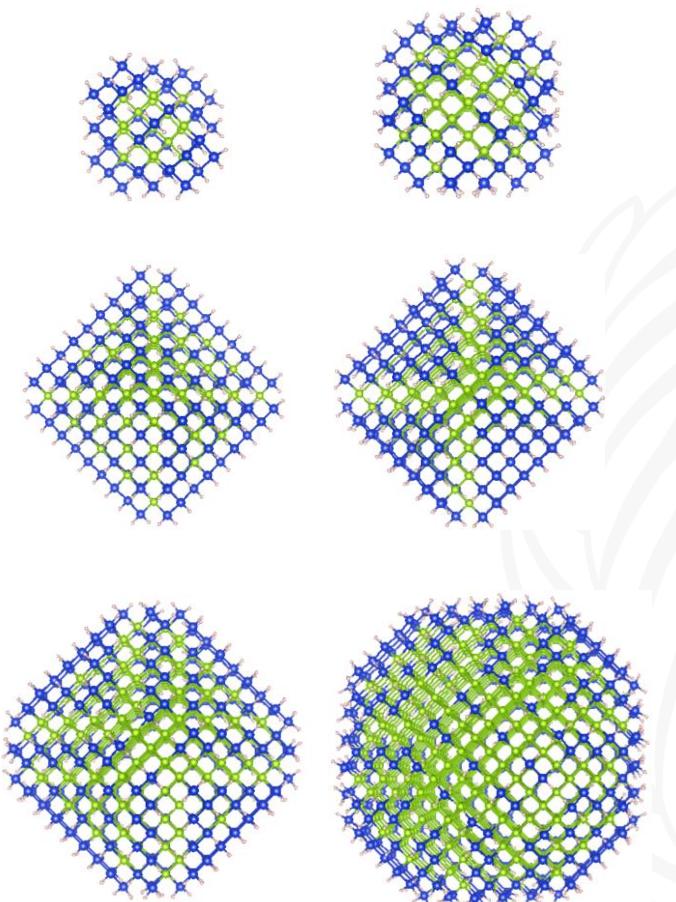


Core vs surface atoms

- By increasing size the surface/core DOS decreases
- Core atoms movements are slower than surface atoms

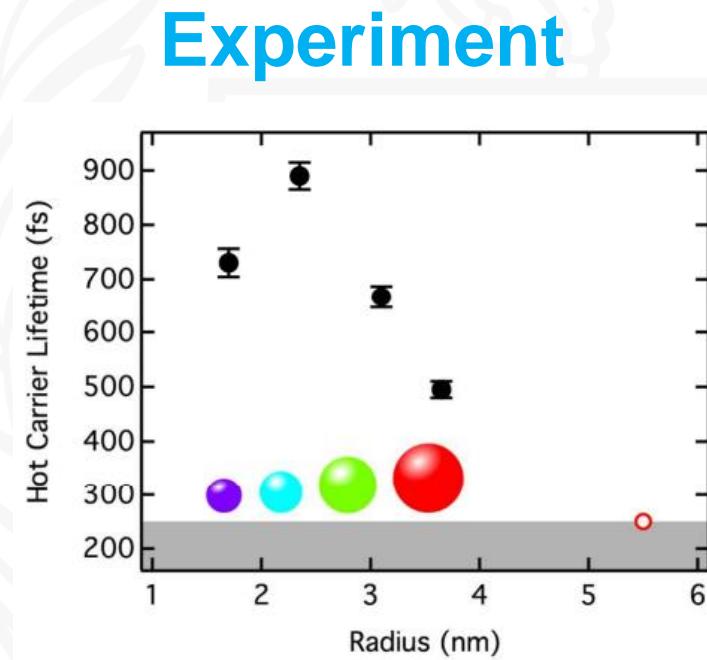
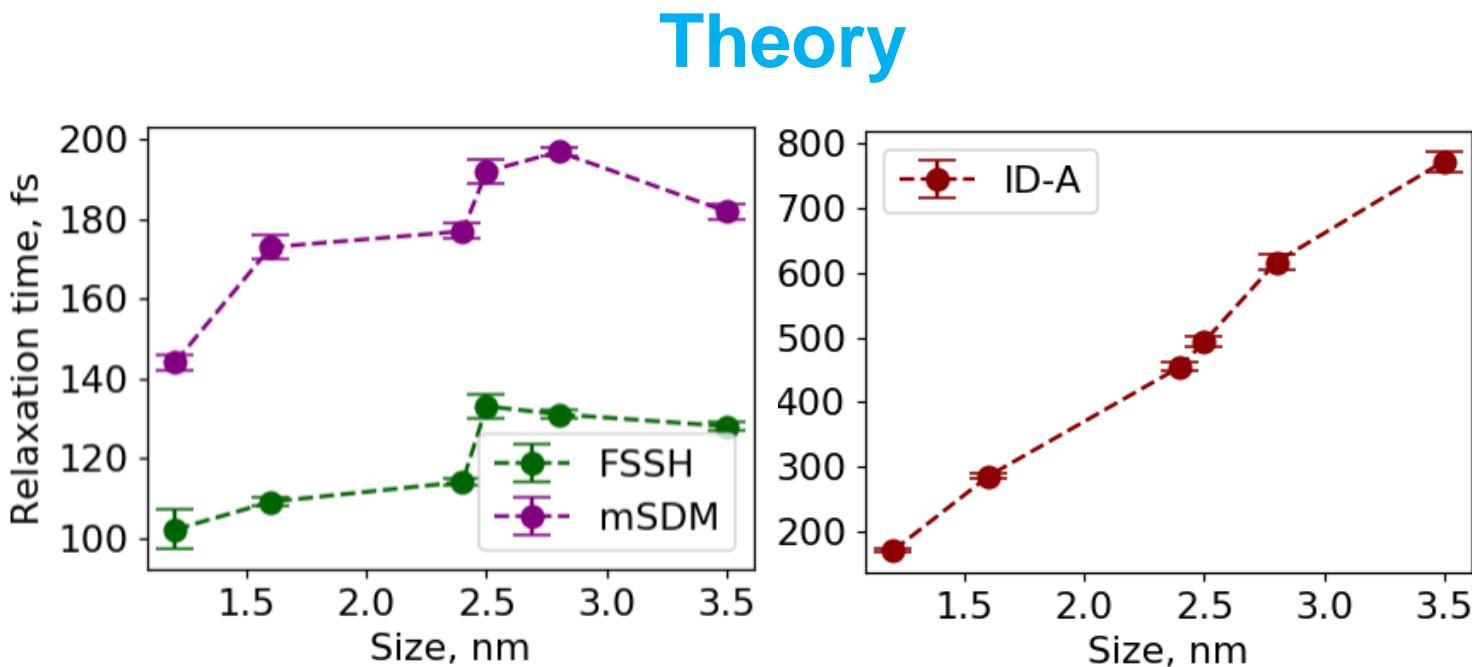
$$\sigma_i = \sqrt{\langle (\vec{r}_i - \langle \vec{r}_i \rangle) \rangle}$$

System	Si-surface	Si-core
$\text{Si}_{59}\text{H}_{60}$	0.273	0.172
$\text{Si}_{123}\text{H}_{100}$	0.152	0.113
$\text{Si}_{265}\text{H}_{140}$	0.144	0.114
$\text{Si}_{329}\text{H}_{172}$	0.186	0.141
$\text{Si}_{501}\text{H}_{228}$	0.262	0.190
$\text{Si}_{1009}\text{H}_{412}$	0.169	0.127



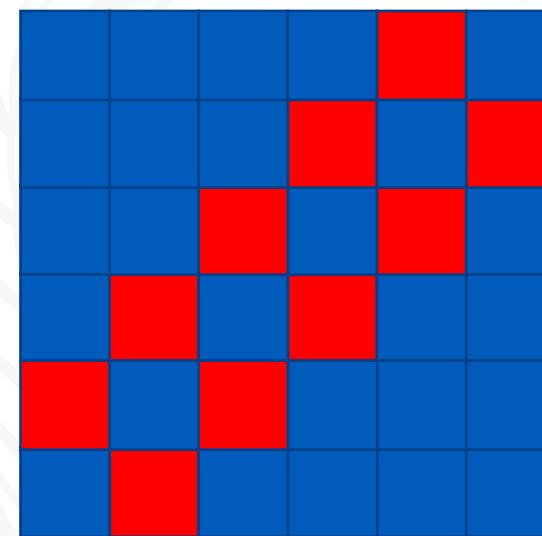
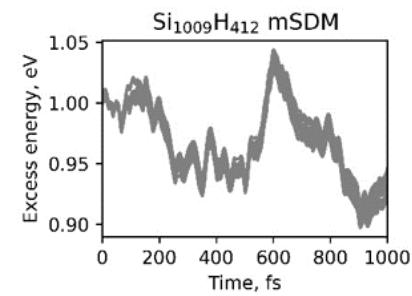
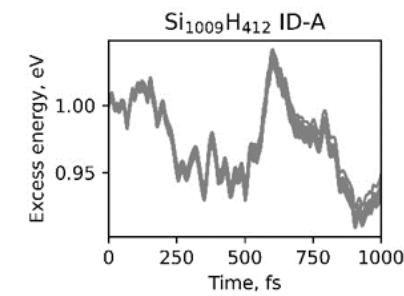
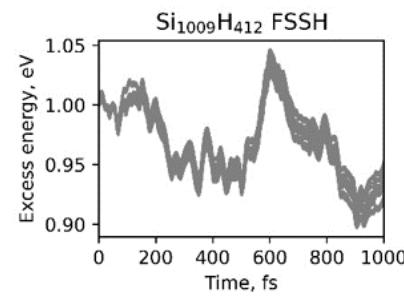
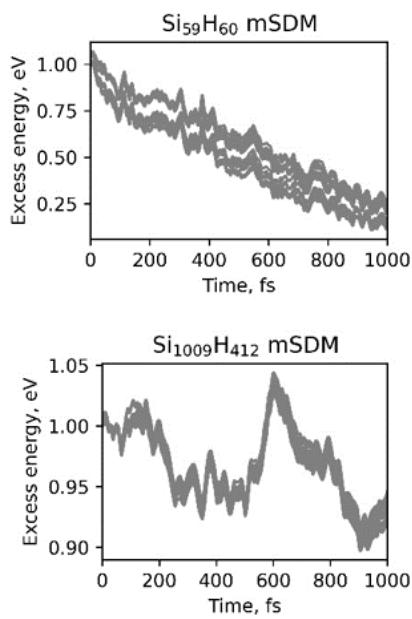
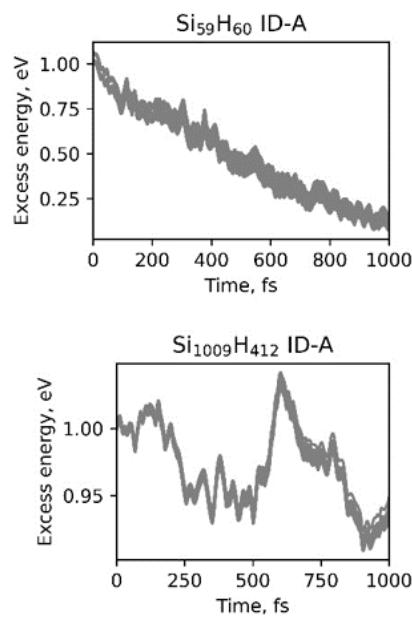
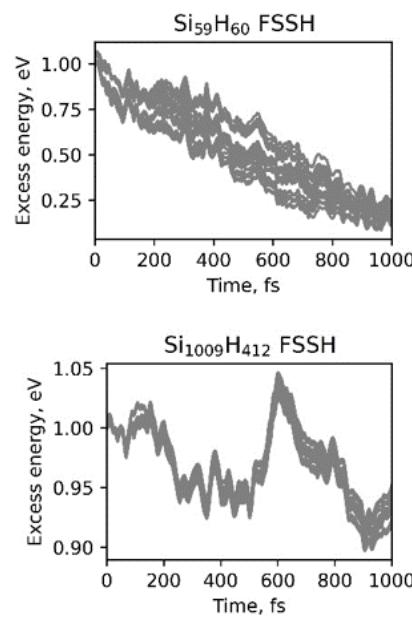
NA-MD results vs experiment

- Experimental data show a non-monotonic dependence of the relaxation time with respect to NC size
- FSSH and mSDM: Non-monotonic dependence of relaxation time on NC size
- ID-A: Monotonic dependence of relaxation time with increasing NC size



NA-MD results vs experiment

- By going to larger NCs, the possibility of relaxation happening through non-adjacent states increase
- NA-MD done with only adjacent state transition allowed does not decay for larger structures



Part I Summary

XTB - NAMD

- A new methodology for NA-MD simulations in large nanostructures and periodic solids is implemented in the open-source Libra code
- The NAC values decrease by increasing Si NC size and C_3N_4 monolayer supercell size
- A non-monotonic dependence of hot-electron relaxation dynamics on Si NC size was observed in FSSH and mSDM in agreement with experiment
- Non-adjacent transitions play an important role in the relaxation dynamics in Si NCs
- By varying charge carrier concentration using different supercell sizes, a saturation of the recombination timescale was observed showing the size-independence of recombination dynamics in very large structures (n -states \rightarrow effective 2-states)

Part II: Nonadiabatic molecular dynamics with machine-learned Kohn- Sham Hamiltonian mapping

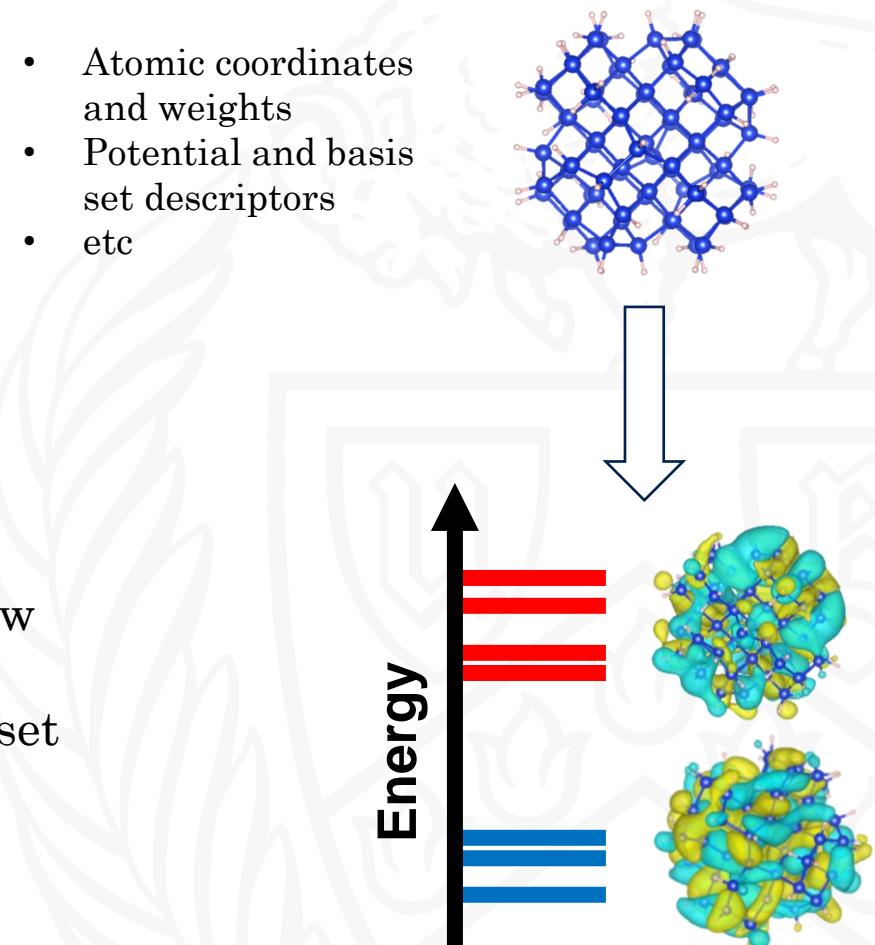


Haters gonna say:
“IT'S FAKE!”

Me and my lovely pet ❤️ 😊

Machine-learning in electronic structure calculations

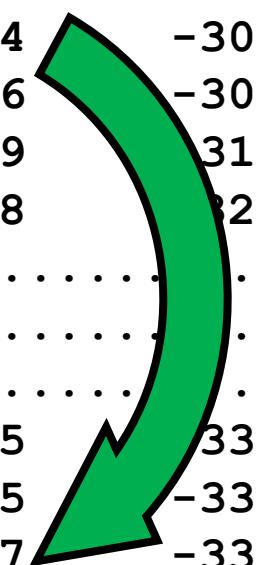
- Single or multiple targets prediction: Band gaps, nonadiabatic couplings, dipole moment etc
- Machine-learning potentials and forcefields, one-electron reduced density matrix prediction
 - SchNorb, Schpacknet, Mlatom, QMLearn, etc
- What they have in common?
 - Trying to “surrogate” quantum chemistry software with ML models
 - Poorly transferrable
 - Not as general as they should be
 - Not applicable to all types of systems and only applicable to few atomic types
 - For large systems, they require the preparation of many data set which is time-consuming
 - Use Neural networks
 - Deep layers with large number of neurons, long training time, large % of training data (up to 90%), cumbersome preprocessing of the data, overfitting problem etc.



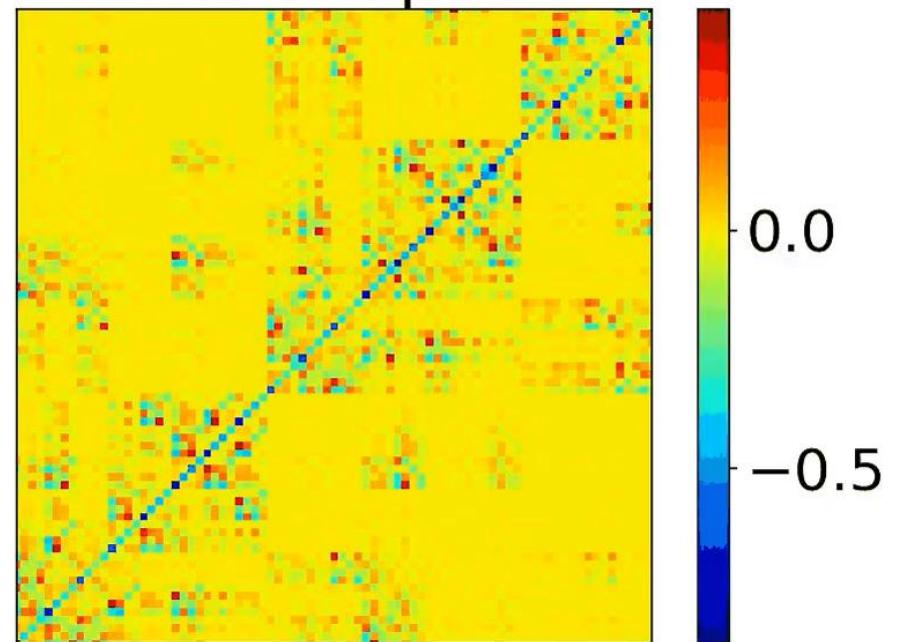
SCF cycle

SCF WAVEFUNCTION OPTIMIZATION - **B3LYP**

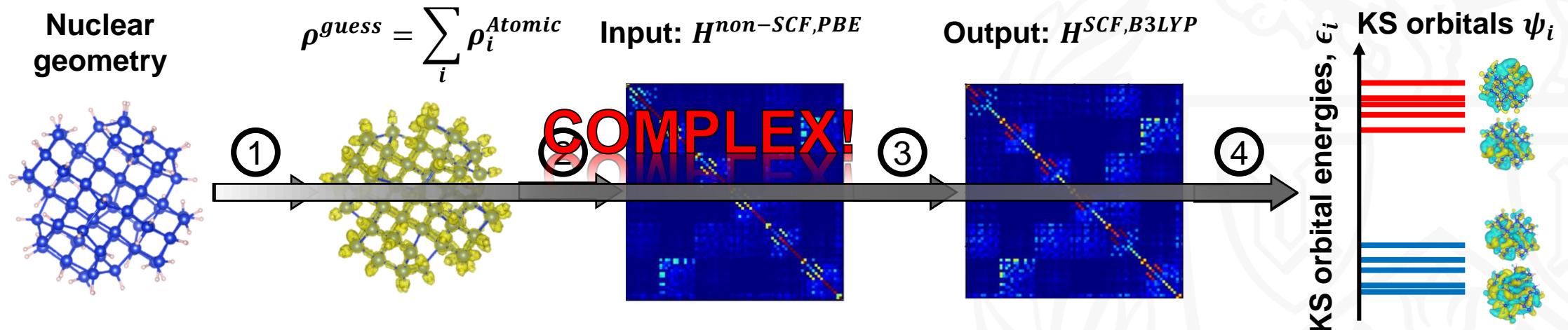
Step	Time (sec)	Convergence
1 Guess/Diag.	5.7	1.59674484
2 Broy./Diag.	127.5	2.77154376
3 Broy./Diag.	127.6	0.72899999
4 Broy./Diag.	128.0	0.12822688
.....
.....
39 Broy./Diag.	129.4	0.00000115
40 Broy./Diag.	129.4	0.00000105
41 Broy./Diag.	128.7	0.00000057



SCF step: 1

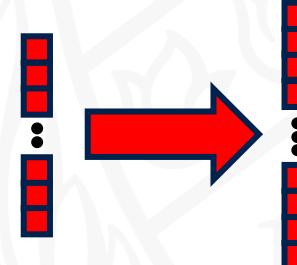
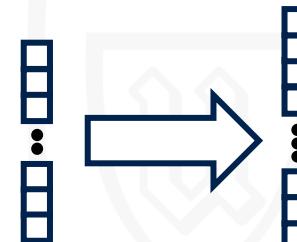
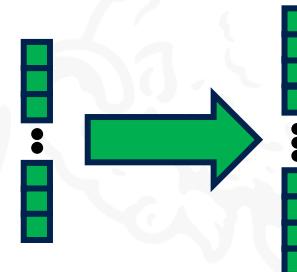
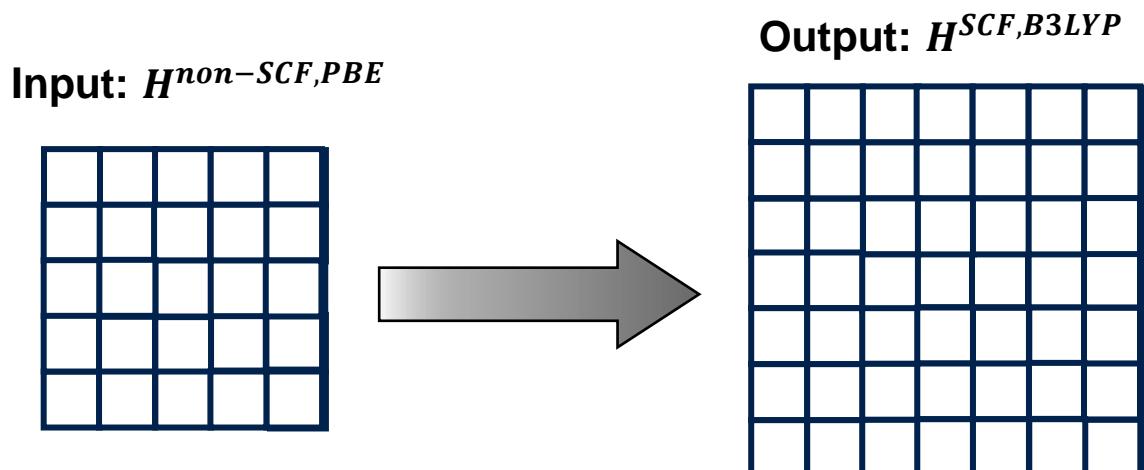


What are the inputs?



Is this efficient?

- Up to millions of elements for very large systems
- Pick the upper triangular part of the KS Hamiltonian matrix due to symmetry
- Split them into multiple partitions
- Train a separate model for each partition → Each model can be separately trained in parallel
- Rebuild the matrix and diagonalize it



Different partitioning methods

Input KS
Hamiltonian matrix

	C ₁	C ₂	H ₁
C ₁	s p _x p _y p _z	s p _x p _y p _z	s
p _x			
p _y			
p _z			
s			
C ₂	p _x		
p _x			
p _y			
p _z			
H ₁	s		



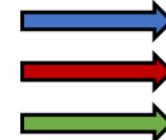
output KS
Hamiltonian matrix

	C ₁			C ₂			H ₁		
C ₁	s	p _x	p _y	p _z	s	p _x	p _y	p _z	s
p _x									
p _y									
p _z									
s									
C ₂	p _x								
p _x									
p _y									
p _z									
H ₁	p _x								
p _x									
p _y									
p _z									



Input KS
Hamiltonian matrix

	C ₁	C ₂	H ₁
C ₁	s p _x p _y p _z	s p _x p _y p _z	s
p _x			
p _y			
p _z			
s			
C ₂	p _x		
p _x			
p _y			
p _z			
H ₁	s		

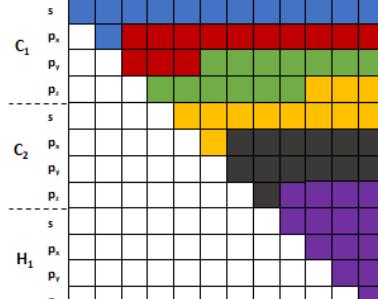


	C ₁			C ₂			H ₁		
C ₁	s	p _x	p _y	p _z	s	p _x	p _y	p _z	s
p _x									
p _y									
p _z									
s									
C ₂	p _x								
p _x									
p _y									
p _z									
H ₁	p _x								
p _x									
p _y									
p _z									



output KS
Hamiltonian matrix

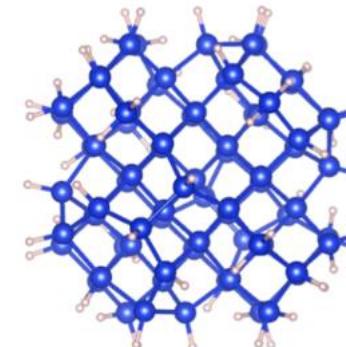
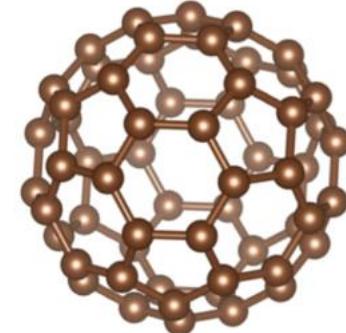
	C ₁			C ₂			H ₁		
C ₁	s	p _x	p _y	p _z	s	p _x	p _y	p _z	s
p _x									
p _y									
p _z									
s									
C ₂	p _x								
p _x									
p _y									
p _z									
H ₁	p _x								
p _x									
p _y									
p _z									



(d)

Models and the systems

- Kernel ridge regressor with a linear kernel
- C₆₀ fullerene with a basis set size of 240
- Si₇₅H₆₄ with a basis set size of 1039
- Step 1:
 - Generate a precomputed nuclear trajectory with 2000 geometries with PBE functional (similar to what is done in typical NA-MD simulations in nanoscale systems)
- Step 2:
 - Equal partitioning of the input and target Hamiltonian matrices
 - 30 partitions just for test!
- Step 3:
 - Train the models for 50 (2.5%), 100 (5%), 250 (12.5%), 500 (25%), 750 (37.5%), 1000 (50%) randomly selected geometries
- Step 4:
 - Use the model to generate the Hamiltonian matrices and molecular orbitals which can be done using high-throughput computation



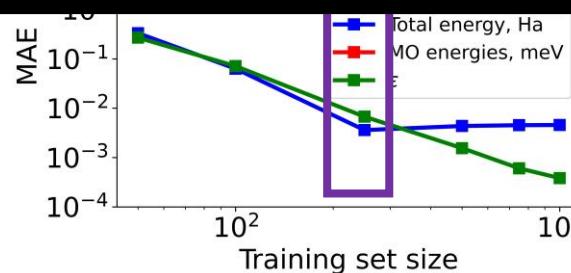
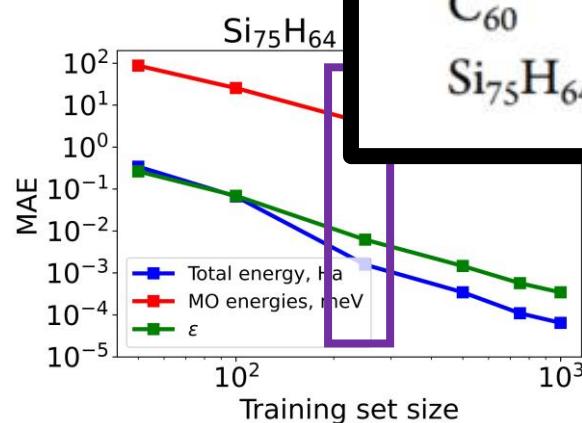
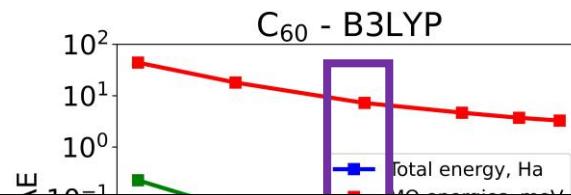
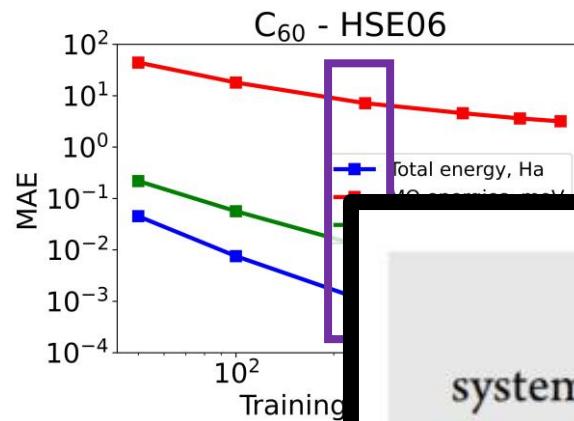
Error measures

- Mean absolute error of the following:
 - 1- Total energy
 - Feed back the ML molecular orbitals to the quantum chemistry software
 - 2- Molecular orbitals energies
 - 3- Overlap of the ML and reference molecular orbitals

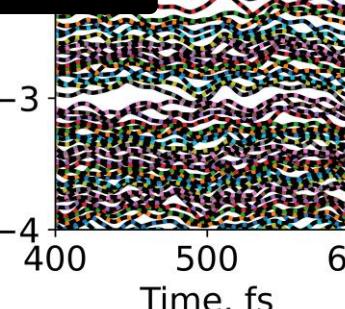
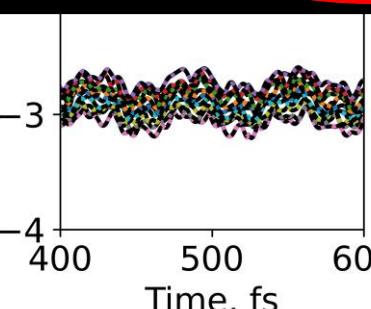
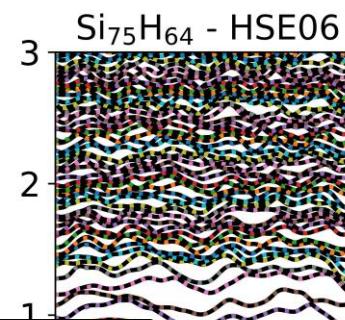
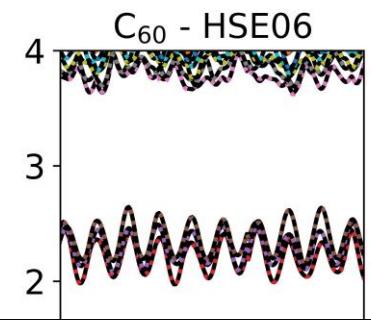
$$\epsilon_{i,overlap} = 1.0 - |\langle \psi_{i,ML} | \psi_{i,ref} \rangle|$$

$$\epsilon = \frac{1}{N_{MO}} \sum_i^{N_{MO}} \epsilon_i$$

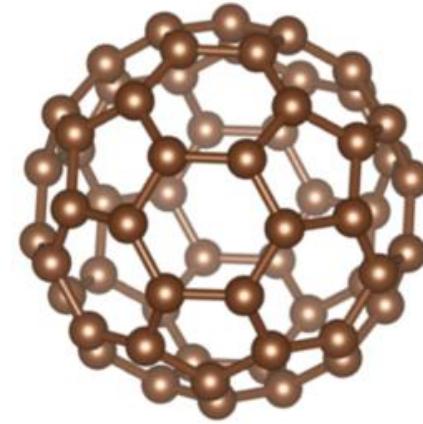
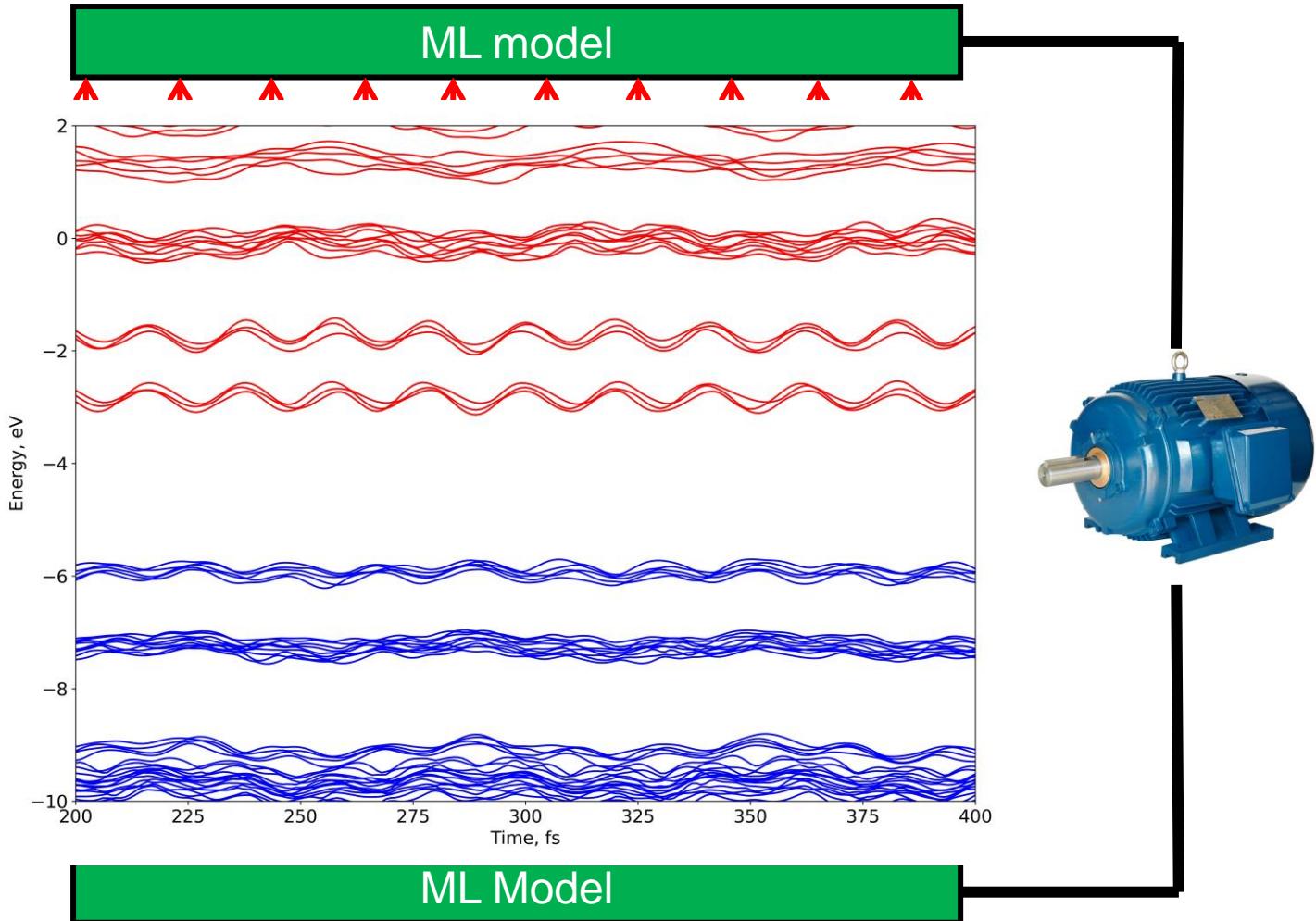
ML results



system	the atomic basis set size	PBE	B3LYP	HSE06
C ₆₀	240	×37	×225	×217
Si ₇₅ H ₆₄	1039	×16	×724	×435



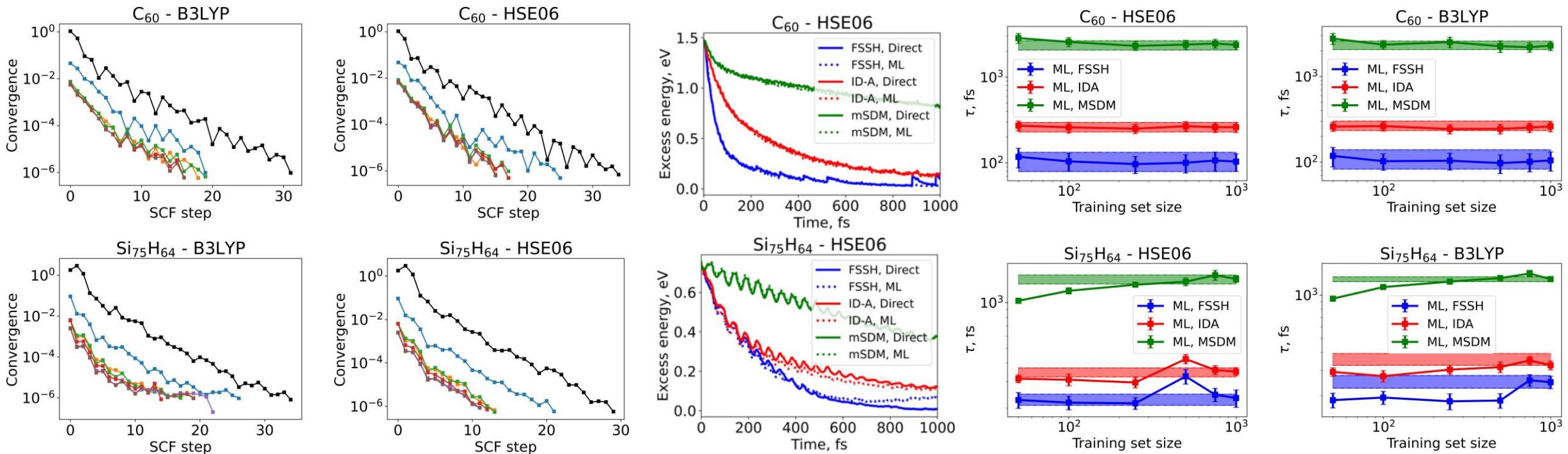
Let's review the idea



- CP2K: PBE atomic guess, 2.17 sec
- CP2K: Converged B3LYP, 529 sec
- ML mapping: 0.08 sec
- Diagonalization: 0.1 sec
- ML training: 12 sec

ML results

- SCF convergence with ML MOs
 - 1.5-2 times faster convergence
 - ML MOs are good guesses!
- Excess energy relaxation dynamics
 - Time scales from dynamics in ML MOs are in within the error margin of the reference time scales

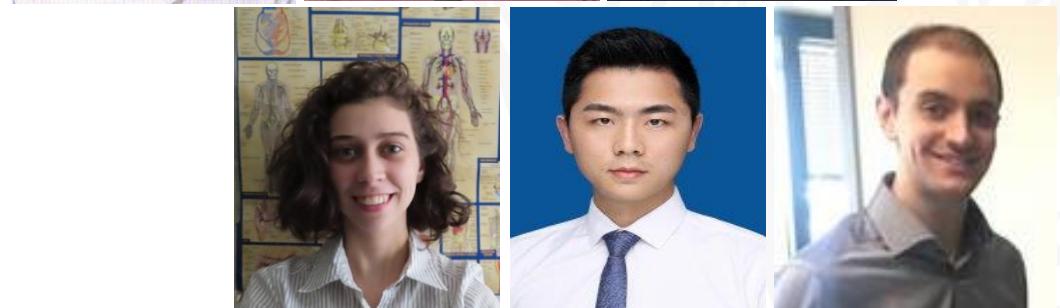
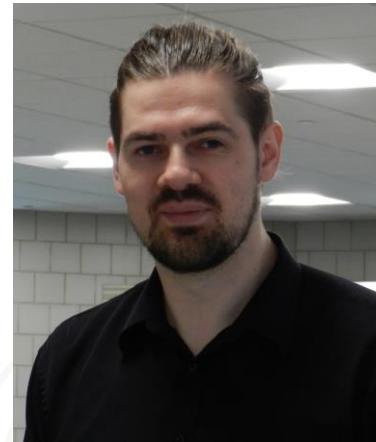


Part II Summary

- A simple, efficient, and scalable ML approach for mapping non-self-consistent Kohn-Sham Hamiltonians constructed with one kind of density functional to the nearly self consistent Hamiltonians constructed with another kind of density functional.
 - Speeds up the calculations by several orders of magnitude
 - Is conceptually simpler than alternative ML approaches
 - Is applicable to different systems and sizes and can be used for mapping Hamiltonians constructed with arbitrary density functionals
 - Requires a modest training data, learns fast, and generates molecular orbitals and their energies with the accuracy nearly matching that of conventional calculations
 - When applied to nonadiabatic dynamics simulation of excitation energy relaxation in large systems yields the corresponding time scales within the margin of error of the conventional calculations

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Thank You!

Questions?

