

# **Advancing Quantum Simulations with Machine Learning and Graph Theory**

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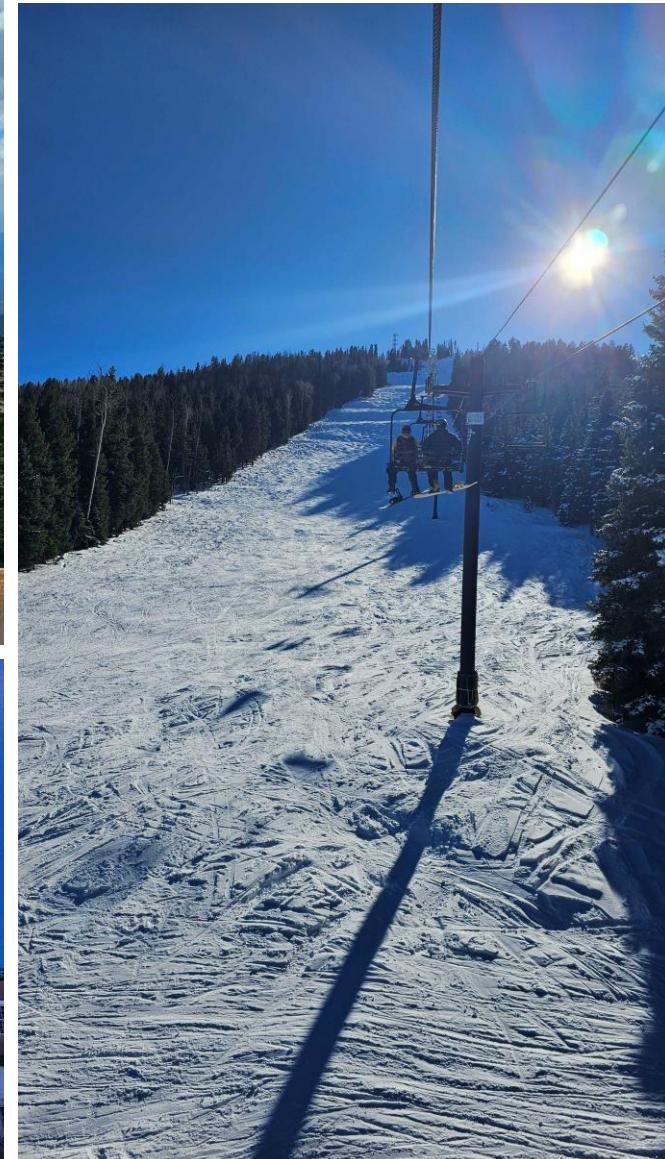
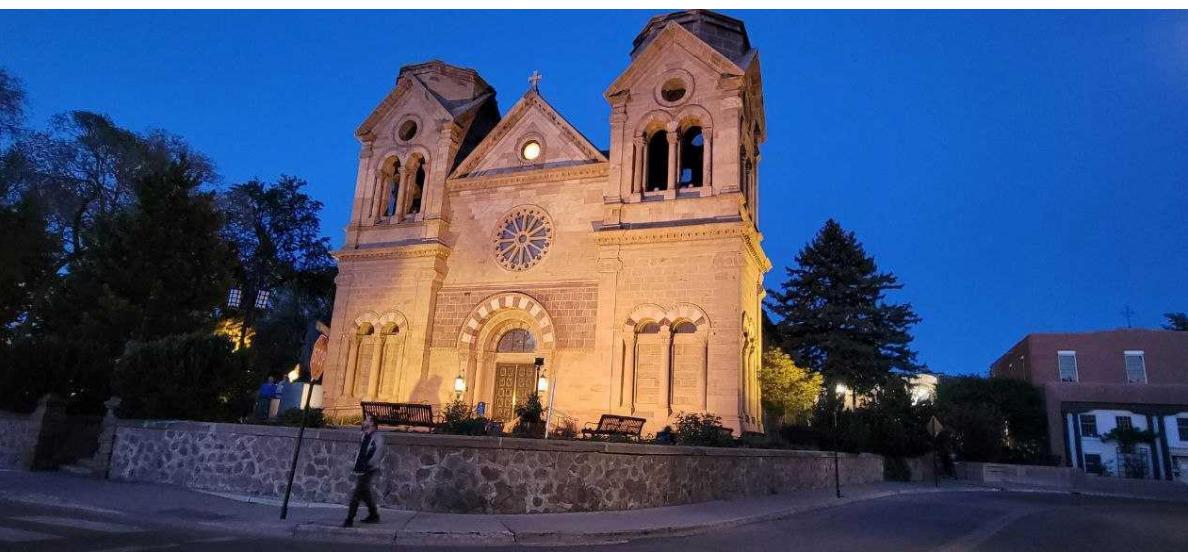


September 4, 2024

LA-UR-24-28802

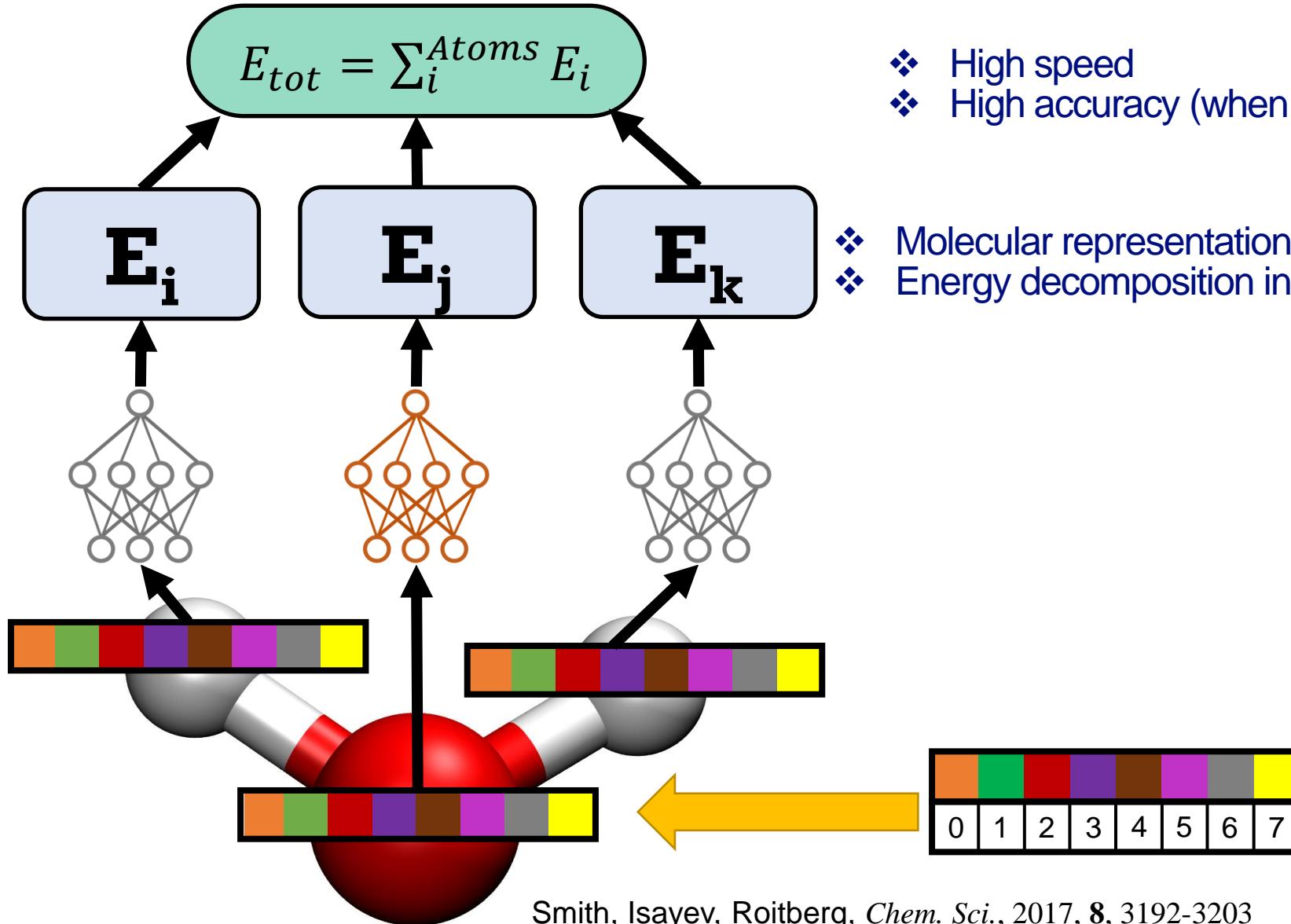


# Northern New Mexico Area

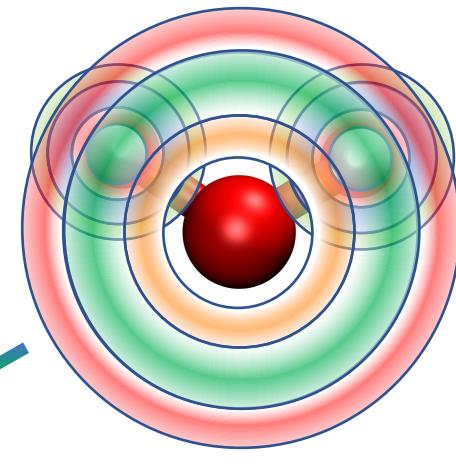


# ML to Replace QM

## The ANI-type Neural Network potential



- ❖ High speed
- ❖ High accuracy (when applied within a domain of training data)
  
- ❖ Molecular representation via local atomic environment descriptors
- ❖ Energy decomposition into atomic contributions

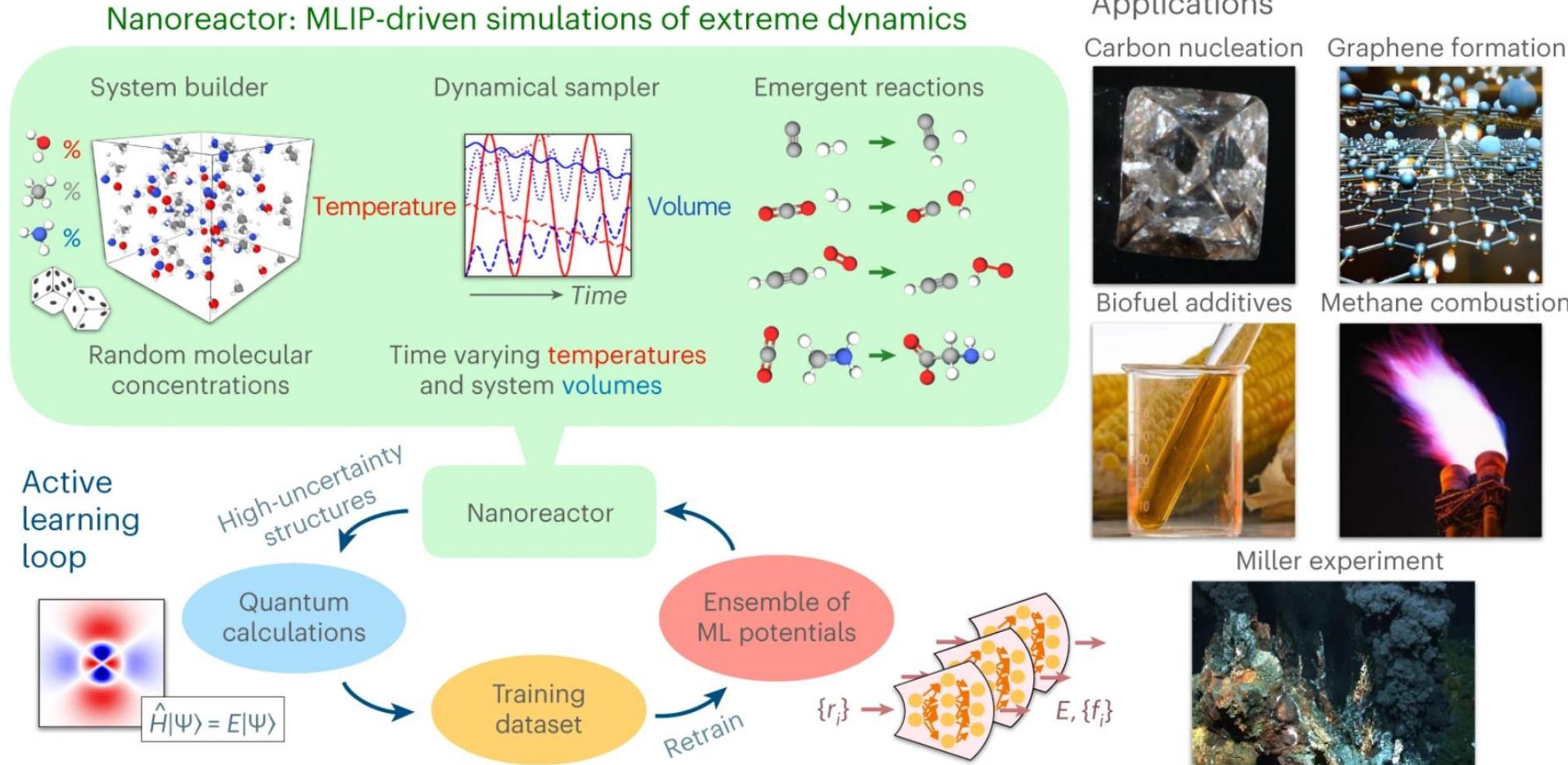


# ML to Replace QM: Large Scale Simulations

Simple models can simulate complex processes when provided with high-quality data.

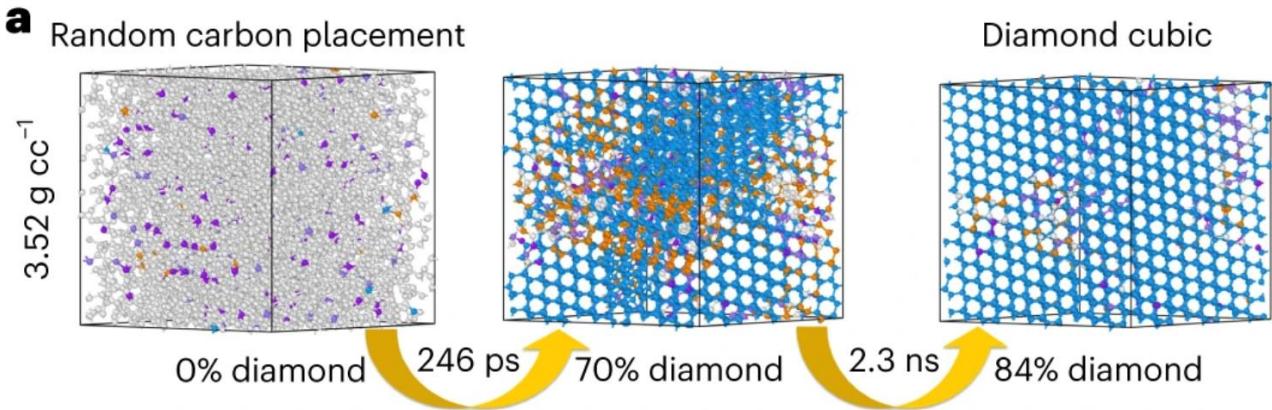
ML potential trained to ANI-1xnr dataset:

Active Learning via high-T non-equilibrium condensed phase MD snapshots. 26K datapoints (Boxes of up to 150 atoms)

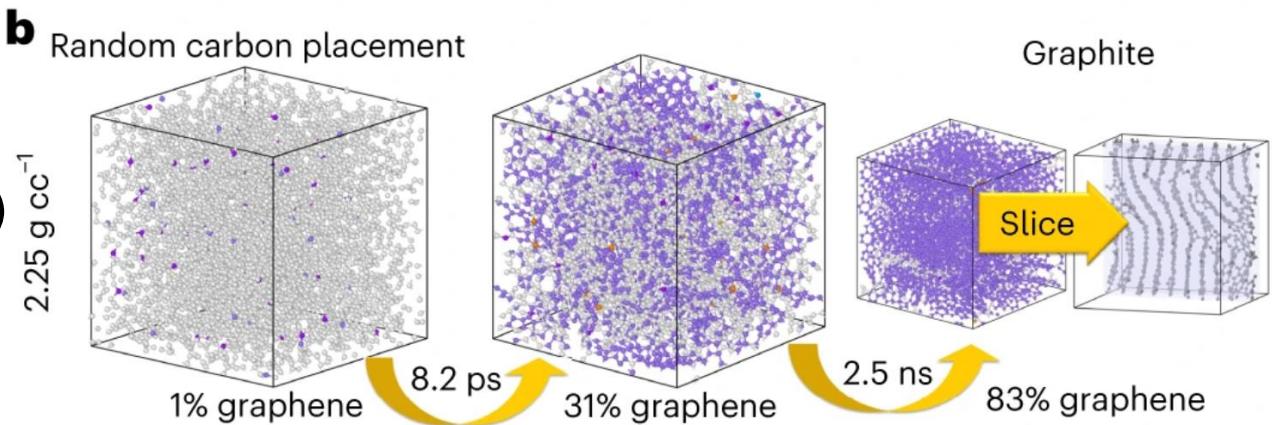


# Carbon solid-phase nucleation simulation

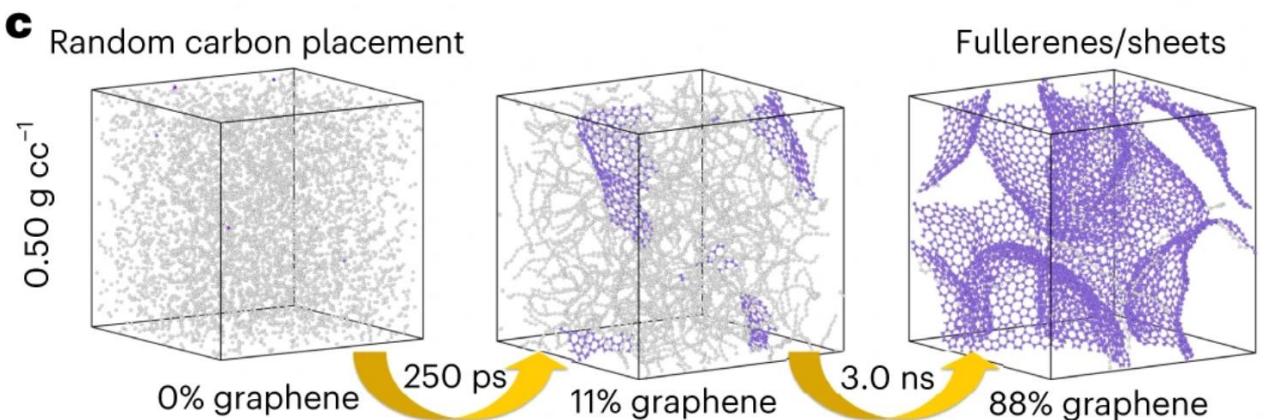
high ( $3.52 \text{ g cc}^{-1}$ )



medium ( $2.25 \text{ g cc}^{-1}$ )

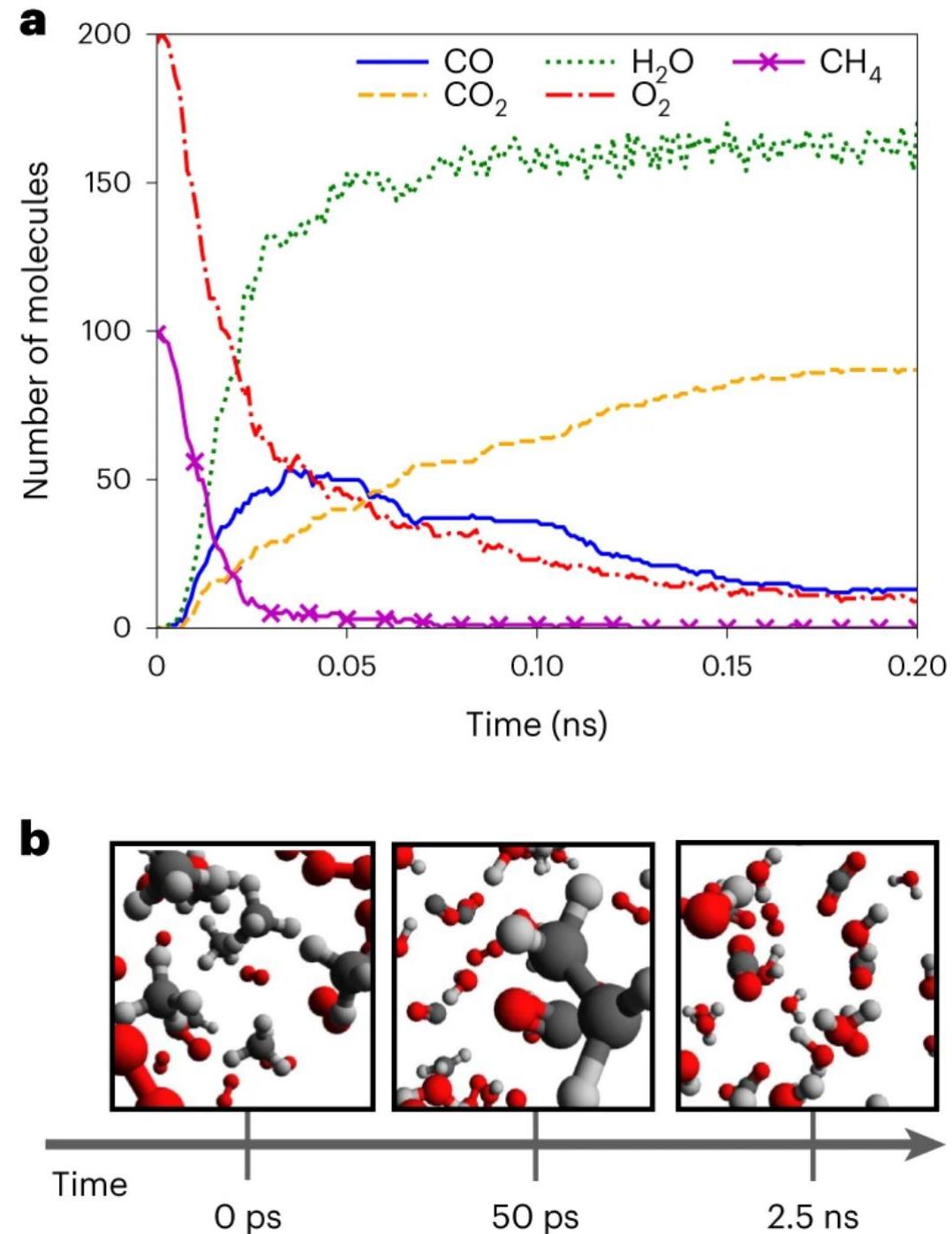


low ( $0.50 \text{ g cc}^{-1}$ )



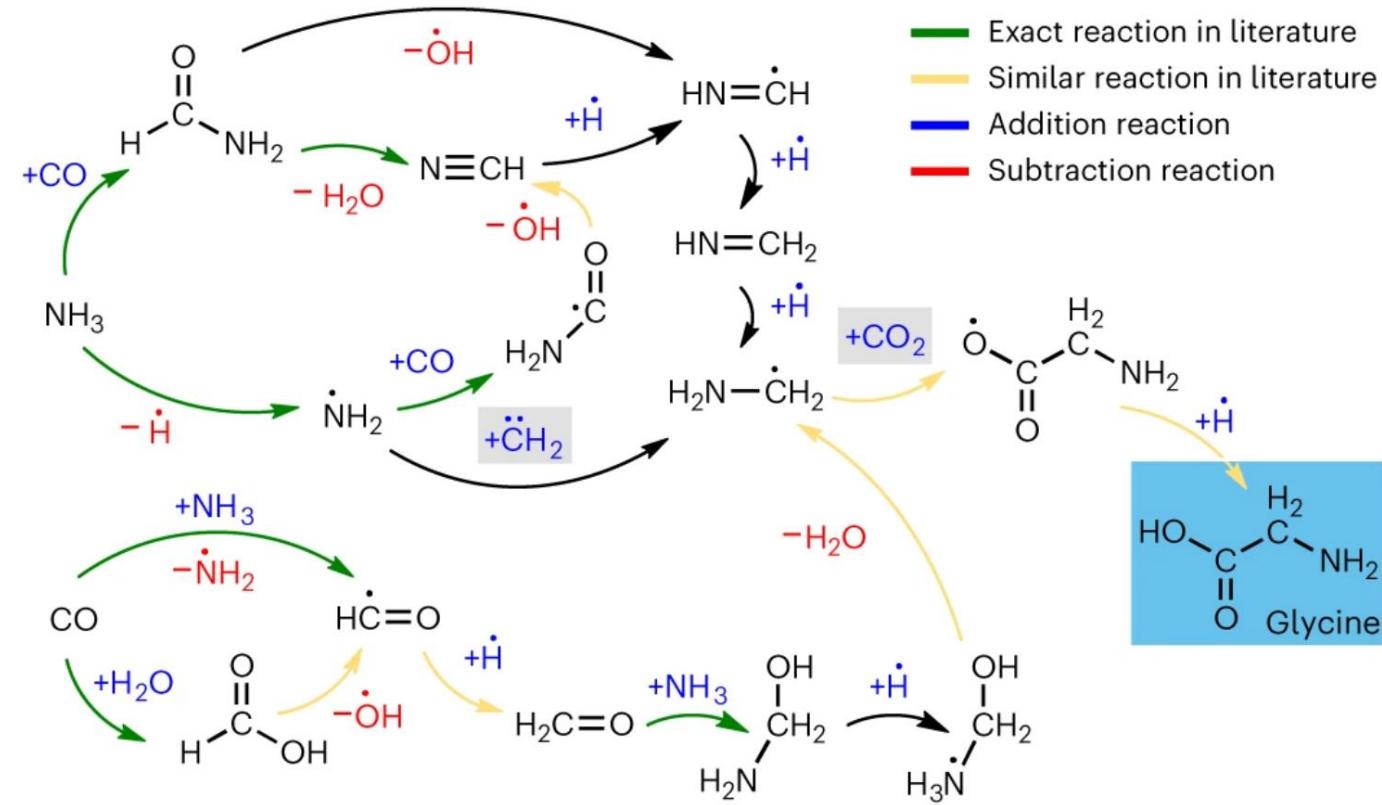
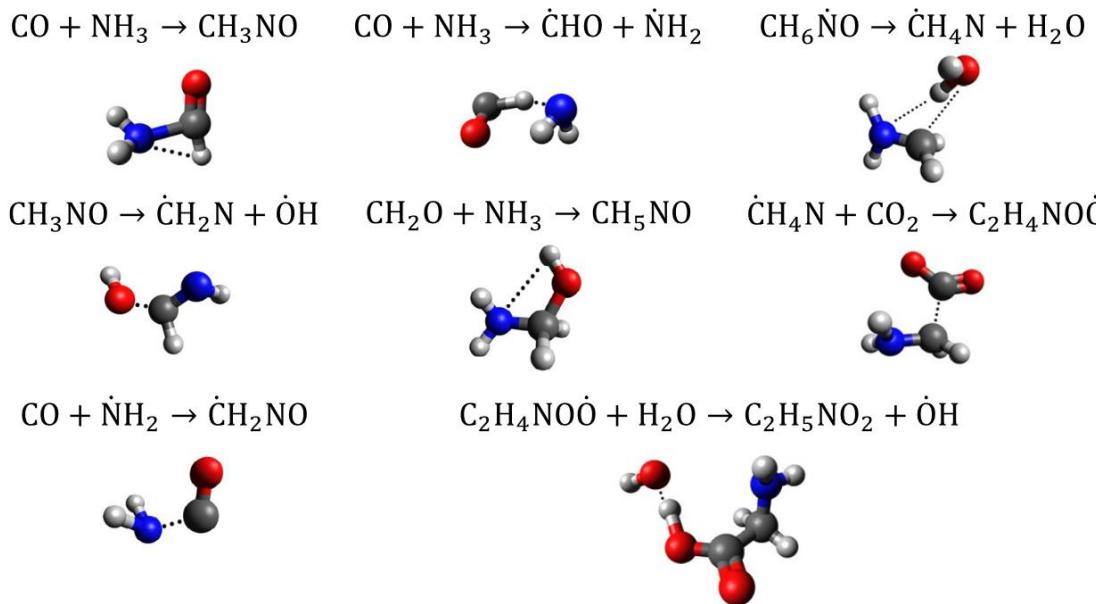
# Methane combustion

- Initial conditions: 100  $\text{CH}_4$  and 200  $\text{O}_2$  molecules, 0.1fs timestep
- ANI-1xnr potential correctly produces major products and species profiles
- Reaction rates depend on the reference DFT level of theory

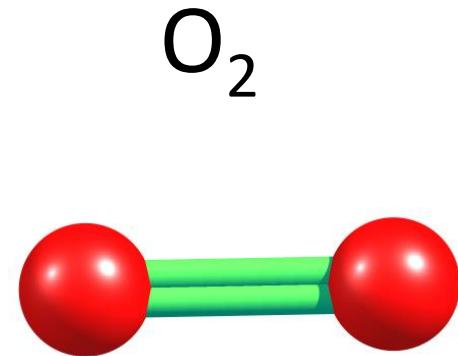


# Miller Experiment (Life Formation)

- Initial conditions: 16 H<sub>2</sub>, 14 H<sub>2</sub>O, 14 CO, 14 NH<sub>3</sub> and 14 CH<sub>4</sub>
- 0.25 fs timestep
- Glycine is formed!



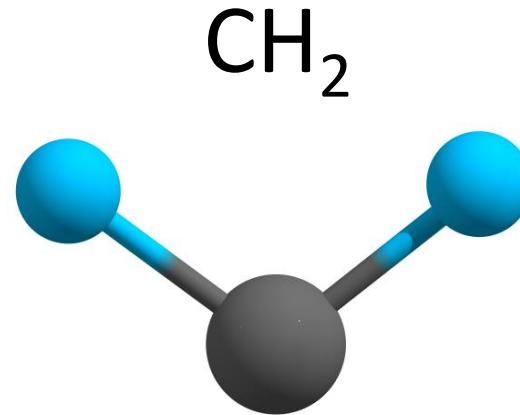
# ML potentials limitations: no electronic structure information



Singlet: 1 eV



Triplet: 0.0 eV

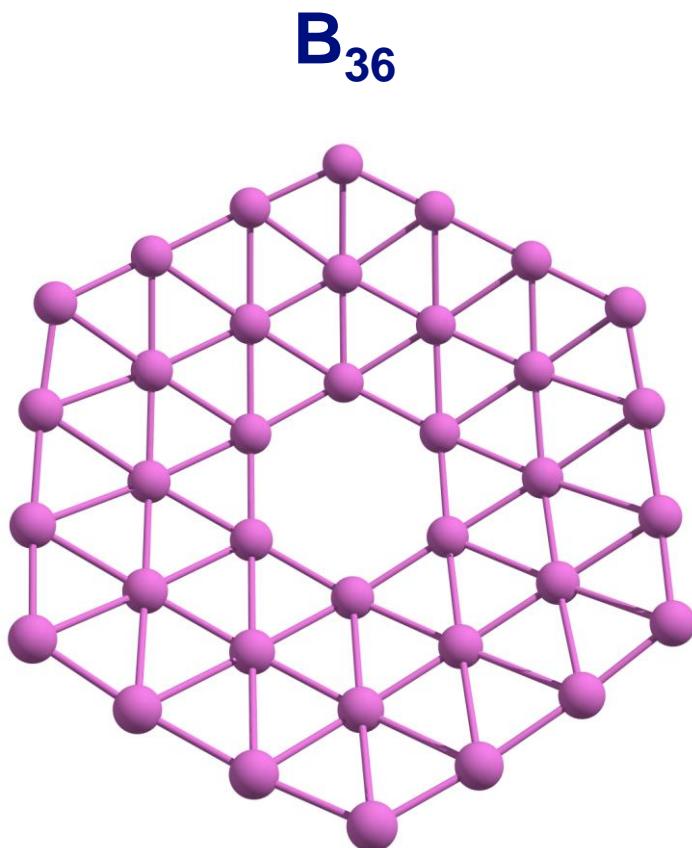


Singlet: 0.5 eV

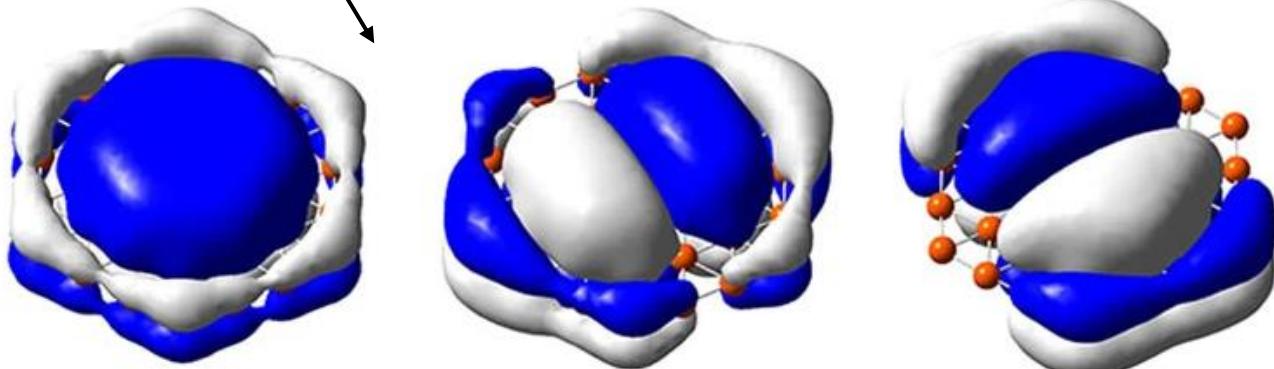


Triplet: 0.0 eV

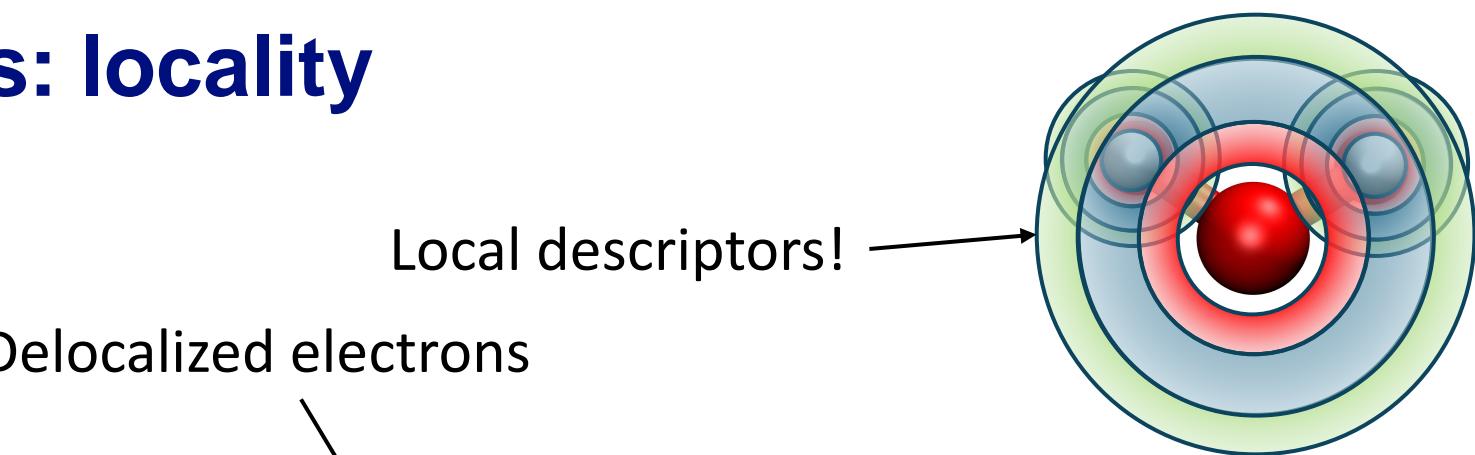
# ML potentials limitations: locality



Delocalized electrons



Local descriptors!



- $B_{36}$  has fully delocalized chemical bonds
- Aromatic (like benzene)  $\rightarrow$  planar

❖ Non-local electronic effects often dictate structural stability

# ML to Assist QM

## Semiempirical Quantum Mechanics (SEQM)

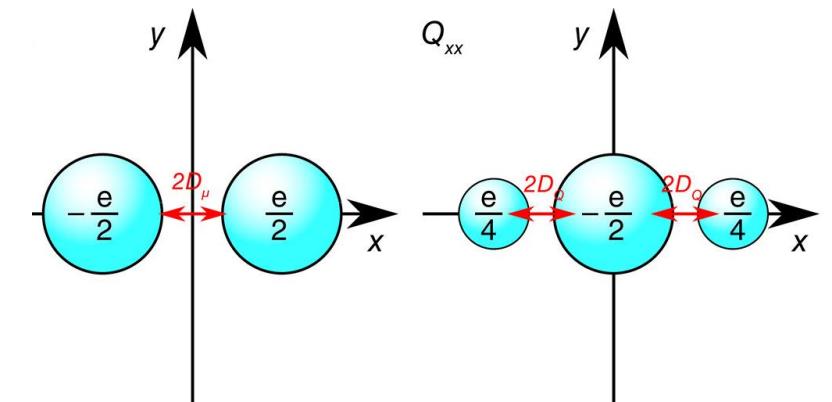
### Neglect of Diatomic Differential Overlap (NDDO):

- Based on Hartree-Fock formalism
- Overlap matrix is neglected
- 3c- and 4c-2e integrals are neglected
- 2c-2e integrals are approximated by multipoles
- Valence shell electrons only, minimal basis set
- 1c-1e and 1c-2e integrals are replaced by static fitted parameters

$$FC = \cancel{SCE}$$

MO coefficients → **FC** ← Fock matrix

Eigenvalues (MO energies) → **FC** ← Overlap matrix (neglected)



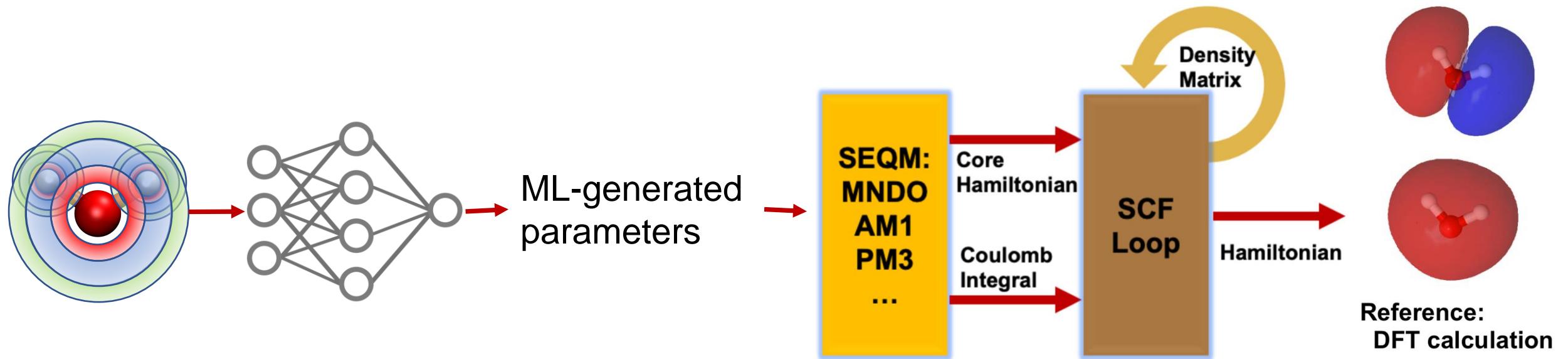
- ❖ The accuracy is compromised
- ❖ The scaling is reduced from quartic  $O(N^4)$  to cubic  $O(N^3)$ , lower prefactor
- ❖ **Electronic structure formalism is retained (charges, multiplicity, non-local effects)**

# SEQM Limitation: Accuracy

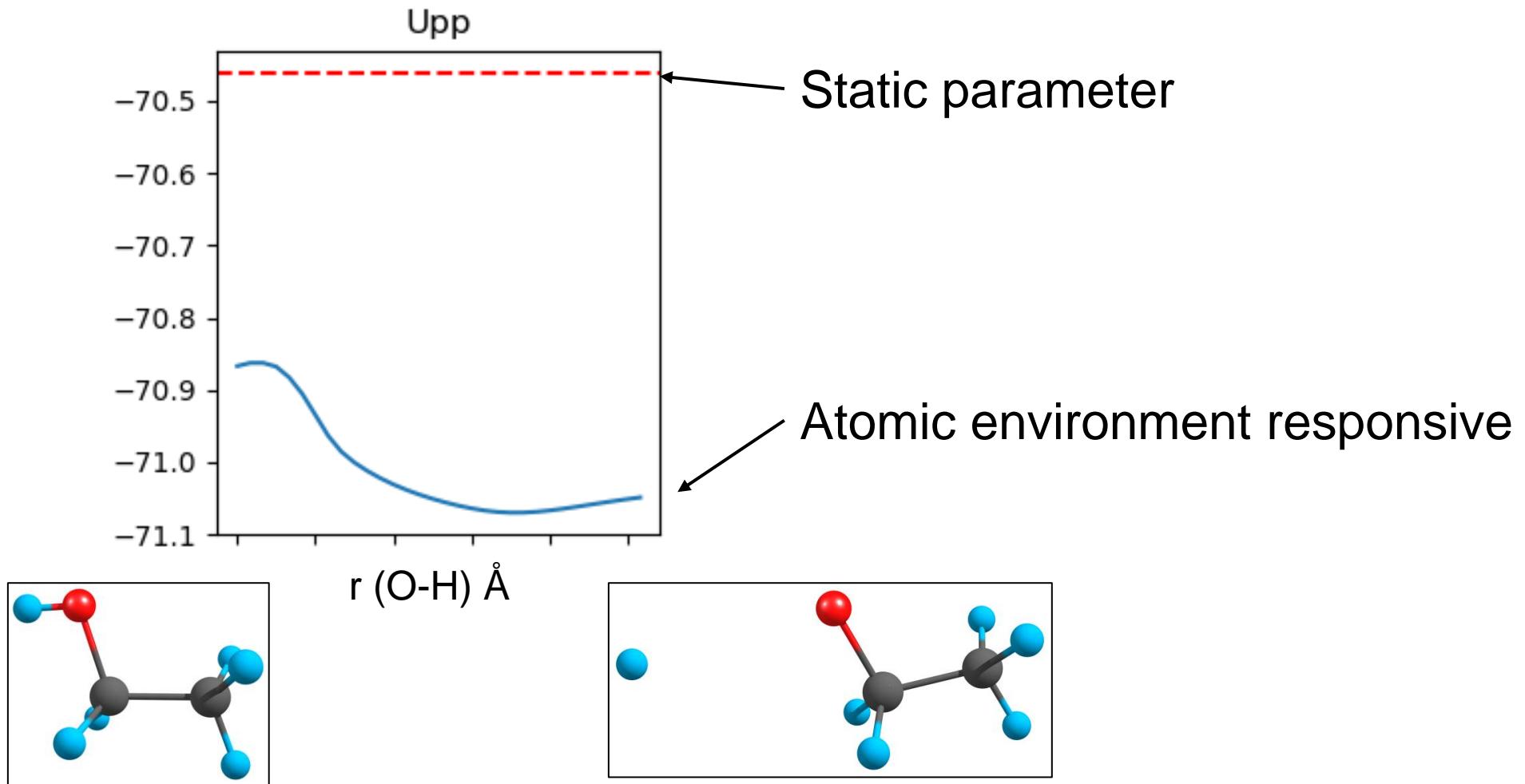
- ❖ Static parameters in Hamiltonian compromise accuracy

# Improving accuracy of SEQM: ML + SEQM

- ❖ Replacement of static parameters in semi-empirical Hamiltonian with dynamically responsive
- ❖ ML model generates parameter values based on spatial descriptors



$U_{pp}$ :  $p$ -AO one-electron one-center integral for O atom



# ML to Assist QM

## Semiempirical Quantum Mechanics (SEQM)

### PySEQM: PyTorch-Based Semi-Empirical Quantum Mechanics

#### Capabilities:

- Neglect of Diatomic Differential Overlap models (PM6, PM3, AM1, MNDO)
- Built-in interfaces for ML re-parametrization
- GPU-accelerated simulations
- Multiple parallel simulations via a batch mode
- Forces and errors calculation via PyTorch backpropagation

<https://github.com/lanl/PYSEQM.git>

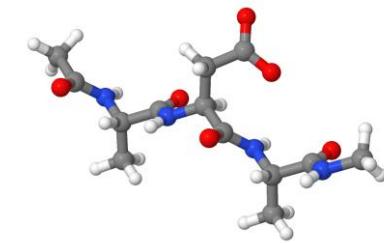
G. Zhou, et. al. PNAS, 2022, 119, e2120333119

M. Kulichenko et al. J. Chem. Theory Comput. 2023, 19, 11, 3209–3222

# ML to Assist QM: Training SEQM to Non-Equilibrium Data

ANI-1x training set

RMSE of Atomization energies Test set: 250 Tripeptides (DFT reference data)			
Method	SEQM (PM3)	ML (HIPNN)	ML+SEQM
RMSE [kcal/mol]/atom	0.6	1.1	<b>0.2</b>



- ❖ ML+SEQM achieves higher accuracy than pure ML and SEQM
- ❖ ML+SEQM needs less training data than pure ML
- ❖ In fact, **ML+SEQM can't have too much data**
  - **Training is expensive because of error backpropagation through SCF loop.**

# ML to Assist QM: Training SEQM to Reactive Data

Robert Stanton et al. Unpublished

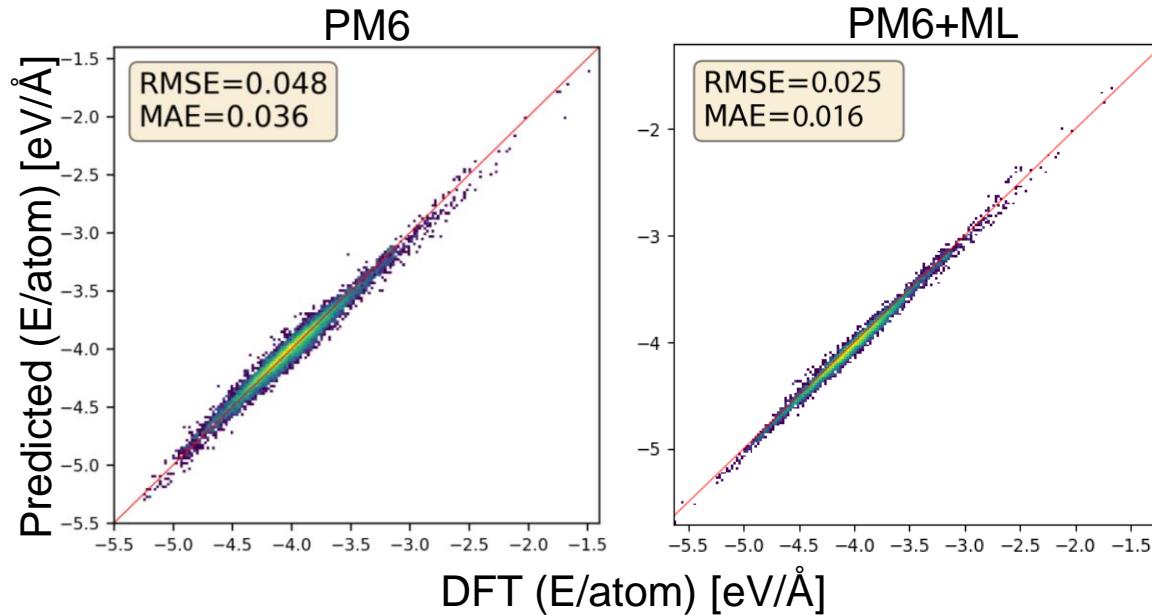
**Training data:** 140k broken-symmetry open shell singlets and doublets

- 60% Transition1x<sup>1</sup> – reaction pathways
- 10% BSE49<sup>2</sup> – bond dissociation paths
- 30% ANI-1x<sup>3</sup> – non-equilibrium geometries

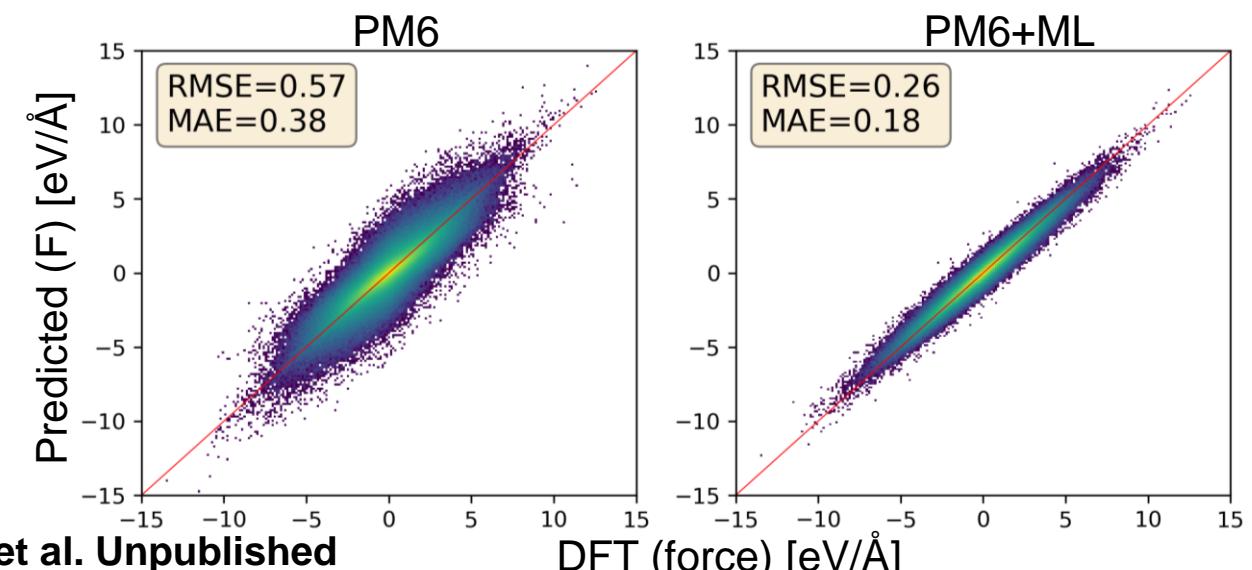
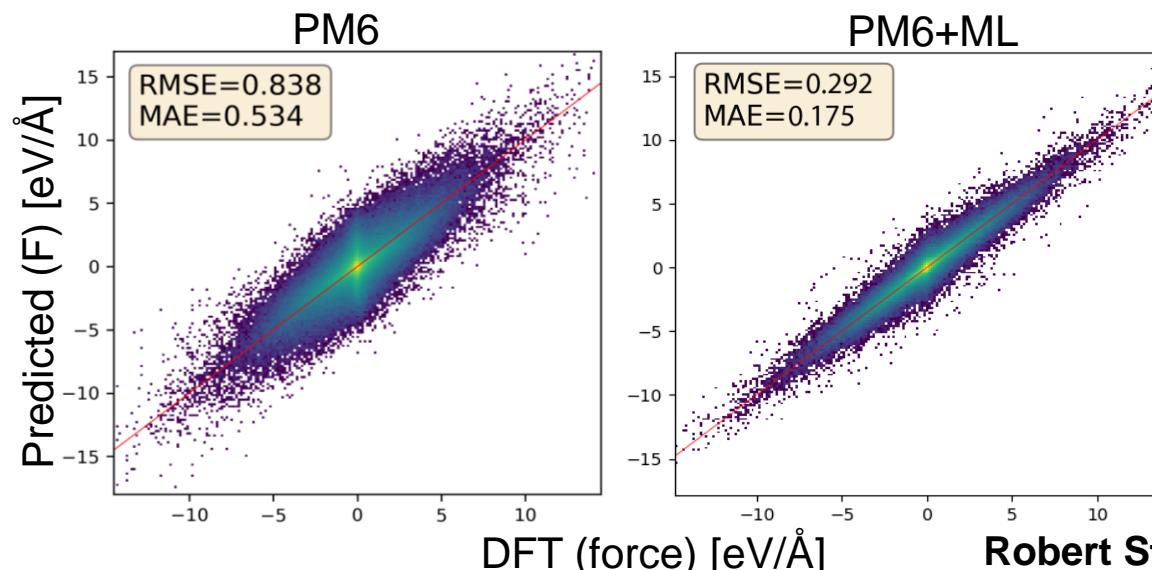
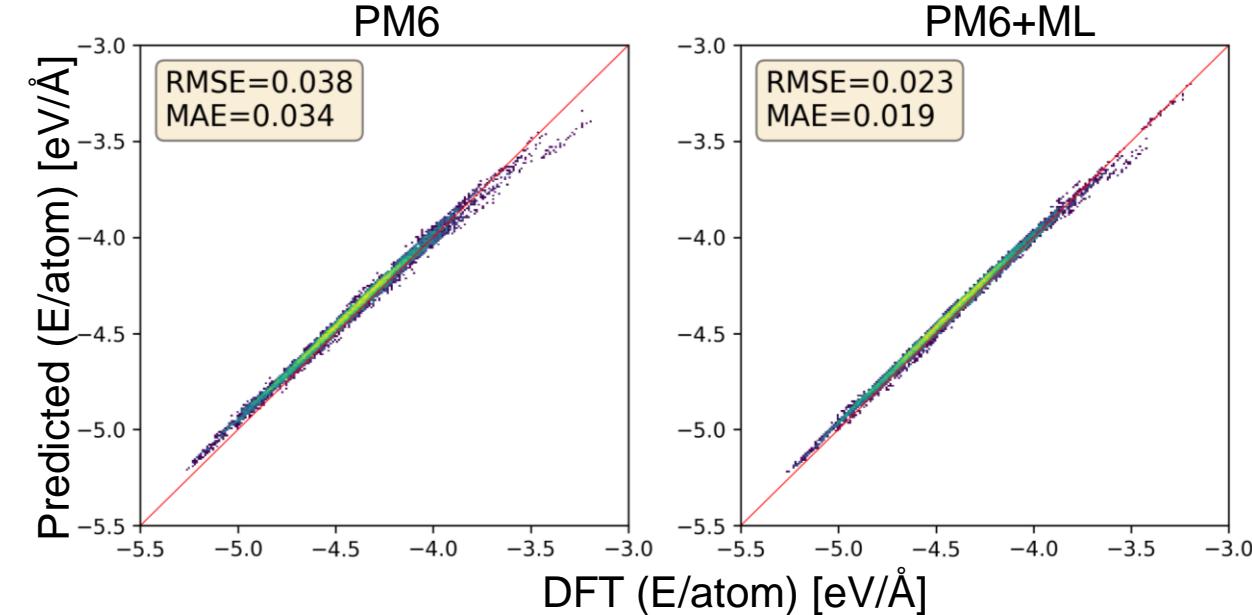
- 1) M. Schreiner et al., Sci Data 2022, 9, 779
- 2) V.K. Prasad et al., Sci Data 2021, 8, 300
- 3) J.S. Smith et al., Sci Data 2020, 7, 134

# ML to Assist QM: Training SEQM to Reactive Data

Held-out Test Set (14k, reactive)

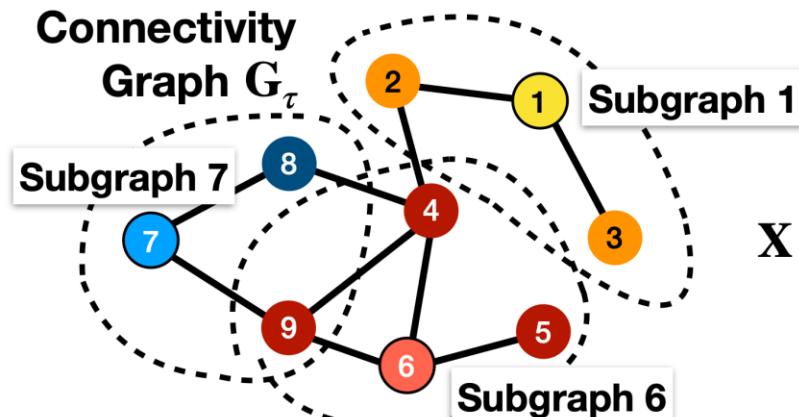


Drug Bank subset (13k, real drug molecules)



# Graph-based Electronic Structure Theory

Non-overlapping cores  
Overlapping halos



$$X = \begin{matrix} 1 & 2 & & & & & & & \\ 2 & 3 & & & & & & & \\ & 3 & 4 & & & & & & \\ & & 4 & 5 & 6 & & & & \\ & & & 5 & 6 & 7 & & & \\ & & & & & 7 & 8 & & \\ & & & & & & 8 & 9 & \\ & & & & & & & 9 & \end{matrix}$$

**Initial Density Matrix**

$$\mathbf{x}^{(1)} = \begin{matrix} 1 & & \\ & 2 & \\ & & 3 \end{matrix}$$

$$f(\mathbf{x}^{(1)}) = \begin{matrix} 1 & & \\ & 2 & \\ & & 3 \end{matrix}$$

$$\mathbf{x}^{(6)} = \begin{matrix} 4 & & & \\ & 5 & & \\ & & 6 & \\ & & & 9 \end{matrix}$$

$$f(\mathbf{x}^{(6)}) = \begin{matrix} 4 & & & \\ & 5 & & \\ & & 6 & \\ & & & 9 \end{matrix}$$

$$\mathbf{x}^{(7)} = \begin{matrix} 7 & & \\ & 8 & \\ & & 9 \end{matrix}$$

$$f(\mathbf{x}^{(7)}) = \begin{matrix} 7 & & \\ & 8 & \\ & & 9 \end{matrix}$$

core halo

**Initial Density SubMatrices**

**Updated Density SubMatrices**

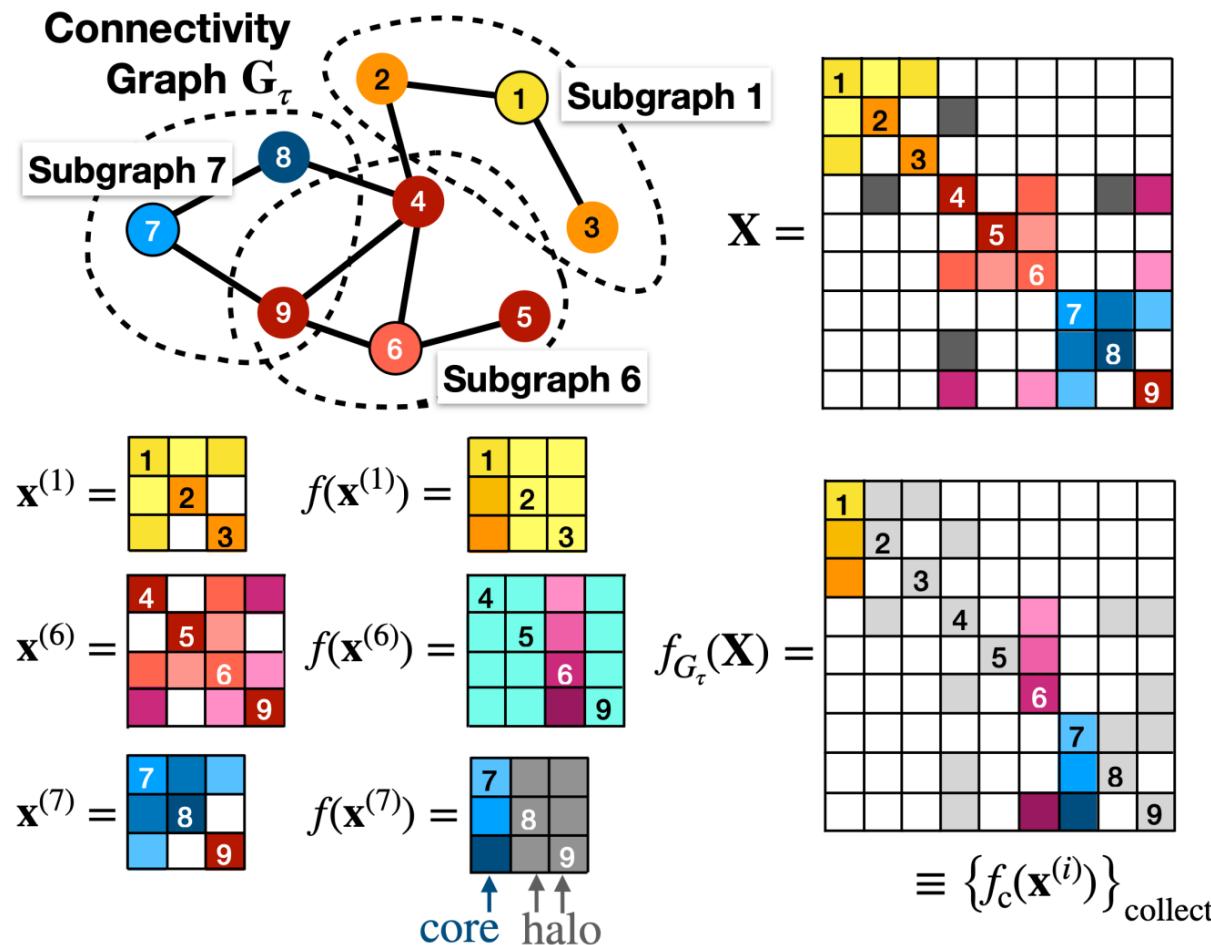
$$f_{G_\tau}(\mathbf{X}) = \begin{matrix} 1 & & & & & & & & \\ 2 & & & & & & & & \\ & 3 & & & & & & & \\ & & 4 & & & & & & \\ & & & 5 & & & & & \\ & & & & 6 & & & & \\ & & & & & 7 & & & \\ & & & & & & 8 & & \\ & & & & & & & 9 & \end{matrix}$$

$\equiv \left\{ f_c(\mathbf{x}^{(i)}) \right\}_{\text{collect}}$

**Updated Density Matrix  
Reconstructed from Subgraphs**

# Graph-based Electronic Structure Theory

- Graph partitioning is adaptive: a new graph is constructed at each MD step or DM optimization step
- Overlap matrix or distances for initialization

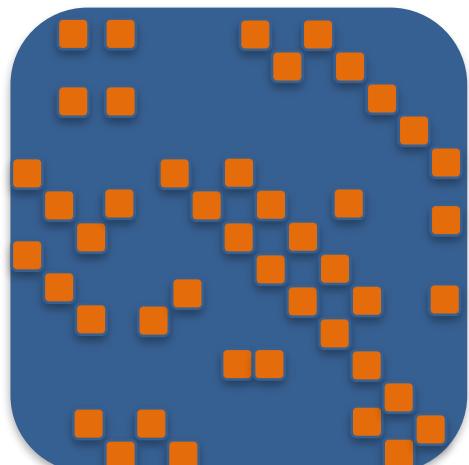


Subgraphs are not isolated!

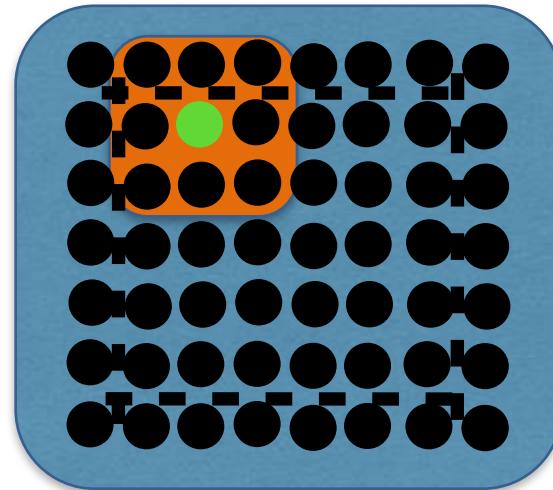
A full (non-local) Coulomb summation is performed when constructing Fock SubMatrices.  
Subgraphs “feel” each other.  
But the eigenvalue problem is solved for a subgraph only.

# Linear Scaling Electronic Structure Theory

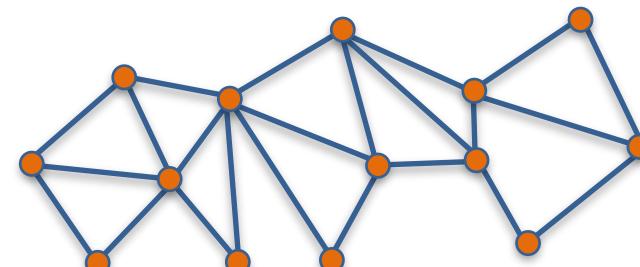
Sparse Matrix Algebra



Divide and Conquer



Graph Theory

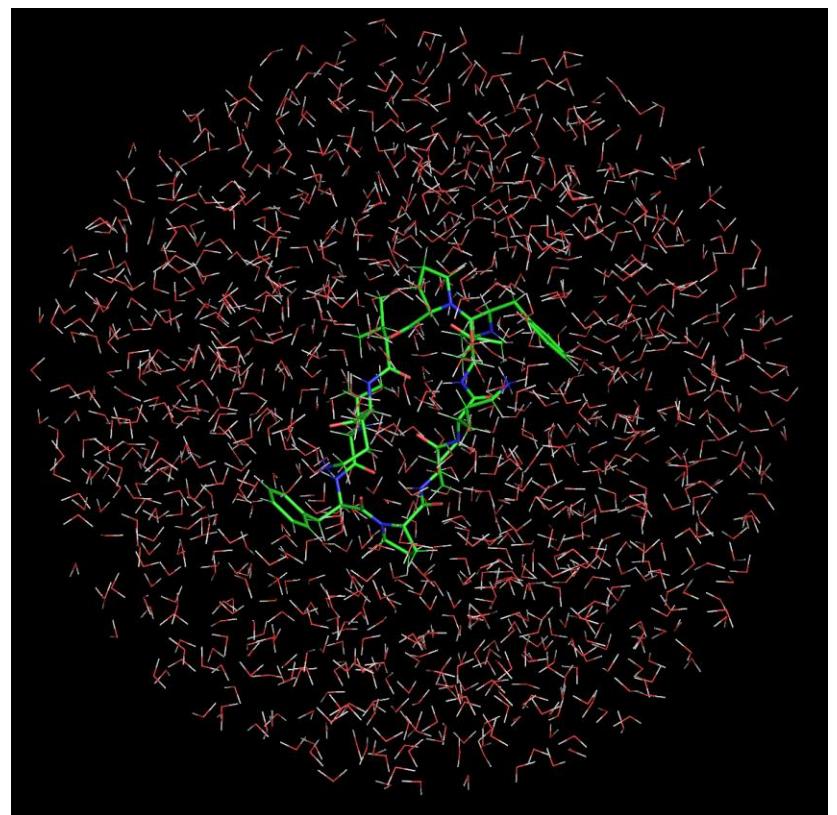


- a) Simple error control
- b) Efficient parallelism on distributed memory
- c) Small overhead

# Density Matrix Optimization of Solvated Gramicidin S

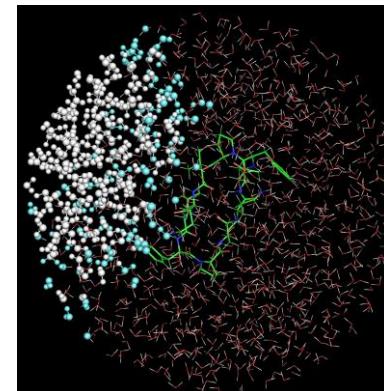
Gramicidin S solvated in water

3605 atoms

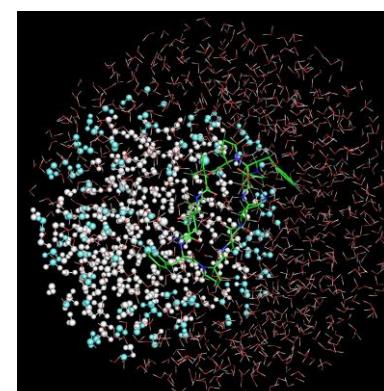


→  
7 subgraphs

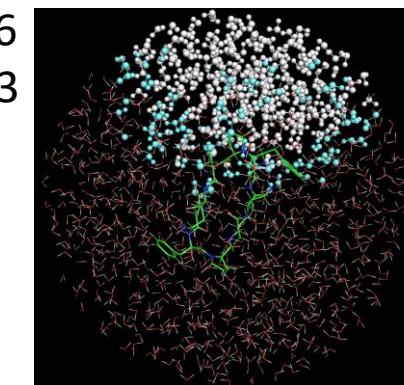
CORE: 443  
HALO: 165



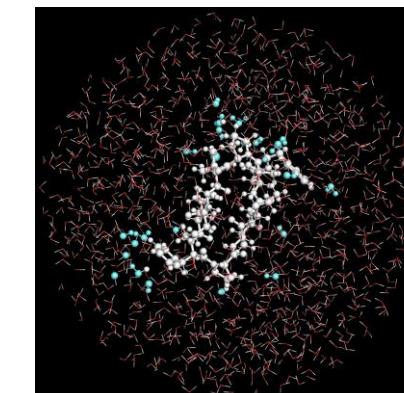
CORE: 556  
HALO: 218



CORE: 639  
HALO: 188

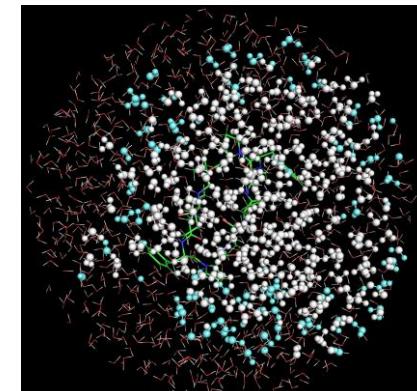


CORE: 180  
HALO: 46



CORE: 527  
HALO: 203

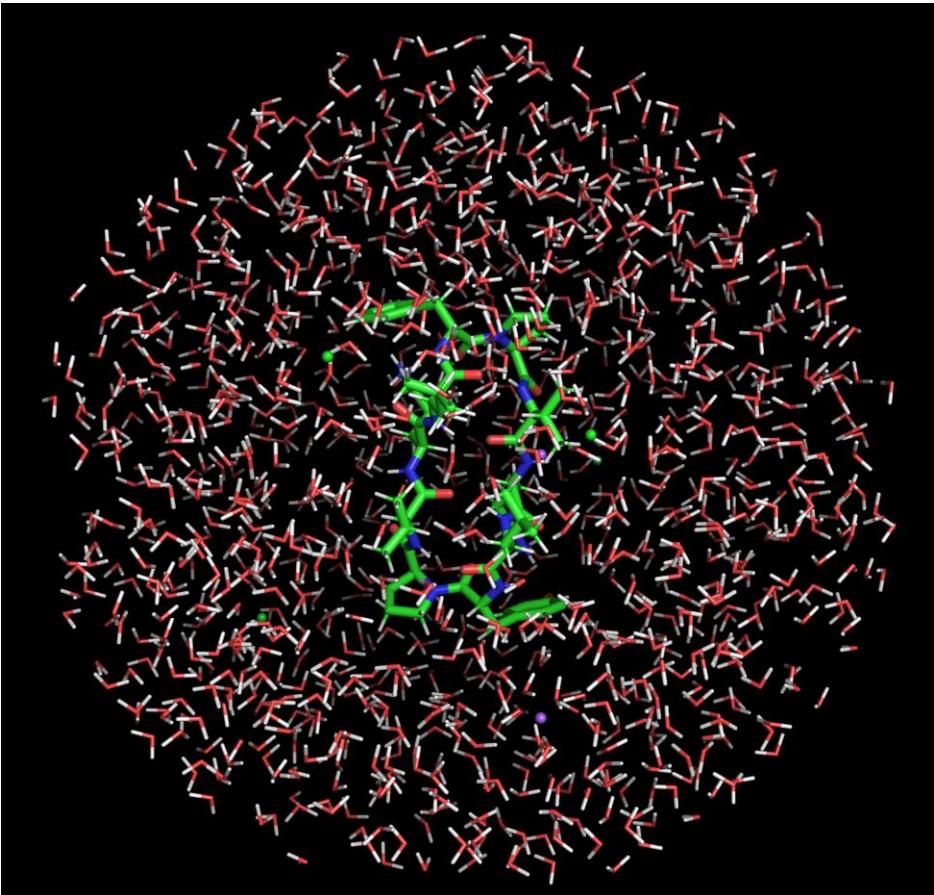
CORE: 624  
HALO: 178



(Built via PACKMOL)

# Density Matrix Optimization of solvated Gramicidin S

Intel(R) Xeon(R) Gold 5218R CPU @ 2.10GHz



3605 atoms

1 part:

Etot: -378831.186 eV

7 parts:

Etot: -378831.191 eV

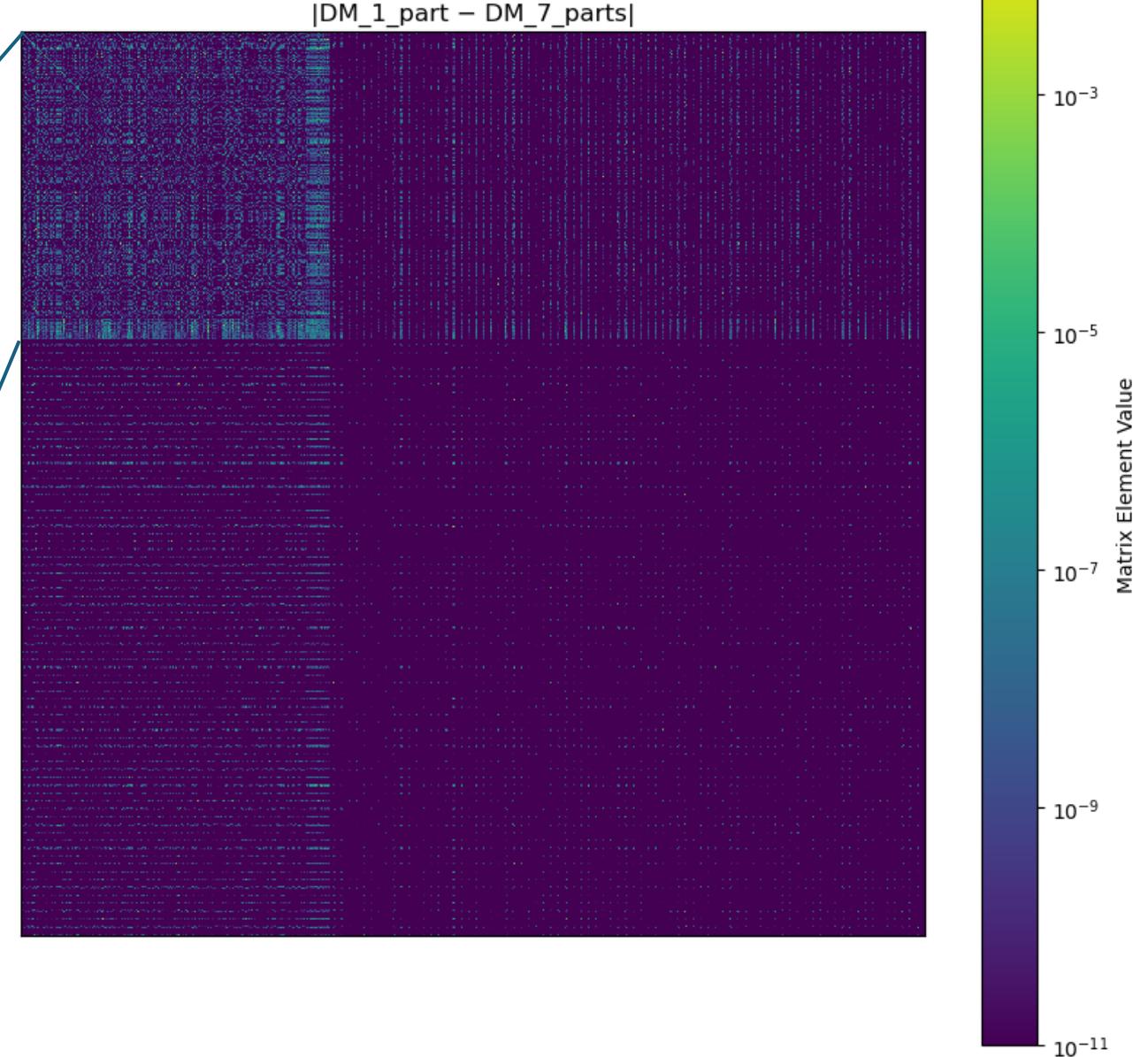
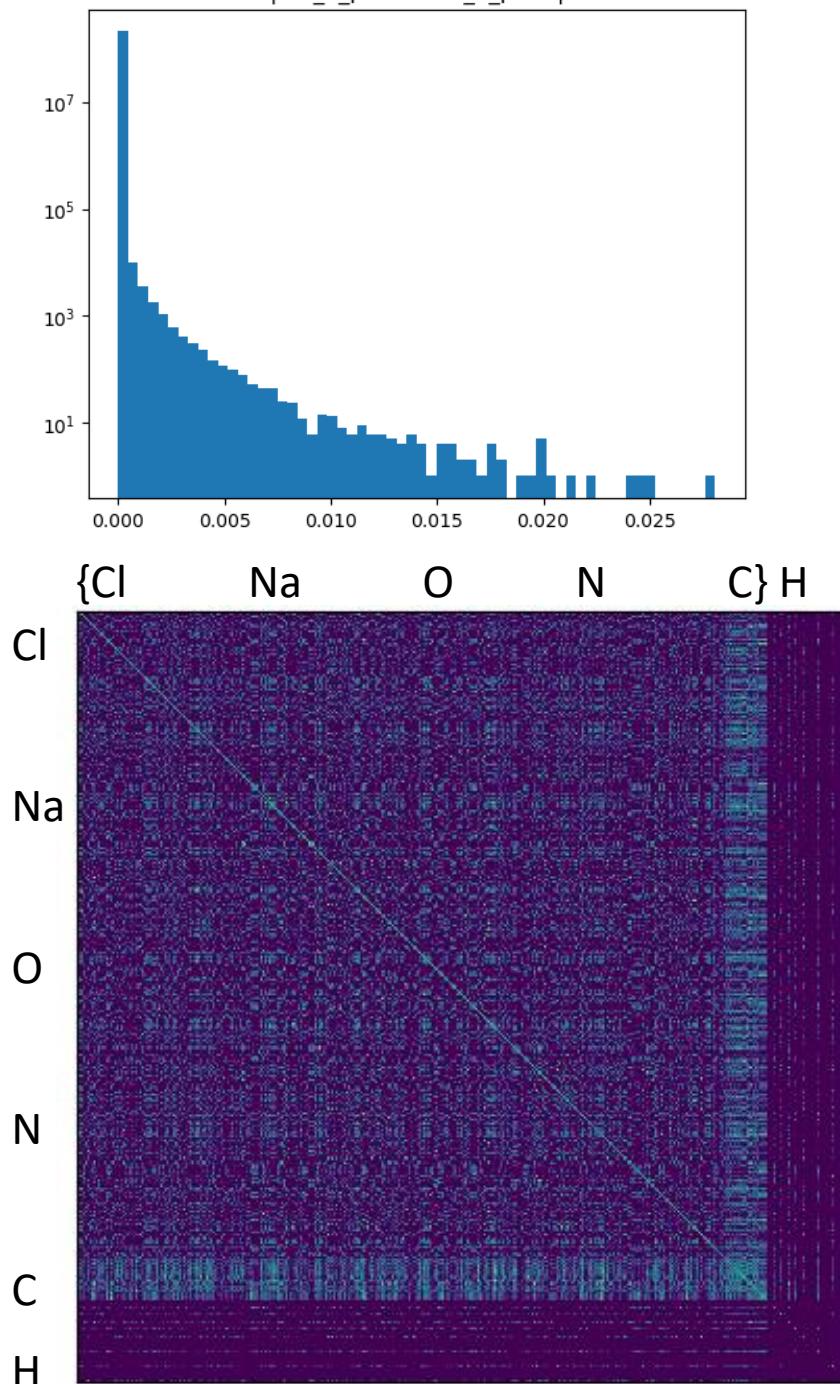
$$\Delta E_{\text{tot}} = 0.005 \text{ eV}$$

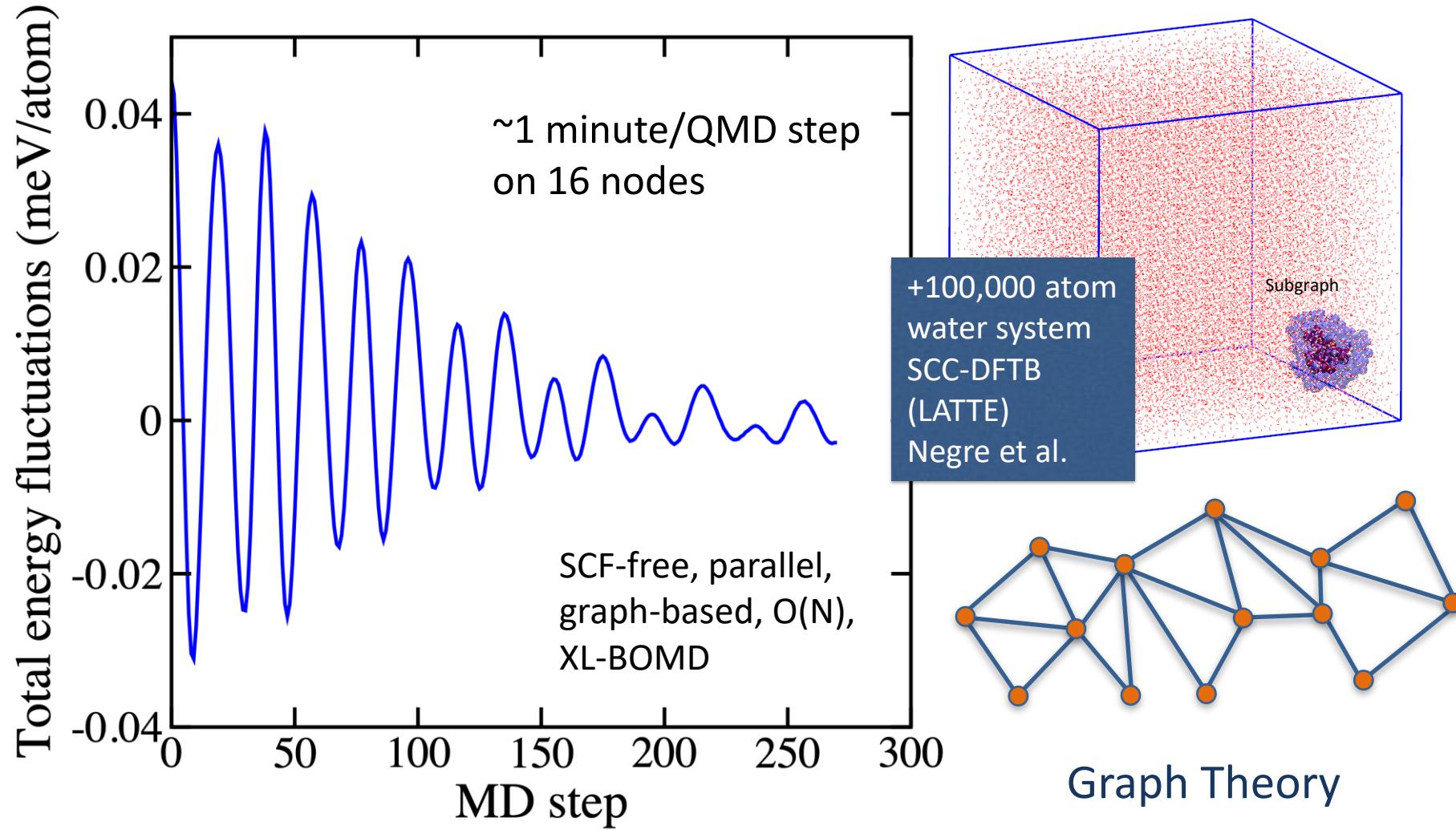
11min 37s

2min 11s

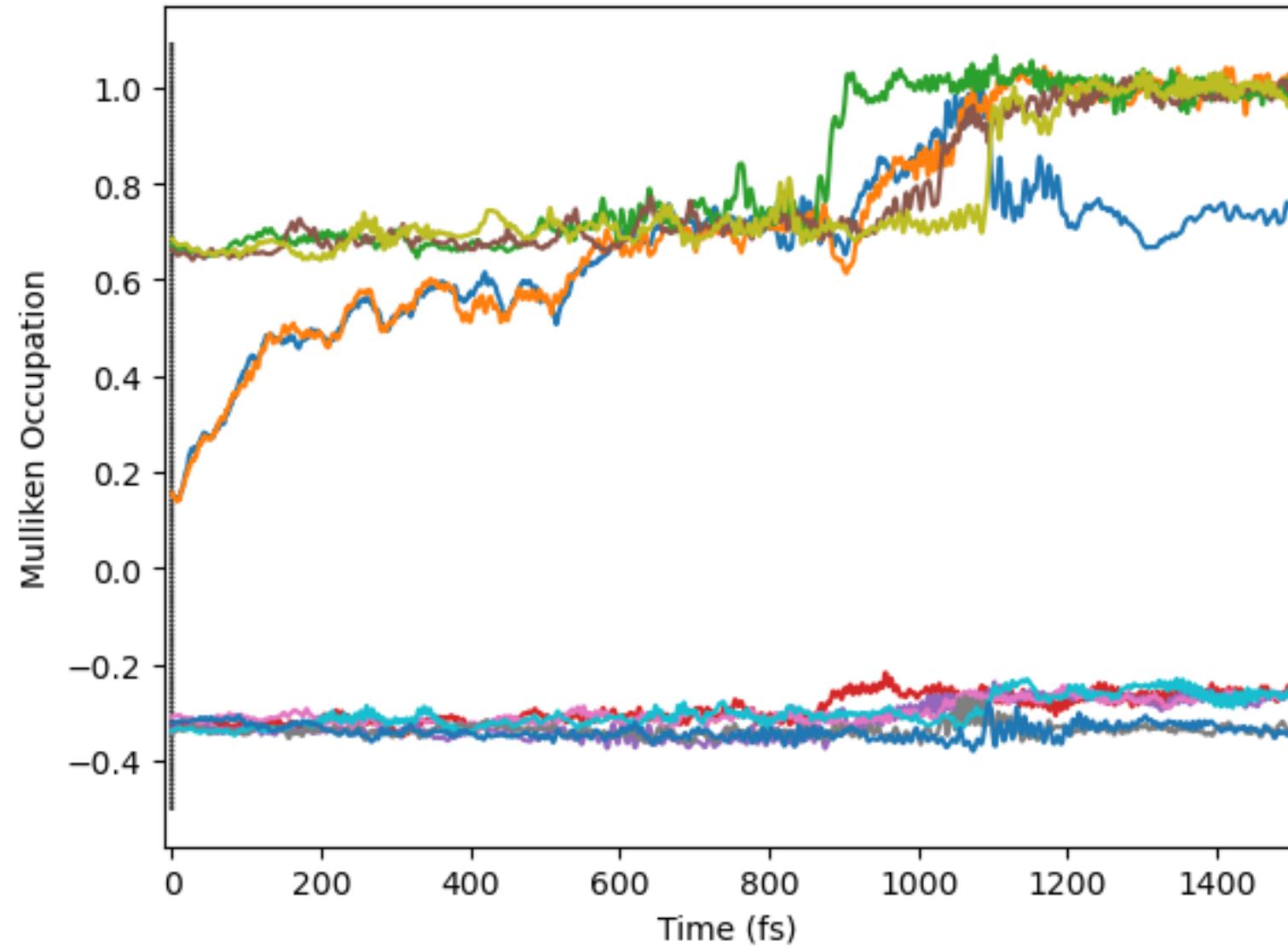
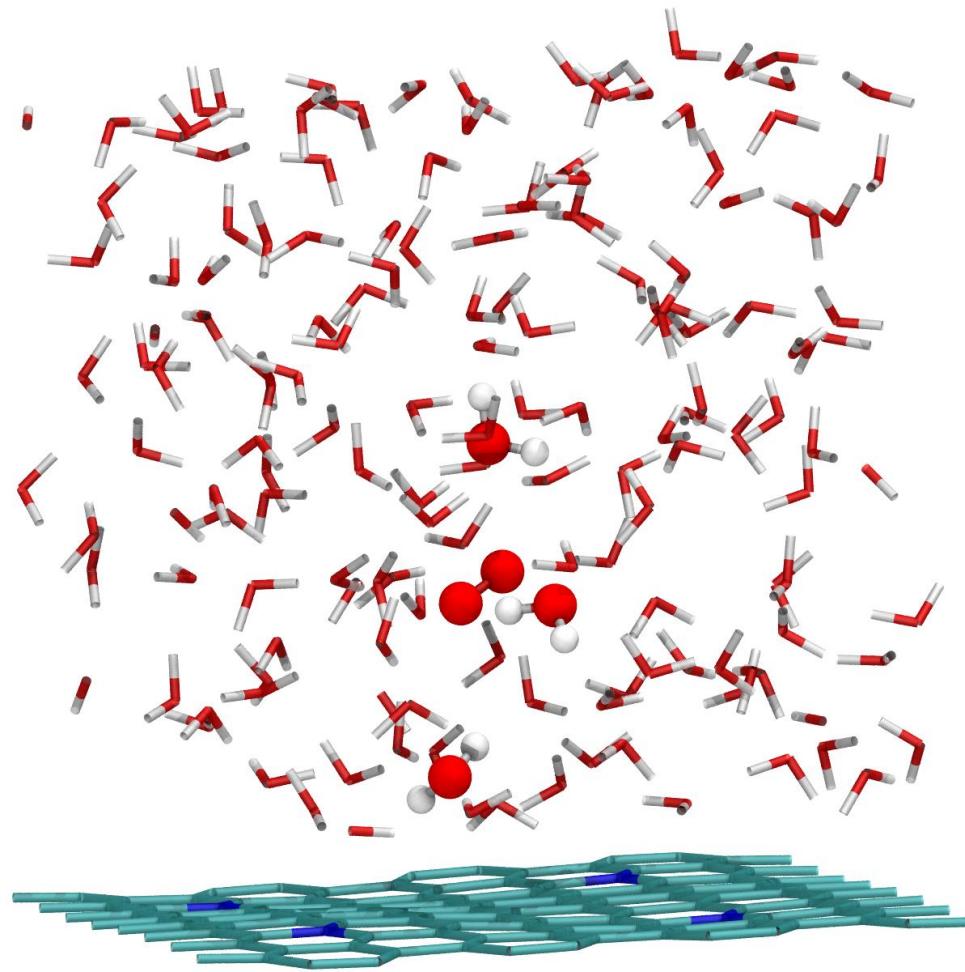
# Density Matrix Comparison

## Whole System vs Subgraphs



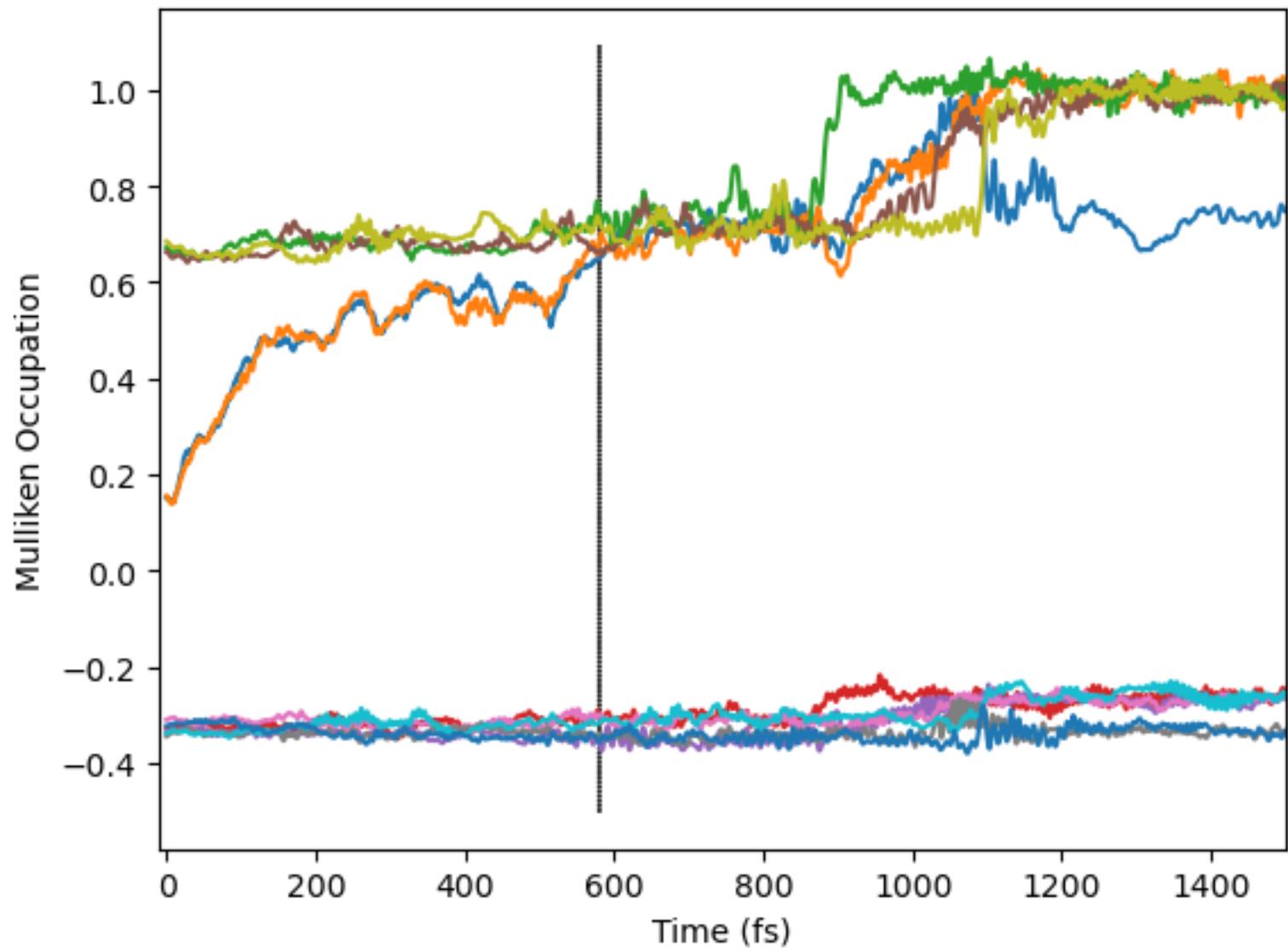
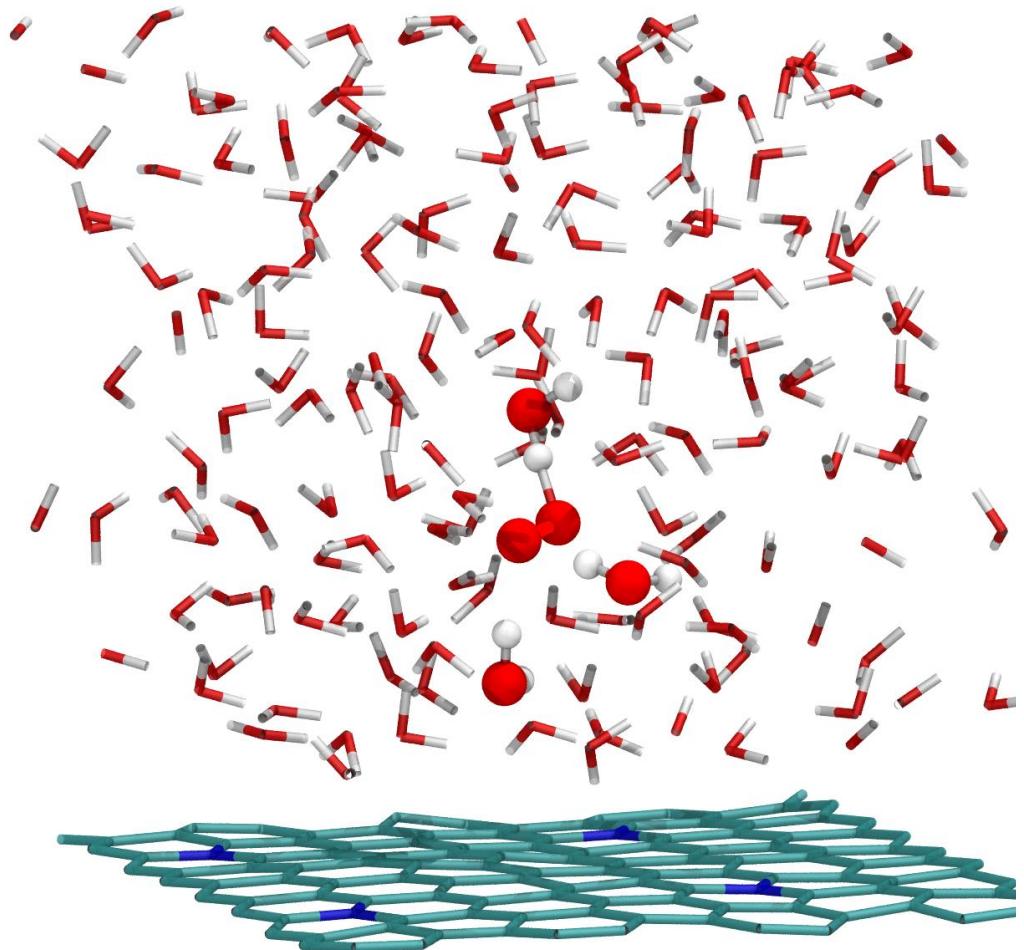


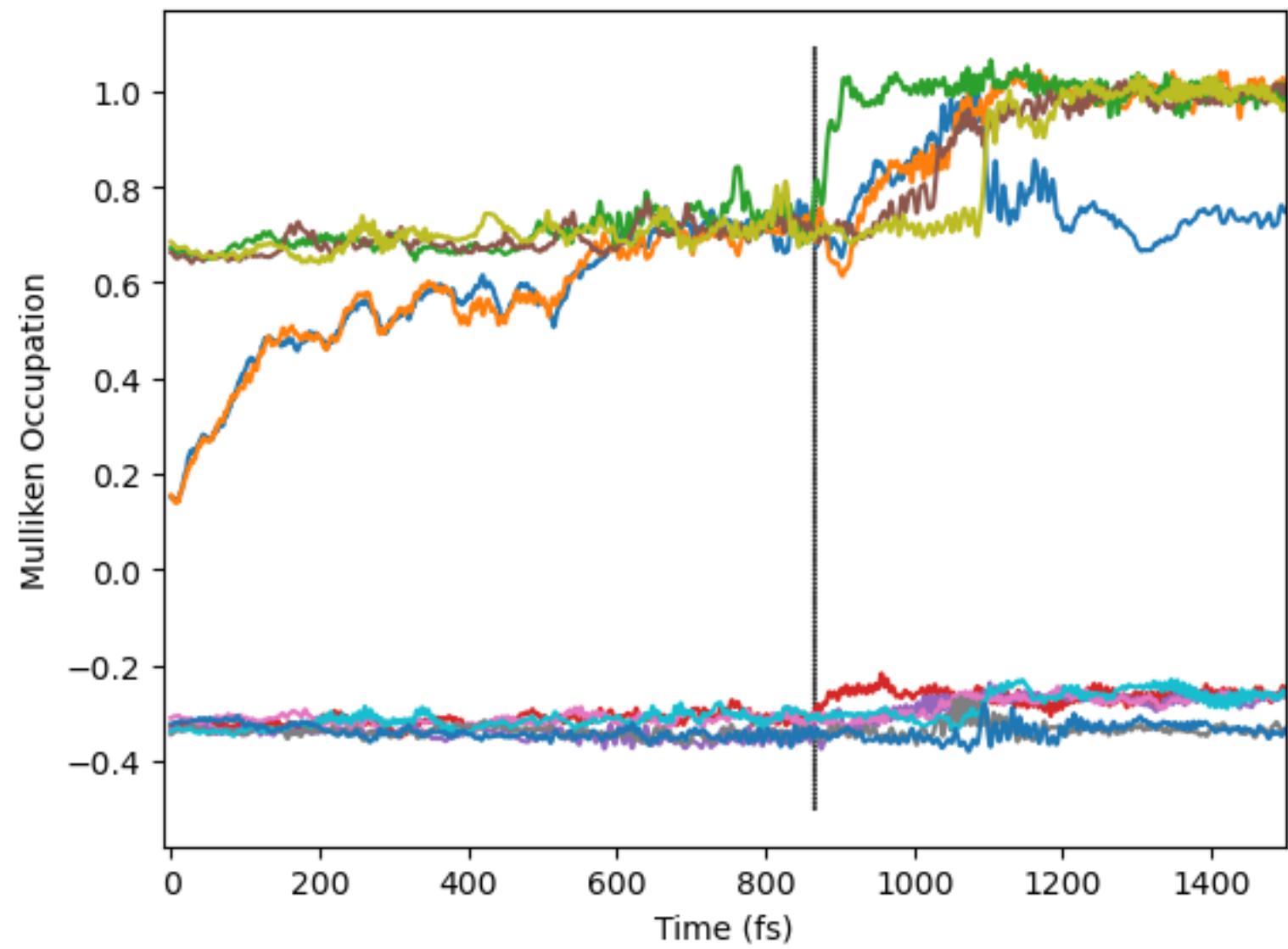
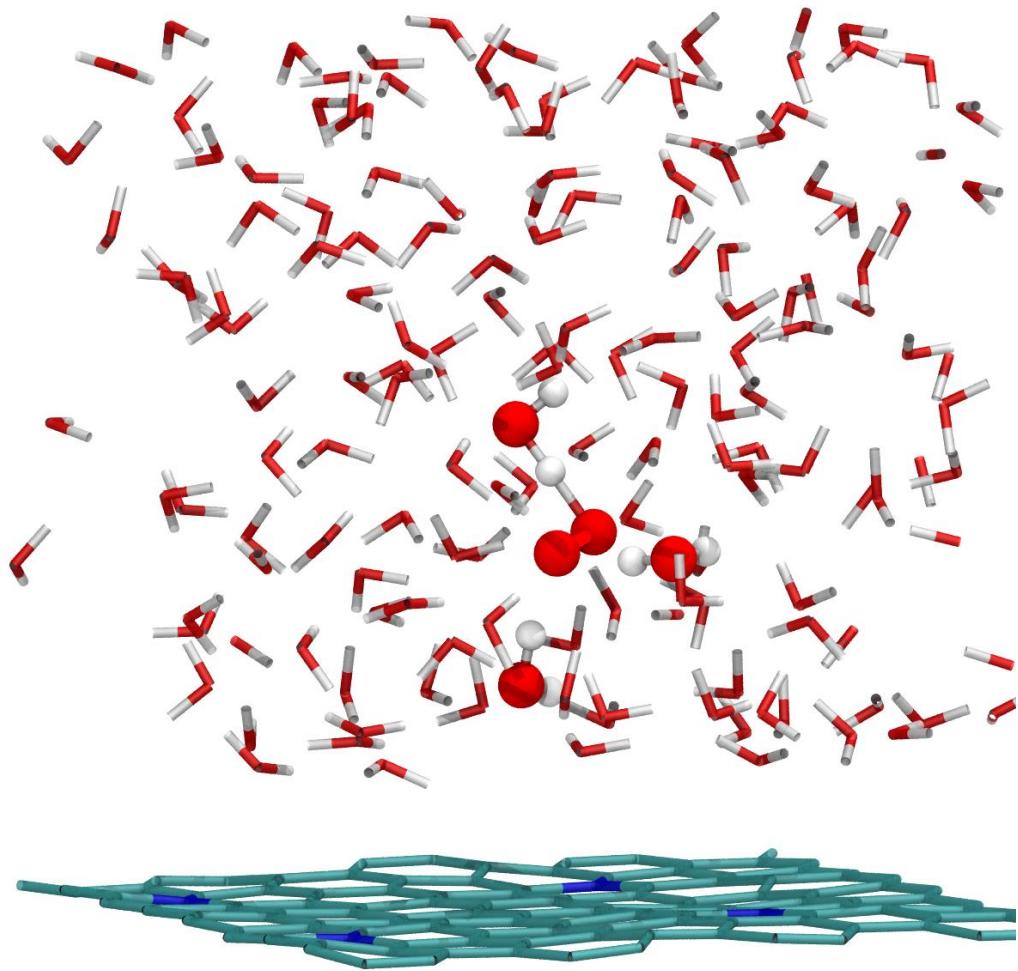
# Oxygen Reduction Reaction

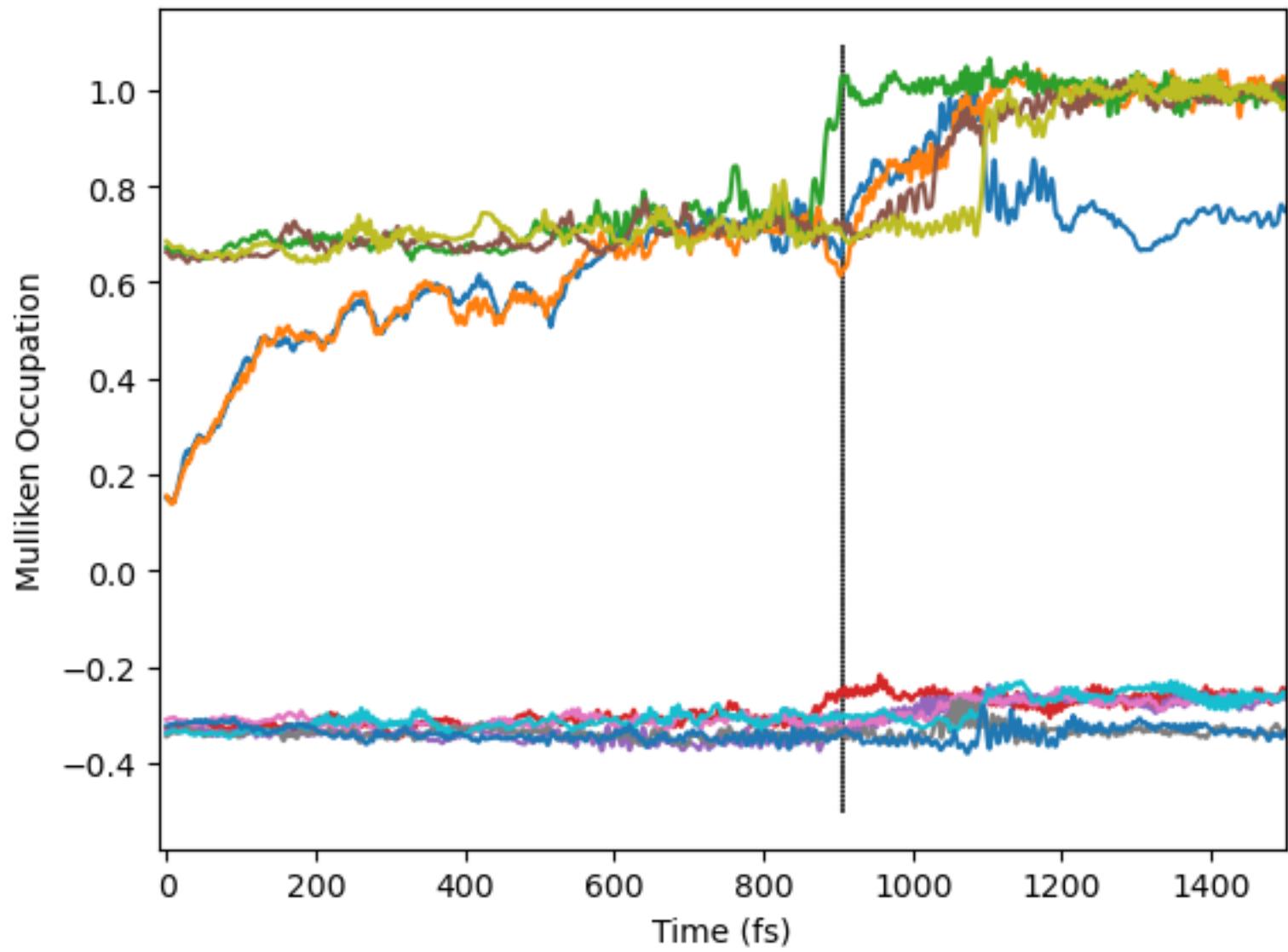
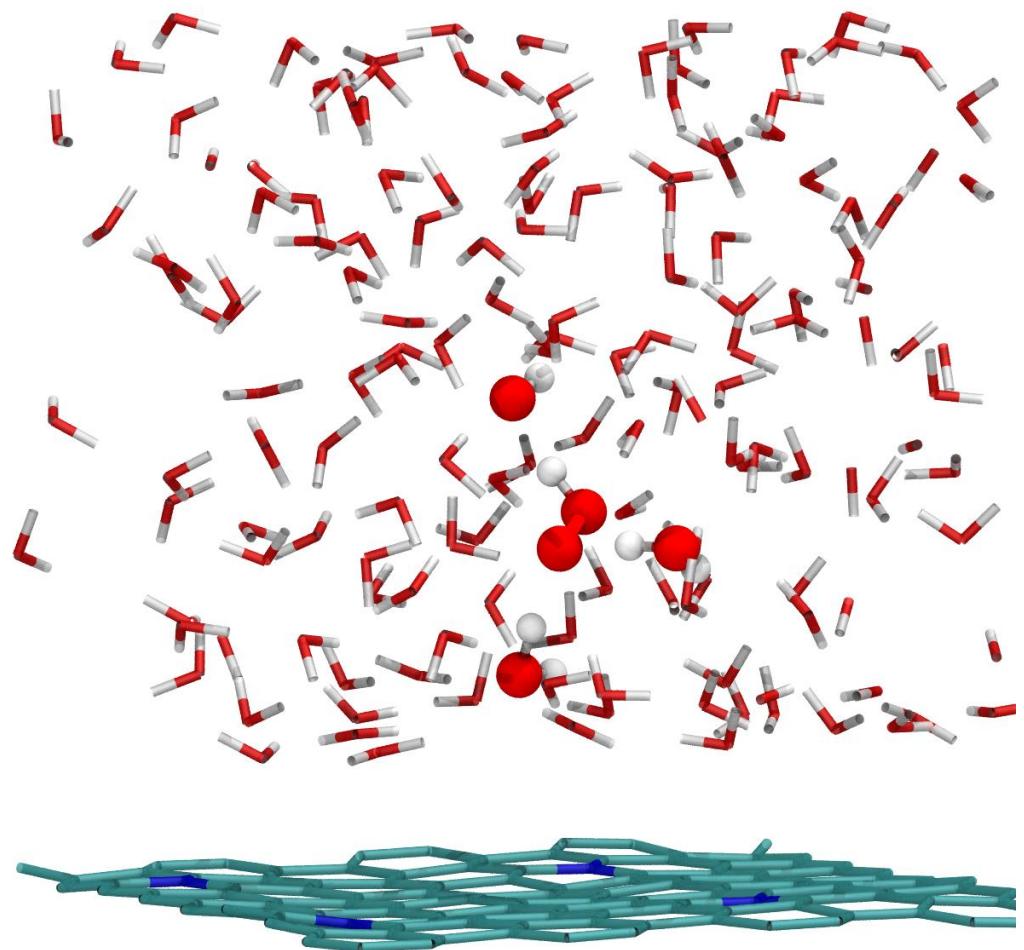


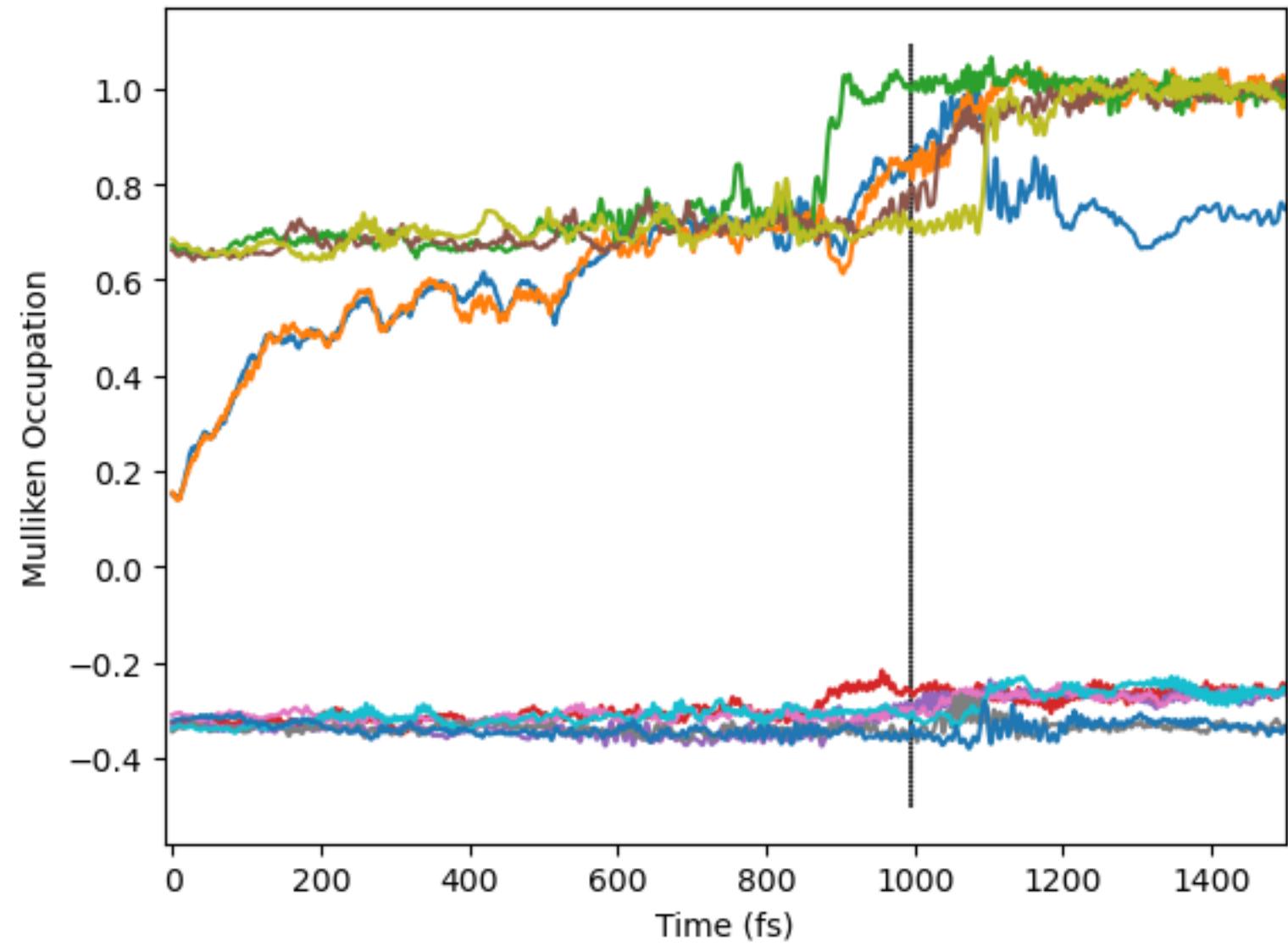
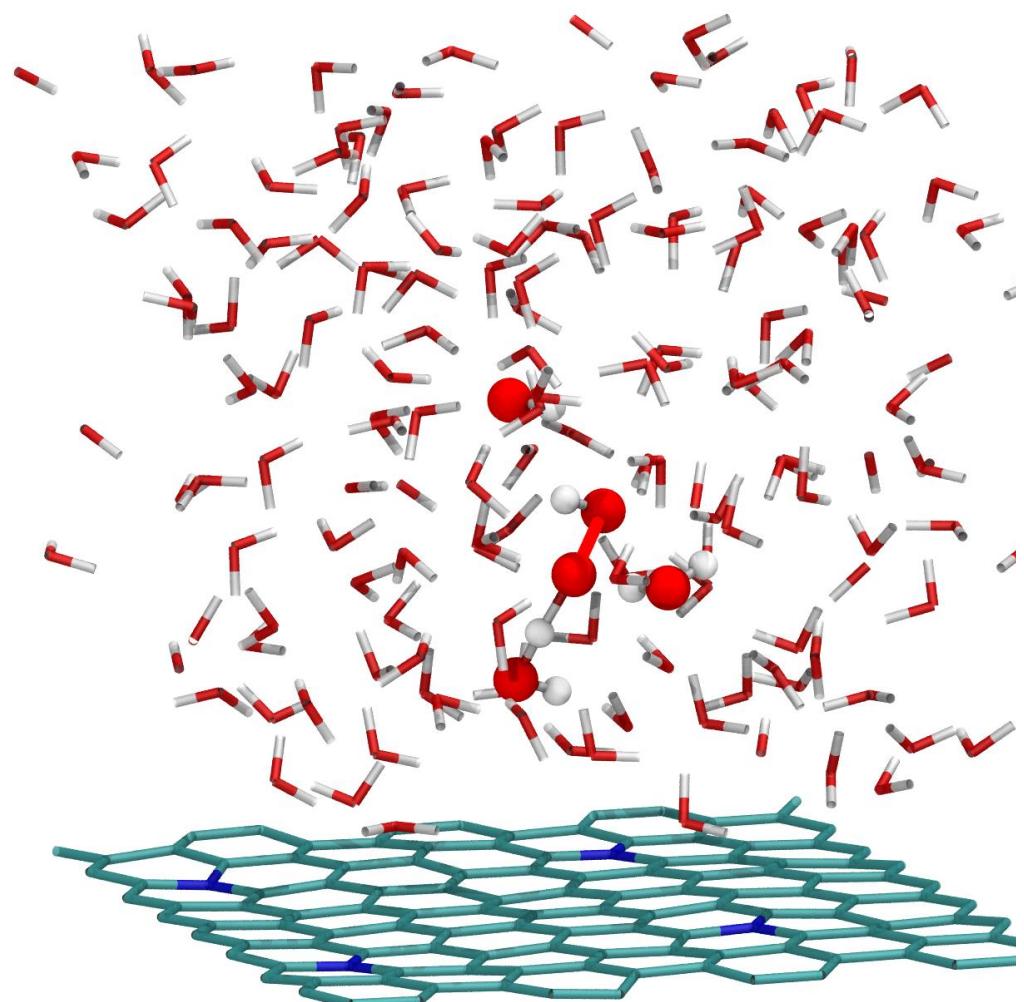
Fundamental cathode reaction in fuel cells/electrochemistry

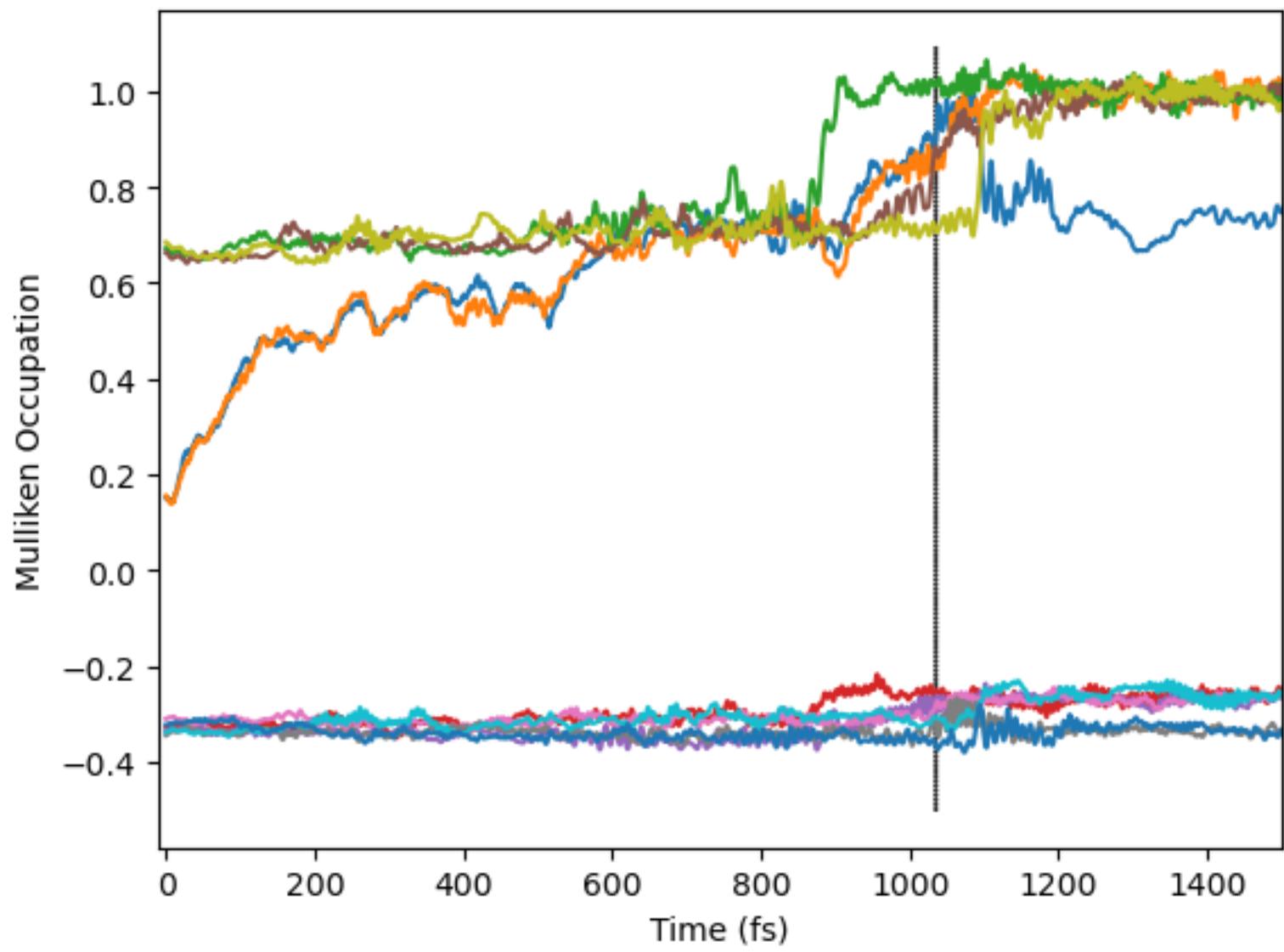
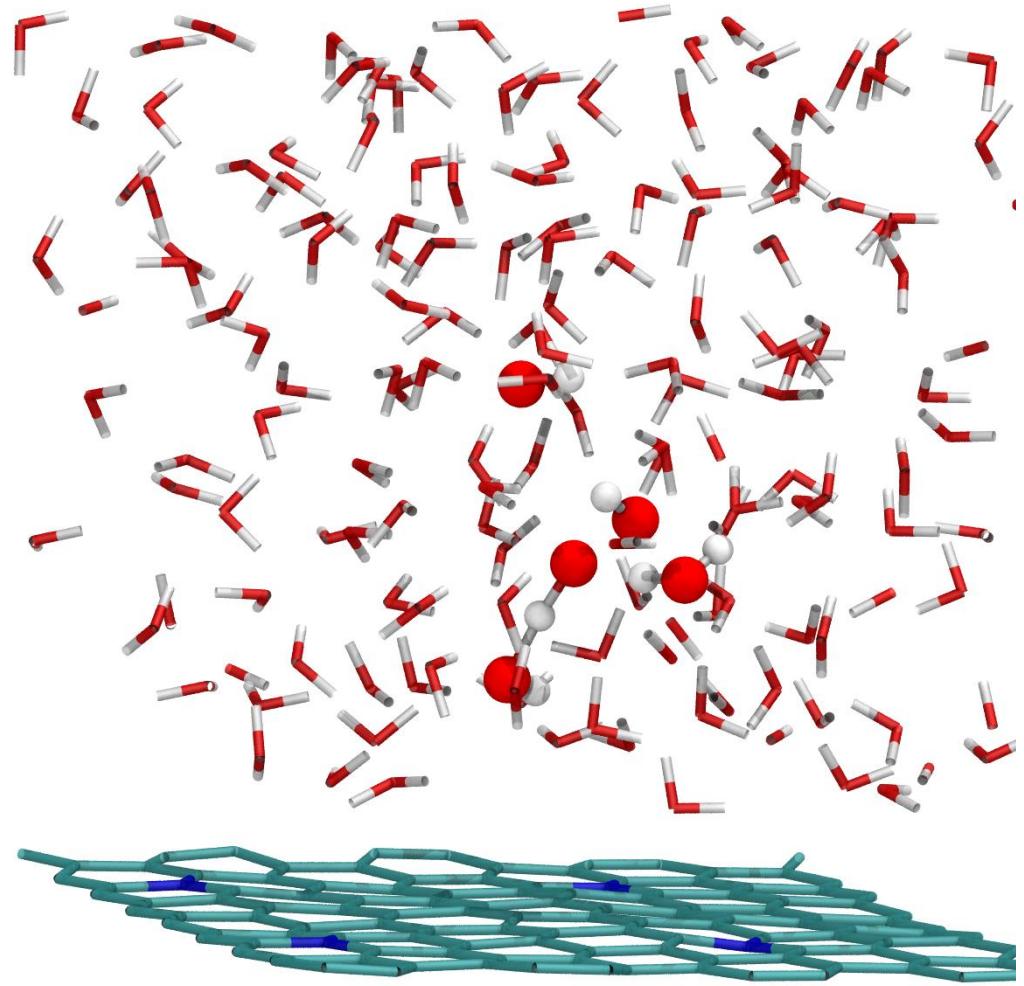
Rae C. Grove et al. Unpublished

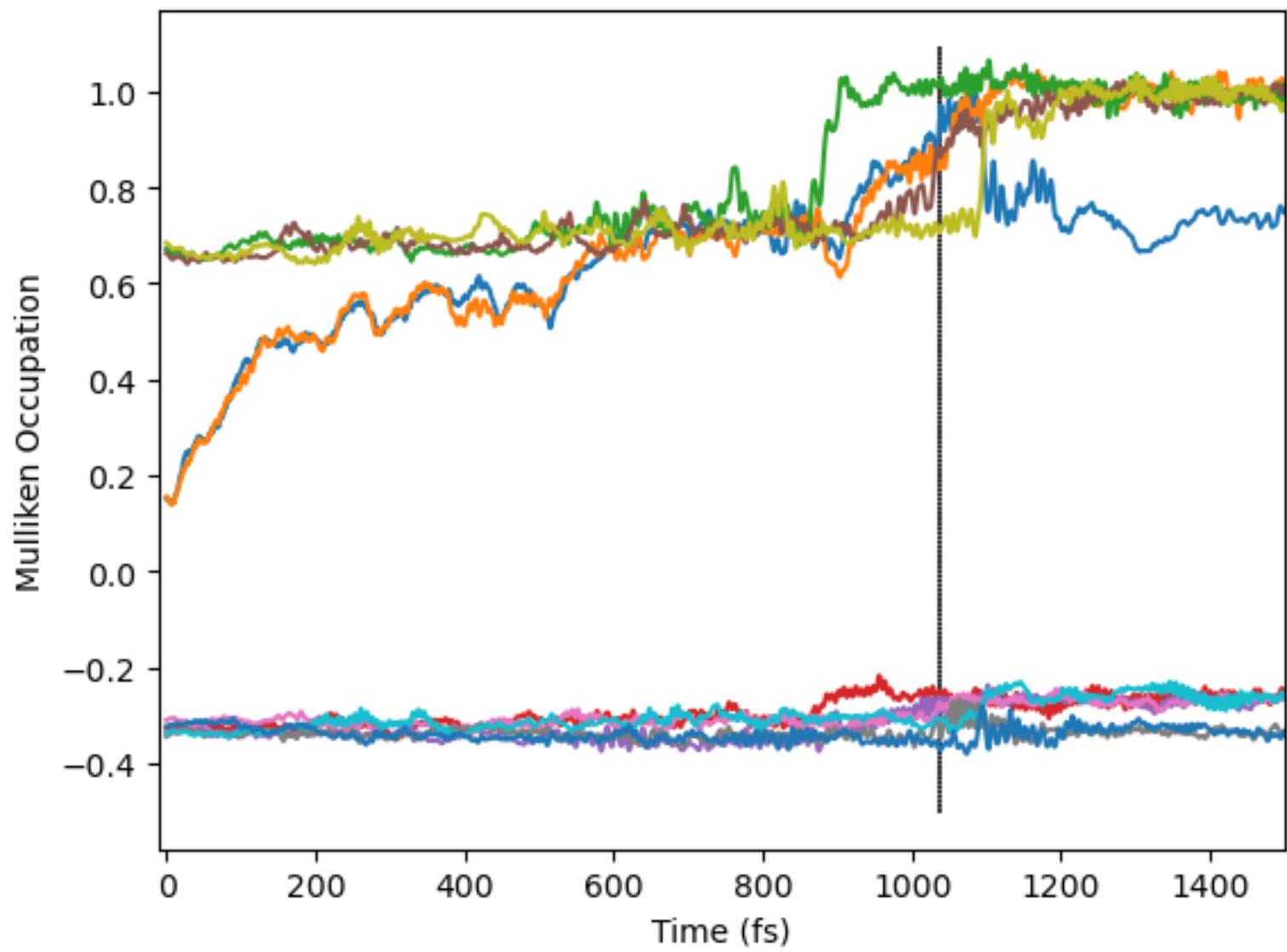
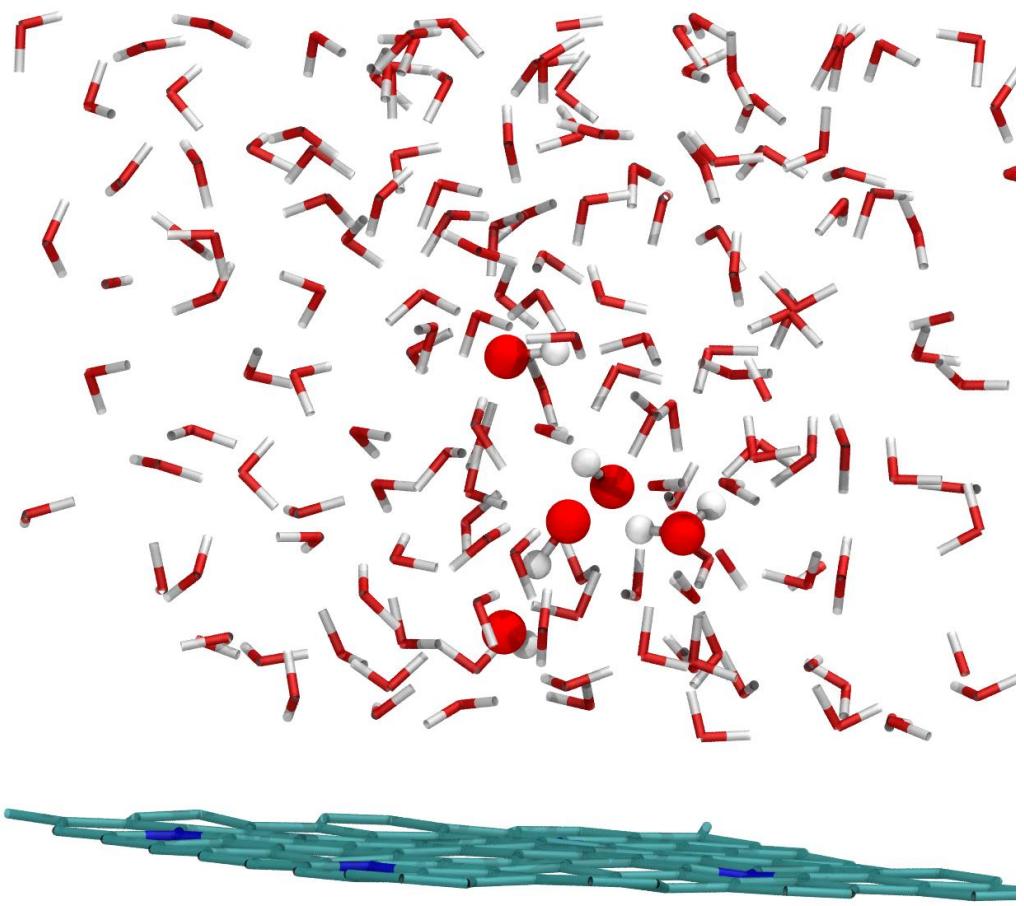


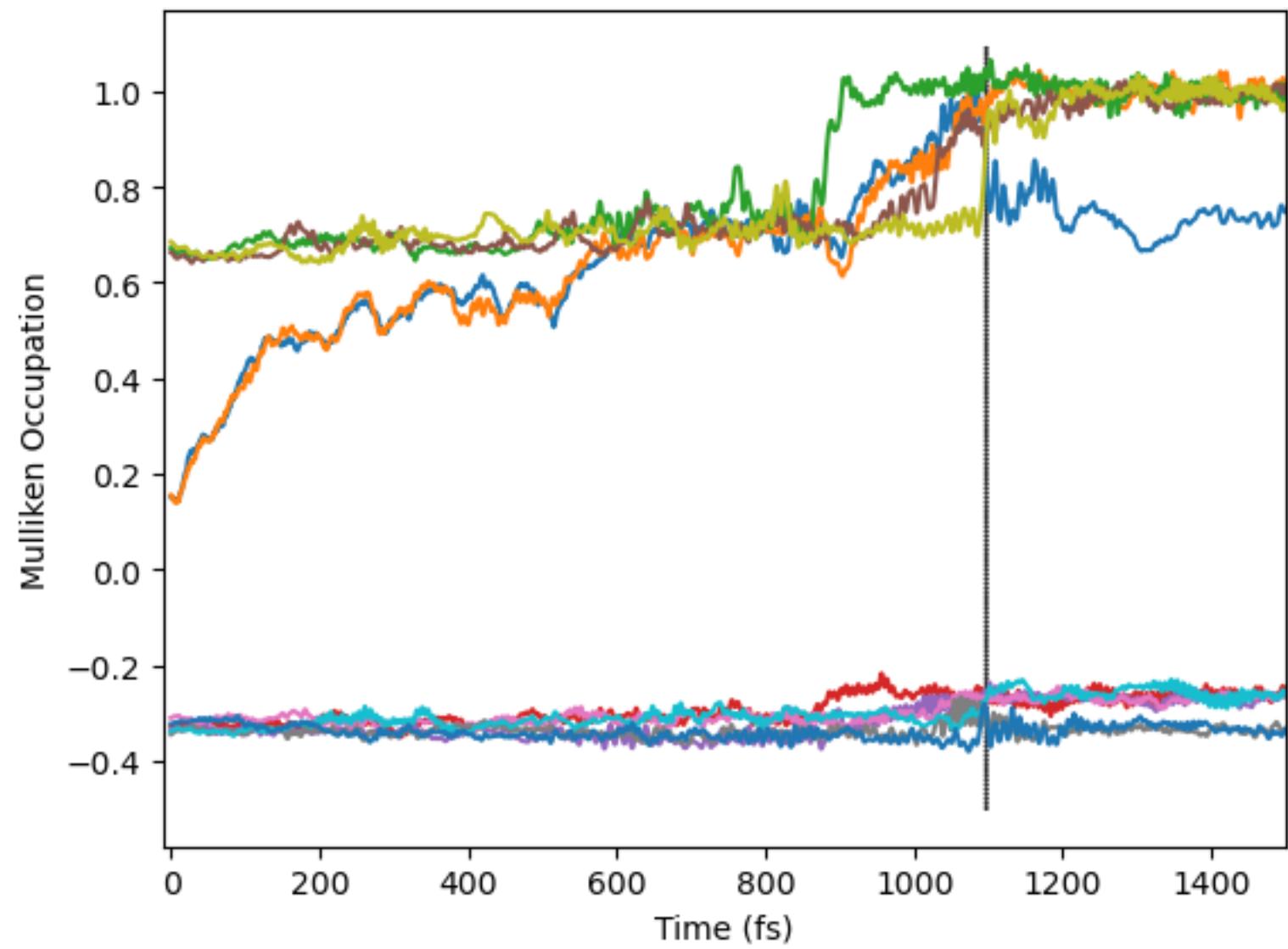
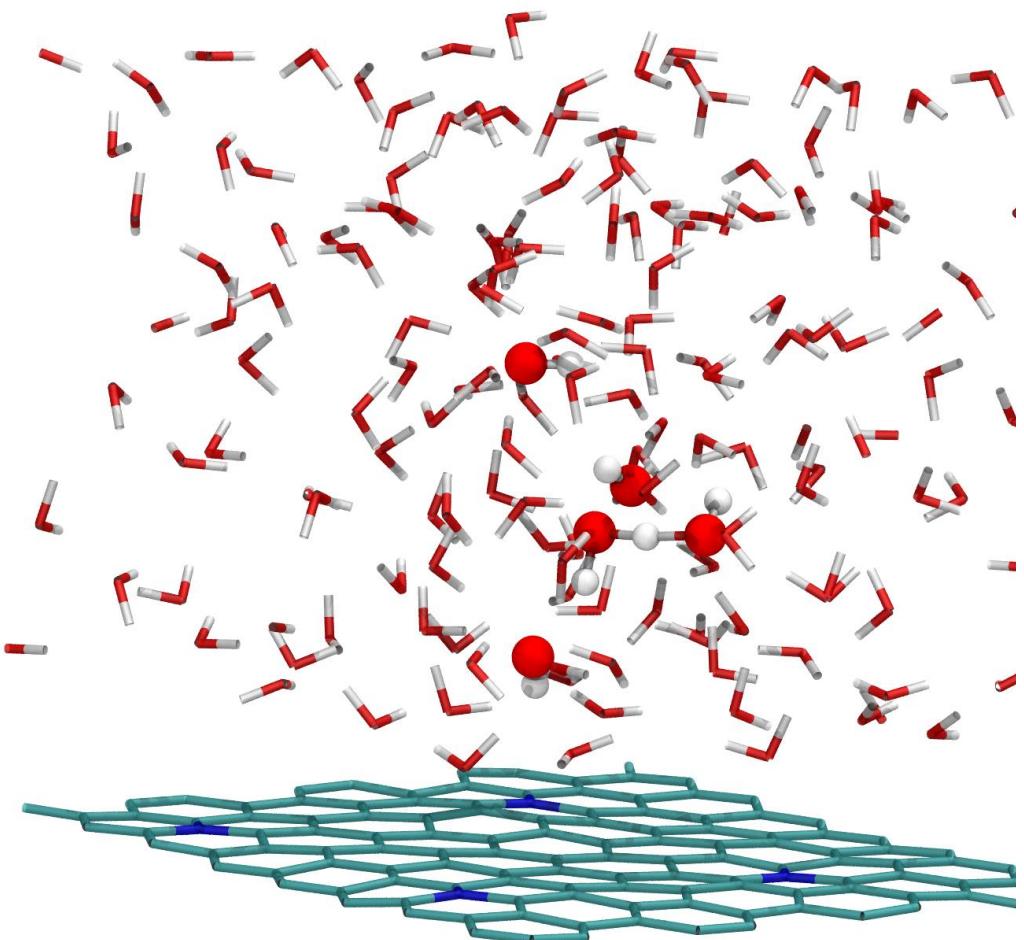


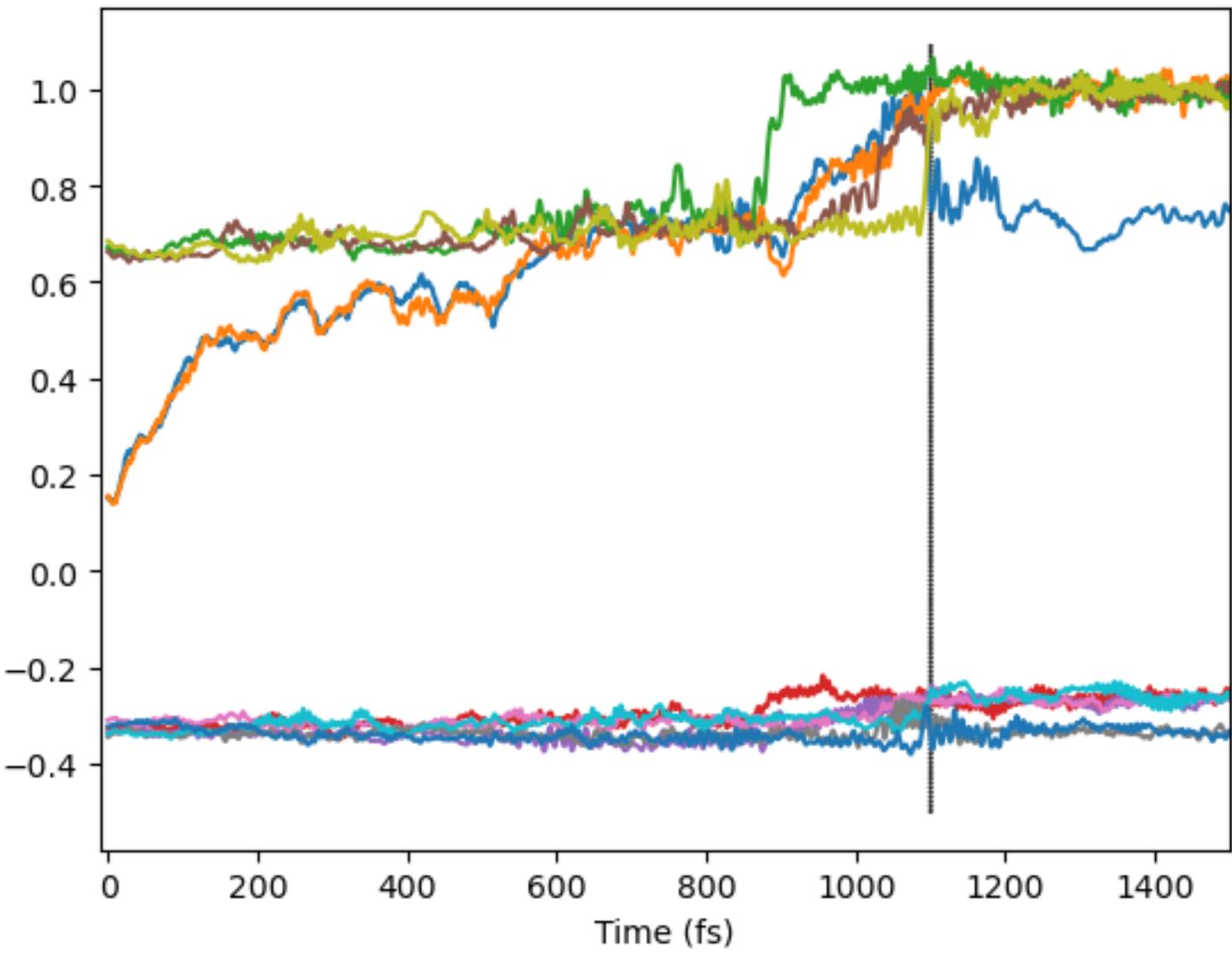
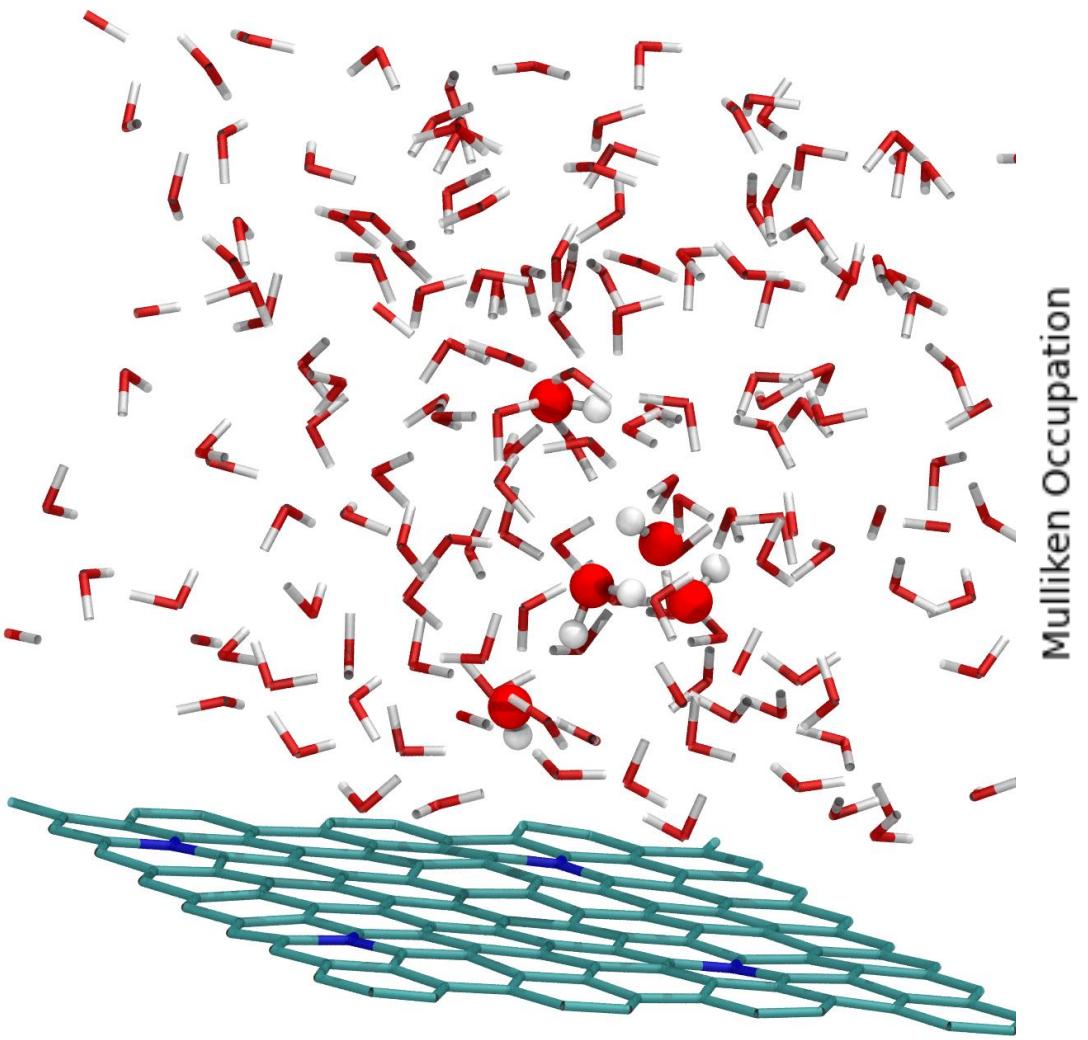


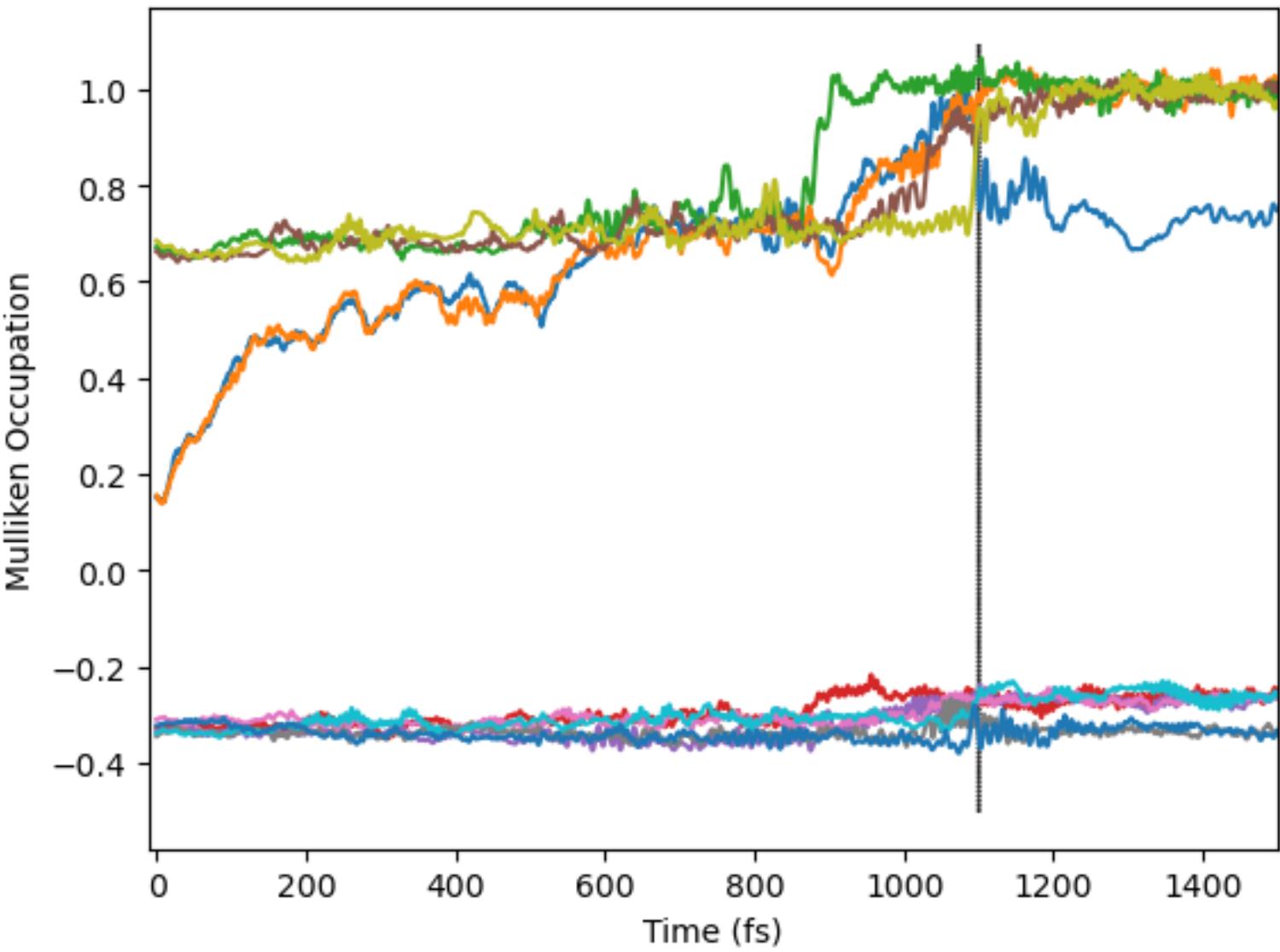
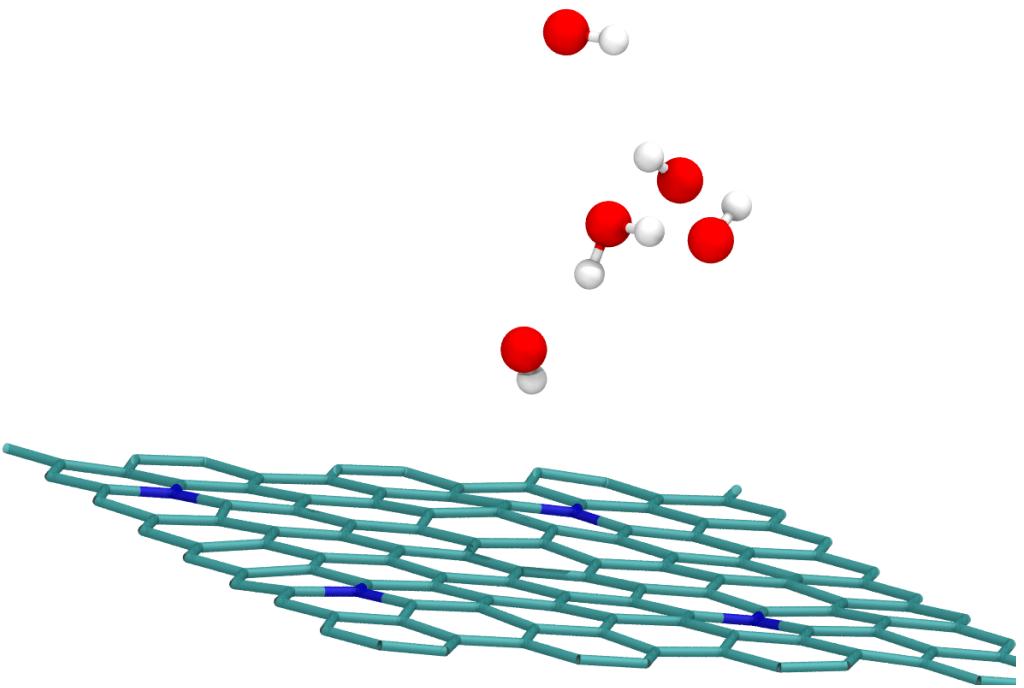






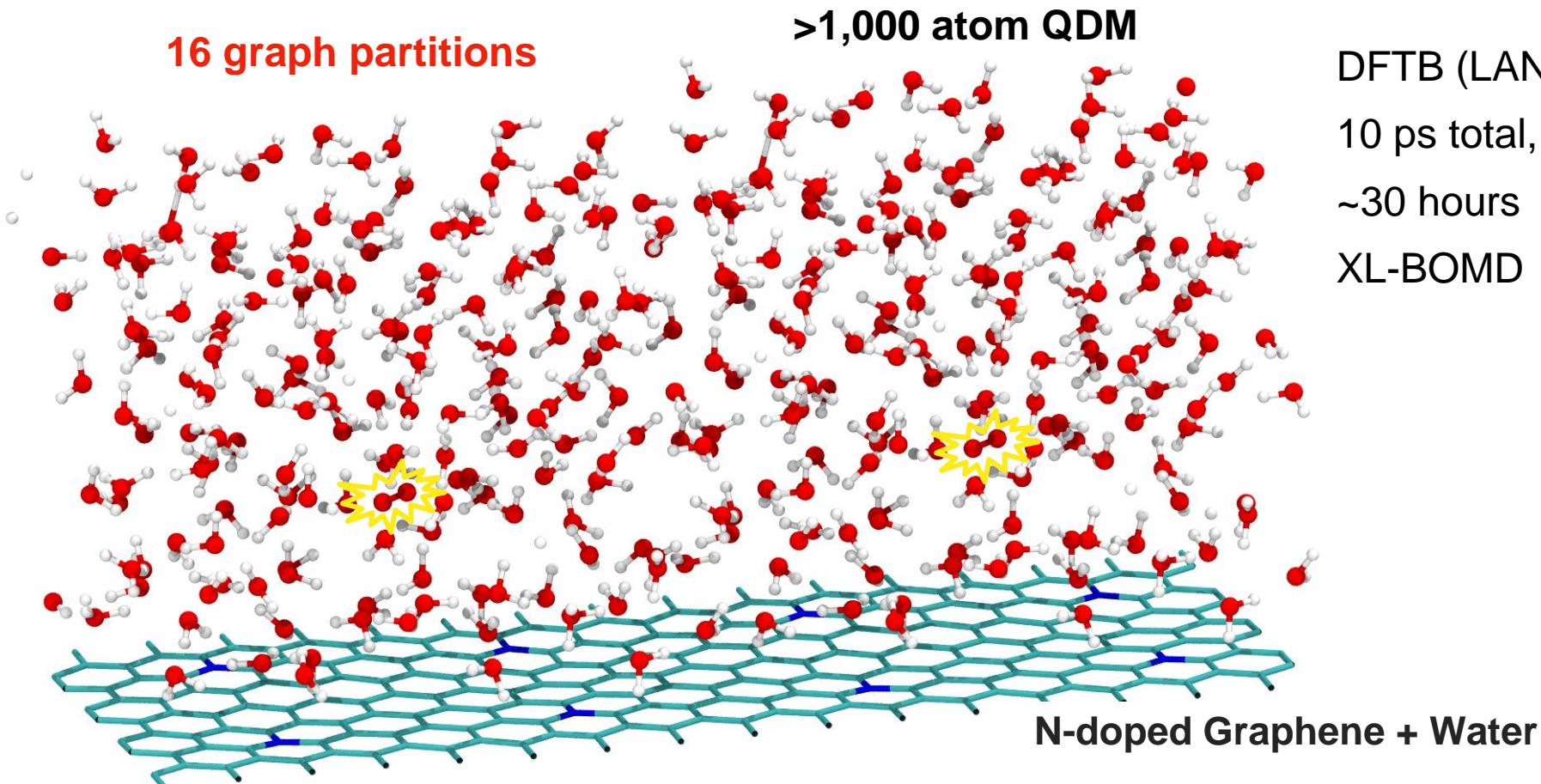






# Graph-Based QMD: Oxygen Reduction Reaction

Non-locality is properly described in graph-based QMD



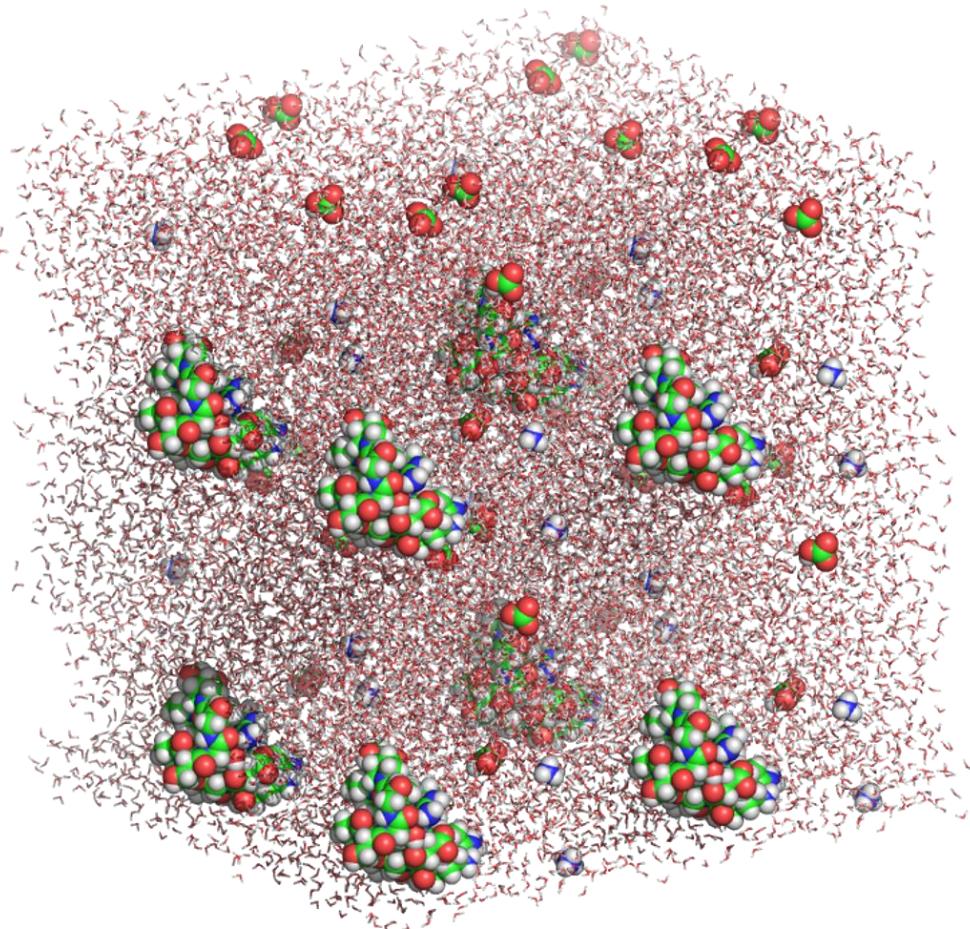
DFTB (LANL 31 parameters)

10 ps total, 0.1 fs timesteps

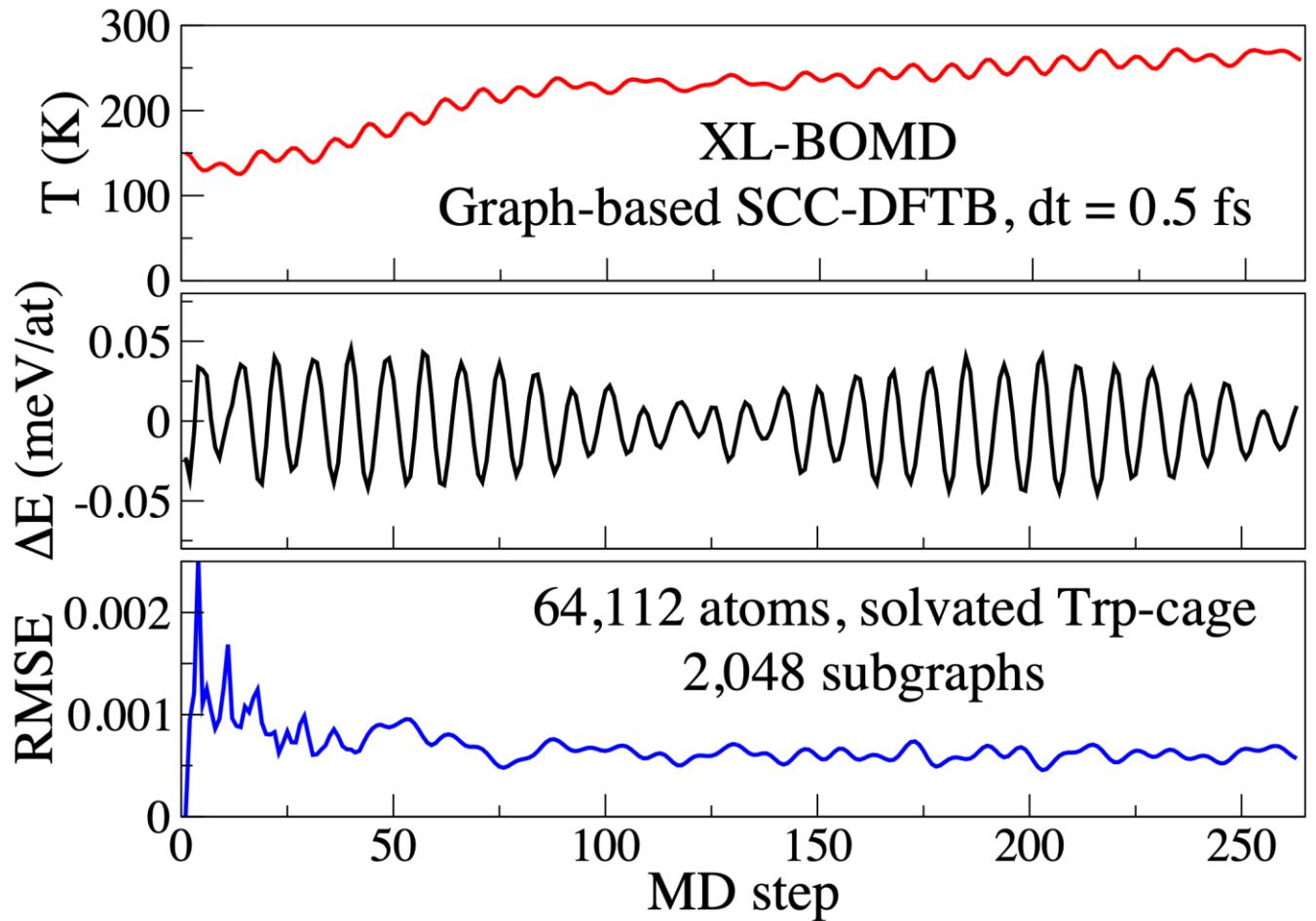
~30 hours

XL-BOMD

64K atoms Trp-cage  
+ ammonium bicarbonate solution  
Partitioned in 2,048 subgraphs  
running on 32 CPU nodes



## Distributed graph-based shadow QMD for reactive & charge sensitive systems (SCC-DFTB, $dt = 0.5$ fs)



Negre, Wall, Niklasson, J. Chem. Phys. 158, 074108 (2023), "Graph-based Quantum-response Theory and Shadow Born-Oppenheimer Molecular Dynamics"

# Summary

## ❖ ML-based interatomic potentials:

- + Fast
- + Accurate (in the domain of training data chemical space)
- Ignore (usually) electronic structure (charge, multiplicity, non-local effects)
- Require a lot of training data

## ❖ SEQM methods:

- + Retain electronic structure formalism (charge, multiplicity, non-local effects)
- ± Faster than *ab initio* but slower than ML
- Compromised accuracy

## ❖ ML+SEQM:

- + Higher accuracy than just ML or SEQM
- + Require less training data than ML
- Training is more challenging than for pure ML (backpropagation through SCF loop)
  - Special data preparation techniques are needed, e.g. Active Learning

## ❖ Graph-based QMD

- + Improves scalability of quantum methods

**Thank You for Your Attention!**

# Acknowledgements

## LANL T-1

Sergei Tretiak  
Ben Nebgen  
Anders Niklasson  
Kipton Barros  
Nick Lubbers  
Richard Messerly  
Robert Stanton  
Rae A. C. Grove  
Nikita Fedik

## LANL CSS

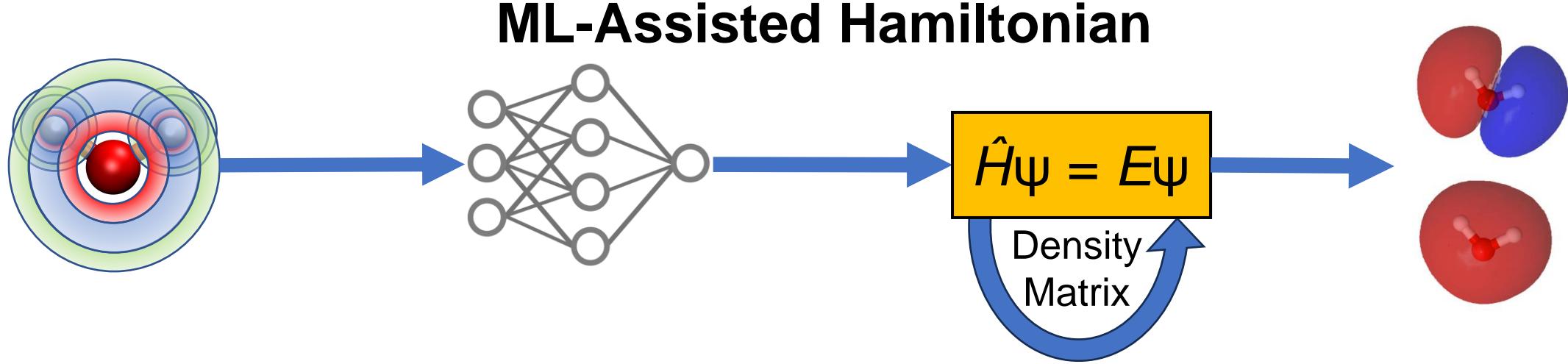
Nick Lubbers  
Ying Wai Li

## NVIDIA

Justin Smith  
Guoqing Zhou







## Linear Scaling via Graphs

