

Orbital-Free Density Functional Theory for Molecular Systems Using Deep Learning

Chang Liu

Microsoft Research Al for Science

Computational Methods for Molecular Science

molecular problems

biomolecule understanding

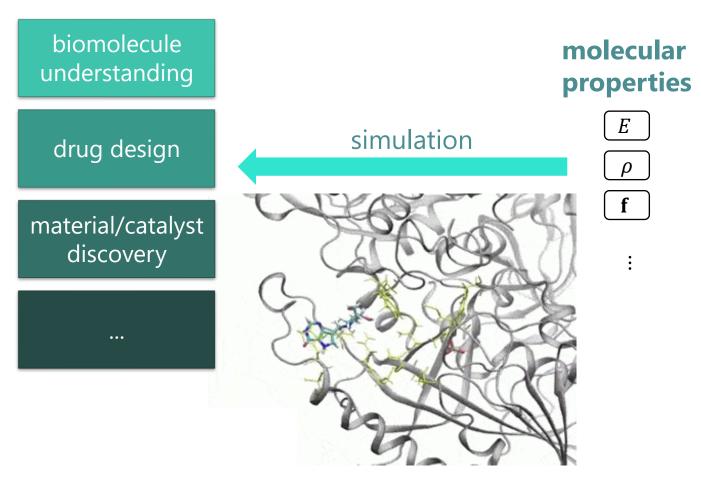
drug design

material/catalyst discovery

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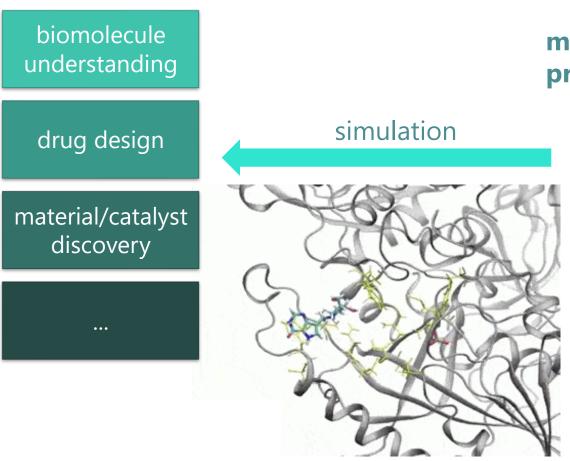
Computational Methods for Molecular Science

molecular problems



Computational Methods for Molecular Science

molecular problems



molecular properties

 \overline{E}

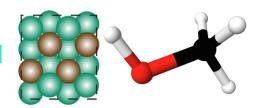
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f

Solve the electronic structure:

Schrödinger equation $\widehat{H}\psi = E\psi$

molecular structure



· To solve the *N*-electron Schrödinger equation $\widehat{H}\psi(\mathbf{r}_1,\cdots,\mathbf{r}_N)=E\psi(\mathbf{r}_1,\cdots,\mathbf{r}_N)$:

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Variational Principle:

$$\min_{\psi} \langle \psi | \widehat{H} | \psi \rangle$$
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One function on \mathbb{R}^{3N}

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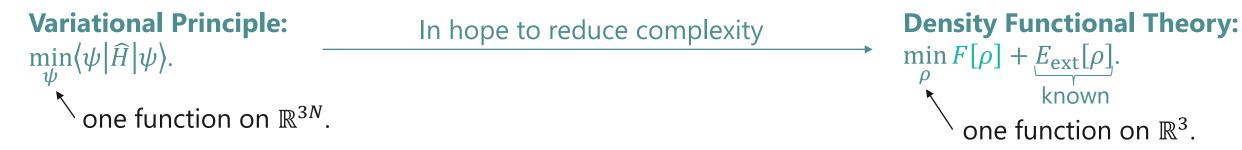
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\min_{\psi} \langle \psi | \widehat{H} | \psi \rangle.

One function on \mathbb{R}^{3N}
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Complexity:

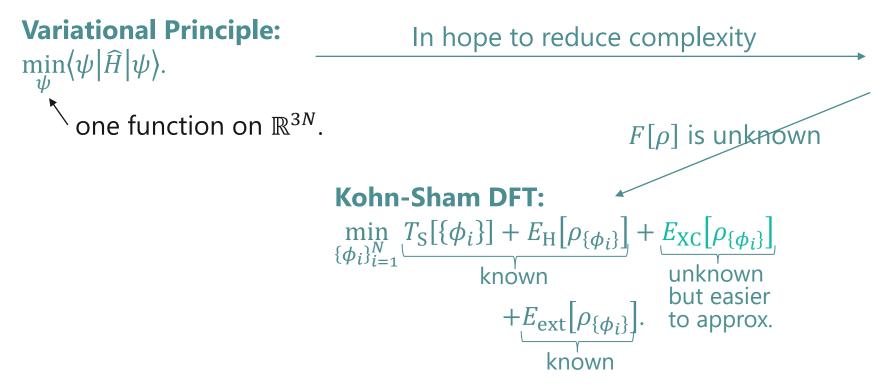
 $O(\exp(N))$

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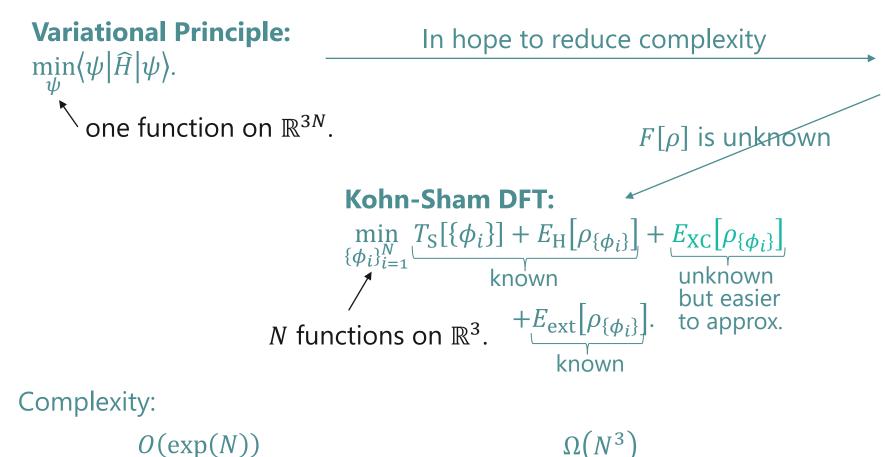
Density Functional Theory:

$$\min_{\rho} F[\rho] + \underbrace{E_{\text{ext}}[\rho]}_{\text{known}}.$$
one function on \mathbb{R}^3 .

Complexity:

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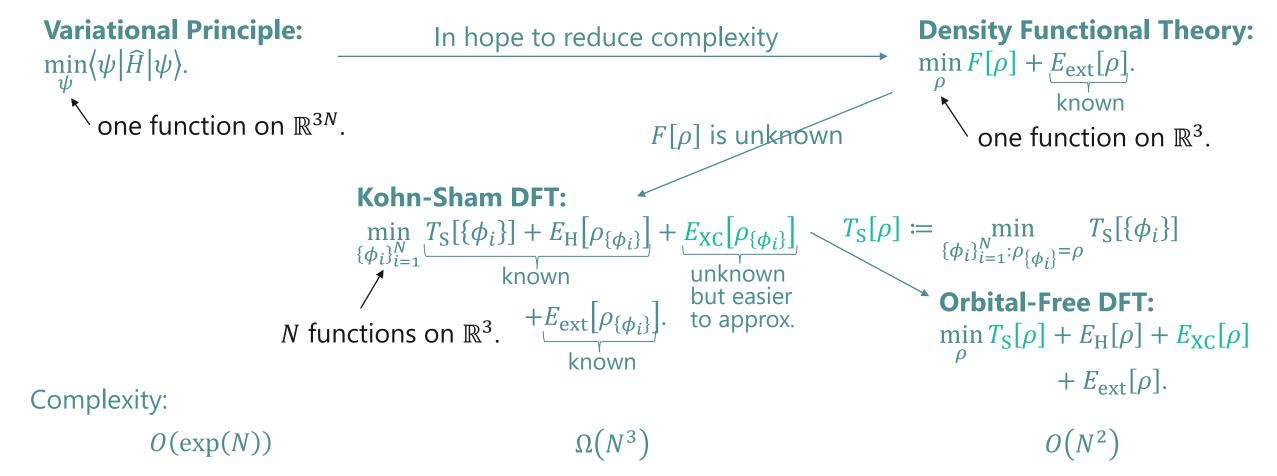
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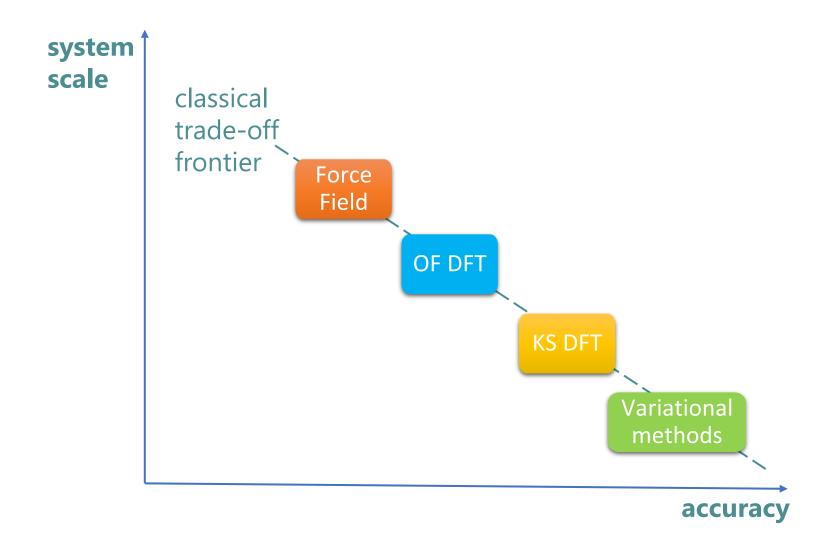


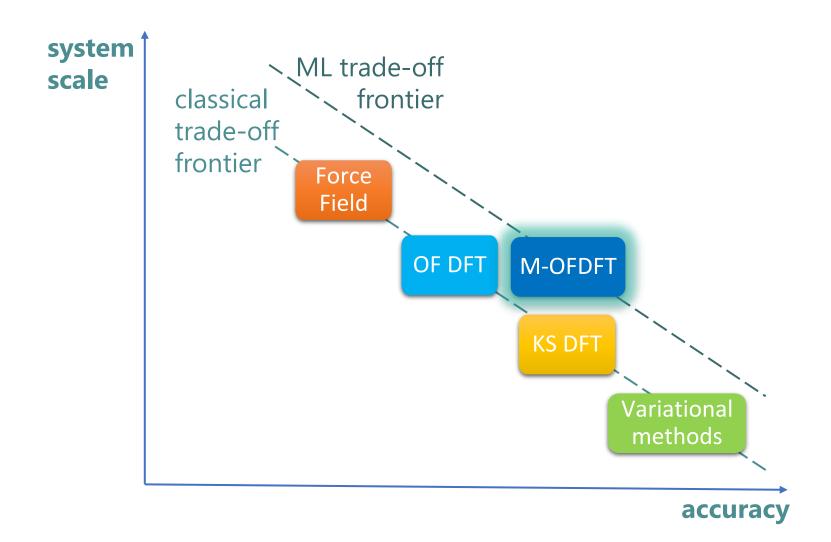
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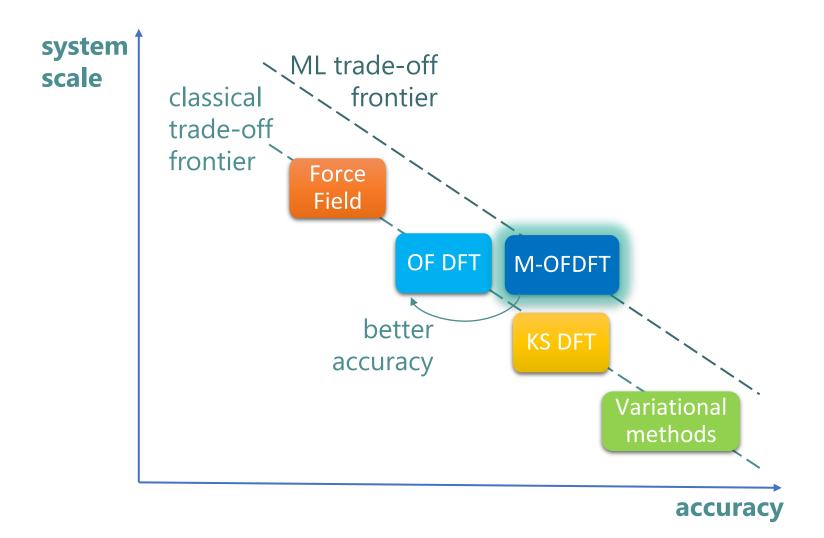
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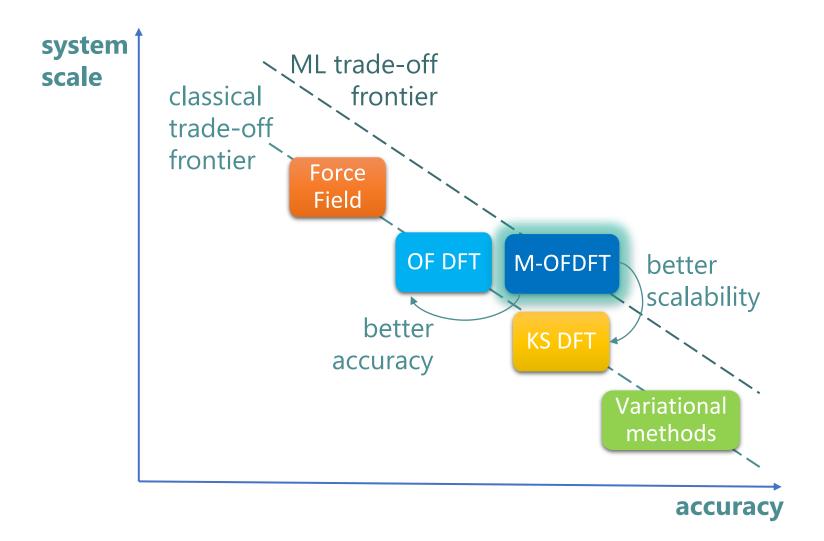
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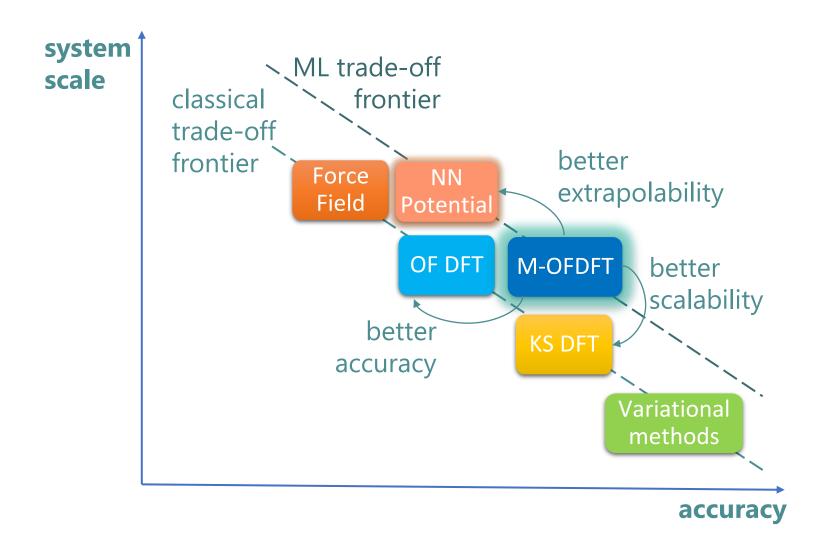










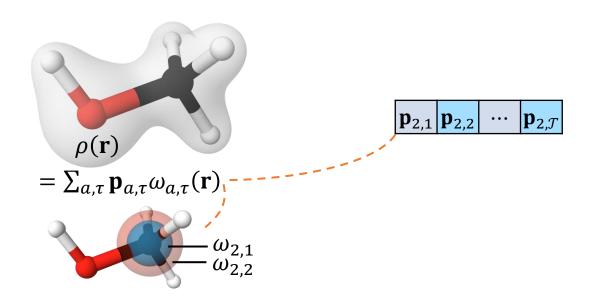


Approximating $T_S[\rho]$

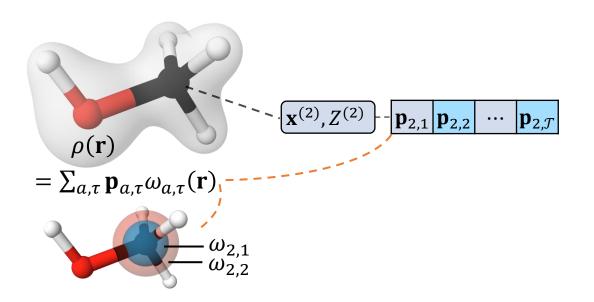
- Density representation
 - Grid-based density representation: nonlocal calculation is expensive on $\sim 10^4 N$ grid points.
 - · Limited to 10~20 atoms.



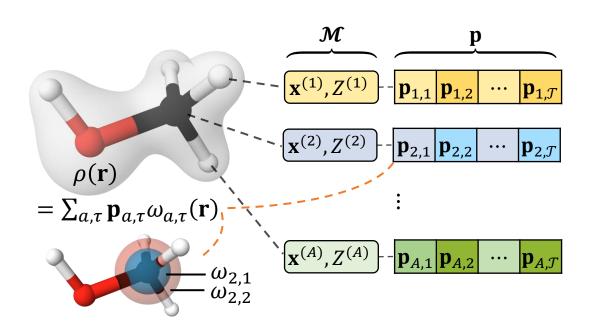
· Density representation using **atomic basis**: Expansion coefficients ${\bf p}$ on atomic basis: ρ represented as $({\bf p},\mathcal{M})$.



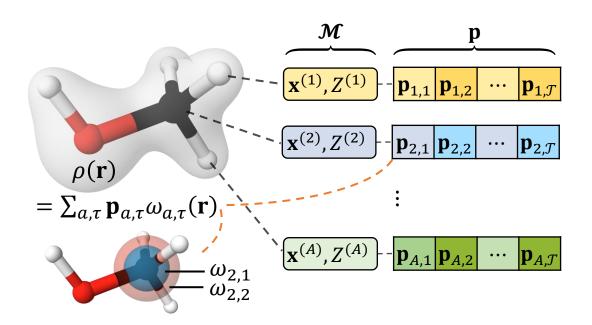
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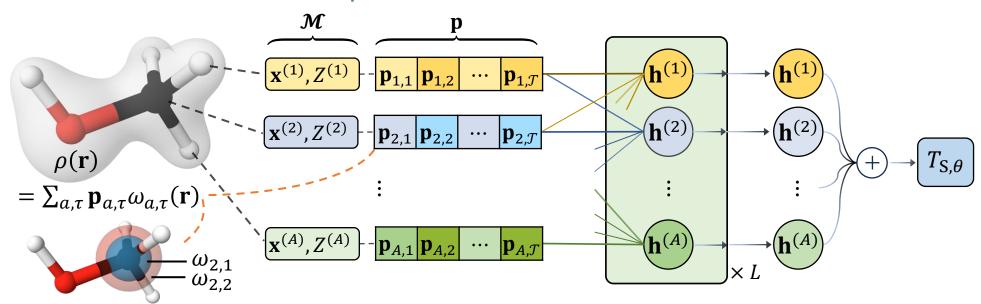
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 - → ~1000 times less dimensions than grid.

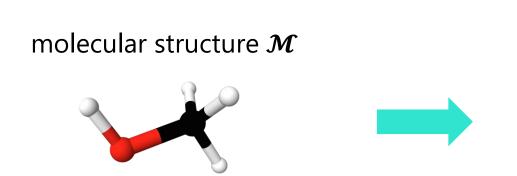


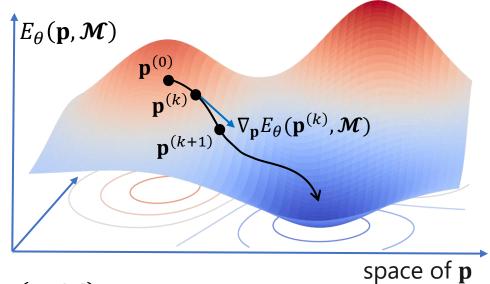
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 - → ~1000 times less dimensions than grid.
- · Explicit **nonlocal** model: Graphormer (Transformer-like model).



M-OFDFT Workflow

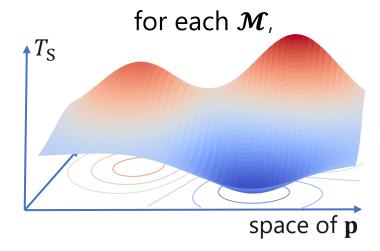
· Density optimization by gradient descent.



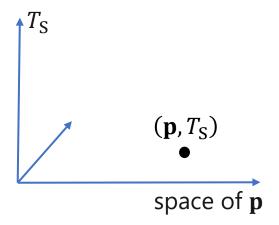


$$E_{\theta}(\mathbf{p}, \mathbf{\mathcal{M}}) := T_{S,\theta}(\mathbf{p}, \mathbf{\mathcal{M}}) + E_{H}(\mathbf{p}, \mathbf{\mathcal{M}}) + E_{XC}(\mathbf{p}, \mathbf{\mathcal{M}}) + E_{ext}(\mathbf{p}, \mathbf{\mathcal{M}})$$

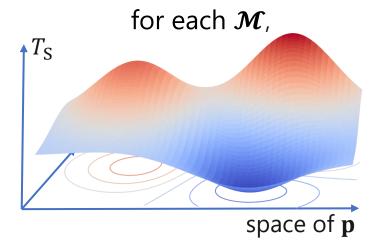
· Learning an objective: capture the whole landscape.



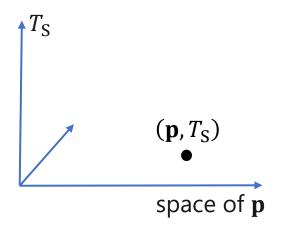
- · Learning an objective: capture the whole landscape.
 - · One datapoint is not enough.



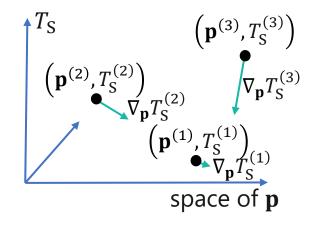
from KSDFT converged solution



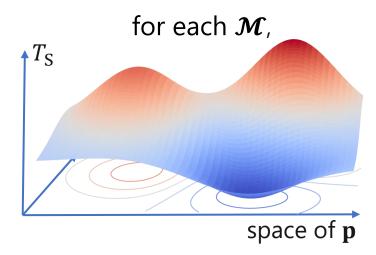
- · Learning an objective: capture the whole landscape.
 - · One datapoint is not enough.
 - · Generate multiple datapoints each with a gradient label.



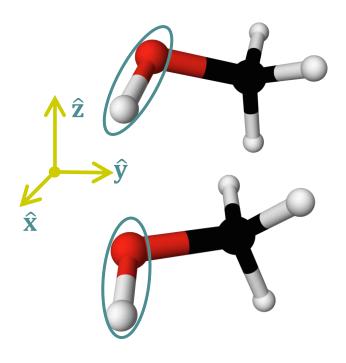
from KSDFT converged solution



from each of KSDFT iterations

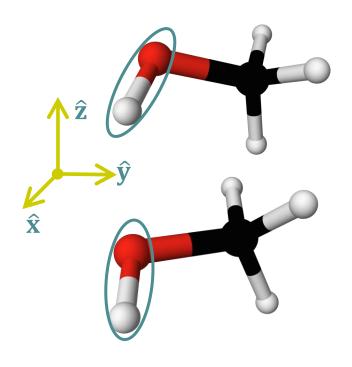


· Geometric invariance: T_S does not change with the rotation of molecule.

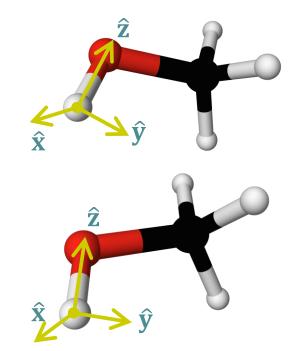


p rotates with molecule.

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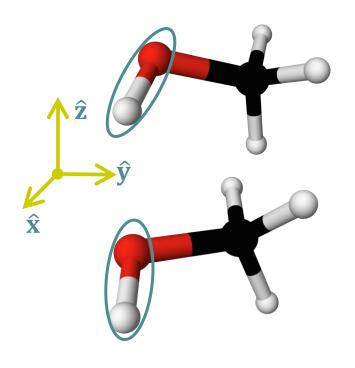


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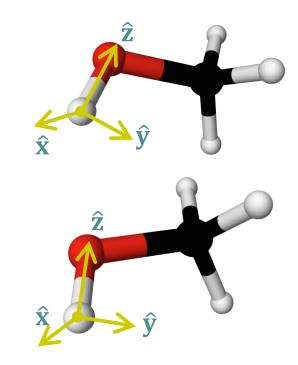


Local frame: **p** remains the same.

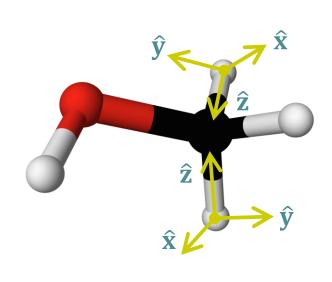
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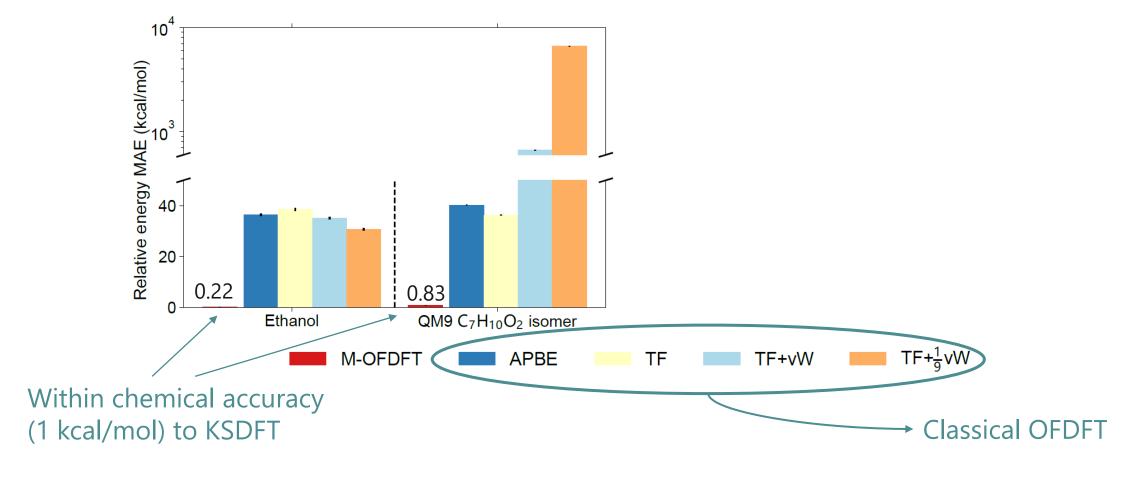


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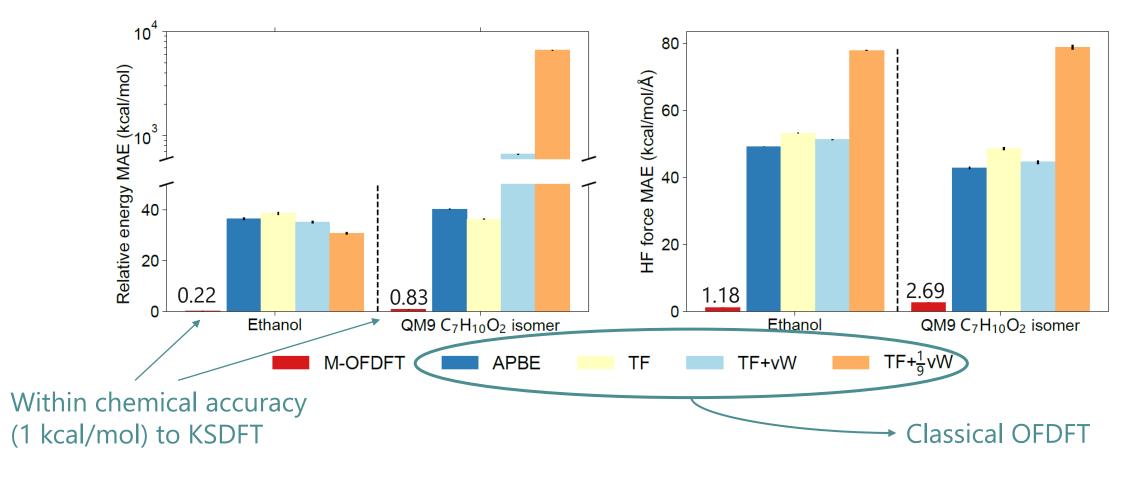


Additional benefit: similar local structures have similar **p**

• Energy and force:

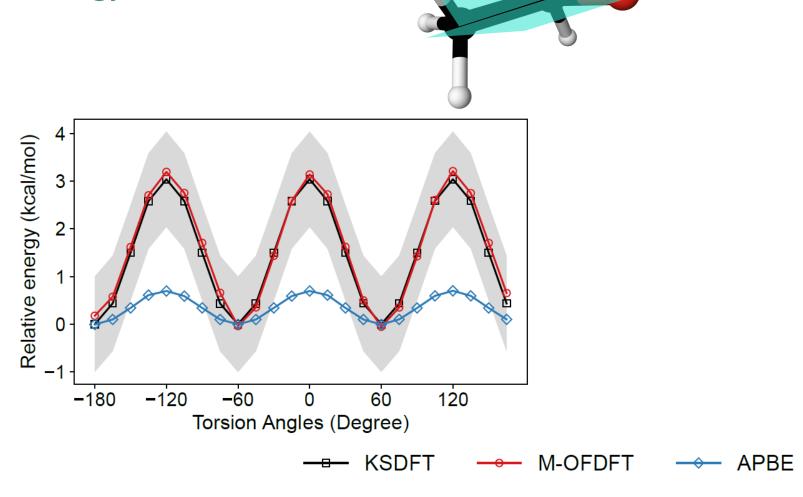


• Energy and force:

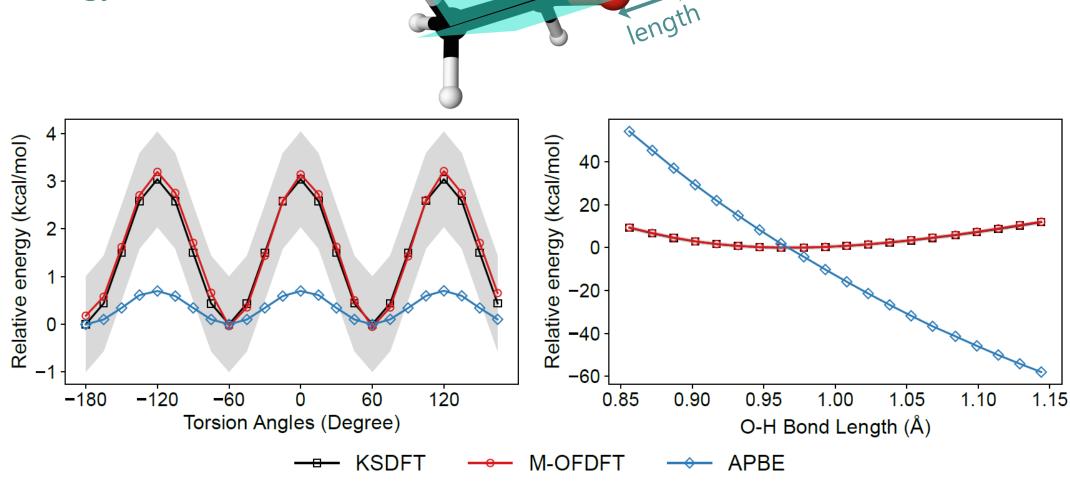


angle

• Energy surface:

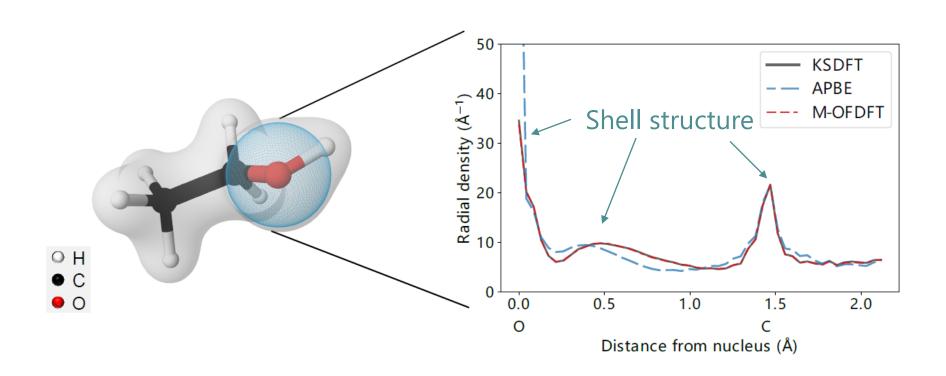


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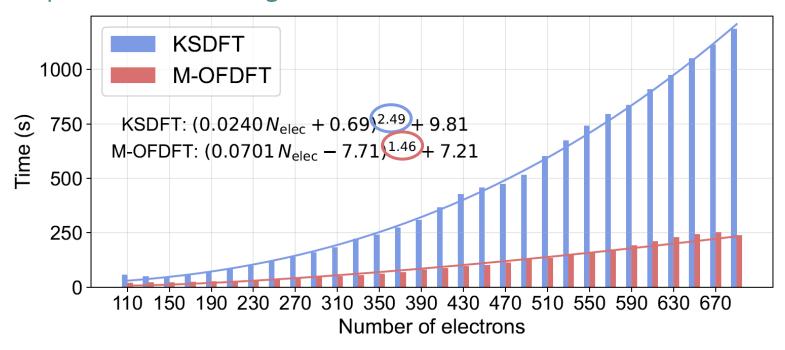
angle

· Electron density:



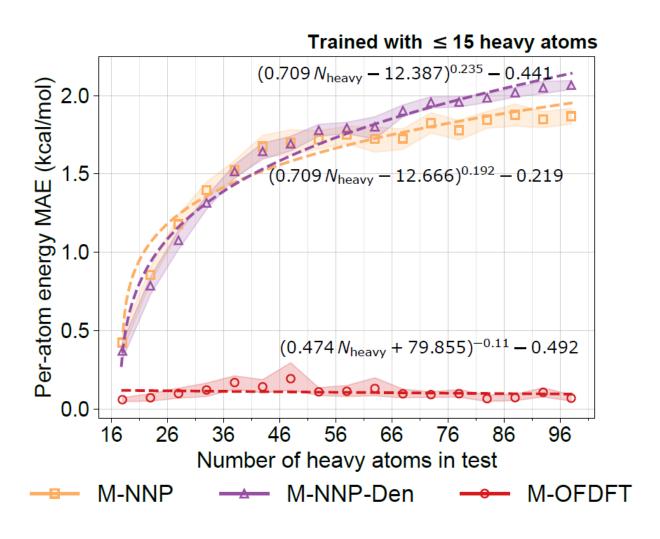
Better Scalability than KSDFT

· Lower empirical cost scaling:



Protein (PDB ID: 1PRB): 738 atoms, 2750 electrons
→ 27.4-fold speed up (0.45 h vs. 12.3 h).

Better Extrapolability than NN Potential



In the Future

- · Large-scale molecular dynamics simulation.
- · Quantum embedding for multi-scale calculation.
- Towards universality by:
 - · Large data and model.
 - · Mathematical properties.

Thank You!