

# HPC+AI: pushing molecular dynamics with ab initio accuracy to 100 million atoms

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New York Scientific Data Summit 2020,  
arXiv: 2005.00223

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# EFFICIENT LONG-RANGE CONVOLUTIONS FOR POINT CLOUDS

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A PREPRINT

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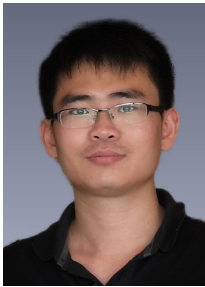
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October 13, 2020

## ABSTRACT

The efficient treatment of long-range interactions for point clouds is a challenging problem in many scientific machine learning applications. To extract global information, one usually needs a large window size, a large number of layers, and/or a large number of channels. This can often significantly increase the computational cost. In this work, we present a novel neural network layer that directly incorporates long-range information for a point cloud. This layer, ~~dubbed the long-range convolutional (LRC)-layer~~, leverages the convolutional theorem coupled with ~~the non-uniform Fourier transform~~. In a nutshell, the LRC-layer mollifies the point cloud to an adequately sized regular grid, computes its Fourier transform, multiplies the result by a set of trainable Fourier multipliers, computes the inverse Fourier transform, and finally interpolates the result back to the point cloud. The resulting global all-to-all convolution operation can be performed in nearly-linear time asymptotically with respect to the number of input points. The LRC-layer is a particularly powerful tool when combined with local convolution as together they offer efficient and seamless treatment of both short and long range interactions. We showcase this framework by introducing a neural network architecture that combines LRC-layers with short-range convolutional layers to accurately learn the energy and force associated with a  $N$ -body potential. We also exploit the induced two-level decomposition and propose an efficient strategy to train the combined architecture with a reduced number of samples.

# Our team



**Weile Jia**  
(Berkeley)



**Han Wang**  
(CAEP)



**Mohan Chen**  
(Peking)



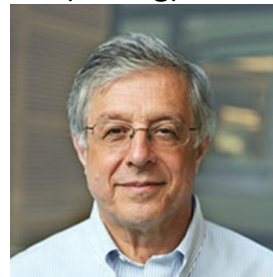
**Denghui Lu**  
(Peking)



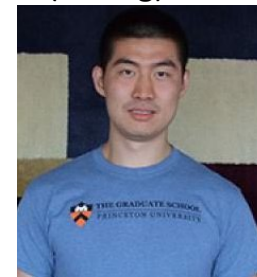
**Lin Lin**  
(Berkeley)



**Weinan E**  
(Princeton)



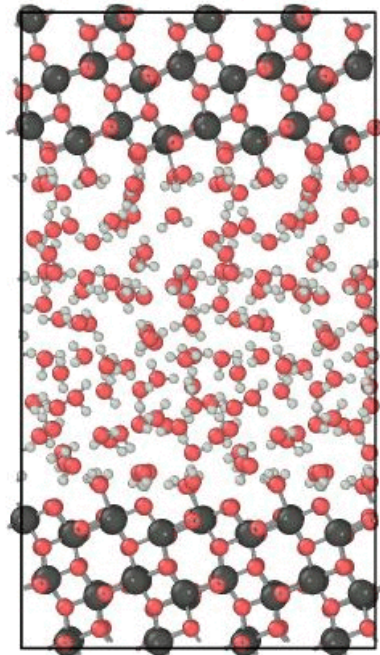
**Roberto Car**  
(Princeton)



**Linfeng Zhang**  
(Princeton)


# Molecular dynamics


$$E = E(R_1, R_2, \dots, R_M)$$
$$M_I \frac{d^2 R_I}{dt^2} = F_I = -\nabla_{R_I} E(R_1, R_2, \dots, R_M)$$



Example: water on TiO2 surface

# MD and COVID-19







Articles

About 16,600 results (0.05 sec)

Any time

Since 2020

Since 2019

Since 2016

Custom range...

Sort by relevance

Sort by date

include patents

include citations

Create alert

Promising inhibitors of main protease of novel corona virus to prevent the spread of **COVID-19** using docking and **molecular dynamics simulation**

[D Kumar](#), [K Kumari](#), [VK Vishvakarma...](#) - ... and **Dynamics**, 2020 - Taylor & Francis

Abstract Coronavirus disease-2019 (**COVID-19**) is a global health emergency and the matter of serious concern, which has been declared a pandemic by WHO. Till date, no potential medicine/drug is available to cure the infected persons from SARS-CoV-2. This deadly virus ...

☆  Cited by 4 All 11 versions Web of Science: 12 Import into BibTeX 

Virtual screening, **molecular dynamics** and structure–activity relationship studies to identify potent approved drugs for **Covid-19** treatment

[MM Rahman](#), [T Saha](#), [KJ Islam](#), [RH Suman...](#) - ... and **Dynamics**, 2020 - Taylor & Francis

Computer-aided drug screening by **molecular** docking, **molecular dynamics** (MD) and structural–activity relationship (SAR) can offer an efficient approach to identify promising drug repurposing candidates for **COVID-19** treatment. In this study, computational screening ...

☆  Cited by 3 All 8 versions Import into BibTeX 

# Two main approaches

Calculate energy  $E$  and force  $F_I$ :

- Computing on the fly using quantum mechanics (e.g. Kohn-Sham density functional theory). Accurate but expensive: *ab initio* molecular dynamics (AIMD)

$$E = \langle \Psi_0 | H_e^{KS} | \Psi_0 \rangle$$

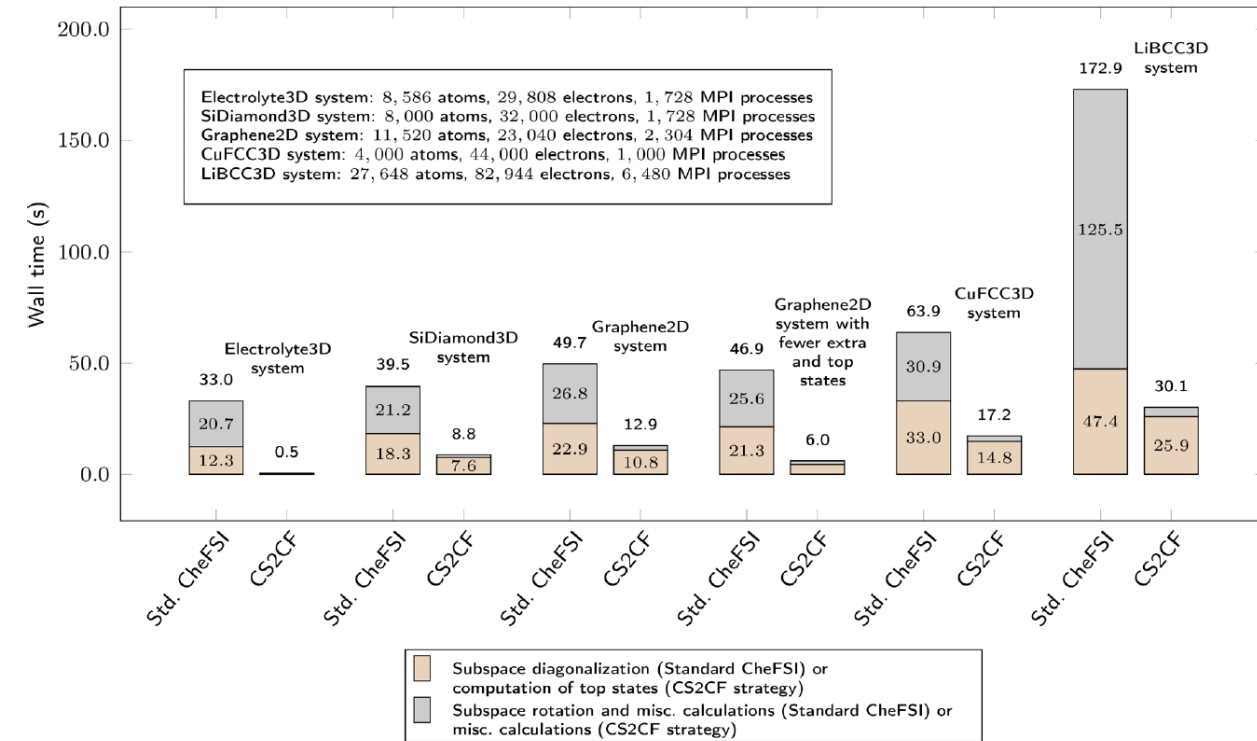
Routinely done for **hundreds of atoms, 1 picosecond ( $10^{-12}$  s) or less per day**

- Empirical potentials: efficient but maybe much less accurate, e.g. TIP3P for water

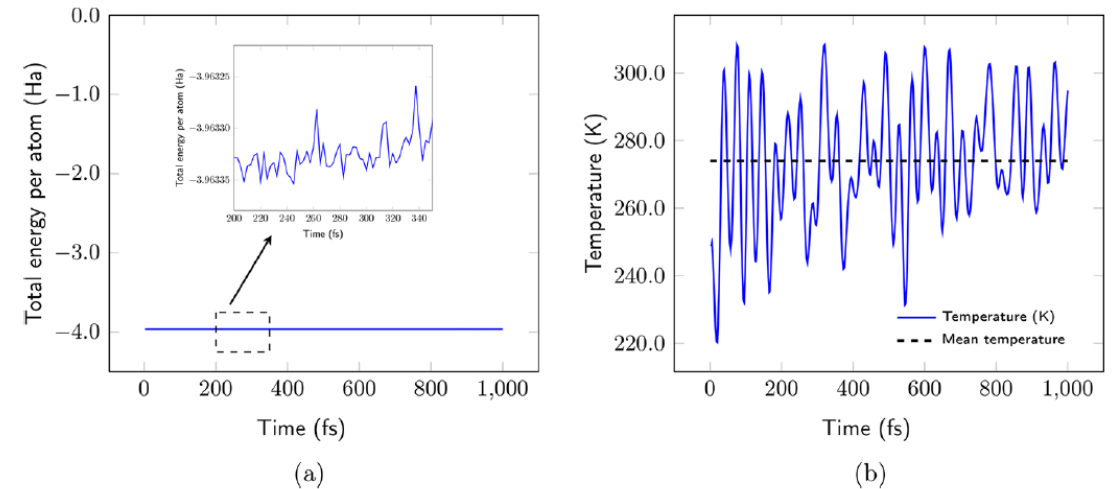
$$E = \sum_i \sum_j \frac{k_C q_i q_j}{r_{ij}} + \frac{A}{r_{00}^{12}} - \frac{B}{r_{00}^6}$$

Routinely done for **millions to billions of atoms, nanosecond ( $10^{-9}$  s) to microsecond ( $10^{-6}$  s) per day**

# Pushing the limit of *ab initio* molecular dynamics with reduced scaling algorithms and supercomputers



CS2CF: Two-level Chebyshev filter based complementary subspace method



AIMD simulation of 8000 Si atoms (32000 electrons) for 1 ps ( $10^{-12}$ s)

Total number of CPU cores: 34560.

28 hour wall clock time

Nearly 1 million CPU hours.

[L., Lu, Ying and E, J. Comput. Phys. 2012]

[Banerjee, L., Suryanarayana, Yang, Pask, J. Chem. Theory Comput. 2018]



# Pole expansion and selected inversion (PEXSI)

- At most  $O(N^2)$  scaling (insulators, semiconductor and metals). Standard method scales as  $O(N^3)$
- Integrated with a number of community electronic structure software packages
- Solve systems > 10000 atoms.
- Efficiently use 10,000-100,000 cores.
- BigDFT
- CP2K
- DFTB+
- DGDFT
- FHI-aims
- QuantumWise AtK
- SIESTA
- “Electronic structure infrastructure” (ELSI) <https://wordpress.elsi-interchange.org/>

<http://www.pexsi.org/>

PEXSI

latest

Search docs

CONTENTS:

- Introduction
- Download
- Installation
- Tutorial
- Further details
- Frequently asked questions
- Troubleshooting

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Indeed Prime's career coaches can help you level up your tech career. Join for free today!

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Docs » Welcome to PEXSI's documentation! [Edit on Bitbucket](#)

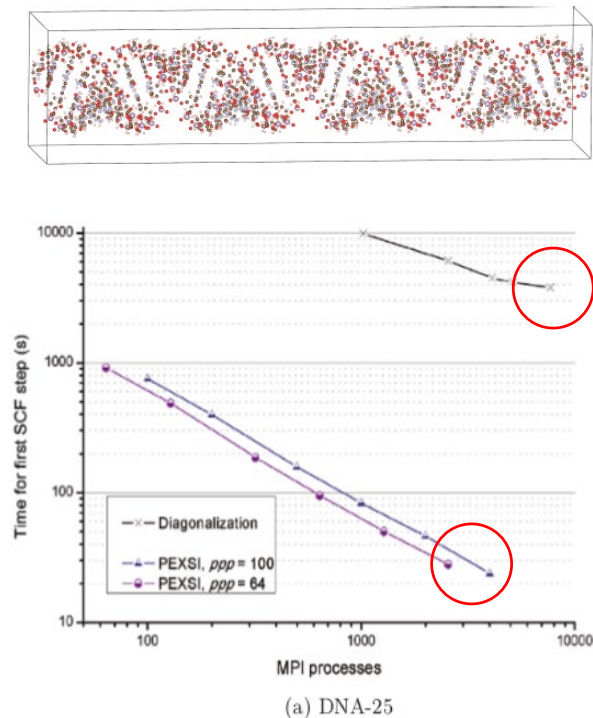
## Welcome to PEXSI's documentation!

### Contents:

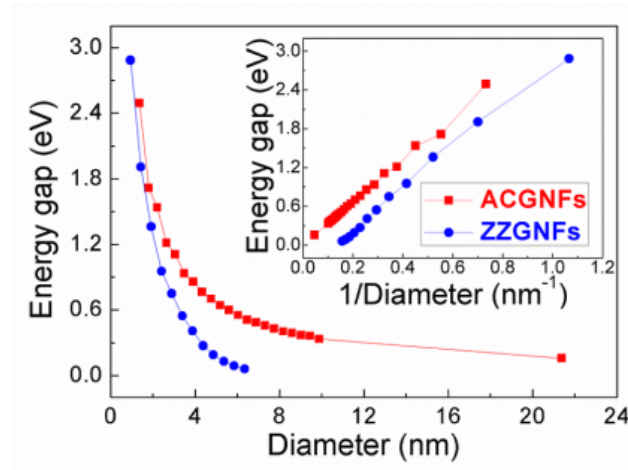
- Introduction
  - Overview
  - PEXSI used in external packages
  - License
  - Contributors
  - Citing PEXSI
  - Developer's documentation
  - PEXSI version history
- Download
- Installation
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  - Build PT-Scotch
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  - Build SuperLU\_DIST
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- Tutorial
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  - Parallel selected inversion for a real symmetric matrix
  - Parallel selected inversion for a complex symmetric matrix
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  - Parallel selected inversion for a complex unsymmetric matrix
  - Solving Kohn-Sham density functional theory: I
  - Solving Kohn-Sham density functional theory: II
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- Further details
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  - Data type
  - C/C++ interface
  - FORTRAN interface
- Frequently asked questions
  - General questions
  - Installation
  - Performance
- Troubleshooting



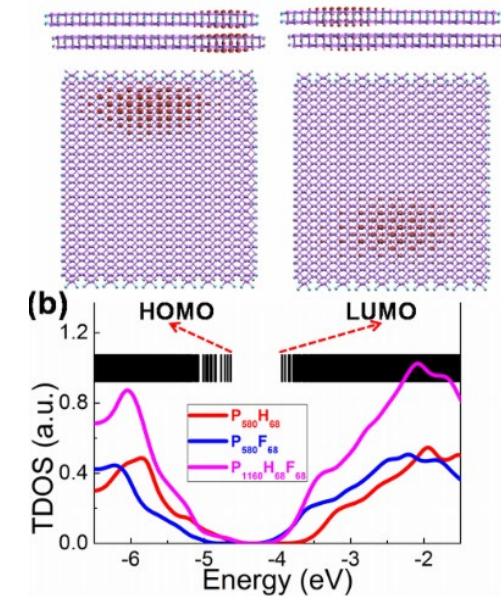
# Solving quantum mechanics with $\sim 10000$ atoms: Pole expansion and selected inversion (PEXSI)



Large scale DNA calculation  
(20000 atoms)



Electronic structure of large scale  
graphene nanoflake (10000 atoms)

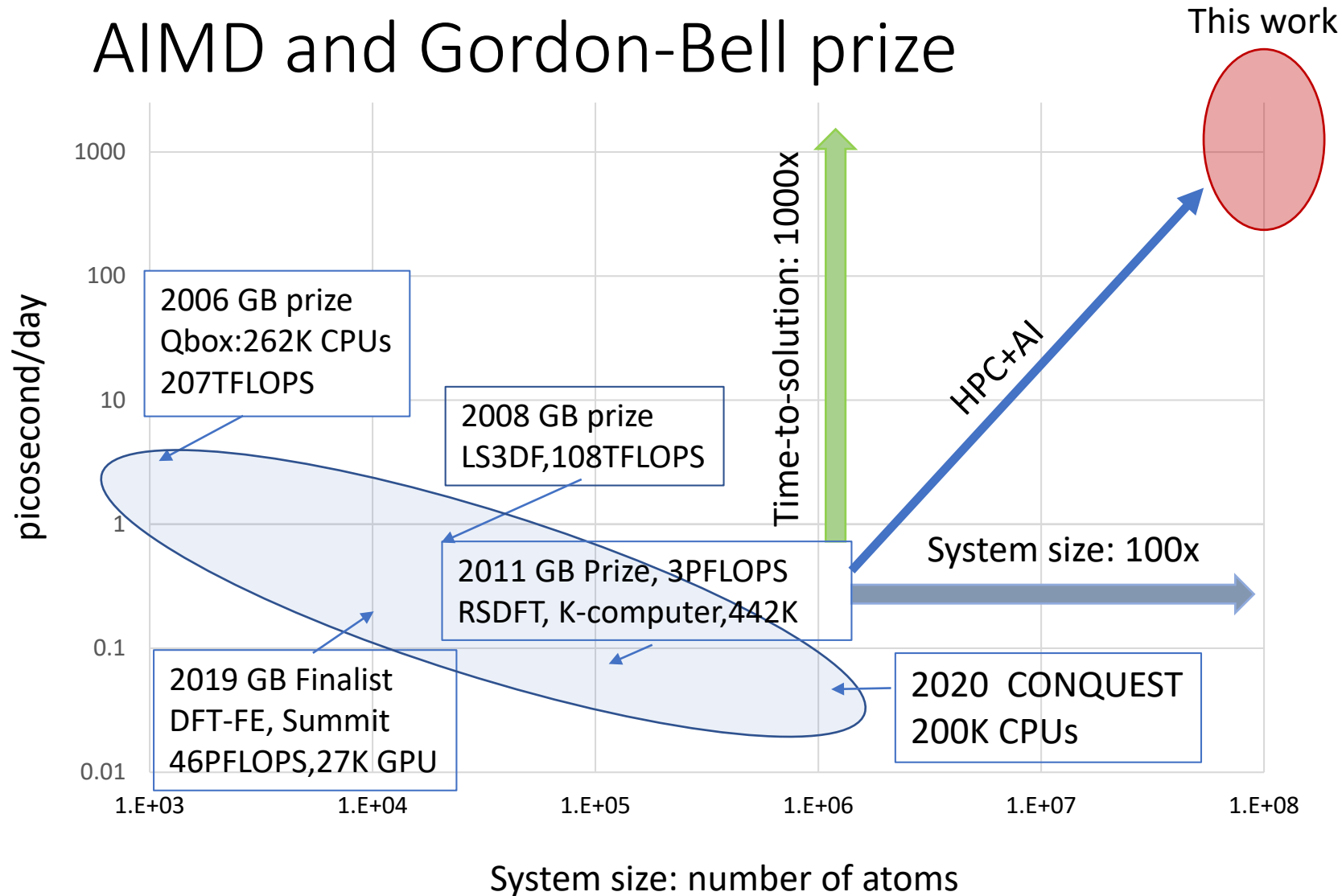


Predict large scale  
phosphorene nanoflake (PNF)  
heterojunction as new  
candidates of solar cells (9000  
atoms)

[L., Lu, Ying, Car and E, Commun. Math. Sci. 2009]  
[L., Garcia, Huhs, Yang, JPCM 2014]  
[Hu, L., Yang, Yang, J. Chem. Phys. 2014]

[Hu, L. and Yang, Phys. Chem. Chem. Phys. 2015]  
[Hu, L., Yang, Dai and Yang, Nano Lett., 2016]

# AIMD and Gordon-Bell prize



**Compared to state-of-the-art**

>10<sup>3</sup> times faster

>10<sup>2</sup> times bigger

DP: 91PFLOPS (45% of the peak)

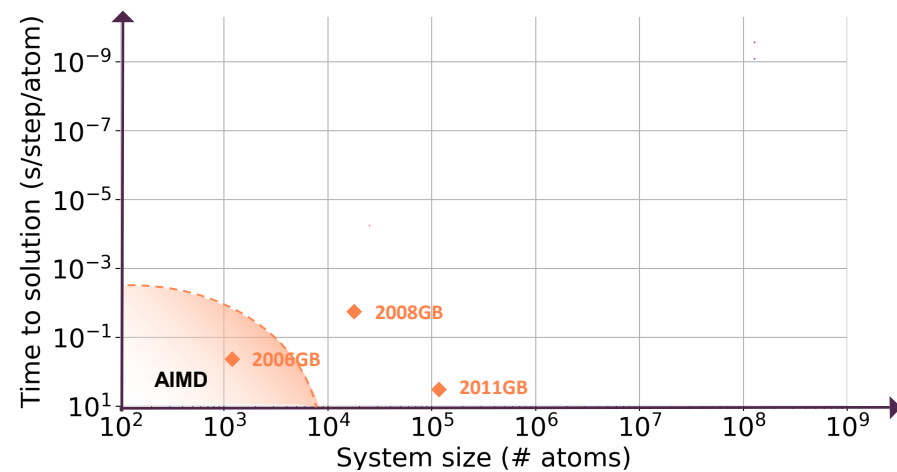
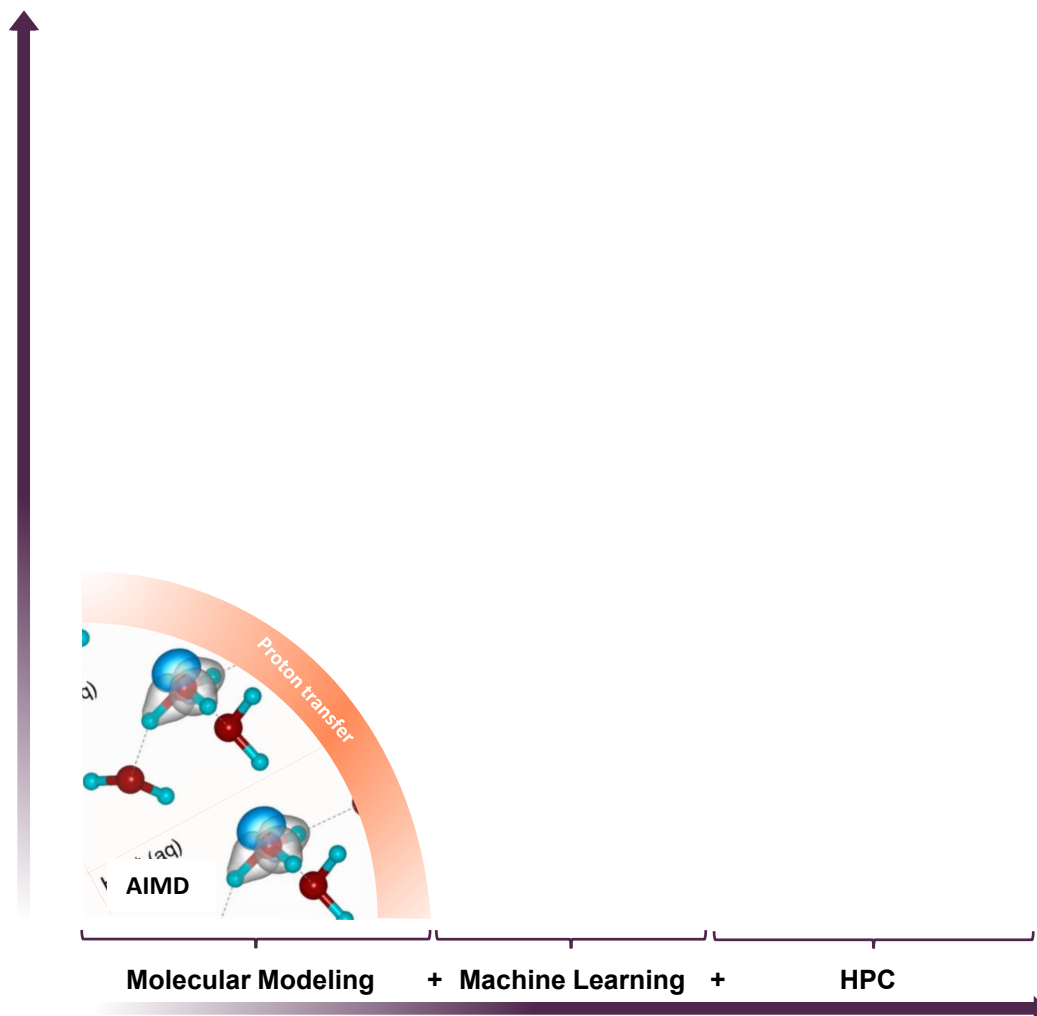
Mixed-SP: 162 PFLOPS

Mixed-HP: 275 PFLOPS

**SC20 Gordon Bell Prize Finalist**

arXiv: 2005.00223

# *Ab initio* Molecular Dynamics (AIMD): Solving DFT “on-the-fly”



**Advantages:** General and accurate

**Limitations:** Time and size scales

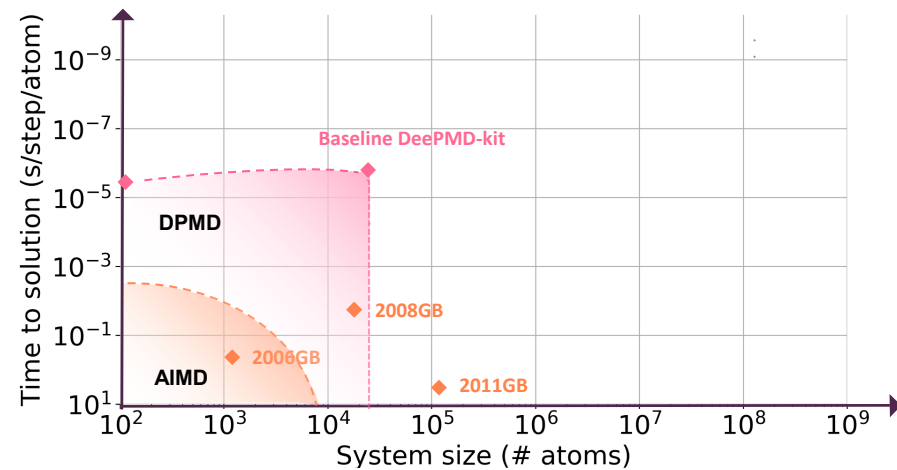
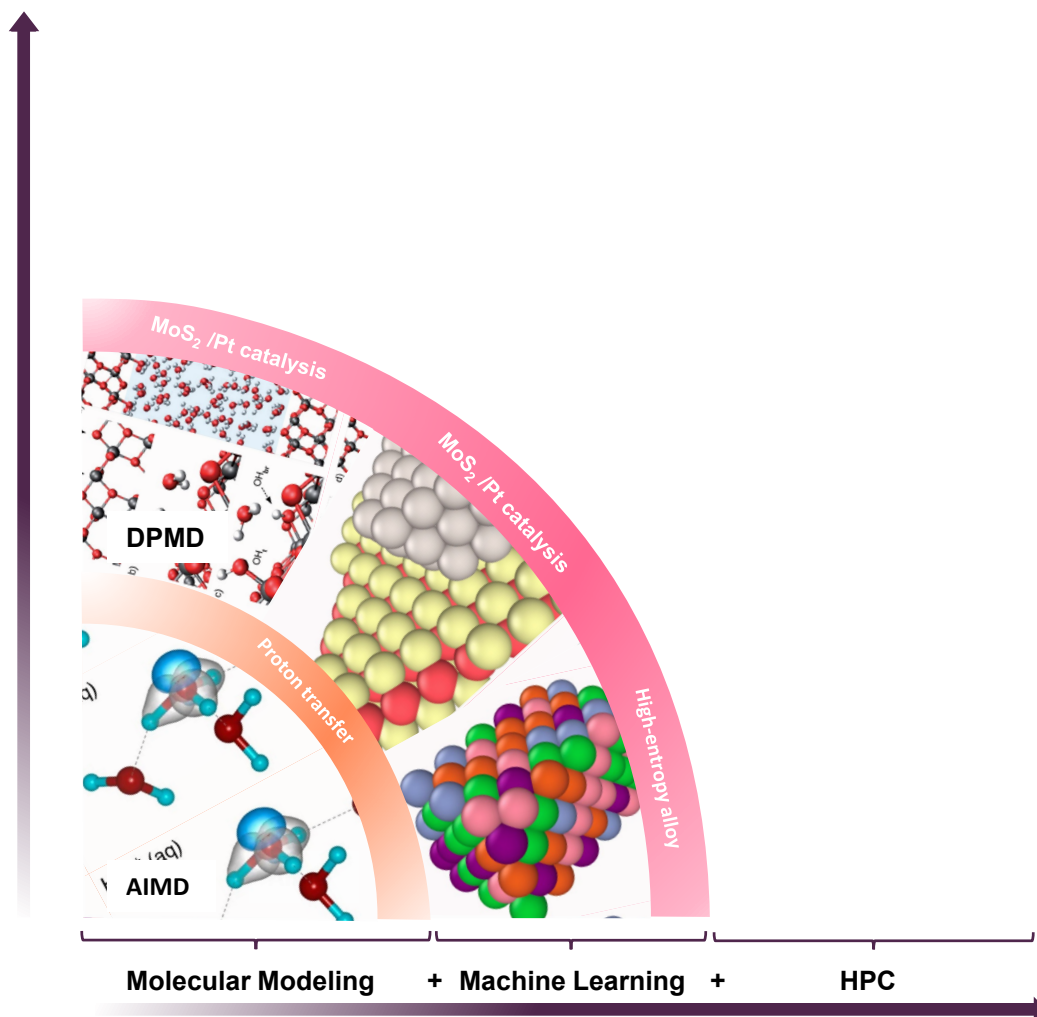
Density Functional  
Theory (DFT) solver

Energy  
Force  
Virial

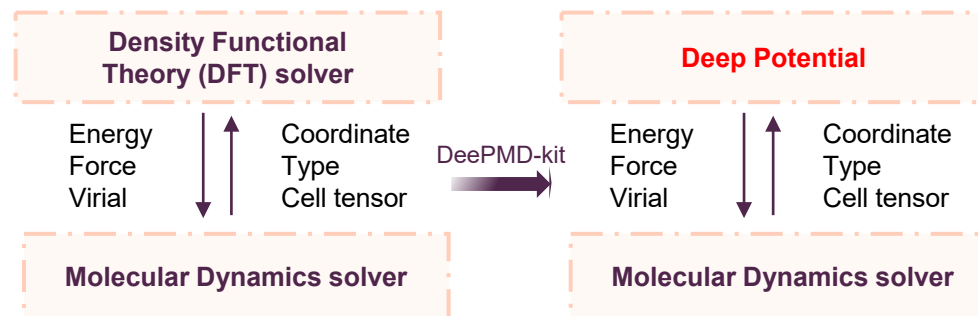
Coordinate  
Type  
Cell tensor

Molecular Dynamics solver

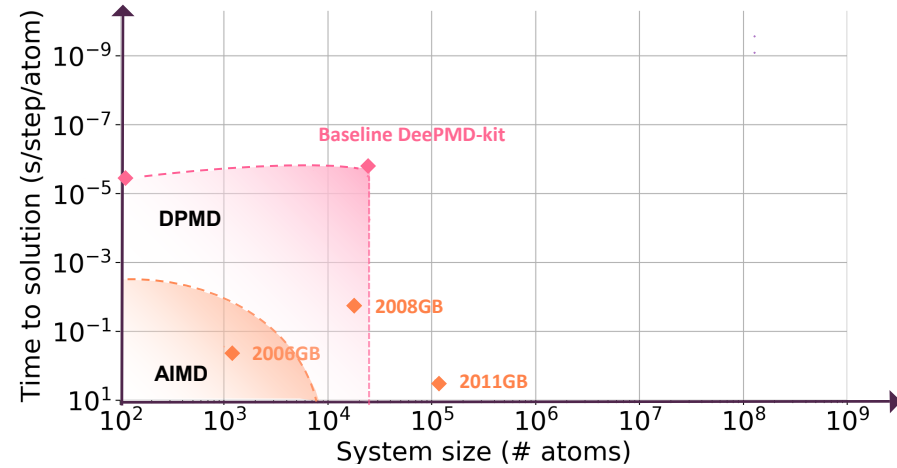
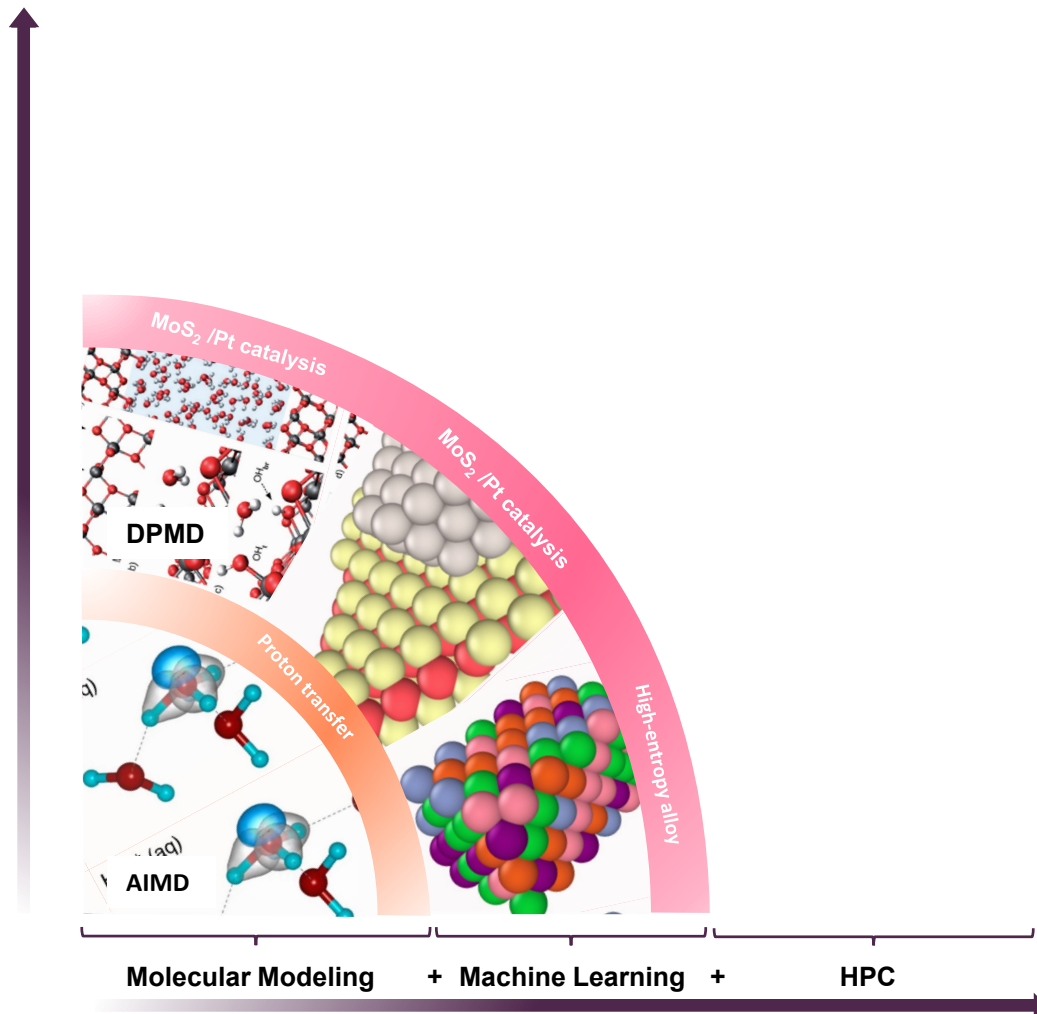
# Deep Potential Molecular Dynamics (DPMD): boosting AIMD with ML



**Deep Potential:**  
Physical requirements + machine learning



# Deep Potential Molecular Dynamics (DPMD): boosting AIMD with ML

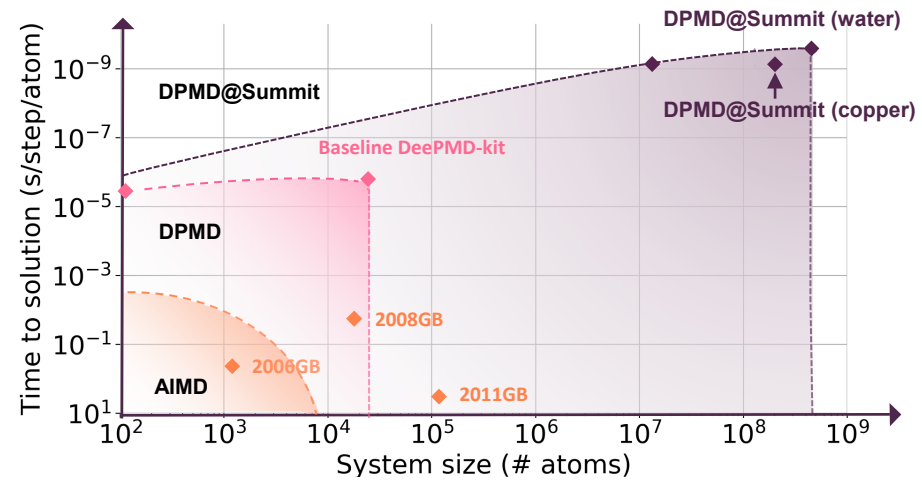
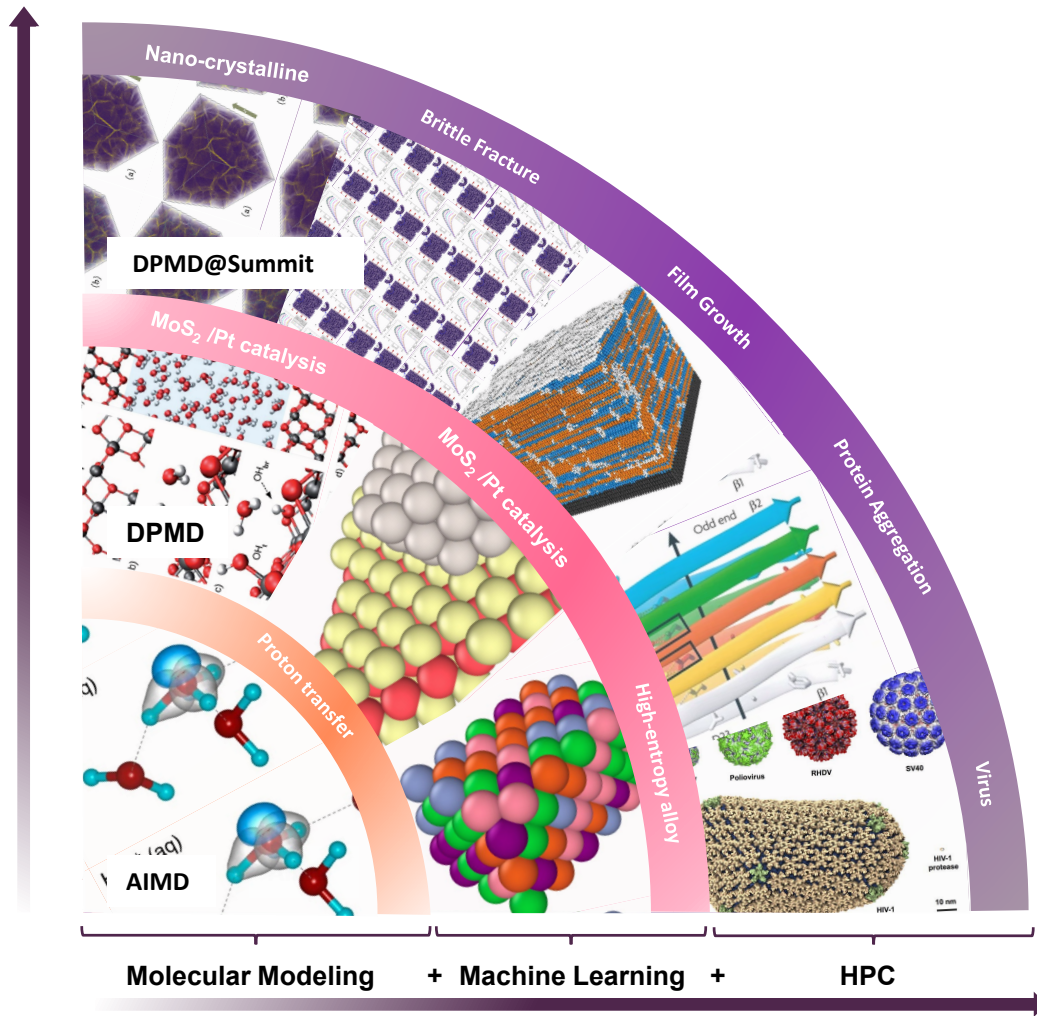


Time and size scales required by important Problems

Problem	Time span [ns]	System size [#atom]
Droplet coalescence	~10	~1e+8
Dynamic fracture	~0.1	~1e+8
Strength of nanocrystalline metal	~0.01	~1e+6
Heterogeneous aqueous interfaces	~100	~1e+6



# This work: molecular modeling + machine learning + HPC



Time and size scales required by important Problems

Problem	Time span [ns]	System size [#atom]
Droplet coalescence	~10	~1e+8
Dynamic fracture	~0.1	~1e+8
Strength of nanocrystalline metal	~0.01	~1e+6
Heterogeneous aqueous interfaces	~100	~1e+6

# Method: Deep Potential Molecular Dynamics

**Machine learning:**  
Representing high-dimensional functions



**Physical principles:**  
Extensive property; Symmetry invariance

**Representation:**

$$\mathcal{F}(\mathbf{x}, \omega) = \mathcal{L}^{\text{out}} \circ \mathcal{L}^2 \circ \mathcal{L}^1 \circ \mathcal{L}^0(\mathbf{x})$$

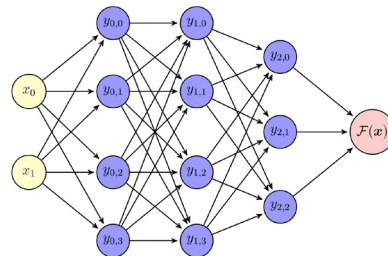
$$\mathcal{L}^i(\mathbf{y}) = \tanh(\mathbf{W}^i \cdot \mathbf{y} + \mathbf{b}^i), \quad i = 0, 1, 2$$

$$\mathcal{L}^{\text{out}}(\mathbf{y}) = \mathbf{W} \cdot \mathbf{y} + \mathbf{b}$$

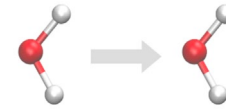
$$\omega = \{\mathbf{W}^i, \mathbf{b}^i, \mathbf{W}, \mathbf{b} \mid i = 0, 1, 2\}$$

**Optimization/Training:**

$$\min_{\omega} \sum_{d \in \mathcal{D}} \|\mathcal{F}(\mathbf{x}_d, \omega) - f(\mathbf{x}_d)\|$$



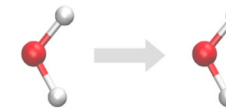
**Translational**



**Rotational**



**Permutational**



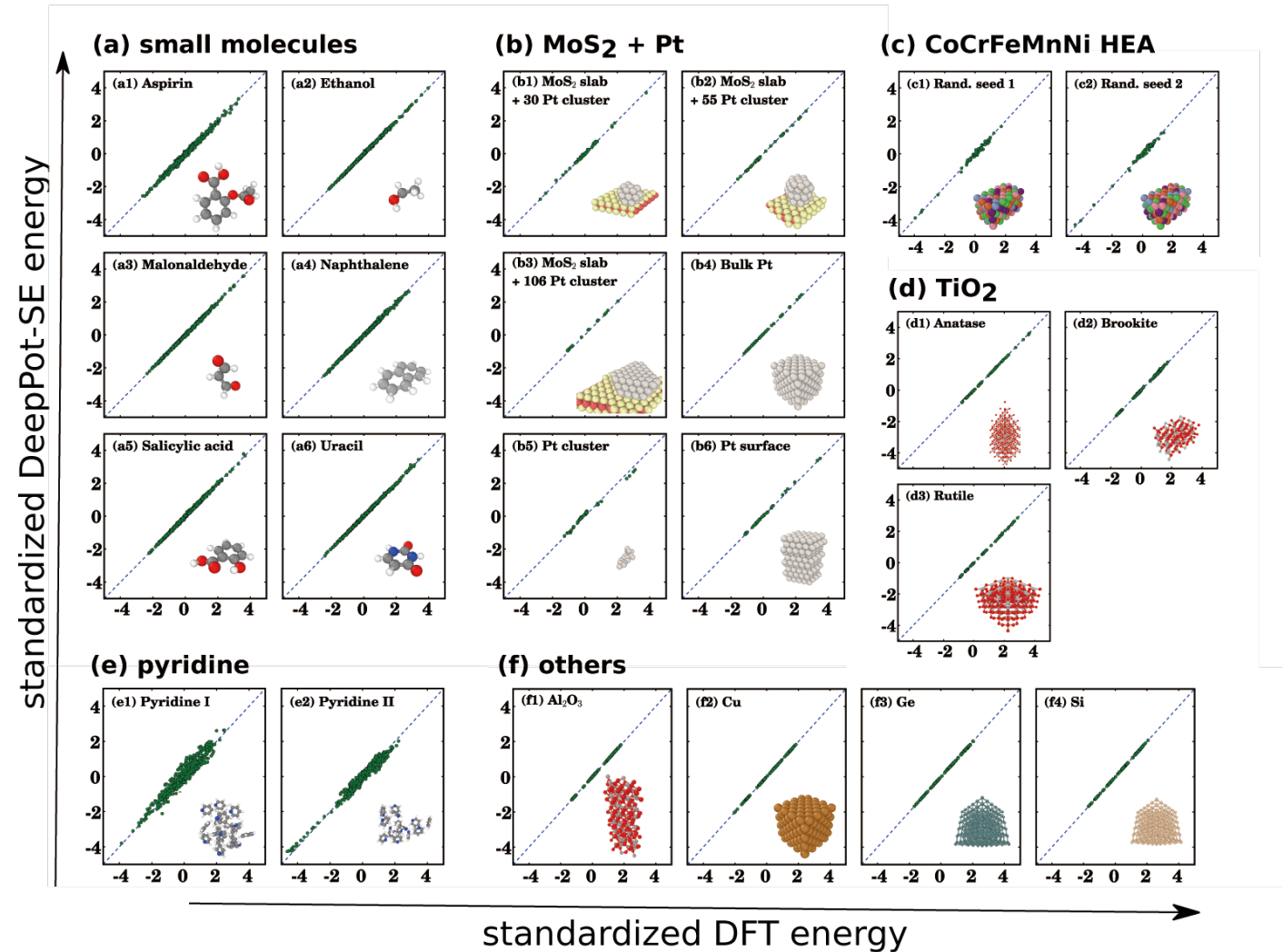
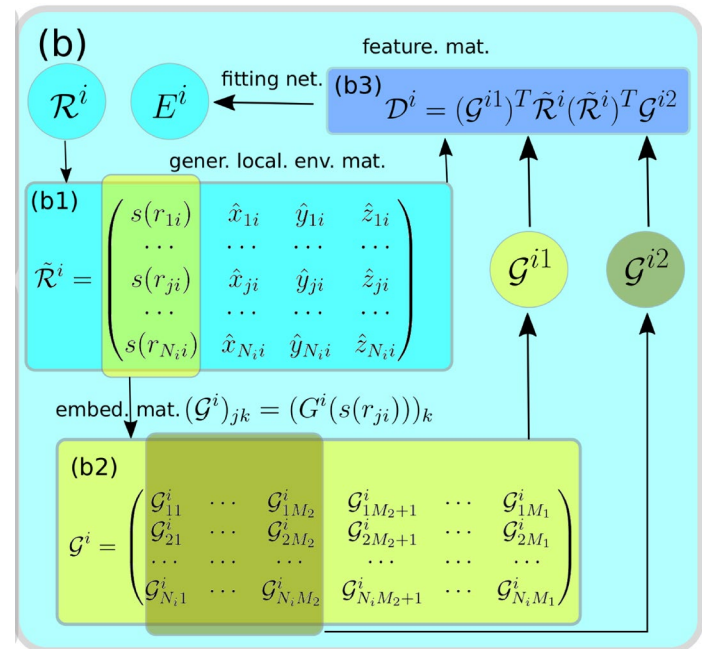
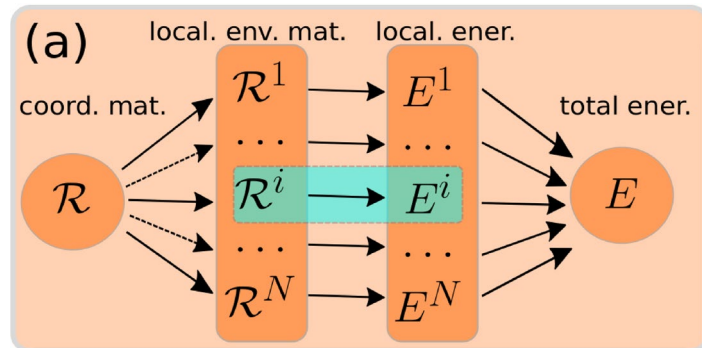
$$E(r_0, r_1, r_2) = E(r_0 + s, r_1 + s, r_2 + s)$$

$$E(r_0, r_1, r_2) = E(Ur_0, Ur_1, Ur_2)$$

$$E(r_0, r_1, r_2) = E(r_0, r_2, r_1)$$



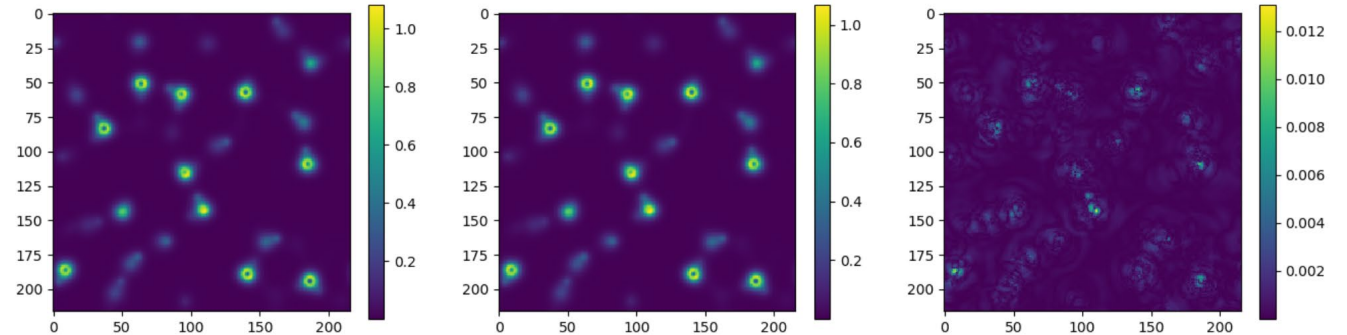
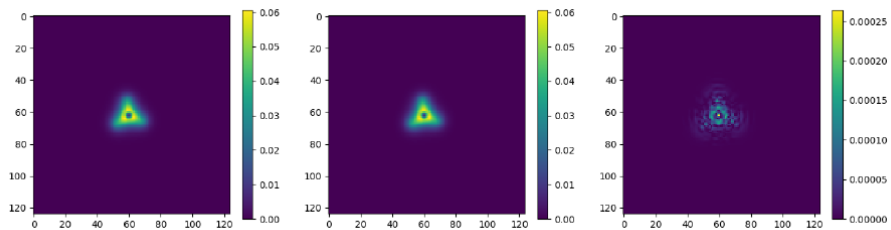
# Method: Deep Potential Molecular Dynamics



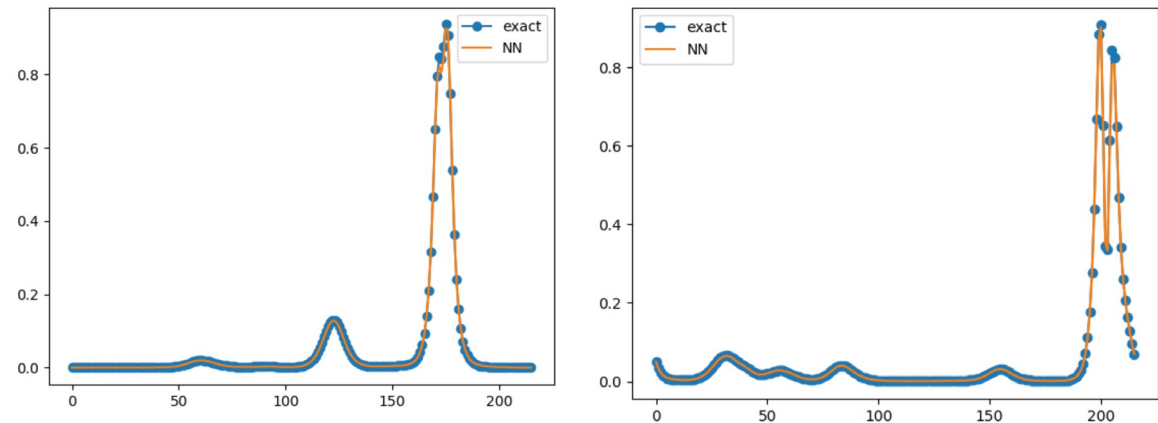
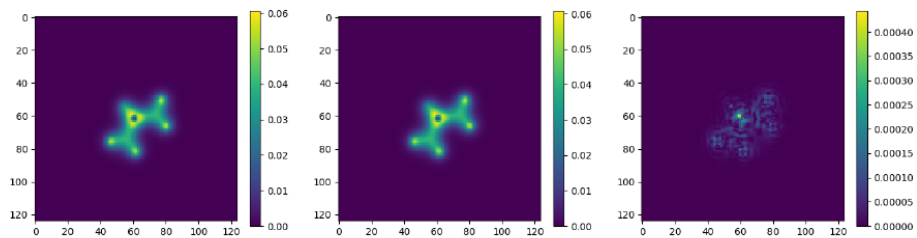
# Machine learning of the electron density

water 256 molecules

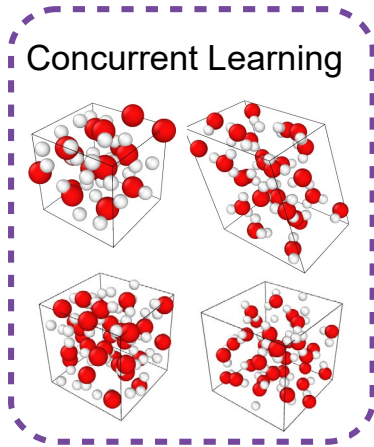
ethane



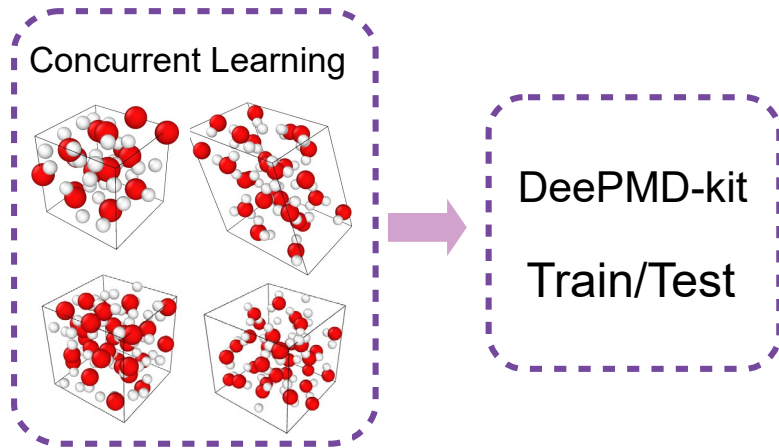
isobutene



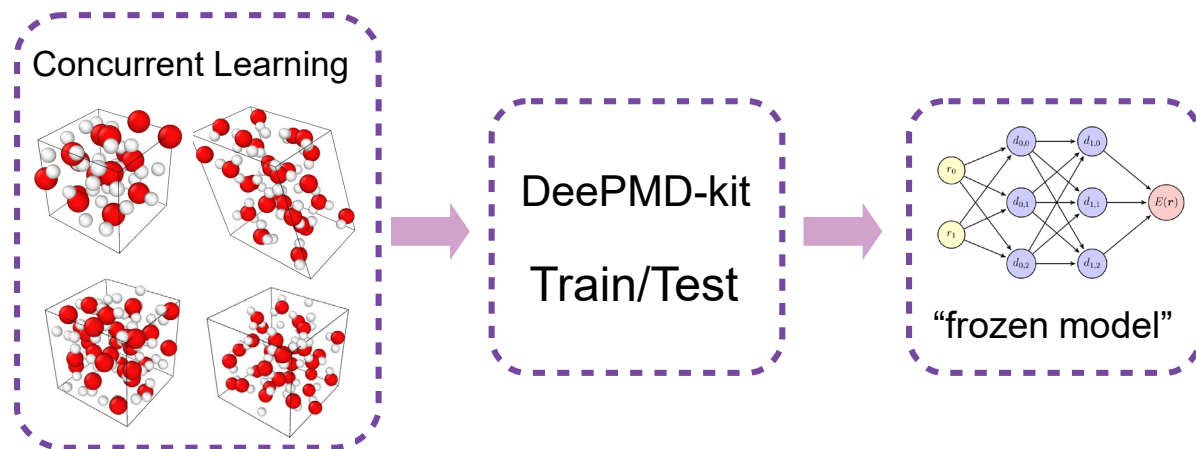
## Method: Deep Potential Molecular Dynamics



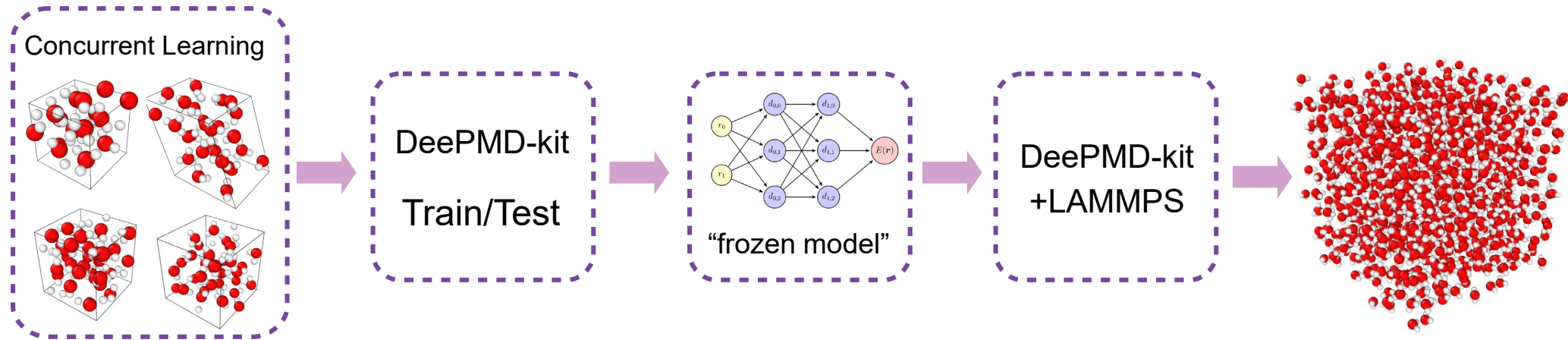
## Method: Deep Potential Molecular Dynamics



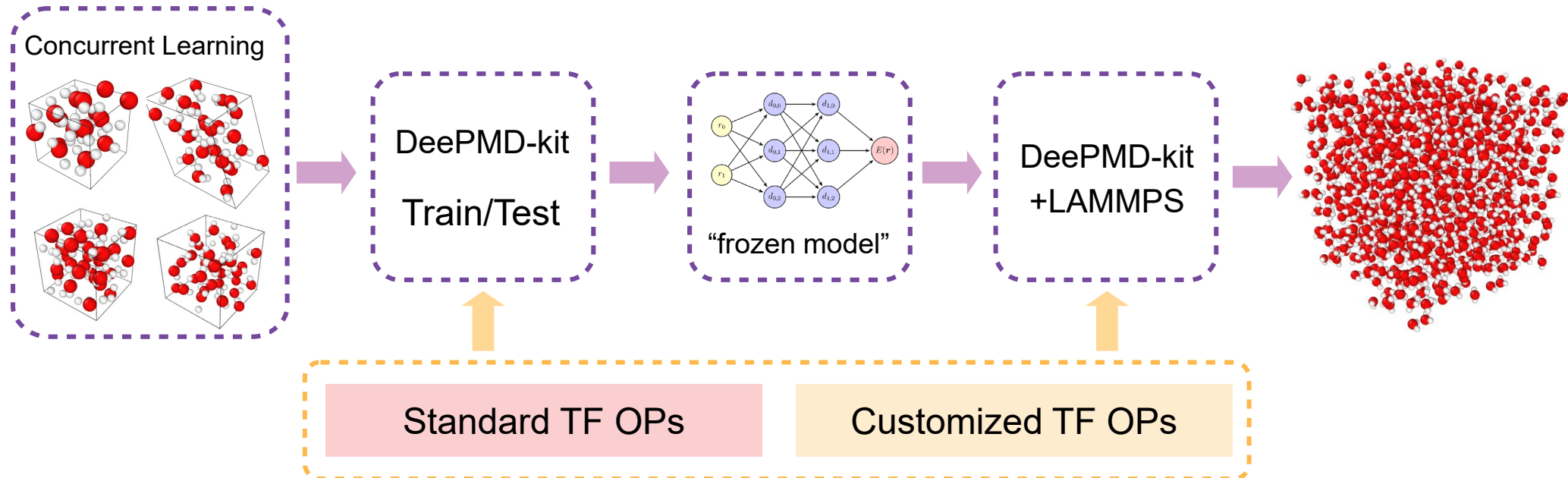
# Method: Deep Potential Molecular Dynamics



# Method: Deep Potential Molecular Dynamics

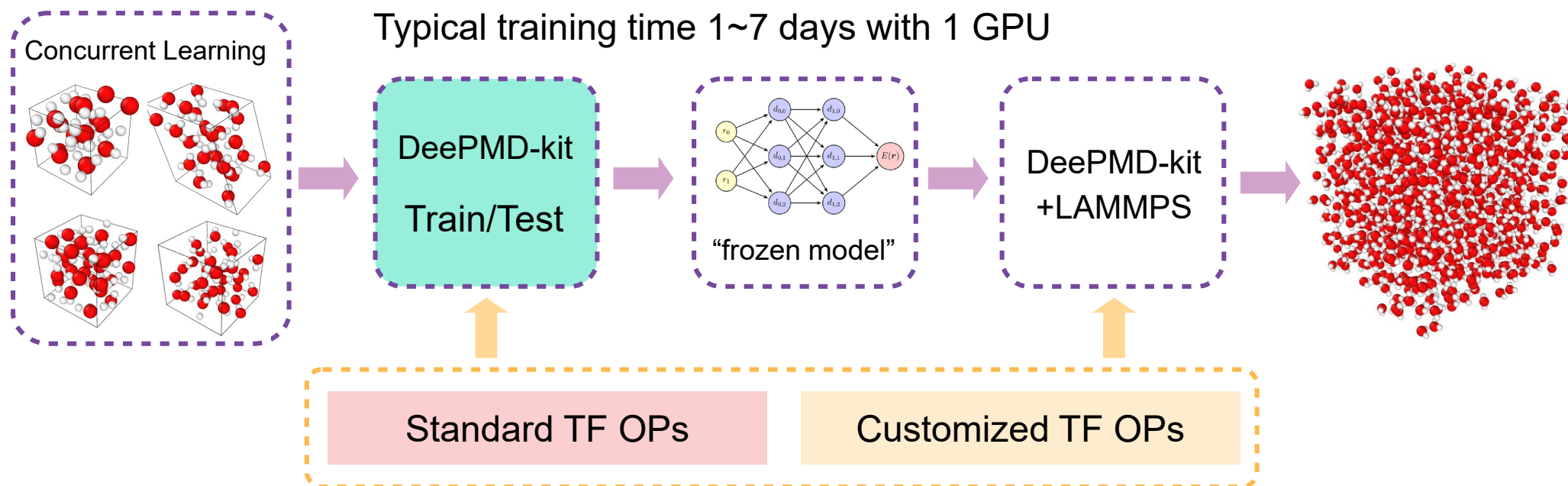


# Method: Deep Potential Molecular Dynamics

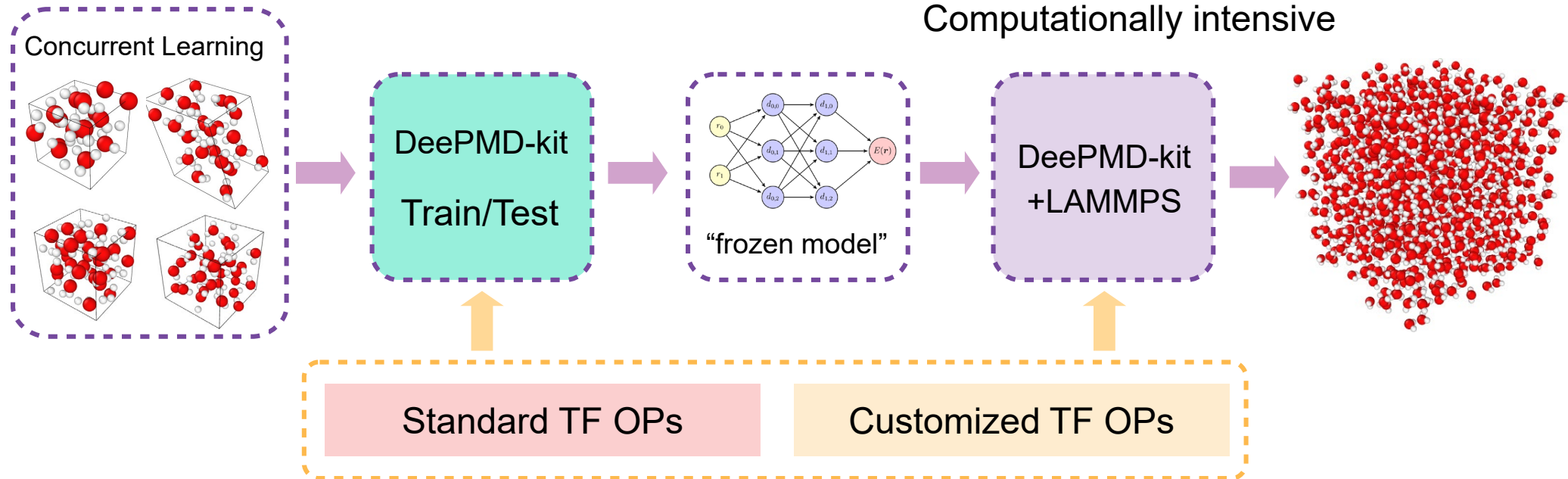




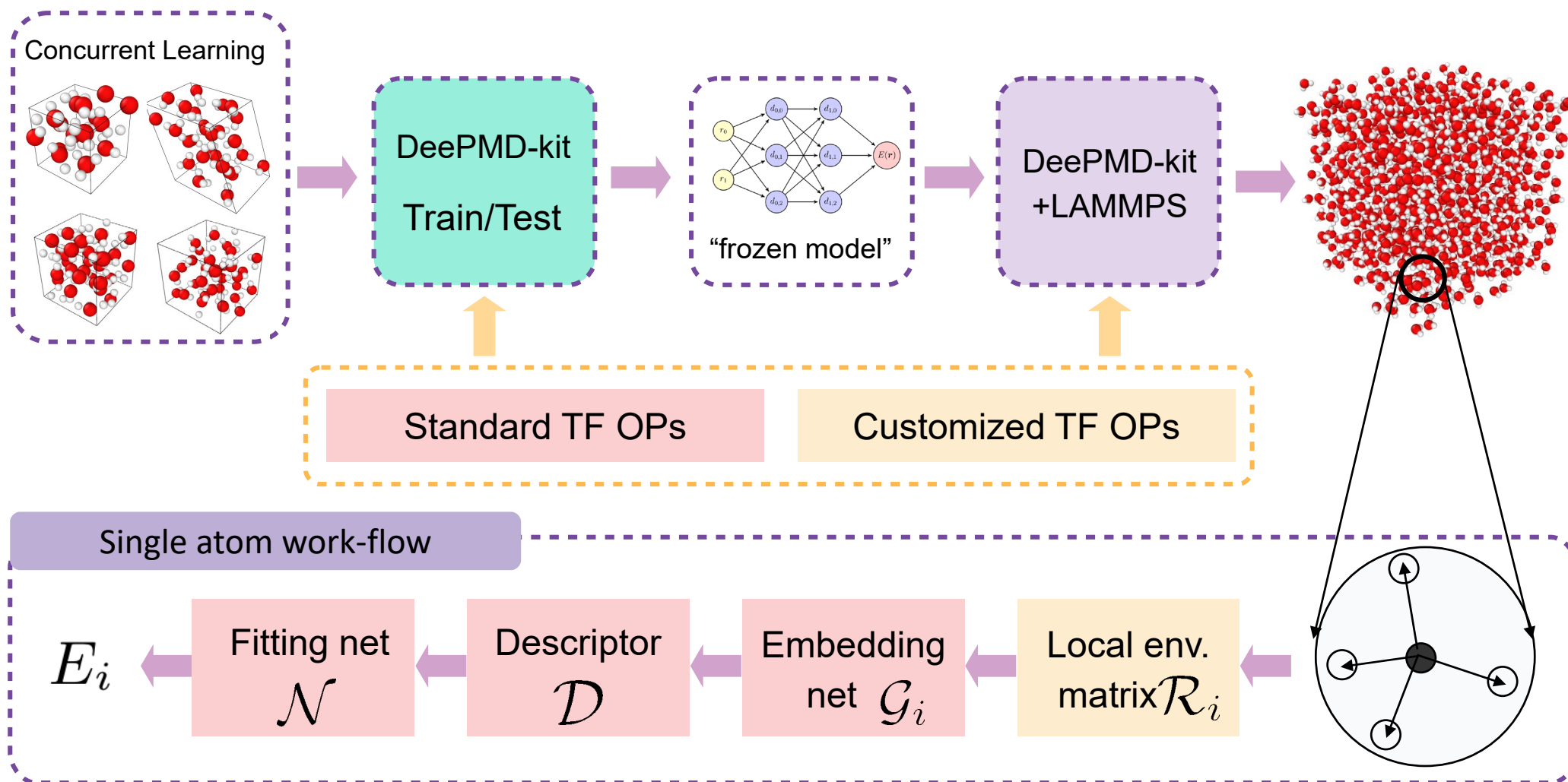
# Method: Deep Potential Molecular Dynamics



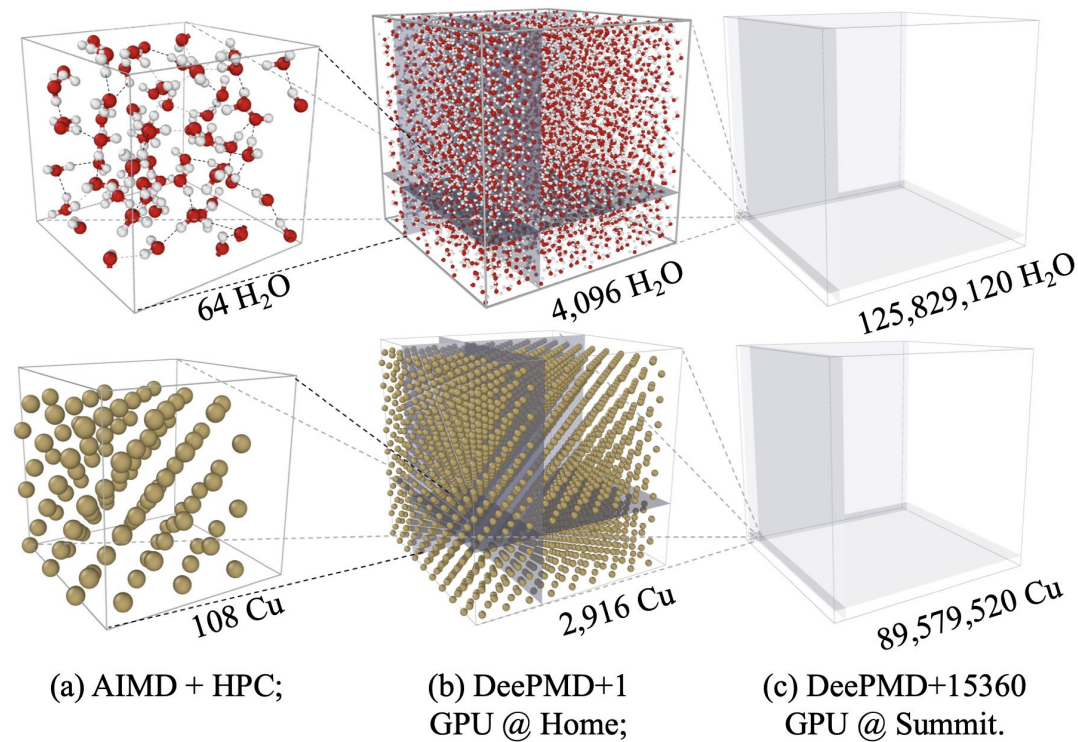
# Method: Deep Potential Molecular Dynamics



# Method: Deep Potential Molecular Dynamics



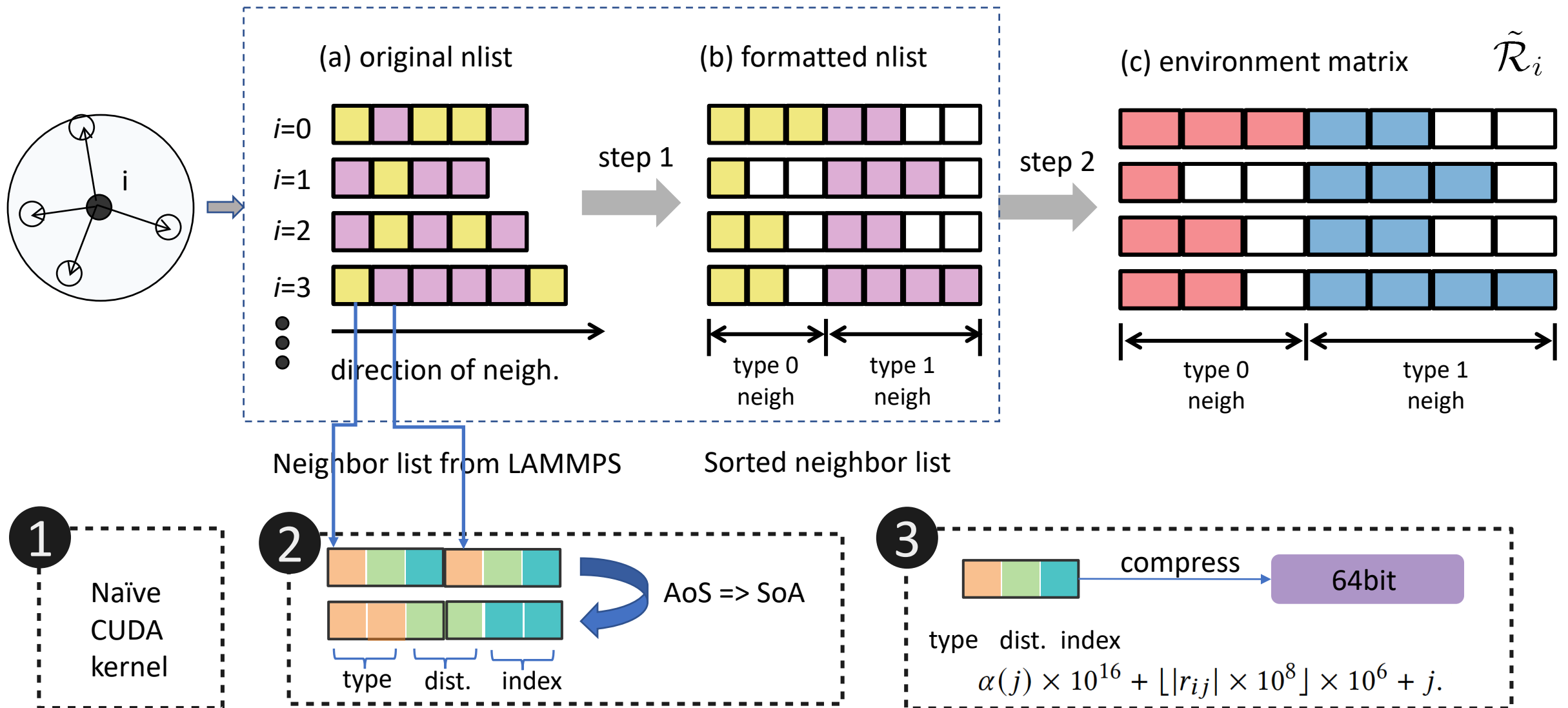
# Physical systems



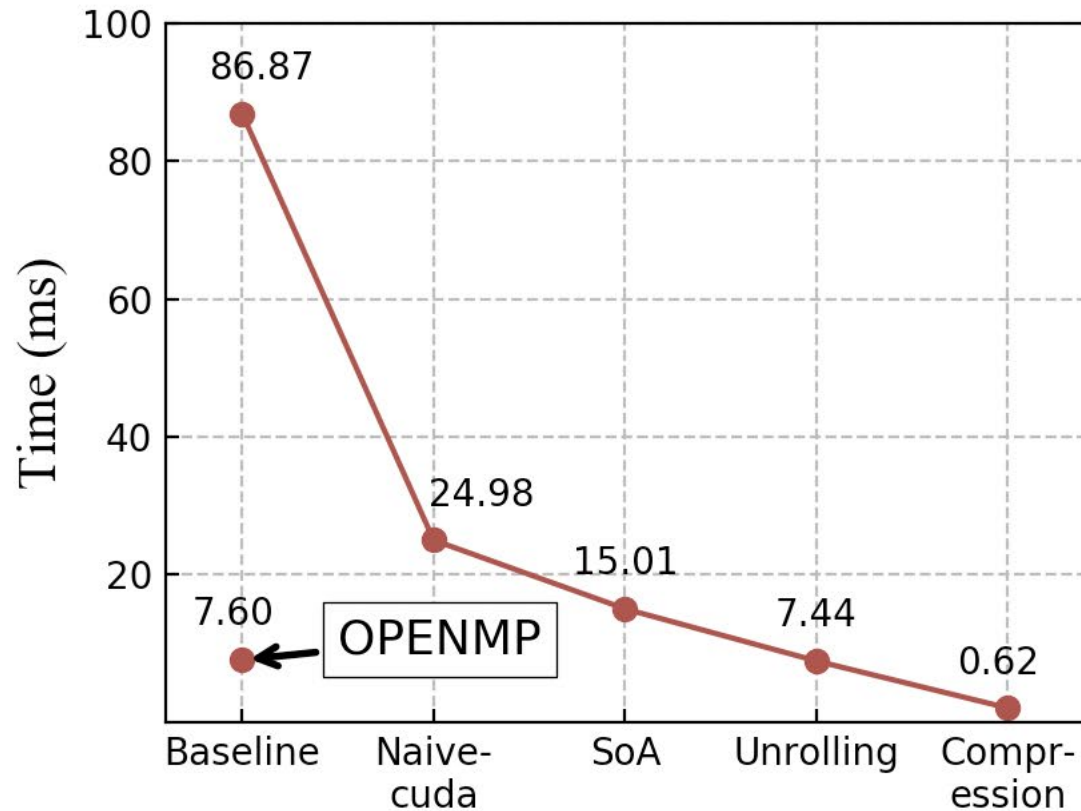
- Single GPU:
  - 8192 H<sub>2</sub>O molecule (24576 atoms)
  - 4860 copper atoms
- Scaling:
  - Strong scaling:
    - Copper: 15,925,248 atoms
    - Water: 12,779,520 atoms
  - Weak scaling:
    - Copper: each GPU holds 4656 atoms
    - Water: each GPU holds 24834 atoms

500 MD steps are simulated in the tests.

# Customized TensorFlow operators

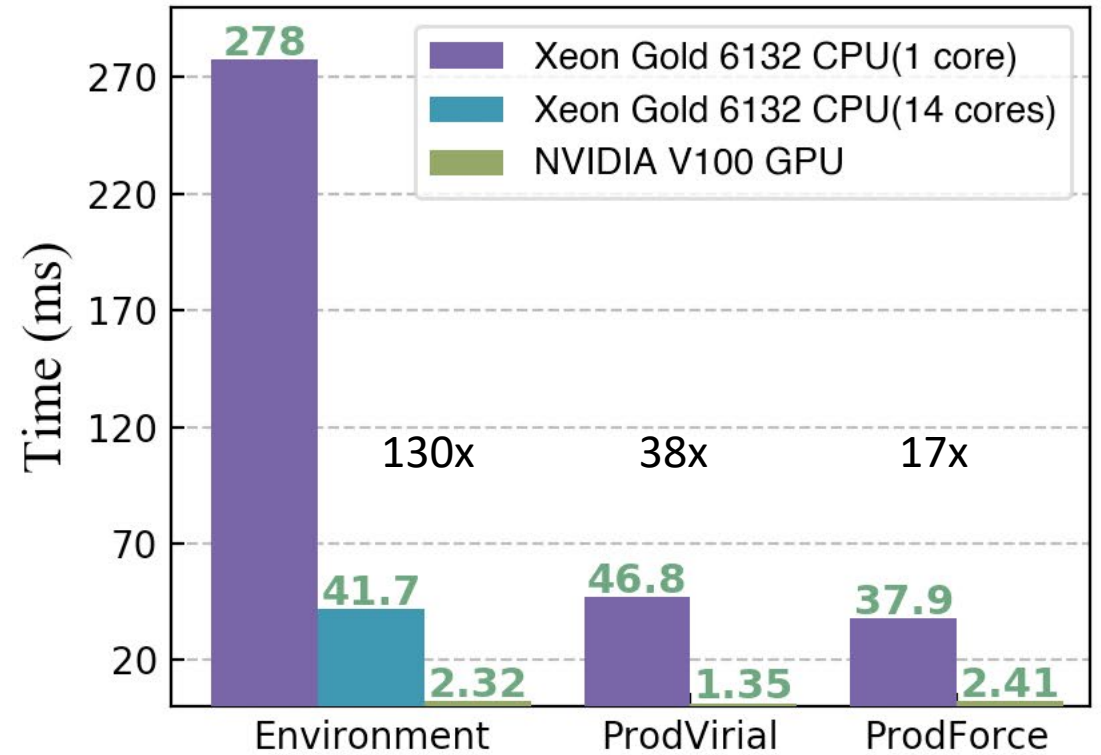


# Customized TensorFlow operators



(a)

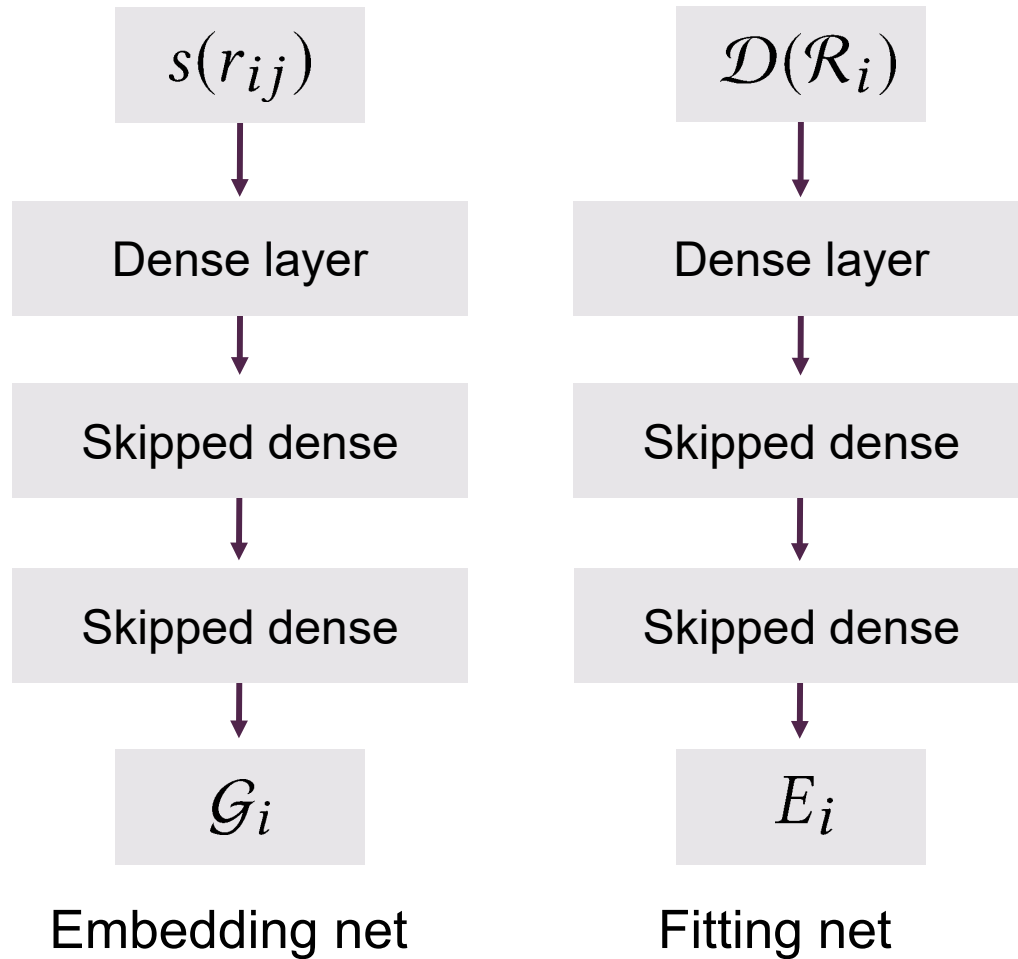
Speedup of formatting neighbor list



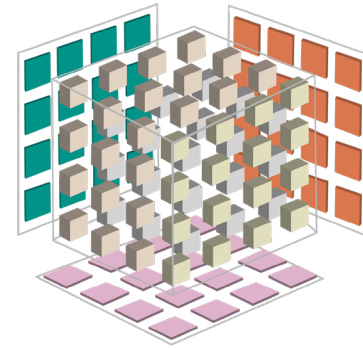
(b)

Speedup of all the customized TensorFlow operators

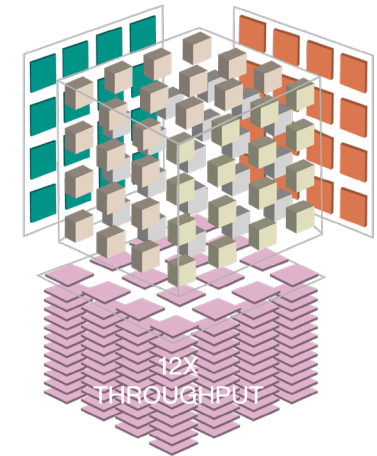
# Mixed precision



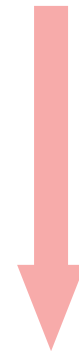
PASCAL



VOLTA TENSOR CORES



Boost performance?



7 TFLOPS (double)

14 TFLOPS (single)

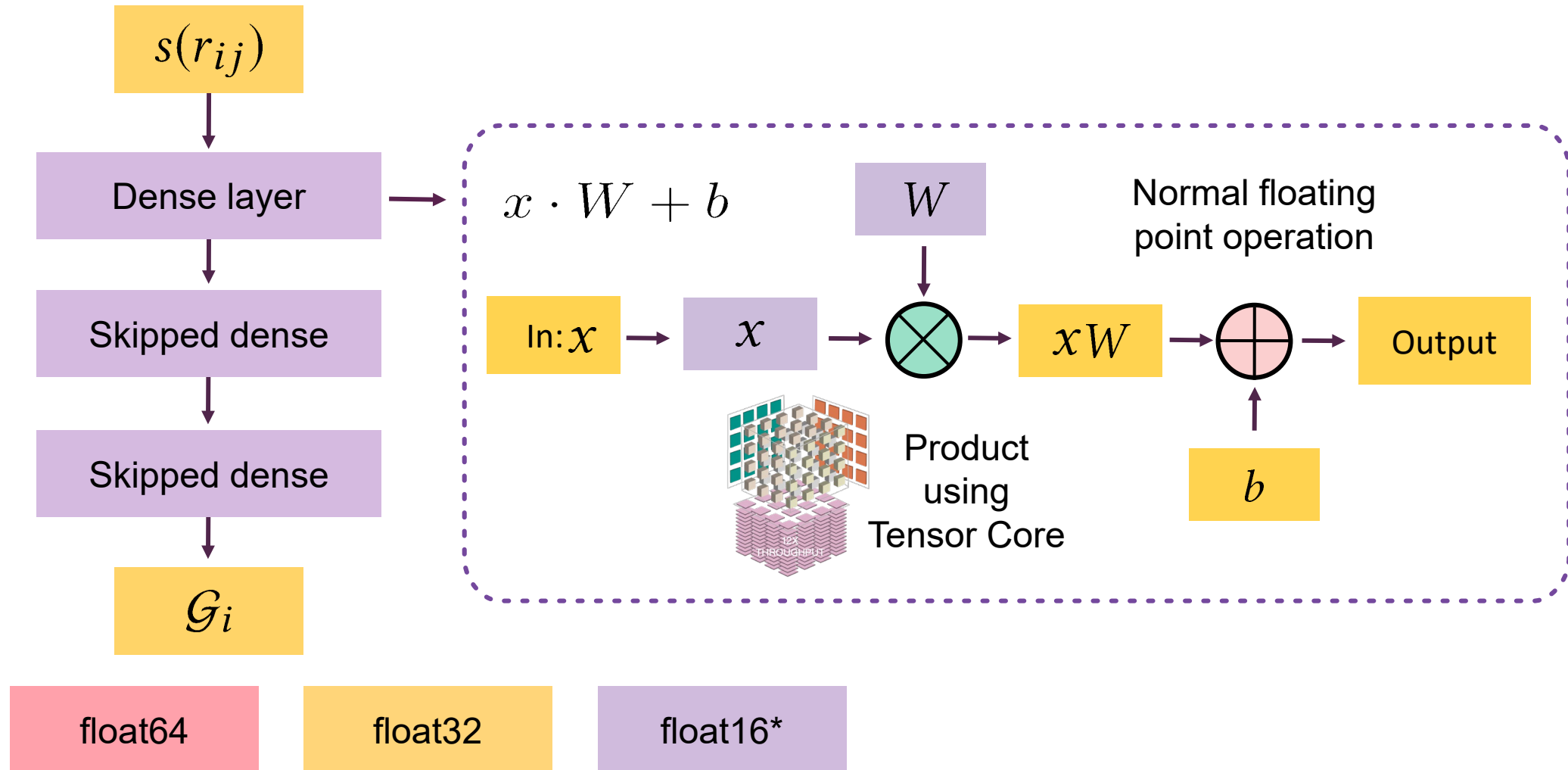
127 TFLOPS (half TensorCore)



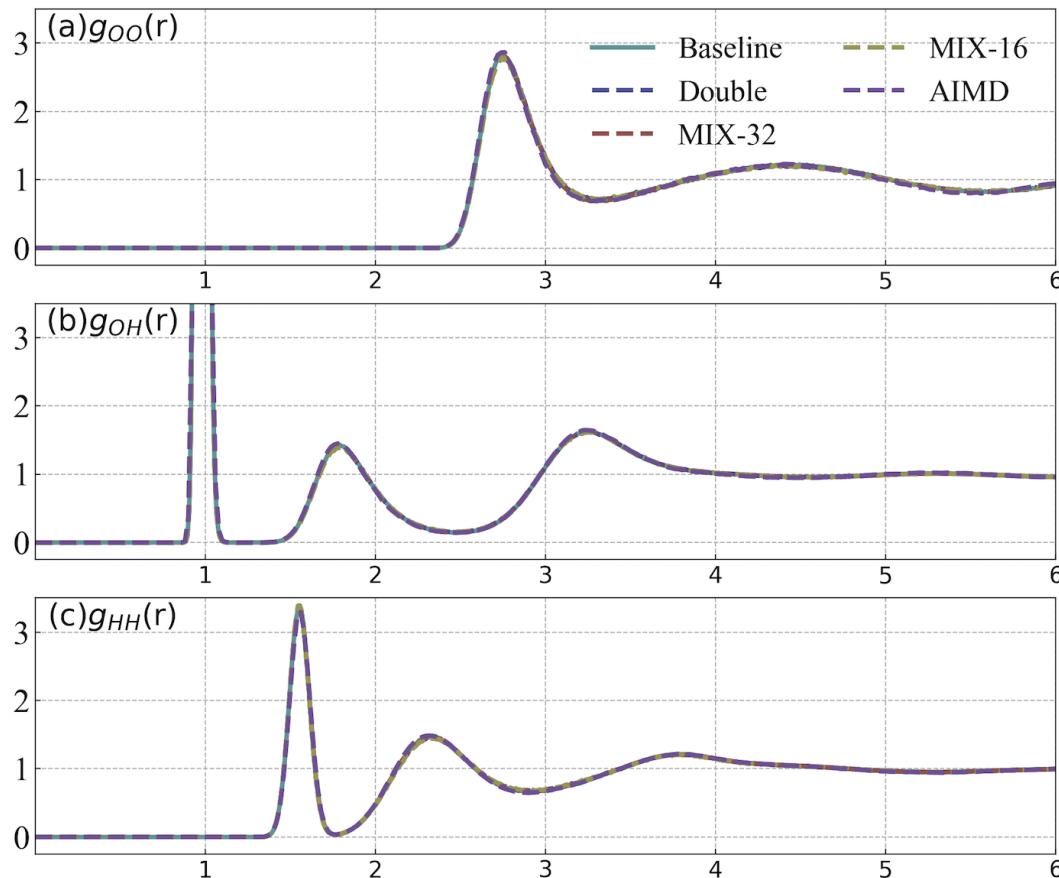
Lose Accuracy?



# Mixed precision



# Mixed precision: accuracy



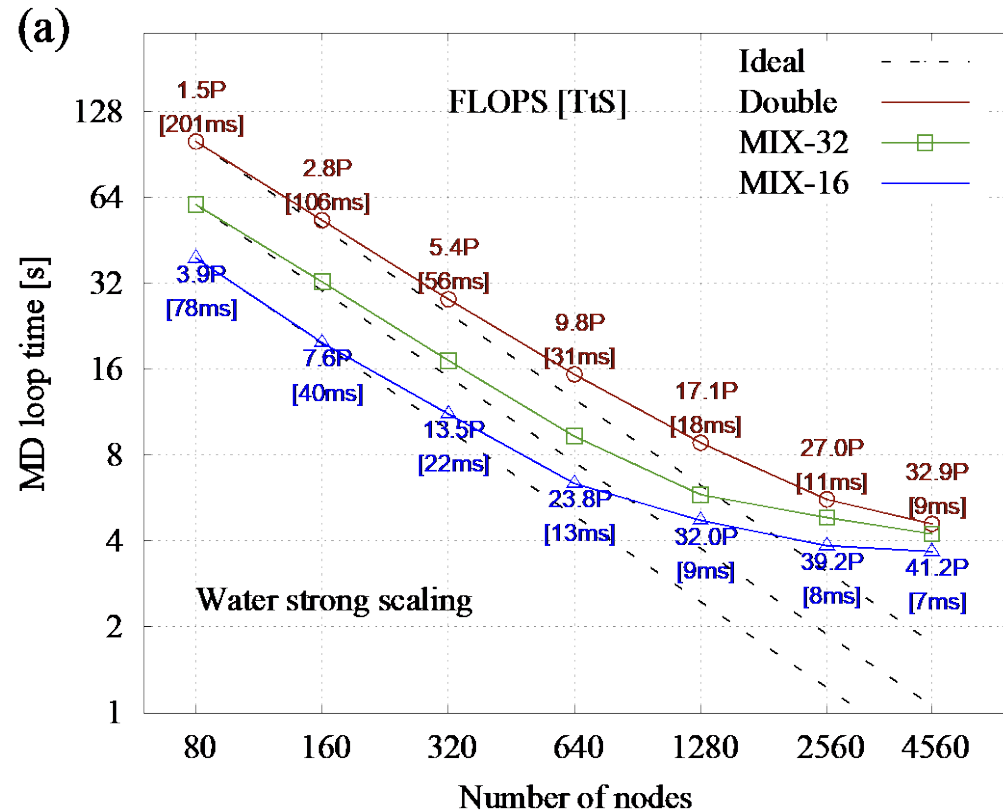
Radial distribution functions  $g_{OO}(r)$ ,  $g_{OH}(r)$ , and  $g_{HH}(r)$  of liquid water at ambient conditions, calculated by AIMD and four DeePMD-kit implementations: baseline, optimized double, MIX-32, and MIX-16

Testing error of 3 different precisions

Precision	Error in energy [eV/molecule]	Error in force [eV/Å]
Double	$1.2 \times 10^{-3}$	$3.7 \times 10^{-2}$
MIX-32	$1.2 \times 10^{-3}$	$3.7 \times 10^{-2}$
MIX-16	$3.6 \times 10^{-3}$	$3.8 \times 10^{-2}$

- Mixed precision can achieve excellent accuracy
- Accuracy of MIX-32 is same as Double

# Strong scaling (I)

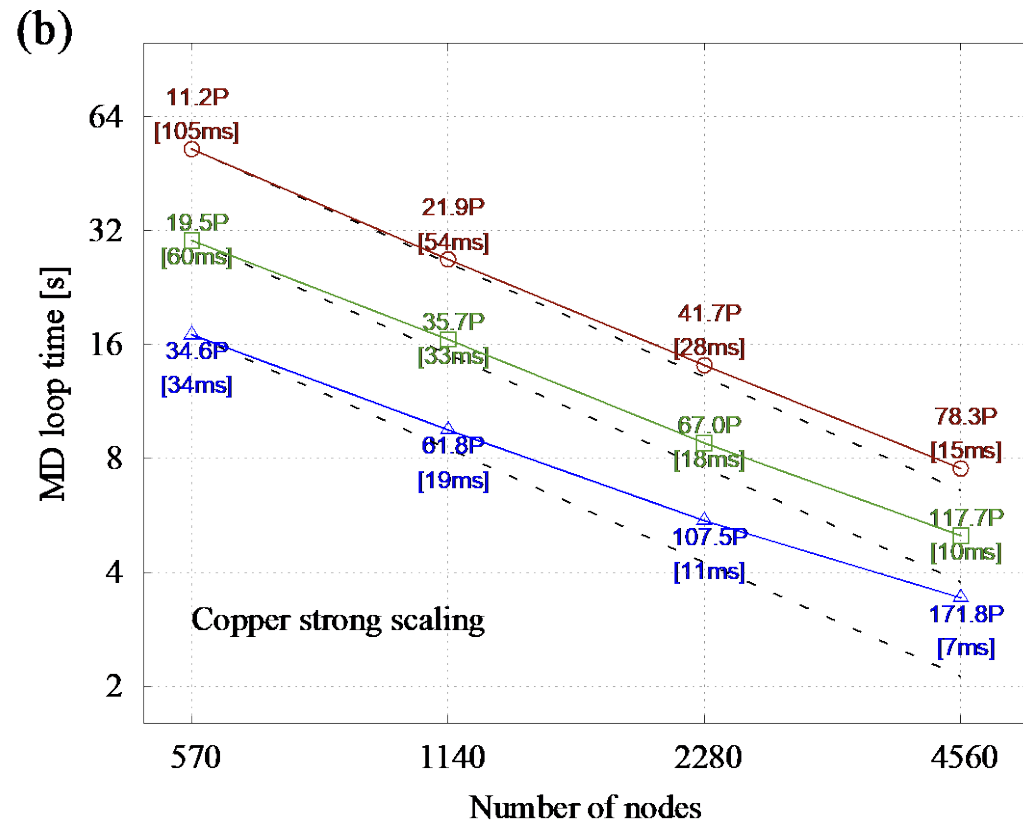


Water: 12,779,520 atoms

#Nodes	80	160	320	640	1280	2560	4560
#GPUs	480	960	1920	3840	7680	15360	27360
#atoms	26624	13312	6656	3328	1664	832	467
#ghosts	25275	17014	11408	7839	5553	3930	3037
MD time	100.4	53.2	28.1	15.4	8.8	5.6	4.6
Efficiency	1.00	0.94	0.89	0.82	0.71	0.56	0.38
PFLOPS	1.51	2.84	5.37	9.84	17.09	26.98	32.90
%of Peak	42.90	40.45	38.26	35.07	30.44	24.03	16.45

Average number of atoms (per GPU), average ghost region size (per GPU), and double precision FLOPS for the 12,779,520 atoms water system.

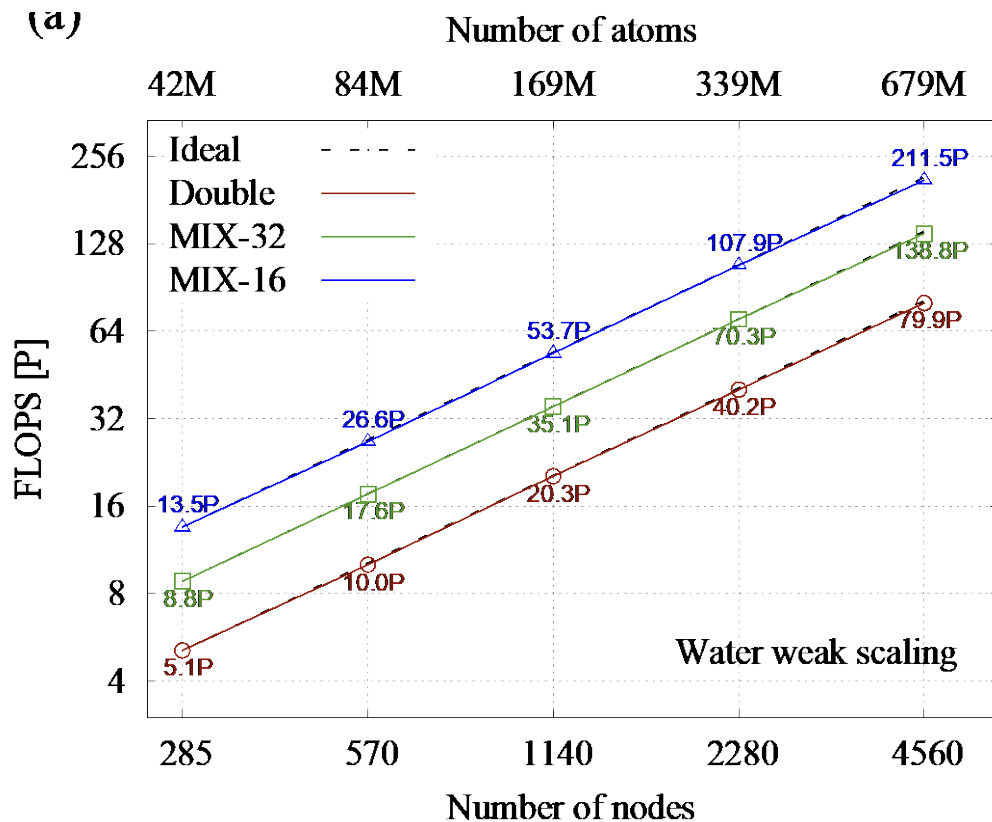
# Strong scaling (II)



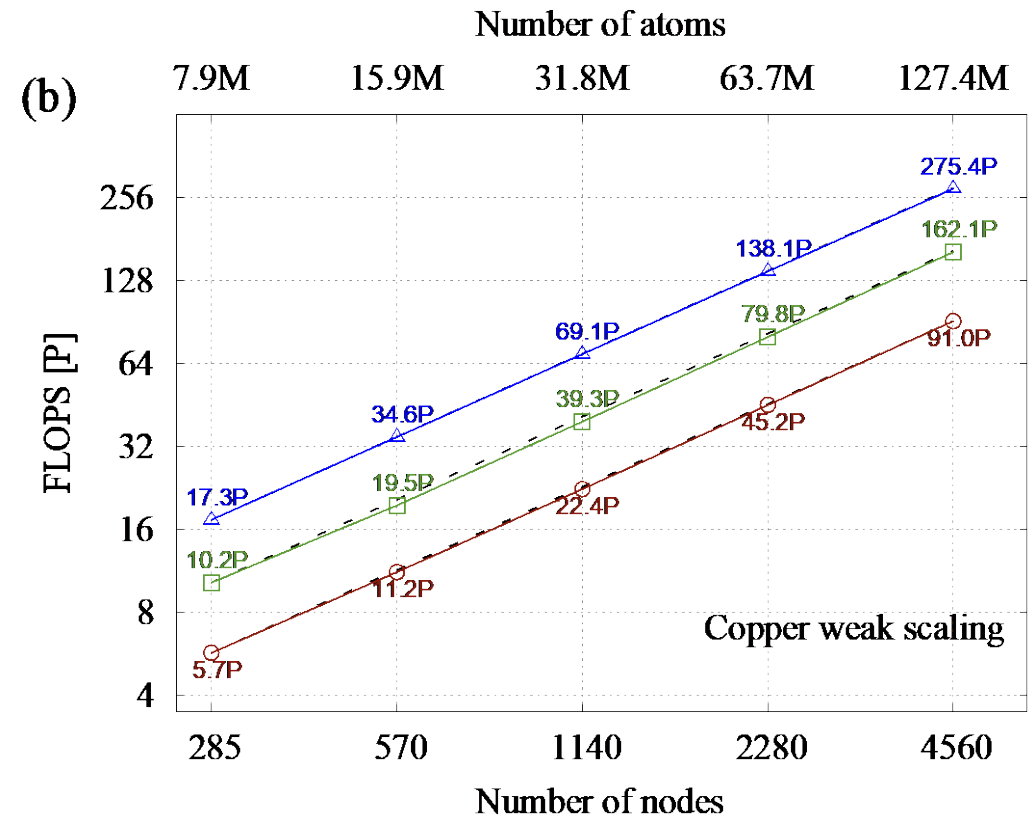
## • Peak performance:

- 78.3/117/171 PFLOPS for double/MIX-32/MIX-16
- Parallel efficiency: 87%/72%/62% using 4560 nodes compared to 570 nodes.
- Double precision scales better because of memory usage
- MIX-16 is 3x faster on 570 nodes, and 2.2x faster on 4560 nodes.

# Weak Scaling: Water and Copper

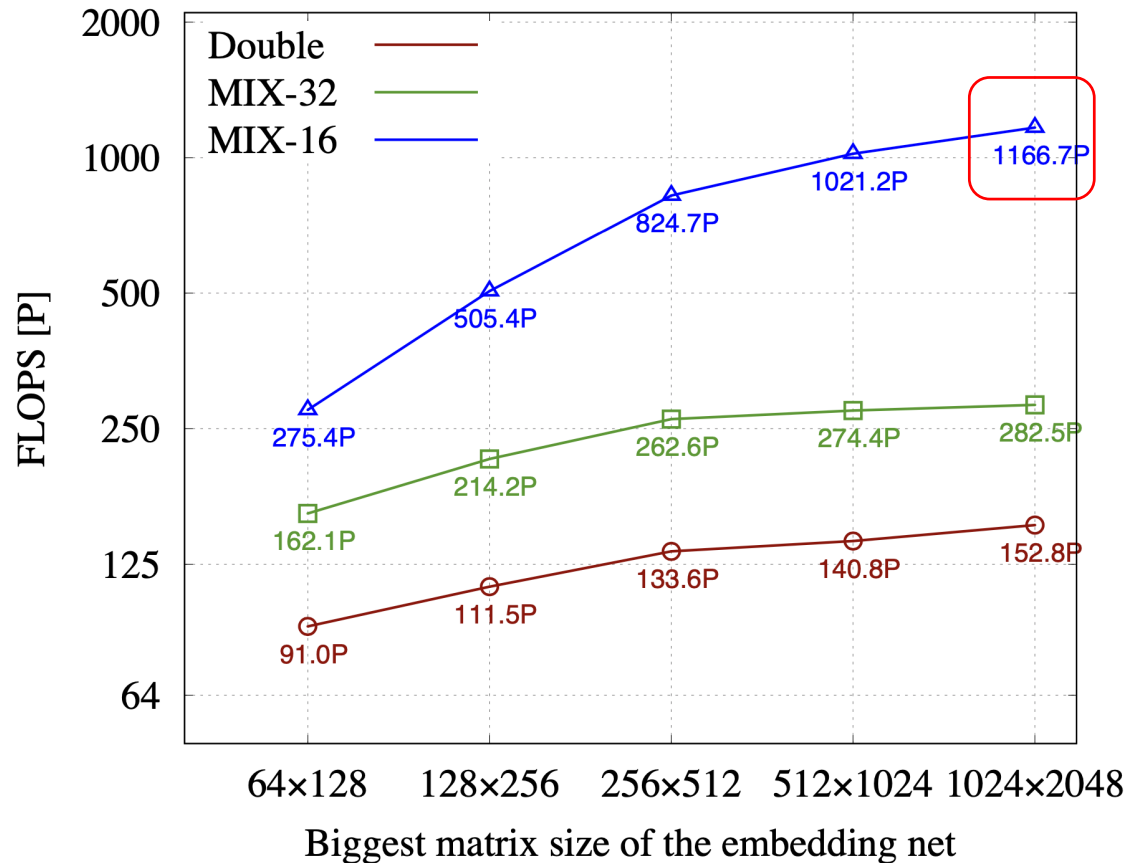


Water: weak scaling from 285 to 4560 nodes  
#atoms ranges from 42M to 679M



Copper: weak scaling from 285 to 4560 nodes  
#atoms ranges from 7.9M to 127.4M

# What if using bigger network?



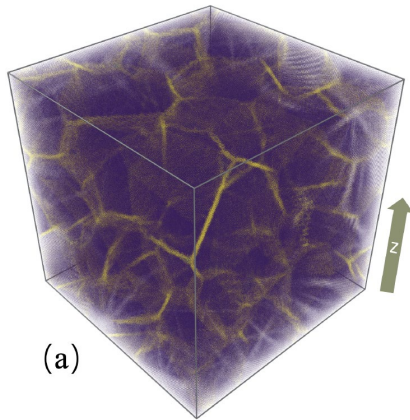
Peak performance of on Summit when using different embedding net size

- Better performance comes with bigger matrix size.
- DeePMD-kit can reach **1.1EFLOPS** with 1024x2048 matrix
- 32x64x128 is enough in terms of accuracy.

MgAlCu System, trained 800w steps				
embedding-net	fitting-net	number of systems	Energy L2err/Natoms	Force L2err
8-16-32	240-240-240	7430	5.909221e-03 eV	5.301006e-02 eV/A
16-32-64	240-240-240	7430	5.393266e-03 eV	5.162859e-02 eV/A
24-48-96	240-240-240	7430	5.272818e-03 eV	5.068834e-02 eV/A
32-64-128	240-240-240	7430	5.071967e-03 eV	5.085757e-02 eV/A

- Computation is bound by hardware FLOP/Byte ratio:
  - V100 GPU, FP-64:  $7\text{TFLOPS} \div 900\text{GB/s} = 7.8\text{FLOP/Byte}$
  - V100 GPU, FP-32:  $14\text{TFLOPS} \div 900\text{GB/s} = 15.5\text{FLOP/Byte}$
  - V100 GPU, HP-16:  $120\text{TFLOPS} \div 900\text{GB/s} = 133\text{FLOP/Byte}$
  - Fujitsu A64FX CPU:  $13.51\text{TFLOPS} \div 1024\text{GB/s} = 13.2\text{FLOP/Byte}$

# Application: nanocrystalline copper



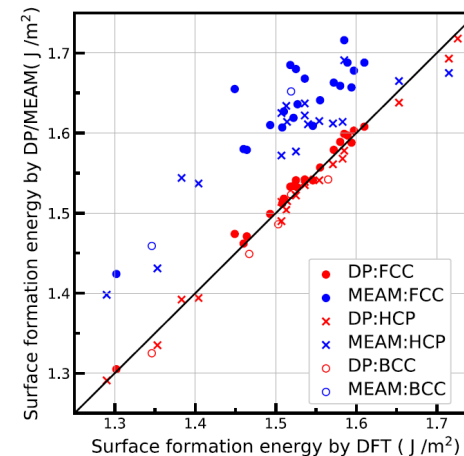
- The strength and hardness of metals can be enhanced by refining their grains into the nanometer scale [1][2]
- MD provides microscopic insights into the underlying mechanism

- A  $50 \times 50 \times 50 \text{ nm}^3$  cube with more than 10 million atoms
- 64 **randomly oriented** crystals with 15-nm averaged grain diameter
- Purple: copper atoms (face-centered-cubic structure);  
Yellow: grain boundaries

## Recent experimental works on nanocrystallines:

[1] Science **360**, 526-530 (2018). [2] Nature **545**, 80 (2017)

A DP model **with DFT accuracy** provides more accurate properties for copper than widely used empirical models (MEAM)

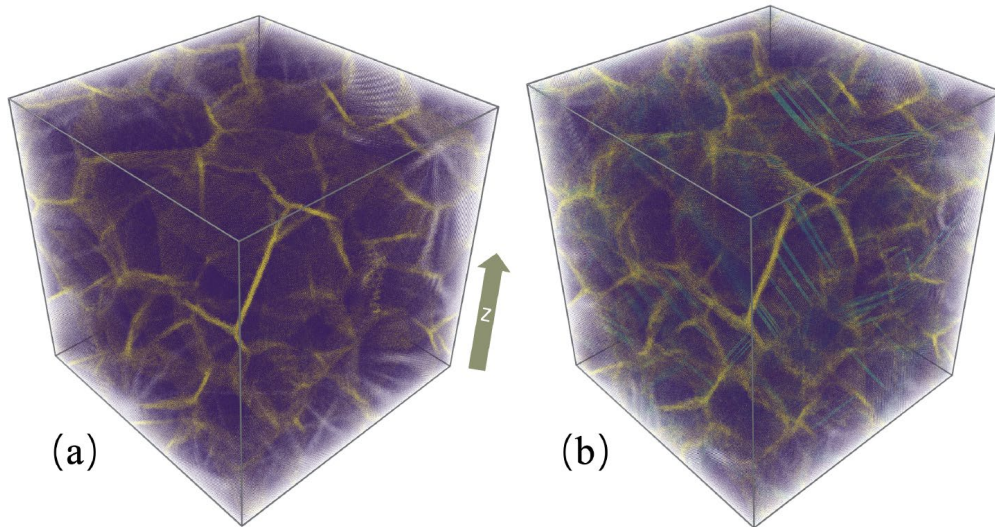


Methods	Stacking fault energy (mJ/m <sup>2</sup> )
EXP	41
DFT	38.08
DP	36(2)
MEAM	72.7

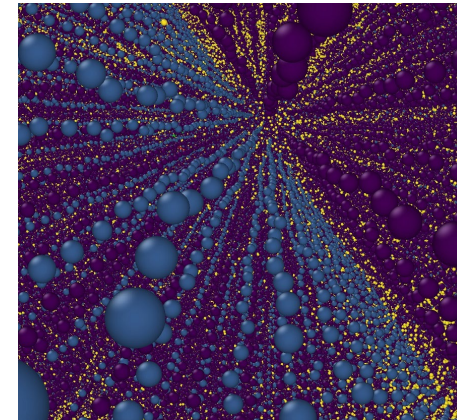
Comp. Phys. Comm. **253**, 107206 (2020)



# Application: nanocrystalline copper



Purple: copper atoms; Yellow: grain boundaries; Cyan: dislocations

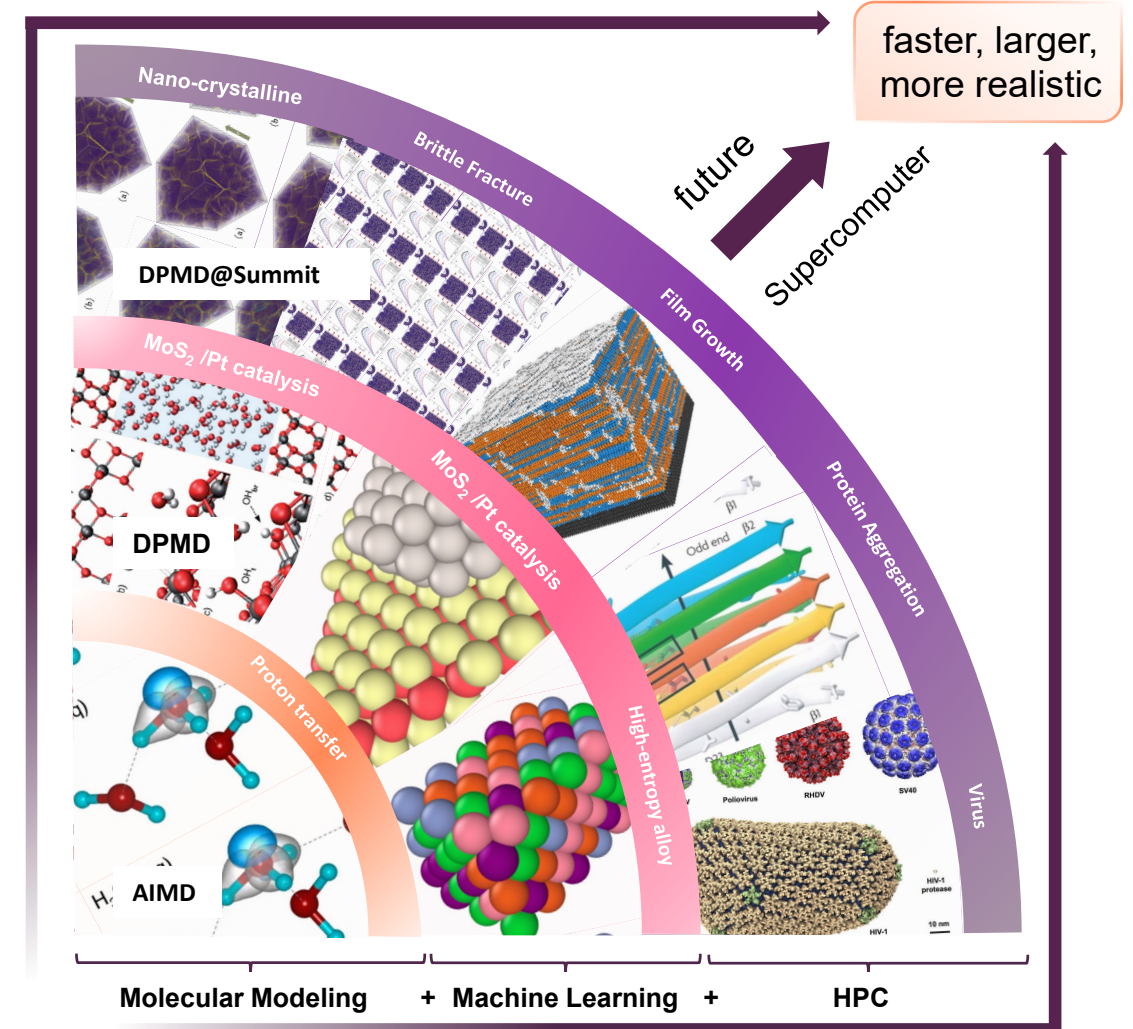


- DPMD simulates the **elongation** of the nanocrystalline copper along the **z** direction (deformation: 10%) to yield the strength of nanocrystalline
- DPMD parameters: 50,000 steps at 300 K with a time-step of 0.5 fs (strain rate of  $5 \times 10^8 \text{s}^{-1}$ ); NPT ensemble

The origins of strength in nanocrystalline is governed by the movements of grain boundaries and dislocations, which can be simulated and analyzed by DPMD.

# Conclusion

- **HPC + AI + Physical models: a new paradigm**
  - >1000x time-to-solution, >100x system size
  - on exa-scale machine: **billions** of atoms
  - Physics-based neural network design
  - AI-specific hardwares in HPC+AI applications
- **Applications**
  - **Materials:** alloy, battery, semiconductor, etc.
  - **Chemistry:** catalysis, combustion, etc.
  - **Biology:** drug design, protein folding, etc.
- **Hardware/Software co-design**
  - New demand from HPC + AI + Physics applications



# Acknowledgement



Lin-Wang Wang

Chao Yang

Jiduan Liu

Junqi Yin

Bronson Messer

**BAI**



**国家自然科学基金委员会**

National Natural Science Foundation of China

Thank you for your attention!