Deep Potential Molecular Dynamics on SUMMIT

Roberto Car Princeton University



OLCF User Meeting (June 22-24) Panel Discussion (June 22)

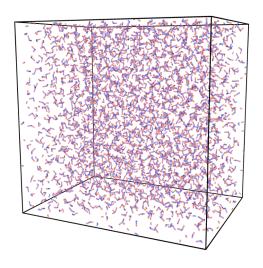




0

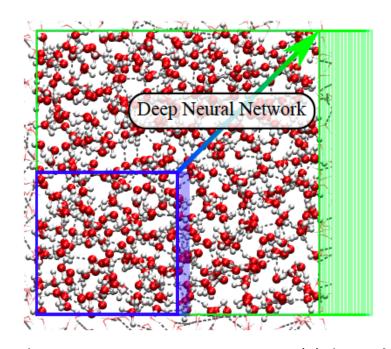
Molecular Dynamics, Ab-initio Molecular Dynamics, and Machine Learning

$$m_k \ddot{\boldsymbol{r}}_k = -\frac{\partial E(\boldsymbol{r}_1, \boldsymbol{r}_2, \boldsymbol{r}_3, \dots, \boldsymbol{r}_N)}{\partial \boldsymbol{r}_k}$$



- *Ab-initio* Molecular Dynamics (AIMD) is MD with forces derived on the fly from the quantum mechanical ground-state of the electrons.
- AIMD is more accurate than MD with empirical force fields (FF), it can describe chemical bond breaking/forming, but it is also much more costly.
- By learning the potential energy surface (PES) from quantum mechanics, Machine Learning (ML) methods make possible simulations of AIMD quality at FF cost.
- One such method, the deep potential (DP) method, uses deep neural networks to model the PES and other ground state properties accessible to AIMD. It was developed in the Ph D thesis of **Linfeng Zhang**, directed by **Weinan E** (Math Dept) and myself. Several other people contributed to the effort.

From AIMD to DPMD: overcoming size and time bottlenecks with Deep Neural Network (DNN) representations



Potential energy, polarization, and polarizability surfaces

$$O(r_1, r_2, r_3, ..., r_N) = \sum_i o_i$$
 $o_i = f(\{r_k \in \mathcal{N}_i\})$

f is a **symmetry preserving continuous and differentiable** function of the atomic coordinates in environments with variable numbers of atoms.

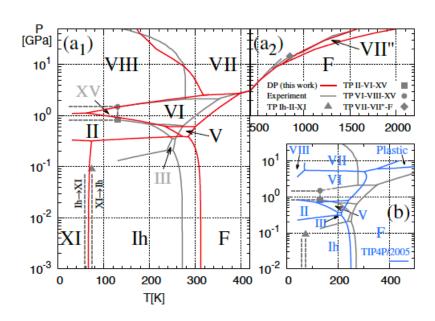
Distinctive features:

- Flexibility of DNN
- Learning on the fly (DP-GEN)
- Computational efficiency and HPC performance

The DP representation uses 2 DNN: (1) the **embedding network** needed to construct the **feature matrix**, which is a general descriptor of the environment, and (2) the actual **fitting network** for the physical property of interest

L. Zhang et al, Phys Rev Lett 120, 143001 (2018); L. Zhang et al., in Advances in Neural Information Processing Systems 31, 4441 (2018)

A DP model for water based on SCAN-DFT



10¹ (a) 10⁰ 10⁻¹ 10⁻² Ice VII -12.8 -12.6 -12.6 -12.8 -12.8 (b) from VII ..from Fluid 1000 1100 1200 1300 1400 1500 1600 1700 T [K] 1210 Enthalpy [eV/H₂O] Ice VII → Ice VII" 432 H₂O a weakly 1st order -12.5 13.9 transition 13.8 13.7 13.6 432 H₂O 13.5 3456 H₀O 1230 1250

< 35,000 DFT minimizations to construct the PES, i.e. 0.05 % of the total configurations visited with DP-GEN Free energy error is approx. 1 meV/mol

L. Zhang, H. Wang, R.C., W.E, Phys Rev Lett 126, 236001 (2021)

Pushing the limit of molecular dynamics with *ab initio* accuracy to 100 million atoms with machine learning

Weile Jia*, Han Wang[†], Mohan Chen[‡], Denghui Lu[‡], Lin Lin*¶, Roberto Car[∥], Weinan E[∥], Linfeng Zhang[∥] §

*University of California, Berkeley, Berkeley, USA

Email: jiaweile@berkeley.edu, linlin@math.berkeley.edu

† Laboratory of Computational Physics, Institute of Applied Physics and Computational Mathematics, Beijing, China Email: wang_han@iapcm.ac.cn

[‡]CAPT, HEDPS,College of Engineering, Peking University, Beijing, China

Email: mohanchen@pku.edu.cn, denghuilu@pku.edu.cn

¶Lawrence Berkeley National Laboratory, Berkeley, USA

Princeton University, Princeton, USA

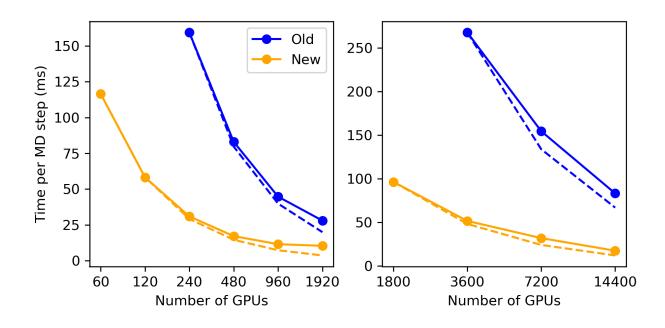
Email: rcar@princeton.edu, weinan@math.princeton.edu,linfengz@princeton.edu

2020 Gordon Bell Prize of the ACM at the SC20 Conference

Performance of Deep Potential Molecular Dynamics (DPMD) on Summit against other MD methods with *ab-initio* (DFT) accuracy

Work	Year	Pot.	System	#atoms	#CPU cores	#GPUs	Machine	Peak[FLOPS]	TtS [s/step/atom]
Qbox [12]	2006	DFT	Mo	1K	262K	_	BlueGene/L	207T	2.8×10^{-1}
LS3DF [14]	2008	LS-DFT	ZnTeO	16K	131K	_	BlueGene/P	108T	1.8×10^{-2}
RSDFT [46]	2011	DFT	Si	107K	442K	_	K-computer	3.1P	2.6×10^{0}
DFT-FE [13]	2019	DFT	Mg	11K	159K	22.8K	Summit	46P	6.5×10^{-2}
CONQUEST [17]	2020	LS-DFT	Si	1M	200K	_	K-computer	?	4.0×10^{-3}
Simple-NN [47]*	2019	BP	SiO_2	14K	80	_	Unknown‡	?	3.6×10^{-5}
Singraber el.al. [48]*	2019	BP	H_2O	9K	512	_	VSC†	?	1.3×10^{-6}
Baseline [45]**	2018	DP	H_2O	25K	1	1	Summit	_	5.6×10^{-5}
This work (double)	2020	DP	H ₂ O	679M	27.3K	27.3K	Summit	80P	3.0×10^{-10}
This work (mixed-half)	2020	DP	H_2O	679M	27.3K	27.3K	Summit	212P	1.1×10^{-10}
This work (double)	2020	DP	Cu	127M	27.3K	27.3K	Summit	91P	8.1×10^{-10}
This work (mixed-half)	2020	DP	Cu	127M	27.3K	27.3K	Summit	275P	2.7×10^{-10}

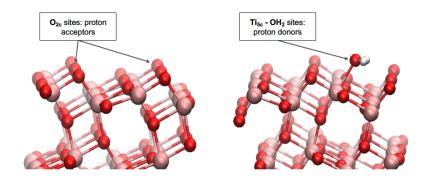
A further optimization: compressed DPMD



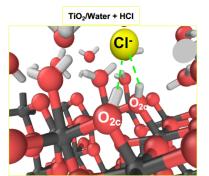
Strong scaling on Summit using new (compressed) and old (non-compressed) DPMD code. Continuous and dashed lines represent the actual and ideal scaling, respectively. Left: 3 million atoms system (900,000 water molecules and 300,000 TiO₂ atoms). Right: 68 million atoms ($^{20.6}$ million water molecules and 6 million TiO2 atoms).

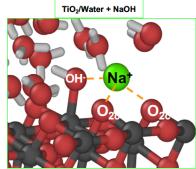
Acidic and basic electrolytic solutions in contact with TiO₂

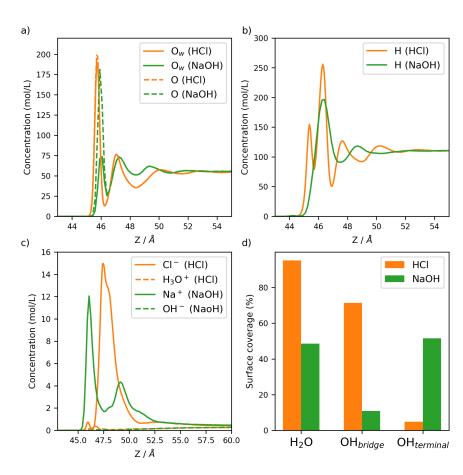
Acid/base sites on the TiO₂ anatase (101) surface



Ion solvation at the TiO₂/Water interface

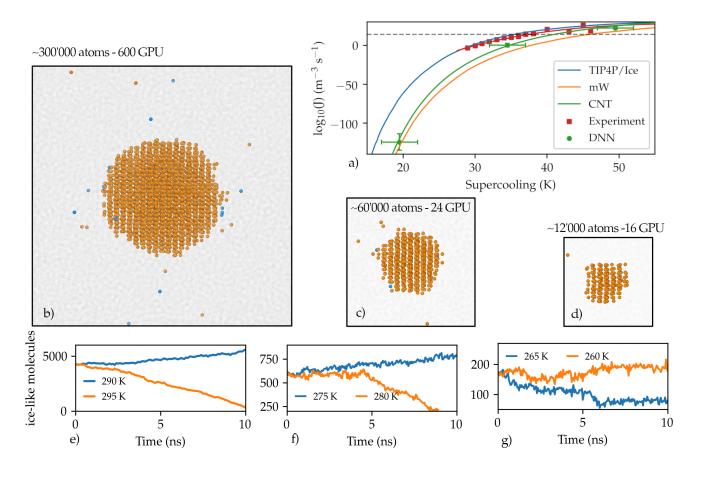


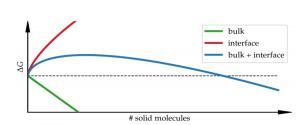




From M. Calegari Andrade et al., (2021)

Homogeneous ice nucleation with the seeding technique





$$\Delta G = \frac{4}{3}\pi R^3 \rho_s \Delta \mu + 4\pi R^2 \gamma$$

$$J = \rho_f Z f^+ \exp(-\Delta G_c / (k_B T)),$$

Homogeneous nucleation limit: 40-41 K (predicted from simulation) 38 K (experiment)

From P. Piaggi et al., (2021)

Conclusions and Outlook

- Long term goals in the two studies that were mentioned: (a) model charge distribution in electrolyte in contact with reactive interface under applied bias; (b) model heterogeneous nucleation (e.g. ice nucleation in the atmosphere)
- New algorithmic implementation/optimization will be necessary
- Properties that were previously out of reach become accessible to firstprinciples calculations, providing a new test ground for quantum mechanical approximations (e.g. DFT)

Acknowledgements

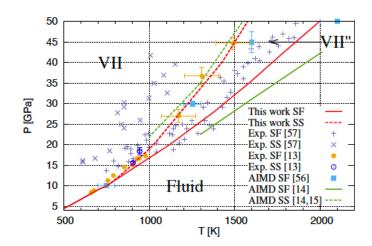




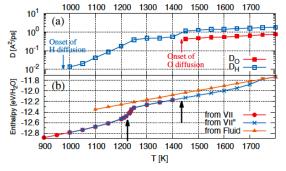
http://chemlabs.princeton.edu/ccsc/

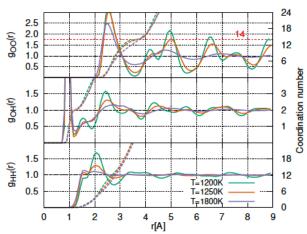
Temperature induced molecular to ionic transition at high

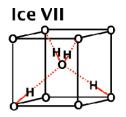
pressure



Melting of ice VII is a 2 step process







Strong covalent fluctuations persist in spite of ice rule breaking Ionic defect (hydronium – hydroxide like) population is approx. 11 % in the fluid at 1450 K