



Full Length Article

TeaNet: Universal neural network interatomic potential inspired by iterative electronic relaxations

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ABSTRACT

A universal interatomic potential for an arbitrary set of chemical elements is urgently needed in computational materials science. Graph convolution neural network (GCN) has rich expressive power, but previously was mainly employed to transport scalars and vectors, not rank ≥ 2 tensors. As classic interatomic potentials were inspired by tight-binding electronic relaxation framework, we want to represent this iterative propagation of rank ≥ 2 tensor information by GCN. Here we propose an architecture called the tensor embedded atom network (TeaNet) where angular interaction is translated into graph convolution through the incorporation of Euclidean tensors, vectors and scalars. By applying the residual network (ResNet) architecture and training with recurrent GCN weights initialization, a much deeper (16 layers) GCN was constructed, whose flow is similar to an iterative electronic relaxation. Our training dataset is generated by density functional theory calculation of mostly chemically and structurally randomized configurations. We demonstrate that arbitrary structures and reactions involving the first 18 elements on the periodic table (H to Ar) can be realized satisfactorily by TeaNet, including C–H molecular structures, metals, amorphous SiO₂, and water, showing surprisingly good performance (energy mean absolute error 19 meV/atom) and robustness for arbitrary chemistries involving elements from H to Ar.

1. Introduction

A universal interatomic potential for atomistic simulations of arbitrary chemical species, structures, transformations and reactions would considerably extend the reach of computational materials. While historically we have used simple analytical expressions [1–3], machine learning (ML) interatomic potentials [4–9] are increasingly invoked to parametrize interatomic interactions.

Deep neural networks (DNN) have proved to be successful in various ML tasks when large datasets are provided. The convolution operation, where identical set of weights are used for nodes “belonging” to different spatial locations, achieves efficient compression. The convolutional weight depends on the relative distance, and not the absolute positions (“translational invariance”). This idea of parametrizing interactions by spatial relationships can be generalized to graphs. The field of graph convolution-based neural networks (GCN) has been expanding rapidly [10–12], in particular for molecular systems, where atoms and bonds are represented by the nodes and edges of the graph. Such network architectures appear natural to both atomistic and electronic-structure modelers. Indeed, as all the atoms/ions of the same chemical

type/valence state and isotopic mass are “indistinguishable particles” in quantum mechanics, the GCN weights assigned to atoms/bonds of the same chemical type(s) but different integer labels i or j , where $i, j = 1, 2, \dots, N$ is the (arbitrarily) assigned index of an atom in the simulation, should obviously also be identical (“permutational invariance”). However, sometimes, there can be a “minus sign” issue. Such “minus sign” can show up in some bond-centered quantities, e.g. if $\mathbf{x}_{ij} \equiv \mathbf{x}_i - \mathbf{x}_j$, then $\mathbf{x}_{ij} = -\mathbf{x}_{ji}$, and how to store certain “bond-centered” quantities thus necessitates the usage of notation $[ij]$ where the order of i, j in the bracket matters, unlike $r_{ij} \equiv |\mathbf{x}_{ij}|$ where the order of i, j does not matter, for which we use the notation (ij) . So we use notation $\mathbf{x}^{[ij]} \equiv \mathbf{x}_{ij}$ to denote a vector that belongs to directed edge labeled by $[ij]$, and $r^{(ij)} \equiv r_{ij}$ to denote a scalar that belongs to undirected edge labeled by (ij) , for “bond-centered” quantities, that can be scalar (rank-0 tensor), vector (rank-1 tensor), matrix (rank-2 tensor), etc. Note in this paper we take “bond” to mean i, j pair relations where $r^{(ij)}$ can nanometers, and not necessarily the so-called first nearest neighbors.

While GCN architecture exploiting translational and permutational invariances remove the dependence on an arbitrary observation-frame

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origin and an arbitrary atomic indexing scheme, how “rotational invariance”, that is, how arbitrary observation-frame orientations affect or not affect certain results, needs to be discussed. In any atomistic calculation of the stress tensor, heat flux vector, etc. based on for instance the Tersoff potential [13], or in assembling the electronic overlap integral and Hamiltonian matrix in the tight-binding/linear combination of atomic orbitals (LCAO) model [14], one has plenty of scalars (rank 0), vectors (rank 1) and matrices (rank 2) in the data flow of a code. In an iterative electronic relaxation or explicit time-dependent density functional theory (TDDFT) [15] calculation, this kind of tensorial data flow can sometime even carry into the (pseudo)time-domain. In all these calculations, the observation-frame orientation does not really matter, as all physical quantities are expressed in rank- M tensors $\tilde{T}_{\alpha_1, \alpha_2, \dots, \alpha_M}$, with tensor transformation law

$$\tilde{T}_{\alpha'_1, \alpha'_2, \dots, \alpha'_M} = Q_{\alpha'_1 \alpha_1} Q_{\alpha'_2 \alpha_2} \dots Q_{\alpha'_M \alpha_M} T_{\alpha_1, \alpha_2, \dots, \alpha_M} \quad (1)$$

where \tilde{T} is the same physical object read in a different observation frame, $Q_{\alpha' \alpha}$ is the rotation matrix between two observation frames, and Einstein summation rule is used. In this paper we use $\alpha, \beta = 1, 2, 3$ to label Cartesian axes, and $i, j, k = 1, 2, \dots, N$ to label atoms. Thus, $T_{\alpha}^{[ij]}$ denotes a rank-1 tensor (vector) that belongs to a bond, or pair of atoms $[ij]$, where the order matters (directed edge), and $T_{\alpha\beta}^{(ij)}$ is a rank-2 tensor (matrix) that belongs to the bond or pair of atoms (ij) where the order does not matter. Similarly, T_{α}^i is a rank-1 tensor (vector) that belongs to the atom i , and $T_{\alpha\beta}^i$ is a rank-2 tensor (matrix) that belongs to the atom i . One could certainly come up with more complex notations like $T_{\alpha\beta}^{(ijk)}$

where the permutation orders of i, j, k does not matter, or something like $T_{\alpha\beta\gamma\delta}^{(ij)(kl)}$ where i, j order does not matter, k, l order does not matter, but (ij) and (kl) order matters. Generally speaking, in this notation the superscript denotes the “owner” of the tensor whose Cartesian indices are in the subscript. In this paper we will only be limited to $M \leq 2$, and owners either $i, (ij)$, or $[ij]$, as these covers the data types of most of the legacy codes. One can thus imagine these kinds of “tensor-typed” and “ownership-stamped” data flowing in respective legacy codes to represent interatomic or electronic-structure interactions.

In addition to the stable molecular structures, currently several GCN models have also succeeded in reproducing the dynamics of specific molecules [6,7,16–18]. However, a universal IP describing bond formation, bond breaking and recombination for arbitrary structures with arbitrary number of elements remains at the developmental stage. Inspired by the nonlinear iterative data flows in a DFT calculation in achieving charge-density convergence, we believe the performance of GCN can be significantly improved by allowing $M \geq 2$ quantities (“tensors” in “tensor embedded atom network (TeaNet)”) to flow in the network, in addition to the $M = 0$ (scalars) and occasional $M = 1$ (vectors) quantities that flow in conventional GCN.

Physically, embedded atom method (EAM) potential incorporates the concept of electron density of metal, while Tersoff-type and modified embedded atom method (MEAM) potentials incorporate the concept of bond order and angular dependence, which can be derived from the tight-binding approximation of the electronic wave function, using local combination of (quasi)atomic orbitals [14]. These IPs have been widely used for simulating extended defects, mechanical deformation and damage, and phase transitions. However, individual potential parameter set is developed to reproduce a certain systems (e.g. FCC metals, silica, organic molecules, etc.). In this paper, we propose a NNIP architecture (see Section 2) that can be considered a superset of MEAM potentials while mimicking electronic total-energy relaxation [19] in a local orbital (tight-binding) basis [14,20,21]. We call this approach the tensor embedded atom network (TeaNet). We modify the architecture of GCN with new components (edge-associated in addition to node-associated variables) that fully represent the corresponding physics-based IP. Rank-2 tensors as well as rank-1 vectors are introduced in the network, so the model can naturally represent propagation of orientation-dependent Hamiltonian information. We have

also adopted residual NN architecture, with recurrent parameter model initially. Such ResNet architecture and recurrent GCN initialization to accelerate computations are found to be quite effective in getting rapid reduction of training error.

Our method is related to previous NNIP efforts. Embedded Atom Neural Network Potential (EANN) [18] extends the EAM potential using NN. This model combines physics-based representation (electron density) and NN-based embedding function $F(\rho)$. This physics-related model provides excellent accuracy for bulk systems while retaining simplicity. There are several works implementing geometric information into NN architecture [22–26]. Among them, spherical harmonics-based models have been actively proposed and applied to the atomistic simulations [22,23,27,28]. One of the key idea is to use Clebsch–Gordan coefficients to hold invariances by any rotations in SO(3) group. In addition, the idea and the theoretical study of using tensor values in the interatomic potential was investigated in Moment Tensor Potentials (MTP) [29]. Although the aim is similar to our model, the geometric information is represented in different ways. Further discussion of the schematic difference and numerical experiences are written in Appendix A.3.

In Section 4, we show the training results of our model for elements 1–18 (H–Ar) on the periodic table, where random combination of these elements in mostly highly disordered structures are used as the training set. We also performed sensitivity analysis and discussed the importance of the different features of our model. In Section 5, we show the general applicability of our method to a wide range of materials including chemical reaction processes. We will demonstrate that our model performs well for liquid water, amorphous silica as well as simple metals and hydrocarbons.

2. TeaNet architecture

The overview of the TeaNet is shown in Fig. 1. We first introduce the notation used in our drawings. In the line-drawing figures, values are illustrated as circles. The filled colors corresponds to the types of the values, where scalar, vector, and tensor are illustrated as gray, light blue, and blue circles, respectively. Operations are illustrated as rectangles. Here, we write the linear layer as $\text{linear}(x)$, the nonlinear activation layer as $\text{activation}(x)$, the concatenation function as $\text{concat}(x, y, \dots)$, vector L2-norm as $\text{norm}(x)$, and the cutoff function as $\text{cutoff}(x)$. We use subscript to denote the dimension of stacked variables, for example s_{128} means 128 scalars, v_{32} means 32 vectors (total 48 real numbers), and t_{16} means 16 matrices, each 3×3 . The 128, 32, and 16 are called number of channels. $\text{linear}(x)$ is always applied channel by channel. It is noted that each $\text{linear}(x)$ appeared in the following equations has different parameters. It is also noted that those parameters are learnable network parameters like in ordinary neural networks.

While the output of TeaNet is the total energy of the system (a scalar), the network is trained to simultaneously compute the atomic forces, providing useful data for training. The atomic forces are calculated by a backpropagation process, and so the training process becomes a double backpropagation. The molecular dynamics simulation requires a smooth activation function. In this study, we employed the integral of the softplus function, which to our knowledge we were first to propose as an activation function. The integral is calculated as follows:

$$\begin{aligned} f(x) &\equiv \int_{-\infty}^x \log(1 + \exp(t)) dt \\ &= -\text{Li}_2(-\exp(x)), \end{aligned} \quad (2)$$

where Li_2 is a second-order polylogarithm function. This function approaches 0 as x tends to $-\infty$ and approaches the curve of $x^2 + C$ at large x , where C is a constant. Using the activation function, we can train a softplus-type network in the second backpropagation process. The comparison of the second derivative of activation functions is shown in Fig. 2. The effect of this change to the prediction accuracy is presented

Overview

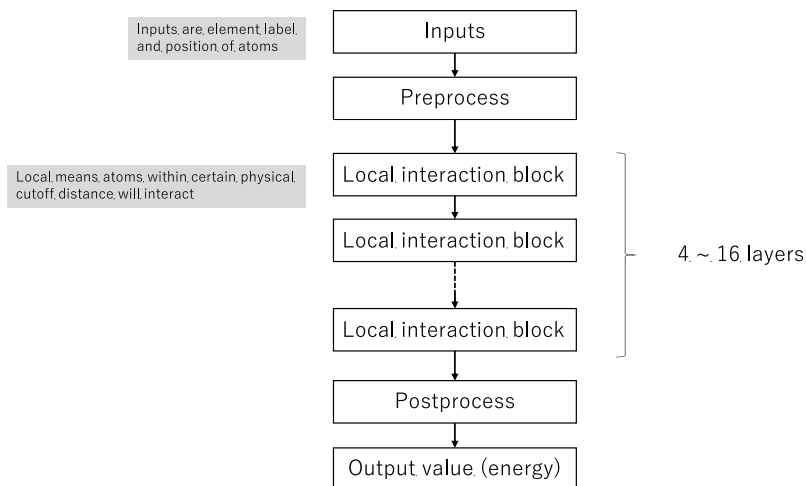


Fig. 1. Overview of the TeaNet NNIP.

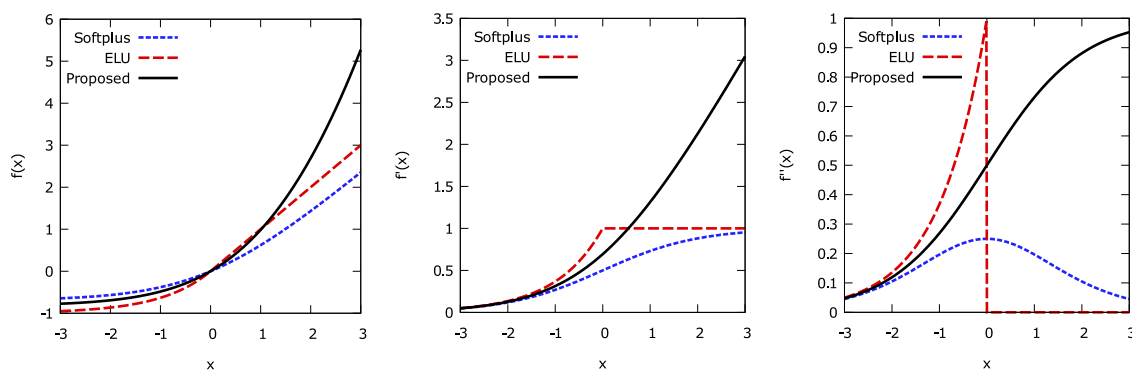


Fig. 2. Left: comparison of activation functions. Softplus and ELU ($\alpha = 1$) functions [30] are also shown. They are shifted so that $f(0)$ becomes 0. Middle: derivative of the activation functions. Right: second derivative of activation functions. In softplus and ELU, second gradient value $f''(x)$ vanishes when x is large.

in Section 4. In addition, when this function is applied to the edge arrays, the activation functions are shifted so that $f(0)$ becomes 0. Thus

$$\text{activation}(x) \equiv f(x) - f(0). \quad (3)$$

The cutoff function $\text{cutoff}(x)$ is a smoothly decaying function. In this work, we use the same function as $\text{activation}(x)$ shifted by linear function,

$$\text{cutoff}(x) \equiv \text{activation}(\text{linear}(x)) + (c_1 x + c_0) \quad (4)$$

where c_0 and c_1 (linear function part) are set to satisfy $\text{cutoff}(x)$ and its derivative are zero when x equals to the cutoff distance.

In TeaNet architecture, the inputs are the list of element label and the list of position of atom. Other predefined information such as bonding or atomic charges are not required. The output value is single scalar value, which corresponds to the energy. The force of the atoms are calculated using normal back propagation. There are three parts in TeaNet. The first part is preprocess. It receives the input values and creates various values which is used for the graph convolution layers. The second part is the internal graph convolution layers which we call local interaction block. The input values and output values of the single layer have the same shapes. Therefore we can stack the layers by arbitrary numbers. The last part is postprocess part, which receives the output values of the graph convolution layer and output single scalar value.

2.1. Preprocess and postprocessing

2.1.1. Preprocessing

Here, we use the character a as atom-related values (corresponding nodes) and b as bond-related values (corresponding bonds).

Bonds are counted only for pair of atoms whose distance is smaller than the cutoff distance. In this paper, the cutoff distance is set to be 6 Å.

There are three types of values for atom-related values which are scalar, vector, and rank-2 tensor. We use the symbols a_s , a_v , and a_t for them. It is noted that each types of values have multiple channels. For example, in this paper, we use 256 dimensions (usually called channels in neural network context) for scalar value and 16 dimensions for both vector and rank-2 tensor value. Therefore, if the number of atoms in the system is 64 and the number of dimension of the space is 3, the shapes of a_s , a_v , and a_t are 64×128 , $64 \times 3 \times 16$, and $64 \times 3 \times 3 \times 16$, respectively (see Fig. 3).

Bonds have scalar and vector values. We use the symbols b_s , b_v as well. In addition, two special constant values for bond-related values are also introduced. One is relative position vector r_v . It is defined by the difference of the position of two corresponding atoms. Another one is bond length r_s , which can be calculated by the l2-norm of r_v . It should be noted that the sign of r_v depends on the order of corresponding two atoms, which is described as “minus sign” issue at the introduction section. Careful consideration is required to use r_v in the following

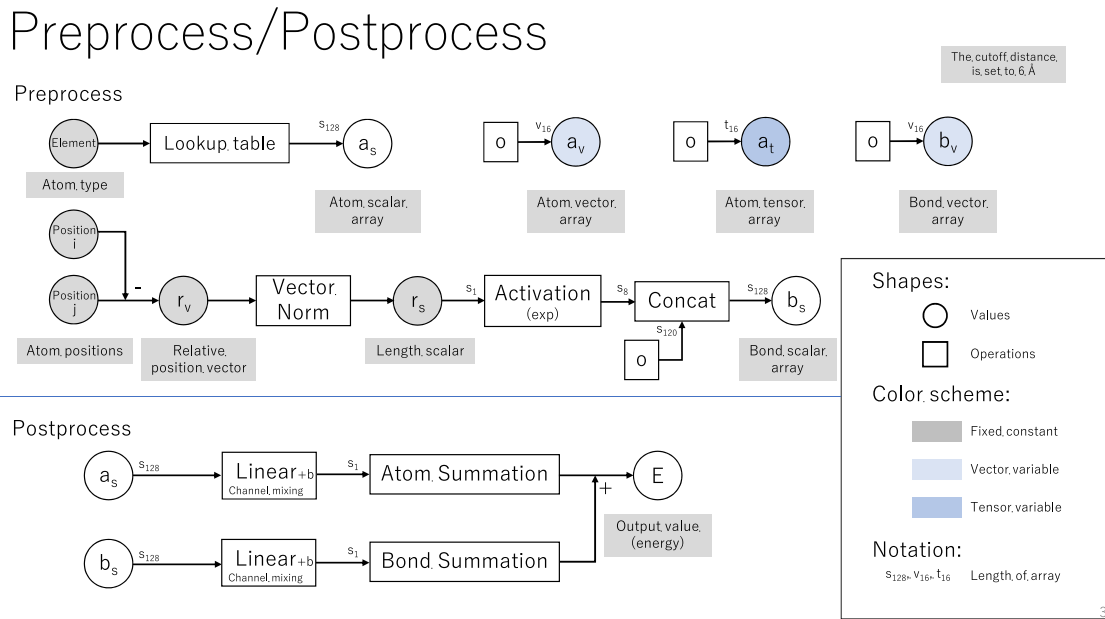


Fig. 3. Preprocess and postprocessing.

Table 1
List of the input values of \mathbf{n}_s .

Element	\mathbf{n}_s
H	[0.5, 0, 0, 0, 0, 0, 0, 0, 0, 0]
He	[1, 0, 0, 0, 0, 0, 0, 0, 0, 0]
Li	[1, 0.5, 0, 0, 0, 0, 0, 0, 0, 0]
Be	[1, 1, 0, 0, 0, 0, 0, 0, 0, 0]
B	[1, 1, 0.5, 0, 0, 0, 0, 0, 0, 0]
C	[1, 1, 1, 0, 0, 0, 0, 0, 0, 0]
N	[1, 1, 1, 0.5, 0, 0, 0, 0, 0, 0]
O	[1, 1, 1, 1, 0, 0, 0, 0, 0, 0]
F	[1, 1, 1, 1, 0.5, 0, 0, 0, 0, 0]
Ne	[1, 1, 1, 1, 1, 0, 0, 0, 0, 0]
Na	[1, 1, 1, 1, 1, 0.5, 0, 0, 0, 0]
Mg	[1, 1, 1, 1, 1, 1, 0, 0, 0, 0]
Al	[1, 1, 1, 1, 1, 1, 0.5, 0, 0, 0]
Si	[1, 1, 1, 1, 1, 1, 1, 0, 0, 0]
P	[1, 1, 1, 1, 1, 1, 1, 0.5, 0, 0]
S	[1, 1, 1, 1, 1, 1, 1, 1, 0, 0]
Cl	[1, 1, 1, 1, 1, 1, 1, 1, 0.5, 0]
Ar	[1, 1, 1, 1, 1, 1, 1, 1, 1, 1]

calculations since the output value should not depend on the order of atoms. We use the character i and j for the label of those two atoms.

Atom scalar a_s is initialized by look-up table. To imitate the occupancy of electron orbitals, the values corresponding to the atomic number are divided by 2 and packed by 1 from the top of the array. The list is shown in Table 1. The remaining channels are set to zero. Atom vector a_v and rank-2 tensor a_t are initialized by zero.

Bond scalar b_s are initialized by Eq. (5),

$$b_s = \exp\{-\text{linear}(r_s)\} + (c'_1 r_s + c'_0), \quad (5)$$

where c'_0 and c'_1 (linear function part) are set to satisfy b_s and its derivative with respect to r_s are zero when r_s equals to the cutoff distance. Eq. (5) is expected to behave like the distance term of the Morse-style IP.

Bond vector b_v is also initialized by zero. Unlike r_v , we make b_v does not depend on the order of atom i and j . The example of physical value corresponding b_v is local electric dipole.

To reiterate, in the preprocess part, a_s , a_v , a_t , b_s , b_v , r_s , and r_v are initialized.

2.1.2. Postprocessing

For the postprocessing part, only a_s and b_s are used to calculate energy. It is noted that a_s and b_s have multiple channels (multiple scalar values for single atom and single bond). First, single scalar values for each atom and bond are calculated by,

$$a_{\text{last}} = \text{linear}(a_s), \quad b_{\text{last}} = \text{linear}(b_s), \quad (6)$$

where the number of channels of a_{last} and b_{last} are one.

Then, a_{last} and b_{last} are summed along all atoms and bonds. The obtained single scalar value is the output value (total energy E) of this model.

$$E = \sum_{\text{atoms}} a_{\text{last}} + \sum_{\text{bonds}} b_{\text{last}}. \quad (7)$$

2.2. Local interaction block: overview

This section shows the overview of the calculation flow of local interaction block. The detail of each calculation block will be described in the later sections.

First, several operations are applied to the atom-wise inputs (a_s , a_v , a_t) and the bond-wise inputs (b_s , b_v). Those newly created values during the local interaction block are named a_{s1} or a_{v1} .

Then, atom-wise values are distributed to the corresponding bonds. It is noted that there are always two atom-wise values for single bond. Those distributed values are concatenated with bond-wise values with keeping required invariances. The bond shape values (r_s , r_v) are also used here. Then, the new bond-wise value named y_{tot} is created using those values (see Fig. 4).

After that, new atom-wise variables and bond-wise variables are created using y_{tot} . Those values are added to the atom input values and bond input values. Finally, the same shapes of values as the input values (a_s , a_v , a_t , b_s , b_v) are returned.

2.3. Local interaction block: preprocessing

As described before, the local interaction block receives a_s , a_v , a_t , b_s , and b_v as inputs. First, several linear and nonlinear functions are

In the middle: Local interaction block

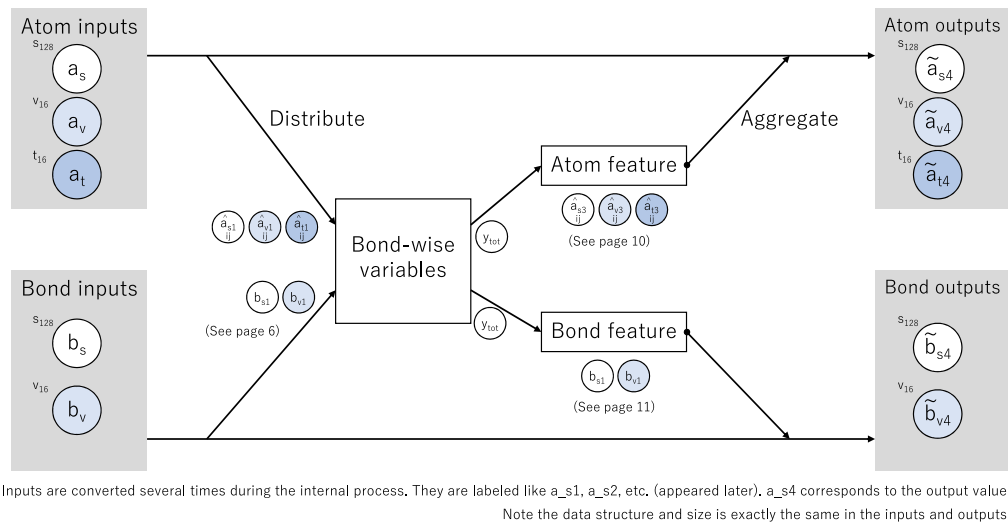


Fig. 4. Local interaction block: overview.

Within local interaction block: Preprocess

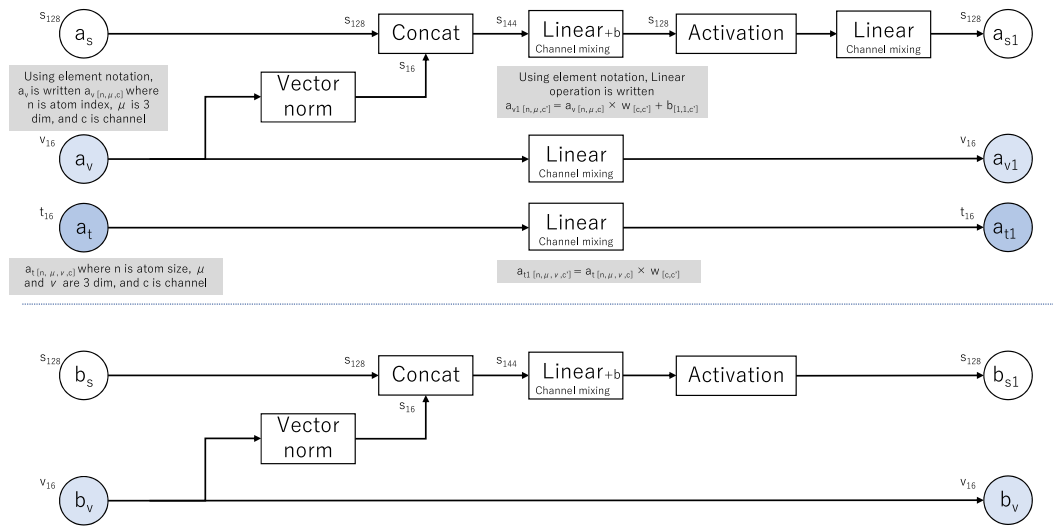


Fig. 5. Local interaction block: preprocessing.

applied for each values.

$$\begin{aligned}
 a_{s1} &= \text{linear}(\text{activation}(\text{linear}(\text{concat}(a_s, \text{norm}(a_v))))), \\
 a_{v1} &= \text{linear}(a_v), \\
 a_{t1} &= \text{linear}(a_t), \\
 b_{s1} &= \text{activation}(\text{linear}(\text{concat}(b_s, \text{norm}(b_v)))).
 \end{aligned}
 \tag{8}$$

Here, concat means the values are concatenated along the channel axis (see Fig. 5).

For linear channel mixing, the linear operation is not applied along the space dimension axis but along the channel axis. It is noted that the raw components of vector and tensor values should not be summed, multiplied independently, or combined with other scalar values since those components depend on the basis vectors of the coordination system. On the other hand, linear function along channel axis, scalar multiplication, inner product (including vector norm), and tensor product are allowed operations.

In this paper, vector norm means the L2-norm of vector along dimension axis. The result values can be treated as the scalar values.

2.4. Local interaction block: distribution

The atom-wise variables a_{s1} , a_{v1} , and a_{t1} are distributed to the corresponding bonds. It is noted that there are always two atom-wise values for single bond. We labeled them by i and j as described before (see Fig. 6).

To clarify that the distributed values corresponds to the bonds, we name the distributed atom-type values as β_{s1} , β_{v1} , and β_{t1} . Since there are two corresponding atoms (i and j) for single bond, there are two β values such as β_{s1i} and β_{s1j} . We write $\beta_{s1\{i,j\}}$ when the same operations are applied along i and j .

We now have $\beta_{s1\{i,j\}}$, $\beta_{v1\{i,j\}}$, $\beta_{t1\{i,j\}}$, b_{s1} , and b_v . Independently, we have r_s and r_v . All of those values are bond-wise values.

Distribute atom values to corresponding bonds

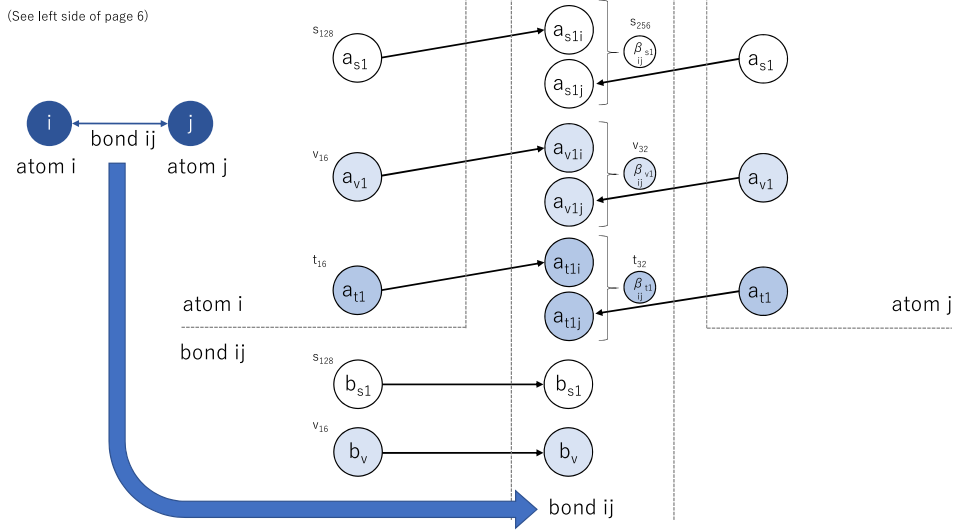


Fig. 6. Local interaction block: distribution.

Create various bond-wise variables (preparation)

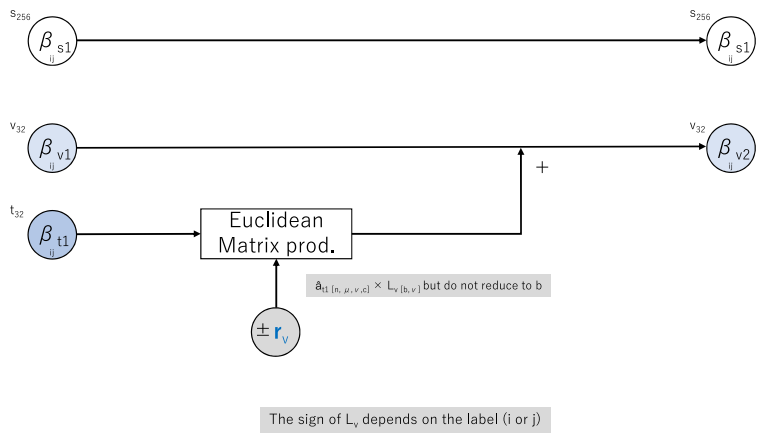


Fig. 7. Create bond-wise values: preparation.

2.5. Create bond-wise values: preparation

Tensor value $\beta_{t1\{i,j\}}$ is squashed into vector values by taking inner product with r_v , and then summed to $\beta_{v1\{i,j\}}$.

$$\beta_{v2\{i,j\}} = \beta_{v1\{i,j\}} \pm_{ij} \beta_{t1\{i,j\}} \cdot r_v. \tag{9}$$

It is noted that the sign of r_v depends on the order of the atomic label (i or j). Therefore, to keep the $i - j$ order invariance, the sign should be flipped when the operation is applied to j -related values. We use the symbol \pm_{ij} for that case. In the figure, the $i - j$ order sensitive values are highlighted as blue characters and lines (see Fig. 7).

2.6. Create bond-wise values: create various intermediate values

Various bond-type scalar values are calculated by taking the inner products of vector values.

$$\begin{aligned} x_{0\{i,j\}} &= \beta_{s\{i,j\}} \text{cutoff}(r_s), \\ x_{1\{i,j\}} &= \pm_{ij} \beta_{v2\{i,j\}} \cdot r_v \text{cutoff}(r_s), \\ x_{2\{i,j\}} &= \beta_{v2\{i,j\}} \cdot b_v, \\ x_3 &= \beta_{v2i} \cdot \beta_{v2j} \text{cutoff}(r_s). \end{aligned} \tag{10}$$

It is noted that \pm_{ij} is used for r_v part again. The cutoff function $\text{cutoff}(r_s)$ is multiplied for $x_{0\{i,j\}}$, $x_{1\{i,j\}}$, and x_3 to ensure that all values are zero when the bond distance equals to the cutoff distance. It does

Create various bond-wise scalar variables

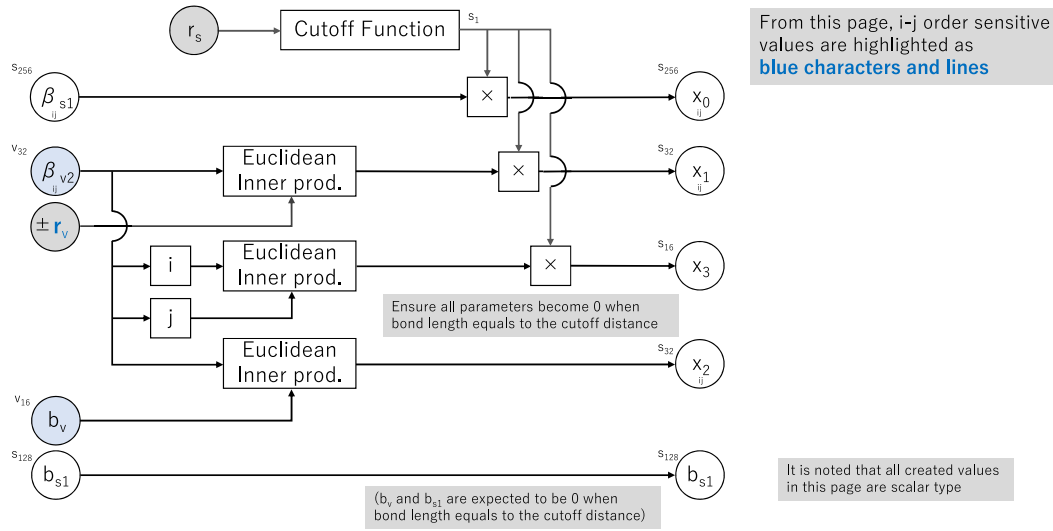


Fig. 8. Create bond-wise values: create various intermediate values.

Concat/Activation (holding bond direction invariance)

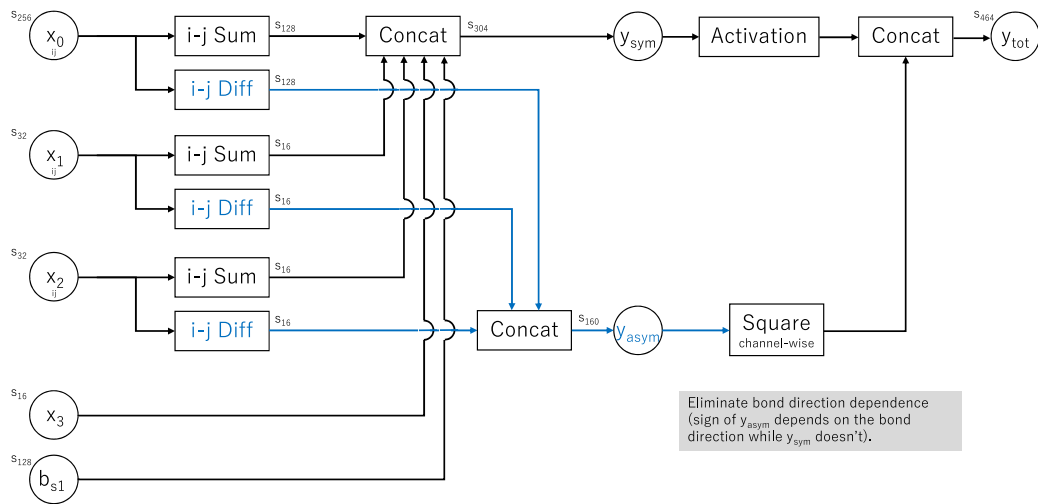


Fig. 9. Create bond-wise values: concatenation.

not be applied to $x_{2\{i,j\}}$ since bond-related value b_v is assumed to have the same nature (see Fig. 8).

2.7. Create bond-wise values: concatenation

The goal of this section is to create the unified bond-wise value y_{tot} from the previously created values. The obtained scalar values are $x_{0\{i,j\}}$, $x_{1\{i,j\}}$, $x_{2\{i,j\}}$, x_3 , and b_{s1} .

The thing left to be done is to eliminate $i - j$ order dependence. It is noted that the values of $x_{0\{i,j\}}$ swap if we swap atom i and j . In this architecture, we first calculate the summation and difference ($x_{0i} + x_{0j}$ and $x_{0i} - x_{0j}$). The former one does not have order dependence and the latter one has order dependence only on its sign. Therefore, applying the even function for the latter one removes the order dependence. Here, we use the square function. The same treatment is carried out

for $x_{1\{i,j\}}$ and $x_{2\{i,j\}}$.

$$\begin{aligned} y_{sym} &= \text{linear}(\text{concat}(x_{0i} + x_{0j}, x_{1i} + x_{1j}, x_{2i} + x_{2j}, x_3, e_{s1})), \\ y_{asym} &= \text{linear}(\text{concat}(x_{0i} - x_{0j}, x_{1i} - x_{1j}, x_{2i} - x_{2j})), \\ y_{tot} &= \text{activation}(y_{sym}) + (y_{asym})^2, \end{aligned} \quad (11)$$

where $(y_{asym})^2$ means element-by-element square. y_{tot} is considered to represent the state of the bond (see Fig. 9).

In the figure, we highlighted the order-sensitive calculation flow as blue characters and lines.

2.8. Local interaction block: create atomic values for update

Using y_{tot} , various values which will be accumulated to atom-wise values and bond-wise values are created. Atom-type variables are

Create atom features

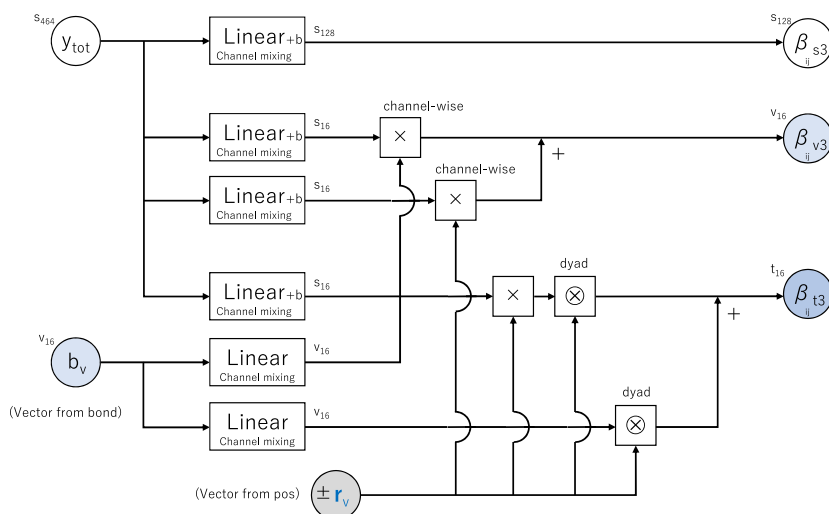


Fig. 10. Local interaction block: create atomic values for update.

Create bond features

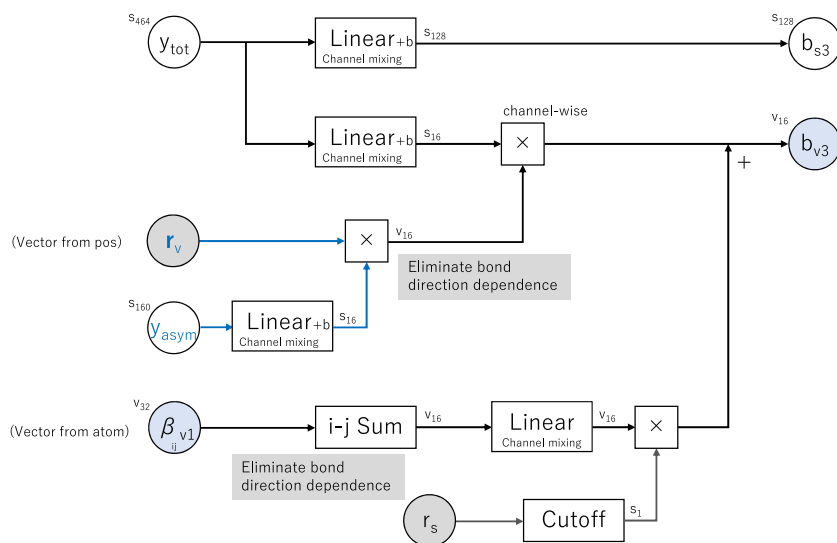


Fig. 11. Local interaction block: create bond values for update.

calculated by (see Fig. 10),

$$\begin{aligned} \beta_{s3\{i,j\}} &= \text{linear}(y_{tot}), \\ \beta_{v3\{i,j\}} &= \text{linear}(y_{tot})\text{linear}(b_v) \pm_{ij} \text{linear}(y_{tot})r_v, \\ \beta_{t3\{i,j\}} &= \text{linear}(y_{tot})r_v \otimes r_v \pm_{ij} \text{linear}(b_v) \otimes r_v. \end{aligned} \quad (12)$$

2.9. Local interaction block: create bond values for update

In the same manner to the atom-wise values, bond-wise values are calculated using y_{tot} .

$$\begin{aligned} b_{s3} &= \text{linear}(y_{tot}), \\ b_{v3} &= \text{linear}(y_{tot})\text{linear}(y_{asym})r_v + \text{linear}(\beta_{v2i} + \beta_{v2j})\text{cutoff}(r_s). \end{aligned} \quad (13)$$

For creating bond vector value b_{v3} , y_{asym} is introduced to eliminate the $i - j$ order dependence (see Fig. 11).

2.10. Local interaction block: aggregation

$\beta_{s3\{i,j\}}$, $\beta_{v3\{i,j\}}$, $\beta_{t3\{i,j\}}$ are intended to update the atom-wise values. However, those values are still bond-wise values and needed to be aggregated to the corresponding atoms. This is done by taking the summation of neighboring bond-wise values to the atoms. This is the inverse calculation flow to the distribution described in Section 2.4

We name the summed atomic values as a_{s3} , a_{v3} , and a_{t3} (see Fig. 12).

Aggregating bond (taking summation) to bond

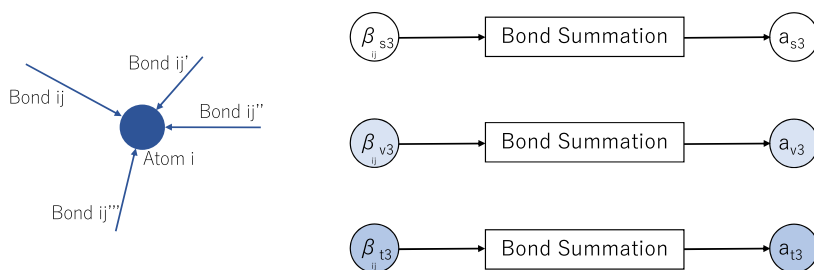


Fig. 12. Local interaction block: aggregation.

Atom output (scalar)

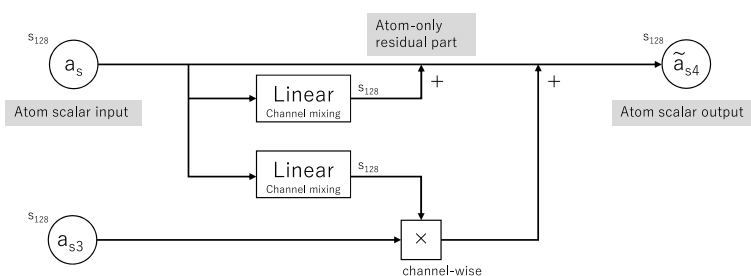


Fig. 13. Local interaction block: output 1.

Atom output (vector, tensor)

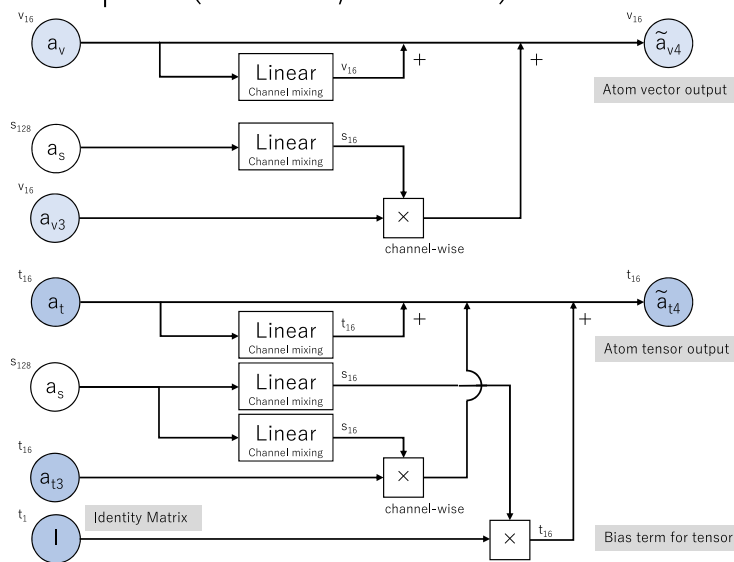


Fig. 14. Local interaction block: output 2.

Bond output

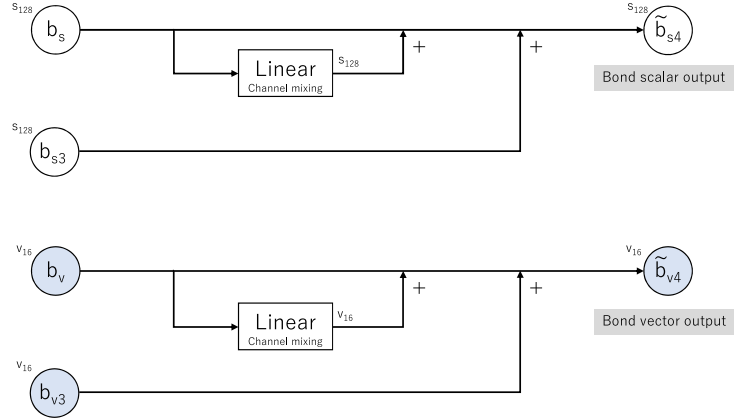


Fig. 15. Local interaction block: output 3.

2.11. Local interaction block: create output values

Finally, node and edge variables are updated by ResNet-style bypass function (see Figs. 13–15).

$$\begin{aligned}
 \tilde{a}_{s4} &= a_s + \text{linear}(a_s) + \text{linear}(a_s)a_{s3}, \\
 \tilde{a}_{v4} &= a_v + \text{linear}(a_v) + \text{linear}(a_s)a_{v3}, \\
 \tilde{a}_{t4} &= a_t + \text{linear}(a_t) + \text{linear}(a_s)a_{t3} + \text{linear}(a_s)\mathbf{I}, \\
 \tilde{b}_{s4} &= b_s + \text{linear}(b_s) + b_{s3}, \\
 \tilde{b}_{v4} &= b_v + \text{linear}(b_v) + b_{v3},
 \end{aligned} \tag{14}$$

where \mathbf{I} is the identity tensor which is used as the bias term. The first term is a residual part and the second term is the structure-independent value update part.

It is noted that $\text{linear}(a_s)$ is multiplied to atom-wise update part. It is considered to work as a node convolution gate function. These variables are the final output of the interaction block and used as the input variables of the next block.

Those five values (\tilde{a}_{s4} , \tilde{a}_{v4} , \tilde{a}_{t4} , \tilde{b}_{s4} , and \tilde{b}_{v4}) are the output values of the local interaction block. They are used for the input values of the next local interaction block or the postprocess layer.

3. TeaNet philosophy and training

With the detailed network laid out in Section 2, we now zoom out and discuss the underlying philosophy of TeaNet. We would like to show the correspondence between existing physics-based potentials (EAM and Tersoff-type angular-dependent potentials) and GCN, in Sections 3.1 and 3.2, respectively. We show that the Tersoff-type angular-dependent bond-order potential can also be rewritten as the graph convolution by incorporating the Euclidean tensor variables into GCN architecture. This means that the rank-2 tensors empower GCN to treat the spatial information naturally while keeping frame-rotation, reflection, and translation equivariances. We also show the necessity of tensor values for transferring spatial information in graph convolution architecture. Then in Section 3.3, we introduce the constraint which enables the model to be stacked deeper and to improve the accuracy. Then we explain the analogy of this constraint with the energy relaxation procedure of the charge-transfer-type IP, which is known as charge equilibration (QE) method [31]

3.1. Rewriting EAM potential as graph convolution

The EAM potential [1] incorporates the concept of electron density in a shallow 1-layer network. In EAM, the total energy, E , is calculated as:

$$\begin{aligned}
 E &= \frac{1}{2} \sum_i \sum_{j \neq i} \phi_{ij}(r_{ij}) + \sum_i F_i(\rho_i), \\
 \rho_i &= \sum_{j \neq i} f_j(r_{ij}),
 \end{aligned} \tag{15}$$

where i, j are the atom labels and ϕ_{ij} , F_i , f_j , and r_{ij} are functions describing the two-body energy, the embedding energy, the electron charge, and the interatomic distance, respectively. In EAM potential, ρ_i which corresponds to the background electron density at atom i is calculated by the summation of pairwise function. It can be expressed as a single-layer graph convolution (see Fig. 16).

The EAM potential can be translated as a shallow GCN as follows: The atomic information (on the nodes) is distributed to the corresponding bonds r_{ij} . Then, the bond-wise values ($\phi_{ij}(r_{ij})$, $f_i(r_{ij})$) are calculated. A part of them ($f_i(r_{ij})$) are summed to the corresponding atoms and atom-site nonlinear function ($F_i(\rho)$) is applied. It is noted that EAM potential has the required invariances such as permutation, pair order, and isometry.

The calculation flow of our graph convolution layer follows the idea of the EAM potential. First, the atom-wise values are calculated. Then, they are distributed into the corresponding bonds and the bond-wise values are calculated by combining atom-wise values and bond-wise values. After that, the calculated bond-wise values are transferred into the corresponding atoms and update the atom-wise values.

To accumulate the edge information ($f_j(r_{ij})$) into nodes, the embedding function (F_i) plays an important role. In EAM potential, F_i represents the interaction between certain atoms and the surrounding electron density. Therefore, from a physics standpoint, the embedding function is essential in the network architecture. We call this the “node gate” function. The effect of the node gate function on prediction accuracy is presented in Section 4.

3.2. Translating bond angle interaction into graph convolution and embedding vector and tensor values

Generally speaking, atomic interactions depend on the bond angle between interacting atoms. For example, H_2O and NH_3 molecules are stabilized at a certain bond angle. Diamond comprises a tetrahedral network. These angular dependencies are generated by the interaction between electron orbitals [14].

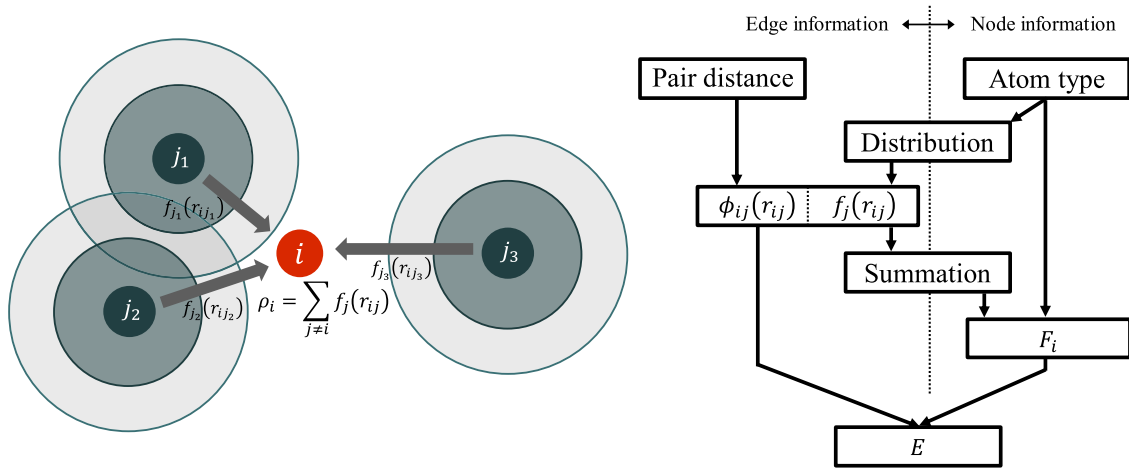


Fig. 16. EAM potential represented as a graph convolution. Left: Schematic of the summation operation. Right: Corresponding network model.

When embedding spatial information in the network architecture, satisfying invariance requirements can be challenging. The energy should be invariant to the rotation of the basis vectors. Invariance is handled differently in different models. One solution is to limit the input data to only the bond length. SchNet [7] and PhysNet [17] uses bond length only. Deep tensor neural networks (DTNN) [6] and deep potential molecular dynamics (DPMD) [16] also maintain the rotational invariance by using bond length. However, bond–bond interactions usually depends on the higher-order geometric information such as bond angle or dihedral angle, and its relation to the bond length can be weak. The detailed discussion is in Appendix A.1. Since the solution of using the raw values of vector components as the input values loses the rotation invariance, it is not appropriate for a molecular dynamics simulation.

Many existing IPs involve bond angles directly. For example, the Stillinger–Weber potential [32] has a three-body energy function. Bond-order-type potentials, such as the Tersoff potential [2,33], possess a bond-order term consisting of the three-body angular-dependent term. Some machine learning-based models give similar solutions. The Behler–Parrinello neural network (BPNN) [4] calculates the three-body symmetry functions. DimeNet++ [34,35] also utilizes three-body angle information and GemNet [36] incorporates four-body dihedral angle.

However, the bond angles correspond to neither nodes nor edges but rather to three-body atom combinations. Therefore, they should be combined and converted into representative node and edge values during the convolution operation, which requires the use of ad-hoc functions such as symmetry functions. Another problem is the lack of long-range interaction in the three-body angle term. In GCN, local information can transfer to farther nodes through the convolutional layers. Transfer of the angle information is also desirable. For example, the directional electronic orbitals of the π bonds can be extensively spread. However, convolution of the angular information at the node crushes the angle information and prevents its propagation.

Here, we show that the angle-dependent three-body convolution algorithm can be naturally expressed as a normal node-and-edge convolution operation using Euclidean vector and second-order tensor values. This means that the model can have local spatial information and propagate it to farther nodes, and to interact with them at nodes while keeping rotational invariances. This is achieved by rewriting the Tersoff-type angle-dependent bond-order function as a convolution operation.

The Tersoff-type angle-dependent term ζ_{ij} can be written as

$$E = \frac{1}{2} \sum_{i,j \neq i} \phi_A(r_{ij}) + \frac{1}{2} \sum_{i,j \neq i} b(\zeta_{ij}) \phi_B(r_{ij}),$$

$$\zeta_{ij} = \sum_{k \neq i,j} G(\theta_{ijk}) H(r_{ij}, r_{ik}),$$
(16)

where i , j , and k are the atom labels; θ_{ijk} is the angle between bonds ij and ik ; r_{ij} and r_{ik} are the bond lengths, and ϕ_A , ϕ_B , b , G , and H are various functions. In some Tersoff-type potentials [3,37], the ζ_{ij} term is expressed as

$$\zeta_{ij} = \sum_{k \neq i,j} \left[c + d \{ h - \cos(\theta_{ijk}) \}^2 \right] f_c(r_{ik}) \exp[\lambda(r_{ij} - r_{ik})],$$
(17)

where f_c is the cutoff function and c , d , h , and λ are the parameters. After expanding the factors and converting the parameters, Eq. (17) is transformed to

$$\begin{aligned} \zeta_{ij} &= \exp(\lambda r_{ij}) \sum_{k \neq i,j} [g_0 + g_1 \cos(\theta_{ijk}) + g_2 \cos^2(\theta_{ijk})] f_c(r_{ik}) \exp(-\lambda r_{ik}) \\ &= \exp(\lambda r_{ij}) \sum_{k \neq i,j} [g_0 + g_1 \hat{\mathbf{r}}_{ij} \cdot \hat{\mathbf{r}}_{ik} + g_2 (\hat{\mathbf{r}}_{ij} \cdot \hat{\mathbf{r}}_{ik})^2] f_c(r_{ik}) \exp(-\lambda r_{ik}) \\ &= \exp(\lambda r_{ij}) \sum_{k \neq i,j} [g_0 + g_1 \hat{\mathbf{r}}_{ij} \cdot \hat{\mathbf{r}}_{ik} + g_2 (\hat{\mathbf{r}}_{ij} \otimes \hat{\mathbf{r}}_{ij}) : (\hat{\mathbf{r}}_{ik} \otimes \hat{\mathbf{r}}_{ik})] \\ &\times f_c(r_{ik}) \exp(-\lambda r_{ik}) \\ &= \exp(\lambda r_{ij}) \sum_{k \neq i} [g_0 + g_1 \hat{\mathbf{r}}_{ij} \cdot \hat{\mathbf{r}}_{ik} + g_2 (\hat{\mathbf{r}}_{ij} \otimes \hat{\mathbf{r}}_{ij}) : (\hat{\mathbf{r}}_{ik} \otimes \hat{\mathbf{r}}_{ik})] \\ &\times f_c(r_{ik}) \exp(-\lambda r_{ik}) \\ &\quad - (g_0 + g_1 + g_2) f_c(r_{ij}) \\ &= g_0 \exp(\lambda r_{ij}) \left[\sum_{k \neq i} f_c(r_{ik}) \exp(-\lambda r_{ik}) \right] \\ &\quad + g_1 \exp(\lambda r_{ij}) \hat{\mathbf{r}}_{ij} \cdot \left[\sum_{k \neq i} \hat{\mathbf{r}}_{ik} f_c(r_{ik}) \exp(-\lambda r_{ik}) \right] \\ &\quad + g_2 \exp(\lambda r_{ij}) (\hat{\mathbf{r}}_{ij} \otimes \hat{\mathbf{r}}_{ij}) : \left[\sum_{k \neq i} (\hat{\mathbf{r}}_{ik} \otimes \hat{\mathbf{r}}_{ik}) f_c(r_{ik}) \exp(-\lambda r_{ik}) \right] \\ &\quad - (g_0 + g_1 + g_2) f_c(r_{ij}), \end{aligned}$$
(18)

where $\hat{\mathbf{r}}_{ij}$ and $\hat{\mathbf{r}}_{ik}$ are the unit vectors. The symbols “ \cdot ”, “ $:$ ”, and “ \otimes ” denote the inner product, the Frobenius inner product, and the tensor product (dyad) of two vectors, respectively. Since all summation terms are written without j , they can be calculated by the convolution operation. As a result, the Tersoff-type potential function can be written as a two-layered neural network. The necessity of the Rank-2 tensors for the angle interaction using convolution operation and its physical meaning and comparison with spherical harmonics-based methods are shown in the Appendix A.2.

Based on this discussion, we introduce both vectors and tensors into the network. Each node array contains scalar, vector, and tensor values, whereas each edge array contains scalar and vector values. A

relative position vector is also provided as an input value. The effects of tensor values on prediction accuracy are presented in Section 4. See Section 2.1 for the details of the implementation.

3.3. Improvement of stacked GCN accuracy inspired of iterative energy minimization process

Like in existing GCNs, the local interaction block can be stacked multiple times. However, as frequently seen in NN training, we observed the increase of the number of layers always brings the instability during the learning procedure. Therefore, it was hard to improve the accuracy by increasing the number of layers of our model in practice.

Here, we found a method to reduce this instability significantly. The key idea is to initialize and to make a constraint that all middle layers have the same NN parameters at the initial stage of training. One can find similarities to the recurrent GCN architecture [10]. Another essential point is to apply the residual network (ResNet) architecture. Interestingly, we found that the accuracy was improved by increasing the number of layers up to 16. (see architectural details in Section 4). It is said that improving the expression power of GCN is hard by increasing the depth size [38]. This was also true in atomistic system in practice. Many GCN models in atomistic system also have up to 6 convolution layers [7,16,17]. In addition, making the constraint to set the all middle layers have the same parameters can be thought to enforce them to behave the identical nonlinear transformation, which seems to reduce the expressive ability of the entire network. Therefore, it is not strange to think that this method does not contribute to the accuracy. It is noted that this constraint was came from an analogy with physics. In this section, we explain the analogy and introduce the insight why the deeply stacked model can improve the accuracy even it is GCN.

Limiting the number of GCN layers to one means the node's information can be determined only by the neighboring nodes. In the analogy with GCN and EAM potential, this corresponds to the assumption that the electron state (density) of the atom can be calculated only by surrounding atoms. Although the assumption works well for certain systems, it is not physically correct picture in general, as seen by the long-ranged nature of the dielectric response function in DFT [39]. The charge transfer effect plays important roles in chemical reactions. The actual electron states are determined so that the energy of the entire system is minimized. DFT calculates the ground state of the electron density by an iterative procedure. To incorporate such long-ranged propagation of information, charge-transfer-type IPs [31,37,40,41], which model the deviation of the electron density and minimize the energy of the system with respect to the charge distribution, are being actively developed.

In charge-transfer-type IPs, the energy minimization involves implicit matrix-vector equations solved by matrix inverse calculation [31,40] or solved by repeatedly updating the charge distribution using the gradient-based method [41]. If the number of iterations is fixed, this iterative procedure could be written as a feed-forward data flow model. It is noted that iterative total energy minimization reproduces the physically reasonable long-range interactions. A well-known example is the Green's function solution that can be represented by a matrix-vector equation $\mathbf{Ax} = \mathbf{b}$: even though \mathbf{A} is a sparse matrix (local interactions), the inverse \mathbf{A}^{-1} is dense and resembles long-range interactions. However, by iteratively solving $\mathbf{Ax} = \mathbf{b}$ with Krylov subspace method $\{\mathbf{b}, \mathbf{A}\mathbf{b}, \mathbf{A}^2\mathbf{b}, \mathbf{A}^3\mathbf{b}, \dots, \mathbf{A}^n\mathbf{b}\}$, one can achieve excellent approximant to the long-range interaction, which is akin to an n -layer neural network with identical weights.

It should be noted the importance of the residual network architecture in the above discussion. The residual network (ResNet) [42] have recently emerged in the fields of image recognition, as have other machine-learning tasks, including object detection [43], machine translation [44], and speech synthesis [45]. ResNet's core idea is to "bypass" the output values from the middle layers and add them directly to the

lower layer to avoid gradient disappearance during back propagation. Interestingly, previous studies interpreted the ResNet architecture as an explicit Euler method of ordinary and partial differential equations [46–48]. In this section, we associated the stack of the local interaction blocks using residual network connection with charge-transfer energy minimization calculation of IPs.

3.4. Data collection

Since our target to develop an universal IP with applicability to arbitrary structures, the dataset is required to cover the wide range of phase space as much as possible. One solution is to increase the number of data points. Another requirement is to secure the diversity of data points.

The dataset is created as follows. First, the simulation box is filled with tens of atoms. The element type is randomly selected from the first three rows of the periodic table (from H to Ar). The number of element types and their ratio in one sample is also widely distributed. The system is heated to high temperature (e.g. 10,000 K), melted for approximately 100 femtoseconds, cooled to a setting temperature, then further annealed for another 100 femtoseconds by classical MD to obtain a snapshot. The timestep is 1 femtosecond. This process is repeated for various temperatures (up to 5000 K) and volumes. Then, the reference energy and atomic forces are obtained by DFT calculations of the snapshots. We consider that this dataset consists of highly disordered structures, including many types of local atomic configurations, and thus presents a challenging task. Furthermore, most of the configurations are far from stable.

In addition, to include realistic structure, we create another dataset by heating the structures of the molecular dataset of the Materials Project repository [49] up to 3000 K. In this work, we merged those two datasets. The entire dataset contains approximately 294,000 structures. The size of the dataset at the double backpropagation process (the corresponding atomic forces of the 294,000 structures) is approximately 7,375,000. Two-hundred randomly selected structures (including 4962×3 atomic force data) are used for the test dataset exclusively.

We used VASP for DFT calculation. To increase the number of data points, the relatively fast settings were used. GGA-PBE was used for the exchange–correlation energy. The Gaussian smearing was used. Spin polarization is considered. The smearing width σ was 0.2 eV. The PREC setting in VASP (used to determine energy cutoff) was set to Medium. One k-point was applied. We used the same settings among structures to ensure the energy surface is consistent. Further expansion of the dataset (e.g. increasing the number of elements, increasing the number of structures, improvement of the computational accuracy) is a future task.

The details of dataset is shown in Appendix A.8.

3.5. Training procedure

The NN hyperparameters are set as follows. The length of the scalar node and edge arrays is set to be 128. The length of the vector node, rank-2 tensor node, and vector edge arrays is each set to 16. The cutoff distance is set to 6 Å. The minibatch size is 100.

The network is trained by optimizing the combined absolute loss function (energies and atomic forces) using the Adam optimizer [50]. As the number of layers increased, frequent fluctuations were observed in the training error. This instability may be explained, at least in part, by the roughness of the DFT-calculated potential energy surface, which is the ground truth of this task. Small atomic displacements, such as the approaching of two neighboring atoms, can potentially cause abrupt energy increases.

To resolve this problem, we constrained the parameters of all intermediate layers in the network to the same values at the initial stage of the training, as described in Section 3.3.

Finally, the models were trained by stochastic gradient descent with a small learning rate (0.1). The numbers of iterations were set to 450,000 (initial), 450,000 (main), and 20,000 (final) in all cases.

Table 2
Regression accuracy of trained networks with various numbers of layers.

# layers	# params	Test loss function [unitless]	Energy MAE [meV/atom]	Force MAE [eV/Å]
2	87,000	2.54	32.5	0.213
4	235,000	1.92	23.9	0.167
8	529,000	1.65	21.4	0.143
16	1,120,000	1.62	19.3	0.142

Table 3
Comparison between the baseline and the four-layer network with one removed component.

	Test loss function	Energy MAE [meV/atom]	Force MAE [eV/Å]
Original four layers	1.84	22.6	0.161
w/o tensor	2.15	25.5	0.190
w/o gate	1.99	24.5	0.174
Softplus	1.89	24.1	0.165

4. Training results

4.1. Dependence of accuracy on the number of NN layers

There are several datasets for atomic systems, without reaction barrier information. For example, QM7 (GDB7-12) [51] and QM9 (GDB9-14) [52] are composed of equilibrium molecular data. In contrast, to reproduce the wide range of energy surface, the model should reproduce a wide range of structures. Therefore, evaluations of highly disordered structures including dangling bonds, overcoordinated atoms, and various disordered bond lengths are required. Therefore, we prepare our own dataset of highly disordered structures using molecular dynamics simulations. The dataset consists of the first three rows of the periodic table (from H to Ar). The details of the data preparation are shown in Section 3.4.

We trained networks of different depths (2, 4, 8, and 16 layers). The hyperparameters and other settings for training are shown in Section 3.5. The results are depicted in Table 2. Increasing the number of layers improved the network accuracy. No overfitting was observed in any system. In the best-performing network (with 16 layers), the mean absolute error (MAE) of the energy was 19.3 meV/atom. Our proposed method enables to construct deeper model which has higher accuracy in the field of GCN.

For further evaluation, we also trained our model for datasets of locally stable atomic configurations (QM9 dataset and Materials Project molecule dataset). In addition, we evaluated the applicability of previous works using our dataset. The results are shown in Appendix A.4.

4.2. Effects of the proposed components of the network

To investigate the effects of the components in our proposed network architecture, we systematically removed their corresponding functions and checked each component effect. The results are presented in Table 3.

First, the network was run without inputting the tensor values (“w/o tensor” row in Table 3). To conduct a fair test, the number of scalar values was increased to maintain the original number of parameters in the network. Then, the network was run without the node convolution gate (“w/o gate” row in Table 3). The number of scalar values was again increased to offset the reduction in the number of parameters. Finally, the proposed activation function was replaced by the softplus function (“Softplus” row in Table 3). A four-layer network without the initial 450,000 iterations was used for comparison.

The largest decrease in accuracy is seen in the case without a tensor value. The second largest decrease is in the case where the node convolution gate was not inserted. Interestingly, the proposed activation function outperformed the softplus function.

Table 4

Top: Structural accuracy on small hydrocarbon molecules. Bottom: calculated lattice constants and cohesive energies of different phases of Na, Al, and Si. The cohesive energies corresponding to the most stable structure are shown in bold.

	C-C length [Å]		C-H length [Å]		H-C-C angle [degree]	
	DFT	TeaNet	DFT	TeaNet	DFT	TeaNet
Acetylene (C ₂ H ₂)	1.21	1.21	1.07	1.06	180°	180°
Ethene (C ₂ H ₄)	1.33	1.34	1.09	1.09	122°	121°
Ethane (C ₂ H ₆)	1.53	1.53	1.10	1.10	112°	112°
Benzene (C ₆ H ₆)	1.40	1.40	1.09	1.09	120°	120°
Cyclohexene (C ₆ H ₁₂)	1.53	1.55	1.10	1.10	110°	110°

		Lattice constant [Å]		Cohesive energy [eV/atom]	
		DFT	TeaNet	DFT	TeaNet
Na	FCC	5.30	5.39	1.10	1.16
	BCC	4.22	4.30	1.09	1.15
	Diamond	7.62	7.29	0.76	0.77
Al	FCC	4.05	4.11	3.42	3.43
	BCC	3.23	3.26	3.27	3.38
	Diamond	6.05	6.30	2.79	2.75
Si	FCC	3.91	4.26	3.97	4.43
	BCC	3.17	3.37	3.93	4.40
	Diamond	5.47	5.47	4.64	4.76

5. Materials applications

5.1. Overview

The universal NNIP should be applicable to arbitrary 3D atomic configurations with any bond types, crystal/molecular structures, and element type (up to Ar in this dataset). We have tested various systems including molecular systems, inorganic crystal structures, water, and aqueous solutions.

In this section, we used the four-layer version of the neural network in consideration of the calculation cost of MD simulations. This is like the embedded-atom potential with embedding applied four times, and with tensors and vectors propagating inside as well. The same parameter set is used throughout this section.

5.2. Intramolecular structure

We tested the reproducibility of the structures of small C-H molecules. The bond lengths and bond angles of typical small hydrocarbon molecules were compared, and the results are listed in Table 4.

Our model can reproduce both the bond lengths and angles with good accuracy. In particular, a variety of C-C bonding (*sp*, *sp*², and *sp*³) is well reproduced. It is noted that ethene forms a planar structure and that ethane forms a staggered conformation. This indicates that our model captures the dihedral angle (4-node) interactions by passing vector and tensor information through the C-C bond. In addition, we confirmed that benzene forms a planar structure while cyclohexene forms a chair-type structure, which is a typical difference in bonding nature between aromaticity and a single bond.

5.3. Bulk properties of metal and semiconductor

Metals have delocalized dielectric response, while materials with bandgap can have exponentially localized response [14]. Table 4 shows TeaNet predictions of Na, Al, and Si. Several crystal structure polymorphs of the same element were evaluated.

5.4. Amorphous silicon dioxide

Since SiO₂ amorphous structure has various bond angles and various coordination numbers, it is treated as a benchmark of the IPs [37,53]. Amorphous SiO₂ configuration including 648 atoms is obtained by

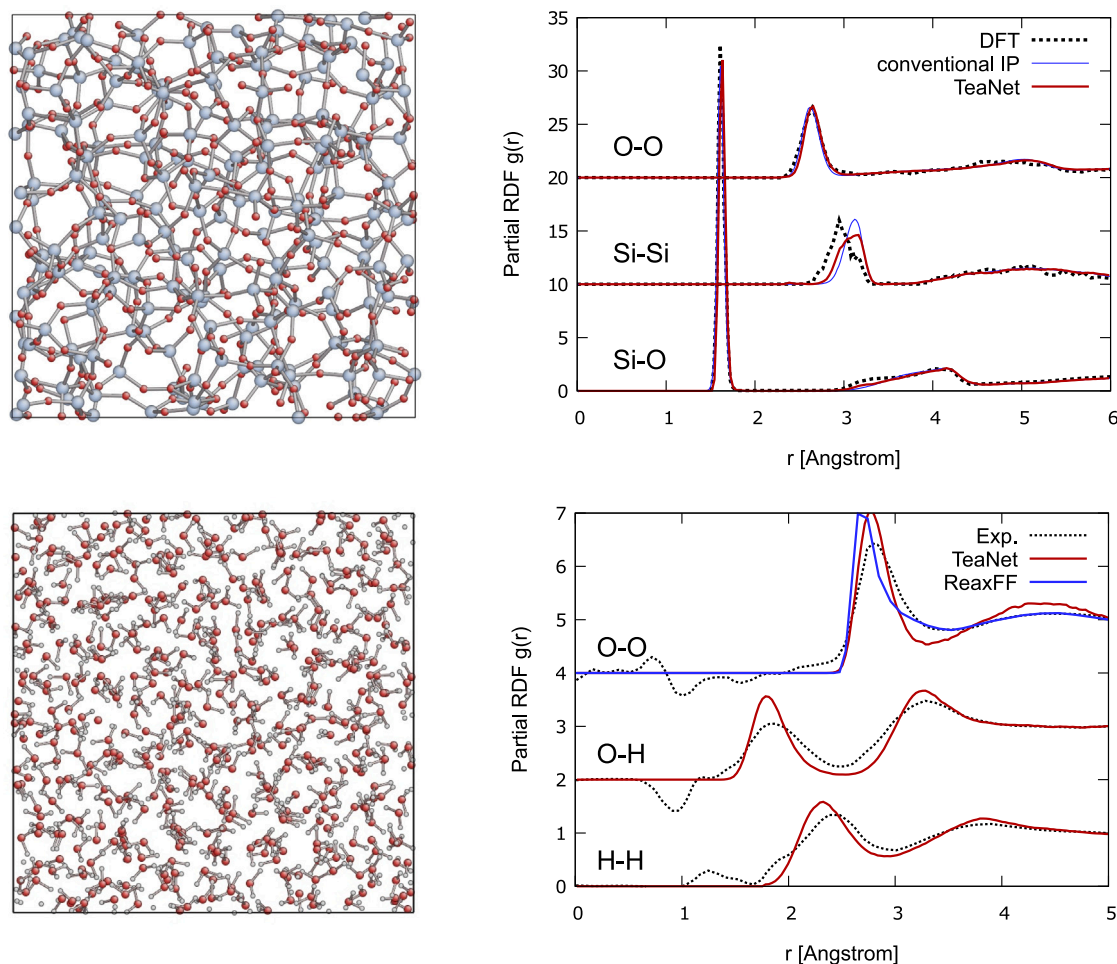


Fig. 17. Top left: obtained SiO_2 amorphous structure. Top right: comparison of partial radial distribution function of amorphous SiO_2 with DFT [54] and conventional IP [37]. Bottom left: snapshot of water. Bottom right: partial radial distribution function of water at 300 K. The experimental data is derived from the merged X-ray and neutron scattering data [56]. It is noted that the intramolecular bonds of H_2O (within 1.20 Å for O-H and 1.77 Å for H-H) are not shown. For O-O, ReaxFF potential result [57] is also shown.

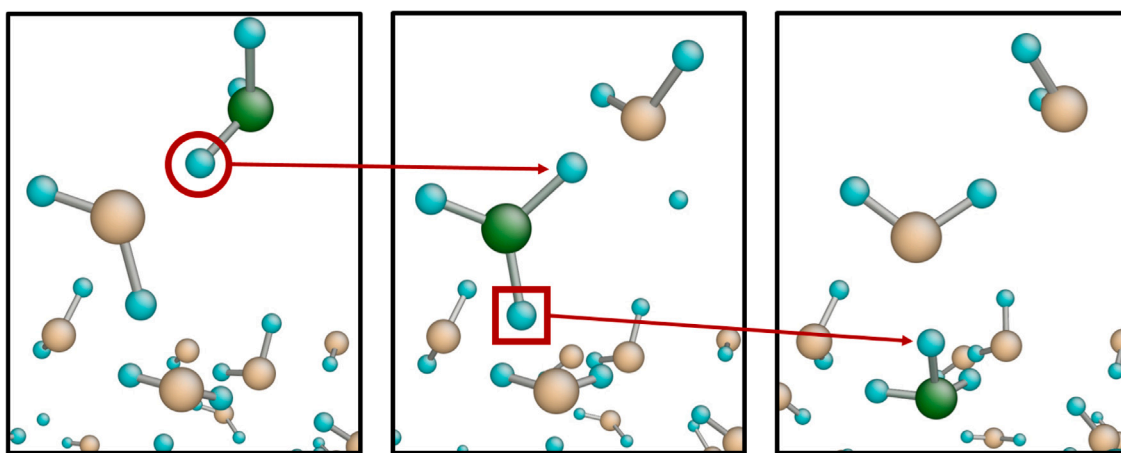


Fig. 18. Snapshots of hopping of H between H_2O molecules. H, 2-coordinate O, and 3-coordinate O are shown by blue, yellow, and green spheres, respectively. (Left): In water, H in H_2O and H_3O are oriented to neighboring O atoms. (Left to middle): An H in H_3O hopped to another O. (Middle to right): Another H in the H_3O molecule hopped to the other H_2O molecule. As a whole, these events were considered as the Grotthuss diffusion of H.

a melt-quench process. The obtained structure and the partial radial distribution functions are shown in Fig. 17. The result is in good agreement with those of previous studies [37,54]. Detailed comparison for silica polymorphs with the other IPs [53,55] are shown in Appendix A.6.

5.5. Properties of water

Water is ubiquitous in chemistry and biochemistry. Atomistic simulation of polar and protic solvent is, therefore, essential for chemistry, biochemistry and electrochemistry. First, the ice (ice Ih) crystal structure was created. The calculated density of ice at 200 K was 0.93 g/cm^3 .

Second, liquid properties were investigated. As an initial structure, an MD cell having 512 H₂O molecules was prepared. It was melted at 800 K for 1 ps under NVT ensemble and then annealed at 300 K and 1 bar for 3 ns under NPT ensemble. The density of liquid water was 1.00 g/cm³. These values are in good agreement with the experimental values (0.92 g/cm³ at 200 K, 1.00 g/cm³ at 300 K), and we confirmed that the density of liquid water is higher than that of ice [58]. Fig. 17 shows a snapshot of TeaNet simulation of a system of water molecules at 300 K, and the partial radial distribution function (RDF) of water predicted by our model compared to the experiment [56]. It is noted that there are IPs which can reproduce the liquid water and ice structures. For example, the calculated density of liquid water and ice using ReaxFF potential [57] are 1.01 g/cm³ and 0.96 g/cm³, respectively. In addition, O–O partial RDF of ReaxFF potential is shown in Fig. 17.

Another important property of water is its high dielectric constant. In MD simulation, the dielectric constant ϵ can be calculated from the fluctuation of the total dipole moment by [59]

$$\epsilon = 1 + \frac{4\pi}{3Vk_B T} (\langle M^2 \rangle - \langle M \rangle^2), \quad (19)$$

where M , V , k_B , and T are the dipole moment, volume, Boltzmann constant, and temperature, respectively. $\langle \rangle$ corresponds to the time average operation. The dipole moment of a single H₂O molecule is set to 1.8546 Debye in this simulation. The calculated dielectric constant was around 52 (Experimental value: 78 at 298 K [58]).

In this simulation, the calculation speed was about 0.14 second/step for 1536 atoms (512 H₂O molecules) using single NVIDIA Titan V GPU.

5.6. Ion dissociation and the Grotthuss proton diffusion mechanism

Next, we investigate ion dissociation, proton transport, and the Grotthuss mechanism by simulating HCl in H₂O. As a result, the HCl molecule dissociated and a single Cl atom and H₃O molecule were created. Here, Cl and H₃O are shown without +/- signs because the charge deviation effect cannot be extracted explicitly. After this, occasionally one H atom in the H₃O was observed to hop to another neighboring O atom, as shown in Fig. 18. This proton transfer process, known as the Grotthuss mechanism, plays an important role in proton diffusion. But previously there was no bonded IP that can reproduce the Grotthuss mechanism. In TeaNet MD, the calculated effective diffusion coefficient of H₃O is 1.5 Å²/ps, which is in good agreement with the previous DFT study (DFT: 1.3 Å²/ps, experiment: 0.93 Å²/ps [60]). It should be noted that ReaxFF potential [57] can reproduce the diffusion coefficient (1.0 Å²/ps). The figures focusing on the Cl atom is shown in Appendix A.7.

6. Conclusion

In this paper, we provided a unified view of GCN and physics-based interatomic potentials. Based on the findings, we proposed a new network model, named the tensor embedded atom network (TeaNet). In this network, the graph convolution is associated with EAM potential and the stacked network model is associated with the iterative electronic total energy relaxation calculation. The Euclidean vectors and tensor values are incorporated into the model to reproduce the propagation of orientation-dependent Hamiltonian information. TeaNet mimics the information flow of nonlinear iterative electronic relaxations (truncating at 5 iterations at present). The proposed model shows great performance for the first 18 elements on the periodic table (H to Ar) even for highly disordered structures. We showed that it can reproduce a diverse range of material properties including C–H molecular structures, metals, amorphous SiO₂, liquid water and ice.

CRedit authorship contribution statement

So Takamoto: Conceptualization, Methodology, Writing – original draft. **Satoshi Izumi:** Supervision. **Ju Li:** Supervision, Writing – review & editing.

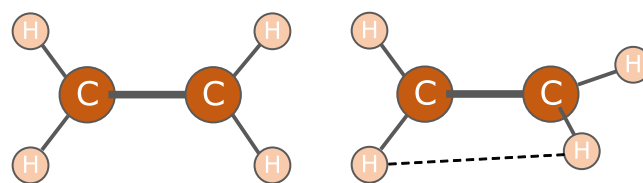


Fig. A.19. Schematic illustration of the rotation of C–C bond in ethylene. Only H–H distance corresponding opposite site (illustrated by dotted line) is different.

Table A.5

Model comparison using proposed highly disordered dataset.

	Cutoff [Å]	Geometric information	# params	Energy MAE [meV/atom]	Force MAE [eV/Å]
SchNet	6.0	$l = 0$	310,000	29.7	0.638
NequIP	4.0	$l = 1$ (32 channels)	468,120	305	0.941
NequIP	6.0	$l = 2$ (16 channels)	281,208	445	0.946
TeaNet (ours)	6.0	rank-2 tensor	235,000	23.9	0.167

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

The raw data and the processed data required to reproduce these findings are available to download from Code Ocean (<https://codeocean.com/capsule/4358608>).

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Appendix

A.1. Examples on the weak correlation between bond length and interactions of atoms

With finite radial cutoff distance, using bond length information only sometimes makes it hard to estimate the interactions of atoms. The simple example is ethylene. The rotation of C–C bond is fixed because of pi-bonding. However, with respect to C–C bond rotation, all angles of the chemical bonds which share the same atom do not change. This is interpreted as the dihedral angle interaction which has important role in organic molecules. It is noted that if the cutoff distance is long enough, there can be seen a difference in H–H distance where two hydrogen atoms are connected to the other side of C atoms. However, the change of H–H distance with respect to the rotation of C–C bond is relatively subtle. In addition, in this case, the length-based method should represent the pi-bond interaction as the distance of H–H length, while there is little direct interaction between them (see Fig. A.19).

Another example is small cluster consisting of three atoms arranged in an equilateral triangle. Accounting the nearest neighbor atoms only, the numbers of neighbor atoms are identical to the infinite chain structure. It means that the length-based model with short cutoff distance cannot tell whether the structure is triangle or chain no matter how many the convolution layer is, while their bond angles are quite different. In other words, the length-based model should represent the angle-dependent interaction by the existence of the second nearest neighbor atoms (see Fig. A.20).

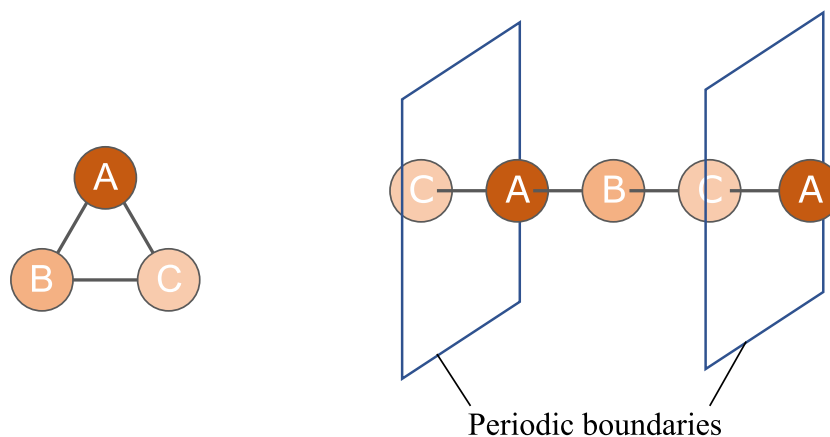


Fig. A.20. Schematic illustration of triangle cluster and infinite chain. They have the same connectivity.

Table A.6

Calculated cohesive energy, relative energy to α -quartz, and density of silica polymorphs. a-Q, a-C, and b-T correspond to α -quartz, α -cristobalite, β -tridymite, respectively.

	Crystal	Cohesive energy [eV/atom]	Relative energy [eV/atom]	Density [g/cm ³]
DFT [61]	a-Q	7.942		2.48
	a-C	7.953	-0.011	2.13
	b-T	7.950	-0.008	2.06
	stishovite	7.730	0.212	4.11
Tersoff [53]	a-Q	6.698		2.42
	a-C	6.697	0.001	2.16
	b-T	6.696	0.002	2.08
	stishovite	6.196	0.502	3.89
ReaxFF [55]	a-Q	-		2.55
	a-C	-	0.001	2.22
	b-T	-	-0.006	2.09
	stishovite	-	0.279	4.29
Ours	a-Q	6.720		2.44
	a-C	6.717	0.003	2.19
	b-T	6.711	0.009	1.92
	stishovite	6.466	0.254	4.12

A.2. The necessity of Rank-2 tensors and its physical meaning

Rank-2 tensors are essential to express the edge–edge interaction through their angle by graph convolution operation. This can be demonstrated in the following example. Let the nodes and edges contain only vector values, and suppose that two edges are connected to a center node, that has point-group symmetry as shown in Fig. A.21. After the convolution, the summed vector values at the node are always $\mathbf{0}$, and the node loses its directional information. If the third edge is connected to the node, no angle dependence is represented. However, if the second-order tensor values are introduced, the point-group symmetric edge pairs have identical (no sign reversal) tensor values; therefore, the directional information can be accumulated on the node. It should be noted that the vector and tensor values are not merely mathematical tricks but express various physical quantities related to the electronic structure. For example, the local charge deviation is expressed by the electric dipole moment. Since the electron orbit of a π bond extends perpendicularly to the bond direction, the dihedral bending is prevented. Polarizability can be expressed by tensor as well. These properties can be naturally expressed using the vector and tensor variables. Higher-order tensor values can also be introduced in the same manner.

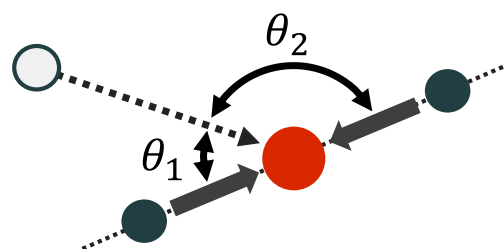


Fig. A.21. Example of the vanishment of directional information when convoluting with vector values only. If a pair of atoms (shown in dark green circles) having the same properties are located on opposite sides of the center atom (shown in orange circle), any vector values summed at the center atom will vanish. Thus, the angular-dependent interaction between another neighbor atom (shown in white circle) and dark green atoms, corresponding to θ_1 and θ_2 , cannot be incorporated in the model.

A.3. Relation between tensor values and spherical harmonics-based methods

Recently, graph neural network models which can treat spherical harmonics-based representation has been proposed and actively applied to the atomistic simulations [22,23,27,28]. The tensor-based model and spherical harmonics-based model have similar trends from a certain point of view. First of all, they have the ability to represent the geometric information while holding the rotation and translation invariances. In addition, they are not limited to the vector representation but can treat the higher-order geometric information using rank- n tensor or higher rotation order l in spherical harmonics.

However, the geometric information is represented in different ways. We can observe it in various points. For example, the tensor-based model has $O(n)$ symmetry while the spherical harmonics-based model has $SO(3)$ symmetry. In other words, the tensor-based model has a mirror-symmetry in natural, while the spherical harmonics-based model can tell mirrored structure. (It is noted that additional restriction can make spherical harmonics-based model to have mirror symmetry.) In addition, the tensor-based model uses inner product and tensor product for spatial information calculation. It means that graphs which are embedded in more than 3 dimensional space can be treated. The nonlinearity is also different between tensor operations and spherical harmonics operations (e.g. Clebsch–Gordan product). It is well known that the nonlinear operations in neural network have significant impact for the performance.

Therefore, they have different expression power and cannot be converted from one model to another. The numerical benchmarks are taken in the below section.

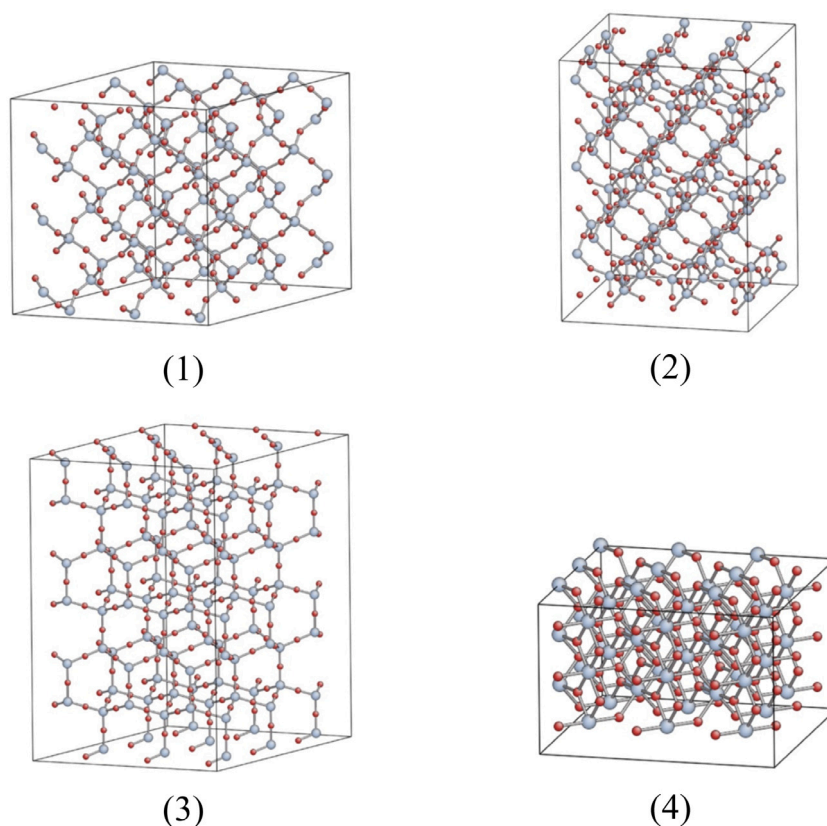


Fig. A.22. Illustration of SiO₂ crystals (1) α -quartz. (2) α -cristobalite. (3) β -tridymite. (4) stishovite. The optimized structure using TeaNet are shown. It is noted that Si and O atoms in stishovite have 6 neighboring atoms and 3 neighboring atoms, respectively.

A.4. Numerical experiments of our model for existing dataset

Although our aim is to reproduce the potential energy of highly disordered atomic configurations and our model and dataset are created for that purpose, we also evaluated our model for datasets of locally stable atomic configurations. First, the QM9 dataset was used. Since QM9 contains only stable structures, it is possible to increase accuracy by retraining. We retrained the four-layer version of the network with the stochastic gradient descent (SGD) optimizer while gradually decreasing the learning rate. The mean squared error of the energy was used as the loss. In this case, we use the original QM9 validation dataset as the test dataset. The MAE of the energy was 13 meV per molecule (1.2 meV/atom) among the QM9 validation dataset. This is similar to the current top scores (14 meV [7], 8 meV [17]), and the other methods (19–130 meV) [5]. It is noted that the error of the dataset with locally stable structures is one magnitude smaller than that of highly disordered structures shown in Table 2.

Second, the Materials Project molecule dataset, which consists of elements in the first three rows of the periodic table, was used. We recalculated the energy of the dataset by DFT to adjust the difference in the method of DFT. We trained the network in the same way as with QM9. The resulting MAE of the energy was 3.1 meV/atom. Our model well succeeds in estimating the energy of locally stable atomic configurations. It is noted that our model does not require the bond types as the input and that we use a relatively short cutoff distances (6 Å).

A.5. Numerical experiments of other models for our dataset

In the previous section, we evaluated our model with existing dataset. Conversely, we evaluate the other models using our highly

disordered dataset and compare their performance in this section. Our dataset contains diverse structure because it is not limited to the stable structure. Therefore, we regard that this task is relatively hard as compared to the existing stable structure dataset. In this section, we especially focused on the force reproducibility since it is the main property for the dynamics simulation task. It is noted that recent studies proposed to take a large loss coefficient for force side for better training [28].

We would like to note that symmetry function-based methods (BPNN [4] and its derivations) is not suitable for this task. Since symmetry function explicitly treats the three-body term of each element, the number of parameters increases dramatically by increasing the number of elements in the dataset. This behavior makes it hard to train the model.

The GNN-based model can be applied to this dataset. We select two architectures here. First, we use SchNet [7] as the current length-based milestone method. Next, we use NequIP [28] as a representative of the spherical harmonics and Clebsch–Gordan product based models.

For SchNet, we use SchNetPack for the evaluation. The specified parameters are below. To align the conditions, we set the number of layer to 4 (original model: 3 and 6) and the cutoff distance to 6.0 Å. We set the parameter ρ (weight of losses) for the energy and the force to 0.001 and 0.999, respectively.

For NequIP, we use the official implementation (<https://github.com/mir-group/nequip>). The provided hyperparameters for examples are also used. The changed points are described below. First, we noticed that the network parameter initialization does not work for this dataset (the loss goes above 10^{35}). We found that this can be suppressed by multiplying 0.1 to the all initial network parameters. The default cutoff is 4.0 Å. We also evaluated 6.0 Å and with the 2nd rotation order 1

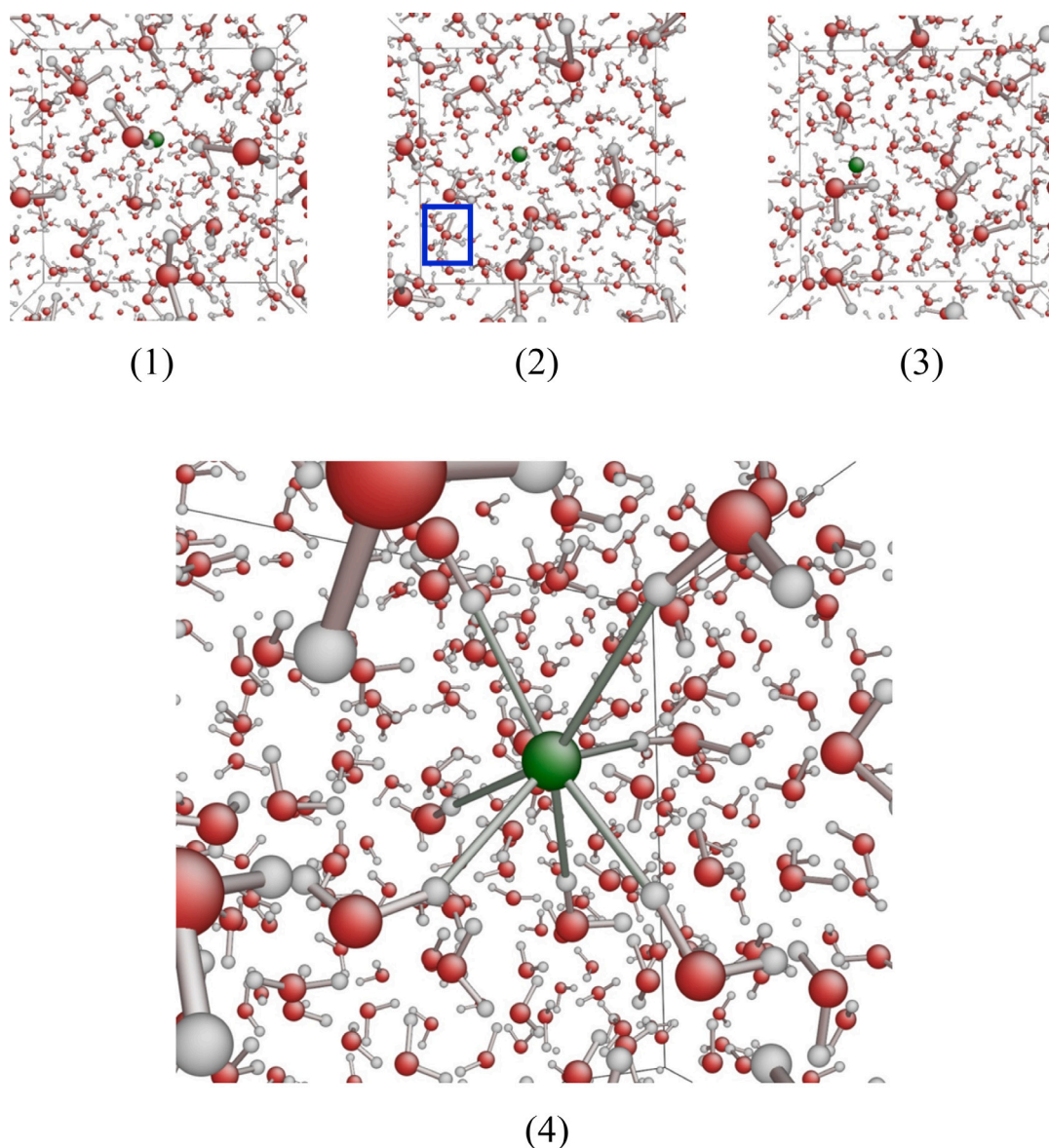


Fig. A.23. (1), (2), and (3): Snapshots of water in which HCl molecule was inserted. The green sphere corresponds to Cl atom. H₃O molecule can be found in the blue box shown in (2). (4): Close snapshot of (3). H–Cl long-range bonds are also shown (visual cutoff distance for H–Cl was set to 3 Å).

to align with TeaNet settings. In this case, we reduced the number of channels from 32 to 16 to keep the number of parameters in a certain range. The loss coefficients are set to 100 for force loss and 1 for per-atom energy loss (they are recommended values for MD simulation tasks). We set the max number of epochs to 100 (6259100 iterations in total).

The result is shown in Table A.5. The result indicates that the force reproduction task in this dataset is quite difficult as compared to the previous benchmarks. For example, NequIP for MD17 task shows good performance for the force reproduction (MAE is less than 0.01 eV/Å for all molecules). We can point out two possible reasons to this difference. The first one is that the structures are far from the stable point. It does not only expand the magnitude of force values but also increase the anharmonicity, which makes it hard to estimate. In other words, the target region (phase space) to estimate is quite larger than the previous datasets. The second one is the difference of the number of element types. It also expands the number of atomic combinations dramatically, which would also contribute to the difficulty of the task.

The result shows that TeaNet performs best for the force reproduction. It indicates that TeaNet makes significant progress for this kind of task. It is noted that, since the nature of this dataset is far from the existing ones, there is a chance that the existing models' hyperparameters were not optimal.

A.6. Silica polymorphs reproducibility

Additional experiments for the reproducibility of silica polymorphs (α -quartz, α -cristobalite, β -tridymite, stishovite) are carried out. The result is shown in Table A.6. The snapshots are shown in Fig. A.22. Overall, our model well reproduces the silica polymorphs including the difference of the energies and the densities. In addition, our model well estimates the difference of the energy of stishovite, which Tersoff-type potential estimates two times larger. In stishovite crystal structure, one Si atom is connected to 6 O atoms and one O atom is connected to 3 Si atoms. It means that the local environment of each atom is far from the

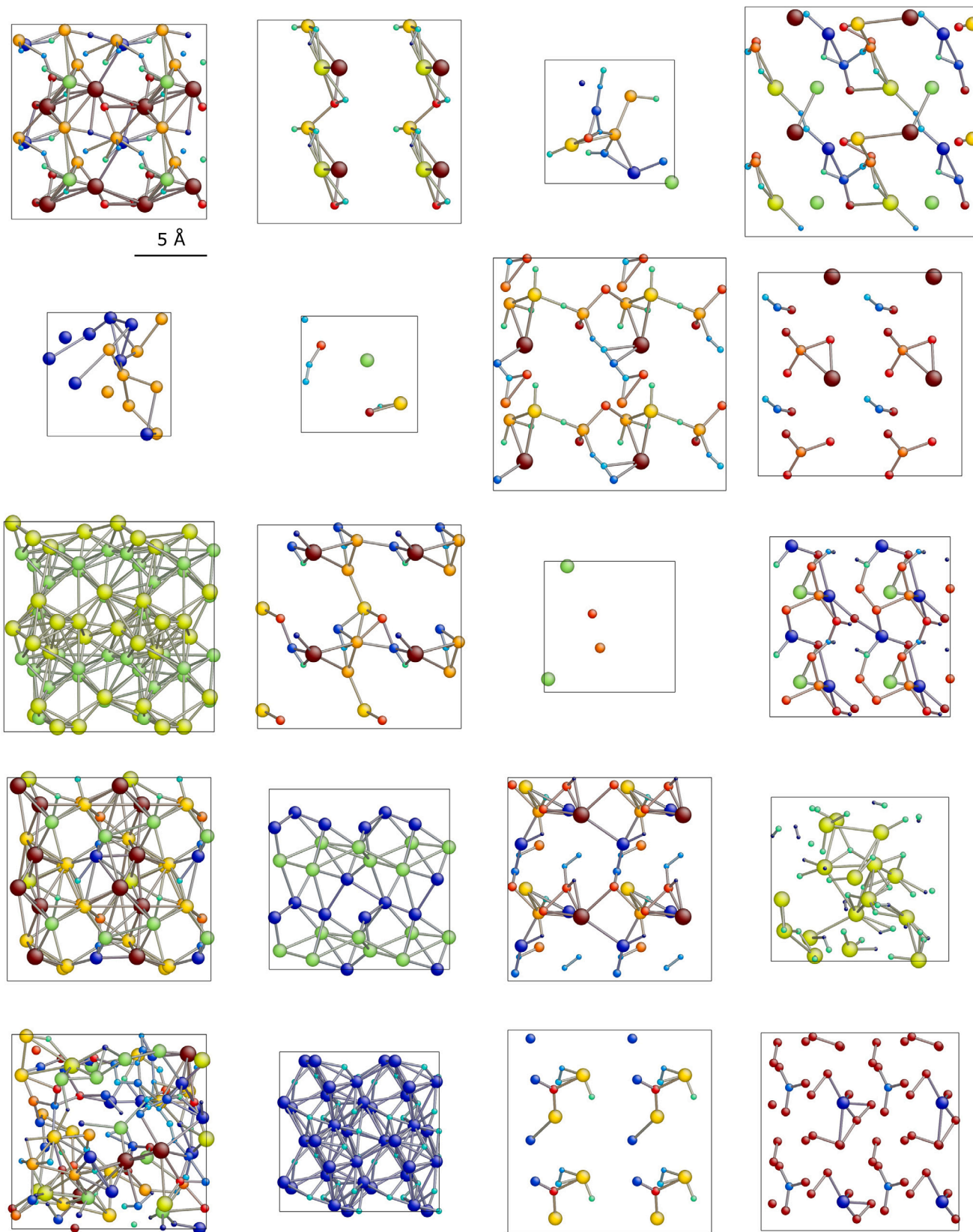


Fig. A.24. The structures of the first 20 samples in Table A.7 are shown (order: top left to right). The colors of the atoms correspond to the element number (H: blue, Ar: red). It is noted that the structures with small box are drawn at a size of 2×2 . See Table A.7 for the details of component.

Table A.7

Content of the test dataset. The number of each element in the test dataset is shown. E corresponds to the total energy of the system calculated by DFT. The zero point of the energy is defined as the sum of the energies of atoms separated in a vacuum. The unit of energy is eV.

H	He	Li	Be	B	C	N	O	F	Ne	Na	Mg	Al	Si	P	S	Cl	Ar	E	E/atom
0	1	1	0	0	3	0	1	3	1	0	0	3	0	0	1	2	2	-32.57	-1.81
1	0	0	0	0	0	0	2	1	0	1	1	0	0	0	1	0	1	-22.14	-2.77
0	1	1	1	2	2	0	2	2	1	0	1	2	0	1	0	0	0	-58.83	-3.68
0	1	1	1	0	1	2	1	1	1	1	1	0	1	1	1	1	1	-53.44	-3.34
0	0	8	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	-30.25	-1.89
0	0	0	0	0	0	3	1	0	1	0	1	0	0	1	0	1	0	-18.42	-2.30
0	0	0	0	1	1	2	0	4	0	0	1	2	1	2	0	1	1	-64.72	-4.05
0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	2	2	1	-22.55	-2.82
0	0	0	0	0	0	0	0	0	9	9	0	0	0	0	0	0	0	0.97	0.05
0	1	0	2	0	0	1	0	1	0	0	1	2	0	1	0	0	1	-25.22	-2.52
0	0	0	0	0	0	0	0	0	2	0	0	0	1	1	0	0	0	-2.54	-0.63
3	0	2	0	0	1	0	0	2	1	0	0	0	1	3	1	2	0	-47.47	-2.97
0	0	1	0	1	0	0	1	1	2	1	4	1	1	0	0	0	3	-26.56	-1.66
0	0	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	-2.99	-0.37
2	0	2	0	1	3	0	1	0	0	0	1	1	1	3	0	0	1	-55.86	-3.49
16	0	0	0	0	0	0	0	32	0	16	0	0	0	0	0	0	0	-197.82	-3.09
9	6	10	12	7	12	9	3	7	9	6	10	5	3	3	7	6	4	-394.97	-3.09
0	0	9	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	-62.79	-3.49
0	0	0	2	0	1	1	0	1	0	0	2	0	0	0	1	0	0	-23.62	-2.95
0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	14	0	-28.70	-1.79
0	0	8	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	-58.89	-3.68
2	0	3	1	1	1	1	0	2	0	0	0	3	0	1	1	0	0	-48.22	-3.01
1	2	2	0	0	1	1	1	0	0	0	3	1	0	0	0	2	2	-27.45	-1.72
2	1	2	1	0	0	0	0	3	3	0	0	2	0	1	1	0	0	-41.19	-2.57
0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	7	1.25	0.16
0	0	0	0	0	0	0	0	0	1	0	15	0	0	0	0	0	0	-0.22	-0.01
0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-28.89	-1.81
10	0	0	0	0	12	2	0	0	0	0	0	0	0	0	0	0	0	-117.52	-4.90
1	1	0	2	1	0	1	2	1	0	2	1	1	1	1	0	1	0	-56.39	-3.52
1	1	0	0	1	0	1	1	1	0	0	0	0	1	2	0	1	0	-36.41	-3.64
1	1	1	0	2	1	0	0	2	1	2	1	0	2	1	1	1	1	-45.35	-2.52
0	3	1	0	0	0	1	3	0	1	0	2	0	0	1	2	2	0	-36.98	-2.31
2	0	2	2	0	2	0	0	1	2	2	0	2	1	2	0	0	2	-34.90	-1.74
0	0	0	0	0	0	0	0	0	9	0	0	0	0	9	0	0	0	-20.54	-1.14
0	0	0	0	1	0	1	1	0	1	0	2	0	1	0	0	1	0	-22.94	-2.87
4	1	2	2	0	0	1	1	1	0	1	1	1	0	1	0	0	0	-35.49	-2.22
1	1	0	1	2	1	1	0	0	1	2	0	1	1	1	2	0	3	-32.36	-1.80
1	0	1	0	0	2	1	0	0	0	1	0	0	0	0	2	0	0	-25.29	-3.16
4	5	2	2	4	5	3	5	1	6	2	4	1	2	2	9	5	2	-220.63	-3.45
0	2	1	1	1	1	0	0	1	1	0	1	0	1	0	0	0	0	-23.16	-2.32
2	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	2	1	-10.70	-1.34
0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	-3.60	-1.80
1	2	0	0	0	2	2	2	1	1	0	1	1	0	1	0	2	0	-60.44	-3.78
1	2	0	0	0	1	0	0	0	1	0	0	1	0	1	1	0	0	-11.70	-1.46
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	10	0	-41.19	-2.06
0	0	15	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	-31.25	-1.95
0	0	2	2	0	1	1	0	0	0	0	2	3	0	0	1	3	1	-44.95	-2.81
0	0	0	0	4	0	0	0	0	0	4	0	0	0	0	0	0	0	-21.54	-2.69
0	0	0	0	1	0	1	1	0	0	1	0	1	1	0	1	1	0	-26.63	-3.33
0	0	0	0	0	0	0	0	0	8	0	8	0	0	0	0	0	0	-5.74	-0.36
1	0	0	0	1	0	1	0	0	1	0	0	2	1	0	0	1	0	-10.77	-1.35
1	0	0	1	0	2	0	0	1	0	0	0	1	0	1	0	0	1	-25.65	-3.21
1	1	0	1	0	1	2	1	2	0	0	1	0	1	0	0	0	1	-46.32	-3.86
5	5	4	4	3	3	3	6	3	4	4	1	5	1	0	3	4	6	-206.37	-3.22
0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	-22.43	-1.40
0	0	0	0	0	0	0	0	0	0	4	0	0	4	0	0	0	0	-16.87	-2.11
6	0	10	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	-36.95	-1.85
0	0	0	0	1	0	1	0	0	0	0	0	0	2	0	0	0	0	-13.41	-3.35
2	0	1	0	1	1	1	0	1	0	1	0	1	1	0	1	1	0	-34.68	-2.89
0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	9	0	-45.46	-2.53
0	0	0	0	0	0	8	0	0	8	0	0	0	0	0	0	0	0	-41.27	-2.58
0	2	2	2	1	0	2	1	1	2	0	0	1	1	0	0	1	0	-43.28	-2.71
0	0	0	0	8	0	0	0	8	0	0	0	0	0	0	0	0	0	-80.56	-5.03
0	1	2	1	0	0	0	2	0	0	0	0	0	0	0	2	0	0	-24.73	-3.09
0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1	-1.31	-0.33
0	2	1	0	2	1	0	3	1	1	0	0	2	1	1	1	2	2	-61.66	-3.08

(continued on next page)

Table A.7 (continued).

H	He	Li	Be	B	C	N	O	F	Ne	Na	Mg	Al	Si	P	S	Cl	Ar	E	E/atom
0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	1	-10.50	-2.62
0	0	0	9	0	0	9	0	0	0	0	0	0	0	0	0	0	0	-71.42	-3.97
2	0	0	0	0	1	1	1	0	0	1	0	1	0	2	2	1	4	-42.65	-2.67
0	3	1	3	0	0	0	0	1	0	0	2	2	0	2	1	1	0	-39.80	-2.49
1	0	1	1	0	0	0	1	0	0	2	0	0	1	0	1	0	0	-22.08	-2.76
5	6	7	10	8	12	14	2	9	10	5	6	3	8	6	9	3	5	-427.13	-3.34
0	0	0	0	0	0	0	0	1	0	0	6	0	0	0	0	1	0	-15.13	-1.89
0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	-88.14	-5.51
2	1	1	1	0	1	1	0	2	1	3	0	0	1	0	1	0	1	-39.07	-2.44
0	0	0	1	1	0	0	2	2	0	1	1	1	0	3	0	0	0	-42.05	-3.50
1	1	2	2	3	0	0	0	0	0	1	1	0	0	0	2	2	1	-39.07	-2.44
0	1	1	1	1	0	0	3	0	1	0	0	1	1	0	0	0	0	-32.15	-3.22
8	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	-71.87	-4.49
1	0	1	1	0	3	5	0	1	0	1	1	1	1	1	1	1	1	-66.54	-3.33
1	1	3	1	0	0	1	2	0	1	1	0	0	2	0	1	1	1	-46.73	-2.92
0	1	0	1	0	2	1	1	0	0	1	1	0	0	0	2	1	1	-38.19	-3.18
0	2	1	1	1	1	1	0	2	0	0	1	1	1	0	1	0	3	-46.10	-2.88
0	0	8	0	16	0	8	16	8	8	0	16	0	32	8	8	0	0	-461.06	-3.60
0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	1	0	0	-44.16	-2.76
11	8	8	6	8	11	6	3	5	12	9	6	6	6	6	4	6	7	-374.90	-2.93
0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	-39.70	-2.48
6	0	0	0	0	8	2	0	0	0	0	0	0	0	0	0	0	0	-75.53	-4.72
1	0	0	1	0	1	1	0	2	0	0	0	2	3	1	2	0	2	-56.83	-3.55
1	1	0	0	0	0	1	2	2	1	1	0	0	0	0	2	5	0	-32.44	-2.03
0	0	1	1	1	0	1	0	0	1	2	0	0	0	0	0	0	1	-7.19	-0.90
0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	-40.96	-5.12
0	2	0	1	0	1	1	1	0	1	0	1	2	1	1	0	4	0	-37.51	-2.34
0	0	0	10	0	10	0	0	0	0	0	0	0	0	0	0	0	0	-93.71	-4.69
1	2	3	1	0	1	1	0	0	2	1	1	0	2	0	2	2	1	-44.09	-2.20
4	0	0	0	0	4	2	2	0	0	0	0	0	0	0	0	0	0	-51.94	-4.33
0	0	0	1	2	0	3	0	1	0	0	1	0	1	2	1	0	0	-53.71	-4.48
0	0	0	0	0	0	0	0	0	4	0	0	0	4	0	0	0	0	-11.15	-1.39
0	1	0	0	0	2	1	3	1	2	0	3	0	1	0	0	0	2	-50.47	-3.15
0	0	8	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	-57.67	-3.60
2	2	0	1	2	1	0	0	0	1	1	0	1	2	0	0	1	2	-29.53	-1.85
14	7	4	0	2	5	13	8	8	7	5	10	5	9	11	7	7	6	-378.64	-2.96
0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	9	0	0	-74.44	-4.14
0	1	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	-6.89	-0.86
0	0	0	0	0	0	9	0	0	0	9	0	0	0	0	0	0	0	-46.17	-2.56
4	7	7	4	4	4	7	3	0	5	2	3	3	3	2	2	3	1	-204.67	-3.20
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	6	-2.18	-0.27
0	4	0	0	0	0	0	0	0	0	0	0	0	0	4	4	0	4	-19.82	-1.24
3	3	1	1	1	2	2	3	3	33	2	3	1	1	2	0	0	3	-92.94	-1.45
1	3	1	2	0	2	2	1	1	0	1	1	0	1	0	2	0	2	-51.51	-2.58
0	0	0	1	2	1	2	0	0	0	2	2	2	3	1	0	0	0	-59.71	-3.73
16	8	16	0	0	0	8	8	0	24	0	0	24	8	0	0	8	8	-266.13	-2.08
2	2	1	1	0	1	0	1	0	0	0	1	1	0	3	2	0	1	-45.98	-2.87
0	2	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	-44.08	-2.45
0	1	0	0	2	0	1	0	1	2	0	2	0	1	2	0	0	0	-24.05	-2.00
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	-47.83	-2.99
8	8	2	8	8	6	10	2	7	8	7	3	11	6	5	9	14	6	-383.19	-2.99
0	0	0	0	8	0	0	0	0	0	0	0	0	0	8	0	0	0	-76.73	-4.80
0	0	2	1	3	1	0	2	1	1	0	0	0	1	1	1	0	2	-59.94	-3.75
0	0	0	0	7	0	1	0	0	0	0	0	0	0	0	0	0	0	-33.89	-4.24
1	0	3	2	1	1	1	0	1	1	0	0	0	0	0	1	0	0	-29.74	-2.48
0	1	0	0	0	0	0	0	0	6	0	0	0	0	1	0	0	0	-0.06	-0.01
7	0	0	0	0	7	0	1	0	0	0	0	0	0	0	1	3	0	-74.36	-3.91
1	0	1	2	2	1	1	0	1	0	1	1	2	2	1	1	1	2	-54.96	-2.75
0	8	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	-22.66	-1.42
0	0	0	0	2	1	1	1	0	1	0	2	1	1	0	0	1	1	-31.12	-2.59
0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	-5.95	-1.98
0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	9	0	-47.85	-2.66
0	0	2	0	1	2	0	0	0	1	2	1	2	1	1	2	1	0	-52.83	-3.30
7	0	0	0	0	0	9	4	0	0	0	0	0	0	0	0	0	0	-60.71	-3.04
0	2	2	0	2	0	1	2	5	2	0	0	0	0	1	0	0	1	-49.48	-2.75
1	2	1	0	1	0	2	1	0	0	0	0	2	1	0	0	1	0	-40.21	-3.35
0	0	16	0	0	0	8	0	8	0	0	8	0	8	0	0	16	0	-185.75	-2.90
1	2	0	2	1	1	1	3	0	2	0	1	2	1	2	0	0	1	-61.69	-3.08
0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	8	0	0	-59.34	-3.71
0	2	0	0	1	0	0	1	2	1	1	0	2	0	1	1	3	1	-42.74	-2.67
1	0	0	1	0	0	1	3	1	1	2	2	0	0	1	0	1	2	-37.49	-2.34
3	0	1	0	0	1	0	0	0	1	0	1	1	0	2	2	4	0	-39.57	-2.47
0	2	0	0	1	2	2	0	0	1	0	2	0	1	0	0	0	1	-33.80	-2.82
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	15	0	-29.37	-1.84
0	0	0	0	8	0	0	0	0	8	0	0	0	0	0	0	0	0	-39.13	-2.45
1	2	0	2	0	0	1	1	1	0	0	2	0	1	0	2	1	2	-45.19	-2.82

(continued on next page)

Table A.7 (continued).

H	He	Li	Be	B	C	N	O	F	Ne	Na	Mg	Al	Si	P	S	Cl	Ar	E	E/atom
0	0	16	0	16	0	0	0	0	0	0	0	0	16	0	0	0	16	-170.52	-2.66
0	8	8	8	16	8	24	8	0	8	16	8	0	8	8	0	0	0	-483.13	-3.77
13	0	0	0	0	7	1	1	0	0	0	0	0	0	0	0	0	0	-88.00	-4.00
0	1	0	0	2	4	0	0	0	1	2	1	1	3	0	1	0	0	-56.86	-3.55
9	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	-38.97	-2.17
0	0	0	2	1	0	1	0	1	1	2	0	1	0	1	1	0	1	-33.08	-2.76
0	1	0	1	0	1	1	0	0	0	0	1	0	0	1	0	0	2	-17.18	-2.15
0	0	1	1	3	1	0	0	2	0	3	1	1	0	1	1	1	2	-45.47	-2.53
0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	9	0	0	-45.55	-2.53
0	0	0	0	1	1	0	0	0	0	0	0	0	2	2	0	0	2	-12.91	-1.61
0	2	0	0	1	1	1	1	1	1	1	3	0	0	1	1	1	1	-44.00	-2.75
9	8	9	8	7	10	8	8	4	6	2	7	8	6	5	10	8	5	-370.09	-2.89
0	0	9	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	-11.95	-0.66
1	0	1	1	2	0	0	0	1	0	0	0	0	0	0	1	1	0	-24.14	-3.02
0	0	0	0	18	0	0	0	0	0	0	0	0	0	0	0	0	2	-83.57	-4.18
0	0	4	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	-31.34	-3.92
0	0	0	0	0	16	0	0	0	0	0	0	32	0	0	0	16	0	-248.64	-3.88
0	6	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	-3.70	-0.46
1	1	0	0	0	0	0	0	0	1	1	0	0	1	0	1	0	2	-7.90	-0.99
1	2	2	0	1	1	2	1	1	0	0	0	0	4	0	3	2	0	-59.84	-2.99
0	0	1	1	0	0	0	1	1	0	1	0	0	2	1	0	0	0	-27.50	-3.44
0	2	0	0	1	2	1	1	0	1	1	2	2	2	0	0	1	0	-37.31	-2.33
0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	6	0	0	-19.17	-2.40
0	1	0	2	2	2	0	1	1	1	1	0	2	1	1	1	0	0	-56.88	-3.55
8	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	-49.09	-3.07
0	0	1	0	1	1	2	1	1	2	0	0	2	1	0	1	1	2	-49.73	-3.11
0	0	2	1	1	0	1	1	0	1	2	1	0	2	1	1	0	2	-42.56	-2.66
0	0	0	0	0	0	0	18	0	2	0	0	0	0	0	0	0	0	-57.64	-2.88
1	1	0	0	1	1	1	0	2	3	0	0	2	0	1	1	1	1	-39.10	-2.44
0	0	0	4	0	0	0	0	0	0	8	0	4	0	0	0	0	0	-18.93	-1.18
0	0	8	16	16	8	8	16	8	16	0	0	8	16	0	0	0	8	-484.78	-3.79
8	8	0	0	0	16	0	16	0	0	8	16	16	0	0	16	16	8	-414.13	-3.24
0	0	0	0	15	0	0	0	0	0	0	1	0	0	0	0	0	0	-81.78	-5.11
0	2	0	1	0	0	0	2	0	2	0	2	0	2	0	1	3	1	-34.70	-2.17
1	0	3	1	0	0	1	1	0	1	3	1	0	1	1	0	2	2	-35.55	-1.98
0	0	1	0	0	0	0	2	0	0	0	3	3	1	2	2	2	0	-50.47	-3.15
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	1	0	-43.11	-2.69
0	0	0	32	0	0	0	0	0	0	0	0	0	32	0	0	0	0	-230.94	-3.61
5	6	6	7	6	6	7	9	5	13	8	5	12	7	3	5	8	10	-326.74	-2.55
1	0	1	0	2	0	2	2	0	1	4	0	1	1	1	1	1	0	-51.42	-2.86
0	8	0	16	8	0	0	0	0	0	0	0	8	0	0	8	8	8	-138.38	-2.16
0	3	0	0	3	3	3	2	2	4	1	0	0	0	6	1	1	3	-68.00	-2.13
0	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	32	0	-219.32	-3.43
0	0	0	0	64	0	0	64	0	0	0	0	0	0	0	0	0	0	-796.72	-6.22
1	3	0	2	1	1	1	1	3	0	0	0	1	0	1	0	1	0	-51.38	-3.21
1	0	1	1	1	0	3	0	0	0	0	0	0	1	0	2	0	0	-41.80	-4.18
0	8	16	0	0	8	0	8	0	0	8	16	0	0	0	0	0	0	-130.89	-2.05
0	0	0	0	0	0	0	0	8	0	0	0	0	0	8	0	0	0	-45.30	-2.83
1	0	1	0	0	1	0	0	1	2	2	1	0	0	2	0	2	3	-35.13	-2.20
0	0	0	0	0	0	0	0	0	10	10	0	0	0	0	0	0	0	-7.75	-0.39
1	0	0	3	0	0	0	0	1	0	0	1	0	1	0	0	1	0	-14.94	-1.87
0	8	8	8	8	0	0	0	0	0	8	8	8	8	0	8	0	0	-148.50	-2.32
0	0	0	0	0	0	0	0	4	0	0	0	0	0	4	0	0	0	-24.20	-3.02
1	0	0	1	0	0	1	1	1	1	0	1	0	0	0	0	0	1	-13.42	-1.68
0	0	0	10	0	0	0	6	0	4	0	0	0	0	0	0	0	0	-75.76	-3.79
0	0	4	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	-17.00	-2.13
0	1	1	1	0	0	0	1	0	1	2	1	0	2	1	3	1	1	-42.95	-2.68
0	0	1	1	1	0	1	1	0	0	1	2	2	1	0	0	0	1	-27.97	-2.33

usual tetrahedral silica crystal structures. It indicates that our model is robust for the change of local environments of atoms.

A.7. Cl atom observation in water

In the simulation of ion dissociation and proton diffusion of water, one HCl molecule was added into H₂O. In this section, the behavior of Cl atom was observed. The snapshots are shown in Fig. A.23. As the HCl molecule dissociated in the water, the individual Cl atom was observed during the MD simulation. The interaction of Cl atom and surrounding water molecules was also shown. Although they are not bonded strictly, H atoms in the surrounding water molecule tend to get closer to the Cl atom. This is in good agreement with the picture of anions in water. It

should be noted that those effects were reproduced without preparing any explicit water-Cl DFT simulations in advance.

A.8. Details of dataset

The details of the test dataset is shown. Since it was made by randomly selecting from the entire dataset, it can be considered to reflect the trend of the entire dataset.

Table A.7 shows the amount of each element in the test dataset. The calculated energy is also shown. The structures of the first 20 samples in Table A.7 are shown in Fig. A.24. Table A.8 shows the number of pairs in the test dataset. As described in the main text, the dataset consists of highly disordered structures.

Table A.8

The number of atom pairs in the test dataset.

	H	He	Li	Be	B	C	N	O	F	Ne	Na	Mg	Al	Si	P	S	Cl	Ar
H	981	403	622	300	277	916	684	1002	564	535	438	327	537	341	741	401	469	372
He		455	582	554	518	594	601	527	401	637	384	598	586	477	500	780	539	501
Li			2091	522	705	543	697	1313	662	676	509	902	741	802	502	432	779	460
Be				1208	671	766	929	590	401	606	414	411	621	1391	283	491	385	442
B					3324	505	739	3514	659	886	459	474	625	824	572	751	448	551
C						1333	681	538	393	554	477	599	841	460	396	868	676	490
N							1068	759	536	927	825	586	525	678	576	433	622	416
O								2745	387	758	404	520	625	462	505	414	506	455
F									815	499	520	369	402	415	488	519	503	372
Ne										1201	717	588	668	621	778	350	498	553
Na											741	451	374	393	295	346	527	321
Mg												917	468	489	302	482	630	383
Al													1515	516	599	1106	510	
Si														1098	297	412	889	451
P															1155	716	408	342
S																1600	738	464
Cl																	1413	469
Ar																		421

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