A1: Interpretability of descriptors in DeePMD-kit

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A1: Interpretability of descriptors in DeePMD-kit

1 Discriptions of 6 given systems with the raw data

1.1 Scripts converting raw data to xyz for visualization

Here we provide a package named raw2pdb which could convert the raw data file to exyz (an extended xyz format) and pdb format. The pbc information was also encoded into these two type files. You can visualize 3D structures with VMD or PyMol.

An example code is show below:

```
from raw2pdb import raw2pdb
2
3
   # path to the raw data
    idir = '/Users/zhuqiang/Documents/My_Jobs@Nanjing/My_Competition/
        deepmd_hackathon/Cu_full/cu.bcc.02 \times 02 \times 02 \times 02/02.md/sys-0016/'deepmd
   # path to the output dir
5
    odir =
6
7
   # output name
   oname = 'cu.bcc.02 \times 02 \times 02.pdb'
   # execute the func
10
   raw2pdb(idir,odir,oname)
```

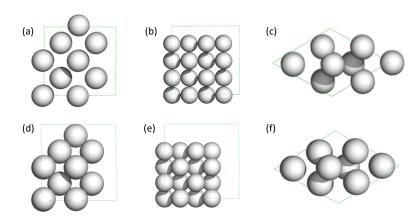


Figure 1: Illustration of the raw data of 6 given systems, namely, Cu (a) bcc, (b) fcc, (c) hcp under normal conditions and (d) bcc, (e) fcc, (f) hcp under high pressure

Once you get the pdb or xyz file, you can visualize it with some state-of-art software. PyMol was utilized here.

1.2 Visualization of the feature spaces

Here we revised two scripts of the code for dumping the feature spaces.

```
1
2
            tf.add_to_collection('coutput',output)
3
            return output, output_qmat
4
5
       – trainer.py <del>----#</del>
                     doutput,_ = run_sess(self.sess, [tf.get_collection('coutput'),
6
        self.train_op], \
7
                     feed_dict=train_feed_dict ,\
8
                     options=prf_options, run_metadata=prf_run_metadata)
9
                     doutput = np.array(doutput)
10
11
                     # dump the feature matrix to doutput.dat
                     if cur\_batch %1000 == 0:
12
```

With the feature matrix $\mathcal{D}_i[1]$ possessed, we want to know the relationship between the feature space and the raw data we provided.

As the feature matrix has a dimensional of M1 * M2. In the Cu system, the parameter of M1 and M2 are specified by the last layer of the *neuron* and *axis_neuron*, respectively, which results dimension of 1200 for a single atom. It is too large to be visualize. The first task is to reduce the dimension. Here, we applied the principle component analysis (PCA) with help of the scikit-learn.[2]

As shown in Figure 2 (a), we plotted top 10 ranked principle components (pcs). The top 3 pcs could cover almost 93 %, which means 1200 dimensions could be reduced to 3 without lossing much information. Subsuquently, we further group the data into 6 groups with the K-Means algorithm supplied by sci-kit learn,[2] and the results were shown in Figure 2 (b).

Why do we choose 6 groups? As we firstly guess, the feature spaces could well separate the 6 Cu systems. The results may somewhat be depressed.

How did the 6 systems look like? if we visualize it with some conventional ways. In the next subsection, the radial distribution functions were applied.

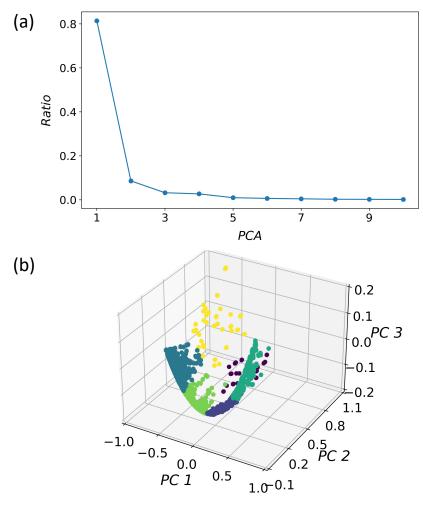


Figure 2: Visualization of the feature space. (a) Ratio of top 10 eigenvalues (b) Feature space of the feature matrix \mathcal{D}_i mapped to the top 3 components and grouped into 6 clusters with KMeans.

1.3 Radial Distribution Functions

Here, the radial distribution functions (rdfs) of 6 Cu systems were calculated with MDTraj.[3] The results are shown in Figure 3. From it, we could see that 6 rdfs could be grouped into 2 large classes, where the first peak changed a lot. These two classes denote the systems under the normal condition (solid lines in Figure 3) and high pressure (dashed lines), respectively. A small shift of the first peak was observed in the *bcc*, *fcc*, and *hcp*. However, little difference could be observed within these two classes. This phenomenon may also be reflected from Figure 2 (b).

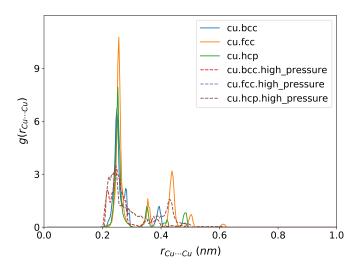


Figure 3: Radial distribution functions of 6 Cu systems.

References

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