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# DeePMD-kit

## Deep Modeling

Mar 07, 2022



# GETTING STARTED

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DeePMD-kit is a package written in Python/C++, designed to minimize the effort required to build deep learning based model of interatomic potential energy and force field and to perform molecular dynamics (MD). This brings new hopes to addressing the accuracy-versus-efficiency dilemma in molecular simulations. Applications of DeePMD-kit span from finite molecules to extended systems and from metallic systems to chemically bonded systems.

---

**Important:** The project DeePMD-kit is licensed under [GNU LGPLv3.0](#). If you use this code in any future publications, please cite this using *Han Wang, Linfeng Zhang, Jiequn Han, and Weinan E. “DeePMD-kit: A deep learning package for many-body potential energy representation and molecular dynamics.” Computer Physics Communications 228 (2018): 178-184.*

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## GETTING STARTED

In this text, we will call the deep neural network that is used to represent the interatomic interactions (Deep Potential) the model. The typical procedure of using DeePMD-kit is

### 1.1 Easy install

There are various easy methods to install DeePMD-kit. Choose one that you prefer. If you want to build by yourself, jump to the next two sections.

After your easy installation, DeePMD-kit (`dp`) and LAMMPS (`lmp`) will be available to execute. You can try `dp -h` and `lmp -h` to see the help. `mpirun` is also available considering you may want to train models or run LAMMPS in parallel.

- *Install off-line packages*
- *Install with conda*
- *Install with docker*

#### 1.1.1 Install off-line packages

Both CPU and GPU version offline packages are available in [the Releases page](#).

Some packages are splitted into two files due to size limit of GitHub. One may merge them into one after downloading:

```
cat deepmd-kit-2.0.0-cuda11.3_gpu-Linux-x86_64.sh.0 deepmd-kit-2.0.0-cuda11.3_gpu-Linux-  
↪x86_64.sh.1 > deepmd-kit-2.0.0-cuda11.3_gpu-Linux-x86_64.sh
```

#### 1.1.2 Install with conda

DeePMD-kit is available with [conda](#). Install [Anaconda](#) or [Miniconda](#) first.

One may create an environment that contains the CPU version of DeePMD-kit and LAMMPS:

```
conda create -n deepmd deepmd-kit=*cpu libdeepmd=*cpu lammps-dp -c https://conda.  
↪deepmodeling.org
```

Or one may want to create a GPU environment containing [CUDA Toolkit](#):

```
conda create -n deepmd deepmd-kit=*gpu libdeepmd=*gpu lammps-dp cudatoolkit=11.3.  
↪horovod -c https://conda.deepmodeling.org
```

One could change the CUDA Toolkit version from 10.1 or 11.3.

One may specify the DeePMD-kit version such as 2.0.0 using

```
conda create -n deepmd deepmd-kit=2.0.0=*cpu libdeepmd=2.0.0=*cpu lammmps-dp=2.0.0_
↳horovod -c https://conda.deepmodeling.org
```

One may enable the environment using

```
conda activate deepmd
```

### 1.1.3 Install with docker

A docker for installing the DeePMD-kit is available [here](#).

To pull the CPU version:

```
docker pull ghcr.io/deepmodeling/deepmd-kit:2.0.0_cpu
```

To pull the GPU version:

```
docker pull ghcr.io/deepmodeling/deepmd-kit:2.0.0_cuda10.1_gpu
```

To pull the ROCm version:

```
docker pull deepmodeling/dpmdkit-rocm:dp2.0.3-rocm4.5.2-tf2.6-lmp29Sep2021
```

## 1.2 Prepare data with dpdata

One can use the a convenient tool [dpdata](#) to convert data directly from the output of first principle packages to the DeePMD-kit format.

To install one can execute

```
pip install dpdata
```

An example of converting data [VASP](#) data in OUTCAR format to DeePMD-kit data can be found at

```
$deepmd_source_dir/examples/data_conv
```

Switch to that directory, then one can convert data by using the following python script

```
import dpdata
dsys = dpdata.LabeledSystem('OUTCAR')
dsys.to('deepmd/npz', 'deepmd_data', set_size = dsys.get_nframes())
```

`get_nframes()` method gets the number of frames in the OUTCAR, and the argument `set_size` enforces that the set size is equal to the number of frames in the system, viz. only one `set` is created in the `system`.

The data in DeePMD-kit format is stored in the folder `deepmd_data`.

A list of all [supported data format](#) and more nice features of `dpdata` can be found at the [official website](#).

## 1.3 Training a model

Several examples of training can be found at the `examples` directory:

```
$ cd $deepmd_source_dir/examples/water/se_e2_a/
```

After switching to that directory, the training can be invoked by

```
$ dp train input.json
```

where `input.json` is the name of the input script.

By default, the verbosity level of the DeePMD-kit is `INFO`, one may see a lot of important information on the code and environment showing on the screen. Among them two pieces of information regarding data systems worth special notice.

```
DEEPMD INFO    ---Summary of DataSystem: training  -----
DEEPMD INFO    found 3 system(s):
DEEPMD INFO
DEEPMD INFO          system  natoms  bch_sz  n_bch  probab_
DEEPMD INFO    ↪ pbc
DEEPMD INFO          ../data_water/data_0/    192    1    80  0.250_
DEEPMD INFO    ↪ T
DEEPMD INFO          ../data_water/data_1/    192    1   160  0.500_
DEEPMD INFO    ↪ T
DEEPMD INFO          ../data_water/data_2/    192    1    80  0.250_
DEEPMD INFO    ↪ T
DEEPMD INFO    -----
DEEPMD INFO    ---Summary of DataSystem: validation  -----
DEEPMD INFO    found 1 system(s):
DEEPMD INFO
DEEPMD INFO          system  natoms  bch_sz  n_bch  probab_
DEEPMD INFO    ↪ pbc
DEEPMD INFO          ../data_water/data_3    192    1    80  1.000_
DEEPMD INFO    ↪ T
DEEPMD INFO    -----
```

The DeePMD-kit prints detailed information on the training and validation data sets. The data sets are defined by "training\_data" and "validation\_data" defined in the "training" section of the input script. The training data set is composed by three data systems, while the validation data set is composed by one data system. The number of atoms, batch size, number of batches in the system and the probability of using the system are all shown on the screen. The last column presents if the periodic boundary condition is assumed for the system.

During the training, the error of the model is tested every `disp_freq` training steps with the batch used to train the model and with `numb_btch` batches from the validating data. The training error and validation error are printed correspondingly in the file `disp_file` (default is `lcurve.out`). The batch size can be set in the input script by the key `batch_size` in the corresponding sections for training and validation data set. An example of the output

```
#  step    rmse_val    rmse_trn    rmse_e_val  rmse_e_trn    rmse_f_val  rmse_f_trn  _
↪      lr
↪      0    3.33e+01    3.41e+01    1.03e+01    1.03e+01    8.39e-01    8.72e-01  _
↪ 1.0e-03
```

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100	2.57e+01	2.56e+01	1.87e+00	1.88e+00	8.03e-01	8.02e-01	↵
↵1.0e-03							
200	2.45e+01	2.56e+01	2.26e-01	2.21e-01	7.73e-01	8.10e-01	↵
↵1.0e-03							
300	1.62e+01	1.66e+01	5.01e-02	4.46e-02	5.11e-01	5.26e-01	↵
↵1.0e-03							
400	1.36e+01	1.32e+01	1.07e-02	2.07e-03	4.29e-01	4.19e-01	↵
↵1.0e-03							
500	1.07e+01	1.05e+01	2.45e-03	4.11e-03	3.38e-01	3.31e-01	↵
↵1.0e-03							

The file contains 8 columns, from left to right, are the training step, the validation loss, training loss, root mean square (RMS) validation error of energy, RMS training error of energy, RMS validation error of force, RMS training error of force and the learning rate. The RMS error (RMSE) of the energy is normalized by number of atoms in the system. One can visualize this file by a simple Python script:

```
import numpy as np
import matplotlib.pyplot as plt

data = np.genfromtxt("lcurve.out", names=True)
for name in data.dtype.names[1:-1]:
    plt.plot(data['step'], data[name], label=name)
plt.legend()
plt.xlabel('Step')
plt.ylabel('Loss')
plt.xscale('symlog')
plt.yscale('log')
plt.grid()
plt.show()
```

Checkpoints will be written to files with prefix `save_ckpt` every `save_freq` training steps.

### 1.3.1 Warning

It is warned that the example water data (in folder `examples/water/data`) is of very limited amount, is provided only for testing purpose, and should not be used to train a production model.

## 1.4 Freeze a model

The trained neural network is extracted from a checkpoint and dumped into a database. This process is called “freezing” a model. The idea and part of our code are from [Morgan](#). To freeze a model, typically one does

```
$ dp freeze -o graph.pb
```

in the folder where the model is trained. The output database is called `graph.pb`.

## 1.5 Test a model

The frozen model can be used in many ways. The most straightforward test can be performed using `dp test`. A typical usage of `dp test` is

```
dp test -m graph.pb -s /path/to/system -n 30
```

where `-m` gives the tested model, `-s` the path to the tested system and `-n` the number of tested frames. Several other command line options can be passed to `dp test`, which can be checked with

```
$ dp test --help
```

An explanation will be provided

```
usage: dp test [-h] [-m MODEL] [-s SYSTEM] [-S SET_PREFIX] [-n NUMB_TEST]
              [-r RAND_SEED] [--shuffle-test] [-d DETAIL_FILE]

optional arguments:
  -h, --help                show this help message and exit
  -m MODEL, --model MODEL    Frozen model file to import
  -s SYSTEM, --system SYSTEM The system dir
  -S SET_PREFIX, --set-prefix SET_PREFIX The set prefix
  -n NUMB_TEST, --numb-test NUMB_TEST The number of data for test
  -r RAND_SEED, --rand-seed RAND_SEED The random seed
  --shuffle-test             Shuffle test data
  -d DETAIL_FILE, --detail-file DETAIL_FILE The file containing details of energy force and virial accuracy
```

## 1.6 Run MD with LAMMPS

Running an MD simulation with LAMMPS is simpler. In the LAMMPS input file, one needs to specify the pair style as follows

```
pair_style      deepmd graph.pb
pair_coeff      * *
```

where `graph.pb` is the file name of the frozen model. It should be noted that LAMMPS counts atom types starting from 1, therefore, all LAMMPS atom type will be firstly subtracted by 1, and then passed into the DeePMD-kit engine to compute the interactions.



## INSTALLATION

### 2.1 Easy install

There are various easy methods to install DeePMD-kit. Choose one that you prefer. If you want to build by yourself, jump to the next two sections.

After your easy installation, DeePMD-kit (dp) and LAMMPS (lmp) will be available to execute. You can try `dp -h` and `lmp -h` to see the help. `mpirun` is also available considering you may want to train models or run LAMMPS in parallel.

- *Install off-line packages*
- *Install with conda*
- *Install with docker*

#### 2.1.1 Install off-line packages

Both CPU and GPU version offline packages are available in [the Releases page](#).

Some packages are splited into two files due to size limit of GitHub. One may merge them into one after downloading:

```
cat deepmd-kit-2.0.0-cuda11.3_gpu-Linux-x86_64.sh.0 deepmd-kit-2.0.0-cuda11.3_gpu-Linux-  
↪x86_64.sh.1 > deepmd-kit-2.0.0-cuda11.3_gpu-Linux-x86_64.sh
```

#### 2.1.2 Install with conda

DeePMD-kit is available with [conda](#). Install [Anaconda](#) or [Miniconda](#) first.

One may create an environment that contains the CPU version of DeePMD-kit and LAMMPS:

```
conda create -n deepmd deepmd-kit=*cpu libdeepmd=*cpu lammgs-dp -c https://conda.  
↪deepmodeling.org
```

Or one may want to create a GPU environment containing [CUDA Toolkit](#):

```
conda create -n deepmd deepmd-kit=*gpu libdeepmd=*gpu lammgs-dp cudatoolkit=11.3.  
↪horovod -c https://conda.deepmodeling.org
```

One could change the CUDA Toolkit version from 10.1 or 11.3.

One may specify the DeePMD-kit version such as 2.0.0 using

```
conda create -n deepmd deepmd-kit=2.0.0=*cpu libdeepmd=2.0.0=*cpu lammmps-dp=2.0.0_
↳horovod -c https://conda.deepmodeling.org
```

One may enable the environment using

```
conda activate deepmd
```

### 2.1.3 Install with docker

A docker for installing the DeePMD-kit is available [here](#).

To pull the CPU version:

```
docker pull ghcr.io/deepmodeling/deepmd-kit:2.0.0_cpu
```

To pull the GPU version:

```
docker pull ghcr.io/deepmodeling/deepmd-kit:2.0.0_cuda10.1_gpu
```

To pull the ROCm version:

```
docker pull deepmodeling/dpmdkit-rocm:dp2.0.3-rocm4.5.2-tf2.6-lmp29Sep2021
```

## 2.2 Install from source code

Please follow our [github](#) webpage to download the [latest released version](#) and [development version](#).

Or get the DeePMD-kit source code by `git clone`

```
cd /some/workspace
git clone --recursive https://github.com/deepmodeling/deepmd-kit.git deepmd-kit
```

The `--recursive` option clones all [submodules](#) needed by DeePMD-kit.

For convenience, you may want to record the location of source to a variable, saying `deepmd_source_dir` by

```
cd deepmd-kit
deepmd_source_dir=`pwd`
```

### 2.2.1 Install the python interface

#### Install the Tensorflow's python interface

First, check the python version on your machine

```
python --version
```

We follow the virtual environment approach to install TensorFlow's Python interface. The full instruction can be found on the official [TensorFlow website](#). Now we assume that the Python interface will be installed to virtual environment directory `$tensorflow_venv`



```
virtualenv -p python3 $tensorflow_venv
source $tensorflow_venv/bin/activate
pip install --upgrade pip
pip install --upgrade tensorflow
```

It is important that everytime a new shell is started and one wants to use DeePMD-kit, the virtual environment should be activated by

```
source $tensorflow_venv/bin/activate
```

if one wants to skip out of the virtual environment, he/she can do

```
deactivate
```

If one has multiple python interpreters named like python3.x, it can be specified by, for example

```
virtualenv -p python3.7 $tensorflow_venv
```

If one does not need the GPU support of deepmd-kit and is concerned about package size, the CPU-only version of TensorFlow should be installed by

```
pip install --upgrade tensorflow-cpu
```

To verify the installation, run

```
python -c "import tensorflow as tf;print(tf.reduce_sum(tf.random.normal([1000, 1000])))"
```

One should remember to activate the virtual environment every time he/she uses deepmd-kit.

## Install the DeePMD-kit's python interface

Execute

```
cd $deepmd_source_dir
pip install .
```

One may set the following environment variables before executing pip:

Environment variables	Allowed value	Default value	Usage
DP_VARIANT	cpu, cuda, rocm	cpu	Build CPU variant or GPU variant with CUDA or ROCM support.
CUDA_TOOLKIT_ROOT_PATH	Path	Detected automatically	The path to the CUDA toolkit directory.
ROCM_ROOT	Path	Detected automatically	The path to the ROCM toolkit directory.

To test the installation, one should firstly jump out of the source directory

```
cd /some/other/workspace
```

then execute

```
dp -h
```

It will print the help information like

```
usage: dp [-h] {train,freeze,test} ...

DeePMD-kit: A deep learning package for many-body potential energy
representation and molecular dynamics

optional arguments:
  -h, --help            show this help message and exit

Valid subcommands:
  {train,freeze,test}
    train               train a model
    freeze              freeze the model
    test                test the model
```

## Install horovod and mpi4py

Horovod and `mpi4py` is used for parallel training. For better performance on GPU, please follow tuning steps in [Horovod on GPU](#).

```
# With GPU, prefer NCCL as a communicator.
HOROVOD_WITHOUT_GLOO=1 HOROVOD_WITH_TENSORFLOW=1 HOROVOD_GPU_OPERATIONS=NCCL HOROVOD_
↪NCCL_HOME=/path/to/nccl pip install horovod mpi4py
```

If your work in CPU environment, please prepare runtime as below:

```
# By default, MPI is used as communicator.
HOROVOD_WITHOUT_GLOO=1 HOROVOD_WITH_TENSORFLOW=1 pip install horovod mpi4py
```

To ensure Horovod has been built with proper framework support enabled, one can invoke the `horovodrun --check-build` command, e.g.,

```
$ horovodrun --check-build
```

Horovod v0.22.1:

Available Frameworks:

```
[X] TensorFlow
[X] PyTorch
[ ] MXNet
```

Available Controllers:

```
[X] MPI
[X] Gloo
```

Available Tensor Operations:

```
[X] NCCL
[ ] DDL
[ ] CCL
```

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```
[X] MPI
[X] Gloo
```

From version 2.0.1, Horovod and mpi4py with MPICH support is shipped with the installer.

If you don't install horovod, DeePMD-kit will fall back to serial mode.

## 2.2.2 Install the C++ interface

If one does not need to use DeePMD-kit with LAMMPS or I-Pi, then the python interface installed in the previous section does everything and he/she can safely skip this section.

### Install the Tensorflow's C++ interface

Check the compiler version on your machine

```
gcc --version
```

The C++ interface of DeePMD-kit was tested with compiler gcc >= 4.8. It is noticed that the I-Pi support is only compiled with gcc >= 4.8.

First the C++ interface of Tensorflow should be installed. It is noted that the version of Tensorflow should be consistent with the python interface. You may follow the instruction to install the corresponding C++ interface.

### Install the DeePMD-kit's C++ interface

Now go to the source code directory of DeePMD-kit and make a build place.

```
cd $deepmd_source_dir/source
mkdir build
cd build
```

I assume you want to install DeePMD-kit into path \$deepmd\_root, then execute cmake

```
cmake -DTENSORFLOW_ROOT=$tensorflow_root -DCMAKE_INSTALL_PREFIX=$deepmd_root ..
```

where the variable tensorflow\_root stores the location where the TensorFlow's C++ interface is installed.

One may add the following arguments to cmake:

CMake arguments	Allowed value	Default value	Usage
- DTENSORFLOW_ROOT=<value>	Path	-	The Path to TensorFlow's C++ interface.
- DCMAKE_INSTALL_PREFIX=<value>	Path	-	The Path where DeePMD-kit will be installed.
- DUSE_CUDA_TOOLKIT=<value>	TRUE FALSE	FALSE	If TRUE, Build GPU support with CUDA toolkit.
- DCUDA_TOOLKIT_ROOT_DIR=<value>	Path	Detected automatically	The path to the CUDA toolkit directory.
- DUSE_ROCM_TOOLKIT=<value>	TRUE FALSE	FALSE	If TRUE, Build GPU support with ROCM toolkit.
- DROCM_ROOT=<value>	Path	Detected automatically	The path to the ROCM toolkit directory.
- DLAMMPS_VERSION_NUMBER=<value>	Num-	20210929	Only necessary for LAMMPS built-in mode. The version number of LAMMPS (yyyymmdd).
- DLAMMPS_SOURCE_ROOT=<value>	Path	-	Only necessary for LAMMPS plugin mode. The path to the LAMMPS source code (later than 8Apr2021). If not assigned, the plugin mode will not be enabled.

If the cmake has been executed successfully, then run the following make commands to build the package:

```
make -j4
make install
```

The option -j4 means using 4 processes in parallel. You may want to use a different number according to your hardware.

If everything works fine, you will have the following executable and libraries installed in \$deepmd\_root/bin and \$deepmd\_root/lib

```
$ ls $deepmd_root/bin
dp_ipi      dp_ipi_low
$ ls $deepmd_root/lib
libdeepmd_cc_low.so  libdeepmd_ipi_low.so  libdeepmd_lmp_low.so  libdeepmd_low.so
↪ libdeepmd_op_cuda.so  libdeepmd_op.so
libdeepmd_cc.so      libdeepmd_ipi.so      libdeepmd_lmp.so      libdeepmd_op_cuda_low.
↪so  libdeepmd_op_low.so  libdeepmd.so
```

## 2.3 Install LAMMPS

There are two ways to install LAMMPS: the built-in mode and the plugin mode. The built-in mode builds LAMMPS along with the DeePMD-kit and DeePMD-kit will be loaded automatically when running LAMMPS. The plugin mode builds LAMMPS and a plugin separately, so one needs to use `plugin load` command to load the DeePMD-kit's LAMMPS plugin library.

### 2.3.1 Install LAMMPS's DeePMD-kit module (built-in mode)

DeePMD-kit provides a module for running MD simulation with LAMMPS. Now make the DeePMD-kit module for LAMMPS.

```
cd $deepmd_source_dir/source/build
make lammps
```

DeePMD-kit will generate a module called USER-DEEPM in the build directory. If you need the low precision version, move `env_low.sh` to `env.sh` in the directory. Now download the LAMMPS code (29Oct2020 or later), and uncompress it:

```
cd /some/workspace
wget https://github.com/lammps/lammps/archive/stable_29Sep2021_update2.tar.gz
tar xf stable_29Sep2021_update2.tar.gz
```

The source code of LAMMPS is stored in directory `lammps-stable_29Sep2021_update2`. Now go into the LAMMPS code and copy the DeePMD-kit module like this

```
cd lammps-stable_29Sep2021_update2/src/
cp -r $deepmd_source_dir/source/build/USER-DEEPM .
```

Now build LAMMPS

```
make yes-kSPACE
make yes-user-deepmd
make mpi -j4
```

If everything works fine, you will end up with an executable `lmp_mpi`.

```
./lmp_mpi -h
```

The DeePMD-kit module can be removed from LAMMPS source code by

```
make no-user-deepmd
```

### 2.3.2 Install LAMMPS (plugin mode)

Starting from 8Apr2021, LAMMPS also provides a plugin mode, allowing one to build LAMMPS and a plugin separately.

Now download the LAMMPS code (8Apr2021 or later), and uncompress it:

```
cd /some/workspace
wget https://github.com/lammps/lammps/archive/stable_29Sep2021_update2.tar.gz
tar xf stable_29Sep2021_update2.tar.gz
```

The source code of LAMMPS is stored in directory `lammps-stable_29Sep2021_update2`. Now go into the LAMMPS directory and create a directory called `build`

```
mkdir -p lammps-stable_29Sep2021_update2/build/  
cd lammps-stable_29Sep2021_update2/build/
```

Now build LAMMPS. Note that `PLUGIN` and `KSPACE` package must be enabled, and `BUILD_SHARED_LIBS` must be set to `yes`. You can install any other package you want.

```
cmake -D PKG_PLUGIN=ON -D PKG_KSPACE=ON -D LAMMPS_INSTALL_RPATH=ON -D BUILD_SHARED_  
↳LIBS=yes -D CMAKE_INSTALL_PREFIX=${deepmd_root} -D CMAKE_INSTALL_LIBDIR=lib -D CMAKE_  
↳INSTALL_FULL_LIBDIR=${deepmd_root}/lib ../cmake  
make -j4  
make install
```

If everything works fine, you will end up with an executable `${deepmd_root}/bin/lmp`.

```
${deepmd_root}/bin/lmp -h
```

## 2.4 Install i-PI

The i-PI works in a client-server model. The i-PI provides the server for integrating the replica positions of atoms, while the DeePMD-kit provides a client named `dp_ipi` that computes the interactions (including energy, force and virial). The server and client communicate via the Unix domain socket or the Internet socket. Full documentation for i-PI can be found [here](#). The source code and a complete installation guide for i-PI can be found [here](#). To use i-PI with already existing drivers, install and update using Pip:

```
pip install -U i-PI
```

Test with Pytest:

```
pip install pytest  
pytest --pyargs ipi.tests
```

## 2.5 Install GROMACS with DeepMD

### 2.5.1 Patch source code of GROMACS

Download source code of a supported gromacs version (2020.2) from <https://manual.gromacs.org/2020.2/download.html>. Run the following command:

```
export PATH=$PATH:${deepmd_kit_root}/bin  
dp_gmx_patch -d $gromacs_root -v $version -p
```

where `deepmd_kit_root` is the directory where the latest version of deepmd-kit is installed, and `gromacs_root` refers to the source code directory of gromacs. And `version` represents the version of gromacs, **only support 2020.2 now**. If attempting to patch another version of gromacs you will still need to set `version` to `2020.2` as this is the only supported version, we cannot guarantee that patching other versions of gromacs will work.

## 2.5.2 Compile GROMACS with deepmd-kit

The C++ interface of deepmd-kit 2.x and tensorflow 2.x are required. And be aware that only deepmd-kit with **high precision** is supported now, since we cannot ensure single precision is enough for a GROMACS simulation. Here is a sample compile script:

```
#!/bin/bash
export CC=/usr/bin/gcc
export CXX=/usr/bin/g++
export CMAKE_PREFIX_PATH="/path/to/fftw-3.3.9" # fftw libraries
mkdir build
cd build

cmake3 .. -DCMAKE_CXX_STANDARD=14 \ # not required, but c++14 seems to be more
↳ compatible with higher version of tensorflow
    -DGMX_MPI=ON \
    -DGMX_GPU=CUDA \ # Gromacs on ROCm has not been fully developed yet
    -DCUDA_TOOLKIT_ROOT_DIR=/path/to/cuda \
    -DCMAKE_INSTALL_PREFIX=/path/to/gromacs-2020.2-deepmd
make -j
make install
```

## 2.6 Building conda packages

One may want to keep both convenience and personalization of the DeePMD-kit. To achieve this goal, one can consider building conda packages. We provide building scripts in [deepmd-kit-recipes organization](#). These building tools are driven by [conda-build](#) and [conda-smithy](#).

For example, if one wants to turn on MPIIO package in LAMMPS, go to [lammps-dp-feedstock](#) repository and modify `recipe/build.sh`. `-D PKG_MPIIO=OFF` should be changed to `-D PKG_MPIIO=ON`. Then go to the main directory and executing

```
./build-locally.py
```

This requires that Docker has been installed. After the building, the packages will be generated in `build_artifacts/linux-64` and `build_artifacts/noarch`, and then one can install then executing

```
conda create -n deepmd lammps-dp -c file:///path/to/build_artifacts -c https://conda.
↳ deepmodeling.org -c nvidia
```

One may also upload packages to one's Anaconda channel, so they can be installed on other machines:

```
anaconda upload /path/to/build_artifacts/linux-64/*.tar.bz2 /path/to/build_artifacts/
↳ noarch/*.tar.bz2
```





## DATA

In this section, we will introduce how to convert the DFT labeled data into the data format used by DeePMD-kit.

The DeePMD-kit organize data in `systems`. Each `system` is composed by a number of `frames`. One may roughly view a `frame` as a snap short on an MD trajectory, but it does not necessary come from an MD simulation. A `frame` records the coordinates and types of atoms, cell vectors if the periodic boundary condition is assumed, energy, atomic forces and virial. It is noted that the `frames` in one `system` share the same number of atoms with the same type.

### 3.1 Data conversion

One needs to provide the following information to train a model: the atom type, the simulation box, the atom coordinate, the atom force, system energy and virial. A snapshot of a system that contains these information is called a **frame**. We use the following convention of units:

Property	Unit
Time	ps
Length	Å
Energy	eV
Force	eV/Å
Virial	eV
Pressure	Bar

The frames of the system are stored in two formats. A raw file is a plain text file with each information item written in one file and one frame written on one line. The default files that provide box, coordinate, force, energy and virial are `box.raw`, `coord.raw`, `force.raw`, `energy.raw` and `virial.raw`, respectively. *We recommend you use these file names.* Here is an example of `force.raw`:

```
$ cat force.raw
-0.724 2.039 -0.951 0.841 -0.464 0.363
6.737 1.554 -5.587 -2.803 0.062 2.222
-1.968 -0.163 1.020 -0.225 -0.789 0.343
```

This `force.raw` contains 3 frames with each frame having the forces of 2 atoms, thus it has 3 lines and 6 columns. Each line provides all the 3 force components of 2 atoms in 1 frame. The first three numbers are the 3 force components of the first atom, while the second three numbers are the 3 force components of the second atom. The coordinate file `coord.raw` is organized similarly. In `box.raw`, the 9 components of the box vectors should be provided on each line. In `virial.raw`, the 9 components of the virial tensor should be provided on each line in the order `XX XY XZ YX YY YZ ZX ZY ZZ`. The number of lines of all raw files should be identical.

We assume that the atom types do not change in all frames. It is provided by `type.raw`, which has one line with the types of atoms written one by one. The atom types should be integers. For example the `type.raw` of a system that has 2 atoms with 0 and 1:

```
$ cat type.raw
0 1
```

Sometimes one needs to map the integer types to atom name. The mapping can be given by the file `type_map.raw`. For example

```
$ cat type_map.raw
0 H
```

The type 0 is named by "O" and the type 1 is named by "H".

The second format is the data sets of numpy binary data that are directly used by the training program. User can use the script `$deepmd_source_dir/data/raw/raw_to_set.sh` to convert the prepared raw files to data sets. For example, if we have a raw file that contains 6000 frames,

```
$ ls
box.raw coord.raw energy.raw force.raw type.raw virial.raw
$ $deepmd_source_dir/data/raw/raw_to_set.sh 2000
nframe is 6000
nline per set is 2000
will make 3 sets
making set 0 ...
making set 1 ...
making set 2 ...
$ ls
box.raw coord.raw energy.raw force.raw set.000 set.001 set.002 type.raw virial.
↪raw
```

It generates three sets `set.000`, `set.001` and `set.002`, with each set contains 2000 frames. One do not need to take care of the binary data files in each of the `set.*` directories. The path containing `set.*` and `type.raw` is called a *system*.

If one needs to train a non-periodic system, an empty `nopbc` file should be put under the system directory. `box.raw` is not necessary in a non-periodic system.

## 3.2 Prepare data with dpdata

One can use the a convenient tool `dpdata` to convert data directly from the output of first principle packages to the DeePMD-kit format.

To install one can execute

```
pip install dpdata
```

An example of converting data `VASP` data in `OUTCAR` format to DeePMD-kit data can be found at

```
$deepmd_source_dir/examples/data_conv
```

Switch to that directory, then one can convert data by using the following python script

```
import dpdata
dsys = dpdata.LabeledSystem('OUTCAR')
dsys.to('deepmd/npz', 'deepmd_data', set_size = dsys.get_nframes())
```

`get_nframes()` method gets the number of frames in the OUTCAR, and the argument `set_size` enforces that the set size is equal to the number of frames in the system, viz. only one set is created in the system.

The data in DeePMD-kit format is stored in the folder `deepmd_data`.

A list of all [supported data format](#) and more nice features of `dpdata` can be found at the [official website](#).



## 4.1 Overall

A model has two parts, a descriptor that maps atomic configuration to a set of symmetry invariant features, and a fitting net that takes descriptor as input and predicts the atomic contribution to the target physical property. It's defined in the `model` section of the `input.json`, for example

```
"model": {
  "type_map":      ["O", "H"],
  "descriptor" : {
    "...": "..."
  },
  "fitting_net" : {
    "...": "..."
  }
}
```

Assume that we are looking for a model for water, we will have two types of atoms. The atom types are recorded as integers. In this example, we denote 0 for oxygen and 1 for hydrogen. A mapping from the atom type to their names is provided by `type_map`.

The model has two subsections `descriptor` and `fitting_net`, which defines the descriptor and the fitting net, respectively. The `type_map` is optional, which provides the element names (but not necessarily to be the element name) of the corresponding atom types.

DeePMD-kit implements the following descriptors:

1. `se_e2_a`: DeepPot-SE constructed from all information (both angular and radial) of atomic configurations. The embedding takes the distance between atoms as input.
2. `se_e2_r`: DeepPot-SE constructed from radial information of atomic configurations. The embedding takes the distance between atoms as input.
3. `se_e3`: DeepPot-SE constructed from all information (both angular and radial) of atomic configurations. The embedding takes angles between two neighboring atoms as input.
4. `loc_frame`: Defines a local frame at each atom, and the compute the descriptor as local coordinates under this frame.
5. `hybrid`: Concatenate a list of descriptors to form a new descriptor.

The fitting of the following physical properties are supported

1. `ener`: Fitting the energy of the system. The force (derivative with atom positions) and the virial (derivative with the box tensor) can also be trained. See the example.

2. *dipole*: The dipole moment.
3. *polar*: The polarizability.

## 4.2 Descriptor "se\_e2\_a"

The notation of `se_e2_a` is short for the Deep Potential Smooth Edition (DeepPot-SE) constructed from all information (both angular and radial) of atomic configurations. The `e2` stands for the embedding with two-atoms information. This descriptor was described in detail in [the DeepPot-SE paper](#).

In this example we will train a DeepPot-SE model for a water system. A complete training input script of this example can be found in the directory.

```
$deepmd_source_dir/examples/water/se_e2_a/input.json
```

With the training input script, data are also provided in the example directory. One may train the model with the DeePMD-kit from the directory.

The construction of the descriptor is given by section `descriptor`. An example of the descriptor is provided as follows

```
"descriptor" :{
  "type":          "se_e2_a",
  "rcut_smth":     0.50,
  "rcut":          6.00,
  "sel":           [46, 92],
  "neuron":        [25, 50, 100],
  "type_one_side": true,
  "axis_neuron":   16,
  "resnet_dt":     false,
  "seed":          1
}
```

- The type of the descriptor is set to `"se_e2_a"`.
- `rcut` is the cut-off radius for neighbor searching, and the `rcut_smth` gives where the smoothing starts.
- `sel` gives the maximum possible number of neighbors in the cut-off radius. It is a list, the length of which is the same as the number of atom types in the system, and `sel[i]` denote the maximum possible number of neighbors with type `i`.
- The `neuron` specifies the size of the embedding net. From left to right the members denote the sizes of each hidden layer from input end to the output end, respectively. If the outer layer is of twice size as the inner layer, then the inner layer is copied and concatenated, then a [ResNet architecture](#) is built between them.
- If the option `type_one_side` is set to `true`, then descriptor will consider the types of neighbor atoms. Otherwise, both the types of centric and neighbor atoms are considered.
- The `axis_neuron` specifies the size of submatrix of the embedding matrix, the axis matrix as explained in the [DeepPot-SE paper](#).
- If the option `resnet_dt` is set `true`, then a timestep is used in the ResNet.
- `seed` gives the random seed that is used to generate random numbers when initializing the model parameters.

### 4.3 Descriptor "se\_e2\_r"

The notation of `se_e2_r` is short for the Deep Potential Smooth Edition (DeepPot-SE) constructed from the radial information of atomic configurations. The `e2` stands for the embedding with two-atom information.

A complete training input script of this example can be found in the directory

```
$deepmd_source_dir/examples/water/se_e2_r/input.json
```

The training input script is very similar to that of `se_e2_a`. The only difference lies in the `descriptor` section

```
"descriptor": {
  "type":          "se_e2_r",
  "sel":           [46, 92],
  "rcut_smth":     0.50,
  "rcut":          6.00,
  "neuron":        [5, 10, 20],
  "resnet_dt":     false,
  "seed":          1,
  "_comment":     " that's all"
},
```

The type of the descriptor is set by the key `"type"`.

### 4.4 Descriptor "se\_e3"

The notation of `se_e3` is short for the Deep Potential Smooth Edition (DeepPot-SE) constructed from all information (both angular and radial) of atomic configurations. The embedding takes angles between two neighboring atoms as input (denoted by `e3`).

A complete training input script of this example can be found in the directory

```
$deepmd_source_dir/examples/water/se_e3/input.json
```

The training input script is very similar to that of `se_e2_a`. The only difference lies in the `descriptor` section

```
"descriptor": {
  "type":          "se_e3",
  "sel":           [40, 80],
  "rcut_smth":     0.50,
  "rcut":          6.00,
  "neuron":        [2, 4, 8],
  "resnet_dt":     false,
  "seed":          1,
  "_comment":     " that's all"
},
```

The type of the descriptor is set by the key `"type"`.

## 4.5 Descriptor "hybrid"

This descriptor hybridize multiple descriptors to form a new descriptor. For example we have a list of descriptor denoted by  $D_1, D_2, \dots, D_N$ , the hybrid descriptor is the concatenation of the list, i.e.  $D = (D_1, D_2, \dots, D_N)$ .

To use the descriptor in DeePMD-kit, one firstly set the `type` to "hybrid", then provide the definitions of the descriptors by the items in the list,

```
"descriptor" : {
  "type": "hybrid",
  "list" : [
    {
      "type" : "se_e2_a",
      ...
    },
    {
      "type" : "se_e2_r",
      ...
    }
  ]
},
```

A complete training input script of this example can be found in the directory

```
$deepmd_source_dir/examples/water/hybrid/input.json
```

## 4.6 Determine sel

All descriptors require to set `sel`, which means the expected maximum number of type- $i$  neighbors of an atom. DeePMD-kit will allocate memory according to `sel`.

`sel` should not be too large or too small. If `sel` is too large, the computing will become much slower and cost more memory. If `sel` is not enough, the energy will be not conserved, making the accuracy of the model worse.

To determine a proper `sel`, one can calculate the neighbor stat of the training data before training:

```
dp neighbor-stat -s data -r 6.0 -t O H
```

where `data` is the directory of data, `6.0` is the cutoff radius, and `O` and `H` is the type map. The program will give the `max_nbor_size`. For example, `max_nbor_size` of the water example is `[38, 72]`, meaning an atom may have 38 O neighbors and 72 H neighbors in the training data.

The `sel` should be set to a higher value than that of the training data, considering there may be some extreme geometries during MD simulations. As a result, we set to `[46, 92]` in the water example.



## 4.7 Fit energy

In this section, we will take `$deepmd_source_dir/examples/water/se_e2_a/input.json` as an example of the input file.

### 4.7.1 Fitting network

The construction of the fitting net is give by section `fitting_net`

```
"fitting_net" : {
  "neuron":           [240, 240, 240],
  "resnet_dt":        true,
  "seed":             1
},
```

- `neuron` specifies the size of the fitting net. If two neighboring layers are of the same size, then a [ResNet architecture](#) is built between them.
- If the option `resnet_dt` is set `true`, then a timestep is used in the ResNet.
- `seed` gives the random seed that is used to generate random numbers when initializing the model parameters.

### 4.7.2 Loss

The loss function for training energy is given by

```
loss = pref_e * loss_e + pref_f * loss_f + pref_v * loss_v
```

where `loss_e`, `loss_f` and `loss_v` denote the loss in energy, force and virial, respectively. `pref_e`, `pref_f` and `pref_v` give the prefactors of the energy, force and virial losses. The prefactors may not be a constant, rather it changes linearly with the learning rate. Taking the force prefactor for example, at training step `t`, it is given by

```
pref_f(t) = start_pref_f * ( lr(t) / start_lr ) + limit_pref_f * ( 1 - lr(t) / start_lr )
```

where `lr(t)` denotes the learning rate at step `t`. `start_pref_f` and `limit_pref_f` specifies the `pref_f` at the start of the training and at the limit of `t -> inf`.

The loss section in the `input.json` is

```
"loss" : {
  "start_pref_e": 0.02,
  "limit_pref_e": 1,
  "start_pref_f": 1000,
  "limit_pref_f": 1,
  "start_pref_v": 0,
  "limit_pref_v": 0
}
```

The options `start_pref_e`, `limit_pref_e`, `start_pref_f`, `limit_pref_f`, `start_pref_v` and `limit_pref_v` determine the start and limit prefactors of energy, force and virial, respectively.

If one does not want to train with virial, then he/she may set the virial prefactors `start_pref_v` and `limit_pref_v` to 0.

## 4.8 Fit tensor like Dipole and Polarizability

Unlike energy which is a scalar, one may want to fit some high dimensional physical quantity, like dipole (vector) and polarizability (matrix, shorted as polar). Deep Potential has provided different API to allow this. In this example we will show you how to train a model to fit them for a water system. A complete training input script of the examples can be found in

```
$deepmd_source_dir/examples/water_tensor/dipole/dipole_input.json
$deepmd_source_dir/examples/water_tensor/polar/polar_input.json
```

The training and validation data are also provided our examples. But note that **the data provided along with the examples are of limited amount, and should not be used to train a production model.**

Similar to the `input.json` used in `ener` mode, training json is also divided into `model`, `learning_rate`, `loss` and `training`. Most keywords remains the same as `ener` mode, and their meaning can be found [here](#). To fit a tensor, one need to modify `model.fitting_net` and `loss`.

### 4.8.1 Fitting Network

The `fitting_net` section tells DP which fitting net to use.

The json of dipole type should be provided like

```
"fitting_net" : {
    "type": "dipole",
    "sel_type": [0],
    "neuron": [100,100,100],
    "resnet_dt": true,
    "seed": 1,
},
```

The json of polar type should be provided like

```
"fitting_net" : {
    "type": "polar",
    "sel_type": [0],
    "neuron": [100,100,100],
    "resnet_dt": true,
    "seed": 1,
},
```

- `type` specifies which type of fitting net should be used. It should be either `dipole` or `polar`. Note that `global_polar` mode in version 1.x is already **deprecated** and is merged into `polar`. To specify whether a system is global or atomic, please see [here](#).
- `sel_type` is a list specifying which type of atoms have the quantity you want to fit. For example, in water system, `sel_type` is `[0]` since 0 represents for atom O. If left unset, all type of atoms will be fitted.
- The rest args has the same meaning as they do in `ener` mode.

## 4.8.2 Loss

DP supports a combinational training of global system (only a global tensor label, i.e. dipole or polar, is provided in a frame) and atomic system (labels for **each** atom included in `sel_type` are provided). In a global system, each frame has just **one** tensor label. For example, when fitting polar, each frame will just provide a 1 x 9 vector which gives the elements of the polarizability tensor of that frame in order XX, XY, XZ, YX, YY, YZ, XZ, ZY, ZZ. By contrast, in a atomic system, each atom in `sel_type` has a tensor label. For example, when fitting dipole, each frame will provide a `#sel_atom` x 3 matrix, where `#sel_atom` is the number of atoms whose type are in `sel_type`.

The loss section tells DP the weight of this two kind of loss, i.e.

```
loss = pref * global_loss + pref_atomic * atomic_loss
```

The loss section should be provided like

```
"loss" : {
    "type":          "tensor",
    "pref":          1.0,
    "pref_atomic":   1.0
},
```

- type should be written as `tensor` as a distinction from `ener` mode.
- `pref` and `pref_atomic` respectively specify the weight of global loss and atomic loss. It can not be left unset. If set to 0, system with corresponding label will NOT be included in the training process.

## 4.8.3 Training Data Preparation

In tensor mode, the identification of label's type (global or atomic) is derived from the file name. The global label should be named as `dipole.npy/raw` or `polarizability.npy/raw`, while the atomic label should be named as `atomic_dipole.npy/raw` or `atomic_polarizability.npy/raw`. If wrongly named, DP will report an error

```
ValueError: cannot reshape array of size xxx into shape (xx,xx). This error may occur
↳ when your label mismatch it's name, i.e. you might store global tensor in `atomic_
↳ tensor.npy` or atomic tensor in `tensor.npy`.
```

In this case, please check the file name of label.

## 4.8.4 Train the Model

The training command is the same as `ener` mode, i.e.

```
dp train input.json
```

The detailed loss can be found in `lcurve.out`:

#	step	rmse_val	rmse_trn	rmse_lc_val	rmse_lc_trn	rmse_gl_val	rmse_gl_trn	lr
	0	8.34e+00	8.26e+00	8.34e+00	8.26e+00	0.00e+00	0.00e+00	1.0e-02
	100	3.51e-02	8.55e-02	0.00e+00	8.55e-02	4.38e-03	0.00e+00	5.0e-03
	200	4.77e-02	5.61e-02	0.00e+00	5.61e-02	5.96e-03	0.00e+00	2.5e-03
	300	5.68e-02	1.47e-02	0.00e+00	0.00e+00	7.10e-03	1.84e-03	1.3e-03
	400	3.73e-02	3.48e-02	1.99e-02	0.00e+00	2.18e-03	4.35e-03	6.3e-04
	500	2.77e-02	5.82e-02	1.08e-02	5.82e-02	2.11e-03	0.00e+00	3.2e-04

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600	2.81e-02	5.43e-02	2.01e-02	0.00e+00	1.01e-03	6.79e-03	1.6e-04
700	2.97e-02	3.28e-02	2.03e-02	0.00e+00	1.17e-03	4.10e-03	7.9e-05
800	2.25e-02	6.19e-02	9.05e-03	0.00e+00	1.68e-03	7.74e-03	4.0e-05
900	3.18e-02	5.54e-02	9.93e-03	5.54e-02	2.74e-03	0.00e+00	2.0e-05
1000	2.63e-02	5.02e-02	1.02e-02	5.02e-02	2.01e-03	0.00e+00	1.0e-05
1100	3.27e-02	5.89e-02	2.13e-02	5.89e-02	1.43e-03	0.00e+00	5.0e-06
1200	2.85e-02	2.42e-02	2.85e-02	0.00e+00	0.00e+00	3.02e-03	2.5e-06
1300	3.47e-02	5.71e-02	1.07e-02	5.71e-02	3.00e-03	0.00e+00	1.3e-06
1400	3.13e-02	5.76e-02	3.13e-02	5.76e-02	0.00e+00	0.00e+00	6.3e-07
1500	3.34e-02	1.11e-02	2.09e-02	0.00e+00	1.57e-03	1.39e-03	3.2e-07
1600	3.11e-02	5.64e-02	3.11e-02	5.64e-02	0.00e+00	0.00e+00	1.6e-07
1700	2.97e-02	5.05e-02	2.97e-02	5.05e-02	0.00e+00	0.00e+00	7.9e-08
1800	2.64e-02	7.70e-02	1.09e-02	0.00e+00	1.94e-03	9.62e-03	4.0e-08
1900	3.28e-02	2.56e-02	3.28e-02	0.00e+00	0.00e+00	3.20e-03	2.0e-08
2000	2.59e-02	5.71e-02	1.03e-02	5.71e-02	1.94e-03	0.00e+00	1.0e-08

One may notice that in each step, some of local loss and global loss will be 0.0. This is because our training data and validation data consist of global system and atomic system, i.e.

```
--training_data
    >atomic_system
    >global_system
--validation_data
    >atomic_system
    >global_system
```

During training, at each step when the lcurve.out is printed, the system used for evaluating the training (validation) error may be either with only global or only atomic labels, thus the corresponding atomic or global errors are missing and are printed as zeros.

## 4.9 Type embedding approach

We generate specific type embedding vector for each atom type, so that we can share one descriptor embedding net and one fitting net in total, which decline training complexity largely.

The training input script is similar to that of se\_e2\_a, but different by adding the type\_embedding section.

### 4.9.1 Type embedding net

The model defines how the model is constructed, adding a section of type embedding net:

```
"model": {
  "type_map":      ["O", "H"],
  "type_embedding":{
    ...
  },
  "descriptor" :{
    ...
  },
  "fitting_net" : {
```

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```

    ...
  }
}

```

Model will automatically apply type embedding approach and generate type embedding vectors. If type embedding vector is detected, descriptor and fitting net would take it as a part of input.

The construction of type embedding net is given by `type_embedding`. An example of `type_embedding` is provided as follows

```

"type_embedding": {
  "neuron": [2, 4, 8],
  "resnet_dt": false,
  "seed": 1
}

```

- The `neuron` specifies the size of the type embedding net. From left to right the members denote the sizes of each hidden layer from input end to the output end, respectively. It takes one-hot vector as input and output dimension equals to the last dimension of the `neuron` list. If the outer layer is of twice size as the inner layer, then the inner layer is copied and concatenated, then a [ResNet architecture](#) is built between them.
- If the option `resnet_dt` is set `true`, then a timestep is used in the ResNet.
- `seed` gives the random seed that is used to generate random numbers when initializing the model parameters.

A complete training input script of this example can be find in the directory.

```
$deepmd_source_dir/examples/water/se_e2_a_tebd/input.json
```

See [here](#) for further explanation of type embedding.

**P.S.: You can't apply compression method while using atom type embedding**

## 4.10 Deep potential long-range (DPLR)

Notice: **The interfaces of DPLR are not stable and subject to change**

The method of DPLR is described in [this paper](#). One is recommended to read the paper before using the DPLR.

In the following, we take the DPLR model for example to introduce the training and LAMMPS simulation with the DPLR model. The DPLR model is training in two steps.

### 4.10.1 Train a deep Wannier model for Wannier centroids

We use the deep Wannier model (DW) to represent the relative position of the Wannier centroid (WC) with the atom to which it is associated. One may consult the introduction of the [dipole model](#) for a detailed introduction. An example input `wc.json` and a small dataset `data` for tutorial purposes can be found in

```
$deepmd_source_dir/examples/water/dplr/train/
```

It is noted that **the tutorial dataset is not enough for training a productive model**. Two settings make the training input script different from an energy training input:

```

    "fitting_net": {
        "type": "dipole",
        "dipole_type": [0],
        "neuron": [128, 128, 128],
        "seed": 1
    },

```

The type of fitting is set to "dipole". The dipole is associate to type 0 atoms (oxygens), by the setting "dipole\_type": [0]. What we trained is the displacement of the WC from the corresponding oxygen atom. It shares the same training input as atomic dipole because both are 3-dimensional vectors defined on atoms. The loss section is provided as follows

```

"loss": {
    "type": "tensor",
    "pref": 0.0,
    "pref_atomic": 1.0
},

```

so that the atomic dipole is trained as labels. Note that the numpy compressed file `atomic_dipole.npy` should be provided in each dataset.

The training and freezing can be started from the example directory by

```
dp train dw.json && dp freeze -o dw.pb
```

#### 4.10.2 Train the DPLR model

The training of the DPLR model is very similar to the standard short-range DP models. An example input script can be found in the example directory. The following section is introduced to compute the long-range energy contribution of the DPLR model, and modify the short-range DP model by this part.

```

"modifier": {
    "type": "dipole_charge",
    "model_name": "dw.pb",
    "model_charge_map": [-8],
    "sys_charge_map": [6, 1],
    "ewald_h": 1.00,
    "ewald_beta": 0.40
},

```

The "model\_name" specifies which DW model is used to predict the position of WCs. "model\_charge\_map" gives the amount of charge assigned to WCs. "sys\_charge\_map" provides the nuclear charge of oxygen (type 0) and hydrogen (type 1) atoms. "ewald\_beta" (unit  $\text{\AA}^{-1}$ ) gives the spread parameter controls the spread of Gaussian charges, and "ewald\_h" (unit  $\text{\AA}$ ) assigns the grid size of Fourier transform. The DPLR model can be trained and frozen by (from the example directory)

```
dp train ener.json && dp freeze -o ener.pb
```

### 4.10.3 Molecular dynamics simulation with DPLR

In MD simulations, the long-range part of the DPLR is calculated by the LAMMPS kspace support. Then the long-range interaction is back-propagated to atoms by DeePMD-kit. This setup is commonly used in classical molecular dynamics simulations as the “virtual site”. Unfortunately, LAMMPS does not natively support virtual sites, so we have to hack the LAMMPS code, which makes the input configuration and script a little wired.

An example of input configuration file and script can be found in

`$deepmd_source_dir/examples/water/dplr/lmp/`

We use `atom_style full` for DPLR simulations. the coordinates of the WCs are explicitly written to the configuration file. Moreover, a virtual bond is established between the oxygens and the WCs to indicate they are associated together. The configuration file containing 128 H2O molecules is thus written as

```
512 atoms
3 atom types
128 bonds
1 bond types

0 16.421037674 xlo xhi
0 16.421037674 ylo yhi
0 16.421037674 zlo zhi
0 0 0 xy xz yz

Masses

1 16
2 2
3 16

Atoms

      1      1 1 6 8.4960699081e+00 7.5073699951e+00 9.6371297836e+00
      2      2 1 6 4.0597701073e+00 6.8156299591e+00 1.2051420212e+01
...
    385      1 3 -8 8.4960699081e+00 7.5073699951e+00 9.6371297836e+00
    386      2 3 -8 4.0597701073e+00 6.8156299591e+00 1.2051420212e+01
...

Bonds

1 1 1 385
2 1 2 386
...
```

The oxygens and hydrogens are assigned with atom types 1 and 2 (corresponding to training atom types 0 and 1), respectively. The WCs are assigned with atom type 3. We want to simulate heavy water so the mass of hydrogens is set to 2.

An example input script is provided in

```
$deepmd_source_dir/examples/water/dplr/lmp/in.lammps
```

Here are some explanations

```
# groups of real and virtual atoms
group          real_atom type 1 2
group          virtual_atom type 3

# bond between real and its corresponding virtual site should be given
# to setup a map between real and virtual atoms. However, no real
# bonded interaction is applied, thus bond_style "zero" is used.
pair_style      deepmd ener.pb
pair_coeff      * *
bond_style      zero
bond_coeff      *
special_bonds   lj/coul 1 1 1 angle no
```

Type 1 and 2 (O and H) are real\_atoms, while type 3 (WCs) are virtual\_atoms. The model file ener.pb stores both the DW and DPLR models, so the position of WCs and the energy can be inferred from it. A virtual bond type is specified by bond\_style zero. The special\_bonds command switches off the exclusion of intramolecular interactions.

```
# kspace_style "pppm/dplr" should be used. in addition the
# gewald(1/distance) should be set the same as that used in
# training. Currently only ik differentiation is supported.
kspace_style    ppm/dplr 1e-5
kspace_modify   gewald ${BETA} diff ik mesh ${KMESH} ${KMESH} ${KMESH}
```

The long-range part is calculated by the kspace support of LAMMPS. The kspace\_style ppm/dplr is required. The spread parameter set by variable BETA should be set the same as that used in training. The KMESH should be set dense enough so the long-range calculation is converged.

```
# "fix dplr" set the position of the virtual atom, and spread the
# electrostatic interaction asserting on the virtual atom to the real
# atoms. "type_associate" associates the real atom type its
# corresponding virtual atom type. "bond_type" gives the type of the
# bond between the real and virtual atoms.
fix             0 all dplr model ener.pb type_associate 1 3 bond_type 1
fix_modify      0 virial yes
```

The fix command dplr calculates the position of WCs by the DW model and back-propagates the long-range interaction on virtual atoms to real atoms.

```
# compute the temperature of real atoms, excluding virtual atom contribution
compute         real_temp real_atom temp
compute         real_press all pressure real_temp
fix             1 real_atom nvt temp ${TEMP} ${TEMP} ${TAU_T}
fix_modify      1 temp real_temp
```

The temperature of the system should be computed from the real atoms. The kinetic contribution in the pressure tensor is also computed from the real atoms. The thermostat is applied to only real atoms. The computed temperature and pressure of real atoms can be accessed by, e.g.



```
fix                                thermo_print all print ${THERMO_FREQ} "$(step) $(pe) $(ke) $(etotal)
↪$(enthalpy) $(c_real_temp) $(c_real_press) $(vol) $(c_real_press[1]) $(c_real_
↪press[2]) $(c_real_press[3])" append thermo.out screen no title "# step pe ke etotal_
↪enthalpy temp press vol pxx pyy pzz"
```

The LAMMPS simulation can be started from the example directory by

```
lmp -i in.lammps
```

If LAMMPS complains that no model file `ener.pb` exists, it can be copied from the training example directory.

The MD simulation lasts for only 20 steps. If one runs a longer simulation, it will blow up, because the model is trained with a very limited dataset for a very short training steps, thus is of poor quality.

Another restriction should be noted is that the energies printed at the zero step is not correct. This is because at the zero step the position of the WC has not been updated with the DW model. The energies printed in later steps are correct.



## TRAINING

### 5.1 Training a model

Several examples of training can be found at the `examples` directory:

```
$ cd $deepmd_source_dir/examples/water/se_e2_a/
```

After switching to that directory, the training can be invoked by

```
$ dp train input.json
```

where `input.json` is the name of the input script.

By default, the verbosity level of the DeePMD-kit is `INFO`, one may see a lot of important information on the code and environment showing on the screen. Among them two pieces of information regarding data systems worth special notice.

```
DEEPMD INFO    ---Summary of DataSystem: training  -----
↪ -----
DEEPMD INFO    found 3 system(s):
DEEPMD INFO                                     system  natoms  bch_sz  n_bch  probab_
↪ pbc
DEEPMD INFO                                     ../data_water/data_0/  192    1    80  0.250_
↪ T
DEEPMD INFO                                     ../data_water/data_1/  192    1   160  0.500_
↪ T
DEEPMD INFO                                     ../data_water/data_2/  192    1    80  0.250_
↪ T
DEEPMD INFO    -----
↪ -----
DEEPMD INFO    ---Summary of DataSystem: validation -----
↪ -----
DEEPMD INFO    found 1 system(s):
DEEPMD INFO                                     system  natoms  bch_sz  n_bch  probab_
↪ pbc
DEEPMD INFO                                     ../data_water/data_3  192    1    80  1.000_
↪ T
DEEPMD INFO    -----
↪ -----
```

The DeePMD-kit prints detailed information on the training and validation data sets. The data sets are defined by "training\_data" and "validation\_data" defined in the "training" section of the input script. The training

data set is composed by three data systems, while the validation data set is composed by one data system. The number of atoms, batch size, number of batches in the system and the probability of using the system are all shown on the screen. The last column presents if the periodic boundary condition is assumed for the system.

During the training, the error of the model is tested every `disp_freq` training steps with the batch used to train the model and with `numb_btch` batches from the validating data. The training error and validation error are printed correspondingly in the file `disp_file` (default is `lcurve.out`). The batch size can be set in the input script by the key `batch_size` in the corresponding sections for training and validation data set. An example of the output

#	step	rmse_val	rmse_trn	rmse_e_val	rmse_e_trn	rmse_f_val	rmse_f_trn	
↪	lr							
	0	3.33e+01	3.41e+01	1.03e+01	1.03e+01	8.39e-01	8.72e-01	└
↪	1.0e-03							
	100	2.57e+01	2.56e+01	1.87e+00	1.88e+00	8.03e-01	8.02e-01	└
↪	1.0e-03							
	200	2.45e+01	2.56e+01	2.26e-01	2.21e-01	7.73e-01	8.10e-01	└
↪	1.0e-03							
	300	1.62e+01	1.66e+01	5.01e-02	4.46e-02	5.11e-01	5.26e-01	└
↪	1.0e-03							
	400	1.36e+01	1.32e+01	1.07e-02	2.07e-03	4.29e-01	4.19e-01	└
↪	1.0e-03							
	500	1.07e+01	1.05e+01	2.45e-03	4.11e-03	3.38e-01	3.31e-01	└
↪	1.0e-03							

The file contains 8 columns, from left to right, are the training step, the validation loss, training loss, root mean square (RMS) validation error of energy, RMS training error of energy, RMS validation error of force, RMS training error of force and the learning rate. The RMS error (RMSE) of the energy is normalized by number of atoms in the system. One can visualize this file by a simple Python script:

```
import numpy as np
import matplotlib.pyplot as plt

data = np.genfromtxt("lcurve.out", names=True)
for name in data.dtype.names[1:-1]:
    plt.plot(data['step'], data[name], label=name)
plt.legend()
plt.xlabel('Step')
plt.ylabel('Loss')
plt.xscale('symlog')
plt.yscale('log')
plt.grid()
plt.show()
```

Checkpoints will be written to files with prefix `save_ckpt` every `save_freq` training steps.

### 5.1.1 Warning

It is warned that the example water data (in folder `examples/water/data`) is of very limited amount, is provided only for testing purpose, and should not be used to train a production model.

## 5.2 Advanced options

In this section, we will take `$deepmd_source_dir/examples/water/se_e2_a/input.json` as an example of the input file.

### 5.2.1 Learning rate

The `learning_rate` section in `input.json` is given as follows

```
"learning_rate" :{
  "type":          "exp",
  "start_lr":      0.001,
  "stop_lr":       3.51e-8,
  "decay_steps":   5000,
  "_comment":      "that's all"
}
```

- `start_lr` gives the learning rate at the beginning of the training.
- `stop_lr` gives the learning rate at the end of the training. It should be small enough to ensure that the network parameters satisfactorily converge.
- During the training, the learning rate decays exponentially from `start_lr` to `stop_lr` following the formula.

$$\text{lr}(t) = \text{start\_lr} * \text{decay\_rate} ^ ( t / \text{decay\_steps} )$$

where `t` is the training step.

### 5.2.2 Training parameters

Other training parameters are given in the `training` section.

```
"training": {
  "training_data": {
    "systems":          ["../data_water/data_0/", "../data_water/data_1/",
    ↪ "../data_water/data_2/"],
    "batch_size":       "auto"
  },
  "validation_data":{
    "systems":          ["../data_water/data_3"],
    "batch_size":       1,
    "numb_btch":        3
  },
  "mixed_precision": {
    "output_prec":      "float32",
    "compute_prec":     "float16"
  }
}
```

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```

    },

    "numb_step":      1000000,
    "seed":           1,
    "disp_file":       "lcurve.out",
    "disp_freq":       100,
    "save_freq":       1000
}

```

The sections "training\_data" and "validation\_data" give the training dataset and validation dataset, respectively. Taking the training dataset for example, the keys are explained below:

- **systems** provide paths of the training data systems. DeePMD-kit allows you to provide multiple systems with different numbers of atoms. This key can be a **list** or a **str**.
  - **list**: **systems** gives the training data systems.
  - **str**: **systems** should be a valid path. DeePMD-kit will recursively search all data systems in this path.
- At each training step, DeePMD-kit randomly pick **batch\_size** frame(s) from one of the systems. The probability of using a system is by default in proportion to the number of batches in the system. More optional are available for automatically determining the probability of using systems. One can set the key **auto\_prob** to
  - "prob\_uniform" all systems are used with the same probability.
  - "prob\_sys\_size" the probability of using a system is in proportional to its size (number of frames).
  - "prob\_sys\_size; sidx\_0:eidx\_0:w\_0; sidx\_1:eidx\_1:w\_1;..." the list of systems are divided into blocks. The block *i* has systems ranging from *sidx\_i* to *eidx\_i*. The probability of using a system from block *i* is in proportional to *w\_i*. Within one block, the probability of using a system is in proportional to its size.
- An example of using "auto\_prob" is given as below. The probability of using **systems[2]** is 0.4, and the sum of the probabilities of using **systems[0]** and **systems[1]** is 0.6. If the number of frames in **systems[1]** is twice as **system[0]**, then the probability of using **system[1]** is 0.4 and that of **system[0]** is 0.2.

```

"training_data": {
    "systems":      ["../data_water/data_0/", "../data_water/data_1/",
→ "../data_water/data_2/"],
    "auto_prob":    "prob_sys_size; 0:2:0.6; 2:3:0.4",
    "batch_size":   "auto"
}

```

- The probability of using systems can also be specified explicitly with key **"sys\_prob"** that is a list having the length of the number of systems. For example

```

"training_data": {
    "systems":      ["../data_water/data_0/", "../data_water/data_1/",
→ "../data_water/data_2/"],
    "sys_prob":     [0.5, 0.3, 0.2],
    "batch_size":   "auto:32"
}

```

- The key **batch\_size** specifies the number of frames used to train or validate the model in a training step. It can be set to
  - **list**: the length of which is the same as the **systems**. The batch size of each system is given by the elements of the list.

- `int`: all systems use the same batch size.
- `"auto"`: the same as `"auto:32"`, see `"auto:N"`
- `"auto:N"`: automatically determines the batch size so that the `batch_size` times the number of atoms in the system is no less than `N`.
- The key `numb_batch` in `validate_data` gives the number of batches of model validation. Note that the batches may not be from the same system

The section `mixed_precision` specifies the mixed precision settings, which will enable the mixed precision training workflow for deepmd-kit. The keys are explained below:

- `output_prec` precision used in the output tensors, only `float32` is supported currently.
- `compute_prec` precision used in the computing tensors, only `float16` is supported currently. Note there are several limitations about the mixed precision training:
- Only `'se_e2_a'` type descriptor is supported by the mixed precision training workflow.
- The precision of embedding net and fitting net are forced to be set to `float32`.

Other keys in the `training` section are explained below:

- `numb_step` The number of training steps.
- `seed` The random seed for getting frames from the training data set.
- `disp_file` The file for printing learning curve.
- `disp_freq` The frequency of printing learning curve. Set in the unit of training steps
- `save_freq` The frequency of saving check point.

### 5.2.3 Options and environment variables

Several command line options can be passed to `dp train`, which can be checked with

```
$ dp train --help
```

An explanation will be provided

```
positional arguments:
  INPUT                the input json database

optional arguments:
  -h, --help            show this help message and exit

  --init-model INIT_MODEL
                        Initialize a model by the provided checkpoint

  --restart RESTART     Restart the training from the provided checkpoint

  --init-frz-model INIT_FRZ_MODEL
                        Initialize the training from the frozen model.

  --skip-neighbor-stat Skip calculating neighbor statistics. Sel checking, automatic_
↪sel, and model compression will be disabled. (default: False)
```

`--init-model model.ckpt`, initializes the model training with an existing model that is stored in the checkpoint `model.ckpt`, the network architectures should match.

**--restart model.ckpt**, continues the training from the checkpoint `model.ckpt`.

**--init-frz-model frozen\_model.pb**, initializes the training with an existing model that is stored in `frozen_model.pb`.

**--skip-neighbor-stat** will skip calculating neighbor statistics if one is concerned about performance. Some features will be disabled.

To get the best performance, one should control the number of threads used by DeePMD-kit. This is achieved by three environmental variables: `OMP_NUM_THREADS`, `TF_INTRA_OP_PARALLELISM_THREADS` and `TF_INTER_OP_PARALLELISM_THREADS`. `OMP_NUM_THREADS` controls the multithreading of DeePMD-kit implemented operations. `TF_INTRA_OP_PARALLELISM_THREADS` and `TF_INTER_OP_PARALLELISM_THREADS` controls `intra_op_parallelism_threads` and `inter_op_parallelism_threads`, which are Tensorflow configurations for multithreading. An explanation is found [here](#).

For example if you wish to use 3 cores of 2 CPUs on one node, you may set the environmental variables and run DeePMD-kit as follows:

```
export OMP_NUM_THREADS=3
export TF_INTRA_OP_PARALLELISM_THREADS=3
export TF_INTER_OP_PARALLELISM_THREADS=2
dp train input.json
```

For a node with 128 cores, it is recommended to start with the following variables:

```
export OMP_NUM_THREADS=16
export TF_INTRA_OP_PARALLELISM_THREADS=16
export TF_INTER_OP_PARALLELISM_THREADS=8
```

It is encouraged to adjust the configurations after empirical testing.

One can set other environmental variables:

Environment ables	vari-	Allowed value	Default value	Usage
DP_INTERFACE_PREC		high, low	high	Control high (double) or low (float) precision of training.

## 5.3 Training Parameters

**Note:** One can load, modify, and export the input file by using our effective web-based tool [DP-GUI](#). All training parameters below can be set in DP-GUI. By clicking “SAVE JSON”, one can download the input file for further training.

**model:**

type: dict  
argument path: `model`

**type\_map:**

type: list, optional  
argument path: `model/type_map`

A list of strings. Give the name to each type of atoms. It is noted that the number of atom type of training system must be less than 128 in a GPU environment.



**data\_stat\_nbatch:**

type: int, optional, default: 10  
 argument path: model/data\_stat\_nbatch

The model determines the normalization from the statistics of the data. This key specifies the number of *frames* in each *system* used for statistics.

**data\_stat\_protect:**

type: float, optional, default: 0.01  
 argument path: model/data\_stat\_protect

Protect parameter for atomic energy regression.

**use\_srtab:**

type: str, optional  
 argument path: model/use\_srtab

The table for the short-range pairwise interaction added on top of DP. The table is a text data file with  $(N_t + 1) * N_t / 2 + 1$  columns. The first column is the distance between atoms. The second to the last columns are energies for pairs of certain types. For example we have two atom types, 0 and 1. The columns from 2nd to 4th are for 0-0, 0-1 and 1-1 correspondingly.

**smin\_alpha:**

type: float, optional  
 argument path: model/smin\_alpha

The short-range tabulated interaction will be swithed according to the distance of the nearest neighbor. This distance is calculated by softmin. This parameter is the decaying parameter in the softmin. It is only required when *use\_srtab* is provided.

**sw\_rmin:**

type: float, optional  
 argument path: model/sw\_rmin

The lower boundary of the interpolation between short-range tabulated interaction and DP. It is only required when *use\_srtab* is provided.

**sw\_rmax:**

type: float, optional  
 argument path: model/sw\_rmax

The upper boundary of the interpolation between short-range tabulated interaction and DP. It is only required when *use\_srtab* is provided.

**type\_embedding:**

type: dict, optional  
 argument path: model/type\_embedding

The type embedding.

**neuron:**

type: list, optional, default: [2, 4, 8]  
 argument path: model/type\_embedding/neuron

Number of neurons in each hidden layers of the embedding net. When two layers are of the same size or one layer is twice as large as the previous layer, a skip connection is built.

**activation\_function:**

type: str, optional, default: tanh

argument path: model/type\_embedding/activation\_function

The activation function in the embedding net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: bool, optional, default: False

argument path: model/type\_embedding/resnet\_dt

Whether to use a “Timestep” in the skip connection

**precision:**

type: str, optional, default: float64

argument path: model/type\_embedding/precision

The precision of the embedding net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**trainable:**

type: bool, optional, default: True

argument path: model/type\_embedding/trainable

If the parameters in the embedding net are trainable

**seed:**

type: int | NoneType, optional

argument path: model/type\_embedding/seed

Random seed for parameter initialization

**descriptor:**

type: dict

argument path: model/descriptor

The descriptor of atomic environment.

Depending on the value of *type*, different sub args are accepted.

**type:**

type: str (flag key)

argument path: model/descriptor/type

possible choices: *loc\_frame*, *se\_e2\_a*, *se\_e3*, *se\_a\_tpe*, *se\_e2\_r*, *hybrid*

The type of the descriptor. See explanation below.

- *loc\_frame*: Defines a local frame at each atom, and the compute the descriptor as local coordinates under this frame.
- *se\_e2\_a*: Used by the smooth edition of Deep Potential. The full relative coordinates are used to construct the descriptor.
- *se\_e2\_r*: Used by the smooth edition of Deep Potential. Only the distance between atoms is used to construct the descriptor.
- *se\_e3*: Used by the smooth edition of Deep Potential. The full relative coordinates are used to construct the descriptor. Three-body embedding will be used by this descriptor.

- *se\_a\_tpe*: Used by the smooth edition of Deep Potential. The full relative coordinates are used to construct the descriptor. Type embedding will be used by this descriptor.
- *hybrid*: Concatenate of a list of descriptors as a new descriptor.

When *type* is set to *loc\_frame*:

**sel\_a:**

type: list

argument path: model/descriptor[loc\_frame]/sel\_a

A list of integers. The length of the list should be the same as the number of atom types in the system. *sel\_a[i]* gives the selected number of type-i neighbors. The full relative coordinates of the neighbors are used by the descriptor.

**sel\_r:**

type: list

argument path: model/descriptor[loc\_frame]/sel\_r

A list of integers. The length of the list should be the same as the number of atom types in the system. *sel\_r[i]* gives the selected number of type-i neighbors. Only relative distance of the neighbors are used by the descriptor. *sel\_a[i] + sel\_r[i]* is recommended to be larger than the maximally possible number of type-i neighbors in the cut-off radius.

**rcut:**

type: float, optional, default: 6.0

argument path: model/descriptor[loc\_frame]/rcut

The cut-off radius. The default value is 6.0

**axis\_rule:**

type: list

argument path: model/descriptor[loc\_frame]/axis\_rule

A list of integers. The length should be 6 times of the number of types.

- *axis\_rule[i\*6+0]*: class of the atom defining the first axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.
- *axis\_rule[i\*6+1]*: type of the atom defining the first axis of type-i atom.
- *axis\_rule[i\*6+2]*: index of the axis atom defining the first axis. Note that the neighbors with the same class and type are sorted according to their relative distance.
- *axis\_rule[i\*6+3]*: class of the atom defining the first axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.
- *axis\_rule[i\*6+4]*: type of the atom defining the second axis of type-i atom.
- *axis\_rule[i\*6+5]*: class of the atom defining the second axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.

When *type* is set to *se\_e2\_a* (or its alias *se\_a*):

**sel:**

type: list | str, optional, default: auto

argument path: model/descriptor[se\_e2\_a]/sel

This parameter set the number of selected neighbors for each type of atom. It can be:

- *List[int]*. The length of the list should be the same as the number of atom types in the system. *sel[i]* gives the selected number of type-i neighbors. *sel[i]* is recommended to be larger than the maximally possible number of type-i neighbors in the cut-off radius. It is noted that the total sel value must be less than 4096 in a GPU environment.
- *str*. Can be “auto:factor” or “auto”. “factor” is a float number larger than 1. This option will automatically determine the *sel*. In detail it counts the maximal number of neighbors with in the cutoff radius for each type of neighbor, then multiply the maximum by the “factor”. Finally the number is wrapped up to 4 divisible. The option “auto” is equivalent to “auto:1.1”.

**rcut:**

type: float, optional, default: 6.0

argument path: model/descriptor[se\_e2\_a]/rcut

The cut-off radius.

**rcut\_smth:**

type: float, optional, default: 0.5

argument path: model/descriptor[se\_e2\_a]/rcut\_smth

Where to start smoothing. For example the  $1/r$  term is smoothed from *rcut* to *rcut\_smth*

**neuron:**

type: list, optional, default: [10, 20, 40]

argument path: model/descriptor[se\_e2\_a]/neuron

Number of neurons in each hidden layers of the embedding net. When two layers are of the same size or one layer is twice as large as the previous layer, a skip connection is built.

**axis\_neuron:**

type: int, optional, default: 4, alias: *n\_axis\_neuron*

argument path: model/descriptor[se\_e2\_a]/axis\_neuron

Size of the submatrix of G (embedding matrix).

**activation\_function:**

type: str, optional, default: tanh

argument path: model/descriptor[se\_e2\_a]/activation\_function

The activation function in the embedding net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: bool, optional, default: False

argument path: model/descriptor[se\_e2\_a]/resnet\_dt

Whether to use a “Timestep” in the skip connection

**type\_one\_side:**

type: bool, optional, default: False

argument path: model/descriptor[se\_e2\_a]/type\_one\_side

Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets

**precision:**

type: str, optional, default: float64

argument path: model/descriptor[se\_e2\_a]/precision

The precision of the embedding net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**trainable:**

type: bool, optional, default: True

argument path: model/descriptor[se\_e2\_a]/trainable

If the parameters in the embedding net is trainable

**seed:**

type: int | NoneType, optional

argument path: model/descriptor[se\_e2\_a]/seed

Random seed for parameter initialization

**exclude\_types:**

type: list, optional, default: []

argument path: model/descriptor[se\_e2\_a]/exclude\_types

The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**set\_davg\_zero:**

type: bool, optional, default: False

argument path: model/descriptor[se\_e2\_a]/set\_davg\_zero

Set the normalization average to zero. This option should be set when *atom\_ener* in the energy fitting is used

When `type` is set to `se_e3` (or its aliases `se_at`, `se_a_3be`, `se_t`):

**sel:**

type: list | str, optional, default: auto

argument path: model/descriptor[se\_e3]/sel

This parameter set the number of selected neighbors for each type of atom. It can be:

- *List[int]*. The length of the list should be the same as the number of atom types in the system. *sel[i]* gives the selected number of type-*i* neighbors. *sel[i]* is recommended to be larger than the maximally possible number of type-*i* neighbors in the cut-off radius. It is noted that the total sel value must be less than 4096 in a GPU environment.
- *str*. Can be “auto:factor” or “auto”. “factor” is a float number larger than 1. This option will automatically determine the *sel*. In detail it counts the maximal number of neighbors within the cutoff radius for each type of neighbor, then multiply the maximum by the “factor”. Finally the number is wrapped up to 4 divisible. The option “auto” is equivalent to “auto:1.1”.

**rcut:**

type: float, optional, default: 6.0

argument path: model/descriptor[se\_e3]/rcut

The cut-off radius.

**rcut\_smth:**

type: float, optional, default: 0.5

argument path: model/descriptor[se\_e3]/rcut\_smth

Where to start smoothing. For example the  $1/r$  term is smoothed from *rcut* to *rcut\_smth*

**neuron:**

type: list, optional, default: [10, 20, 40]  
argument path: model/descriptor[se\_e3]/neuron

Number of neurons in each hidden layers of the embedding net. When two layers are of the same size or one layer is twice as large as the previous layer, a skip connection is built.

**activation\_function:**

type: str, optional, default: tanh  
argument path: model/descriptor[se\_e3]/activation\_function

The activation function in the embedding net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: bool, optional, default: False  
argument path: model/descriptor[se\_e3]/resnet\_dt

Whether to use a “Timestep” in the skip connection

**precision:**

type: str, optional, default: float64  
argument path: model/descriptor[se\_e3]/precision

The precision of the embedding net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**trainable:**

type: bool, optional, default: True  
argument path: model/descriptor[se\_e3]/trainable

If the parameters in the embedding net are trainable

**seed:**

type: int | NoneType, optional  
argument path: model/descriptor[se\_e3]/seed

Random seed for parameter initialization

**set\_davg\_zero:**

type: bool, optional, default: False  
argument path: model/descriptor[se\_e3]/set\_davg\_zero

Set the normalization average to zero. This option should be set when *atom\_ener* in the energy fitting is used

When `type` is set to `se_a_tpe` (or its alias `se_a_ebd`):

**sel:**

type: list | str, optional, default: auto  
argument path: model/descriptor[se\_a\_tpe]/sel

This parameter set the number of selected neighbors for each type of atom. It can be:

- `List[int]`. The length of the list should be the same as the number of atom types in the system. `sel[i]` gives the selected number of type-*i* neighbors. `sel[i]` is recommended to be larger than the

maximally possible number of type-*i* neighbors in the cut-off radius. It is noted that the total *sel* value must be less than 4096 in a GPU environment.

- *str*. Can be “auto:factor” or “auto”. “factor” is a float number larger than 1. This option will automatically determine the *sel*. In detail it counts the maximal number of neighbors within the cutoff radius for each type of neighbor, then multiply the maximum by the “factor”. Finally the number is wrapped up to 4 divisible. The option “auto” is equivalent to “auto:1.1”.

**rcut:**

type: float, optional, default: 6.0

argument path: model/descriptor[se\_a\_tpe]/rcut

The cut-off radius.

**rcut\_smth:**

type: float, optional, default: 0.5

argument path: model/descriptor[se\_a\_tpe]/rcut\_smth

Where to start smoothing. For example the  $1/r$  term is smoothed from *rcut* to *rcut\_smth*

**neuron:**

type: list, optional, default: [10, 20, 40]

argument path: model/descriptor[se\_a\_tpe]/neuron

Number of neurons in each hidden layers of the embedding net. When two layers are of the same size or one layer is twice as large as the previous layer, a skip connection is built.

**axis\_neuron:**

type: int, optional, default: 4, alias: *n\_axis\_neuron*

argument path: model/descriptor[se\_a\_tpe]/axis\_neuron

Size of the submatrix of G (embedding matrix).

**activation\_function:**

type: str, optional, default: tanh

argument path: model/descriptor[se\_a\_tpe]/activation\_function

The activation function in the embedding net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: bool, optional, default: False

argument path: model/descriptor[se\_a\_tpe]/resnet\_dt

Whether to use a “Timestep” in the skip connection

**type\_one\_side:**

type: bool, optional, default: False

argument path: model/descriptor[se\_a\_tpe]/type\_one\_side

Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets

**precision:**

type: str, optional, default: float64

argument path: model/descriptor[se\_a\_tpe]/precision

The precision of the embedding net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**trainable:**

type: bool, optional, default: True

argument path: model/descriptor[se\_a\_tpe]/trainable

If the parameters in the embedding net is trainable

**seed:**

type: int | NoneType, optional

argument path: model/descriptor[se\_a\_tpe]/seed

Random seed for parameter initialization

**exclude\_types:**

type: list, optional, default: []

argument path: model/descriptor[se\_a\_tpe]/exclude\_types

The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**set\_davg\_zero:**

type: bool, optional, default: False

argument path: model/descriptor[se\_a\_tpe]/set\_davg\_zero

Set the normalization average to zero. This option should be set when *atom\_ener* in the energy fitting is used

**type\_nchanl:**

type: int, optional, default: 4

argument path: model/descriptor[se\_a\_tpe]/type\_nchanl

number of channels for type embedding

**type\_nlayer:**

type: int, optional, default: 2

argument path: model/descriptor[se\_a\_tpe]/type\_nlayer

number of hidden layers of type embedding net

**numb\_aparam:**

type: int, optional, default: 0

argument path: model/descriptor[se\_a\_tpe]/numb\_aparam

dimension of atomic parameter. if set to a value > 0, the atomic parameters are embedded.

When `type` is set to `se_e2_r` (or its alias `se_r`):

**sel:**

type: list | str, optional, default: auto

argument path: model/descriptor[se\_e2\_r]/sel

This parameter set the number of selected neighbors for each type of atom. It can be:

- `List[int]`. The length of the list should be the same as the number of atom types in the system. `sel[i]` gives the selected number of type-*i* neighbors. `sel[i]` is recommended to be larger than the



maximally possible number of type-*i* neighbors in the cut-off radius. It is noted that the total *sel* value must be less than 4096 in a GPU environment.

- *str*. Can be “auto:factor” or “auto”. “factor” is a float number larger than 1. This option will automatically determine the *sel*. In detail it counts the maximal number of neighbors within the cutoff radius for each type of neighbor, then multiply the maximum by the “factor”. Finally the number is wrapped up to 4 divisible. The option “auto” is equivalent to “auto:1.1”.

**rcut:**

type: float, optional, default: 6.0

argument path: model/descriptor[se\_e2\_r]/rcut

The cut-off radius.

**rcut\_smth:**

type: float, optional, default: 0.5

argument path: model/descriptor[se\_e2\_r]/rcut\_smth

Where to start smoothing. For example the  $1/r$  term is smoothed from *rcut* to *rcut\_smth*

**neuron:**

type: list, optional, default: [10, 20, 40]

argument path: model/descriptor[se\_e2\_r]/neuron

Number of neurons in each hidden layers of the embedding net. When two layers are of the same size or one layer is twice as large as the previous layer, a skip connection is built.

**activation\_function:**

type: str, optional, default: tanh

argument path: model/descriptor[se\_e2\_r]/activation\_function

The activation function in the embedding net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: bool, optional, default: False

argument path: model/descriptor[se\_e2\_r]/resnet\_dt

Whether to use a “Timestep” in the skip connection

**type\_one\_side:**

type: bool, optional, default: False

argument path: model/descriptor[se\_e2\_r]/type\_one\_side

Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets

**precision:**

type: str, optional, default: float64

argument path: model/descriptor[se\_e2\_r]/precision

The precision of the embedding net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**trainable:**

type: bool, optional, default: True

argument path: model/descriptor[se\_e2\_r]/trainable

If the parameters in the embedding net are trainable

**seed:**

type: `int` | `NoneType`, optional

argument path: `model/descriptor[se_e2_r]/seed`

Random seed for parameter initialization

**exclude\_types:**

type: `list`, optional, default: `[]`

argument path: `model/descriptor[se_e2_r]/exclude_types`

The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**set\_davg\_zero:**

type: `bool`, optional, default: `False`

argument path: `model/descriptor[se_e2_r]/set_davg_zero`

Set the normalization average to zero. This option should be set when *atom\_ener* in the energy fitting is used

When `type` is set to `hybrid`:

**list:**

type: `list`

argument path: `model/descriptor[hybrid]/list`

A list of descriptor definitions

**fitting\_net:**

type: `dict`

argument path: `model/fitting_net`

The fitting of physical properties.

Depending on the value of *type*, different sub args are accepted.

**type:**

type: `str` (flag key), default: `ener`

argument path: `model/fitting_net/type`

possible choices: *ener*, *dipole*, *polar*

The type of the fitting. See explanation below.

- *ener*: Fit an energy model (potential energy surface).
- *dipole*: Fit an atomic dipole model. Global dipole labels or atomic dipole labels for all the selected atoms (see *sel\_type*) should be provided by *dipole.npy* in each data system. The file either has number of frames lines and 3 times of number of selected atoms columns, or has number of frames lines and 3 columns. See *loss* parameter.
- *polar*: Fit an atomic polarizability model. Global polarizability labels or atomic polarizability labels for all the selected atoms (see *sel\_type*) should be provided by *polarizability.npy* in each data system. The file either has number of frames lines and 9 times of number of selected atoms columns, or has number of frames lines and 9 columns. See *loss* parameter.

When `type` is set to `ener`:

**numb\_fparam:**

type: int, optional, default: 0

argument path: `model/fitting_net[ener]/numb_fparam`

The dimension of the frame parameter. If set to >0, file *fparam.npy* should be included to provided the input fparams.

**numb\_aparam:**

type: int, optional, default: 0

argument path: `model/fitting_net[ener]/numb_aparam`

The dimension of the atomic parameter. If set to >0, file *aparam.npy* should be included to provided the input aparams.

**neuron:**

type: list, optional, default: [120, 120, 120], alias: *n\_neuron*

argument path: `model/fitting_net[ener]/neuron`

The number of neurons in each hidden layers of the fitting net. When two hidden layers are of the same size, a skip connection is built.

**activation\_function:**

type: str, optional, default: tanh

argument path: `model/fitting_net[ener]/activation_function`

The activation function in the fitting net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**precision:**

type: str, optional, default: float64

argument path: `model/fitting_net[ener]/precision`

The precision of the fitting net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**resnet\_dt:**

type: bool, optional, default: True

argument path: `model/fitting_net[ener]/resnet_dt`

Whether to use a “Timestep” in the skip connection

**trainable:**

type: list | bool, optional, default: True

argument path: `model/fitting_net[ener]/trainable`

Whether the parameters in the fitting net are trainable. This option can be

- bool: True if all parameters of the fitting net are trainable, False otherwise.
- list of bool: Specifies if each layer is trainable. Since the fitting net is composed by hidden layers followed by a output layer, the length of tihs list should be equal to  $\text{len}(\text{neuron})+1$ .

**rcond:**

type: float, optional, default: 0.001

argument path: `model/fitting_net[ener]/rcond`

The condition number used to determine the inital energy shift for each type of atoms.

**seed:**

type: `int` | `NoneType`, optional  
argument path: `model/fitting_net[ener]/seed`  
Random seed for parameter initialization of the fitting net

**atom\_ener:**

type: `list`, optional, default: `[]`  
argument path: `model/fitting_net[ener]/atom_ener`  
Specify the atomic energy in vacuum for each type

When `type` is set to `dipole`:

**neuron:**

type: `list`, optional, default: `[120, 120, 120]`, alias: `n_neuron`  
argument path: `model/fitting_net[dipole]/neuron`  
The number of neurons in each hidden layers of the fitting net. When two hidden layers are of the same size, a skip connection is built.

**activation\_function:**

type: `str`, optional, default: `tanh`  
argument path: `model/fitting_net[dipole]/activation_function`  
The activation function in the fitting net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: `bool`, optional, default: `True`  
argument path: `model/fitting_net[dipole]/resnet_dt`  
Whether to use a “Timestep” in the skip connection

**precision:**

type: `str`, optional, default: `float64`  
argument path: `model/fitting_net[dipole]/precision`  
The precision of the fitting net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**sel\_type:**

type: `list` | `int` | `NoneType`, optional, alias: `dipole_type`  
argument path: `model/fitting_net[dipole]/sel_type`  
The atom types for which the atomic dipole will be provided. If not set, all types will be selected.

**seed:**

type: `int` | `NoneType`, optional  
argument path: `model/fitting_net[dipole]/seed`  
Random seed for parameter initialization of the fitting net

When `type` is set to `polar`:

**neuron:**

type: `list`, optional, default: `[120, 120, 120]`, alias: `n_neuron`

argument path: `model/fitting_net[polar]/neuron`

The number of neurons in each hidden layers of the fitting net. When two hidden layers are of the same size, a skip connection is built.

**activation\_function:**

type: `str`, optional, default: `tanh`

argument path: `model/fitting_net[polar]/activation_function`

The activation function in the fitting net. Supported activation functions are “relu”, “relu6”, “softplus”, “sigmoid”, “tanh”, “gelu”.

**resnet\_dt:**

type: `bool`, optional, default: `True`

argument path: `model/fitting_net[polar]/resnet_dt`

Whether to use a “Timestep” in the skip connection

**precision:**

type: `str`, optional, default: `float64`

argument path: `model/fitting_net[polar]/precision`

The precision of the fitting net parameters, supported options are “default”, “float16”, “float32”, “float64”.

**fit\_diag:**

type: `bool`, optional, default: `True`

argument path: `model/fitting_net[polar]/fit_diag`

Fit the diagonal part of the rotational invariant polarizability matrix, which will be converted to normal polarizability matrix by contracting with the rotation matrix.

**scale:**

type: `list | float`, optional, default: `1.0`

argument path: `model/fitting_net[polar]/scale`

The output of the fitting net (polarizability matrix) will be scaled by `scale`

**shift\_diag:**

type: `bool`, optional, default: `True`

argument path: `model/fitting_net[polar]/shift_diag`

Whether to shift the diagonal of polar, which is beneficial to training. Default is true.

**sel\_type:**

type: `list | int | NoneType`, optional, alias: `pol_type`

argument path: `model/fitting_net[polar]/sel_type`

The atom types for which the atomic polarizability will be provided. If not set, all types will be selected.

**seed:**

type: `int | NoneType`, optional

argument path: `model/fitting_net[polar]/seed`

Random seed for parameter initialization of the fitting net

**modifier:**

type: dict, optional

argument path: `model/modifier`

The modifier of model output.

Depending on the value of *type*, different sub args are accepted.

**type:**

type: str (flag key)

argument path: `model/modifier/type`

possible choices: *dipole\_charge*

The type of modifier. See explanation below.

*-dipole\_charge*: Use WFCC to model the electronic structure of the system. Correct the long-range interaction

When *type* is set to *dipole\_charge*:

**model\_name:**

type: str

argument path: `model/modifier[dipole_charge]/model_name`

The name of the frozen dipole model file.

**model\_charge\_map:**

type: list

argument path: `model/modifier[dipole_charge]/model_charge_map`

The charge of the WFCC. The list length should be the same as the *sel\_type*.

**sys\_charge\_map:**

type: list

argument path: `model/modifier[dipole_charge]/sys_charge_map`

The charge of real atoms. The list length should be the same as the *type\_map*

**ewald\_beta:**

type: float, optional, default: 0.4

argument path: `model/modifier[dipole_charge]/ewald_beta`

The splitting parameter of Ewald sum. Unit is  $\text{\AA}^{-1}$

**ewald\_h:**

type: float, optional, default: 1.0

argument path: `model/modifier[dipole_charge]/ewald_h`

The grid spacing of the FFT grid. Unit is  $\text{\AA}$

**compress:**

type: dict, optional

argument path: `model/compress`

Model compression configurations

Depending on the value of *type*, different sub args are accepted.

**type:**

type: str (flag key), default: *se\_e2\_a*

argument path: `model/compress/type`

possible choices: `se_e2_a`

The type of model compression, which should be consistent with the descriptor type.

When `type` is set to `se_e2_a` (or its alias `se_a`):

**model\_file:**

type: `str`

argument path: `model/compress[se_e2_a]/model_file`

The input model file, which will be compressed by the DeePMD-kit.

**table\_config:**

type: `list`

argument path: `model/compress[se_e2_a]/table_config`

The arguments of model compression, including `extrapolate`(scale of model extrapolation), `stride`(uniform stride of tabulation's first and second table), and `frequency`(frequency of tabulation overflow check).

**min\_nbor\_dist:**

type: `float`

argument path: `model/compress[se_e2_a]/min_nbor_dist`

The nearest distance between neighbor atoms saved in the frozen model.

**loss:**

type: `dict`, optional

argument path: `loss`

The definition of loss function. The loss type should be set to *tensor*, *ener* or left unset. .

Depending on the value of *type*, different sub args are accepted.

**type:**

type: `str` (flag key), default: `ener`

argument path: `loss/type`

possible choices: `ener`, `tensor`

The type of the loss. When the fitting type is *ener*, the loss type should be set to *ener* or left unset. When the fitting type is *dipole* or *polar*, the loss type should be set to *tensor*. .

When `type` is set to `ener`:

**start\_pref\_e:**

type: `float` | `int`, optional, default: `0.02`

argument path: `loss[ener]/start_pref_e`

The prefactor of energy loss at the start of the training. Should be larger than or equal to 0. If set to none-zero value, the energy label should be provided by file `energy.npy` in each data system. If both `start_pref_energy` and `limit_pref_energy` are set to 0, then the energy will be ignored.

**limit\_pref\_e:**

type: `float` | `int`, optional, default: `1.0`

argument path: `loss[ener]/limit_pref_e`

The prefactor of energy loss at the limit of the training, Should be larger than or equal to 0. i.e. the training step goes to infinity.

**start\_pref\_f:**

type: float | int, optional, default: 1000

argument path: loss[ener]/start\_pref\_f

The prefactor of force loss at the start of the training. Should be larger than or equal to 0. If set to none-zero value, the force label should be provided by file force.npy in each data system. If both start\_pref\_force and limit\_pref\_force are set to 0, then the force will be ignored.

**limit\_pref\_f:**

type: float | int, optional, default: 1.0

argument path: loss[ener]/limit\_pref\_f

The prefactor of force loss at the limit of the training, Should be larger than or equal to 0. i.e. the training step goes to infinity.

**start\_pref\_v:**

type: float | int, optional, default: 0.0

argument path: loss[ener]/start\_pref\_v

The prefactor of virial loss at the start of the training. Should be larger than or equal to 0. If set to none-zero value, the virial label should be provided by file virial.npy in each data system. If both start\_pref\_virial and limit\_pref\_virial are set to 0, then the virial will be ignored.

**limit\_pref\_v:**

type: float | int, optional, default: 0.0

argument path: loss[ener]/limit\_pref\_v

The prefactor of virial loss at the limit of the training, Should be larger than or equal to 0. i.e. the training step goes to infinity.

**start\_pref\_ae:**

type: float | int, optional, default: 0.0

argument path: loss[ener]/start\_pref\_ae

The prefactor of atom\_ener loss at the start of the training. Should be larger than or equal to 0. If set to none-zero value, the atom\_ener label should be provided by file atom\_ener.npy in each data system. If both start\_pref\_atom\_ener and limit\_pref\_atom\_ener are set to 0, then the atom\_ener will be ignored.

**limit\_pref\_ae:**

type: float | int, optional, default: 0.0

argument path: loss[ener]/limit\_pref\_ae

The prefactor of atom\_ener loss at the limit of the training, Should be larger than or equal to 0. i.e. the training step goes to infinity.

**start\_pref\_pf:**

type: float | int, optional, default: 0.0

argument path: loss[ener]/start\_pref\_pf

The prefactor of atom\_pref loss at the start of the training. Should be larger than or equal to 0. If set to none-zero value, the atom\_pref label should be provided by file atom\_pref.npy in each data system. If both start\_pref\_atom\_pref and limit\_pref\_atom\_pref are set to 0, then the atom\_pref will be ignored.

**limit\_pref\_pf:**



type: float | int, optional, default: 0.0  
 argument path: loss[ener]/limit\_pref\_pf

The prefactor of atom\_pref loss at the limit of the training, Should be larger than or equal to 0. i.e. the training step goes to infinity.

#### relative\_f:

type: float | NoneType, optional  
 argument path: loss[ener]/relative\_f

If provided, relative force error will be used in the loss. The difference of force will be normalized by the magnitude of the force in the label with a shift given by *relative\_f*, i.e.  $DF_i / (\|F\| + \text{relative\_f})$  with  $DF$  denoting the difference between prediction and label and  $\|F\|$  denoting the L2 norm of the label.

When *type* is set to *tensor*:

#### pref:

type: float | int  
 argument path: loss[tensor]/pref

The prefactor of the weight of global loss. It should be larger than or equal to 0. It controls the weight of loss corresponding to global label, i.e. 'polarizability.npy' or *dipole.npy*, whose shape should be #frames x [9 or 3]. If it's larger than 0.0, this npy should be included.

#### pref\_atomic:

type: float | int  
 argument path: loss[tensor]/pref\_atomic

The prefactor of the weight of atomic loss. It should be larger than or equal to 0. It controls the weight of loss corresponding to atomic label, i.e. *atomic\_polarizability.npy* or *atomic\_dipole.npy*, whose shape should be #frames x ([9 or 3] x #selected atoms). If it's larger than 0.0, this npy should be included. Both *pref* and *pref\_atomic* should be provided, and either can be set to 0.0.

#### learning\_rate:

type: dict  
 argument path: learning\_rate

The definition of learning rate

#### scale\_by\_worker:

type: str, optional, default: linear  
 argument path: learning\_rate/scale\_by\_worker

When parallel training or batch size scaled, how to alter learning rate. Valid values are *linear* (default), *sqrt* or *none*.

Depending on the value of *type*, different sub args are accepted.

#### type:

type: str (flag key), default: exp  
 argument path: learning\_rate/type  
 possible choices: *exp*

The type of the learning rate.

When *type* is set to *exp*:

#### start\_lr:

type: float, optional, default: 0.001  
argument path: learning\_rate[exp]/start\_lr

The learning rate the start of the training.

**stop\_lr:**

type: float, optional, default: 1e-08  
argument path: learning\_rate[exp]/stop\_lr

The desired learning rate at the end of the training.

**decay\_steps:**

type: int, optional, default: 5000  
argument path: learning\_rate[exp]/decay\_steps

The learning rate is decaying every this number of training steps.

**training:**

type: dict  
argument path: training

The training options.

**training\_data:**

type: dict  
argument path: training/training\_data

Configurations of training data.

**systems:**

type: list | str  
argument path: training/training\_data/systems

The data systems for training. This key can be provided with a list that specifies the systems, or be provided with a string by which the prefix of all systems are given and the list of the systems is automatically generated.

**set\_prefix:**

type: str, optional, default: set  
argument path: training/training\_data/set\_prefix

The prefix of the sets in the *systems*.

**batch\_size:**

type: list | str | int, optional, default: auto  
argument path: training/training\_data/batch\_size

This key can be

- list: the length of which is the same as the *systems*. The batch size of each system is given by the elements of the list.
- int: all *systems* use the same batch size.
- string “auto”: automatically determines the batch size so that the batch\_size times the number of atoms in the system is no less than 32.
- string “auto:N”: automatically determines the batch size so that the batch\_size times the number of atoms in the system is no less than N.

**auto\_prob:**

type: `str`, optional, default: `prob_sys_size`, alias: `auto_prob_style`

argument path: `training/training_data/auto_prob`

Determine the probability of systems automatically. The method is assigned by this key and can be

- “`prob_uniform`”: the probability all the systems are equal, namely  $1.0/\text{self.get\_nsystems}()$
- “`prob_sys_size`”: the probability of a system is proportional to the number of batches in the system
- “`prob_sys_size;stt_idx:end_idx:weight;stt_idx:end_idx:weight;...`”: the list of systems is divided into blocks. A block is specified by `stt_idx:end_idx:weight`, where `stt_idx` is the starting index of the system, `end_idx` is then ending (not including) index of the system, the probabilities of the systems in this block sums up to `weight`, and the relatively probabilities within this block is proportional to the number of batches in the system.

**sys\_probs:**

type: `list` | `NoneType`, optional, default: `None`, alias: `sys_weights`

argument path: `training/training_data/sys_probs`

A list of float if specified. Should be of the same length as `systems`, specifying the probability of each system.

**validation\_data:**

type: `dict` | `NoneType`, optional, default: `None`

argument path: `training/validation_data`

Configurations of validation data. Similar to that of training data, except that a `numb_btch` argument may be configured

**systems:**

type: `list` | `str`

argument path: `training/validation_data/systems`

The data systems for validation. This key can be provided with a list that specifies the systems, or be provided with a string by which the prefix of all systems are given and the list of the systems is automatically generated.

**set\_prefix:**

type: `str`, optional, default: `set`

argument path: `training/validation_data/set_prefix`

The prefix of the sets in the `systems`.

**batch\_size:**

type: `list` | `str` | `int`, optional, default: `auto`

argument path: `training/validation_data/batch_size`

This key can be

- `list`: the length of which is the same as the `systems`. The batch size of each system is given by the elements of the list.
- `int`: all `systems` use the same batch size.
- string “`auto`”: automatically determines the batch size so that the `batch_size` times the number of atoms in the system is no less than 32.

- string “auto:N”: automatically determines the batch size so that the `batch_size` times the number of atoms in the system is no less than N.

**auto\_prob:**

type: `str`, optional, default: `prob_sys_size`, alias: `auto_prob_style`

argument path: `training/validation_data/auto_prob`

Determine the probability of systems automatically. The method is assigned by this key and can be

- “`prob_uniform`”: the probability all the systems are equal, namely  $1.0/\text{self.get\_nsystems}()$
- “`prob_sys_size`”: the probability of a system is proportional to the number of batches in the system
- “`prob_sys_size;stt_idx:end_idx:weight;stt_idx:end_idx:weight;...`”: the list of systems is divided into blocks. A block is specified by `stt_idx:end_idx:weight`, where `stt_idx` is the starting index of the system, `end_idx` is then ending (not including) index of the system, the probabilities of the systems in this block sums up to `weight`, and the relatively probabilities within this block is proportional to the number of batches in the system.

**sys\_probs:**

type: `list` | `NoneType`, optional, default: `None`, alias: `sys_weights`

argument path: `training/validation_data/sys_probs`

A list of float if specified. Should be of the same length as `systems`, specifying the probability of each system.

**numb\_btch:**

type: `int`, optional, default: 1, alias: `numb_batch`

argument path: `training/validation_data/numb_btch`

An integer that specifies the number of systems to be sampled for each validation period.

**mixed\_precision:**

type: `dict`, optional

argument path: `training/mixed_precision`

Configurations of mixed precision.

**output\_prec:**

type: `str`, optional, default: `float32`

argument path: `training/mixed_precision/output_prec`

The precision for mixed precision params. ” “The trainable variables precision during the mixed precision training process, ” “supported options are float32 only currently.

**compute\_prec:**

type: `str`

argument path: `training/mixed_precision/compute_prec`

The precision for mixed precision compute. ” “The compute precision during the mixed precision training process, ” “supported options are float16 only currently.

**numb\_steps:**

type: `int`, alias: `stop_batch`

argument path: `training/numb_steps`

Number of training batch. Each training uses one batch of data.

**seed:**

type: int | NoneType, optional  
argument path: `training/seed`

The random seed for getting frames from the training data set.

**disp\_file:**

type: str, optional, default: `lcurve.out`  
argument path: `training/disp_file`

The file for printing learning curve.

**disp\_freq:**

type: int, optional, default: `1000`  
argument path: `training/disp_freq`

The frequency of printing learning curve.

**save\_freq:**

type: int, optional, default: `1000`  
argument path: `training/save_freq`

The frequency of saving check point.

**save\_ckpt:**

type: str, optional, default: `model.ckpt`  
argument path: `training/save_ckpt`

The file name of saving check point.

**disp\_training:**

type: bool, optional, default: `True`  
argument path: `training/disp_training`

Displaying verbose information during training.

**time\_training:**

type: bool, optional, default: `True`  
argument path: `training/time_training`

Timing during training.

**profiling:**

type: bool, optional, default: `False`  
argument path: `training/profiling`

Profiling during training.

**profiling\_file:**

type: str, optional, default: `timeline.json`  
argument path: `training/profiling_file`

Output file for profiling.

**enable\_profiler:**

type: bool, optional, default: `False`

argument path: `training/enable_profiler`

Enable TensorFlow Profiler (available in TensorFlow 2.3) to analyze performance. The log will be saved to `tensorboard_log_dir`.

**tensorboard:**

type: bool, optional, default: False

argument path: `training/tensorboard`

Enable tensorboard

**tensorboard\_log\_dir:**

type: str, optional, default: log

argument path: `training/tensorboard_log_dir`

The log directory of tensorboard outputs

**tensorboard\_freq:**

type: int, optional, default: 1

argument path: `training/tensorboard_freq`

The frequency of writing tensorboard events.

## 5.4 Parallel training

Currently, parallel training is enabled in a synchronized way with help of [Horovod](#). Depend on the number of training processes (according to MPI context) and number of GPU cards available, DeePMD-kit will decide whether to launch the training in parallel (distributed) mode or in serial mode. Therefore, no additional options is specified in your JSON/YAML input file.

### 5.4.1 Tuning learning rate

Horovod works in the data-parallel mode, resulting in a larger global batch size. For example, the real batch size is 8 when `batch_size` is set to 2 in the input file and you launch 4 workers. Thus, `learning_rate` is automatically scaled by the number of workers for better convergence. Technical details of such heuristic rule are discussed at [Accurate, Large Minibatch SGD: Training ImageNet in 1 Hour](#).

The number of decay steps required to achieve same accuracy can decrease by the number of cards (e.g., 1/2 of steps in the above case), but needs to be scaled manually in the input file.

In some cases, it won't work well when scale learning rate by worker count in a linear way. Then you can try `sqrt` or `none` by setting argument `scale_by_worker` like below.

```
"learning_rate" :{
  "scale_by_worker": "none",
  "type": "exp"
}
```

### 5.4.2 Scaling test

Testing `examples/water/se_e2_a` on a 8-GPU host, linear acceleration can be observed with increasing number of cards.

Num of GPU cards	Seconds every 100 samples	Samples per second	Speed up
1	1.4515	68.89	1.00
2	1.5962	62.65*2	1.82
4	1.7635	56.71*4	3.29
8	1.7267	57.91*8	6.72

### 5.4.3 How to use

Training workers can be launched with `horovodrun`. The following command launches 4 processes on the same host:

```
CUDA_VISIBLE_DEVICES=4,5,6,7 horovodrun -np 4 \
dp train --mpi-log=workers input.json
```

Need to mention, environment variable `CUDA_VISIBLE_DEVICES` must be set to control parallelism on the occupied host where one process is bound to one GPU card.

Note that `OMP_NUM_THREADS`, `TF_INTRA_OP_PARALLELISM_THREADS`, and `TF_INTER_OP_PARALLELISM_THREADS` should be carefully adjusted to achieve the best performance.

When using MPI with Horovod, `horovodrun` is a simple wrapper around `mpirun`. In the case where fine-grained control over options passed to `mpirun`, `mpirun` can be invoked directly, and it will be detected automatically by Horovod, e.g.,

```
CUDA_VISIBLE_DEVICES=4,5,6,7 mpirun -l -launcher=fork -hosts=localhost -np 4 \
dp train --mpi-log=workers input.json
```

this is sometimes necessary on HPC environment.

Whether distributed workers are initiated can be observed at the “Summary of the training” section in the log (`world size > 1`, and distributed).

```
[0] DEEPM INFO    ---Summary of the training-----
[0] DEEPM INFO    distributed
[0] DEEPM INFO    world size:          4
[0] DEEPM INFO    my rank:              0
[0] DEEPM INFO    node list:           ['exp-13-57']
[0] DEEPM INFO    running on:         exp-13-57
[0] DEEPM INFO    computing device:   gpu:0
[0] DEEPM INFO    CUDA_VISIBLE_DEVICES: 0,1,2,3
[0] DEEPM INFO    Count of visible GPU: 4
[0] DEEPM INFO    num_intra_threads:   0
[0] DEEPM INFO    num_inter_threads:   0
[0] DEEPM INFO    -----
```

## 5.4.4 Logging

What's more, 2 command-line arguments are defined to control the logging behavior when performing parallel training with MPI.

optional arguments:

```
-l LOG_PATH, --log-path LOG_PATH
    set log file to log messages to disk, if not
    specified, the logs will only be output to console
    (default: None)
-m {master,collect,workers}, --mpi-log {master,collect,workers}
    Set the manner of logging when running with MPI.
    'master' logs only on main process, 'collect'
    broadcasts logs from workers to master and 'workers'
    means each process will output its own log (default:
    master)
```

## 5.5 TensorBoard Usage

TensorBoard provides the visualization and tooling needed for machine learning experimentation. A full instruction of tensorboard can be found [here](#).

### 5.5.1 Highlighted features

DeePMD-kit can now use most of the interesting features enabled by tensorboard!

- **Tracking and visualizing metrics**, such as l2\_loss, l2\_energy\_loss and l2\_force\_loss
- **Visualizing the model graph** (ops and layers)
- **Viewing histograms of weights, biases, or other tensors as they change over time.**
- **Viewing summaries of trainable variables**

### 5.5.2 How to use Tensorboard with DeePMD-kit

Before running TensorBoard, make sure you have generated summary data in a log directory by modifying the the input script, set “tensorboard” true in training subsection will enable the tensorboard data analysis. eg. **water\_se\_a.json**.

```
"training" : {
  "systems":      ["../data/"],
  "set_prefix":    "set",
  "stop_batch":    1000000,
  "batch_size":    1,

  "seed":          1,

  "_comment": " display and restart",
  "_comment": " frequencies counted in batch",
  "disp_file":     "lcurve.out",
  "disp_freq":     100,
  "numb_test":     10,
```

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```

    "save_freq":      1000,
    "save_ckpt":      "model.ckpt",

    "disp_training": true,
    "time_training": true,
    "tensorboard":    true,
    "tensorboard_log_dir": "log",
    "tensorboard_freq": 1000,
    "profiling":      false,
    "profiling_file": "timeline.json",
    "_comment":       "that's all"
}

```

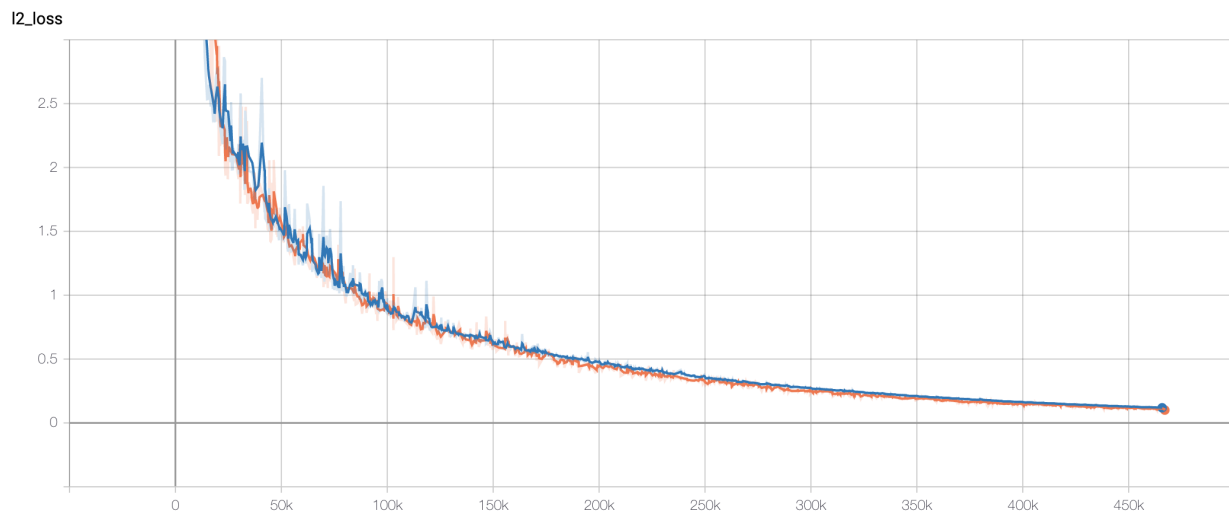
Once you have event files, run TensorBoard and provide the log directory. This should print that TensorBoard has started. Next, connect to `http://tensorboard_server_ip:6006`.

TensorBoard requires a logdir to read logs from. For info on configuring TensorBoard, run `tensorboard --help`. One can easily change the log name with “`tensorboard_log_dir`” and the sampling frequency with “`tensorboard_freq`”.

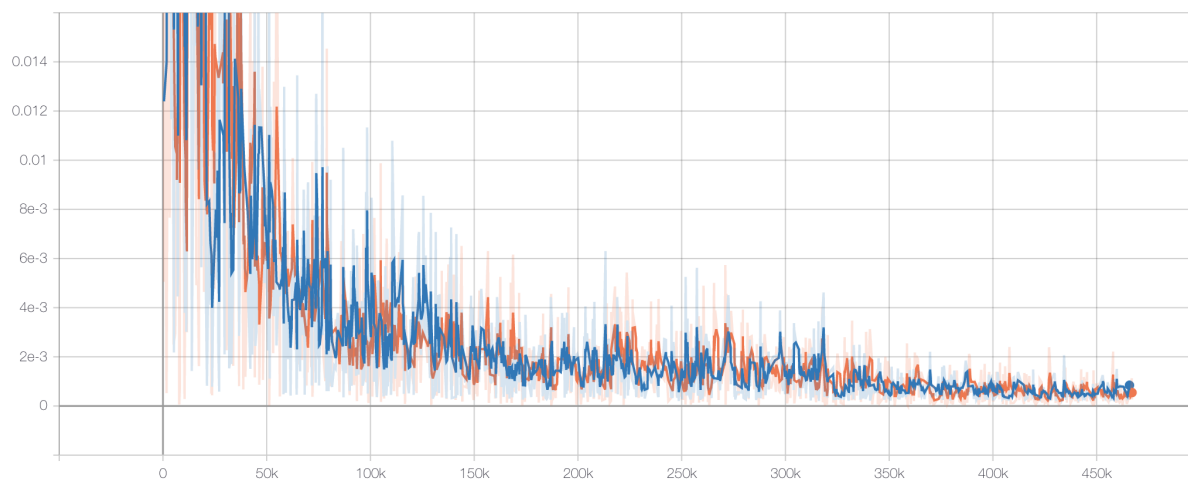
```
tensorboard --logdir path/to/logs
```

### 5.5.3 Examples

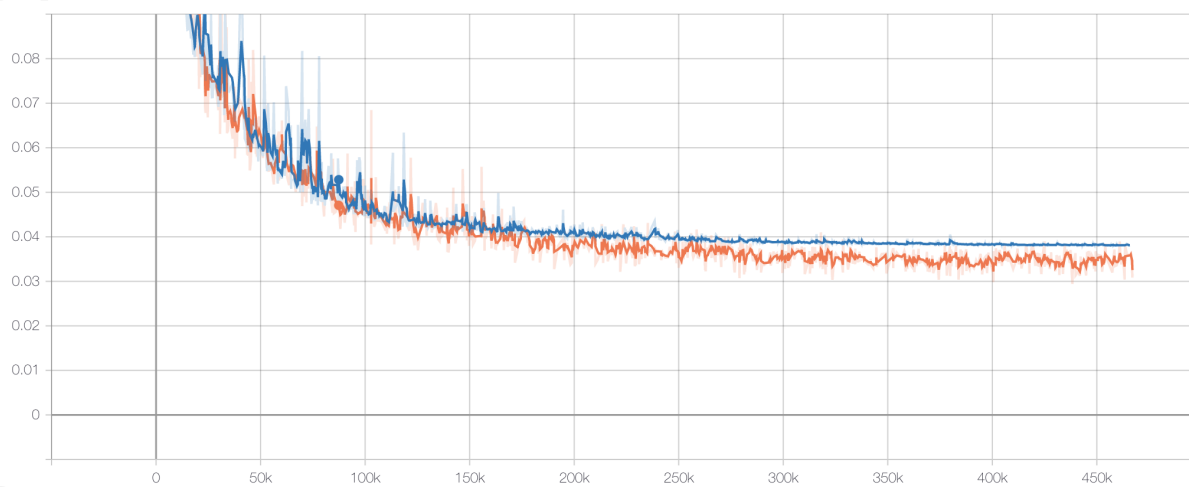
#### Tracking and visualizing loss metrics(red:train, blue:test)



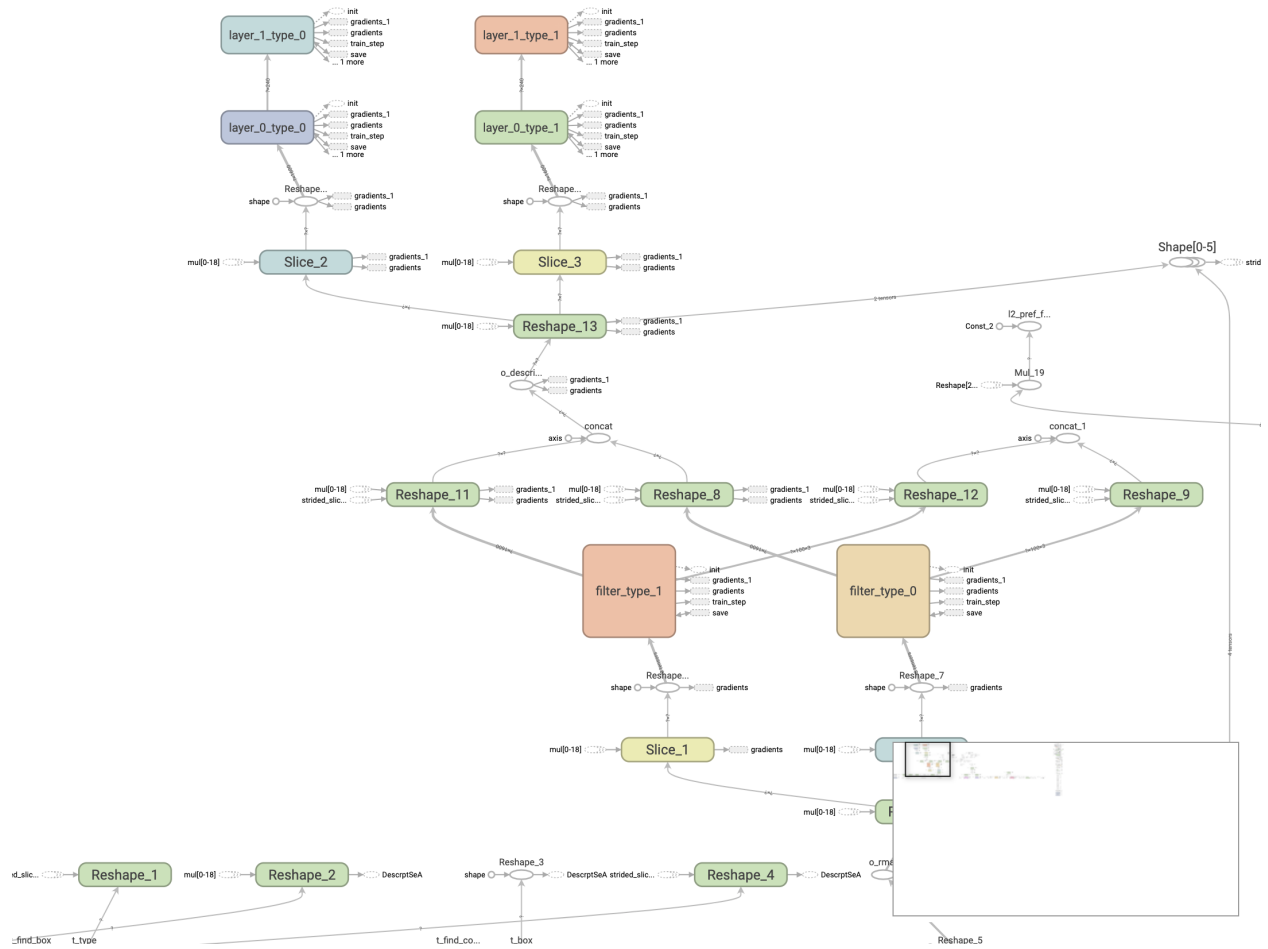
l2\_ener\_loss



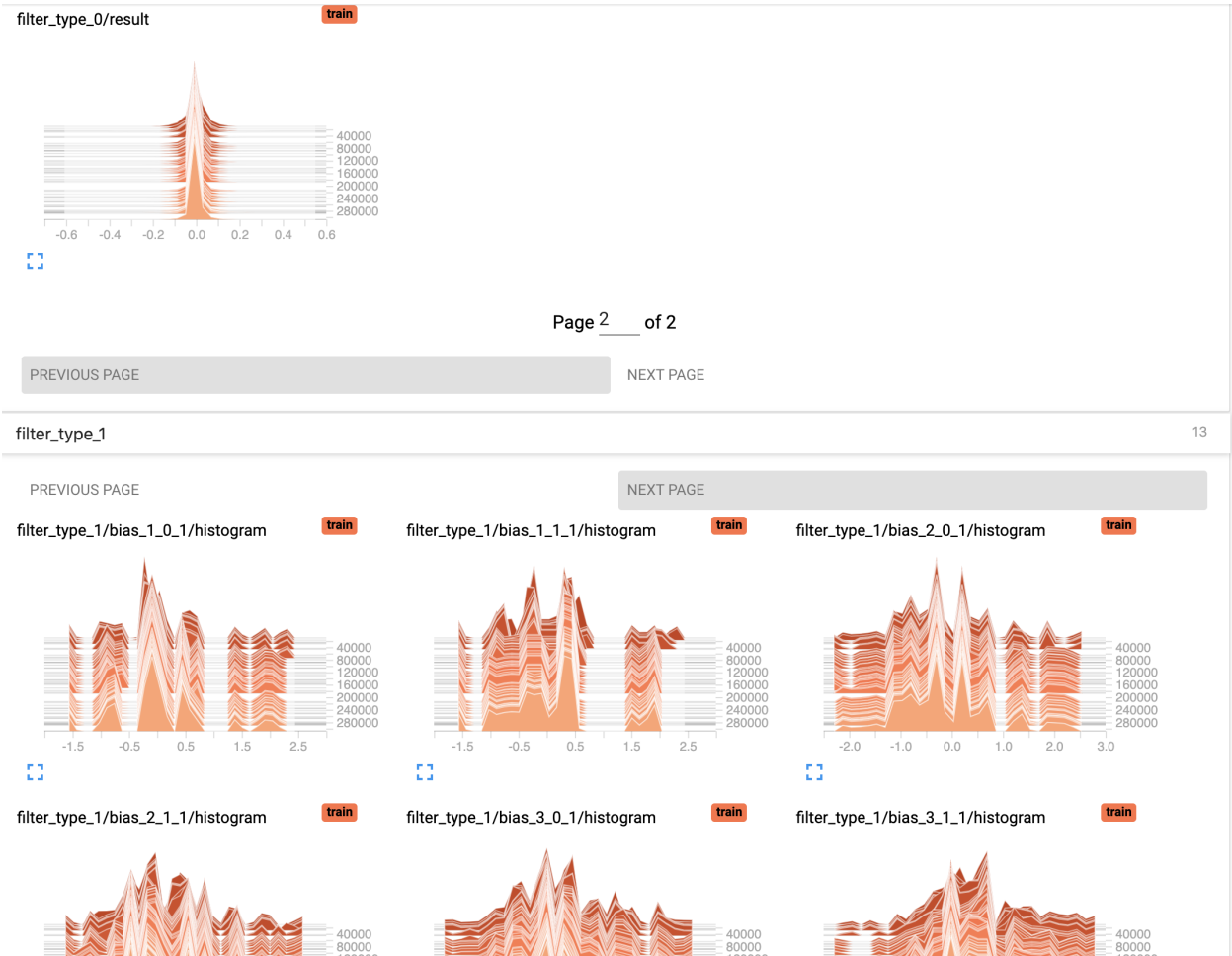
l2\_force\_loss



## Visualizing deepmd-kit model graph



Viewing histograms of weights, biases, or other tensors as they change over time



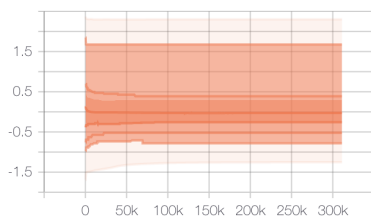
filter\_type\_0

13

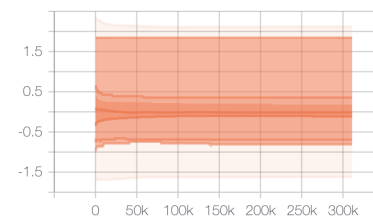
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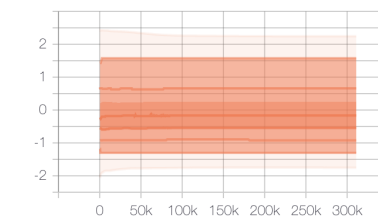
filter\_type\_0/bias\_1\_0\_1/histogram



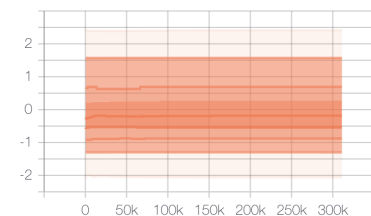
train filter\_type\_0/bias\_1\_1\_1/histogram



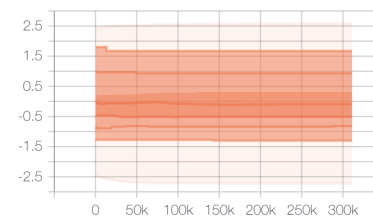
train filter\_type\_0/bias\_2\_0\_1/histogram



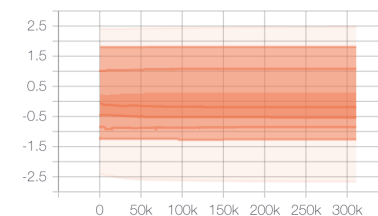
filter\_type\_0/bias\_2\_1\_1/histogram



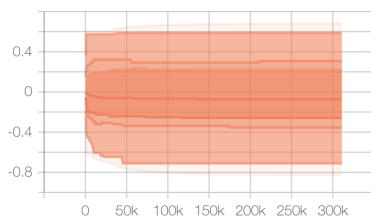
train filter\_type\_0/bias\_3\_0\_1/histogram



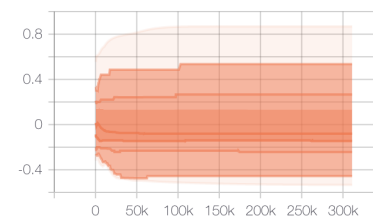
train filter\_type\_0/bias\_3\_1\_1/histogram



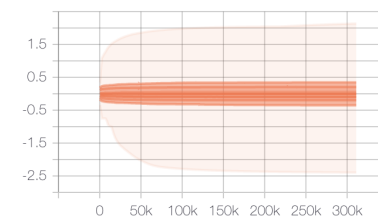
filter\_type\_0/matrix\_1\_0\_1/histogram



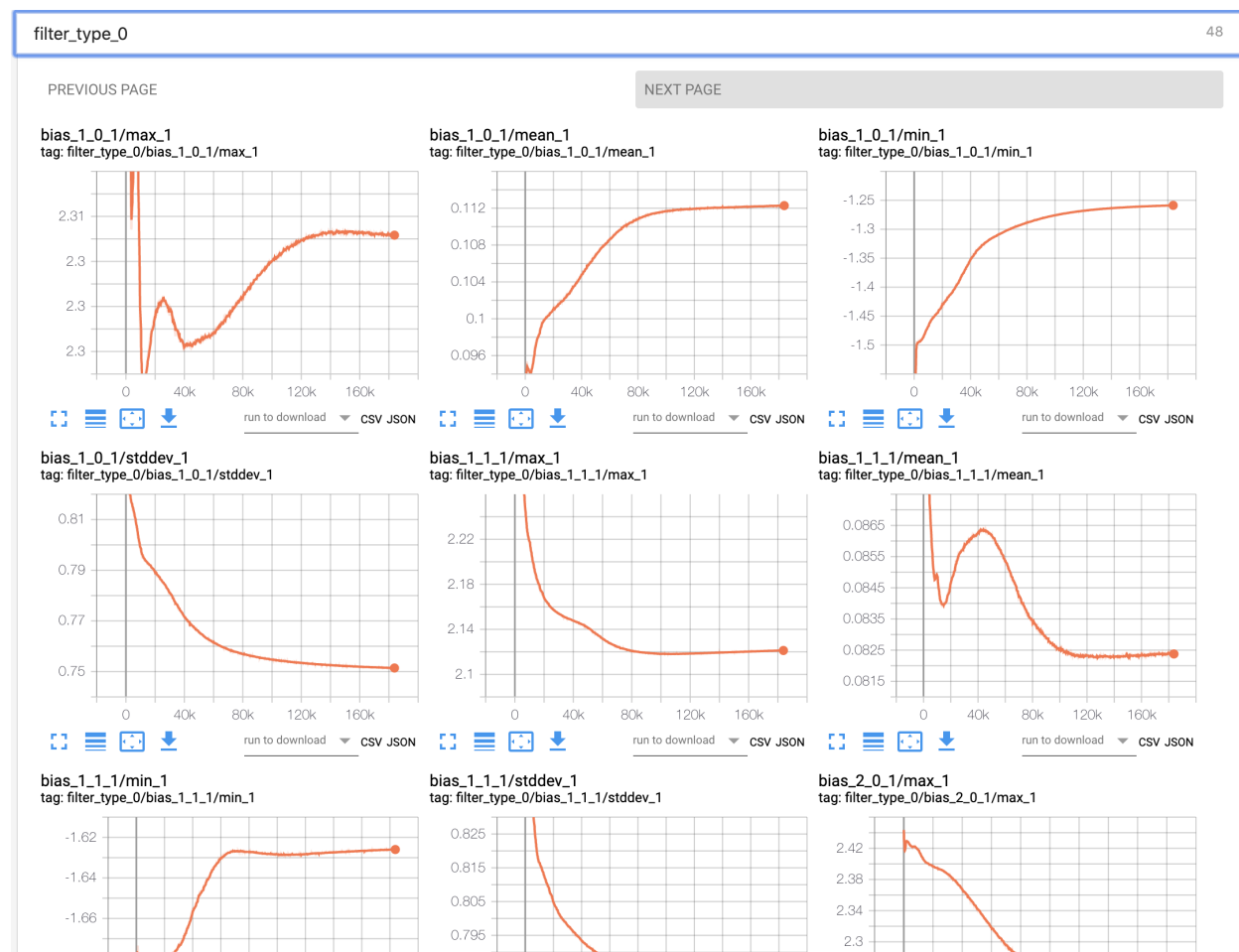
train filter\_type\_0/matrix\_1\_1\_1/histogram



train filter\_type\_0/matrix\_2\_0\_1/histogram



## Viewing summaries of trainable variables



## 5.5.4 Attention

Allowing the tensorboard analysis will takes extra execution time.(eg, 15% increasing @Nvidia GTX 1080Ti double precision with default water sample)

TensorBoard can be used in Google Chrome or Firefox. Other browsers might work, but there may be bugs or performance issues.

## 5.6 Known limitations of using GPUs

If you use deepmd-kit in a GPU environment, the acceptable value range of some variables are additionally restricted compared to the CPU environment due to the software's GPU implementations:

1. The number of atom type of a given system must be less than 128.
2. The maximum distance between an atom and it's neighbors must be less than 128. It can be controlled by setting the rcut value of training parameters.
3. Theoretically, the maximum number of atoms that a single GPU can accept is about 10,000,000. However, this value is actually limited by the GPU memory size currently, usually within 1000,000 atoms even at the model

compression mode.

4. The total sel value of training parameters(in model/descriptor section) must be less than 4096.
5. The size of the last layer of embedding net must be less than 1024 during the model compression process.





## FREEZE AND COMPRESS

### 6.1 Freeze a model

The trained neural network is extracted from a checkpoint and dumped into a database. This process is called “freezing” a model. The idea and part of our code are from [Morgan](#). To freeze a model, typically one does

```
$ dp freeze -o graph.pb
```

in the folder where the model is trained. The output database is called `graph.pb`.

### 6.2 Compress a model

Once the frozen model is obtained from deepmd-kit, we can get the neural network structure and its parameters (weights, biases, etc.) from the trained model, and compress it in the following way:

```
dp compress -i graph.pb -o graph-compress.pb
```

where `-i` gives the original frozen model, `-o` gives the compressed model. Several other command line options can be passed to `dp compress`, which can be checked with

```
$ dp compress --help
```

An explanation will be provided

```
usage: dp compress [-h] [-v {DEBUG,3,INFO,2,WARNING,1,ERROR,0}] [-l LOG_PATH]
                  [-m {master,collect,workers}] [-i INPUT] [-o OUTPUT]
                  [-s STEP] [-e EXTRAPOLATE] [-f FREQUENCY]
                  [-c CHECKPOINT_FOLDER]

optional arguments:
  -h, --help            show this help message and exit
  -v {DEBUG,3,INFO,2,WARNING,1,ERROR,0}, --log-level {DEBUG,3,INFO,2,WARNING,1,ERROR,0}
                        set verbosity level by string or number, 0=ERROR,
                        1=WARNING, 2=INFO and 3=DEBUG (default: INFO)
  -l LOG_PATH, --log-path LOG_PATH
                        set log file to log messages to disk, if not
                        specified, the logs will only be output to console
                        (default: None)
  -m {master,collect,workers}, --mpi-log {master,collect,workers}
```

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```

Set the manner of logging when running with MPI.
'master' logs only on main process, 'collect'
broadcasts logs from workers to master and 'workers'
means each process will output its own log (default:
master)

-i INPUT, --input INPUT
    The original frozen model, which will be compressed by
    the code (default: frozen_model.pb)

-o OUTPUT, --output OUTPUT
    The compressed model (default:
    frozen_model_compressed.pb)

-s STEP, --step STEP
    Model compression uses fifth-order polynomials to
    interpolate the embedding-net. It introduces two
    tables with different step size to store the
    parameters of the polynomials. The first table covers
    the range of the training data, while the second table
    is an extrapolation of the training data. The domain
    of each table is uniformly divided by a given step
    size. And the step(parameter) denotes the step size of
    the first table and the second table will use 10 *
    step as it's step size to save the memory. Usually the
    value ranges from 0.1 to 0.001. Smaller step means
    higher accuracy and bigger model size (default: 0.01)

-e EXTRAPOLATE, --extrapolate EXTRAPOLATE
    The domain range of the first table is automatically
    detected by the code: [d_low, d_up]. While the second
    table ranges from the first table's upper
    boundary(d_up) to the extrapolate(parameter) * d_up:
    [d_up, extrapolate * d_up] (default: 5)

-f FREQUENCY, --frequency FREQUENCY
    The frequency of tabulation overflow check(Whether the
    input environment matrix overflow the first or second
    table range). By default do not check the overflow
    (default: -1)

-c CHECKPOINT_FOLDER, --checkpoint-folder CHECKPOINT_FOLDER
    path to checkpoint folder (default: .)

-t TRAINING_SCRIPT, --training-script TRAINING_SCRIPT
    The training script of the input frozen model
    (default: None)

```

### Parameter explanation

Model compression, which including tabulating the embedding-net. The table is composed of fifth-order polynomial coefficients and is assembled from two sub-tables. For model descriptor with `se_e2_a` type, the first sub-table takes the `stride(parameter)` as it's uniform stride, while the second sub-table takes `10 * stride` as it's uniform stride; For model descriptor with `se_e3` type, the first sub-table takes `10 * stride` as it's uniform stride, while the second sub-table takes `100 * stride` as it's uniform stride. The range of the first table is automatically detected by deepmd-kit, while the second table ranges from the first table's upper boundary(`upper`) to the `extrapolate(parameter) * upper`. Finally, we added a check frequency parameter. It indicates how often the program checks for overflow(if the input environment matrix overflow the first or second table range) during the MD inference.

### Justification of model compression

Model compression, with little loss of accuracy, can greatly speed up MD inference time. According to different

simulation systems and training parameters, the speedup can reach more than 10 times at both CPU and GPU devices. At the same time, model compression can greatly change the memory usage, reducing as much as 20 times under the same hardware conditions.

#### **Acceptable original model version**

The model compression interface requires the version of deepmd-kit used in original model generation should be 2.0.0-alpha.0 or above. If one has a frozen 1.2 or 1.3 model, one can upgrade it through the `dp convert-from` interface.(eg: `dp convert-from 1.2/1.3 -i old_frozen_model.pb -o new_frozen_model.pb`)

#### **Acceptable descriptor type**

Descriptors with `se_e2_a`, `se_e3`, `'se_e2_r'` type are supported by the model compression feature. Hybrid mixed with above descriptors is also supported.

#### **Available activation functions for descriptor:**

- tanh
- gelu
- relu
- relu6
- softplus
- sigmoid



## 7.1 Test a model

The frozen model can be used in many ways. The most straightforward test can be performed using `dp test`. A typical usage of `dp test` is

```
dp test -m graph.pb -s /path/to/system -n 30
```

where `-m` gives the tested model, `-s` the path to the tested system and `-n` the number of tested frames. Several other command line options can be passed to `dp test`, which can be checked with

```
$ dp test --help
```

An explanation will be provided

```
usage: dp test [-h] [-m MODEL] [-s SYSTEM] [-S SET_PREFIX] [-n NUMB_TEST]
              [-r RAND_SEED] [--shuffle-test] [-d DETAIL_FILE]

optional arguments:
  -h, --help                show this help message and exit
  -m MODEL, --model MODEL    Frozen model file to import
  -s SYSTEM, --system SYSTEM The system dir
  -S SET_PREFIX, --set-prefix SET_PREFIX The set prefix
  -n NUMB_TEST, --numb-test NUMB_TEST The number of data for test
  -r RAND_SEED, --rand-seed RAND_SEED The random seed
  --shuffle-test             Shuffle test data
  -d DETAIL_FILE, --detail-file DETAIL_FILE The file containing details of energy force and virial accuracy
```

## 7.2 Calculate Model Deviation

One can also use a subcommand to calculate deviation of predicted forces or virials for a bunch of models in the following way:

```
dp model-devi -m graph.000.pb graph.001.pb graph.002.pb graph.003.pb -s ./data -o model_
devi.out
```

where `-m` specifies graph files to be calculated, `-s` gives the data to be evaluated, `-o` the file to which model deviation results is dumped. Here is more information on this sub-command:

```
usage: dp model-devi [-h] [-v {DEBUG,3,INFO,2,WARNING,1,ERROR,0}]
                    [-l LOG_PATH] [-m MODELS [MODELS ...]] [-s SYSTEM]
                    [-S SET_PREFIX] [-o OUTPUT] [-f FREQUENCY] [-i ITEMS]

optional arguments:
  -h, --help                show this help message and exit
  -v {DEBUG,3,INFO,2,WARNING,1,ERROR,0}, --log-level {DEBUG,3,INFO,2,WARNING,1,ERROR,0}
                        set verbosity level by string or number, 0=ERROR,
                        1=WARNING, 2=INFO and 3=DEBUG (default: INFO)
  -l LOG_PATH, --log-path LOG_PATH
                        set log file to log messages to disk, if not
                        specified, the logs will only be output to console
                        (default: None)
  -m MODELS [MODELS ...], --models MODELS [MODELS ...]
                        Frozen models file to import (default:
                        ['graph.000.pb', 'graph.001.pb', 'graph.002.pb',
                        'graph.003.pb'])
  -s SYSTEM, --system SYSTEM
                        The system directory, not support recursive detection.
                        (default: .)
  -S SET_PREFIX, --set-prefix SET_PREFIX
                        The set prefix (default: set)
  -o OUTPUT, --output OUTPUT
                        The output file for results of model deviation
                        (default: model_devi.out)
  -f FREQUENCY, --frequency FREQUENCY
                        The trajectory frequency of the system (default: 1)
```

For more details with respect to definition of model deviation and its application, please refer to Yuzhi Zhang, Haidi Wang, Weijie Chen, Jinzhe Zeng, Linfeng Zhang, Han Wang, and Weinan E, DP-GEN: A concurrent learning platform for the generation of reliable deep learning based potential energy models, Computer Physics Communications, 2020, 253, 107206.

## INFERENCE

Note that the model for inference is required to be compatible with the DeePMD-kit package. See [Model compatibility](#) for details.

### 8.1 Python interface

One may use the python interface of DeePMD-kit for model inference, an example is given as follows

```
from deepmd.infer import DeepPot
import numpy as np
dp = DeepPot('graph.pb')
coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
cell = np.diag(10 * np.ones(3)).reshape([1, -1])
atype = [1,0,1]
e, f, v = dp.eval(coord, cell, atype)
```

where e, f and v are predicted energy, force and virial of the system, respectively.

Furthermore, one can use the python interface to calculate model deviation.

```
from deepmd.infer import calc_model_devi
from deepmd.infer import DeepPot as DP
import numpy as np

coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
cell = np.diag(10 * np.ones(3)).reshape([1, -1])
atype = [1,0,1]
graphs = [DP("graph.000.pb"), DP("graph.001.pb")]
model_devi = calc_model_devi(coord, cell, atype, graphs)
```

### 8.2 C++ interface

The C++ interface of DeePMD-kit is also available for model interface, which is considered faster than Python interface. An example `infer_water.cpp` is given below:

```
#include "deepmd/DeepPot.h"

int main(){
```

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```
deepmd::DeepPot dp ("graph.pb");
std::vector<double> coord = {1., 0., 0., 0., 0., 1.5, 1., 0., 3.};
std::vector<double> cell = {10., 0., 0., 0., 10., 0., 0., 0., 10.};
std::vector<int> atype = {1, 0, 1};
double e;
std::vector<double> f, v;
dp.compute (e, f, v, coord, atype, cell);
}
```

where  $e$ ,  $f$  and  $v$  are predicted energy, force and virial of the system, respectively.

You can compile `infer_water.cpp` using `gcc`:

```
gcc infer_water.cpp -D HIGH_PREC -L $deepmd_root/lib -L $tensorflow_root/lib -I $deepmd_
↪root/include -I $tensorflow_root/include -Wl,--no-as-needed -ldeepmd_cc -lstdc++ -
↪ltensorflow_cc -Wl,-rpath=$deepmd_root/lib -Wl,-rpath=$tensorflow_root/lib -o infer_
↪water
```

and then run the program:

```
./infer_water
```



## INTEGRATE WITH THIRD-PARTY PACKAGES

Note that the model for inference is required to be compatible with the DeePMD-kit package. See [Model compatibility](#) for details.

### 9.1 Use deep potential with ASE

Deep potential can be set up as a calculator with ASE to obtain potential energies and forces.

```
from ase import Atoms
from deepmd.calculator import DP

water = Atoms('H2O',
               positions=[(0.7601, 1.9270, 1),
                           (1.9575, 1, 1),
                           (1., 1., 1.)],
               cell=[100, 100, 100],
               calculator=DP(model="frozen_model.pb"))
print(water.get_potential_energy())
print(water.get_forces())
```

Optimization is also available:

```
from ase.optimize import BFGS
dyn = BFGS(water)
dyn.run(fmax=1e-6)
print(water.get_positions())
```

### 9.2 Run MD with LAMMPS

Running an MD simulation with LAMMPS is simpler. In the LAMMPS input file, one needs to specify the pair style as follows

```
pair_style      deepmd graph.pb
pair_coeff      * *
```

where `graph.pb` is the file name of the frozen model. It should be noted that LAMMPS counts atom types starting from 1, therefore, all LAMMPS atom type will be firstly subtracted by 1, and then passed into the DeePMD-kit engine to compute the interactions.

## 9.3 LAMMPS commands

### 9.3.1 Enable DeePMD-kit plugin (plugin mode)

If you are using the plugin mode, enable DeePMD-kit package in LAMMPS with `plugin` command:

```
plugin load libdeepmd_lmp.so
```

The built-in mode doesn't need this step.

### 9.3.2 pair\_style deepmd

The DeePMD-kit package provides the `pair_style deepmd`

```
pair_style deepmd models ... keyword value ...
```

- `deepmd` = style of this `pair_style`
- `models` = frozen model(s) to compute the interaction. If multiple models are provided, then only the first model serves to provide energy and force prediction for each timestep of molecular dynamics, and the model deviation will be computed among all models every `out_freq` timesteps.
- `keyword` = `out_file` or `out_freq` or `fparam` or `atomic` or `relative`

### Examples

```
pair_style deepmd graph.pb
pair_style deepmd graph.pb fparam 1.2
pair_style deepmd graph_0.pb graph_1.pb graph_2.pb out_file md.out out_freq 10 atomic_
↪relative 1.0
```

### Description

Evaluate the interaction of the system by using [Deep Potential](#) or [Deep Potential Smooth Edition](#). It is noticed that deep potential is not a “pairwise” interaction, but a multi-body interaction.

This pair style takes the deep potential defined in a model file that usually has the `.pb` extension. The model can be trained and frozen by package [DeePMD-kit](#).

The model deviation evaluate the consistency of the force predictions from multiple models. By default, only the maximal, minimal and average model deviations are output. If the key `atomic` is set, then the model deviation of force prediction of each atom will be output.

By default, the model deviation is output in absolute value. If the keyword `relative` is set, then the relative model deviation will be output. The relative model deviation of the force on atom `i` is defined by

$$Ef_i = \frac{|Df_i|}{|f_i| + level}$$

where `Df_i` is the absolute model deviation of the force on atom `i`, `|f_i|` is the norm of the the force and `level` is provided as the parameter of the keyword `relative`.

## Restrictions

- The `deepmd` pair style is provided in the USER-DEEPMO package, which is compiled from the DeePMD-kit, visit the [DeePMD-kit website](#) for more information.

### 9.3.3 Compute tensorial properties

The DeePMD-kit package provide the compute `deeptensor/atom` for computing atomic tensorial properties.

```
compute ID group-ID deeptensor/atom model_file
```

- ID: user-assigned name of the computation
- group-ID: ID of the group of atoms to compute
- `deeptensor/atom`: the style of this compute
- `model_file`: the name of the binary model file.

## Examples

```
compute          dipole all deeptensor/atom dipole.pb
```

The result of the compute can be dump to trajectory file by

```
dump              1 all custom 100 water.dump id type c_dipole[1] c_dipole[2] c_dipole[3]
```

## Restrictions

- The `deeptensor/atom` compute is provided in the USER-DEEPMO package, which is compiled from the DeePMD-kit, visit the [DeePMD-kit website](#) for more information.

### 9.3.4 Long-range interaction

The reciprocal space part of the long-range interaction can be calculated by LAMMPS command `kpace_style`. To use it with DeePMD-kit, one writes

```
pair_style        deepmd graph.pb
pair_coeff
kpace_style       pppm 1.0e-5
kpace_modify      gewald 0.45
```

Please notice that the DeePMD does nothing to the direct space part of the electrostatic interaction, because this part is assumed to be fitted in the DeePMD model (the direct space cut-off is thus the cut-off of the DeePMD model). The splitting parameter `gewald` is modified by the `kpace_modify` command.

### 9.3.5 Use of the centroid/stress/atom to get the full 3x3 “atomic-virial”

The DeePMD-kit allows also the computation of per-atom stress tensor defined as:

Where is the atomic position of nth atom, velocity of atom and the derivative of the atomic energy.

In LAMMPS one can get the per-atom stress using the command `centroid/stress/atom`:

```
compute ID group-ID centroid/stress/atom NULL virial
```

see [LAMMPS doc page](#) for more details on the meaning of the keywords.

#### Examples

In order of computing the 9-component per-atom stress

```
compute stress all centroid/stress/atom NULL virial
```

Thus `c_stress` is an array with 9 component in the order `xx,yy,zz,xy,xz,yz,yx,zx,zy`.

If you use this feature please cite D. Tisi, L. Zhang, R. Bertossa, H. Wang, R. Car, S. Baroni - arXiv preprint [arXiv:2108.10850](#), 2021

### 9.3.6 Computation of heat flux

Using per-atom stress tensor one can, for example, compute the heat flux defined as:

to compute the heat flux with LAMMPS:

```
compute ke_ID all ke/atom
compute pe_ID all pe/atom
compute stress_ID group-ID centroid/stress/atom NULL virial
compute flux_ID all heat/flux ke_ID pe_ID stress_ID
```

#### Examples

```
compute ke all ke/atom
compute pe all pe/atom
compute stress all centroid/stress/atom NULL virial
compute flux all heat/flux ke pe stress
```

`c_flux` is a global vector of length 6. The first three components are the x, y and z components of the full heat flux vector. The others are the components of the so-called convective portion, see [LAMMPS doc page](#) for more details.

If you use these features please cite D. Tisi, L. Zhang, R. Bertossa, H. Wang, R. Car, S. Baroni - arXiv preprint [arXiv:2108.10850](#), 2021

## 9.4 Run path-integral MD with i-PI

The i-PI works in a client-server model. The i-PI provides the server for integrating the replica positions of atoms, while the DeePMD-kit provides a client named `dp_ipi` (or `dp_ipi_low` for low precision) that computes the interactions (including energy, force and virial). The server and client communicates via the Unix domain socket or the Internet socket. Installation instructions of i-PI can be found [here](#). The client can be started by

```
i-pi input.xml &
dp_ipi water.json
```

It is noted that multiple instances of the client is allow for computing, in parallel, the interactions of multiple replica of the path-integral MD.

`water.json` is the parameter file for the client `dp_ipi`, and an example is provided:

```
{
  "verbose":          false,
  "use_unix":         true,
  "port":             31415,
  "host":             "localhost",
  "graph_file":       "graph.pb",
  "coord_file":       "conf.xyz",
  "atom_type" : {
    "OW":             0,
    "HW1":            1,
    "HW2":            1
  }
}
```

The option `use_unix` is set to `true` to activate the Unix domain socket, otherwise, the Internet socket is used.

The option `port` should be the same as that in `input.xml`:

```
<port>31415</port>
```

The option `graph_file` provides the file name of the frozen model.

The `dp_ipi` gets the atom names from an `XYZ` file provided by `coord_file` (meanwhile ignores all coordinates in it), and translates the names to atom types by rules provided by `atom_type`.

## 9.5 Running MD with GROMACS

### 9.5.1 DP/MM Simulation

This part gives a simple tutorial on how to run a DP/MM simulation for methane in water, which means using DP for methane and TIP3P for water. All relevant files can be found in `examples/methane`.

## Topology Preparation

Similar to QM/MM simulation, the internal interactions (including bond, angle, dihedrals, LJ, Columb) of the region descibed by a neural network potential (NNP) have to be **turned off**. In GROMACS, bonded interactions can be turned off by modifying [ bonds ], [ angles ], [ dihedrals ] and [ pairs ] sections. And LJ and Columb interactions must be turned off by [ exclusions ] section.

For example, if one wants to simulate ethane in water, using DeepPotential for methane and TIP3P for water, the topology of methane should be like the following (as presented in `examples/methane/methane.itp`):

```
[ atomtypes ]
;name btype mass charge ptype sigma epsilon
c3 c3 0.0 0.0 A 0.339771 0.451035
hc hc 0.0 0.0 A 0.260018 0.087027

[ moleculetype ]
;name nrexcl
methane 3

[ atoms ]
; nr type resnr residue atom cgnr charge mass
1 c3 1 MOL C1 1 -0.1068 12.010
2 hc 1 MOL H1 2 0.0267 1.008
3 hc 1 MOL H2 3 0.0267 1.008
4 hc 1 MOL H3 4 0.0267 1.008
5 hc 1 MOL H4 5 0.0267 1.008

[ bonds ]
; i j func b0 kb
1 2 5
1 3 5
1 4 5
1 5 5

[ exclusions ]
; ai aj1 aj2 aj3 aj4
1 2 3 4 5
2 1 3 4 5
3 1 2 4 5
4 1 2 3 5
5 1 2 3 4
```

For comparson, the original topology file genearted by acpype will be:

```
; methane_GMX.itp created by acpype (v: 2021-02-05T22:15:50CET) on Wed Sep 8 01:21:53
→2021

[ atomtypes ]
;name bond_type mass charge ptype sigma epsilon Amb
c3 c3 0.000000 0.000000 A 3.39771e-01 4.51035e-01 ; 1.91 0.1078
hc hc 0.000000 0.000000 A 2.60018e-01 8.70272e-02 ; 1.46 0.0208

[ moleculetype ]
;name nrexcl
```

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```

methane          3

[ atoms ]
;  nr  type  resi  res  atom  cgnr      charge      mass      ; qtot  bond_type
   1   c3    1    MOL   C1    1    -0.106800    12.01000 ; qtot -0.107
   2   hc    1    MOL   H1    2     0.026700     1.00800 ; qtot -0.080
   3   hc    1    MOL   H2    3     0.026700     1.00800 ; qtot -0.053
   4   hc    1    MOL   H3    4     0.026700     1.00800 ; qtot -0.027
   5   hc    1    MOL   H4    5     0.026700     1.00800 ; qtot  0.000

[ bonds ]
;  ai    aj  funct    r          k
   1     2    1    1.0970e-01  3.1455e+05 ;    C1 - H1
   1     3    1    1.0970e-01  3.1455e+05 ;    C1 - H2
   1     4    1    1.0970e-01  3.1455e+05 ;    C1 - H3
   1     5    1    1.0970e-01  3.1455e+05 ;    C1 - H4

[ angles ]
;  ai    aj    ak    funct    theta      cth
   2     1     3     1    1.0758e+02  3.2635e+02 ;    H1 - C1    - H2
   2     1     4     1    1.0758e+02  3.2635e+02 ;    H1 - C1    - H3
   2     1     5     1    1.0758e+02  3.2635e+02 ;    H1 - C1    - H4
   3     1     4     1    1.0758e+02  3.2635e+02 ;    H2 - C1    - H3
   3     1     5     1    1.0758e+02  3.2635e+02 ;    H2 - C1    - H4
   4     1     5     1    1.0758e+02  3.2635e+02 ;    H3 - C1    - H4

```

## DeepMD Settings

Before running simulation, we need to tell GROMACS to use DeepPotential by setting environment variable `GMX_DEEPMO_INPUT_JSON`:

```
export GMX_DEEPMO_INPUT_JSON=input.json
```

Then, in your working directories, we have to write `input.json` file:

```

{
  "graph_file": "/path/to/graph.pb",
  "type_file": "type.raw",
  "index_file": "index.raw",
  "lambda": 1.0,
  "pbc": false
}

```

Here is an explanation for these settings:

- `graph_file`: The graph file (with suffix `.pb`) generated by `dp freeze` command
- `type_file`: File to specify DP atom types (in space-separated format). Here, `type.raw` looks like

```
1 0 0 0 0
```

- `index_file`: File containing indices of DP atoms (in space-separated format), which should be in consistent with indices' order in `.gro` file but **starting from zero**. Here, `index.raw` looks like

0 1 2 3 4

- `lambda`: Optional, default 1.0. Used in alchemical calculations.
- `pbcs`: Optional, default true. If true, the GROMACS periodic condition is passed to DeepMD.

## Run Simulation

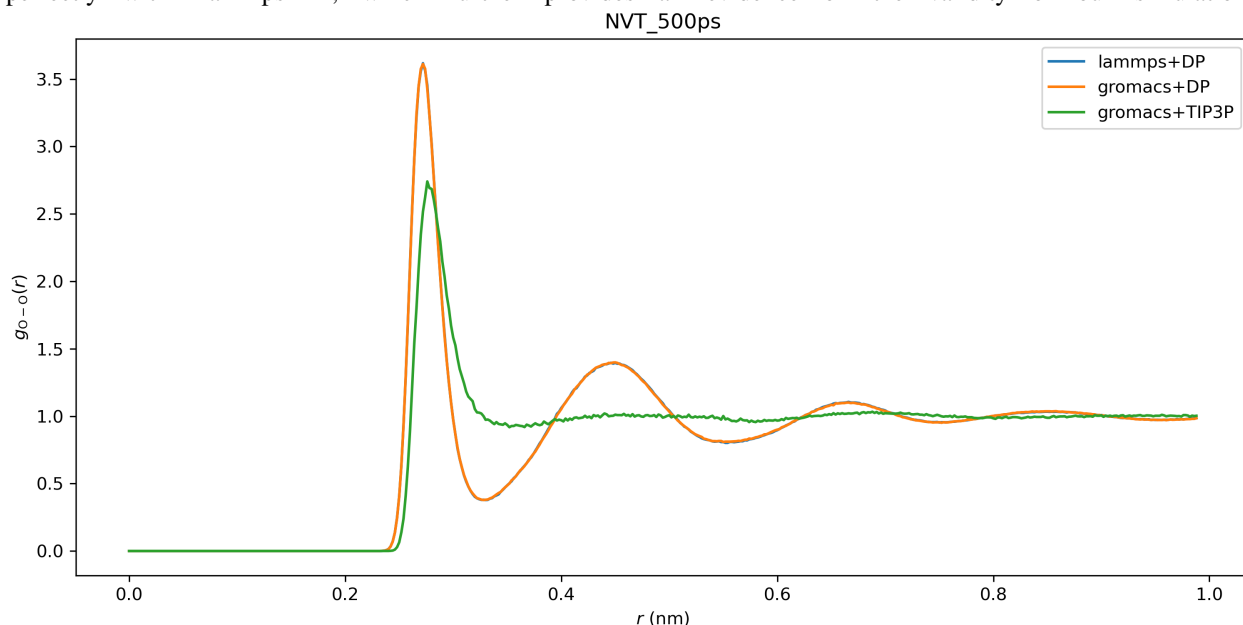
Finally, you can run GROMACS using `gmx mdrun` as usual.

### 9.5.2 All-atom DP Simulation

This part gives an example on how to run a simulation with all atoms described by a DeepPotential with Gromacs, taking water as an example. Instead of using `[ exclusions ]` to turn off the non-bonded energies, we can simply do this by setting LJ parameters (i.e. `epsilon` and `sigma`) and partial charges to 0, as shown in `examples/water/gmx/water.top`:

```
[ atomtypes ]
; name      at.num  mass    charge ptype  sigma    epsilon
HW          1       1.008   0.0000  A    0.000000e+00  0.000000e+00
OW          8       16.00   0.0000  A    0.000000e+00  0.000000e+00
```

As mentioned in the above section, `input.json` and relevant files (`index.raw`, `type.raw`) should also be created. Then, we can start the simulation under NVT ensemble and plot the radial distribution function (RDF) by `gmx rdf` command. We can see that the RDF given by Gromacs+DP matches perfectly with LAMMPS+DP, which further provides an evidence on the validity of our simulation.



However, we still recommend you run all-atom DP simulation using LAMMPS since it is more stable and efficient.



In consequence of various differences of computers or systems, problems may occur. Some common circumstances are listed as follows. In addition, some frequently asked questions about parameters setting are listed as follows. If other unexpected problems occur, you're welcome to contact us for help.

## 10.1 How to tune Fitting/embedding-net size ?

Here are some test forms on fitting-net size tuning or embedding-net size tuning performed on several different systems.

### 10.1.1 Al2O3

**Fitting net size tuning form on Al2O3: (embedding-net size: [25,50,100])**

Fitting-net size	Energy L2err(eV)	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[240,240,240]	1.742252e-02	7.259383e-05	4.014115e-02
[80,80,80]	1.799349e-02	7.497287e-05	4.042977e-02
[40,40,40]	1.799036e-02	7.495984e-05	4.068806e-02
[20,20,20]	1.834032e-02	7.641801e-05	4.094784e-02
[10,10,10]	1.913058e-02	7.971073e-05	4.154775e-02
[5,5,5]	1.932914e-02	8.053808e-05	4.188052e-02
[4,4,4]	1.944832e-02	8.103467e-05	4.217826e-02
[3,3,3]	2.068631e-02	8.619296e-05	4.300497e-02
[2,2,2]	2.267962e-02	9.449840e-05	4.413609e-02
[1,1,1]	2.813596e-02	1.172332e-04	4.781115e-02
[]	3.135002e-02	1.306251e-04	5.373120e-02

*[] means no hidden layer, but there is still a linear output layer. This situation is equal to the linear regression.*

**Embedding net size tuning form on Al<sub>2</sub>O<sub>3</sub>: (Fitting-net size: [240,240,240])**

Embedding-net size	Energy L2err(eV)	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[25,50,100]	1.742252e-02	7.259383e-05	4.014115e-02
[10,20,40]	2.909990e-02	1.212496e-04	4.734667e-02
[5,10,20]	3.357767e-02	1.399070e-04	5.706385e-02
[4,8,16]	6.060367e-02	2.525153e-04	7.333304e-02
[3,6,12]	5.656043e-02	2.356685e-04	7.793539e-02
[2,4,8]	5.277023e-02	2.198759e-04	7.459995e-02
[1,2,4]	1.302282e-01	5.426174e-04	9.672238e-02

**10.1.2 Cu****Fitting net size tuning form on Cu: (embedding-net size: [25,50,100])**

Fitting-net size	Energy L2err(eV)	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[240,240,240]	4.135548e-02	1.615449e-04	8.940946e-02
[20,20,20]	4.323858e-02	1.689007e-04	8.955762e-02
[10,10,10]	4.399364e-02	1.718502e-04	8.962891e-02
[5,5,5]	4.468404e-02	1.745470e-04	8.970111e-02
[4,4,4]	4.463580e-02	1.743586e-04	8.972011e-02
[3,3,3]	4.493758e-02	1.755374e-04	8.971303e-02
[2,2,2]	4.500736e-02	1.758100e-04	8.973878e-02
[1,1,1]	4.542073e-02	1.774247e-04	8.964761e-02
[]	4.545168e-02	1.775456e-04	8.983201e-02

**Embedding net size tuning form on Cu: (Fitting-net size: [240,240,240])**

Embedding-net size	Energy L2err(eV)	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[25,50,100]	4.135548e-02	1.615449e-04	8.940946e-02
[20,40,80]	4.203562e-02	1.642016e-04	8.925881e-02
[15,30,60]	4.146672e-02	1.619794e-04	8.936911e-02
[10,20,40]	4.263060e-02	1.665258e-04	8.955818e-02
[5,10,20]	4.994913e-02	1.951138e-04	9.007786e-02
[4,8,16]	1.022157e-01	3.992802e-04	9.532119e-02
[3,6,12]	1.362098e-01	5.320695e-04	1.073860e-01
[2,4,8]	7.061800e-02	2.758515e-04	9.126418e-02
[1,2,4] && seed = 1	9.843161e-02	3.844985e-04	9.348505e-02
[1,2,4] && seed = 2	9.404335e-02	3.673568e-04	9.304089e-02
[1,2,4] && seed = 3	1.508016e-01	5.890688e-04	1.382356e-01
[1,2,4] && seed = 4	9.686949e-02	3.783965e-04	9.294820e-02

### 10.1.3 Water

Fitting net size tuning form on water: (embedding-net size: [25,50,100])

Fitting-net size	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[240,240,240]	9.1589E-04	5.1540E-02
[200,200,200]	9.3221E-04	5.2366E-02
[160,160,160]	9.4274E-04	5.3403E-02
[120,120,120]	9.5407E-04	5.3093E-02
[80,80,80]	9.4605E-04	5.3402E-02
[40,40,40]	9.8533E-04	5.5790E-02
[20,20,20]	1.0057E-03	5.8232E-02
[10,10,10]	1.0466E-03	6.2279E-02
[5,5,5]	1.1154E-03	6.7994E-02
[4,4,4]	1.1289E-03	6.9613E-02
[3,3,3]	1.2368E-03	7.9786E-02
[2,2,2]	1.3558E-03	9.7042E-02
[1,1,1]	1.4633E-03	1.1265E-01
[]	1.5193E-03	1.2136E-01

Embedding net size tuning form on water: (Fitting-net size: [240,240,240])

Embedding-net size	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[25,50,100]	9.1589E-04	5.1540E-02
[20,40,80]	9.5080E-04	5.3593E-02
[15,30,60]	9.7996E-04	5.6338E-02
[10,20,40]	1.0353E-03	6.2776E-02
[5,10,20]	1.1254E-03	7.3195E-02
[4,8,16]	1.2495E-03	8.0371E-02
[3,6,12]	1.3604E-03	9.9883E-02
[2,4,8]	1.4358E-03	9.7389E-02
[1,2,4]	2.1765E-03	1.7276E-01

## 10.1.4 Mg-Al

Fitting net size tuning form on Mg-Al: (embedding-net size: [25,50,100])

Fitting-net size	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[240,240,240]	3.9606e-03	1.6289e-02
[200,200,200]	3.9449e-03	1.6471e-02
[160,160,160]	4.0947e-03	1.6413e-02
[120,120,120]	3.9234e-03	1.6283e-02
[80,80,80]	3.9758e-03	1.6506e-02
[40,40,40]	3.9142e-03	1.6348e-02
[20,20,20]	4.1302e-03	1.7006e-02
[10,10,10]	4.3433e-03	1.7524e-02
[5,5,5]	5.3154e-03	1.9716e-02
[4,4,4]	5.4210e-03	1.9710e-02
[2,2,2]	6.2667e-03	2.2568e-02
[1,1,1]	7.3676e-03	2.6375e-02
[]	7.3999e-03	2.6097e-02

Embedding net size tuning form on Mg-Al: (Fitting-net size: [240,240,240])

Embedding-net size	Energy L2err/Natoms(eV)	Force L2err(eV/Angstrom)
[25,50,100]	3.9606e-03	1.6289e-02
[20,40,80]	4.0292e-03	1.6555e-02
[15,30,60]	4.1743e-03	1.7026e-02
[10,20,40]	4.8138e-03	1.8516e-02
[5,10,20]	5.6052e-03	2.0709e-02
[4,8,16]	6.1335e-03	2.1450e-02
[3,6,12]	6.6469e-03	2.3003e-02
[2,4,8]	6.8222e-03	2.6318e-02
[1,2,4]	1.0678e-02	3.9559e-02

## 10.2 How to control the number of nodes used by a job ?

Set the number of CPU nodes used by DP algorithms with:

```
mpirun -np $num_nodes dp
```

Set the number of threads used by DP algorithms with:

```
export OMP_NUM_THREADS=$num_threads
```

Set the number of CPU nodes used by TF kernels with:

```
export TF_INTRA_OP_PARALLELISM_THREADS=$num_nodes
export TF_INTER_OP_PARALLELISM_THREADS=$num_nodes
```

## 10.3 Do we need to set $rcut < \text{half boxsize}$ ?

When seeking the neighbors of atom  $i$  under periodic boundary condition, deepmd-kit considers all  $j$  atoms within cutoff  $rcut$  from atom  $i$  in all mirror cells.

So, so there is no limitation on the setting of  $rcut$ .

PS: The reason why some softwares require  $rcut < \text{half boxsize}$  is that they only consider the nearest mirrors from the center cell. Deepmd-kit is totally different from them.

## 10.4 How to set $sel$ ?

$sel$  is short for “selected number of atoms in  $rcut$ ”.

$sel\_a[i]$  is a list of integers. The length of the list should be the same as the number of atom types in the system.

$sel\_a[i]$  gives the number of selected number of type  $i$  neighbors within  $rcut$ . To ensure that the results are strictly accurate,  $sel\_a[i]$  should be larger than the largest number of type  $i$  neighbors in the  $rcut$ .

However, the computation overhead increases with  $sel\_a[i]$ , therefore,  $sel\_a[i]$  should be as small as possible.

The setting of  $sel\_a[i]$  should balance the above two considerations.

## 10.5 Installation

### 10.5.1 Inadequate versions of gcc/g++

Sometimes you may use a gcc/g++ of version  $< 4.8$ . In this way, you can still compile all the parts of TensorFlow and most of the parts of DeePMD-kit, but i-Pi and GROMACS plugin will be disabled automatically. Or if you have a gcc/g++ of version  $> 4.8$ , say, 7.2.0, you may choose to use it by doing

```
export CC=/path/to/gcc-7.2.0/bin/gcc
export CXX=/path/to/gcc-7.2.0/bin/g++
```

### 10.5.2 Build files left in DeePMD-kit

When you try to build a second time when installing DeePMD-kit, files produced before may contribute to failure. Thus, you may clear them by

```
cd build
rm -r *
```

and redo the cmake process.

## 10.6 The temperature undulates violently during early stages of MD

This is probably because your structure is too far from the equilibrium configuration.

Although, to make sure the potential model is truly accurate, we recommend to check model deviation.

## 10.7 MD: cannot run LAMMPS after installing a new version of DeePMD-kit

This typically happens when you install a new version of DeePMD-kit and copy directly the generated USER-DEEPM to a LAMMPS source code folder and re-install LAMMPS.

To solve this problem, it suffices to first remove USER-DEEPM from LAMMPS source code by

```
make no-user-deepmd
```

and then install the new USER-DEEPM.

If this does not solve your problem, try to decompress the LAMMPS source tarball and install LAMMPS from scratch again, which typically should be very fast.

## 10.8 Model compatibility

When the version of DeePMD-kit used to training model is different from the that of DeePMD-kit running MDs, one has the problem of model compatibility.

DeePMD-kit guarantees that the codes with the same major and minor revisions are compatible. That is to say v0.12.5 is compatible to v0.12.0, but is not compatible to v0.11.0 nor v1.0.0.

One can execute `dp convert-from` to convert an old model to a new one.

Model version	v0.12	v1.0	v1.1	v1.2	v1.3	v2.0	v2.1
Compatibility							

### Legend:

- : The model is compatible with the DeePMD-kit package.
- : The model is incompatible with the DeePMD-kit package, but one can execute `dp convert-from` to convert an old model to v2.1.
- : The model is incompatible with the DeePMD-kit package, and there is no way to convert models.

## CODING CONVENTIONS

### 11.1 Preface

The aim of these coding standards is to help create a codebase with defined and consistent coding style that every contributor can get easily familiar with. This will enhance code readability as there will be no different coding styles from different contributors and everything will be documented. Also PR diffs will be smaller because of unified coding style. Finally static typing will help in hunting down potential bugs before the code is even run.

Contributed code will not be refused merely because it does not strictly adhere to these conditions; as long as it's internally consistent, clean, and correct, it probably will be accepted. But don't be surprised if the "offending" code gets fiddled over time to conform to these conventions.

There are also github actions CI checks for python code style which will annotate the PR diff for you to see the areas where your code is lacking compared to the set standard.

### 11.2 Rules

The code must be compatible with the oldest supported version of python which is 3.6

The project follows the generic coding conventions as specified in the [Style Guide for Python Code](#), [Docstring Conventions](#) and [Typing Conventions](#) PEPs, clarified and extended as follows:

- Do not use "\*" imports such as `from module import *`. Instead, list imports explicitly.
- Use 4 spaces per indentation level. No tabs.
- No one-liner compound statements (i.e., no `if x: return`: use two lines).
- Maximum line length is 88 characters as recommended by [black](#) which is less strict than [Docstring Conventions](#) suggests.
- Use "StudlyCaps" for class names.
- Use "lowercase" or "lowercase\_with\_underscores" for function, method, variable names and module names. For short names, joined lowercase may be used (e.g. "tagname"). Choose what is most readable.
- No single-character variable names, except indices in loops that encompass a very small number of lines (`for i in range(5): ...`).
- Avoid lambda expressions. Use named functions instead.
- Avoid functional constructs (filter, map, etc.). Use list comprehensions instead.
- Use "double quotes" for string literals, and `"""triple double quotes"""` for docstring's. Single quotes are OK for something like

```
f"something {'this' if x else 'that'}"
```

- Use f-strings `s = f"{x:.2f}"` instead of old style formatting with `"%f" % x`. string format method `"{x:.2f}".format()` may be used sparsely where it is more convenient than f-strings.

## 11.3 Whitespace

Python is not C/C++ so whitespace should be used sparingly to maintain code readability

- Read the *Whitespace in Expressions and Statements* section of [PEP8](#).
- Avoid [trailing whitespaces](#).
- Do not use excessive whitespace in your expressions and statements.
- You should have blank spaces after commas, colons, and semi-colons if it isn't trailing next to the end of a bracket, brace, or parentheses.
- With any operators you should use a space in on both sides of the operator.
- Colons for slicing are considered a binary operator, and should not have any spaces between them.
- You should have parentheses with no space, directly next to the function when calling functions `function()`.
- When indexing or slicing the brackets should be directly next to the collection with no space `collection["index"]`.
- Whitespace used to line up variable values is not recommended.
- Make sure you are consistent with the formats you choose when optional choices are available.

## 11.4 General advice

- Get rid of as many `break` and `continue` statements as possible.
- Write short functions. All functions should fit within a standard screen.
- Use descriptive variable names.

## 11.5 Writing documentation in the code

Here is an example of how to write good docstrings:

<https://github.com/numpy/numpy/blob/master/doc/example.py>

The numpy doctring documentation can be found [here](#)

It is a good practice to run [pydocstyle](#) check on your code or use a text editor that does it automatically):

```
$ pydocstyle filename.py
```



## 11.6 Run pycodestyle on your code

It's a good idea to run `pycodestyle` on your code (or use a text editor that does it automatically):

```
$ pycodestyle filename.py
```

## 11.7 Run mypy on your code

It's a good idea to run `mypy` on your code (or use a text editor that does it automatically):

```
$ mypy filename.py
```

## 11.8 Run pydocstyle on your code

It's a good idea to run `pycodestyle` on your code (or use a text editor that does it automatically):

```
$ pycodestyle filename.py --max-line-length=88
```

## 11.9 Run black on your code

Another method of enforcing `PEP8` is using a tool such as `black`. These tools tend to be very effective at cleaning up code, but should be used carefully and code should be retested after cleaning it. Try:

```
$ black --help
```



## CREATE A MODEL

If you'd like to create a new model that isn't covered by the existing DeePMD-kit library, but reuse DeePMD-kit's other efficient module such as data processing, trainer, etc, you may want to read this section.

To incorporate your custom model you'll need to:

1. Register and implement new components (e.g. descriptor) in a Python file. You may also want to register new TensorFlow OPs if necessary.
2. Register new arguments for user inputs.
3. Package new codes into a Python package.
4. Test new models.

### 12.1 Design a new component

When creating a new component, take descriptor as the example, you should inherit `deepmd.descriptor.descriptor.Descriptor` class and override several methods. Abstract methods such as `deepmd.descriptor.descriptor.Descriptor.build` must be implemented and others are not. You should keep arguments of these methods unchanged.

After implementation, you need to register the component with a key:

```
from deepmd.descriptor import Descriptor

@Descriptor.register("some_descrpt")
class SomeDescriptor(Descriptor):
    def __init__(self, arg1: bool, arg2: float) -> None:
        pass
```

### 12.2 Register new arguments

To let some one uses your new component in their input file, you need to create a new methods that returns some Argument of your new component, and then register new arguments. For example, the code below

```
from typing import List

from dargs import Argument
from deepmd.utils.argcheck import descrpt_args_plugin
```

(continues on next page)

(continued from previous page)

```
@descrpt_args_plugin.register("some_descrpt")
def descrpt_some_args() -> List[Argument]:
    return [
        Argument("arg1", bool, optional=False, doc="balabala"),
        Argument("arg2", float, optional=True, default=6.0, doc="haha"),
    ]
```

allows one to use your new descriptor as below:

```
"descriptor" :{
    "type": "some_descrpt",
    "arg1": true,
    "arg2": 6.0
}
```

The arguments here should be consistent with the class arguments of your new component.

## 12.3 Package new codes

You may use `setuptools` to package new codes into a new Python package. It's critical to add your new component to `entry_points['deepmd']` in `setup.py`:

```
entry_points={
    'deepmd': [
        'some_descrpt=deepmd_some_descrpt:SomeDescript',
    ],
},
```

where `deepmd_some_descrpt` is the module of your codes. It is equivalent to `from deepmd_some_descrpt import SomeDescript`.

If you place `SomeDescript` and `descrpt_some_args` into different modules, you are also expected to add `descrpt_some_args` to `entry_points`.

After you install your new package, you can now use `dp train` to run your new model.

## ATOM TYPE EMBEDDING

### 13.1 Overview

Here is an overview of the deepmd-kit algorithm. Given a specific centric atom, we can obtain the matrix describing its local environment, named as  $R$ . It consists of the distance between centric atom and its neighbors, as well as a direction vector. We can embed each distance into a vector of  $M1$  dimension by an **embedding net**, so the environment matrix  $R$  can be embedded into matrix  $G$ . We can thus extract a descriptor vector (of  $M1*M2$  dim) of the centric atom from the  $G$  by some matrix multiplication, and put the descriptor into **fitting net** to get predicted energy  $E$ . The vanilla version of deepmd-kit builds **embedding net** and **fitting net** relying on the atom type, resulting in  $O(N)$  memory usage. After applying atom type embedding, in deepmd-kit v2.0, we can share one **embedding net** and one **fitting net** in total, which declines training complexity largely.

### 13.2 Preliminary

In the following chart, you can find the meaning of symbols used to clarify the atom type embedding algorithm.

Symbol	Meaning
$i$	Type of centric atom
$j$	Type of neighbor atom
$s_{ij}$	Distance between centric atom and neighbor atom
$G_{ij}(\cdot)$	Origin embedding net, take $s_{ij}$ as input and output embedding vector of $M1$ dim
$G(\cdot)$	Shared embedding net
$\text{Multi}(\cdot)$	Matrix multiplication and flattening, output the descriptor vector of $M1*M2$ dim
$F_i(\cdot)$	Origin fitting net, take the descriptor vector as input and output energy
$F(\cdot)$	Shared fitting net
$A(\cdot)$	Atom type embedding net, input is atom type, output is type embedding vector of dim <code>nchan1</code>

So, we can formulate the training process as follows. Vanilla deepmd-kit algorithm:

$$\text{Energy} = F_i(\text{Multi}(G_{ij}(s_{ij})) )$$

Deepmd-kit applying atom type embedding:

$$\text{Energy} = F( [\text{Multi}(G([s_{ij}, A(i), A(j)]))], A(j)) )$$

or

$$\text{Energy} = F( [\text{Multi}(G([s_{ij}, A(j)]))], A(j)) )$$

The difference between two variants above is whether using the information of centric atom when generating the descriptor. Users can choose by modifying the `type_one_side` hyper-parameter in the input json file.

## 13.3 How to use

A detailed introduction can be found at `se_e2_a_tebd`. Looking for a fast start up, you can simply add a `type_embedding` section in the input json file as displayed in the following, and the algorithm will adopt atom type embedding algorithm automatically. An example of `type_embedding` is like

```
"type_embedding":{
  "neuron":      [2, 4, 8],
  "resnet_dt":   false,
  "seed":        1
}
```

## 13.4 Code Modification

Atom type embedding can be applied to varied `embedding net` and `fitting net`, as a result we build a class `TypeEmbedNet` to support this free combination. In the following, we will go through the execution process of the code to explain our code modification.

### 13.4.1 trainer (train/trainer.py)

In `trainer.py`, it will parse the parameter from the input json file. If a `type_embedding` section is detected, it will build a `TypeEmbedNet`, which will be later input in the `model`. `model` will be built in the function `_build_network`.

### 13.4.2 model (model/ener.py)

When building the operation graph of the `model` in `model.build`. If a `TypeEmbedNet` is detected, it will build the operation graph of `type embed net`, `embedding net` and `fitting net` by order. The building process of `type embed net` can be found in `TypeEmbedNet.build`, which output the type embedding vector of each atom type (of `[ntypes * nchan]` dimension). We then save the type embedding vector into `input_dict`, so that they can be fetched later in `embedding net` and `fitting net`.

### 13.4.3 embedding net (descriptor/se\*.py)

In `embedding net`, we shall take local environment `R` as input and output matrix `G`. Functions called in this process by order is

```
build -> _pass_filter -> _filter -> _filter_lower
```

- `_pass_filter`: It will first detect whether an atom type embedding exists, if so, it will apply atom type embedding algorithm and doesn't divide the input by type.
- `_filter`: It will call `_filter_lower` function to obtain the result of matrix multiplication ( $G^T \cdot R$ ), do further multiplication involved in `Multi()`, and finally output the result of descriptor vector of  $M1 \cdot M2$  dim.

- `_filter_lower`: The main function handling input modification. If type embedding exists, it will call `_concat_type_embedding` function to concat the first column of input R (the column of `s_ij`) with the atom type embedding information. It will decide whether using the atom type embedding vector of centric atom according to the value of `type_one_side` (if set **True**, then we only use the vector of the neighbor atom). The modified input will be put into the `fitting_net` to get G for further matrix multiplication stage.

#### 13.4.4 fitting net (fit/ener.py)

In `fitting_net`, it take the descriptor vector as input, whose dimension is  $[n_{\text{atoms}}, (M1 * M2)]$ . Because we need to involve information of centric atom in this step, we need to generate a matrix named as `atype_embed` (of dim  $[n_{\text{atoms}}, n_{\text{chanl}}]$ ), in which each row is the type embedding vector of the specific centric atom. The input is sorted by type of centric atom, we also know the number of a particular atom type (stored in `natoms[2+i]`), thus we get the type vector of centric atom. In the build phrase of fitting net, it will check whether type embedding exist in `input_dict` and fetch them. After that calling `embed_atom_type` function to lookup embedding vector for type vector of centric atom to obtain `atype_embed`, and concat input with it (`[input, atype_embed]`). The modified input go through `fitting_net` to get predicted energy.

**P.S.: You can't apply compression method while using atom type embedding**





## 14.1 deepmd package

Root of the deepmd package, exposes all public classes and submodules.

```
class deepmd.DeepEval(model_file: Path, load_prefix: str = 'load', default_tf_graph: bool = False,  
                      auto_batch_size: Union[bool, int, deepmd.utils.batch_size.AutoBatchSize] = False)
```

Bases: `object`

Common methods for DeepPot, DeepWFC, DeepPolar, ...

### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix: str** The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**auto\_batch\_size** [bool or int or AutomaticBatchSize, default: False] If True, automatic batch size will be used. If int, it will be used as the initial batch size.

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

### Methods

<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**load\_prefix:** `str`

**make\_natoms\_vec**(atom\_types: `numpy.ndarray`) → `numpy.ndarray`

Make the natom vector used by deepmd-kit.

### Parameters

**atom\_types** The type of atoms

### Returns

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < Ntypes+2$ , number of type i atoms

**property model\_type:** `str`

Get type of model.

:type:str

**property model\_version:** `str`

Get version of model.

**Returns**

`str` version of model

**static reverse\_map**(*vec: numpy.ndarray, imap: List[int]*)  $\rightarrow$  `numpy.ndarray`

Reverse mapping of a vector according to the index map

**Parameters**

**vec** Input vector. Be of shape [nframes, natoms, -1]

**imap** Index map. Be of shape [natoms]

**Returns**

**vec\_out** Reverse mapped vector.

**static sort\_input**(*coord: numpy.ndarray, atom\_type: numpy.ndarray, sel\_atoms: Optional[List[int]] = None*)

Sort atoms in the system according their types.

**Parameters**

**coord** The coordinates of atoms. Should be of shape [nframes, natoms, 3]

**atom\_type** The type of atoms Should be of shape [natoms]

**sel\_atom** The selected atoms by type

**Returns**

**coord\_out** The coordinates after sorting

**atom\_type\_out** The atom types after sorting

**idx\_map** The index mapping from the input to the output. For example coord\_out = coord[:,idx\_map,:]

**sel\_atom\_type** Only output if sel\_atoms is not None The sorted selected atom types

**sel\_idx\_map** Only output if sel\_atoms is not None The index mapping from the selected atoms to sorted selected atoms.

**deepmd.DeepPotential**(*model\_file: Union[str, pathlib.Path], load\_prefix: str = 'load', default\_tf\_graph: bool = False*)  $\rightarrow$  Union[`deepmd.infer.deep_dipole.DeepDipole`, `deepmd.infer.deep_polar.DeepGlobalPolar`, `deepmd.infer.deep_polar.DeepPolar`, `deepmd.infer.deep_pot.DeepPot`, `deepmd.infer.deep_wfc.DeepWFC`]

Factory function that will initialize appropriate potential read from *model\_file*.

**Parameters**

**model\_file:** `str` The name of the frozen model file.

**load\_prefix:** `str` The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

### Returns

**Union**[DeepDipole, DeepGlobalPolar, DeepPolar, DeepPot, DeepWFC] one of the available potentials

### Raises

**RuntimeError** if model file does not correspond to any implemented potential

**class** deepmd.DipoleChargeModifier(*model\_name: str, model\_charge\_map: List[float], sys\_charge\_map: List[float], ewald\_h: float = 1, ewald\_beta: float = 1*)

Bases: *deepmd.infer.deep\_dipole.DeepDipole*

### Parameters

**model\_name** The model file for the DeepDipole model

**model\_charge\_map** Gives the amount of charge for the wfcc

**sys\_charge\_map** Gives the amount of charge for the real atoms

**ewald\_h** Grid spacing of the reciprocal part of Ewald sum. Unit: Å

**ewald\_beta** Splitting parameter of the Ewald sum. Unit: Å<sup>-1</sup>

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

### Methods

<i>build_fv_graph()</i>	Build the computational graph for the force and virial inference.
<i>eval</i> (coord, box, atype[, eval_fv])	Evaluate the modification
<i>eval_full</i> (coords, cells, atom_types[, ...])	Evaluate the model with interface similar to the energy model.
<i>get_dim_aparam</i> ()	Unsupported in this model.
<i>get_dim_fparam</i> ()	Unsupported in this model.
<i>get_ntypes</i> ()	Get the number of atom types of this model.
<i>get_rcut</i> ()	Get the cut-off radius of this model.
<i>get_sel_type</i> ()	Get the selected atom types of this model.
<i>get_type_map</i> ()	Get the type map (element name of the atom types) of this model.
<i>make_natoms_vec</i> (atom_types)	Make the natom vector used by deepmd-kit.
<i>modify_data</i> (data)	Modify data.
<i>reverse_map</i> (vec, imap)	Reverse mapping of a vector according to the index map
<i>sort_input</i> (coord, atom_type[, sel_atoms])	Sort atoms in the system according their types.

**build\_fv\_graph()** → tensorflow.python.framework.ops.Tensor  
Build the computational graph for the force and virial inference.

**eval**(*coord*: *numpy.ndarray*, *box*: *numpy.ndarray*, *atype*: *numpy.ndarray*, *eval\_fv*: *bool* = *True*) → *Tuple*[*numpy.ndarray*, *numpy.ndarray*, *numpy.ndarray*]  
Evaluate the modification

#### Parameters

**coord** The coordinates of atoms  
**box** The simulation region. PBC is assumed  
**atype** The atom types  
**eval\_fv** Evaluate force and virial

#### Returns

**tot\_e** The energy modification  
**tot\_f** The force modification  
**tot\_v** The virial modification

**load\_prefix:** *str*

**modify\_data**(*data*: *dict*) → *None*

Modify data.

#### Parameters

**data** Internal data of DeepmdData. Be a dict, has the following keys - *coord* coordinates - *box* simulation box - *type* atom types - *find\_energy* tells if data has energy - *find\_force* tells if data has force - *find\_virial* tells if data has virial - *energy* energy - *force* force - *virial* virial

## 14.1.1 Subpackages

### deepmd.cluster package

Module that reads node resources, auto detects if running local or on SLURM.

**deepmd.cluster.get\_resource**() → *Tuple*[*str*, *List*[*str*], *Optional*[*List*[*int*]]]

Get local or slurm resources: nodename, nodelist, and gpus.

#### Returns

*Tuple*[*str*, *List*[*str*], *Optional*[*List*[*int*]]] nodename, nodelist, and gpus

### Submodules

#### deepmd.cluster.local module

Get local GPU resources.

**deepmd.cluster.local.get\_gpus**()

Get available IDs of GPU cards at local. These IDs are valid when used as the TensorFlow device ID.

#### Returns

*Optional*[*List*[*int*]] List of available GPU IDs. Otherwise, None.

**deepmd.cluster.local.get\_resource**() → *Tuple*[*str*, *List*[*str*], *Optional*[*List*[*int*]]]

Get local resources: nodename, nodelist, and gpus.

**Returns**

`Tuple[str, List[str], Optional[List[int]]]` nodename, nodelist, and gpus

**deepmd.cluster.slurm module**

Module to get resources on SLURM cluster.

**References**

[https://github.com/deepsense-ai/tensorflow\\_on\\_slurm](https://github.com/deepsense-ai/tensorflow_on_slurm) ####

`deepmd.cluster.slurm.get_resource()` → `Tuple[str, List[str], Optional[List[int]]]`

Get SLURM resources: nodename, nodelist, and gpus.

**Returns**

`Tuple[str, List[str], Optional[List[int]]]` nodename, nodelist, and gpus

**Raises**

**RuntimeError** if number of nodes could not be retrieved

**ValueError** list of nodes is not of the same length as number of nodes

**ValueError** if current nodename is not found in node list

**deepmd.descriptor package****Submodules****deepmd.descriptor.descriptor module**

**class** `deepmd.descriptor.descriptor.Descriptor(*args, **kwargs)`

Bases: `deepmd.utils.plugin.PluginVariant`

The abstract class for descriptors. All specific descriptors should be based on this class.

The descriptor  $\mathcal{D}$  describes the environment of an atom, which should be a function of coordinates and types of its neighbour atoms.

**Notes**

Only methods and attributes defined in this class are generally public, that can be called by other classes.

## Examples

```
>>> descriptor = Descriptor(type="se_e2_a", rcut=6., rcut_smth=0.5, sel=[50])
>>> type(descriptor)
<class 'deepmd.descriptor.se_a.DescriptSeA'>
```

## Methods

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor.
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statistics (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statistics (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor.
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	Returns neighbor information.
<code>get_ntypes()</code>	Returns the number of atom types.
<code>get_rcut()</code>	Returns the cut-off radius.
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given dict
<code>pass_tensors_from_frz_model(*tensors)</code>	Pass the descript_reshape tensor as well as descript_deriv tensor from the frz graph_def
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial.
<code>register(key)</code>	Register a descriptor plugin.

**abstract build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *Dict[str, Any]*, *reuse*: *Optional[bool]* = None, *suffix*: *str* = "") → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor.

### Parameters

**coord\_** [*tf.Tensor*] The coordinate of atoms

**atype\_** [*tf.Tensor*] The type of atoms

**natoms** [*tf.Tensor*] The number of atoms. This tensor has the length of Ntypes + 2  
 natoms[0]: number of local atoms  
 natoms[1]: total number of atoms held by this processor  
 natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

**box** [*tf.Tensor*] The box of frames

**mesh** [*tf.Tensor*] For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** [*dict[str, Any]*] Dictionary for additional inputs

**reuse** [*bool*, optional] The weights in the networks should be reused when get the variable.

**suffix** [*str*, optional] Name suffix to identify this descriptor

**Returns**

**descriptor:** `tf.Tensor` The output descriptor

**Notes**

This method must be implemented, as it's called by other classes.

```
abstract compute_input_stats(data_coord: List[numpy.ndarray], data_box: List[numpy.ndarray],
                             data_atype: List[numpy.ndarray], natoms_vec: List[numpy.ndarray],
                             mesh: List[numpy.ndarray], input_dict: Dict[str, List[numpy.ndarray]])
    → None
```

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

**Parameters**

**data\_coord** [List[`np.ndarray`]] The coordinates. Can be generated by `deepmd.model.model_stat.make_stat_input()`

**data\_box** [List[`np.ndarray`]] The box. Can be generated by `deepmd.model.model_stat.make_stat_input()`

**data\_atype** [List[`np.ndarray`]] The atom types. Can be generated by `deepmd.model.model_stat.make_stat_input()`

**natoms\_vec** [List[`np.ndarray`]] The vector for the number of atoms of the system and different types of atoms. Can be generated by `deepmd.model.model_stat.make_stat_input()`

**mesh** [List[`np.ndarray`]] The mesh for neighbor searching. Can be generated by `deepmd.model.model_stat.make_stat_input()`

**input\_dict** [Dict[str, List[`np.ndarray`]]] Dictionary for additional input

**Notes**

This method must be implemented, as it's called by other classes.

```
enable_compression(min_nbor_dist: float, model_file: str = 'frozen_model.pb', table_extrapolate: float =
                    5.0, table_stride_1: float = 0.01, table_stride_2: float = 0.1, check_frequency: int = -
                    1, suffix: str = "") → None
```

Reveive the statistics (distance, max\_nbor\_size and env\_mat\_range) of the training data.

**Parameters**

**min\_nbor\_dist** [float] The nearest distance between atoms

**model\_file** [str, default: 'frozen\_model.pb'] The original frozen model, which will be compressed by the program

**table\_extrapolate** [float, default: 5.] The scale of model extrapolation

**table\_stride\_1** [float, default: 0.01] The uniform stride of the first table

**table\_stride\_2** [float, default: 0.1] The uniform stride of the second table

**check\_frequency** [int, default: -1] The overflow check frequency

**suffix** [str, optional] The suffix of the scope

## Notes

This method is called by others when the descriptor supported compression.

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict]* = *None*) → *None*

Reveive the mixed precision setting.

### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

## Notes

This method is called by others when the descriptor supported compression.

**abstract get\_dim\_out**() → *int*

Returns the output dimension of this descriptor.

### Returns

*int* the output dimension of this descriptor

## Notes

This method must be implemented, as it's called by other classes.

**get\_dim\_rot\_mat\_1**() → *int*

Returns the first dimension of the rotation matrix. The rotation is of shape dim\_1 x 3

### Returns

*int* the first dimension of the rotation matrix

**get\_feed\_dict**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*:  
*tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*,  
*box*: *tensorflow.python.framework.ops.Tensor*, *mesh*:  
*tensorflow.python.framework.ops.Tensor*) → *Dict[str,*  
*tensorflow.python.framework.ops.Tensor]*

Generate the feed\_dict for current descriptor

### Parameters

**coord\_** [*tf.Tensor*] The coordinate of atoms

**atype\_** [*tf.Tensor*] The type of atoms

**natoms** [*tf.Tensor*] The number of atoms. This tensor has the length of Ntypes + 2  
natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor  
natoms[i]: 2 <= i < Ntypes+2, number of type i atoms

**box** [*tf.Tensor*] The box. Can be generated by `deepmd.model.make_stat_input`

**mesh** [*tf.Tensor*] For historical reasons, only the length of the Tensor matters. if size of  
mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

### Returns

**feed\_dict** [*dict[str, tf.Tensor]*] The output feed\_dict of current descriptor

**get\_nlist**() → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*,  
*List[int]*, *List[int]*]

Returns neighbor information.



**Returns****nlist** [`tf.Tensor`] Neighbor list**rij** [`tf.Tensor`] The relative distance between the neighbor and the center atom.**sel\_a** [`list[int]`] The number of neighbors with full information**sel\_r** [`list[int]`] The number of neighbors with only radial information**abstract get\_ntypes()** → `int`

Returns the number of atom types.

**Returns**`int` the number of atom types**Notes**

This method must be implemented, as it's called by other classes.

**abstract get\_rcut()** → `float`

Returns the cut-off radius.

**Returns**`float` the cut-off radius**Notes**

This method must be implemented, as it's called by other classes.

**get\_tensor\_names**(*suffix*: `str` = "") → `Tuple[str]`

Get names of tensors.

**Parameters****suffix** [`str`] The suffix of the scope**Returns**`Tuple[str]` Names of tensors**init\_variables**(*model\_file*: `str`, *suffix*: `str` = "") → `None`

Init the embedding net variables with the given dict

**Parameters****model\_file** [`str`] The input model file**suffix** [`str`, optional] The suffix of the scope

## Notes

This method is called by others when the descriptor supported initialization from the given variables.

**pass\_tensors\_from\_frz\_model**(\*tensors: *tensorflow.python.framework.ops.Tensor*) → *None*

Pass the descrpt\_reshape tensor as well as descrpt\_deriv tensor from the frz graph\_def

### Parameters

**\*tensors** [*tf.Tensor*] passed tensors

## Notes

The number of parameters in the method must be equal to the numbers of returns in *get\_tensor\_names()*.

**abstract prod\_force\_virial**(atom\_ener: *tensorflow.python.framework.ops.Tensor*, natoms: *tensorflow.python.framework.ops.Tensor*) → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*]

Compute force and virial.

### Parameters

**atom\_ener** [*tf.Tensor*] The atomic energy

**natoms** [*tf.Tensor*] The number of atoms. This tensor has the length of Ntypes + 2  
 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor  
 natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

### Returns

**force** [*tf.Tensor*] The force on atoms

**virial** [*tf.Tensor*] The total virial

**atom\_virial** [*tf.Tensor*] The atomic virial

**static register**(key: *str*) → *deepmd.descriptor.descriptor.Descriptor*

Register a descriptor plugin.

### Parameters

**key** [*str*] the key of a descriptor

### Returns

*Descriptor* the registered descriptor

## Examples

```
>>> @Descriptor.register("some_descrpt")
class SomeDescript(Descriptor):
    pass
```

## deepmd.descriptor.hybrid module

**class** deepmd.descriptor.hybrid.DescriptHybrid(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.descriptor.Descriptor](#)

Concat a list of descriptors to form a new descriptor.

### Parameters

**list** [[list](#)] Build a descriptor from the concatenation of the list of descriptors.

### Methods

<a href="#">build</a> (coord_, atype_, natoms, box_, mesh, ...)	Build the computational graph for the descriptor
<a href="#">compute_input_stats</a> (data_coord, data_box, ...)	Compute the statisitcs (avg and std) of the training data.
<a href="#">enable_compression</a> (min_nbor_dist[, ...])	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<a href="#">enable_mixed_precision</a> ([mixed_prec])	Reveive the mixed precision setting.
<a href="#">get_dim_out</a> ()	Returns the output dimension of this descriptor
<a href="#">get_dim_rot_mat_1</a> ()	Returns the first dimension of the rotation matrix.
<a href="#">get_feed_dict</a> (coord_, atype_, natoms, box, mesh)	Generate the feed_dict for current descriptor
<a href="#">get_nlist</a> ()	Returns neighbor information.
<a href="#">get_nlist_i</a> (ii)	Get the neighbor information of the ii-th descriptor
<a href="#">get_ntypes</a> ()	Returns the number of atom types
<a href="#">get_rcut</a> ()	Returns the cut-off radius
<a href="#">get_tensor_names</a> ([suffix])	Get names of tensors.
<a href="#">init_variables</a> (model_file[, suffix])	Init the embedding net variables with the given dict
<a href="#">pass_tensors_from_frz_model</a> (*tensors)	Pass the descript_reshape tensor as well as descript_deriv tensor from the frz graph_def
<a href="#">prod_force_virial</a> (atom_ener, natoms)	Compute force and virial
<a href="#">register</a> (key)	Register a descriptor plugin.

**build**(coord\_: [tensorflow.python.framework.ops.Tensor](#), atype\_: [tensorflow.python.framework.ops.Tensor](#), natoms: [tensorflow.python.framework.ops.Tensor](#), box\_: [tensorflow.python.framework.ops.Tensor](#), mesh: [tensorflow.python.framework.ops.Tensor](#), input\_dict: [dict](#), reuse: [Optional\[bool\]](#) = None, suffix: [str](#) = '') → [tensorflow.python.framework.ops.Tensor](#)

Build the computational graph for the descriptor

### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 <= i < Ntypes+2, number of type i atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord: list, data\_box: list, data\_atype: list, natoms\_vec: list, mesh: list, input\_dict: dict*) → *None*

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms.  
Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

**enable\_compression**(*min\_nbor\_dist: float, model\_file: str = 'frozen\_model.pb', table\_extrapolate: float = 5.0, table\_stride\_1: float = 0.01, table\_stride\_2: float = 0.1, check\_frequency: int = -1, suffix: str = ''*) → *None*

Receive the statistics (distance, max\_nbor\_size and env\_mat\_range) of the training data.

### Parameters

**min\_nbor\_dist** [*float*] The nearest distance between atoms

**model\_file** [*str*, default: 'frozen\_model.pb'] The original frozen model, which will be compressed by the program

**table\_extrapolate** [*float*, default: 5.] The scale of model extrapolation

**table\_stride\_1** [*float*, default: 0.01] The uniform stride of the first table

**table\_stride\_2** [*float*, default: 0.1] The uniform stride of the second table

**check\_frequency** [*int*, default: -1] The overflow check frequency

**suffix** [*str*, optional] The suffix of the scope

**enable\_mixed\_precision**(*mixed\_prec: Optional[dict] = None*) → *None*

Receive the mixed precision setting.

### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_dim\_out**() → *int*

Returns the output dimension of this descriptor

**get\_nlist\_i**(*ii: int*) → *Tuple[tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor, List[int], List[int]]*

Get the neighbor information of the ii-th descriptor

### Parameters

**ii** [*int*] The index of the descriptor

### Returns

**nlist** Neighbor list  
**rij** The relative distance between the neighbor and the center atom.  
**sel\_a** The number of neighbors with full information  
**sel\_r** The number of neighbors with only radial information

**get\_ntypes()** → **int**

Returns the number of atom types

**get\_rcut()** → **float**

Returns the cut-off radius

**get\_tensor\_names(suffix: str = "")** → **Tuple[str]**

Get names of tensors.

#### Parameters

**suffix** [**str**] The suffix of the scope

#### Returns

**Tuple[str]** Names of tensors

**init\_variables(model\_file: str, suffix: str = "")** → **None**

Init the embedding net variables with the given dict

#### Parameters

**model\_file** [**str**] The input frozen model file

**suffix** [**str**, optional] The suffix of the scope

**pass\_tensors\_from\_frz\_model(\*tensors: tensorflow.python.framework.ops.Tensor)** → **None**

Pass the descrpt\_reshape tensor as well as descrpt\_deriv tensor from the frz graph\_def

#### Parameters

**\*tensors** [**tf.Tensor**] passed tensors

**prod\_force\_virial(atom\_ener: tensorflow.python.framework.ops.Tensor, natoms:**

**tensorflow.python.framework.ops.Tensor)** →

**Tuple[tensorflow.python.framework.ops.Tensor,**

**tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor]**

Compute force and virial

#### Parameters

**atom\_ener** The atomic energy

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

#### Returns

**force** The force on atoms

**virial** The total virial

**atom\_virial** The atomic virial

## deepmd.descriptor.loc\_frame module

**class** deepmd.descriptor.loc\_frame.DescriptLocFrame(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.descriptor.Descriptor](#)

Defines a local frame at each atom, and the compute the descriptor as local coordinates under this frame.

**Parameters**

**rcut** The cut-off radius

**sel\_a** [[list](#)[[str](#)]] The length of the list should be the same as the number of atom types in the system. *sel\_a[i]* gives the selected number of type-i neighbors. The full relative coordinates of the neighbors are used by the descriptor.

**sel\_r** [[list](#)[[str](#)]] The length of the list should be the same as the number of atom types in the system. *sel\_r[i]* gives the selected number of type-i neighbors. Only relative distance of the neighbors are used by the descriptor. *sel\_a[i] + sel\_r[i]* is recommended to be larger than the maximally possible number of type-i neighbors in the cut-off radius.

**axis\_rule**: [list](#)[[int](#)] The length should be 6 times of the number of types. - *axis\_rule[i\*6+0]*: class of the atom defining the first axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.

- *axis\_rule[i\*6+1]*: type of the atom defining the first axis of type-i atom.
- *axis\_rule[i\*6+2]*: index of the axis atom defining the first axis. Note that the neighbors with the same class and type are sorted according to their relative distance.
- *axis\_rule[i\*6+3]*: class of the atom defining the first axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.
- *axis\_rule[i\*6+4]*: type of the atom defining the second axis of type-i atom.
- *axis\_rule[i\*6+5]*: class of the atom defining the second axis of type-i atom. 0 for neighbors with full coordinates and 1 for neighbors only with relative distance.

**Methods**

<a href="#">build</a> (coord_, atype_, natoms, box_, mesh, ...)	Build the computational graph for the descriptor
<a href="#">compute_input_stats</a> (data_coord, data_box, ...)	Compute the statisitcs (avg and std) of the training data.
<a href="#">enable_compression</a> (min_nbor_dist[, ...])	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<a href="#">enable_mixed_precision</a> ([mixed_prec])	Reveive the mixed precision setting.
<a href="#">get_dim_out</a> ()	Returns the output dimension of this descriptor
<a href="#">get_dim_rot_mat_1</a> ()	Returns the first dimension of the rotation matrix.
<a href="#">get_feed_dict</a> (coord_, atype_, natoms, box, mesh)	Generate the feed_dict for current descriptor
<a href="#">get_nlist</a> ()	

**Returns**

<a href="#">get_ntypes</a> ()	Returns the number of atom types
<a href="#">get_rcut</a> ()	Returns the cut-off radisu
<a href="#">get_rot_mat</a> ()	Get rotational matrix
<a href="#">get_tensor_names</a> ([suffix])	Get names of tensors.

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Table 5 – continued from previous page

<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model
<code>pass_tensors_from_frz_model(*tensors)</code>	Pass the <code>descript_reshape</code> tensor as well as <code>descript_deriv</code> tensor from the <code>frz_graph_def</code>
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *dict*, *reuse*: *Optional[bool]* = *None*, *suffix*: *str* = '') → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor

#### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of `Ntypes + 2` `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type `i` atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord*: *list*, *data\_box*: *list*, *data\_atype*: *list*, *natoms\_vec*: *list*, *mesh*: *list*, *input\_dict*: *dict*) → *None*

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

#### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms. Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

**get\_dim\_out**() → *int*

Returns the output dimension of this descriptor

**get\_nlist**() → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*, *List*[*int*], *List*[*int*]]

#### Returns

**nlist** Neighbor list  
**rij** The relative distance between the neighbor and the center atom.  
**sel\_a** The number of neighbors with full information  
**sel\_r** The number of neighbors with only radial information

**get\_ntypes()** → `int`  
 Returns the number of atom types

**get\_rcut()** → `float`  
 Returns the cut-off radius

**get\_rot\_mat()** → `tensorflow.python.framework.ops.Tensor`  
 Get rotational matrix

**init\_variables**(*model\_file*: `str`, *suffix*: `str` = "") → `None`  
 Init the embedding net variables with the given frozen model

#### Parameters

**model\_file** [`str`] The input frozen model file  
**suffix** [`str`, optional] The suffix of the scope

**prod\_force\_virial**(*atom\_ener*: `tensorflow.python.framework.ops.Tensor`, *natoms*:  
`tensorflow.python.framework.ops.Tensor`) →  
`Tuple`[`tensorflow.python.framework.ops.Tensor`,  
`tensorflow.python.framework.ops.Tensor`, `tensorflow.python.framework.ops.Tensor`]  
 Compute force and virial

#### Parameters

**atom\_ener** The atomic energy  
**natoms** The number of atoms. This tensor has the length of `Ntypes + 2` `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type *i* atoms

#### Returns

**force** The force on atoms  
**virial** The total virial  
**atom\_virial** The atomic virial

### deepmd.descriptor.se module

**class** `deepmd.descriptor.se.DescriptSe`(\*args, \*\*kwargs)  
 Bases: `deepmd.descriptor.descriptor.Descriptor`  
 A base class for smooth version of descriptors.



## Notes

All of these descriptors have an environmental matrix and an embedding network (`deepmd.utils.network.embedding_net()`), so they can share some similar methods without defining them twice.

### Attributes

**embedding\_net\_variables** [`dict`] initial embedding network variables

**descript\_reshape** [`tf.Tensor`] the reshaped descriptor

**descript\_deriv** [`tf.Tensor`] the descriptor derivative

**rij** [`tf.Tensor`] distances between two atoms

**nlist** [`tf.Tensor`] the neighbor list

### Methods

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor.
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statisitcs (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor.
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	Returns neighbor information.
<code>get_ntypes()</code>	Returns the number of atom types.
<code>get_rcut()</code>	Returns the cut-off radius.
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model
<code>pass_tensors_from_frz_model(descript_reshape, ...)</code>	Pass the descript_reshape tensor as well as descript_deriv tensor from the frz_graph_def
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial.
<code>register(key)</code>	Register a descriptor plugin.

**get\_tensor\_names**(*suffix: str = ""*) → `Tuple[str]`  
Get names of tensors.

#### Parameters

**suffix** [`str`] The suffix of the scope

#### Returns

`Tuple[str]` Names of tensors

**init\_variables**(*model\_file: str, suffix: str = ""*) → `None`  
Init the embedding net variables with the given frozen model

#### Parameters

**model\_file** [`str`] The input frozen model file

**suffix** [`str`, optional] The suffix of the scope

**pass\_tensors\_from\_frz\_model**(*descript\_reshape*: tensorflow.python.framework.ops.Tensor, *descript\_deriv*: tensorflow.python.framework.ops.Tensor, *rij*: tensorflow.python.framework.ops.Tensor, *nlist*: tensorflow.python.framework.ops.Tensor)

Pass the *descript\_reshape* tensor as well as *descript\_deriv* tensor from the *frz\_graph\_def*

#### Parameters

**descript\_reshape** The passed *descript\_reshape* tensor

**descript\_deriv** The passed *descript\_deriv* tensor

**rij** The passed *rij* tensor

**nlist** The passed *nlist* tensor

**property precision:** tensorflow.python.framework.dtypes.DType

Precision of filter network.

### deepmd.descriptor.se\_a module

**class** deepmd.descriptor.se\_a.DescriptSeA(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.se.DescriptSe](#)

DeepPot-SE constructed from all information (both angular and radial) of atomic configurations. The embedding takes the distance between atoms as input.

The descriptor  $\mathcal{D}^i \in \mathcal{R}^{M_1 \times M_2}$  is given by [1]

$$\mathcal{D}^i = (\mathcal{G}^i)^T \mathcal{R}^i (\mathcal{R}^i)^T \mathcal{G}_{<}^i$$

where  $\mathcal{R}^i \in \mathbb{R}^{N \times 4}$  is the coordinate matrix, and each row of  $\mathcal{R}^i$  can be constructed as follows

$$(\mathcal{R}^i)_j = \begin{bmatrix} \frac{s(r_{ji})}{r_{ji}} \\ \frac{s(r_{ji})x_{ji}}{r_{ji}^2} \\ \frac{s(r_{ji})y_{ji}}{r_{ji}^2} \\ \frac{s(r_{ji})z_{ji}}{r_{ji}^2} \end{bmatrix}$$

where  $\mathbf{R}_{ji} = \mathbf{R}_j - \mathbf{R}_i = (x_{ji}, y_{ji}, z_{ji})$  is the relative coordinate and  $r_{ji} = \|\mathbf{R}_{ji}\|$  is its norm. The switching function  $s(r)$  is defined as:

$$s(r) = \begin{cases} \frac{1}{r}, & r < r_s \\ \frac{1}{r} \left\{ \left( \frac{r-r_s}{r_c-r_s} \right)^3 \left( -6 \left( \frac{r-r_s}{r_c-r_s} \right)^2 + 15 \frac{r-r_s}{r_c-r_s} - 10 \right) + 1 \right\}, & r_s \leq r < r_c \\ 0, & r \geq r_c \end{cases}$$

Each row of the embedding matrix  $\mathcal{G}^i \in \mathbb{R}^{N \times M_1}$  consists of outputs of a embedding network  $\mathcal{N}$  of  $s(r_{ji})$ :

$$(\mathcal{G}^i)_j = \mathcal{N}(s(r_{ji}))$$

$\mathcal{G}_{<}^i \in \mathbb{R}^{N \times M_2}$  takes first  $M_2$  columns of  $\mathcal{G}^i$ . The equation of embedding network  $\mathcal{N}$  can be found at [deepmd.utils.network.embedding\\_net\(\)](#).

#### Parameters

**rcut** The cut-off radius  $r_c$

**rcut\_smth** From where the environment matrix should be smoothed  $r_s$

**sel** [[list](#)][[str](#)]] sel[i] specifies the maximum number of type i atoms in the cut-off radius

**neuron** [`list[int]`] Number of neurons in each hidden layers of the embedding net  $\mathcal{N}$

**axis\_neuron** Number of the axis neuron  $M_2$  (number of columns of the sub-matrix of the embedding matrix)

**resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$

**trainable** If the weights of embedding net are trainable.

**seed** Random seed for initializing the network parameters.

**type\_one\_side** Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets

**exclude\_types** [`List[List[int]]`] The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**set\_davg\_zero** Set the shift of embedding net input to zero.

**activation\_function** The activation function in the embedding net. Supported options are {0}

**precision** The precision of the embedding net parameters. Supported options are {1}

**uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

## References

[1]

## Attributes

**precision** Precision of filter network.

## Methods

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statisitcs (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	

## Returns

<code>get_ntypes()</code>	Returns the number of atom types
<code>get_rcut()</code>	Returns the cut-off radius
<code>get_rot_mat()</code>	Get rotational matrix
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model

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Table 7 – continued from previous page

<code>pass_tensors_from_frz_model(descrpt_reshape, ...)</code>	Pass the <code>descrpt_reshape</code> tensor as well as <code>descrpt_deriv</code> tensor from the <code>frz_graph_def</code>
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *dict*, *reuse*: *Optional[bool]* = *None*, *suffix*: *str* = *''*) → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor

#### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of `Ntypes + 2` `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type *i* atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord*: *list*, *data\_box*: *list*, *data\_atype*: *list*, *natoms\_vec*: *list*, *mesh*: *list*, *input\_dict*: *dict*) → *None*

Compute the statisitcs (avg and std) of the training data. The input will be normalized by the statistics.

#### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms. Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

**enable\_compression**(*min\_nbor\_dist*: *float*, *model\_file*: *str* = *'frozen\_model.pb'*, *table\_extrapolate*: *float* = *5*, *table\_stride\_1*: *float* = *0.01*, *table\_stride\_2*: *float* = *0.1*, *check\_frequency*: *int* = *-1*, *suffix*: *str* = *''*) → *None*

Reveive the statisitcs (distance, max\_nbor\_size and env\_mat\_range) of the training data.

#### Parameters

**min\_nbor\_dist** The nearest distance between atoms

**model\_file** The original frozen model, which will be compressed by the program

**table\_extrapolate** The scale of model extrapolation

**table\_stride\_1** The uniform stride of the first table

**table\_stride\_2** The uniform stride of the second table

**check\_frequency** The overflow check frequency

**suffix** [*str*, optional] The suffix of the scope

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict] = None*) → *None*

Reveive the mixed precision setting.

#### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_dim\_out**() → *int*

Returns the output dimension of this descriptor

**get\_dim\_rot\_mat\_1**() → *int*

Returns the first dimension of the rotation matrix. The rotation is of shape dim\_1 x 3

**get\_nlist**() → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*,  
*List[int]*, *List[int]*]

#### Returns

**nlist** Neighbor list

**rij** The relative distance between the neighbor and the center atom.

**sel\_a** The number of neighbors with full information

**sel\_r** The number of neighbors with only radial information

**get\_ntypes**() → *int*

Returns the number of atom types

**get\_rcut**() → *float*

Returns the cut-off radius

**get\_rot\_mat**() → *tensorflow.python.framework.ops.Tensor*

Get rotational matrix

**prod\_force\_virial**(*atom\_ener*: *tensorflow.python.framework.ops.Tensor*, *natoms*:  
*tensorflow.python.framework.ops.Tensor*) →  
*Tuple*[*tensorflow.python.framework.ops.Tensor*,  
*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*]

Compute force and virial

#### Parameters

**atom\_ener** The atomic energy

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 <= i < Ntypes+2, number of type i atoms

#### Returns

**force** The force on atoms

**virial** The total virial

**atom\_virial** The atomic virial

**deepmd.descriptor.se\_a\_ebd module**

**class** deepmd.descriptor.se\_a\_ebd.**DescriptSeAEbd**(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.se\\_a.DescriptSeA](#)

DeepPot-SE descriptor with type embedding approach.

**Parameters**

- rcut** The cut-off radius
- rcut\_smth** From where the environment matrix should be smoothed
- sel** [[list](#)[[str](#)]] sel[i] specifies the maximum number of type i atoms in the cut-off radius
- neuron** [[list](#)[[int](#)]] Number of neurons in each hidden layers of the embedding net
- axis\_neuron** Number of the axis neuron (number of columns of the sub-matrix of the embedding matrix)
- resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$
- trainable** If the weights of embedding net are trainable.
- seed** Random seed for initializing the network parameters.
- type\_one\_side** Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets
- type\_nchanl** Number of channels for type representation
- type\_nlayer** Number of hidden layers for the type embedding net (skip connected).
- numb\_aparam** Number of atomic parameters. If >0 it will be embedded with atom types.
- set\_davg\_zero** Set the shift of embedding net input to zero.
- activation\_function** The activation function in the embedding net. Supported options are {0}
- precision** The precision of the embedding net parameters. Supported options are {1}
- exclude\_types** [[List](#)[[List](#)[[int](#)]]] The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**Attributes**

- precision** Precision of filter network.

**Methods**

<a href="#">build</a> (coord_, atype_, natoms, box_, mesh, ...)	Build the computational graph for the descriptor
<a href="#">compute_input_stats</a> (data_coord, data_box, ...)	Compute the statisitcs (avg and std) of the training data.
<a href="#">enable_compression</a> (min_nbor_dist[, ...])	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<a href="#">enable_mixed_precision</a> ([mixed_prec])	Reveive the mixed precision setting.
<a href="#">get_dim_out</a> ()	Returns the output dimension of this descriptor
<a href="#">get_dim_rot_mat_1</a> ()	Returns the first dimension of the rotation matrix.
<a href="#">get_feed_dict</a> (coord_, atype_, natoms, box, mesh)	Generate the feed_dict for current descriptor

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Table 8 – continued from previous page

<code>get_nlist()</code>	<b>Returns</b>
<code>get_ntypes()</code>	Returns the number of atom types
<code>get_rcut()</code>	Returns the cut-off radius
<code>get_rot_mat()</code>	Get rotational matrix
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model
<code>pass_tensors_from_frz_model(descrpt_reshape, ...)</code>	Pass the <code>descrpt_reshape</code> tensor as well as <code>descrpt_deriv</code> tensor from the <code>frz_graph_def</code>
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *dict*, *reuse*: *Optional[bool]* = *None*, *suffix*: *str* = *''*) → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor

#### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of `Ntypes + 2` `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type *i* atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**descriptor** The output descriptor

### deepmd.descriptor.se\_a\_ef module

**class** `deepmd.descriptor.se_a_ef.DescriptSeAEf(*args, **kwargs)`

Bases: `deepmd.descriptor.descriptor.Descriptor`

#### Parameters

**rcut** The cut-off radius

**rcut\_smth** From where the environment matrix should be smoothed

**sel** [*list[str]*] `sel[i]` specifies the maxmum number of type *i* atoms in the cut-off radius

**neuron** [*list[int]*] Number of neurons in each hidden layers of the embedding net

**axis\_neuron** Number of the axis neuron (number of columns of the sub-matrix of the embedding matrix)

- resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$
- trainable** If the weights of embedding net are trainable.
- seed** Random seed for initializing the network parameters.
- type\_one\_side** Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets
- exclude\_types** `[List[List[int]]]` The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.
- set\_davg\_zero** Set the shift of embedding net input to zero.
- activation\_function** The activation function in the embedding net. Supported options are {0}
- precision** The precision of the embedding net parameters. Supported options are {1}
- uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

## Methods

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statistics (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statistics (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	

### Returns

<code>get_ntypes()</code>	Returns the number of atom types
<code>get_rcut()</code>	Returns the cut-off radius
<code>get_rot_mat()</code>	Get rotational matrix
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given dict
<code>pass_tensors_from_frz_model(*tensors)</code>	Pass the descrpt_reshape tensor as well as descrpt_deriv tensor from the frz_graph_def
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *dict*, *reuse*: *Optional[bool]* = None, *suffix*: *str* = "") → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor

### Parameters

- coord\_** The coordinate of atoms
- atype\_** The type of atoms



**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < \text{Ntypes} + 2$ , number of type i atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs. Should have 'efield'.

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(data\_coord: *list*, data\_box: *list*, data\_atype: *list*, natoms\_vec: *list*, mesh: *list*, input\_dict: *dict*) → *None*

Compute the statisitcs (avg and std) of the training data. The input will be normalized by the statistics.

### Parameters

**data\_coord** The coordinates. Can be generated by deepmd.model.make\_stat\_input

**data\_box** The box. Can be generated by deepmd.model.make\_stat\_input

**data\_atype** The atom types. Can be generated by deepmd.model.make\_stat\_input

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms. Can be generated by deepmd.model.make\_stat\_input

**mesh** The mesh for neighbor searching. Can be generated by deepmd.model.make\_stat\_input

**input\_dict** Dictionary for additional input

**get\_dim\_out**() → *int*

Returns the output dimension of this descriptor

**get\_dim\_rot\_mat\_1**() → *int*

Returns the first dimension of the rotation matrix. The rotation is of shape dim\_1 x 3

**get\_nlist**() → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*, *List*[*int*], *List*[*int*]]

### Returns

**nlist** Neighbor list

**rij** The relative distance between the neighbor and the center atom.

**sel\_a** The number of neighbors with full information

**sel\_r** The number of neighbors with only radial information

**get\_ntypes**() → *int*

Returns the number of atom types

**get\_rcut**() → *float*

Returns the cut-off radisu

**get\_rot\_mat**() → *tensorflow.python.framework.ops.Tensor*

Get rotational matrix

**prod\_force\_virial**(*atom\_ener*: tensorflow.python.framework.ops.Tensor, *natoms*: tensorflow.python.framework.ops.Tensor) → Tuple[tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor]

Compute force and virial

#### Parameters

**atom\_ener** The atomic energy

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

#### Returns

**force** The force on atoms

**virial** The total virial

**atom\_virial** The atomic virial

**class** deepmd.descriptor.se\_a\_ef.DescriptSeAEfLower(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.se\\_a.DescriptSeA](#)

Helper class for implementing DescriptSeAEf

#### Attributes

**precision** Precision of filter network.

#### Methods

<a href="#">build</a> (coord_, atype_, natoms, box_, mesh, ...)	Build the computational graph for the descriptor
<a href="#">compute_input_stats</a> (data_coord, data_box, ...)	Compute the statisitcs (avg and std) of the training data.
<a href="#">enable_compression</a> (min_nbor_dist[, ...])	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<a href="#">enable_mixed_precision</a> ([mixed_prec])	Reveive the mixed precision setting.
<a href="#">get_dim_out</a> ()	Returns the output dimension of this descriptor
<a href="#">get_dim_rot_mat_1</a> ()	Returns the first dimension of the rotation matrix.
<a href="#">get_feed_dict</a> (coord_, atype_, natoms, box, mesh)	Generate the feed_dict for current descriptor
<a href="#">get_nlist</a> ()	

#### Returns

<a href="#">get_ntypes</a> ()	Returns the number of atom types
<a href="#">get_rcut</a> ()	Returns the cut-off radius
<a href="#">get_rot_mat</a> ()	Get rotational matrix
<a href="#">get_tensor_names</a> ([suffix])	Get names of tensors.
<a href="#">init_variables</a> (model_file[, suffix])	Init the embedding net variables with the given frozen model
<a href="#">pass_tensors_from_frz_model</a> (descript_reshape, ...)	Pass the descript_reshape tensor as well as descript_deriv tensor from the frz graph_def
<a href="#">prod_force_virial</a> (atom_ener, natoms)	Compute force and virial
<a href="#">register</a> (key)	Register a descriptor plugin.

**build**(*coord\_*, *atype\_*, *natoms*, *box\_*, *mesh*, *input\_dict*, *suffix*="", *reuse*=None)

Build the computational graph for the descriptor

#### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < Ntypes+2$ , number of type i atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord*, *data\_box*, *data\_atype*, *natoms\_vec*, *mesh*, *input\_dict*)

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

#### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms. Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

### deepmd.descriptor.se\_r module

**class** `deepmd.descriptor.se_r.DescriptSeR`(\*args, \*\*kwargs)

Bases: `deepmd.descriptor.se.DescriptSe`

DeepPot-SE constructed from radial information of atomic configurations.

The embedding takes the distance between atoms as input.

#### Parameters

**rcut** The cut-off radius

**rcut\_smth** From where the environment matrix should be smoothed

**sel** [`list[str]`] `sel[i]` specifies the maximum number of type i atoms in the cut-off radius

**neuron** [`list[int]`] Number of neurons in each hidden layers of the embedding net

**resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$

**trainable** If the weights of embedding net are trainable.

**seed** Random seed for initializing the network parameters.

**type\_one\_side** Try to build  $N_{\text{types}}$  embedding nets. Otherwise, building  $N_{\text{types}}^2$  embedding nets

**exclude\_types** `[List[List[int]]]` The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**activation\_function** The activation function in the embedding net. Supported options are {0}

**precision** The precision of the embedding net parameters. Supported options are {1}

**uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

#### Attributes

**precision** Precision of filter network.

#### Methods

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statisitcs (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	

#### Returns

<code>get_ntypes()</code>	Returns the number of atom types
<code>get_rcut()</code>	Returns the cut-off radius
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model
<code>pass_tensors_from_frz_model(descrpt_reshape, ...)</code>	Pass the descrpt_reshape tensor as well as descrpt_deriv tensor from the frz graph_def
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: `tensorflow.python.framework.ops.Tensor`, *atype\_*: `tensorflow.python.framework.ops.Tensor`, *natoms*: `tensorflow.python.framework.ops.Tensor`, *box\_*: `tensorflow.python.framework.ops.Tensor`, *mesh*: `tensorflow.python.framework.ops.Tensor`, *input\_dict*: `dict`, *reuse*: `Optional[bool]` = None, *suffix*: `str` = "") → `tensorflow.python.framework.ops.Tensor`

Build the computational graph for the descriptor

#### Parameters

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < \text{Ntypes} + 2$ , number of type i atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

### Returns

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord*, *data\_box*, *data\_atype*, *natoms\_vec*, *mesh*, *input\_dict*)

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms. Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

**enable\_compression**(*min\_nbor\_dist*: *float*, *model\_file*: *str* = 'frozen\_model.pb', *table\_extrapolate*: *float* = 5, *table\_stride\_1*: *float* = 0.01, *table\_stride\_2*: *float* = 0.1, *check\_frequency*: *int* = -1, *suffix*: *str* = '') → *None*

Receive the statistics (distance, max\_nbor\_size and env\_mat\_range) of the training data.

### Parameters

**min\_nbor\_dist** The nearest distance between atoms

**model\_file** The original frozen model, which will be compressed by the program

**table\_extrapolate** The scale of model extrapolation

**table\_stride\_1** The uniform stride of the first table

**table\_stride\_2** The uniform stride of the second table

**check\_frequency** The overflow check frequency

**suffix** [*str*, optional] The suffix of the scope

**get\_dim\_out**()

Returns the output dimension of this descriptor

**get\_nlist**()

### Returns

**nlist** Neighbor list

**rij** The relative distance between the neighbor and the center atom.

**sel\_a** The number of neighbors with full information  
**sel\_r** The number of neighbors with only radial information

**get\_ntypes()**

Returns the number of atom types

**get\_rcut()**

Returns the cut-off radius

**prod\_force\_virial**(*atom\_ener*: tensorflow.python.framework.ops.Tensor, *natoms*: tensorflow.python.framework.ops.Tensor) → Tuple[tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor]

Compute force and virial

#### Parameters

**atom\_ener** The atomic energy  
**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

#### Returns

**force** The force on atoms  
**virial** The total virial  
**atom\_virial** The atomic virial

### deepmd.descriptor.se\_t module

**class** deepmd.descriptor.se\_t.DescriptSeT(\*args, \*\*kwargs)

Bases: [deepmd.descriptor.se.DescriptSe](#)

DeepPot-SE constructed from all information (both angular and radial) of atomic configurations.

The embedding takes angles between two neighboring atoms as input.

#### Parameters

**rcut** The cut-off radius  
**rcut\_smth** From where the environment matrix should be smoothed  
**sel** [list[str]] sel[i] specifies the maximum number of type i atoms in the cut-off radius  
**neuron** [list[int]] Number of neurons in each hidden layers of the embedding net  
**resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$   
**trainable** If the weights of embedding net are trainable.  
**seed** Random seed for initializing the network parameters.  
**set\_davg\_zero** Set the shift of embedding net input to zero.  
**activation\_function** The activation function in the embedding net. Supported options are {0}  
**precision** The precision of the embedding net parameters. Supported options are {1}  
**uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

**Attributes**

**precision** Precision of filter network.

**Methods**

<code>build(coord_, atype_, natoms, box_, mesh, ...)</code>	Build the computational graph for the descriptor
<code>compute_input_stats(data_coord, data_box, ...)</code>	Compute the statisitcs (avg and std) of the training data.
<code>enable_compression(min_nbor_dist[, ...])</code>	Reveive the statisitcs (distance, max_nbor_size and env_mat_range) of the training data.
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_dim_out()</code>	Returns the output dimension of this descriptor
<code>get_dim_rot_mat_1()</code>	Returns the first dimension of the rotation matrix.
<code>get_feed_dict(coord_, atype_, natoms, box, mesh)</code>	Generate the feed_dict for current descriptor
<code>get_nlist()</code>	

**Returns**

<code>get_ntypes()</code>	Returns the number of atom types
<code>get_rcut()</code>	Returns the cut-off radisu
<code>get_tensor_names([suffix])</code>	Get names of tensors.
<code>init_variables(model_file[, suffix])</code>	Init the embedding net variables with the given frozen model
<code>pass_tensors_from_frz_model(descrpt_reshape, ...)</code>	Pass the descrpt_reshape tensor as well as descrpt_deriv tensor from the frz_graph_def
<code>prod_force_virial(atom_ener, natoms)</code>	Compute force and virial
<code>register(key)</code>	Register a descriptor plugin.

**build**(*coord\_*: *tensorflow.python.framework.ops.Tensor*, *atype\_*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *box\_*: *tensorflow.python.framework.ops.Tensor*, *mesh*: *tensorflow.python.framework.ops.Tensor*, *input\_dict*: *dict*, *reuse*: *Optional[bool]* = *None*, *suffix*: *str* = '') → *tensorflow.python.framework.ops.Tensor*

Build the computational graph for the descriptor

**Parameters**

**coord\_** The coordinate of atoms

**atype\_** The type of atoms

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type *i* atoms

**mesh** For historical reasons, only the length of the Tensor matters. if size of mesh == 6, pbc is assumed. if size of mesh == 0, no-pbc is assumed.

**input\_dict** Dictionary for additional inputs

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

**Returns**

**descriptor** The output descriptor

**compute\_input\_stats**(*data\_coord: list, data\_box: list, data\_atype: list, natoms\_vec: list, mesh: list, input\_dict: dict*) → *None*

Compute the statistics (avg and std) of the training data. The input will be normalized by the statistics.

#### Parameters

**data\_coord** The coordinates. Can be generated by `deepmd.model.make_stat_input`

**data\_box** The box. Can be generated by `deepmd.model.make_stat_input`

**data\_atype** The atom types. Can be generated by `deepmd.model.make_stat_input`

**natoms\_vec** The vector for the number of atoms of the system and different types of atoms.  
Can be generated by `deepmd.model.make_stat_input`

**mesh** The mesh for neighbor searching. Can be generated by `deepmd.model.make_stat_input`

**input\_dict** Dictionary for additional input

**enable\_compression**(*min\_nbor\_dist: float, model\_file: str = 'frozen\_model.pb', table\_extrapolate: float = 5, table\_stride\_1: float = 0.01, table\_stride\_2: float = 0.1, check\_frequency: int = -1, suffix: str = ''*) → *None*

Reveive the statisitcs (distance, max\_nbor\_size and env\_mat\_range) of the training data.

#### Parameters

**min\_nbor\_dist** The nearest distance between atoms

**model\_file** The original frozen model, which will be compressed by the program

**table\_extrapolate** The scale of model extrapolation

**table\_stride\_1** The uniform stride of the first table

**table\_stride\_2** The uniform stride of the second table

**check\_frequency** The overflow check frequency

**suffix** [*str*, optional] The suffix of the scope

**get\_dim\_out**() → *int*

Returns the output dimension of this descriptor

**get\_nlist**() → *Tuple*[*tensorflow.python.framework.ops.Tensor*, *tensorflow.python.framework.ops.Tensor*, *List*[*int*], *List*[*int*]]

#### Returns

**nlist** Neighbor list

**rij** The relative distance between the neighbor and the center atom.

**sel\_a** The number of neighbors with full information

**sel\_r** The number of neighbors with only radial information

**get\_ntypes**() → *int*

Returns the number of atom types

**get\_rcut**() → *float*

Returns the cut-off radisu



**prod\_force\_virial**(*atom\_ener*: tensorflow.python.framework.ops.Tensor, *natoms*: tensorflow.python.framework.ops.Tensor) → Tuple[tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor, tensorflow.python.framework.ops.Tensor]

Compute force and virial

#### Parameters

**atom\_ener** The atomic energy

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

#### Returns

**force** The force on atoms

**virial** The total virial

**atom\_virial** The atomic virial

### deepmd.entrypoints package

Submodule that contains all the DeePMD-Kit entry point scripts.

**deepmd.entrypoints.compress**(\*, *input*: str, *output*: str, *extrapolate*: int, *step*: float, *frequency*: str, *checkpoint\_folder*: str, *training\_script*: str, *mpi\_log*: str, *log\_path*: Optional[str], *log\_level*: int, \*\*kwargs)

Compress model.

The table is composed of fifth-order polynomial coefficients and is assembled from two sub-tables. The first table takes the step parameter as the domain's uniform step size, while the second table takes 10 \* step as its uniform step size. The range of the first table is automatically detected by the code, while the second table ranges from the first table's upper boundary(upper) to the extrapolate(parameter) \* upper.

#### Parameters

**input** [str] frozen model file to compress

**output** [str] compressed model filename

**extrapolate** [int] scale of model extrapolation

**step** [float] uniform step size of the tabulation's first table

**frequency** [str] frequency of tabulation overflow check

**checkpoint\_folder** [str] training checkpoint folder for freezing

**training\_script** [str] training script of the input frozen model

**mpi\_log** [str] mpi logging mode for training

**log\_path** [Optional[str]] if specified log will be written to this file

**log\_level** [int] logging level

**deepmd.entrypoints.config**(\*, *output*: str, \*\*kwargs)

Auto config file generator.

#### Parameters

**output**: str file to write config file

**Raises**

**RuntimeError** if user does not input any systems

**ValueError** if output file is of wrong type

deepmd.entrypoints.**convert**(\**FROM: str*, *input\_model: str*, *output\_model: str*, \*\**kwargs*)

deepmd.entrypoints.**doc\_train\_input**(\**out\_type: str = 'rst'*, \*\**kwargs*)

Print out training input arguments to console.

deepmd.entrypoints.**freeze**(\**checkpoint\_folder: str*, *output: str*, *node\_names: Optional[str] = None*, \*\**kwargs*)

Freeze the graph in supplied folder.

**Parameters**

**checkpoint\_folder** [*str*] location of the folder with model

**output** [*str*] output file name

**node\_names** [*Optional[str]*, *optional*] names of nodes to output, by default None

deepmd.entrypoints.**make\_model\_devi**(\**models: list*, *system: str*, *set\_prefix: str*, *output: str*, *frequency: int*, \*\**kwargs*)

Make model deviation calculation

**Parameters**

**models: list** A list of paths of models to use for making model deviation

**system: str** The path of system to make model deviation calculation

**set\_prefix: str** The set prefix of the system

**output: str** The output file for model deviation results

**frequency: int** The number of steps that elapse between writing coordinates in a trajectory by a MD engine (such as Gromacs / Lammmps). This paramter is used to determine the index in the output file.

deepmd.entrypoints.**neighbor\_stat**(\**system: str*, *rcut: float*, *type\_map: List[str]*, \*\**kwargs*)

Calculate neighbor statistics.

**Parameters**

**system** [*str*] system to stat

**rcut** [*float*] cutoff radius

**type\_map** [*list[str]*] type map

**Examples**

```
>>> neighbor_stat(system='.', rcut=6., type_map=["C", "H", "O", "N", "P", "S", "Mg",
→ "Na", "HW", "OW", "mNa", "mCl", "mC", "mH", "mMg", "mN", "mO", "mP"])
min_nbor_dist: 0.6599510670195264
max_nbor_size: [23, 26, 19, 16, 2, 2, 1, 1, 72, 37, 5, 0, 31, 29, 1, 21, 20, 5]
```

deepmd.entrypoints.**test**(\**model: str*, *system: str*, *set\_prefix: str*, *numb\_test: int*, *rand\_seed: Optional[int]*, *shuffle\_test: bool*, *detail\_file: str*, *atomic: bool*, \*\**kwargs*)

Test model predictions.

**Parameters**

**model** [**str**] path where model is stored  
**system** [**str**] system directory  
**set\_prefix** [**str**] string prefix of set  
**numb\_test** [**int**] number of tests to do  
**rand\_seed** [**Optional**[**int**]] seed for random generator  
**shuffle\_test** [**bool**] whether to shuffle tests  
**detail\_file** [**Optional**[**str**]] file where test details will be output  
**atomic** [**bool**] whether per atom quantities should be computed

**Raises**

**RuntimeError** if no valid system was found

`deepmd.entrypoints.train_dp(*, INPUT: str, init_model: Optional[str], restart: Optional[str], output: str, init_frz_model: str, mpi_log: str, log_level: int, log_path: Optional[str], is_compress: bool = False, skip_neighbor_stat: bool = False, **kwargs)`

Run DeePMD model training.

**Parameters**

**INPUT** [**str**] json/yaml control file  
**init\_model** [**Optional**[**str**]] path to checkpoint folder or None  
**restart** [**Optional**[**str**]] path to checkpoint folder or None  
**output** [**str**] path for dump file with arguments  
**init\_frz\_model** [**str**] path to frozen model or None  
**mpi\_log** [**str**] mpi logging mode  
**log\_level** [**int**] logging level defined by int 0-3  
**log\_path** [**Optional**[**str**]] logging file path or None if logs are to be output only to stdout  
**is\_compress: bool** indicates whether in the model compress mode  
**skip\_neighbor\_stat** [**bool**, default=False] skip checking neighbor statistics

**Raises**

**RuntimeError** if distributed training job nem is wrong

`deepmd.entrypoints.transfer(*, old_model: str, raw_model: str, output: str, **kwargs)`

Transfer operation from old from graph to new prepared raw graph.

**Parameters**

**old\_model** [**str**] frozen old graph model  
**raw\_model** [**str**] new model that will accept ops from old model  
**output** [**str**] new model with transferred parameters will be saved to this location

## Submodules

### deepmd.entrypoints.compress module

Compress a model, which including tabulating the embedding-net.

```
deepmd.entrypoints.compress.compress(*, input: str, output: str, extrapolate: int, step: float, frequency: str,  
                                     checkpoint_folder: str, training_script: str, mpi_log: str, log_path:  
                                     Optional[str], log_level: int, **kwargs)
```

Compress model.

The table is composed of fifth-order polynomial coefficients and is assembled from two sub-tables. The first table takes the step parameter as the domain's uniform step size, while the second table takes  $10 * \text{step}$  as its uniform step size. The range of the first table is automatically detected by the code, while the second table ranges from the first table's upper boundary(upper) to the extrapolate(parameter) \* upper.

#### Parameters

**input** [str] frozen model file to compress  
**output** [str] compressed model filename  
**extrapolate** [int] scale of model extrapolation  
**step** [float] uniform step size of the tabulation's first table  
**frequency** [str] frequency of tabulation overflow check  
**checkpoint\_folder** [str] trining checkpoint folder for freezing  
**training\_script** [str] training script of the input frozen model  
**mpi\_log** [str] mpi logging mode for training  
**log\_path** [Optional[str]] if speccified log will be written to this file  
**log\_level** [int] logging level

### deepmd.entrypoints.config module

Quickly create a configuration file for smooth model.

```
deepmd.entrypoints.config.config(*, output: str, **kwargs)
```

Auto config file generator.

#### Parameters

**output: str** file to write config file

#### Raises

**RuntimeError** if user does not input any systems  
**ValueError** if output file is of wrong type

### deepmd.entrypoints.convert module

deepmd.entrypoints.convert.**convert**(\**FROM: str*, *input\_model: str*, *output\_model: str*, \*\**kwargs*)

### deepmd.entrypoints.doc module

Module that prints train input arguments docstrings.

deepmd.entrypoints.doc.**doc\_train\_input**(\**out\_type: str = 'rst'*, \*\**kwargs*)  
Print out training input arguments to console.

### deepmd.entrypoints.freeze module

Script for freezing TF trained graph so it can be used with LAMMPS and i-PI.

### References

<https://blog.metaflow.fr/tensorflow-how-to-freeze-a-model-and-serve-it-with-a-python-api-d4f3596b3adc>

deepmd.entrypoints.freeze.**freeze**(\**checkpoint\_folder: str*, *output: str*, *node\_names: Optional[str] = None*, \*\**kwargs*)

Freeze the graph in supplied folder.

#### Parameters

**checkpoint\_folder** [*str*] location of the folder with model

**output** [*str*] output file name

**node\_names** [*Optional[str]*, *optional*] names of nodes to output, by default None

### deepmd.entrypoints.main module

DeePMD-Kit entry point module.

deepmd.entrypoints.main.**get\_ll**(*log\_level: str*) → *int*  
Convert string to python logging level.

#### Parameters

**log\_level** [*str*] allowed input values are: DEBUG, INFO, WARNING, ERROR, 3, 2, 1, 0

#### Returns

*int* one of python logging module log levels - 10, 20, 30 or 40

deepmd.entrypoints.main.**main**()  
DeePMD-Kit entry point.

#### Raises

**RuntimeError** if no command was input

deepmd.entrypoints.main.**parse\_args**(*args: Optional[List[str]] = None*)  
DeePMD-Kit commandline options argument parser.

#### Parameters

**args: List[str]** list of command line arguments, main purpose is testing default option None takes arguments from sys.argv

### deepmd.entrypoints.neighbor\_stat module

deepmd.entrypoints.neighbor\_stat.**neighbor\_stat**(\*, system: *str*, rcut: *float*, type\_map: *List[str]*, \*\*kwargs)

Calculate neighbor statistics.

#### Parameters

**system** [str] system to stat

**rcut** [float] cutoff radius

**type\_map** [list[str]] type map

#### Examples

```
>>> neighbor_stat(system='.', rcut=6., type_map=["C", "H", "O", "N", "P", "S", "Mg",
→ "Na", "HW", "OW", "mNa", "mCl", "mC", "mH", "mMg", "mN", "mO", "mP"])
min_nbor_dist: 0.6599510670195264
max_nbor_size: [23, 26, 19, 16, 2, 2, 1, 1, 72, 37, 5, 0, 31, 29, 1, 21, 20, 5]
```

### deepmd.entrypoints.test module

Test trained DeePMD model.

deepmd.entrypoints.test.**test**(\*, model: *str*, system: *str*, set\_prefix: *str*, numb\_test: *int*, rand\_seed: *Optional[int]*, shuffle\_test: *bool*, detail\_file: *str*, atomic: *bool*, \*\*kwargs)

Test model predictions.

#### Parameters

**model** [str] path where model is stored

**system** [str] system directory

**set\_prefix** [str] string prefix of set

**numb\_test** [int] number of tests to do

**rand\_seed** [Optional[int]] seed for random generator

**shuffle\_test** [bool] whether to shuffle tests

**detail\_file** [Optional[str]] file where test details will be output

**atomic** [bool] whether per atom quantities should be computed

#### Raises

**RuntimeError** if no valid system was found

## deepmd.entrypoints.train module

DeePMD training entrypoint script.

Can handle local or distributed training.

```
deepmd.entrypoints.train.train(*, INPUT: str, init_model: Optional[str], restart: Optional[str], output: str,
                                init_frz_model: str, mpi_log: str, log_level: int, log_path: Optional[str],
                                is_compress: bool = False, skip_neighbor_stat: bool = False, **kwargs)
```

Run DeePMD model training.

### Parameters

**INPUT** [*str*] json/yaml control file

**init\_model** [*Optional[str]*] path to checkpoint folder or None

**restart** [*Optional[str]*] path to checkpoint folder or None

**output** [*str*] path for dump file with arguments

**init\_frz\_model** [*str*] path to frozen model or None

**mpi\_log** [*str*] mpi logging mode

**log\_level** [*int*] logging level defined by int 0-3

**log\_path** [*Optional[str]*] logging file path or None if logs are to be output only to stdout

**is\_compress: bool** indicates whether in the model compress mode

**skip\_neighbor\_stat** [*bool*, default=False] skip checking neighbor statistics

### Raises

**RuntimeError** if distributed training job nem is wrong

## deepmd.entrypoints.transfer module

Module used for transferring parameters between models.

```
deepmd.entrypoints.transfer.transfer(*, old_model: str, raw_model: str, output: str, **kwargs)
```

Transfer operation from old from graph to new prepared raw graph.

### Parameters

**old\_model** [*str*] frozen old graph model

**raw\_model** [*str*] new model that will accept ops from old model

**output** [*str*] new model with transfered parameters will be saved to this location

## deepmd.fit package

## Submodules

## deepmd.fit.dipole module

**class** deepmd.fit.dipole.DipoleFittingSea

Bases: [deepmd.fit.fitting.Fitting](#)

Fit the atomic dipole with descriptor se\_a

## Parameters

**descript** [[tf.Tensor](#)] The descriptor

**neuron** [[List\[int\]](#)] Number of neurons in each hidden layer of the fitting net

**resnet\_dt** [[bool](#)] Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$

**sel\_type** [[List\[int\]](#)] The atom types selected to have an atomic dipole prediction. If is None, all atoms are selected.

**seed** [[int](#)] Random seed for initializing the network parameters.

**activation\_function** [[str](#)] The activation function in the embedding net. Supported options are {0}

**precision** [[str](#)] The precision of the embedding net parameters. Supported options are {1}

**uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

## Attributes

**precision** Precision of fitting network.

## Methods

<a href="#">build</a> (input_d, rot_mat, natoms[, reuse, suffix])	Build the computational graph for fitting net
<a href="#">enable_mixed_precision</a> ([mixed_prec])	Reveive the mixed precision setting.
<a href="#">get_out_size</a> ()	Get the output size.
<a href="#">get_sel_type</a> ()	Get selected type
<a href="#">init_variables</a> (model_file)	Init the fitting net variables with the given frozen model

**build**(input\_d: [tensorflow.python.framework.ops.Tensor](#), rot\_mat: [tensorflow.python.framework.ops.Tensor](#), natoms: [tensorflow.python.framework.ops.Tensor](#), reuse: [bool](#) = None, suffix: [str](#) = '') → [tensorflow.python.framework.ops.Tensor](#)

Build the computational graph for fitting net

## Parameters

**input\_d** The input descriptor

**rot\_mat** The rotation matrix from the descriptor.

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < Ntypes+2$ , number of type i atoms



**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

### Returns

**dipole** The atomic dipole.

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict] = None*) → *None*

Reveive the mixed precision setting.

### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_out\_size**() → *int*

Get the output size. Should be 3

**get\_sel\_type**() → *int*

Get selected type

**init\_variables**(*model\_file*: *str*) → *None*

Init the fitting net variables with the given frozen model

### Parameters

**model\_file** [*str*] The input frozen model file

## deepmd.fit.ener module

**class** deepmd.fit.ener.EnerFitting

Bases: *deepmd.fit.fitting.Fitting*

Fitting the energy of the system. The force and the virial can also be trained.

The potential energy  $E$  is a fitting network function of the descriptor  $\mathcal{D}$ :

$$E(\mathcal{D}) = \mathcal{L}^{(n)} \circ \mathcal{L}^{(n-1)} \circ \dots \circ \mathcal{L}^{(1)} \circ \mathcal{L}^{(0)}$$

The first  $n$  hidden layers  $\mathcal{L}^{(0)}, \dots, \mathcal{L}^{(n-1)}$  are given by

$$\mathbf{y} = \mathcal{L}(\mathbf{x}; \mathbf{w}, \mathbf{b}) = \phi(\mathbf{x}^T \mathbf{w} + \mathbf{b})$$

where  $\mathbf{x} \in \mathbb{R}^{N_1}$  is the input vector and  $\mathbf{y} \in \mathbb{R}^{N_2}$  is the output vector.  $\mathbf{w} \in \mathbb{R}^{N_1 \times N_2}$  and  $\mathbf{b} \in \mathbb{R}^{N_2}$  are weights and biases, respectively, both of which are trainable if *trainable[i]* is *True*.  $\phi$  is the activation function.

The output layer  $\mathcal{L}^{(n)}$  is given by

$$\mathbf{y} = \mathcal{L}^{(n)}(\mathbf{x}; \mathbf{w}, \mathbf{b}) = \mathbf{x}^T \mathbf{w} + \mathbf{b}$$

where  $\mathbf{x} \in \mathbb{R}^{N_{n-1}}$  is the input vector and  $\mathbf{y} \in \mathbb{R}$  is the output scalar.  $\mathbf{w} \in \mathbb{R}^{N_{n-1}}$  and  $\mathbf{b} \in \mathbb{R}$  are weights and bias, respectively, both of which are trainable if *trainable[n]* is *True*.

### Parameters

**descript** The descriptor  $\mathcal{D}$

**neuron** Number of neurons  $N$  in each hidden layer of the fitting net

**resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$

**numb\_fparam** Number of frame parameter

**numb\_aparam** Number of atomic parameter

- rcond** The condition number for the regression of atomic energy.
- tot\_ener\_zero** Force the total energy to zero. Useful for the charge fitting.
- trainable** If the weights of fitting net are trainable. Suppose that we have  $N_l$  hidden layers in the fitting net, this list is of length  $N_l + 1$ , specifying if the hidden layers and the output layer are trainable.
- seed** Random seed for initializing the network parameters.
- atom\_ener** Specifying atomic energy contribution in vacuum. The *set\_davg\_zero* key in the descriptor should be set.
- activation\_function** The activation function  $\phi$  in the embedding net. Supported options are {0}
- precision** The precision of the embedding net parameters. Supported options are {1}
- uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

#### Attributes

- precision** Precision of fitting network.

#### Methods

<i>build</i> (inputs, natoms[, input_dict, reuse, ...])	Build the computational graph for fitting net
<i>compute_input_stats</i> (all_stat[, protection])	Compute the input statistics
<i>compute_output_stats</i> (all_stat)	Compute the output statistics
<i>enable_compression</i> (model_file[, suffix])	Set the fitting net attributes from the frozen model_file when fparam or aparam is not zero
<i>enable_mixed_precision</i> ([mixed_prec])	Reveive the mixed precision setting.
<i>get_numb_aparam</i> ()	Get the number of atomic parameters
<i>get_numb_fparam</i> ()	Get the number of frame parameters
<i>init_variables</i> (model_file)	Init the fitting net variables with the given frozen model

**build**(inputs: tensorflow.python.framework.ops.Tensor, natoms: tensorflow.python.framework.ops.Tensor, input\_dict: dict = None, reuse: bool = None, suffix: str = '') → tensorflow.python.framework.ops.Tensor  
Build the computational graph for fitting net

#### Parameters

- inputs** The input descriptor
- input\_dict** Additional dict for inputs. if numbfparam > 0, should have input\_dict['fparam']  
if numbaparam > 0, should have input\_dict['aparam']
- natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms
- reuse** The weights in the networks should be reused when get the variable.
- suffix** Name suffix to identify this descriptor

#### Returns

- ener** The system energy

**compute\_input\_stats**(*all\_stat*: *dict*, *protection*: *float* = 0.01) → *None*

Compute the input statistics

#### Parameters

**all\_stat** if `numb_fparam > 0` must have `all_stat['fparam']` if `numb_aparam > 0` must have `all_stat['aparam']` can be prepared by `model.make_stat_input`

**protection** Divided-by-zero protection

**compute\_output\_stats**(*all\_stat*: *dict*) → *None*

Compute the output statistics

#### Parameters

**all\_stat** must have the following components: `all_stat['energy']` of shape `n_sys x n_batch x n_frame` can be prepared by `model.make_stat_input`

**enable\_compression**(*model\_file*: *str*, *suffix*: *str* = "") → *None*

Set the fitting net attributes from the frozen `model_file` when `fparam` or `aparam` is not zero

#### Parameters

**model\_file** [*str*] The input frozen model file

**suffix** [*str*, optional] The suffix of the scope

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict]* = *None*) → *None*

Receive the mixed precision setting.

#### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_numb\_aparam**() → *int*

Get the number of atomic parameters

**get\_numb\_fparam**() → *int*

Get the number of frame parameters

**init\_variables**(*model\_file*: *str*) → *None*

Init the fitting net variables with the given frozen model

#### Parameters

**model\_file** [*str*] The input frozen model file

## deepmd.fit.fitting module

**class** `deepmd.fit.fitting.Fitting`

Bases: `object`

#### Attributes

**precision** Precision of fitting network.

**property precision:** `tensorflow.python.framework.dtypes.DType`

Precision of fitting network.

**deepmd.fit.polar module**

**class** deepmd.fit.polar.GlobalPolarFittingSea

Bases: `object`

Fit the system polarizability with descriptor `se_a`

**Parameters**

**descript** [`tf.Tensor`] The descriptor

**neuron** [`List[int]`] Number of neurons in each hidden layer of the fitting net

**resnet\_dt** [`bool`] Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$

**sel\_type** [`List[int]`] The atom types selected to have an atomic polarizability prediction

**fit\_diag** [`bool`] Fit the diagonal part of the rotational invariant polarizability matrix, which will be converted to normal polarizability matrix by contracting with the rotation matrix.

**scale** [`List[float]`] The output of the fitting net (polarizability matrix) for type  $i$  atom will be scaled by `scale[i]`

**diag\_shift** [`List[float]`] The diagonal part of the polarizability matrix of type  $i$  will be shifted by `diag_shift[i]`. The shift operation is carried out after scale.

**seed** [`int`] Random seed for initializing the network parameters.

**activation\_function** [`str`] The activation function in the embedding net. Supported options are {0}

**precision** [`str`] The precision of the embedding net parameters. Supported options are {1}

**Methods**

<code>build(input_d, rot_mat, natoms[, reuse, suffix])</code>	Build the computational graph for fitting net
<code>enable_mixed_precision([mixed_prec])</code>	Reveive the mixed precision setting.
<code>get_out_size()</code>	Get the output size.
<code>get_sel_type()</code>	Get selected atom types
<code>init_variables(model_file)</code>	Init the fitting net variables with the given frozen model

**build**(`input_d, rot_mat, natoms, reuse=None, suffix=""`)  $\rightarrow$  tensorflow.python.framework.ops.Tensor  
Build the computational graph for fitting net

**Parameters**

**input\_d** The input descriptor

**rot\_mat** The rotation matrix from the descriptor.

**natoms** The number of atoms. This tensor has the length of `Ntypes + 2` `natoms[0]`: number of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < Ntypes+2$ , number of type  $i$  atoms

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

**Returns**

**polar** The system polarizability

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict]* = *None*) → *None*

Reveive the mixed precision setting.

#### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_out\_size**() → *int*

Get the output size. Should be 9

**get\_sel\_type**() → *int*

Get selected atom types

**init\_variables**(*model\_file*: *str*) → *None*

Init the fitting net variables with the given frozen model

#### Parameters

**model\_file** [*str*] The input frozen model file

**class** deepmd.fit.polar.PolarFittingLocFrame(*jdata*, *descript*)

Bases: *object*

Fitting polarizability with local frame descriptor.

Deprecated since version 2.0.0: This class is not supported any more.

#### Methods

<b>build</b>	
<b>get_out_size</b>	
<b>get_sel_type</b>	

**build**(*input\_d*, *rot\_mat*, *natoms*, *reuse*=*None*, *suffix*='')

**get\_out\_size**()

**get\_sel\_type**()

**class** deepmd.fit.polar.PolarFittingSeA

Bases: *deepmd.fit.fitting.Fitting*

Fit the atomic polarizability with descriptor se\_a

#### Attributes

**precision** Precision of fitting network.

#### Methods

<i>build</i> ( <i>input_d</i> , <i>rot_mat</i> , <i>natoms</i> [, <i>reuse</i> , <i>suffix</i> ])	Build the computational graph for fitting net
<i>compute_input_stats</i> ( <i>all_stat</i> [, <i>protection</i> ])	Compute the input statistics
<i>enable_mixed_precision</i> ([ <i>mixed_prec</i> ])	Reveive the mixed precision setting.
<i>get_out_size</i> ()	Get the output size.
<i>get_sel_type</i> ()	Get selected atom types
<i>init_variables</i> ( <i>model_file</i> )	Init the fitting net variables with the given frozen model

**build**(*input\_d*: *tensorflow.python.framework.ops.Tensor*, *rot\_mat*: *tensorflow.python.framework.ops.Tensor*, *natoms*: *tensorflow.python.framework.ops.Tensor*, *reuse*: *bool* = *None*, *suffix*: *str* = "")

Build the computational graph for fitting net

#### Parameters

**input\_d** The input descriptor

**rot\_mat** The rotation matrix from the descriptor.

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

**reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**atomic\_polar** The atomic polarizability

**compute\_input\_stats**(*all\_stat*, *protection*=0.01)

Compute the input statistics

#### Parameters

**all\_stat** Dictionary of inputs. can be prepared by model.make\_stat\_input

**protection** Divided-by-zero protection

**enable\_mixed\_precision**(*mixed\_prec*: *Optional[dict]* = *None*) → *None*

Reveive the mixed precision setting.

#### Parameters

**mixed\_prec** The mixed precision setting used in the embedding net

**get\_out\_size**() → *int*

Get the output size. Should be 9

**get\_sel\_type**() → *List[int]*

Get selected atom types

**init\_variables**(*model\_file*: *str*) → *None*

Init the fitting net variables with the given frozen model

#### Parameters

**model\_file** [*str*] The input frozen model file

## deepmd.fit.wfc module

**class** deepmd.fit.wfc.**WFCFitting**(*jdata*, *descript*)

Bases: *object*

Fitting Wannier function centers (WFCs) with local frame descriptor.

Deprecated since version 2.0.0: This class is not supported any more.

## Methods

<b>build</b>	
<b>get_out_size</b>	
<b>get_sel_type</b>	
<b>get_wfc_num</b>	

**build**(*input\_d*, *rot\_mat*, *natoms*, *reuse=None*, *suffix=""*)

**get\_out\_size**()

**get\_sel\_type**()

**get\_wfc\_num**()

## deepmd.infer package

Submodule containing all the implemented potentials.

**class** `deepmd.infer.DeepDipole`(*model\_file*: *Path*, *load\_prefix*: *str* = 'load', *default\_tf\_graph*: *bool* = *False*)  
 Bases: `deepmd.infer.deep_tensor.DeepTensor`

Constructor.

### Parameters

**model\_file** [*Path*] The name of the frozen model file.

**load\_prefix**: *str* The prefix in the load computational graph

**default\_tf\_graph** [*bool*] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.

continues on next page

Table 17 – continued from previous page

<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

`get_dim_aparam()` → `int`  
Unsupported in this model.

`get_dim_fparam()` → `int`  
Unsupported in this model.

`load_prefix:` `str`

`class deepmd.infer.DeepEval(model_file: Path, load_prefix: str = 'load', default_tf_graph: bool = False, auto_batch_size: Union[bool, int, deepmd.utils.batch_size.AutoBatchSize] = False)`

Bases: `object`

Common methods for DeepPot, DeepWFC, DeepPolar, ...

#### Parameters

**model\_file** [`Path`] The name of the frozen model file.

**load\_prefix:** `str` The prefix in the load computational graph

**default\_tf\_graph** [`bool`] If uses the default tf graph, otherwise build a new tf graph for evaluation

**auto\_batch\_size** [`bool` or `int` or `AutomaticBatchSize`, default: `False`] If True, automatic batch size will be used. If int, it will be used as the initial batch size.

#### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

#### Methods

<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

`load_prefix:` `str`

`make_natoms_vec(atom_types: numpy.ndarray) → numpy.ndarray`  
Make the natom vector used by deepmd-kit.

#### Parameters

**atom\_types** The type of atoms

#### Returns

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number



of local atoms `natoms[1]`: total number of atoms held by this processor `natoms[i]`:  $2 \leq i < N_{\text{types}}+2$ , number of type  $i$  atoms

**property** `model_type`: `str`

Get type of model.

:type: `str`

**property** `model_version`: `str`

Get version of model.

**Returns**

`str` version of model

**static** `reverse_map`(*vec*: `numpy.ndarray`, *imap*: `List[int]`) → `numpy.ndarray`

Reverse mapping of a vector according to the index map

**Parameters**

**vec** Input vector. Be of shape `[nframes, natoms, -1]`

**imap** Index map. Be of shape `[natoms]`

**Returns**

**vec\_out** Reverse mapped vector.

**static** `sort_input`(*coord*: `numpy.ndarray`, *atom\_type*: `numpy.ndarray`, *sel\_atoms*: `Optional[List[int]]` = `None`)

Sort atoms in the system according their types.

**Parameters**

**coord** The coordinates of atoms. Should be of shape `[nframes, natoms, 3]`

**atom\_type** The type of atoms Should be of shape `[natoms]`

**sel\_atom** The selected atoms by type

**Returns**

**coord\_out** The coordinates after sorting

**atom\_type\_out** The atom types after sorting

**idx\_map** The index mapping from the input to the output. For example `coord_out = coord[:, idx_map, :]`

**sel\_atom\_type** Only output if `sel_atoms` is not `None` The sorted selected atom types

**sel\_idx\_map** Only output if `sel_atoms` is not `None` The index mapping from the selected atoms to sorted selected atoms.

**class** `deepmd.infer.DeepGlobalPolar`(*model\_file*: `str`, *load\_prefix*: `str` = `'load'`, *default\_tf\_graph*: `bool` = `False`)

Bases: `deepmd.infer.deep_tensor.DeepTensor`

Constructor.

**Parameters**

**model\_file** [`str`] The name of the frozen model file.

**load\_prefix**: `str` The prefix in the load computational graph

**default\_tf\_graph** [`bool`] If uses the default tf graph, otherwise build a new tf graph for evaluation

### Attributes

**model\_type** Get type of model.  
**model\_version** Get version of model.

### Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**eval**(*coords*: *numpy.ndarray*, *cells*: *numpy.ndarray*, *atom\_types*: *List[int]*, *atomic*: *bool* = *False*, *fparam*: *Optional[numpy.ndarray]* = *None*, *aparam*: *Optional[numpy.ndarray]* = *None*, *efield*: *Optional[numpy.ndarray]* = *None*) → *numpy.ndarray*  
 Evaluate the model.

### Parameters

**coords** The coordinates of atoms. The array should be of size nframes x natoms x 3  
**cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size nframes x 9  
**atom\_types** The atom types The list should contain natoms ints  
**atomic** Not used in this model  
**fparam** Not used in this model  
**aparam** Not used in this model  
**efield** Not used in this model

### Returns

**tensor** The returned tensor If *atomic* == *False* then of size nframes x variable\_dof else of size nframes x natoms x variable\_dof

**get\_dim\_aparam()** → *int*  
 Unsupported in this model.

**get\_dim\_fparam()** → *int*  
 Unsupported in this model.

**load\_prefix:** *str*

**class** `deepmd.infer.DeepPolar`(*model\_file*: *Path*, *load\_prefix*: *str* = 'load', *default\_tf\_graph*: *bool* = *False*)  
 Bases: `deepmd.infer.deep_tensor.DeepTensor`

Constructor.

### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix: str** The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

### Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**get\_dim\_aparam()** → int  
Unsupported in this model.

**get\_dim\_fparam()** → int  
Unsupported in this model.

**load\_prefix:** str

```
class deepmd.infer.DeepPot(model_file: Path, load_prefix: str = 'load', default_tf_graph: bool = False,
                           auto_batch_size: Union[bool, int, deepmd.utils.batch_size.AutoBatchSize] =
                           True)
```

Bases: `deepmd.infer.deep_eval.DeepEval`

Constructor.

### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix: str** The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**auto\_batch\_size** [bool or int or AutomaticBatchSize, default: True] If True, automatic batch size will be used. If int, it will be used as the initial batch size.

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

## Examples

```
>>> from deepmd.infer import DeepPot
>>> import numpy as np
>>> dp = DeepPot('graph.pb')
>>> coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
>>> cell = np.diag(10 * np.ones(3)).reshape([1, -1])
>>> atype = [1,0,1]
>>> e, f, v = dp.eval(coord, cell, atype)
```

where  $e$ ,  $f$  and  $v$  are predicted energy, force and virial of the system, respectively.

## Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the energy, force and virial by using this DP.
<code>eval_descriptor(coords, cells, atom_types[, ...])</code>	Evaluate descriptors by using this DP.
<code>get_dim_aparam()</code>	Get the number (dimension) of atomic parameters of this DP.
<code>get_dim_fparam()</code>	Get the number (dimension) of frame parameters of this DP.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Unsupported in this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**eval**(*coords*: *numpy.ndarray*, *cells*: *numpy.ndarray*, *atom\_types*: *List[int]*, *atomic*: *bool* = *False*, *fparam*: *Optional[numpy.ndarray]* = *None*, *aparam*: *Optional[numpy.ndarray]* = *None*, *efield*: *Optional[numpy.ndarray]* = *None*) → *Tuple[numpy.ndarray, ...]*  
Evaluate the energy, force and virial by using this DP.

## Parameters

**coords** The coordinates of atoms. The array should be of size nframes x natoms x 3

**cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size nframes x 9

**atom\_types** The atom types The list should contain natoms ints

**atomic** Calculate the atomic energy and virial

**fparam** The frame parameter. The array can be of size : - nframes x dim\_fparam. - dim\_fparam. Then all frames are assumed to be provided with the same fparam.

**aparam** The atomic parameter The array can be of size : - nframes x natoms x dim\_aparam. - natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. - dim\_aparam. Then all frames and atoms are provided with the same aparam.

**efield** The external field on atoms. The array should be of size nframes x natoms x 3

#### Returns

**energy** The system energy.

**force** The force on each atom

**virial** The virial

**atom\_energy** The atomic energy. Only returned when atomic == True

**atom\_virial** The atomic virial. Only returned when atomic == True

**eval\_descriptor**(*coords: numpy.ndarray, cells: numpy.ndarray, atom\_types: List[int], fparam: Optional[numpy.ndarray] = None, aparam: Optional[numpy.ndarray] = None, efield: Optional[numpy.ndarray] = None*) → numpy.array

Evaluate descriptors by using this DP.

#### Parameters

**coords** The coordinates of atoms. The array should be of size nframes x natoms x 3

**cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size nframes x 9

**atom\_types** The atom types The list should contain natoms ints

**fparam** The frame parameter. The array can be of size : - nframes x dim\_fparam. - dim\_fparam. Then all frames are assumed to be provided with the same fparam.

**aparam** The atomic parameter The array can be of size : - nframes x natoms x dim\_aparam. - natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. - dim\_aparam. Then all frames and atoms are provided with the same aparam.

**efield** The external field on atoms. The array should be of size nframes x natoms x 3

#### Returns

**descriptor** Descriptors.

**get\_dim\_aparam**() → int

Get the number (dimension) of atomic parameters of this DP.

**get\_dim\_fparam**() → int

Get the number (dimension) of frame parameters of this DP.

**get\_ntypes**() → int

Get the number of atom types of this model.

**get\_rcut()** → float

Get the cut-off radius of this model.

**get\_sel\_type()** → List[int]

Unsupported in this model.

**get\_type\_map()** → List[int]

Get the type map (element name of the atom types) of this model.

**load\_prefix:** str

**deepmd.infer.DeepPotential**(*model\_file*: Union[str, pathlib.Path], *load\_prefix*: str = 'load', *default\_tf\_graph*: bool = False) → Union[deepmd.infer.deep\_dipole.DeepDipole, deepmd.infer.deep\_polar.DeepGlobalPolar, deepmd.infer.deep\_polar.DeepPolar, deepmd.infer.deep\_pot.DeepPot, deepmd.infer.deep\_wfc.DeepWFC]

Factory function that will initialize appropriate potential read from *model\_file*.

#### Parameters

**model\_file:** str The name of the frozen model file.

**load\_prefix:** str The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

#### Returns

Union[DeepDipole, DeepGlobalPolar, DeepPolar, DeepPot, DeepWFC] one of the available potentials

#### Raises

RuntimeError if model file does not correspond to any implemented potential

**class** deepmd.infer.DeepWFC(*model\_file*: Path, *load\_prefix*: str = 'load', *default\_tf\_graph*: bool = False)

Bases: deepmd.infer.deep\_tensor.DeepTensor

Constructor.

#### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix:** str The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

#### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

`get_dim_aparam()` → int  
Unsupported in this model.

`get_dim_fparam()` → int  
Unsupported in this model.

**load\_prefix:** str

**class** deepmd.infer.DipoleChargeModifier(*model\_name: str, model\_charge\_map: List[float], sys\_charge\_map: List[float], ewald\_h: float = 1, ewald\_beta: float = 1*)

Bases: *deepmd.infer.deep\_dipole.DeepDipole*

### Parameters

**model\_name** The model file for the DeepDipole model

**model\_charge\_map** Gives the amount of charge for the wfcc

**sys\_charge\_map** Gives the amount of charge for the real atoms

**ewald\_h** Grid spacing of the reciprocal part of Ewald sum. Unit: Å

**ewald\_beta** Splitting parameter of the Ewald sum. Unit: Å<sup>-1</sup>

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>build_fv_graph()</code>	Build the computational graph for the force and virial inference.
<code>eval(coord, box, atype[, eval_fv])</code>	Evaluate the modification
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.

continues on next page

Table 23 – continued from previous page

<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>modify_data(data)</code>	Modify data.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**build\_fv\_graph()** → tensorflow.python.framework.ops.Tensor

Build the computational graph for the force and virial inference.

**eval**(*coord*: *numpy.ndarray*, *box*: *numpy.ndarray*, *atype*: *numpy.ndarray*, *eval\_fv*: *bool = True*) →  
 Tuple[*numpy.ndarray*, *numpy.ndarray*, *numpy.ndarray*]

Evaluate the modification

#### Parameters

**coord** The coordinates of atoms

**box** The simulation region. PBC is assumed

**atype** The atom types

**eval\_fv** Evaluate force and virial

#### Returns

**tot\_e** The energy modification

**tot\_f** The force modification

**tot\_v** The virial modification

**load\_prefix:** *str*

**modify\_data**(*data*: *dict*) → *None*

Modify data.

#### Parameters

**data** Internal data of DeepmdData. Be a dict, has the following keys - *coord* coordinates - *box* simulation box - *type* atom types - *find\_energy* tells if data has energy - *find\_force* tells if data has force - *find\_virial* tells if data has virial - *energy* energy - *force* force - *virial* virial

**class** `deepmd.infer.EwaldRecp`(*hh*, *beta*)

Bases: *object*

Evaluate the reciprocal part of the Ewald sum



## Methods

---

<code>eval(coord, charge, box)</code>	Evaluate
---------------------------------------	----------

---

**eval**(*coord*: `numpy.ndarray`, *charge*: `numpy.ndarray`, *box*: `numpy.ndarray`) → `Tuple[numpy.ndarray, numpy.ndarray, numpy.ndarray]`

Evaluate

### Parameters

**coord** The coordinates of atoms  
**charge** The atomic charge  
**box** The simulation region. PBC is assumed

### Returns

**e** The energy  
**f** The force  
**v** The virial

`deepmd.infer.calc_model_devi(coord, box, atype, models, fname=None, frequency=1, nopbc=True)`

Python interface to calculate model deviation

### Parameters

**coord** [`numpy.ndarray`,  $n\_frames \times n\_atoms \times 3$ ] Coordinates of system to calculate  
**box** [`numpy.ndarray` or `None`,  $n\_frames \times 3 \times 3$ ] Box to specify periodic boundary condition. If `None`, no pbc will be used  
**atype** [`numpy.ndarray`,  $n\_atoms \times 1$ ] Atom types  
**models** [`list` of `DeepPot` models] Models used to evaluate deviation  
**fname** [`str` or `None`] File to dump results, default `None`  
**frequency** [`int`] Steps between frames (if the system is given by molecular dynamics engine), default 1  
**nopbc** [`bool`] Whether to use pbc conditions

### Returns

**model\_devi** [`numpy.ndarray`,  $n\_frames \times 7$ ] Model deviation results. The first column is index of steps, the other 6 columns are `max_devi_v`, `min_devi_v`, `avg_devi_v`, `max_devi_f`, `min_devi_f`, `avg_devi_f`.

## Examples

```
>>> from deepmd.infer import calc_model_devi
>>> from deepmd.infer import DeepPot as DP
>>> import numpy as np
>>> coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
>>> cell = np.diag(10 * np.ones(3)).reshape([1, -1])
>>> atype = [1,0,1]
>>> graphs = [DP("graph.000.pb"), DP("graph.001.pb")]
>>> model_devi = calc_model_devi(coord, cell, atype, graphs)
```

## Submodules

## deepmd.infer.data\_modifier module

```
class deepmd.infer.data_modifier.DipoleChargeModifier(model_name: str, model_charge_map:
                                                    List[float], sys_charge_map: List[float],
                                                    ewald_h: float = 1, ewald_beta: float = 1)
```

Bases: `deepmd.infer.deep_dipole.DeepDipole`

## Parameters

**model\_name** The model file for the DeepDipole model

**model\_charge\_map** Gives the amount of charge for the wfcc

**sys\_charge\_map** Gives the amount of charge for the real atoms

**ewald\_h** Grid spacing of the reciprocal part of Ewald sum. Unit: Å

**ewald\_beta** Splitting parameter of the Ewald sum. Unit: Å<sup>-1</sup>

## Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>build_fv_graph()</code>	Build the computational graph for the force and virial inference.
<code>eval(coord, box, atype[, eval_fv])</code>	Evaluate the modification
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_agraph()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>modify_data(data)</code>	Modify data.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**build\_fv\_graph()** → `tensorflow.python.framework.ops.Tensor`  
Build the computational graph for the force and virial inference.

**eval**(*coord*: `numpy.ndarray`, *box*: `numpy.ndarray`, *atype*: `numpy.ndarray`, *eval\_fv*: `bool = True`) →  
`Tuple[numpy.ndarray, numpy.ndarray, numpy.ndarray]`  
Evaluate the modification

## Parameters

**coord** The coordinates of atoms

**box** The simulation region. PBC is assumed

**atype** The atom types

**eval\_fv** Evaluate force and virial

#### Returns

**tot\_e** The energy modification

**tot\_f** The force modification

**tot\_v** The virial modification

**load\_prefix:** `str`

**modify\_data**(*data: dict*) → `None`

Modify data.

#### Parameters

**data** Internal data of DeepmdData. Be a dict, has the following keys - coord coordinates - box simulation box - type atom types - find\_energy tells if data has energy - find\_force tells if data has force - find\_virial tells if data has virial - energy energy - force force - virial virial

### deepmd.infer.deep\_dipole module

**class** deepmd.infer.deep\_dipole.**DeepDipole**(*model\_file: Path*, *load\_prefix: str = 'load'*, *default\_tf\_graph: bool = False*)

Bases: `deepmd.infer.deep_tensor.DeepTensor`

Constructor.

#### Parameters

**model\_file** [`Path`] The name of the frozen model file.

**load\_prefix: str** The prefix in the load computational graph

**default\_tf\_graph** [`bool`] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

#### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

`get_dim_aparam() → int`  
Unsupported in this model.

`get_dim_fparam() → int`  
Unsupported in this model.

`load_prefix: str`

## deepmd.infer.deep\_eval module

```
class deepmd.infer.deep_eval.DeepEval(model_file: Path, load_prefix: str = 'load', default_tf_graph: bool = False, auto_batch_size: Union[bool, int, deepmd.utils.batch_size.AutoBatchSize] = False)
```

Bases: `object`

Common methods for DeepPot, DeepWFC, DeepPolar, ...

### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix: str** The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**auto\_batch\_size** [bool or int or AutomaticBatchSize, default: False] If True, automatic batch size will be used. If int, it will be used as the initial batch size.

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

## Methods

<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**load\_prefix:** `str`

**make\_natoms\_vec**(*atom\_types*: `numpy.ndarray`) → `numpy.ndarray`

Make the natom vector used by deepmd-kit.

### Parameters

**atom\_types** The type of atoms

### Returns

**natoms** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

**property model\_type:** `str`

Get type of model.

:type:str

**property model\_version:** `str`

Get version of model.

### Returns

`str` version of model

**static reverse\_map**(*vec*: `numpy.ndarray`, *imap*: `List[int]`) → `numpy.ndarray`

Reverse mapping of a vector according to the index map

### Parameters

**vec** Input vector. Be of shape [nframes, natoms, -1]

**imap** Index map. Be of shape [natoms]

### Returns

**vec\_out** Reverse mapped vector.

**static sort\_input**(*coord*: `numpy.ndarray`, *atom\_type*: `numpy.ndarray`, *sel\_atoms*: `Optional[List[int]]` = `None`)

Sort atoms in the system according their types.

### Parameters

**coord** The coordinates of atoms. Should be of shape [nframes, natoms, 3]

**atom\_type** The type of atoms Should be of shape [natoms]

**sel\_atom** The selected atoms by type

### Returns

**coord\_out** The coordinates after sorting

**atom\_type\_out** The atom types after sorting

**idx\_map** The index mapping from the input to the output. For example `coord_out = coord[:,idx_map,:]`

**sel\_atom\_type** Only output if `sel_atoms` is not `None` The sorted selected atom types

**sel\_idx\_map** Only output if `sel_atoms` is not `None` The index mapping from the selected atoms to sorted selected atoms.

## deepmd.infer.deep\_polar module

```
class deepmd.infer.deep_polar.DeepGlobalPolar(model_file: str, load_prefix: str = 'load',
                                              default_tf_graph: bool = False)
```

Bases: `deepmd.infer.deep_tensor.DeepTensor`

Constructor.

### Parameters

**model\_file** [`str`] The name of the frozen model file.

**load\_prefix**: `str` The prefix in the load computational graph

**default\_tf\_graph** [`bool`] If uses the default tf graph, otherwise build a new tf graph for evaluation

### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

### Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**eval**(*coords*: `numpy.ndarray`, *cells*: `numpy.ndarray`, *atom\_types*: `List[int]`, *atomic*: `bool` = `False`, *fparam*: `Optional[numpy.ndarray]` = `None`, *aparam*: `Optional[numpy.ndarray]` = `None`, *efield*: `Optional[numpy.ndarray]` = `None`) → `numpy.ndarray`  
Evaluate the model.

### Parameters

**coords** The coordinates of atoms. The array should be of size `nframes x natoms x 3`

**cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size nframes x 9

**atom\_types** The atom types The list should contain natoms ints

**atomic** Not used in this model

**fparam** Not used in this model

**aparam** Not used in this model

**efield** Not used in this model

#### Returns

**tensor** The returned tensor If atomic == False then of size nframes x variable\_dof else of size nframes x natoms x variable\_dof

**get\_dim\_aparam()** → int  
Unsupported in this model.

**get\_dim\_fparam()** → int  
Unsupported in this model.

**load\_prefix:** str

**class** deepmd.infer.deep\_polar.**DeepPolar**(*model\_file*: Path, *load\_prefix*: str = 'load', *default\_tf\_graph*: bool = False)

Bases: [deepmd.infer.deep\\_tensor.DeepTensor](#)

Constructor.

#### Parameters

**model\_file** [Path] The name of the frozen model file.

**load\_prefix**: str The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

#### Attributes

**model\_type** Get type of model.

**model\_version** Get version of model.

#### Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.

continues on next page

Table 29 – continued from previous page

<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

`get_dim_aparam()` → `int`  
 Unsupported in this model.

`get_dim_fparam()` → `int`  
 Unsupported in this model.

`load_prefix:` `str`

### deepmd.infer.deep\_pot module

**class** `deepmd.infer.deep_pot.DeepPot`(*model\_file*: `Path`, *load\_prefix*: `str` = 'load', *default\_tf\_graph*: `bool` = `False`, *auto\_batch\_size*: `Union[bool, int, deepmd.utils.batch_size.AutoBatchSize]` = `True`)

Bases: `deepmd.infer.deep_eval.DeepEval`

Constructor.

#### Parameters

**model\_file** [`Path`] The name of the frozen model file.

**load\_prefix**: `str` The prefix in the load computational graph

**default\_tf\_graph** [`bool`] If uses the default tf graph, otherwise build a new tf graph for evaluation

**auto\_batch\_size** [`bool` or `int` or `AutomaticBatchSize`, default: `True`] If `True`, automatic batch size will be used. If `int`, it will be used as the initial batch size.

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

### Examples

```
>>> from deepmd.infer import DeepPot
>>> import numpy as np
>>> dp = DeepPot('graph.pb')
>>> coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
>>> cell = np.diag(10 * np.ones(3)).reshape([1, -1])
>>> atype = [1,0,1]
>>> e, f, v = dp.eval(coord, cell, atype)
```

where  $e$ ,  $f$  and  $v$  are predicted energy, force and virial of the system, respectively.

#### Attributes



**model\_type** Get type of model.  
**model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the energy, force and virial by using this DP.
<code>eval_descriptor(coords, cells, atom_types[, ...])</code>	Evaluate descriptors by using this DP.
<code>get_dim_aparam()</code>	Get the number (dimension) of atomic parameters of this DP.
<code>get_dim_fparam()</code>	Get the number (dimension) of frame parameters of this DP.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Unsupported in this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**eval**(*coords*: *numpy.ndarray*, *cells*: *numpy.ndarray*, *atom\_types*: *List[int]*, *atomic*: *bool* = *False*, *fparam*: *Optional[numpy.ndarray]* = *None*, *aparam*: *Optional[numpy.ndarray]* = *None*, *efield*: *Optional[numpy.ndarray]* = *None*) → *Tuple[numpy.ndarray, ...]*  
 Evaluate the energy, force and virial by using this DP.

## Parameters

**coords** The coordinates of atoms. The array should be of size *nframes* x *natoms* x 3  
**cells** The cell of the region. If *None* then non-PBC is assumed, otherwise using PBC. The array should be of size *nframes* x 9  
**atom\_types** The atom types The list should contain *natoms* ints  
**atomic** Calculate the atomic energy and virial  
**fparam** The frame parameter. The array can be of size : - *nframes* x *dim\_fparam*. - *dim\_fparam*. Then all frames are assumed to be provided with the same *fparam*.  
**aparam** The atomic parameter The array can be of size : - *nframes* x *natoms* x *dim\_aparam*. - *natoms* x *dim\_aparam*. Then all frames are assumed to be provided with the same *aparam*. - *dim\_aparam*. Then all frames and atoms are provided with the same *aparam*.  
**efield** The external field on atoms. The array should be of size *nframes* x *natoms* x 3

## Returns

**energy** The system energy.  
**force** The force on each atom  
**virial** The virial  
**atom\_energy** The atomic energy. Only returned when *atomic* == *True*  
**atom\_virial** The atomic virial. Only returned when *atomic* == *True*

**eval\_descriptor**(*coords: numpy.ndarray, cells: numpy.ndarray, atom\_types: List[int], fparam: Optional[numpy.ndarray] = None, aparam: Optional[numpy.ndarray] = None, efield: Optional[numpy.ndarray] = None*) → *numpy.array*

Evaluate descriptors by using this DP.

#### Parameters

- coords** The coordinates of atoms. The array should be of size *nframes* x *natoms* x 3
- cells** The cell of the region. If *None* then non-PBC is assumed, otherwise using PBC. The array should be of size *nframes* x 9
- atom\_types** The atom types The list should contain *natoms* ints
- fparam** The frame parameter. The array can be of size : - *nframes* x *dim\_fparam*. - *dim\_fparam*. Then all frames are assumed to be provided with the same *fparam*.
- aparam** The atomic parameter The array can be of size : - *nframes* x *natoms* x *dim\_aparam*. - *natoms* x *dim\_aparam*. Then all frames are assumed to be provided with the same *aparam*. - *dim\_aparam*. Then all frames and atoms are provided with the same *aparam*.
- efield** The external field on atoms. The array should be of size *nframes* x *natoms* x 3

#### Returns

**descriptor** Descriptors.

**get\_dim\_aparam**() → *int*

Get the number (dimension) of atomic parameters of this DP.

**get\_dim\_fparam**() → *int*

Get the number (dimension) of frame parameters of this DP.

**get\_ntypes**() → *int*

Get the number of atom types of this model.

**get\_rcut**() → *float*

Get the cut-off radius of this model.

**get\_sel\_type**() → *List[int]*

Unsupported in this model.

**get\_type\_map**() → *List[int]*

Get the type map (element name of the atom types) of this model.

**load\_prefix:** *str*

### deepmd.infer.deep\_tensor module

**class** *deepmd.infer.deep\_tensor.DeepTensor*(*model\_file: Path, load\_prefix: str = 'load', default\_tf\_graph: bool = False*)

Bases: *deepmd.infer.deep\_eval.DeepEval*

Evaluates a tensor model.

#### Parameters

- model\_file: str** The name of the frozen model file.
- load\_prefix: str** The prefix in the load computational graph
- default\_tf\_graph [bool]** If uses the default tf graph, otherwise build a new tf graph for evaluation

## Attributes

- model\_type** Get type of model.
- model\_version** Get version of model.

## Methods

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Get the number (dimension) of atomic parameters of this DP.
<code>get_dim_fparam()</code>	Get the number (dimension) of frame parameters of this DP.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**eval**(*coords*: *numpy.ndarray*, *cells*: *numpy.ndarray*, *atom\_types*: *List[int]*, *atomic*: *bool = True*, *fparam*: *Optional[numpy.ndarray] = None*, *aparam*: *Optional[numpy.ndarray] = None*, *efield*: *Optional[numpy.ndarray] = None*) → *numpy.ndarray*  
 Evaluate the model.

## Parameters

- coords** The coordinates of atoms. The array should be of size *nframes* x *natoms* x 3
- cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size *nframes* x 9
- atom\_types** The atom types The list should contain *natoms* ints
- atomic** If True (default), return the atomic tensor Otherwise return the global tensor
- fparam** Not used in this model
- aparam** Not used in this model
- efield** Not used in this model

## Returns

- tensor** The returned tensor If *atomic* == False then of size *nframes* x *output\_dim* else of size *nframes* x *natoms* x *output\_dim*

**eval\_full**(*coords*: *numpy.ndarray*, *cells*: *numpy.ndarray*, *atom\_types*: *List[int]*, *atomic*: *bool = False*, *fparam*: *Optional[numpy.array] = None*, *aparam*: *Optional[numpy.array] = None*, *efield*: *Optional[numpy.array] = None*) → *Tuple[numpy.ndarray, ...]*

Evaluate the model with interface similar to the energy model. Will return global tensor, component-wise force and virial and optionally atomic tensor and atomic virial.

## Parameters

**coords** The coordinates of atoms. The array should be of size nframes x natoms x 3

**cells** The cell of the region. If None then non-PBC is assumed, otherwise using PBC. The array should be of size nframes x 9

**atom\_types** The atom types The list should contain natoms ints

**atomic** Whether to calculate atomic tensor and virial

**fparam** Not used in this model

**aparam** Not used in this model

**efield** Not used in this model

#### Returns

**tensor** The global tensor. shape: [nframes x nout]

**force** The component-wise force (negative derivative) on each atom. shape: [nframes x nout x natoms x 3]

**virial** The component-wise virial of the tensor. shape: [nframes x nout x 9]

**atom\_tensor** The atomic tensor. Only returned when atomic == True shape: [nframes x natoms x nout]

**atom\_virial** The atomic virial. Only returned when atomic == True shape: [nframes x nout x natoms x 9]

**get\_dim\_aparam()** → int

Get the number (dimension) of atomic parameters of this DP.

**get\_dim\_fparam()** → int

Get the number (dimension) of frame parameters of this DP.

**get\_ntypes()** → int

Get the number of atom types of this model.

**get\_rcut()** → float

Get the cut-off radius of this model.

**get\_sel\_type()** → List[int]

Get the selected atom types of this model.

**get\_type\_map()** → List[int]

Get the type map (element name of the atom types) of this model.

**load\_prefix:** str

```
tensors = {'t_box': 't_box:0', 't_coord': 't_coord:0', 't_mesh': 't_mesh:0',
't_natoms': 't_natoms:0', 't_ntypes': 'descrpt_attr/ntypes:0', 't_output_dim':
'model_attr/output_dim:0', 't_rcut': 'descrpt_attr/rcut:0', 't_sel_type':
'model_attr/sel_type:0', 't_tmap': 'model_attr/tmap:0', 't_type': 't_type:0'}
```

**deepmd.infer.deep\_wfc module**

**class** deepmd.infer.deep\_wfc.**DeepWFC**(*model\_file*: Path, *load\_prefix*: str = 'load', *default\_tf\_graph*: bool = False)

Bases: [deepmd.infer.deep\\_tensor.DeepTensor](#)

Constructor.

**Parameters**

**model\_file** [Path] The name of the frozen model file.

**load\_prefix**: str The prefix in the load computational graph

**default\_tf\_graph** [bool] If uses the default tf graph, otherwise build a new tf graph for evaluation

**Warning:** For developers: *DeepTensor* initializer must be called at the end after *self.tensors* are modified because it uses the data in *self.tensors* dict. Do not change the order!

**Attributes**

**model\_type** Get type of model.

**model\_version** Get version of model.

**Methods**

<code>eval(coords, cells, atom_types[, atomic, ...])</code>	Evaluate the model.
<code>eval_full(coords, cells, atom_types[, ...])</code>	Evaluate the model with interface similar to the energy model.
<code>get_dim_aparam()</code>	Unsupported in this model.
<code>get_dim_fparam()</code>	Unsupported in this model.
<code>get_ntypes()</code>	Get the number of atom types of this model.
<code>get_rcut()</code>	Get the cut-off radius of this model.
<code>get_sel_type()</code>	Get the selected atom types of this model.
<code>get_type_map()</code>	Get the type map (element name of the atom types) of this model.
<code>make_natoms_vec(atom_types)</code>	Make the natom vector used by deepmd-kit.
<code>reverse_map(vec, imap)</code>	Reverse mapping of a vector according to the index map
<code>sort_input(coord, atom_type[, sel_atoms])</code>	Sort atoms in the system according their types.

**get\_dim\_aparam()** → int  
Unsupported in this model.

**get\_dim\_fparam()** → int  
Unsupported in this model.

**load\_prefix:** str

**deepmd.infer.ewald\_recip module**

**class** deepmd.infer.ewald\_recip.**EwaldRecp**(*hh, beta*)

Bases: `object`

Evaluate the reciprocal part of the Ewald sum

**Methods**


---

<code>eval</code> (coord, charge, box)	Evaluate
--	----------

---

**eval**(*coord: numpy.ndarray, charge: numpy.ndarray, box: numpy.ndarray*) → `Tuple[numpy.ndarray, numpy.ndarray, numpy.ndarray]`  
 Evaluate

**Parameters**

**coord** The coordinates of atoms  
**charge** The atomic charge  
**box** The simulation region. PBC is assumed

**Returns**

**e** The energy  
**f** The force  
**v** The virial

**deepmd.infer.model\_devi module**

deepmd.infer.model\_devi.**calc\_model\_devi**(*coord, box, atype, models, fname=None, frequency=1, nopbc=True*)

Python interface to calculate model deviation

**Parameters**

**coord** [`numpy.ndarray`, *n\_frames* × *n\_atoms* × 3] Coordinates of system to calculate  
**box** [`numpy.ndarray` or `None`, *n\_frames* × 3 × 3] Box to specify periodic boundary condition. If `None`, no pbc will be used  
**atype** [`numpy.ndarray`, *n\_atoms* × 1] Atom types  
**models** [`list` of DeepPot models] Models used to evaluate deviation  
**fname** [`str` or `None`] File to dump results, default `None`  
**frequency** [`int`] Steps between frames (if the system is given by molecular dynamics engine), default 1  
**nopbc** [`bool`] Whether to use pbc conditions

**Returns**

**model\_devi** [`numpy.ndarray`, *n\_frames* × 7] Model deviation results. The first column is index of steps, the other 6 columns are max\_devi\_v, min\_devi\_v, avg\_devi\_v, max\_devi\_f, min\_devi\_f, avg\_devi\_f.

## Examples

```
>>> from deepmd.infer import calc_model_devi
>>> from deepmd.infer import DeepPot as DP
>>> import numpy as np
>>> coord = np.array([[1,0,0], [0,0,1.5], [1,0,3]]).reshape([1, -1])
>>> cell = np.diag(10 * np.ones(3)).reshape([1, -1])
>>> atype = [1,0,1]
>>> graphs = [DP("graph.000.pb"), DP("graph.001.pb")]
>>> model_devi = calc_model_devi(coord, cell, atype, graphs)
```

deepmd.infer.model\_devi.**calc\_model\_devi\_e**(es: *numpy.ndarray*)

### Parameters

es [*numpy.ndarray*] size of  $n\_models \times n\_frames \times n\_atoms$

deepmd.infer.model\_devi.**calc\_model\_devi\_f**(fs: *numpy.ndarray*)

### Parameters

fs [*numpy.ndarray*] size of  $n\_models \times n\_frames \times n\_atoms \times 3$

deepmd.infer.model\_devi.**calc\_model\_devi\_v**(vs: *numpy.ndarray*)

### Parameters

vs [*numpy.ndarray*] size of  $n\_models \times n\_frames \times 9$

deepmd.infer.model\_devi.**make\_model\_devi**(\*, models: *list*, system: *str*, set\_prefix: *str*, output: *str*, frequency: *int*, \*\*kwargs)

Make model deviation calculation

### Parameters

**models: list** A list of paths of models to use for making model deviation

**system: str** The path of system to make model deviation calculation

**set\_prefix: str** The set prefix of the system

**output: str** The output file for model deviation results

**frequency: int** The number of steps that elapse between writing coordinates in a trajectory by a MD engine (such as Gromacs / LAMMPS). This parameter is used to determine the index in the output file.

deepmd.infer.model\_devi.**write\_model\_devi\_out**(devi: *numpy.ndarray*, fname: *str*)

### Parameters

devi [*numpy.ndarray*] the first column is the steps index

fname [*str*] the file name to dump

## deepmd.loggers package

Module taking care of logging duties.

`deepmd.loggers.set_log_handles`(*level*: *int*, *log\_path*: *Optional*[*Path*] = *None*, *mpi\_log*: *Optional*[*str*] = *None*)

Set desired level for package loggers and add file handlers.

### Parameters

**level**: *int* logging level

**log\_path**: *Optional*[*str*] path to log file, if *None* logs will be send only to console. If the parent directory does not exist it will be automatically created, by default *None*

**mpi\_log** [*Optional*[*str*], *optional*] mpi log type. Has three options. *master* will output logs to file and console only from rank==0. *collect* will write messages from all ranks to one file opened under rank==0 and to console. *workers* will open one log file for each worker designated by its rank, console behaviour is the same as for *collect*. If this argument is specified, package 'mpi4py' must be already installed. by default *None*

### Raises

**RuntimeError** If the argument *mpi\_log* is specified, package *mpi4py* is not installed.

### Notes

Logging levels:

	our notation	python logging	tensorflow cpp	OpenMP
debug	10	10	0	1/on/true/yes
info	20	20	1	0/off/false/no
warning	30	30	2	0/off/false/no
error	40	40	3	0/off/false/no

### References

<https://groups.google.com/g/mpi4py/c/SaNzc8bdj6U35869137/avoid-tensorflow-print-on-standard-error-suppress-openmp-debug-messages-when-running-tensorflow-on-cpu>

<https://stackoverflow.com/questions/35869137/avoid-tensorflow-print-on-standard-error>  
<https://stackoverflow.com/questions/56085015/suppress-openmp-debug-messages-when-running-tensorflow-on-cpu>

## Submodules

### deepmd.loggers.loggers module

Logger initialization for package.

`deepmd.loggers.loggers.set_log_handles`(*level*: *int*, *log\_path*: *Optional*[*Path*] = *None*, *mpi\_log*: *Optional*[*str*] = *None*)

Set desired level for package loggers and add file handlers.

### Parameters

**level**: *int* logging level



**log\_path:** `Optional[str]` path to log file, if None logs will be send only to console. If the parent directory does not exist it will be automatically created, by default None

**mpi\_log** [`Optional[str]`, `optional`] mpi log type. Has three options. *master* will output logs to file and console only from rank==0. *collect* will write messages from all ranks to one file opened under rank==0 and to console. *workers* will open one log file for each worker designated by its rank, console behaviour is the same as for *collect*. If this argument is specified, package 'mpi4py' must be already installed. by default None

#### Raises

**RuntimeError** If the argument *mpi\_log* is specified, package *mpi4py* is not installed.

#### Notes

Logging levels:

	our notation	python logging	tensorflow cpp	OpenMP
debug	10	10	0	1/on/true/yes
info	20	20	1	0/off/false/no
warning	30	30	2	0/off/false/no
error	40	40	3	0/off/false/no

#### References

<https://groups.google.com/g/mpi4py/c/SaNzc8bdj6U35869137/avoid-tensorflow-print-on-standard-error-suppress-openmp-debug-messages-when-running-tensorflow-on-cpu>

<https://stackoverflow.com/questions/35869137/avoid-tensorflow-print-on-standard-error>  
<https://stackoverflow.com/questions/56085015/suppress-openmp-debug-messages-when-running-tensorflow-on-cpu>

### deepmd.loss package

#### Submodules

#### deepmd.loss.ener module

**class** `deepmd.loss.ener.EnerDipoleLoss`(*starter\_learning\_rate*: *float*, *start\_pref\_e*: *float* = 0.1, *limit\_pref\_e*: *float* = 1.0, *start\_pref\_ed*: *float* = 1.0, *limit\_pref\_ed*: *float* = 1.0)

Bases: `object`

#### Methods

<b>build</b>	
<b>eval</b>	
<b>print_header</b>	
<b>print_on_training</b>	

**build**(*learning\_rate*, *natoms*, *model\_dict*, *label\_dict*, *suffix*)

**eval**(*sess*, *feed\_dict*, *natoms*)

**static print\_header**()

**print\_on\_training**(*tb\_writer, cur\_batch, sess, natoms, feed\_dict\_test, feed\_dict\_batch*)

**class** deepmd.loss.ener.**EnerStdLoss**(*starter\_learning\_rate: float, start\_pref\_e: float = 0.02, limit\_pref\_e: float = 1.0, start\_pref\_f: float = 1000, limit\_pref\_f: float = 1.0, start\_pref\_v: float = 0.0, limit\_pref\_v: float = 0.0, start\_pref\_ae: float = 0.0, limit\_pref\_ae: float = 0.0, start\_pref\_pf: float = 0.0, limit\_pref\_pf: float = 0.0, relative\_f: Optional[float] = None*)

Bases: `object`

Standard loss function for DP models

## Methods

<b>build</b>	
<b>eval</b>	
<b>print_header</b>	
<b>print_on_training</b>	

**build**(*learning\_rate, natoms, model\_dict, label\_dict, suffix*)

**eval**(*sess, feed\_dict, natoms*)

**print\_header**()

**print\_on\_training**(*tb\_writer, cur\_batch, sess, natoms, feed\_dict\_test, feed\_dict\_batch*)

## deepmd.loss.tensor module

**class** deepmd.loss.tensor.**TensorLoss**(*jdata, \*\*kwarg*)

Bases: `object`

Loss function for tensorial properties.

## Methods

<b>build</b>	
<b>eval</b>	
<b>print_header</b>	
<b>print_on_training</b>	

**build**(*learning\_rate, natoms, model\_dict, label\_dict, suffix*)

**eval**(*sess, feed\_dict, natoms*)

**print\_header**()

**print\_on\_training**(*tb\_writer, cur\_batch, sess, natoms, feed\_dict\_test, feed\_dict\_batch*)

## deepmd.model package

### Submodules

#### deepmd.model.ener module

```
class deepmd.model.ener.EnerModel(descript, fitting, typeebd=None, type_map: Optional[List[str]] = None,
                                   data_stat_nbatch: int = 10, data_stat_protect: float = 0.01, use_srtab:
                                   Optional[str] = None, smin_alpha: Optional[float] = None, sw_rmin:
                                   Optional[float] = None, sw_rmax: Optional[float] = None)
```

Bases: `object`

Energy model.

#### Parameters

**descript** Descriptor

**fitting** Fitting net

**type\_map** Mapping atom type to the name (str) of the type. For example `type_map[1]` gives the name of the type 1.

**data\_stat\_nbatch** Number of frames used for data statistic

**data\_stat\_protect** Protect parameter for atomic energy regression

**use\_srtab** The table for the short-range pairwise interaction added on top of DP. The table is a text data file with  $(N_t + 1) * N_t / 2 + 1$  columns. The first column is the distance between atoms. The second to the last columns are energies for pairs of certain types. For example we have two atom types, 0 and 1. The columns from 2nd to 4th are for 0-0, 0-1 and 1-1 correspondingly.

**smin\_alpha** The short-range tabulated interaction will be swithed according to the distance of the nearest neighbor. This distance is calculated by softmin. This parameter is the decaying parameter in the softmin. It is only required when `use_srtab` is provided.

**sw\_rmin** The lower boundary of the interpolation between short-range tabulated interaction and DP. It is only required when `use_srtab` is provided.

**sw\_rmin** The upper boundary of the interpolation between short-range tabulated interaction and DP. It is only required when `use_srtab` is provided.

#### Methods

<b>build</b>	
<b>data_stat</b>	
<b>get_ntypes</b>	
<b>get_rcut</b>	
<b>get_type_map</b>	

**build**(coord\_, atype\_, natoms, box, mesh, input\_dict, frz\_model=None, suffix="", reuse=None)

**data\_stat**(data)

**get\_ntypes**()

**get\_rcut**()

```
get_type_map()
model_type = 'ener'
```

### deepmd.model.model\_stat module

`deepmd.model.model_stat.make_stat_input(data, nbatches, merge_sys=True)`

pack data for statistics Parameters ——— data:

The data

**merge\_sys: bool (True)** Merge system data

**all\_stat:** A dictionary of list of list storing data for stat. if `merge_sys == False` data can be accessed by

`all_stat[key][sys_idx][batch_idx][frame_idx]`

**else `merge_sys == True` can be accessed by** `all_stat[key][batch_idx][frame_idx]`

`deepmd.model.model_stat.merge_sys_stat(all_stat)`

### deepmd.model.tensor module

**class** `deepmd.model.tensor.DipoleModel`(*descript*, *fitting*, *type\_map*: *Optional[List[str]] = None*,  
*data\_stat\_nbatch*: *int = 10*, *data\_stat\_protect*: *float = 0.01*)

Bases: `deepmd.model.tensor.TensorModel`

#### Methods

<b>build</b>	
<b>data_stat</b>	
<b>get_ntypes</b>	
<b>get_out_size</b>	
<b>get_rcut</b>	
<b>get_sel_type</b>	
<b>get_type_map</b>	

**class** `deepmd.model.tensor.GlobalPolarModel`(*descript*, *fitting*, *type\_map*: *Optional[List[str]] = None*,  
*data\_stat\_nbatch*: *int = 10*, *data\_stat\_protect*: *float = 0.01*)

Bases: `deepmd.model.tensor.TensorModel`

#### Methods

<b>build</b>	
<b>data_stat</b>	
<b>get_ntypes</b>	
<b>get_out_size</b>	
<b>get_rcut</b>	
<b>get_sel_type</b>	
<b>get_type_map</b>	

```
class deepmd.model.tensor.PolarModel(descrpt, fitting, type_map: Optional[List[str]] = None,
                                     data_stat_nbatch: int = 10, data_stat_protect: float = 0.01)
    Bases: deepmd.model.tensor.TensorModel
```

## Methods

<b>build</b>	
<b>data_stat</b>	
<b>get_ntypes</b>	
<b>get_out_size</b>	
<b>get_rcut</b>	
<b>get_sel_type</b>	
<b>get_type_map</b>	

```
class deepmd.model.tensor.TensorModel(tensor_name: str, descrpt, fitting, type_map: Optional[List[str]] =
None, data_stat_nbatch: int = 10, data_stat_protect: float = 0.01)
```

Bases: `object`

Tensor model.

### Parameters

**tensor\_name** Name of the tensor.

**descrpt** Descriptor

**fitting** Fitting net

**type\_map** Mapping atom type to the name (str) of the type. For example `type_map[1]` gives the name of the type 1.

**data\_stat\_nbatch** Number of frames used for data statistic

**data\_stat\_protect** Protect parameter for atomic energy regression

## Methods

<b>build</b>	
<b>data_stat</b>	
<b>get_ntypes</b>	
<b>get_out_size</b>	
<b>get_rcut</b>	
<b>get_sel_type</b>	
<b>get_type_map</b>	

**build**(coord\_, atype\_, natoms, box, mesh, input\_dict, frz\_model=None, suffix="", reuse=None)

**data\_stat**(data)

**get\_ntypes**()

**get\_out\_size**()

**get\_rcut**()

**get\_sel\_type**()

`get_type_map()`

```
class deepmd.model.tensor.WFCModel(descript, fitting, type_map: Optional[List[str]] = None,
                                   data_stat_nbatch: int = 10, data_stat_protect: float = 0.01)
```

Bases: `deepmd.model.tensor.TensorModel`

## Methods

<code>build</code>	
<code>data_stat</code>	
<code>get_ntypes</code>	
<code>get_out_size</code>	
<code>get_rcut</code>	
<code>get_sel_type</code>	
<code>get_type_map</code>	

## deepmd.op package

This module will house cust Tf OPs after CMake installation.

`deepmd.op.import_ops()`

Import all custom TF ops that are present in this submodule.

## deepmd.utils package

### Submodules

#### deepmd.utils.argcheck module

```
class deepmd.utils.argcheck.ArgsPlugin
```

Bases: `object`

## Methods

<code>get_all_argument()</code>	Get all arguments.
<code>register(name[, alias])</code>	Register a descriptor argument plugin.

`get_all_argument()` → `List[dargs.dargs.Argument]`

Get all arguments.

### Returns

`List[Argument]` all arguments

`register(name: str, alias: Optional[List[str]] = None)` → `Callable[[], List[dargs.dargs.Argument]]`

Register a descriptor argument plugin.

### Parameters

**name** `[str]` the name of a descriptor

**alias** `[List[str], optional]` the list of aliases of this descriptor

**Returns**

`Callable[[], List[Argument]]` the registered descriptor argument method

**Examples**

```
>>> some_plugin = ArgsPlugin()
>>> @some_plugin.register("some_descrpt")
    def descrpt_some_descrpt_args():
        return []
```

```
deepmd.utils.argcheck.descrpt_hybrid_args()
deepmd.utils.argcheck.descrpt_local_frame_args()
deepmd.utils.argcheck.descrpt_se_a_args()
deepmd.utils.argcheck.descrpt_se_a_tpe_args()
deepmd.utils.argcheck.descrpt_se_r_args()
deepmd.utils.argcheck.descrpt_se_t_args()
deepmd.utils.argcheck.descrpt_variant_type_args()
deepmd.utils.argcheck.fitting_dipole()
deepmd.utils.argcheck.fitting_ener()
deepmd.utils.argcheck.fitting_polar()
deepmd.utils.argcheck.fitting_variant_type_args()
deepmd.utils.argcheck.gen_doc(*, make_anchor=True, make_link=True, **kwargs)
deepmd.utils.argcheck.gen_json(**kwargs)
deepmd.utils.argcheck.learning_rate_args()
deepmd.utils.argcheck.learning_rate_exp()
deepmd.utils.argcheck.learning_rate_variant_type_args()
deepmd.utils.argcheck.limit_pref(item)
deepmd.utils.argcheck.list_to_doc(xx)
deepmd.utils.argcheck.loss_args()
deepmd.utils.argcheck.loss_ener()
deepmd.utils.argcheck.loss_tensor()
deepmd.utils.argcheck.loss_variant_type_args()
deepmd.utils.argcheck.make_index(keys)
deepmd.utils.argcheck.make_link(content, ref_key)
deepmd.utils.argcheck.mixed_precision_args()
deepmd.utils.argcheck.model_args()
deepmd.utils.argcheck.model_compression()
deepmd.utils.argcheck.model_compression_type_args()
```

```

deepmd.utils.argcheck.modifier_dipole_charge()
deepmd.utils.argcheck.modifier_variant_type_args()
deepmd.utils.argcheck.normalize(data)
deepmd.utils.argcheck.normalize_hybrid_list(hy_list)
deepmd.utils.argcheck.start_pref(item)
deepmd.utils.argcheck.training_args()
deepmd.utils.argcheck.training_data_args()
deepmd.utils.argcheck.type_embedding_args()
deepmd.utils.argcheck.validation_data_args()

```

### deepmd.utils.batch\_size module

```

class deepmd.utils.batch_size.AutoBatchSize(initial_batch_size: int = 1024, factor: float = 2.0)
    Bases: object

```

This class allows DeePMD-kit to automatically decide the maximum batch size that will not cause an OOM error.

#### Parameters

**initial\_batch\_size** [`int`, default: 1024] initial batch size (number of total atoms)

**factor** [`float`, default: 2.] increased factor

#### Notes

We assume all OOM error will raise `metd: `OutOfMemoryError``.

#### Attributes

**current\_batch\_size** [`int`] current batch size (number of total atoms)

**maximum\_working\_batch\_size** [`int`] maximum working batch size

**minimal\_not\_working\_batch\_size** [`int`] minimal not working batch size

#### Methods

<code>execute</code> (callable, start_index, natoms)	Excuate a method with given batch size.
<code>execute_all</code> (callable, total_size, natoms, ...)	Excuate a method with all given data.

**execute**(callable: *Callable*, start\_index: *int*, natoms: *int*) → *Tuple*[*int*, *tuple*]  
 Excuate a method with given batch size.

#### Parameters

**callable** [`Callable`] The method should accept the batch size and start\_index as parameters, and returns executed batch size and data.

**start\_index** [`int`] start index

**natoms** [`int`] natoms

#### Returns



**int** executed batch size \* number of atoms

**tuple** result from callable, None if failing to execute

#### Raises

**OutOfMemoryError** OOM when batch size is 1

**execute\_all**(callable: *Callable*, total\_size: *int*, natoms: *int*, \*args, \*\*kwargs) → *Tuple[numpy.ndarray]*

Execute a method with all given data.

#### Parameters

**callable** [*Callable*] The method should accept \*args and \*\*kwargs as input and return the similar array.

**total\_size** [*int*] Total size

**natoms** [*int*] The number of atoms

**\*\*kwargs** If 2D np.ndarray, assume the first axis is batch; otherwise do nothing.

### deepmd.utils.compat module

Module providing compatibility between 0.x.x and 1.x.x input versions.

deepmd.utils.compat.**convert\_input\_v0\_v1**(jdata: *Dict[str, Any]*, warning: *bool* = *True*, dump: *Optional[Union[str, pathlib.Path]]* = *None*) → *Dict[str, Any]*

Convert input from v0 format to v1.

#### Parameters

**jdata** [*Dict[str, Any]*] loaded json/yaml file

**warning** [*bool*, optional] whether to show deprecation warning, by default *True*

**dump** [*Optional[Union[str, Path]]*, optional] whether to dump converted file, by default *None*

#### Returns

*Dict[str, Any]* converted output

deepmd.utils.compat.**convert\_input\_v1\_v2**(jdata: *Dict[str, Any]*, warning: *bool* = *True*, dump: *Optional[Union[str, pathlib.Path]]* = *None*) → *Dict[str, Any]*

deepmd.utils.compat.**deprecate\_numb\_test**(jdata: *Dict[str, Any]*, warning: *bool* = *True*, dump: *Optional[Union[str, pathlib.Path]]* = *None*) → *Dict[str, Any]*

Deprecate *numb\_test* since v2.1. It has taken no effect since v2.0.

See #1243.

#### Parameters

**jdata** [*Dict[str, Any]*] loaded json/yaml file

**warning** [*bool*, optional] whether to show deprecation warning, by default *True*

**dump** [*Optional[Union[str, Path]]*, optional] whether to dump converted file, by default *None*

#### Returns

*Dict[str, Any]* converted output

`deepmd.utils.compat.remove_decay_rate(jdata: Dict[str, Any])`  
 convert decay\_rate to stop\_lr.

#### Parameters

**jdata: Dict[str, Any]** input data

`deepmd.utils.compat.update_deepmd_input(jdata: Dict[str, Any], warning: bool = True, dump: Optional[Union[str, pathlib.Path]] = None) → Dict[str, Any]`

### deepmd.utils.convert module

`deepmd.utils.convert.convert_12_to_21(input_model: str, output_model: str)`

`deepmd.utils.convert.convert_13_to_21(input_model: str, output_model: str)`

`deepmd.utils.convert.convert_20_to_21(input_model: str, output_model: str)`

`deepmd.utils.convert.convert_dp12_to_dp13(file)`

`deepmd.utils.convert.convert_dp13_to_dp20(fname: str)`

`deepmd.utils.convert.convert_dp20_to_dp21(fname: str)`

`deepmd.utils.convert.convert_pb_to_pbtxt(pbfile: str, pbtxtfile: str)`

`deepmd.utils.convert.convert_pbtxt_to_pb(pbtxtfile: str, pbfile: str)`

### deepmd.utils.data module

**class** `deepmd.utils.data.DataSets(sys_path, set_prefix, seed=None, shuffle_test=True)`

Bases: `object`

Outdated class for one data system.

Deprecated since version 2.0.0: This class is not maintained any more.

#### Methods

<code>get_batch(batch_size)</code>	returned property prefector [4] in order: energy, force, virial, atom_ener
<code>get_test()</code>	returned property prefector [4] in order: energy, force, virial, atom_ener
<code>load_energy(set_name, nframes, nvalues, ...)</code>	return : coeff_ener, ener, coeff_atom_ener, atom_ener

<b>check_batch_size</b>	
<b>check_test_size</b>	
<b>get_ener</b>	
<b>get_natoms</b>	
<b>get_natoms_2</b>	
<b>get_natoms_vec</b>	
<b>get_numb_set</b>	
<b>get_set</b>	
<b>get_sys_numb_batch</b>	
<b>get_type_map</b>	
<b>load_batch_set</b>	
<b>load_data</b>	
<b>load_set</b>	
<b>load_test_set</b>	
<b>load_type</b>	
<b>load_type_map</b>	
<b>numb_aparam</b>	
<b>numb_fparam</b>	
<b>reset_iter</b>	
<b>set_numb_batch</b>	
<b>stats_energy</b>	

**check\_batch\_size**(*batch\_size*)

**check\_test\_size**(*test\_size*)

**get\_batch**(*batch\_size*)

returned property prefector [4] in order: energy, force, virial, atom\_ener

**get\_ener**()

**get\_natoms**()

**get\_natoms\_2**(*ntypes*)

**get\_natoms\_vec**(*ntypes*)

**get\_numb\_set**()

**get\_set**(*data, idx=None*)

**get\_sys\_numb\_batch**(*batch\_size*)

**get\_test**()

returned property prefector [4] in order: energy, force, virial, atom\_ener

**get\_type\_map**()

**load\_batch\_set**(*set\_name*)

**load\_data**(*set\_name, data\_name, shape, is\_necessary=True*)

**load\_energy**(*set\_name, nframes, nvalues, energy\_file, atom\_energy\_file*)

return : coeff\_ener, ener, coeff\_atom\_ener, atom\_ener

**load\_set**(*set\_name, shuffle=True*)

**load\_test\_set**(*set\_name, shuffle\_test*)

**load\_type**(*sys\_path*)

```

load_type_map(sys_path)
numb_aparam()
numb_fparam()
reset_iter()
set_numb_batch(batch_size)
stats_energy()
class deepmd.utils.data.DeepmdData(sys_path: str, set_prefix: str = 'set', shuffle_test: bool = True,
                                   type_map: Optional[List[str]] = None, modifier=None, trn_all_set:
                                   bool = False)

```

Bases: `object`

Class for a data system.

It loads data from hard disk, and maintains the data as a *data\_dict*

### Parameters

**sys\_path** Path to the data system

**set\_prefix** Prefix for the directories of different sets

**shuffle\_test** If the test data are shuffled

**type\_map** Gives the name of different atom types

**modifier** Data modifier that has the method *modify\_data*

**trn\_all\_set** Use all sets as training dataset. Otherwise, if the number of sets is more than 1, the last set is left for test.

### Methods

<code>add(key, ndof[, atomic, must, high_prec, ...])</code>	Add a data item that to be loaded
<code>avg(key)</code>	Return the average value of an item.
<code>check_batch_size(batch_size)</code>	Check if the system can get a batch of data with <i>batch_size</i> frames.
<code>check_test_size(test_size)</code>	Check if the system can get a test dataset with <i>test_size</i> frames.
<code>get_atom_type()</code>	Get atom types
<code>get_batch(batch_size)</code>	Get a batch of data with <i>batch_size</i> frames.
<code>get_data_dict()</code>	Get the <i>data_dict</i>
<code>get_natoms()</code>	Get number of atoms
<code>get_natoms_vec(ntypes)</code>	Get number of atoms and number of atoms in different types
<code>get_ntypes()</code>	Number of atom types in the system
<code>get_numb_batch(batch_size, set_idx)</code>	Get the number of batches in a set.
<code>get_numb_set()</code>	Get number of training sets
<code>get_sys_numb_batch(batch_size)</code>	Get the number of batches in the data system.
<code>get_test([ntests])</code>	Get the test data with <i>ntests</i> frames.
<code>get_type_map()</code>	Get the type map
<code>reduce(key_out, key_in)</code>	Generate a new item from the reduction of another atom

reset_get_batch	
-----------------	--

**add**(*key: str, ndof: int, atomic: bool = False, must: bool = False, high\_prec: bool = False, type\_sel: Optional[List[int]] = None, repeat: int = 1*)  
 Add a data item that to be loaded

**Parameters**

- key** The key of the item. The corresponding data is stored in *sys\_path/set.\*/key.npy*
- ndof** The number of dof
- atomic** The item is an atomic property. If False, the size of the data should be nframes x ndof If True, the size of data should be nframes x natoms x ndof
- must** The data file *sys\_path/set.\*/key.npy* must exist. If must is False and the data file does not exist, the *data\_dict[find\_key]* is set to 0.0
- high\_prec** Load the data and store in float64, otherwise in float32
- type\_sel** Select certain type of atoms
- repeat** The data will be repeated *repeat* times.

**avg**(*key*)

Return the average value of an item.

**check\_batch\_size**(*batch\_size*)

Check if the system can get a batch of data with *batch\_size* frames.

**check\_test\_size**(*test\_size*)

Check if the system can get a test dataset with *test\_size* frames.

**get\_atom\_type**() → List[int]

Get atom types

**get\_batch**(*batch\_size: int*) → dict

Get a batch of data with *batch\_size* frames. The frames are randomly picked from the data system.

**Parameters**

- batch\_size** size of the batch

**get\_data\_dict**() → dict

Get the *data\_dict*

**get\_natoms**()

Get number of atoms

**get\_natoms\_vec**(*ntypes: int*)

Get number of atoms and number of atoms in different types

**Parameters**

- ntypes** Number of types (may be larger than the actual number of types in the system).

**Returns**

- natoms** natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]: 2 ≤ i < Ntypes+2, number of type i atoms

**get\_ntypes**() → int

Number of atom types in the system

**get\_numb\_batch**(*batch\_size: int, set\_idx: int*) → *int*

Get the number of batches in a set.

**get\_numb\_set**() → *int*

Get number of training sets

**get\_sys\_numb\_batch**(*batch\_size: int*) → *int*

Get the number of batches in the data system.

**get\_test**(*ntests: int = -1*) → *dict*

Get the test data with *ntests* frames.

#### Parameters

**ntests** Size of the test data set. If *ntests* is -1, all test data will be get.

**get\_type\_map**() → *List[str]*

Get the type map

**reduce**(*key\_out: str, key\_in: str*)

Generate a new item from the reduction of another atom

#### Parameters

**key\_out** The name of the reduced item

**key\_in** The name of the data item to be reduced

**reset\_get\_batch**()

### deepmd.utils.data\_system module

**class** deepmd.utils.data\_system.**DataSystem**(*systems, set\_prefix, batch\_size, test\_size, rcut, run\_opt=None*)

Bases: *object*

Outdated class for the data systems.

Deprecated since version 2.0.0: This class is not maintained any more.

#### Methods

<b>check_type_map_consistency</b>	
<b>compute_energy_shift</b>	
<b>format_name_length</b>	
<b>get_batch</b>	
<b>get_batch_size</b>	
<b>get_nbatches</b>	
<b>get_nsystems</b>	
<b>get_ntypes</b>	
<b>get_sys</b>	
<b>get_test</b>	
<b>get_type_map</b>	
<b>numb_fparam</b>	
<b>print_summary</b>	
<b>process_sys_weights</b>	

**check\_type\_map\_consistency**(*type\_map\_list*)

```

compute_energy_shift()
format_name_length(name, width)
get_batch(sys_idx=None, sys_weights=None, style='prob_sys_size')
get_batch_size()
get_nbatches()
get_nsystems()
get_ntypes()
get_sys(sys_idx)
get_test(sys_idx=None)
get_type_map()
numb_fparam()
print_summary()
process_sys_weights(sys_weights)

```

```

class deepmd.utils.data_system.DeepmdDataSystem(systems: List[str], batch_size: int, test_size: int, rcut:
float, set_prefix: str = 'set', shuffle_test: bool = True,
type_map: Optional[List[str]] = None,
modifier=None, trn_all_set=False, sys_probs=None,
auto_prob_style='prob_sys_size')

```

Bases: `object`

Class for manipulating many data systems.

It is implemented with the help of DeepmdData

## Methods

<code>add(key, ndof[, atomic, must, high_prec, ...])</code>	Add a data item that to be loaded
<code>add_dict(adict)</code>	Add items to the data system by a <i>dict</i> . <i>adict</i> should have items like <code>adict[key] = { 'ndof': ndof, 'atomic': atomic, 'must': must, 'high_prec': high_prec, 'type_sel': type_sel, 'repeat': repeat, }</code> For the explanation of the keys see <i>add</i> .
<code>get_batch([sys_idx])</code>	Get a batch of data from the data systems
<code>get_batch_size()</code>	Get the batch size
<code>get_nbatches()</code>	Get the total number of batches
<code>get_nsystems()</code>	Get the number of data systems
<code>get_ntypes()</code>	Get the number of types
<code>get_sys(idx)</code>	Get a certain data system
<code>get_sys_nctest([sys_idx])</code>	Get number of tests for the currently selected system,
<code>get_test([sys_idx, n_test])</code>	Get test data from the the data systems.
<code>get_type_map()</code>	Get the type map
<code>reduce(key_out, key_in)</code>	Generate a new item from the reduction of another atom

<b>compute_energy_shift</b>	
<b>get_data_dict</b>	
<b>print_summary</b>	
<b>set_sys_probs</b>	

**add**(*key: str, ndof: int, atomic: bool = False, must: bool = False, high\_prec: bool = False, type\_sel: Optional[List[int]] = None, repeat: int = 1*)  
Add a data item that to be loaded

#### Parameters

- key** The key of the item. The corresponding data is stored in *sys\_path/set.\*/key.npy*
- ndof** The number of dof
- atomic** The item is an atomic property. If False, the size of the data should be nframes x ndof If True, the size of data should be nframes x natoms x ndof
- must** The data file *sys\_path/set.\*/key.npy* must exist. If must is False and the data file does not exist, the *data\_dict[find\_key]* is set to 0.0
- high\_prec** Load the data and store in float64, otherwise in float32
- type\_sel** Select certain type of atoms
- repeat** The data will be repeated *repeat* times.

**add\_dict**(*adict: dict*) → None

Add items to the data system by a *dict*. *adict* should have items like *adict[key] = {*

*‘ndof’: ndof, ‘atomic’: atomic, ‘must’: must, ‘high\_prec’: high\_prec, ‘type\_sel’: type\_sel, ‘repeat’: repeat,*

*}* For the explanation of the keys see *add*

**compute\_energy\_shift**(*rcond=0.001, key='energy'*)

**get\_batch**(*sys\_idx: Optional[int] = None*)

Get a batch of data from the data systems

#### Parameters

- sys\_idx: int** The index of system from which the batch is get. If *sys\_idx* is not None, *sys\_probs* and *auto\_prob\_style* are ignored If *sys\_idx* is None, automatically determine the system according to *sys\_probs* or *auto\_prob\_style*, see the following.

**get\_batch\_size**() → int

Get the batch size

**get\_data\_dict**(*ii: int = 0*) → dict

**get\_nbatchs**() → int

Get the total number of batches

**get\_nsystems**() → int

Get the number of data systems

**get\_ntypes**() → int

Get the number of types

**get\_sys**(*idx: int*) → *deepmd.utils.data.DeepmdData*

Get a certain data system

**get\_sys\_nctest**(*sys\_idx=None*)



**Get number of tests for the currently selected system,** or one defined by `sys_idx`.

**get\_test**(`sys_idx`: *Optional*[`int`] = `None`, `n_test`: `int` = -1)

Get test data from the the data systems.

#### Parameters

**sys\_idx** The test dat of system with index `sys_idx` will be returned. If is `None`, the currently selected system will be returned.

**n\_test** Number of test data. If set to -1 all test data will be get.

**get\_type\_map**() → `List`[`str`]

Get the type map

**print\_summary**(`name`)

**reduce**(`key_out`, `key_in`)

Generate a new item from the reduction of another atom

#### Parameters

**key\_out** The name of the reduced item

**key\_in** The name of the data item to be reduced

**set\_sys\_probs**(`sys_probs`=`None`, `auto_prob_style`: `str` = 'prob\_sys\_size')

## deepmd.utils.errors module

**exception** `deepmd.utils.errors.GraphTooLargeError`

Bases: `Exception`

The graph is too large, exceeding protobuf's hard limit of 2GB.

**exception** `deepmd.utils.errors.GraphWithoutTensorError`

Bases: `Exception`

**exception** `deepmd.utils.errors.OutOfMemoryError`

Bases: `Exception`

This error is caused by out-of-memory (OOM).

## deepmd.utils.graph module

`deepmd.utils.graph.get_embedding_net_nodes`(`model_file`: `str`, `suffix`: `str` = "") → `Dict`

Get the embedding net nodes with the given frozen model(`model_file`)

#### Parameters

**model\_file** The input frozen model path

**suffix** [`str`, optional] The suffix of the scope

#### Returns

`Dict` The embedding net nodes with the given frozen model

`deepmd.utils.graph.get_embedding_net_nodes_from_graph_def`(`graph_def`: `tensorflow.core.framework.graph_pb2.GraphDef`, `suffix`: `str` = "") → `Dict`

Get the embedding net nodes with the given `tf.GraphDef` object

**Parameters**

**graph\_def** The input `tf.GraphDef` object  
**suffix** [`str`, optional] The scope suffix

**Returns**

**Dict** The embedding net nodes within the given `tf.GraphDef` object

`deepmd.utils.graph.get_embedding_net_variables(model_file: str, suffix: str = "") → Dict`  
Get the embedding net variables with the given frozen model(`model_file`)

**Parameters**

**model\_file** The input frozen model path  
**suffix** [`str`, optional] The suffix of the scope

**Returns**

**Dict** The embedding net variables within the given frozen model

`deepmd.utils.graph.get_embedding_net_variables_from_graph_def(graph_def: tensorflow.core.framework.graph_pb2.GraphDef, suffix: str = "") → Dict`  
Get the embedding net variables with the given `tf.GraphDef` object

**Parameters**

**graph\_def** The input `tf.GraphDef` object  
**suffix** [`str`, optional] The suffix of the scope

**Returns**

**Dict** The embedding net variables within the given `tf.GraphDef` object

`deepmd.utils.graph.get_fitting_net_nodes(model_file: str) → Dict`  
Get the fitting net nodes with the given frozen model(`model_file`)

**Parameters**

**model\_file** The input frozen model path

**Returns**

**Dict** The fitting net nodes with the given frozen model

`deepmd.utils.graph.get_fitting_net_nodes_from_graph_def(graph_def: tensorflow.core.framework.graph_pb2.GraphDef) → Dict`  
Get the fitting net nodes with the given `tf.GraphDef` object

**Parameters**

**graph\_def** The input `tf.GraphDef` object

**Returns**

**Dict** The fitting net nodes within the given `tf.GraphDef` object

`deepmd.utils.graph.get_fitting_net_variables(model_file: str) → Dict`  
Get the fitting net variables with the given frozen model(`model_file`)

**Parameters**

**model\_file** The input frozen model path

**Returns**

**Dict** The fitting net variables within the given frozen model

`deepmd.utils.graph.get_fitting_net_variables_from_graph_def`(*graph\_def: tensorflow.core.framework.graph\_pb2.GraphDef*)  
→ **Dict**

Get the fitting net variables with the given tf.GraphDef object

**Parameters**

**graph\_def** The input tf.GraphDef object

**Returns**

**Dict** The fitting net variables within the given tf.GraphDef object

`deepmd.utils.graph.get_pattern_nodes_from_graph_def`(*graph\_def: tensorflow.core.framework.graph\_pb2.GraphDef*,  
*pattern: str*) → **Dict**

Get the pattern nodes with the given tf.GraphDef object

**Parameters**

**graph\_def** The input tf.GraphDef object

**pattern** The node pattern within the graph\_def

**Returns**

**Dict** The fitting net nodes within the given tf.GraphDef object

`deepmd.utils.graph.get_tensor_by_name`(*model\_file: str*, *tensor\_name: str*) →  
tensorflow.python.framework.ops.Tensor

Load tensor value from the frozen model(model\_file)

**Parameters**

**model\_file** [**str**] The input frozen model path

**tensor\_name** [**str**] Indicates which tensor which will be loaded from the frozen model

**Returns**

**tf.Tensor** The tensor which was loaded from the frozen model

**Raises**

**GraphWithoutTensorError** Whether the tensor\_name is within the frozen model

`deepmd.utils.graph.get_tensor_by_name_from_graph`(*graph: tensorflow.python.framework.ops.Graph*,  
*tensor\_name: str*) →  
tensorflow.python.framework.ops.Tensor

Load tensor value from the given tf.Graph object

**Parameters**

**graph** [**tf.Graph**] The input TensorFlow graph

**tensor\_name** [**str**] Indicates which tensor which will be loaded from the frozen model

**Returns**

**tf.Tensor** The tensor which was loaded from the frozen model

**Raises**

**GraphWithoutTensorError** Whether the tensor\_name is within the frozen model

`deepmd.utils.graph.get_tensor_by_type`(*node*, *data\_type*: *numpy.dtype*) → `tensorflow.python.framework.ops.Tensor`

Get the tensor value within the given node according to the input *data\_type*

**Parameters**

**node** The given tensorflow graph node

**data\_type** The data type of the node

**Returns**

**tf.Tensor** The tensor value of the given node

`deepmd.utils.graph.load_graph_def`(*model\_file*: *str*) → `Tuple`[`tensorflow.python.framework.ops.Graph`, `tensorflow.core.framework.graph_pb2.GraphDef`]

Load graph as well as the graph\_def from the frozen model(*model\_file*)

**Parameters**

**model\_file** [*str*] The input frozen model path

**Returns**

**tf.Graph** The graph loaded from the frozen model

**tf.GraphDef** The graph\_def loaded from the frozen model

## deepmd.utils.learning\_rate module

**class** `deepmd.utils.learning_rate.LearningRateExp`(*start\_lr*: *float*, *stop\_lr*: *float* = *5e-08*, *decay\_steps*: *int* = *5000*, *decay\_rate*: *float* = *0.95*)

Bases: `object`

The exponentially decaying learning rate.

The learning rate at step *t* is given by

$$\alpha(t) = \alpha_0 \lambda^{t/\tau}$$

where  $\alpha$  is the learning rate,  $\alpha_0$  is the starting learning rate,  $\lambda$  is the decay rate, and  $\tau$  is the decay steps.

**Parameters**

**start\_lr** Starting learning rate  $\alpha_0$

**stop\_lr** Stop learning rate  $\alpha_1$

**decay\_steps** Learning rate decay every this number of steps  $\tau$

**decay\_rate** The decay rate  $\lambda$ . If *stop\_step* is provided in *build*, then it will be determined automatically and overwritten.

## Methods

<code>build(global_step[, stop_step])</code>	Build the learning rate
<code>start_lr()</code>	Get the start lr
<code>value(step)</code>	Get the lr at a certain step

**build**(*global\_step*: `tensorflow.python.framework.ops.Tensor`, *stop\_step*: `Optional[int] = None`) → `tensorflow.python.framework.ops.Tensor`  
Build the learning rate

### Parameters

**global\_step** The tf Tensor providing the global training step

**stop\_step** The stop step. If provided, the decay\_rate will be determined automatically and overwritten.

### Returns

**learning\_rate** The learning rate

**start\_lr**() → `float`

Get the start lr

**value**(*step*: `int`) → `float`

Get the lr at a certain step

## deepmd.utils.neighbor\_stat module

**class** `deepmd.utils.neighbor_stat.NeighborStat`(*ntypes*: `int`, *rcut*: `float`)

Bases: `object`

Class for getting training data information.

It loads data from `DeepmdData` object, and measures the data info, including nearest nbor distance between atoms, max nbor size of atoms and the output data range of the environment matrix.

### Parameters

**ntypes** The num of atom types

**rcut** The cut-off radius

## Methods

<code>get_stat(data)</code>	get the data statistics of the training data, including nearest nbor distance between atoms, max nbor size of atoms
-----------------------------	---

**get\_stat**(*data*: `deepmd.utils.data_system.DeepmdDataSystem`) → `Tuple[float, List[int]]`

get the data statistics of the training data, including nearest nbor distance between atoms, max nbor size of atoms

### Parameters

**data** Class for manipulating many data systems. It is implemented with the help of `DeepmdData`.

**Returns****min\_nbor\_dist** The nearest distance between neighbor atoms**max\_nbor\_size** A list with ntypes integers, denotes the actual achieved max sel**deepmd.utils.network module**

deepmd.utils.network.**embedding\_net**(*xx, network\_size, precision, activation\_fn=<function tanh>, resnet\_dt=False, name\_suffix="", stddev=1.0, bavg=0.0, seed=None, trainable=True, uniform\_seed=False, initial\_variables=None, mixed\_prec=None*)

The embedding network.

The embedding network function  $\mathcal{N}$  is constructed by is the composition of multiple layers  $\mathcal{L}^{(i)}$ :

$$\mathcal{N} = \mathcal{L}^{(n)} \circ \mathcal{L}^{(n-1)} \circ \dots \circ \mathcal{L}^{(1)}$$

A layer  $\mathcal{L}$  is given by one of the following forms, depending on the number of nodes: [1]

$$\mathbf{y} = \mathcal{L}(\mathbf{x}; \mathbf{w}, \mathbf{b}) = \begin{cases} \phi(\mathbf{x}^T \mathbf{w} + \mathbf{b}) + \mathbf{x}, & N_2 = N_1 \\ \phi(\mathbf{x}^T \mathbf{w} + \mathbf{b}) + (\mathbf{x}, \mathbf{x}), & N_2 = 2N_1 \\ \phi(\mathbf{x}^T \mathbf{w} + \mathbf{b}), & \text{otherwise} \end{cases}$$

where  $\mathbf{x} \in \mathbb{R}^{N_1}$  is the input vector and  $\mathbf{y} \in \mathbb{R}^{N_2}$  is the output vector.  $\mathbf{w} \in \mathbb{R}^{N_1 \times N_2}$  and  $\mathbf{b} \in \mathbb{R}^{N_2}$  are weights and biases, respectively, both of which are trainable if *trainable* is *True*.  $\phi$  is the activation function.

**Parameters****xx** [Tensor] Input tensor  $\mathbf{x}$  of shape [-1,1]**network\_size**: list of int Size of the embedding network. For example [16,32,64]**precision**: Precision of network weights. For example, tf.float64**activation\_fn**: Activation function  $\phi$ **resnet\_dt**: boolean Using time-step in the ResNet construction**name\_suffix**: str The name suffix append to each variable.**stddev**: float Standard deviation of initializing network parameters**bavg**: float Mean of network initial bias**seed**: int Random seed for initializing network parameters**trainable**: boolean If the network is trainable**uniform\_seed** [bool] Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed**initial\_variables** [dict] The input dict which stores the embedding net variables**mixed\_prec** The input dict which stores the mixed precision setting for the embedding net

## References

[1]

```
deepmd.utils.network.embedding_net_rand_seed_shift(network_size)

deepmd.utils.network.one_layer(inputs, outputs_size, activation_fn=<function tanh>, precision=tf.float64,
                               stddev=1.0, bavg=0.0, name='linear', reuse=None, seed=None,
                               use_timestep=False, trainable=True, useBN=False, uniform_seed=False,
                               initial_variables=None, mixed_prec=None, final_layer=False)

deepmd.utils.network.one_layer_rand_seed_shift()

deepmd.utils.network.variable_summaries(var: tensorflow.python.ops.variables.VariableV1, name: str)
    Attach a lot of summaries to a Tensor (for TensorBoard visualization).
```

### Parameters

**var** [`tf.Variable`] [description]  
**name** [`str`] variable name

## deepmd.utils.pair\_tab module

```
class deepmd.utils.pair_tab.PairTab(filename: str)
    Bases: object
```

### Parameters

**filename** File name for the short-range tabulated potential. The table is a text data file with  $(N_t + 1) * N_t / 2 + 1$  columns. The first column is the distance between atoms. The second to the last columns are energies for pairs of certain types. For example we have two atom types, 0 and 1. The columns from 2nd to 4th are for 0-0, 0-1 and 1-1 correspondingly.

## Methods

<code>get()</code>	Get the serialized table.
<code>reinit(filename)</code>	Initialize the tabulated interaction

`get()` → `Tuple`[`numpy.array`, `numpy.array`]  
 Get the serialized table.

`reinit(filename: str)` → `None`  
 Initialize the tabulated interaction

### Parameters

**filename** File name for the short-range tabulated potential. The table is a text data file with  $(N_t + 1) * N_t / 2 + 1$  columns. The first column is the distance between atoms. The second to the last columns are energies for pairs of certain types. For example we have two atom types, 0 and 1. The columns from 2nd to 4th are for 0-0, 0-1 and 1-1 correspondingly.

**deepmd.utils.path module**

**class** `deepmd.utils.path.DPH5Path(path: str)`

Bases: `deepmd.utils.path.DPPPath`

The path class to data system (DeepmdData) for HDF5 files.

**Parameters**

**path** [*str*] path

**Notes**

**OS - HDF5 relationship:** directory - Group file - Dataset

**Methods**

<code>glob(pattern)</code>	Search path using the glob pattern.
<code>is_dir()</code>	Check if self is directory.
<code>is_file()</code>	Check if self is file.
<code>load_numpy()</code>	Load NumPy array.
<code>load_txt([dtype])</code>	Load NumPy array from text.
<code>rglob(pattern)</code>	This is like calling <code>:metd:`DPPPath.glob()`</code> with <code>**/</code> added in front of the given relative pattern.

**glob**(*pattern: str*) → `List[deepmd.utils.path.DPPPath]`

Search path using the glob pattern.

**Parameters**

**pattern** [*str*] glob pattern

**Returns**

`List[DPPPath]` list of paths

**is\_dir**() → `bool`

Check if self is directory.

**is\_file**() → `bool`

Check if self is file.

**load\_numpy**() → `numpy.ndarray`

Load NumPy array.

**Returns**

`np.ndarray` loaded NumPy array

**load\_txt**(*dtype: Optional[numpy.dtype] = None, \*\*kwargs*) → `numpy.ndarray`

Load NumPy array from text.

**Returns**

`np.ndarray` loaded NumPy array

**rglob**(*pattern: str*) → `List[deepmd.utils.path.DPPPath]`

This is like calling `:metd:`DPPPath.glob()`` with `**/` added in front of the given relative pattern.



**Parameters****pattern** [`str`] glob pattern**Returns**`List[DPPath]` list of paths**class** `deepmd.utils.path.DPOSPath(path: str)`Bases: `deepmd.utils.path.DPPath`

The OS path class to data system (DeepmdData) for real directories.

**Parameters****path** [`str`] path**Methods**

<code>glob(pattern)</code>	Search path using the glob pattern.
<code>is_dir()</code>	Check if self is directory.
<code>is_file()</code>	Check if self is file.
<code>load_numpy()</code>	Load NumPy array.
<code>load_txt(**kwargs)</code>	Load NumPy array from text.
<code>rglob(pattern)</code>	This is like calling <code>:metd:`DPPath.glob()`</code> with <code>**/</code> added in front of the given relative pattern.

**glob**(*pattern: str*) → `List[deepmd.utils.path.DPPath]`

Search path using the glob pattern.

**Parameters****pattern** [`str`] glob pattern**Returns**`List[DPPath]` list of paths**is\_dir**() → `bool`

Check if self is directory.

**is\_file**() → `bool`

Check if self is file.

**load\_numpy**() → `numpy.ndarray`

Load NumPy array.

**Returns**`np.ndarray` loaded NumPy array**load\_txt**(*\*\*kwargs*) → `numpy.ndarray`

Load NumPy array from text.

**Returns**`np.ndarray` loaded NumPy array**rglob**(*pattern: str*) → `List[deepmd.utils.path.DPPath]`This is like calling `:metd:`DPPath.glob()`` with `**/` added in front of the given relative pattern.**Parameters**

**pattern** [`str`] glob pattern

#### Returns

`List[DPPath]` list of paths

**class** `deepmd.utils.path.DPPath(path: str)`

Bases: `abc.ABC`

The path class to data system (DeepmdData).

#### Parameters

**path** [`str`] path

#### Methods

<code>glob(pattern)</code>	Search path using the glob pattern.
<code>is_dir()</code>	Check if self is directory.
<code>is_file()</code>	Check if self is file.
<code>load_numpy()</code>	Load NumPy array.
<code>load_txt(**kwargs)</code>	Load NumPy array from text.
<code>rglob(pattern)</code>	This is like calling <code>:metd:`DPPath.glob()`</code> with <code>**/</code> added in front of the given relative pattern.

**abstract** `glob(pattern: str) → List[deepmd.utils.path.DPPath]`

Search path using the glob pattern.

#### Parameters

**pattern** [`str`] glob pattern

#### Returns

`List[DPPath]` list of paths

**abstract** `is_dir() → bool`

Check if self is directory.

**abstract** `is_file() → bool`

Check if self is file.

**abstract** `load_numpy() → numpy.ndarray`

Load NumPy array.

#### Returns

`np.ndarray` loaded NumPy array

**abstract** `load_txt(**kwargs) → numpy.ndarray`

Load NumPy array from text.

#### Returns

`np.ndarray` loaded NumPy array

**abstract** `rglob(pattern: str) → List[deepmd.utils.path.DPPath]`

This is like calling `:metd:`DPPath.glob()`` with `**/` added in front of the given relative pattern.

#### Parameters

**pattern** [`str`] glob pattern

**Returns**`List[DPPath]` list of paths**deepmd.utils.plugin module**

Base of plugin systems.

**class** `deepmd.utils.plugin.Plugin`

Bases: `object`

A class to register and restore plugins.

**Examples**

```
>>> plugin = Plugin()
>>> @plugin.register("xx")
def xxx():
    pass
>>> print(plugin.plugins['xx'])
```

**Attributes**

**plugins** [`Dict[str, object]`] plugins

**Methods**

<code>get_plugin(key)</code>	Visit a plugin by key.
<code>register(key)</code>	Register a plugin.

**get\_plugin**(*key*) → `object`

Visit a plugin by key.

**Parameters**

**key** `str` key of the plugin

**Returns**

`object` the plugin

**register**(*key: str*) → `Callable[[object], object]`

Register a plugin.

**Returns**

`Callable[[object], object]` decorator

**class** `deepmd.utils.plugin.PluginVariant(*args, **kwargs)`

Bases: `object`

A class to remove *type* from input arguments.

**class** `deepmd.utils.plugin.VariantABCMeta(name, bases, namespace, **kwargs)`

Bases: `deepmd.utils.plugin.VariantMeta`, `abc.ABCMeta`

## Methods

<code>__call__(*args, **kwargs)</code>	Remove <i>type</i> and keys that starts with underline.
<code>mro()</code>	Return a type's method resolution order.
<code>register(subclass)</code>	Register a virtual subclass of an ABC.

**class** `deepmd.utils.plugin.VariantMeta`  
Bases: `object`

## Methods

<code>__call__(*args, **kwargs)</code>	Remove <i>type</i> and keys that starts with underline.
--	---

## deepmd.utils.random module

`deepmd.utils.random.choice(a: numpy.ndarray, p: Optional[numpy.ndarray] = None)`  
Generates a random sample from a given 1-D array.

### Parameters

- a** [`np.ndarray`] A random sample is generated from its elements.
- p** [`np.ndarray`] The probabilities associated with each entry in a.

### Returns

`np.ndarray` arrays with results and their shapes

`deepmd.utils.random.random(size=None)`  
Return random floats in the half-open interval [0.0, 1.0).

### Parameters

- size** Output shape.

### Returns

`np.ndarray` Arrays with results and their shapes.

`deepmd.utils.random.seed(val: Optional[int] = None)`  
Seed the generator.

### Parameters

- val** [`int`] Seed.

`deepmd.utils.random.shuffle(x: numpy.ndarray)`  
Modify a sequence in-place by shuffling its contents.

### Parameters

- x** [`np.ndarray`] The array or list to be shuffled.

## deepmd.utils.sess module

`deepmd.utils.sess.run_sess(sess: tensorflow.python.client.session.Session, *args, **kwargs)`

Run session with errors caught.

### Parameters

**sess**: `tf.Session` TensorFlow Session

### Returns

the result of `sess.run()`

## deepmd.utils.tabulate module

**class** `deepmd.utils.tabulate.DPTabulate`(*descript: deepmd.descriptor.descriptor.Descriptor, neuron: typing.List[int], model\_file: str, type\_one\_side: bool = False, exclude\_types: typing.List[typing.List[int]] = [], activation\_fn: typing.Callable[[tensorflow.python.framework.ops.Tensor], tensorflow.python.framework.ops.Tensor] = <function tanh>, suffix: str = ''*)

Bases: `object`

Class for tabulation.

Compress a model, which including tabulating the embedding-net. The table is composed of fifth-order polynomial coefficients and is assembled from two sub-tables. The first table takes the stride(parameter) as its uniform stride, while the second table takes  $10 * \text{stride}$  as its uniform stride. The range of the first table is automatically detected by deepmd-kit, while the second table ranges from the first table's upper boundary(upper) to the  $\text{extrapolate}(\text{parameter}) * \text{upper}$ .

### Parameters

**descript** Descriptor of the original model

**neuron** Number of neurons in each hidden layers of the embedding net  $\mathcal{N}$

**model\_file** The frozen model

**type\_one\_side** Try to build  $N_{\text{types}}$  tables. Otherwise, building  $N_{\text{types}}^2$  tables

**exclude\_types** `[List[List[int]]]` The excluded pairs of types which have no interaction with each other. For example, `[[0, 1]]` means no interaction between type 0 and type 1.

**activation\_function** The activation function in the embedding net. Supported options are {"tanh", "gelu"} in common.ACTIVATION\_FN\_DICT.

**suffix** `[str, optional]` The suffix of the scope

## Methods

---

<code>build(min_nbor_dist, extrapolate, stride0, ...)</code>	Build the tables for model compression
--	--

---

**build**(*min\_nbor\_dist*: *float*, *extrapolate*: *float*, *stride0*: *float*, *stride1*: *float*) → `Tuple[int, int]`

Build the tables for model compression

### Parameters

- min\_nbor\_dist** The nearest distance between neighbor atoms
- extrapolate** The scale of model extrapolation
- stride0** The uniform stride of the first table
- stride1** The uniform stride of the second table
- neuron** Number of neurons in each hidden layers of the embedding net  $\mathcal{N}$

### Returns

- lower** The lower boundary of environment matrix
- upper** The upper boundary of environment matrix

## deepmd.utils.type\_embed module

**class** `deepmd.utils.type_embed.TypeEmbedNet`

Bases: `object`

### Parameters

- neuron** [`list[int]`] Number of neurons in each hidden layers of the embedding net
- resnet\_dt** Time-step  $dt$  in the resnet construction:  $y = x + dt * \phi(Wx + b)$
- activation\_function** The activation function in the embedding net. Supported options are {0}
- precision** The precision of the embedding net parameters. Supported options are {1}
- trainable** If the weights of embedding net are trainable.
- seed** Random seed for initializing the network parameters.
- uniform\_seed** Only for the purpose of backward compatibility, retrieves the old behavior of using the random seed

## Methods

---

<code>build(ntypes[, reuse, suffix])</code>	Build the computational graph for the descriptor
---	--

---

**build**(*ntypes*: *int*, *reuse*=*None*, *suffix*='')

Build the computational graph for the descriptor

### Parameters

- ntypes** Number of atom types.
- reuse** The weights in the networks should be reused when get the variable.

**suffix** Name suffix to identify this descriptor

#### Returns

**embedded\_types** The computational graph for embedded types

`deepmd.utils.type_embed.embed_atom_type(ntypes: int, natoms: tensorflow.python.framework.ops.Tensor, type_embedding: tensorflow.python.framework.ops.Tensor)`

Make the embedded type for the atoms in system. The atoms are assumed to be sorted according to the type, thus their types are described by a *tf.Tensor* natoms, see explanation below.

#### Parameters

**ntypes:** Number of types.

**natoms:** The number of atoms. This tensor has the length of Ntypes + 2 natoms[0]: number of local atoms natoms[1]: total number of atoms held by this processor natoms[i]:  $2 \leq i < \text{Ntypes} + 2$ , number of type i atoms

**type\_embedding:** The type embedding. It has the shape of [ntypes, embedding\_dim]

#### Returns

**atom\_embedding** The embedded type of each atom. It has the shape of [numb\_atoms, embedding\_dim]

### deepmd.utils.weight\_avg module

`deepmd.utils.weight_avg.weighted_average(errors: List[Dict[str, Tuple[float, float]]]) → Dict`

Compute wighted average of prediction errors for model.

#### Parameters

**errors** [*List[Dict[str, Tuple[float, float]]]*] List: the error of systems Dict: the error of quantities, name given by the key Tuple: (error, weight)

#### Returns

*Dict* weighted averages

## 14.1.2 Submodules

### 14.1.3 deepmd.calculator module

ASE calculator interface module.

**class** `deepmd.calculator.DP(model: Union[str, pathlib.Path], label: str = 'DP', type_dict: Optional[Dict[str, int]] = None, **kwargs)`

Bases: `ase.calculators.calculator.Calculator`

Implementation of ASE deepmd calculator.

Implemented propertie are *energy*, *forces* and *stress*

#### Parameters

**model** [*Union[str, Path]*] path to the model

**label** [*str*, optional] calculator label, by default “DP”

**type\_dict** [*Dict[str, int]*, optional] mapping of element types and their numbers, best left None and the calculator will infer this information from model, by default None

## Examples

Compute potential energy

```
>>> from ase import Atoms
>>> from deepmd.calculator import DP
>>> water = Atoms('H2O',
>>>               positions=[(0.7601, 1.9270, 1),
>>>                           (1.9575, 1, 1),
>>>                           (1., 1., 1.)],
>>>               cell=[100, 100, 100],
>>>               calculator=DP(model="frozen_model.pb"))
>>> print(water.get_potential_energy())
>>> print(water.get_forces())
```

Run BFGS structure optimization

```
>>> from ase.optimize import BFGS
>>> dyn = BFGS(water)
>>> dyn.run(fmax=1e-6)
>>> print(water.get_positions())
```

## Attributes

directory

label

## Methods

<code>band_structure()</code>	Create band-structure object for plotting.
<code>calculate([atoms, properties, system_changes])</code>	Run calculation with deepmd model.
<code>calculate_numerical_forces(atoms[, d])</code>	Calculate numerical forces using finite difference.
<code>calculate_numerical_stress(atoms[, d, voigt])</code>	Calculate numerical stress using finite difference.
<code>calculate_properties(atoms, properties)</code>	This method is experimental; currently for internal use.
<code>check_state(atoms[, tol])</code>	Check for any system changes since last calculation.
<code>get_magnetic_moments([atoms])</code>	Calculate magnetic moments projected onto atoms.
<code>get_property(name[, atoms, allow_calculation])</code>	Get the named property.
<code>get_stresses([atoms])</code>	the calculator should return intensive stresses, i.e., such that <code>stresses.sum(axis=0) == stress</code>
<code>read(label)</code>	Read atoms, parameters and calculated properties from output file.
<code>reset()</code>	Clear all information from old calculation.
<code>set(**kwargs)</code>	Set parameters like <code>set(key1=value1, key2=value2, ...)</code> .
<code>set_label(label)</code>	Set label and convert label to directory and prefix.



<b>calculation_required</b>	
<b>export_properties</b>	
<b>get_atoms</b>	
<b>get_charges</b>	
<b>get_default_parameters</b>	
<b>get_dipole_moment</b>	
<b>get_forces</b>	
<b>get_magnetic_moment</b>	
<b>get_potential_energies</b>	
<b>get_potential_energy</b>	
<b>get_stress</b>	
<b>read_atoms</b>	
<b>todict</b>	

**calculate**(atoms: *Optional*[Atoms] = None, properties: *List*[str] = ['energy', 'forces', 'virial'], system\_changes: *List*[str] = ['positions', 'numbers', 'cell', 'pbc', 'initial\_charges', 'initial\_magnoms'])

Run calculation with deepmd model.

#### Parameters

**atoms** [*Optional*[Atoms], optional] atoms object to run the calculation on, by default None

**properties** [*List*[str], optional] unused, only for function signature compatibility, by default ["energy", "forces", "stress"]

**system\_changes** [*List*[str], optional] unused, only for function signature compatibility, by default all\_changes

**implemented\_properties:** *List*[str] = ['energy', 'forces', 'virial', 'stress']  
Properties calculator can handle (energy, forces, ...)

**name** = 'DP'

### 14.1.4 deepmd.common module

Collection of functions and classes used throughout the whole package.

**class** deepmd.common.ClassArg

Bases: *object*

Class that take care of input json/yaml parsing.

The rules for parsing are defined by the *add* method, than *parse* is called to process the supplied dict

#### Attributes

**arg\_dict:** *Dict*[str, Any] dictionary containing parsing rules

**alias\_map:** *Dict*[str, Any] dictionary with keyword aliases

## Methods

<code>add(key, types_, alias, default, must)</code>	Add key to be parsed.
<code>get_dict()</code>	Get dictionary built from rules defined by add method.
<code>parse(jdata)</code>	Parse input dictionary, use the rules defined by add method.

**add**(key: *str*, types\_: *Union[type, List[type]]*, alias: *Optional[Union[str, List[str]]] = None*, default: *Optional[Any] = None*, must: *bool = False*) → *deepmd.common.ClassArg*  
Add key to be parsed.

### Parameters

**key** [*str*] key name  
**types\_** [*Union[type, List[type]]*] list of allowed key types  
**alias** [*Optional[Union[str, List[str]]]*, *optional*] alias for the key, by default None  
**default** [*Any*, *optional*] default value for the key, by default None  
**must** [*bool*, *optional*] if the key is mandatory, by default False

### Returns

*ClassArg* instance with added key

**get\_dict**() → *Dict[str, Any]*  
Get dictionary built from rules defined by add method.

### Returns

*Dict[str, Any]* settings dictionary with default values

**parse**(jdata: *Dict[str, Any]*) → *Dict[str, Any]*  
Parse input dictionary, use the rules defined by add method.

### Parameters

**jdata** [*Dict[str, Any]*] loaded json/yaml data

### Returns

*Dict[str, Any]* parsed dictionary

**deepmd.common.add\_data\_requirement**(key: *str*, ndof: *int*, atomic: *bool = False*, must: *bool = False*, high\_prec: *bool = False*, type\_sel: *Optional[bool] = None*, repeat: *int = 1*)

Specify data requirements for training.

### Parameters

**key** [*str*] type of data stored in corresponding \*.*np*y file e.g. *forces* or *energy*  
**ndof** [*int*] number of the degrees of freedom, this is tied to *atomic* parameter e.g. *forces* have *atomic=True* and *ndof=3*  
**atomic** [*bool*, *optional*] specifies whwther the *ndof* keyworrd applies to per atom quantity or not, by default False  
**must** [*bool*, *optional*] specifi if the \*.*np*y data file must exist, by default False  
**high\_prec** [*bool*, *optional*] if tru load data to *np.float64* else *np.float32*, by default False

**type\_sel** [**bool**, optional] select only certain type of atoms, by default None

**repeat** [**int**, optional] if specify repeat data *repeat* times, by default 1

deepmd.common.**cast\_precision**(*func*: *Callable*) → *Callable*

A decorator that casts and casts back the input and output tensor of a method.

The decorator should be used in a classmethod.

The decorator will do the following thing: (1) It casts input Tensors from *GLOBAL\_TF\_FLOAT\_PRECISION* to precision defined by property *precision*. (2) It casts output Tensors from *precision* to *GLOBAL\_TF\_FLOAT\_PRECISION*. (3) It checks inputs and outputs and only casts when input or output is a Tensor and its dtype matches *GLOBAL\_TF\_FLOAT\_PRECISION* and *precision*, respectively. If it does not match (e.g. it is an integer), the decorator will do nothing on it.

#### Returns

**Callable** a decorator that casts and casts back the input and output tensor of a method

### Examples

```
>>> class A:
...     @property
...     def precision(self):
...         return tf.float32
...
...     @cast_precision
...     def f(x: tf.Tensor, y: tf.Tensor) -> tf.Tensor:
...         return x ** 2 + y
```

deepmd.common.**docstring\_parameter**(\**sub*: *Tuple[str, ...]*)

Add parameters to object docstring.

#### Parameters

**sub**: **Tuple[str, ...]** list of strings that will be inserted into prepared locations in docstring.

deepmd.common.**expand\_sys\_str**(*root\_dir*: *Union[str, pathlib.Path]*) → *List[str]*

Recursively iterate over directories taking those that contain *type.raw* file.

#### Parameters

**root\_dir** [**Union[str, Path]**] starting directory

#### Returns

**List[str]** list of string pointing to system directories

deepmd.common.**gelu**(*x*: *tensorflow.python.framework.ops.Tensor*) → *tensorflow.python.framework.ops.Tensor*  
Gaussian Error Linear Unit.

This is a smoother version of the RELU.

#### Parameters

**x** [**tf.Tensor**] float Tensor to perform activation

#### Returns

**x with the GELU activation applied**

## References

Original paper <https://arxiv.org/abs/1606.08415>

`deepmd.common.get_activation_func(activation_fn: _ACTIVATION) → Callable[[tensorflow.python.framework.ops.Tensor], tensorflow.python.framework.ops.Tensor]`

Get activation function callable based on string name.

### Parameters

**activation\_fn** [\_ACTIVATION] one of the defined activation functions

### Returns

`Callable[[tf.Tensor], tf.Tensor]` correspondingg TF callable

### Raises

`RuntimeError` if unknown activation function is specified

`deepmd.common.get_np_precision(precision: _PRECISION) → numpy.dtype`

Get numpy precision constant from string.

### Parameters

**precision** [\_PRECISION] string name of numpy constant or default

### Returns

`np.dtype` numpy presicion constant

### Raises

`RuntimeError` if string is invalid

`deepmd.common.get_precision(precision: _PRECISION) → Any`

Convert str to TF DType constant.

### Parameters

**precision** [\_PRECISION] one of the allowed precisions

### Returns

`tf.python.framework.dtypes.DType` appropriate TF constant

### Raises

`RuntimeError` if supplied precision string does not have acoresponding TF constant

`deepmd.common.j_loader(filename: Union[str, pathlib.Path]) → Dict[str, Any]`

Load yaml or json settings file.

### Parameters

**filename** [Union[str, Path]] path to file

### Returns

`Dict[str, Any]` loaded dictionary

### Raises

`TypeError` if the supplied file is of unsupported type

`deepmd.common.j_must_have(jdata: Dict[str, _DICT_VAL], key: str, deprecated_key: List[str] = []) → _DICT_VAL`

Assert that supplied dictionary contains specified key.

#### Returns

`_DICT_VAL` value that was stored under supplied key

#### Raises

`RuntimeError` if the key is not present

`deepmd.common.make_default_mesh(test_box: numpy.ndarray, cell_size: float = 3.0) → numpy.ndarray`  
Get number of cells of size=`cell\_size` fit into average box.

#### Parameters

`test_box` [`np.ndarray`] numpy array with cells of shape Nx9

`cell_size` [`float`, optional] length of one cell, by default 3.0

#### Returns

`np.ndarray` mesh for supplied boxes, how many cells fit in each direction

`deepmd.common.safe_cast_tensor(input: tensorflow.python.framework.ops.Tensor, from_precision: tensorflow.python.framework.dtypes.DType, to_precision: tensorflow.python.framework.dtypes.DType) → tensorflow.python.framework.ops.Tensor`

Convert a Tensor from a precision to another precision.

If input is not a Tensor or without the specific precision, the method will not cast it.

#### Parameters

`input: tf.Tensor` input tensor

`precision` [`tf.DType`] Tensor data type that casts to

#### Returns

`tf.Tensor` casted Tensor

`deepmd.common.select_idx_map(atom_types: numpy.ndarray, select_types: numpy.ndarray) → numpy.ndarray`  
Build map of indices for element supplied element types from all atoms list.

#### Parameters

`atom_types` [`np.ndarray`] array specifying type for each atom as integer

`select_types` [`np.ndarray`] types of atoms you want to find indices for

#### Returns

`np.ndarray` indices of types of atoms defined by `select_types` in `atom_types` array

**Warning:** `select_types` array will be sorted before finding indices in `atom_types`

### 14.1.5 deepmd.env module

Module that sets tensorflow working environment and exports important constants.

`deepmd.env.GLOBAL_ENER_FLOAT_PRECISION`

alias of `numpy.float64`

`deepmd.env.GLOBAL_NP_FLOAT_PRECISION`

alias of `numpy.float64`

`deepmd.env.global_cvt_2_ener_float`(*xx: tensorflow.python.framework.ops.Tensor*) →  
tensorflow.python.framework.ops.Tensor

Cast tensor to globally set energy precision.

**Parameters**

**xx** [`tf.Tensor`] input tensor

**Returns**

`tf.Tensor` output tensor cast to `GLOBAL_ENER_FLOAT_PRECISION`

`deepmd.env.global_cvt_2_tf_float`(*xx: tensorflow.python.framework.ops.Tensor*) →  
tensorflow.python.framework.ops.Tensor

Cast tensor to globally set TF precision.

**Parameters**

**xx** [`tf.Tensor`] input tensor

**Returns**

`tf.Tensor` output tensor cast to `GLOBAL_TF_FLOAT_PRECISION`

`deepmd.env.reset_default_tf_session_config`(*cpu\_only: bool*)

Limit tensorflow session to CPU or not.

**Parameters**

**cpu\_only** [`bool`] If enabled, no GPU device is visible to the TensorFlow Session.

## 15.1 Class Hierarchy

- *Namespace deepmd*
  - *Struct deepmd\_exception*
  - *Struct InputNlist*
  - *Struct NeighborListData*
  - *Struct tf\_exception*
  - *Template Class AtomMap*
  - *Class DeepPot*
  - *Class DeepPotModelDevi*
  - *Class DeepTensor*
  - *Class DipoleChargeModifier*

## 15.2 File Hierarchy

- **dir\_source**
  - **dir\_source\_api\_cc**
    - \* **dir\_source\_api\_cc\_include**
      - file\_source\_api\_cc\_include\_AtomMap.h
      - file\_source\_api\_cc\_include\_common.h
      - file\_source\_api\_cc\_include\_DataModifier.h
      - file\_source\_api\_cc\_include\_DeepPot.h
      - file\_source\_api\_cc\_include\_DeepTensor.h

## 15.3 Full API

### 15.3.1 Namespaces

#### Namespace deepmd

##### Contents

- *Classes*
- *Functions*
- *Typedefs*

##### Classes

- *Struct* `deepmd_exception`
- *Struct* `InputNlist`
- *Struct* `NeighborListData`
- *Struct* `tf_exception`
- *Template Class* `AtomMap`
- *Class* `DeepPot`
- *Class* `DeepPotModelDevi`
- *Class* `DeepTensor`
- *Class* `DipoleChargeModifier`

##### Functions

- *Function* `deepmd::check_status`
- *Function* `deepmd::get_env_nthreads`
- *Function* `deepmd::load_op_library`
- *Function* `deepmd::model_compatible`
- *Function* `deepmd::name_prefix`
- *Function* `deepmd::select_by_type`
- *Template Function* `deepmd::select_map(std::vector<VT>&, const std::vector<VT>&, const std::vector<int>&, const int&)`
- *Template Function* `deepmd::select_map(typename std::vector<VT>::iterator, const typename std::vector<VT>::const_iterator, const std::vector<int>&, const int&)`
- *Template Function* `deepmd::select_map_inv(std::vector<VT>&, const std::vector<VT>&, const std::vector<int>&, const int&)`



- *Template Function* `deepmd::select_map_inv`(typename `std::vector<VT>::iterator`, `const` typename `std::vector<VT>::const_iterator`, `const` `std::vector<int>&`, `const` `int&`)
- *Function* `deepmd::select_real_atoms`
- *Template Function* `deepmd::session_get_scalar`
- *Template Function* `deepmd::session_get_vector`
- *Function* `deepmd::session_input_tensors`(`std::vector<std::pair<std::string, tensorflow::Tensor>>&`, `const` `std::vector<VALUETYPE>&`, `const` `int&`, `const` `std::vector<int>&`, `const` `std::vector<VALUETYPE>&`, `const` `VALUETYPE&`, `const` `std::vector<VALUETYPE>&`, `const` `std::vector<VALUETYPE>&`, `const` `deepmd::AtomMap<VALUETYPE>&`, `const` `std::string`)
- *Function* `deepmd::session_input_tensors`(`std::vector<std::pair<std::string, tensorflow::Tensor>>&`, `const` `std::vector<VALUETYPE>&`, `const` `int&`, `const` `std::vector<int>&`, `const` `std::vector<VALUETYPE>&`, `InputNlist&`, `const` `std::vector<VALUETYPE>&`, `const` `std::vector<VALUETYPE>&`, `const` `deepmd::AtomMap<VALUETYPE>&`, `const` `int`, `const` `int`, `const` `std::string`)

## Typedefs

- *Typedef* `deepmd::ENERGYTYPE`
- *Typedef* `deepmd::STRINGTYPE`
- *Typedef* `deepmd::VALUETYPE`

## 15.3.2 Classes and Structs

### Struct `deepmd_exception`

- Defined in `file_source_api_cc_include_common.h`

### Inheritance Relationships

#### Derived Type

- `public` `deepmd::tf_exception` (*Struct* `tf_exception`)

### Struct Documentation

struct **deepmd\_exception**  
 Subclassed by `deepmd::tf_exception`

## Struct InputNlist

- Defined in file\_source\_api\_cc\_include\_common.h

## Struct Documentation

struct deepmd::InputNlist

Construct *InputNlist* with the input LAMMPS nbor list info.

### Public Functions

inline InputNlist()

inline InputNlist(int inum\_, int \*ilist\_, int \*numneigh\_, int \*\*firstneigh\_)

inline ~InputNlist()

### Public Members

int inum

Number of core region atoms.

int \*ilist

Array stores the core region atom's index.

int \*numneigh

Array stores the core region atom's neighbor atom number.

int \*\*firstneigh

Array stores the core region atom's neighbor index.

## Struct NeighborListData

- Defined in file\_source\_api\_cc\_include\_common.h

## Struct Documentation

struct deepmd::NeighborListData

## Public Functions

```
void copy_from_nlist(const InputNlist &inlist)

void shuffle(const std::vector<int> &fwd_map)

void shuffle(const deepmd::AtomMap<VALUETYPE> &map)

void shuffle_exclude_empty(const std::vector<int> &fwd_map)

void make_inlist(InputNlist &inlist)
```

## Public Members

```
std::vector<int> ilist
    Array stores the core region atom's index.

std::vector<std::vector<int>>> jlist
    Array stores the core region atom's neighbor index.

std::vector<int> numneigh
    Array stores the number of neighbors of core region atoms.

std::vector<int*> firstneigh
    Array stores the the location of the first neighbor of core region atoms.
```

## Struct `tf_exception`

- Defined in `file_source_api_cc_include_common.h`

## Inheritance Relationships

### Base Type

- public `deepmd_exception` (*Struct `deepmd_exception`*)

## Struct Documentation

```
struct deepmd::tf_exception : public deepmd_exception
    Throw exception if TensorFlow doesn't work.
```

## Public Functions

inline **tf\_exception**()

inline **tf\_exception**(const std::string &msg)

## Template Class AtomMap

- Defined in file\_source\_api\_cc\_include\_AtomMap.h

## Class Documentation

template<typename **VALUETYPE**>

class deepmd::**AtomMap**

## Public Functions

**AtomMap**()

**AtomMap**(const std::vector<int>::const\_iterator in\_begin, const std::vector<int>::const\_iterator in\_end)

void **forward**(typename std::vector<*VALUETYPE*>::iterator out, const typename std::vector<*VALUETYPE*>::const\_iterator in, const int stride = 1) const

void **backward**(typename std::vector<*VALUETYPE*>::iterator out, const typename std::vector<*VALUETYPE*>::const\_iterator in, const int stride = 1) const

inline const std::vector<int> &**get\_type**() const

inline const std::vector<int> &**get\_fwd\_map**() const

inline const std::vector<int> &**get\_bkw\_map**() const

## Class DeepPot

- Defined in file\_source\_api\_cc\_include\_DeepPot.h

## Class Documentation

class `deepmd::DeepPot`  
Deep Potential.

### Public Functions

**DeepPot()**

DP constructor without initialization.

**~DeepPot()**

**DeepPot**(const std::string &model, const int &gpu\_rank = 0, const std::string &file\_content = "")

DP constructor with initialization.

#### Parameters

- **model** – [in] The name of the frozen model file.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The content of the model file. If it is not empty, DP will read from the string instead of the file.

void **init**(const std::string &model, const int &gpu\_rank = 0, const std::string &file\_content = "")

Initialize the DP.

#### Parameters

- **model** – [in] The name of the frozen model file.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The content of the model file. If it is not empty, DP will read from the string instead of the file.

void **print\_summary**(const std::string &pre) const

Print the DP summary to the screen.

**Parameters** **pre** – [in] The prefix to each line.

void **compute**(*ENERGYTYPE* &ener, std::vector<*VALUETYPE*> &force, std::vector<*VALUETYPE*> &virial, const std::vector<*VALUETYPE*> &coord, const std::vector<int> &atype, const std::vector<*VALUETYPE*> &box, const std::vector<*VALUETYPE*> &fparam = std::vector<*VALUETYPE*>(), const std::vector<*VALUETYPE*> &aparam = std::vector<*VALUETYPE*>())

Evaluate the energy, force and virial by using this DP.

#### Parameters

- **ener** – [out] The system energy.
- **force** – [out] The force on each atom.
- **virial** – [out] The virial.
- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.

- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter. The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

```
void compute(ENERGYTYPE &ener, std::vector<VALUETYPE> &force, std::vector<VALUETYPE> &virial,
const std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const
std::vector<VALUETYPE> &box, const int nghost, const InputNlist &inlist, const int &ago,
const std::vector<VALUETYPE> &fparam = std::vector<VALUETYPE>(), const
std::vector<VALUETYPE> &aparam = std::vector<VALUETYPE>())
```

Evaluate the energy, force and virial by using this DP.

#### Parameters

- **ener** – [out] The system energy.
- **force** – [out] The force on each atom.
- **virial** – [out] The virial.
- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.
- **nghost** – [in] The number of ghost atoms.
- **inlist** – [in] The input neighbour list.
- **ago** – [in] Update the internal neighbour list if ago is 0.
- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter. The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

```
void compute(ENERGYTYPE &ener, std::vector<VALUETYPE> &force, std::vector<VALUETYPE> &virial,
std::vector<VALUETYPE> &atom_energy, std::vector<VALUETYPE> &atom_virial, const
std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const
std::vector<VALUETYPE> &box, const std::vector<VALUETYPE> &fparam =
std::vector<VALUETYPE>(), const std::vector<VALUETYPE> &aparam =
std::vector<VALUETYPE>())
```

Evaluate the energy, force, virial, atomic energy, and atomic virial by using this DP.

#### Parameters

- **ener** – [out] The system energy.
- **force** – [out] The force on each atom.
- **virial** – [out] The virial.
- **atom\_energy** – [out] The atomic energy.
- **atom\_virial** – [out] The atomic virial.

- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.
- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

```
void compute(ENERGYTYPE &ener, std::vector<VALUETYPE> &force, std::vector<VALUETYPE> &virial,
std::vector<VALUETYPE> &atom_energy, std::vector<VALUETYPE> &atom_virial, const
std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const
std::vector<VALUETYPE> &box, const int nghost, const InputNlist &imp_list, const int &ago,
const std::vector<VALUETYPE> &fparam = std::vector<VALUETYPE>(), const
std::vector<VALUETYPE> &aparam = std::vector<VALUETYPE>())
```

Evaluate the energy, force, virial, atomic energy, and atomic virial by using this DP.

#### Parameters

- **ener** – [out] The system energy.
- **force** – [out] The force on each atom.
- **virial** – [out] The virial.
- **atom\_energy** – [out] The atomic energy.
- **atom\_virial** – [out] The atomic virial.
- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.
- **nghost** – [in] The number of ghost atoms.
- **imp\_list** – [in] The input neighbour list.
- **ago** – [in] Update the internal neighbour list if ago is 0.
- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

```
inline VALUETYPE cutoff() const
    Get the cutoff radius.
```

**Returns** The cutoff radius.

```
inline int numb_types() const
    Get the number of types.
```

**Returns** The number of types.

inline int **dim\_fparam**() const

Get the dimension of the frame parameter.

**Returns** The dimension of the frame parameter.

inline int **dim\_aparam**() const

Get the dimension of the atomic parameter.

**Returns** The dimension of the atomic parameter.

void **get\_type\_map**(std::string &type\_map)

Get the type map (element name of the atom types) of this model.

**Parameters** **type\_map** – [out] The type map of this model.

## Class DeepPotModelDevi

- Defined in file\_source\_api\_cc\_include\_DeepPot.h

## Class Documentation

class deepmd: **DeepPotModelDevi**

### Public Functions

**DeepPotModelDevi**()

DP model deviation constructor without initialization.

**~DeepPotModelDevi**()

**DeepPotModelDevi**(const std::vector<std::string> &models, const int &gpu\_rank = 0, const std::vector<std::string> &file\_contents = std::vector<std::string>())

DP model deviation constructor with initialization.

#### Parameters

- **model** – [in] The names of the frozen model files.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The contents of the model files. If it is not empty, DP will read from the strings instead of the files.

void **init**(const std::vector<std::string> &models, const int &gpu\_rank = 0, const std::vector<std::string> &file\_contents = std::vector<std::string>())

Initialize the DP model deviation contructor.

#### Parameters

- **model** – [in] The names of the frozen model files.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The contents of the model files. If it is not empty, DP will read from the strings instead of the files.



```
void compute(std::vector<ENERGYTYPE> &all_ener, std::vector<std::vector<VALUETYPE>> &all_force,
             std::vector<std::vector<VALUETYPE>> &all_virial, const std::vector<VALUETYPE> &coord,
             const std::vector<int> &atype, const std::vector<VALUETYPE> &box, const int nghost, const
             InputNlist &imp_list, const int &ago, const std::vector<VALUETYPE> &fparam =
             std::vector<VALUETYPE>(), const std::vector<VALUETYPE> &aparam =
             std::vector<VALUETYPE>())
```

Evaluate the energy, force and virial by using these DP models.

#### Parameters

- **all\_ener** – [out] The system energies of all models.
- **all\_force** – [out] The forces on each atom of all models.
- **all\_virial** – [out] The virials of all models.
- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.
- **nghost** – [in] The number of ghost atoms.
- **imp\_list** – [in] The input neighbour list.
- **ago** – [in] Update the internal neighbour list if ago is 0.
- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter. The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

```
void compute(std::vector<ENERGYTYPE> &all_ener, std::vector<std::vector<VALUETYPE>> &all_force,
             std::vector<std::vector<VALUETYPE>> &all_virial, std::vector<std::vector<VALUETYPE>>
             &all_atom_energy, std::vector<std::vector<VALUETYPE>> &all_atom_virial, const
             std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const
             std::vector<VALUETYPE> &box, const int nghost, const InputNlist &imp_list, const int &ago,
             const std::vector<VALUETYPE> &fparam = std::vector<VALUETYPE>(), const
             std::vector<VALUETYPE> &aparam = std::vector<VALUETYPE>())
```

Evaluate the energy, force, virial, atomic energy, and atomic virial by using these DP models.

#### Parameters

- **all\_ener** – [out] The system energies of all models.
- **all\_force** – [out] The forces on each atom of all models.
- **all\_virial** – [out] The virials of all models.
- **all\_atom\_energy** – [out] The atomic energies of all models.
- **all\_atom\_virial** – [out] The atomic virials of all models.
- **coord** – [in] The coordinates of atoms. The array should be of size nframes x natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size nframes x 9.

- **nghost** – [in] The number of ghost atoms.
- **lmp\_list** – [in] The input neighbour list.
- **ago** – [in] Update the internal neighbour list if ago is 0.
- **fparam** – [in] The frame parameter. The array can be of size : nframes x dim\_fparam. dim\_fparam. Then all frames are assumed to be provided with the same fparam.
- **aparam** – [in] The atomic parameter. The array can be of size : nframes x natoms x dim\_aparam. natoms x dim\_aparam. Then all frames are assumed to be provided with the same aparam. dim\_aparam. Then all frames and atoms are provided with the same aparam.

inline *VALUETYPE* **cutoff**() const  
Get the cutoff radius.

**Returns** The cutoff radius.

inline int **numb\_types**() const  
Get the number of types.

**Returns** The number of types.

inline int **dim\_fparam**() const  
Get the dimension of the frame parameter.

**Returns** The dimension of the frame parameter.

inline int **dim\_aparam**() const  
Get the dimension of the atomic parameter.

**Returns** The dimension of the atomic parameter.

void **compute\_avg**(*ENERGYTYPE* &dener, const std::vector<*ENERGYTYPE*> &all\_energy)  
Compute the average energy.

**Parameters**

- **dener** – [out] The average energy.
- **all\_energy** – [in] The energies of all models.

void **compute\_avg**(*VALUETYPE* &dener, const std::vector<*VALUETYPE*> &all\_energy)  
Compute the average energy.

**Parameters**

- **dener** – [out] The average energy.
- **all\_energy** – [in] The energies of all models.

void **compute\_avg**(std::vector<*VALUETYPE*> &avg, const std::vector<std::vector<*VALUETYPE*>> &xx)  
Compute the average of vectors.

**Parameters**

- **avg** – [out] The average of vectors.
- **xx** – [in] The vectors of all models.

void **compute\_std**(std::vector<*VALUETYPE*> &std, const std::vector<*VALUETYPE*> &avg, const  
std::vector<std::vector<*VALUETYPE*>> &xx, const int &stride)  
Compute the standard deviation of vectors.

**Parameters**

- **std** – [out] The standard deviation of vectors.
- **avg** – [in] The average of vectors.
- **xx** – [in] The vectors of all models.
- **stride** – [in] The stride to compute the deviation.

```
void compute_relative_std(std::vector<VALUETYPE> &std, const std::vector<VALUETYPE> &avg,
                        const VALUETYPE eps, const int &stride)
```

Compute the relative standard deviation of vectors.

#### Parameters

- **std** – [out] The standard deviation of vectors.
- **avg** – [in] The average of vectors.
- **eps** – [in] The level parameter for computing the deviation.
- **stride** – [in] The stride to compute the deviation.

```
void compute_std_e(std::vector<VALUETYPE> &std, const std::vector<VALUETYPE> &avg, const
                  std::vector<std::vector<VALUETYPE>> &xx)
```

Compute the standard deviation of atomic energies.

#### Parameters

- **std** – [out] The standard deviation of atomic energies.
- **avg** – [in] The average of atomic energies.
- **xx** – [in] The vectors of all atomic energies.

```
void compute_std_f(std::vector<VALUETYPE> &std, const std::vector<VALUETYPE> &avg, const
                  std::vector<std::vector<VALUETYPE>> &xx)
```

Compute the standard deviation of forces.

#### Parameters

- **std** – [out] The standard deviation of forces.
- **avg** – [in] The average of forces.
- **xx** – [in] The vectors of all forces.

```
void compute_relative_std_f(std::vector<VALUETYPE> &std, const std::vector<VALUETYPE> &avg,
                           const VALUETYPE eps)
```

Compute the relative standard deviation of forces.

#### Parameters

- **std** – [out] The relative standard deviation of forces.
- **avg** – [in] The relative average of forces.
- **eps** – [in] The level parameter for computing the deviation.

## Class DeepTensor

- Defined in file\_source\_api\_cc\_include\_DeepTensor.h

## Class Documentation

class deepmd: **DeepTensor**  
Deep Tensor.

### Public Functions

#### **DeepTensor()**

Deep Tensor constructor without initialization.

**DeepTensor**(const std::string &model, const int &gpu\_rank = 0, const std::string &name\_scope = "")

Deep Tensor constructor with initialization..

#### Parameters

- **model** – [in] The name of the frozen model file.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The content of the model file. If it is not empty, DP will read from the string instead of the file.

void **init**(const std::string &model, const int &gpu\_rank = 0, const std::string &name\_scope = "")

Initialize the Deep Tensor.

#### Parameters

- **model** – [in] The name of the frozen model file.
- **gpu\_rank** – [in] The GPU rank. Default is 0.
- **file\_content** – [in] The content of the model file. If it is not empty, DP will read from the string instead of the file.

void **print\_summary**(const std::string &pre) const

Print the DP summary to the screen.

**Parameters pre** – [in] The prefix to each line.

void **compute**(std::vector<VALUETYPE> &value, const std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const std::vector<VALUETYPE> &box)

Evaluate the value by using this model.

#### Parameters

- **value** – [out] The value to evalute, usually would be the atomic tensor.
- **coord** – [in] The coordinates of atoms. The array should be of size natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size 9.

void **compute**(std::vector<VALUETYPE> &value, const std::vector<VALUETYPE> &coord, const std::vector<int> &atype, const std::vector<VALUETYPE> &box, const int nghost, const *InputNlist* &inlist)

Evaluate the value by using this model.

**Parameters**

- **value** – [out] The value to evaluate, usually would be the atomic tensor.
- **coord** – [in] The coordinates of atoms. The array should be of size `natoms x 3`.
- **atype** – [in] The atom types. The list should contain `natoms` ints.
- **box** – [in] The cell of the region. The array should be of size 9.
- **nghost** – [in] The number of ghost atoms.
- **inlist** – [in] The input neighbour list.

```
void compute(std::vector<VALUETYPE> &global_tensor, std::vector<VALUETYPE> &force,
            std::vector<VALUETYPE> &virial, const std::vector<VALUETYPE> &coord, const
            std::vector<int> &atype, const std::vector<VALUETYPE> &box)
```

Evaluate the global tensor and component-wise force and virial.

**Parameters**

- **global\_tensor** – [out] The global tensor to evaluate.
- **force** – [out] The component-wise force of the global tensor, size `odim x natoms x 3`.
- **virial** – [out] The component-wise virial of the global tensor, size `odim x 9`.
- **coord** – [in] The coordinates of atoms. The array should be of size `natoms x 3`.
- **atype** – [in] The atom types. The list should contain `natoms` ints.
- **box** – [in] The cell of the region. The array should be of size 9.

```
void compute(std::vector<VALUETYPE> &global_tensor, std::vector<VALUETYPE> &force,
            std::vector<VALUETYPE> &virial, const std::vector<VALUETYPE> &coord, const
            std::vector<int> &atype, const std::vector<VALUETYPE> &box, const int nghost, const
            InputNlist &inlist)
```

Evaluate the global tensor and component-wise force and virial.

**Parameters**

- **global\_tensor** – [out] The global tensor to evaluate.
- **force** – [out] The component-wise force of the global tensor, size `odim x natoms x 3`.
- **virial** – [out] The component-wise virial of the global tensor, size `odim x 9`.
- **coord** – [in] The coordinates of atoms. The array should be of size `natoms x 3`.
- **atype** – [in] The atom types. The list should contain `natoms` ints.
- **box** – [in] The cell of the region. The array should be of size 9.
- **nghost** – [in] The number of ghost atoms.
- **inlist** – [in] The input neighbour list.

```
void compute(std::vector<VALUETYPE> &global_tensor, std::vector<VALUETYPE> &force,
            std::vector<VALUETYPE> &virial, std::vector<VALUETYPE> &atom_tensor,
            std::vector<VALUETYPE> &atom_virial, const std::vector<VALUETYPE> &coord, const
            std::vector<int> &atype, const std::vector<VALUETYPE> &box)
```

Evaluate the global tensor and component-wise force and virial.

**Parameters**

- **global\_tensor** – [out] The global tensor to evaluate.
- **force** – [out] The component-wise force of the global tensor, size odim x natoms x 3.
- **virial** – [out] The component-wise virial of the global tensor, size odim x 9.
- **atom\_tensor** – [out] The atomic tensor value of the model, size natoms x odim.
- **atom\_virial** – [out] The component-wise atomic virial of the global tensor, size odim x natoms x 9.
- **coord** – [in] The coordinates of atoms. The array should be of size natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size 9.

```
void compute(std::vector<VALUETYPE> &global_tensor, std::vector<VALUETYPE> &force,
             std::vector<VALUETYPE> &virial, std::vector<VALUETYPE> &atom_tensor,
             std::vector<VALUETYPE> &atom_virial, const std::vector<VALUETYPE> &coord, const
             std::vector<int> &atype, const std::vector<VALUETYPE> &box, const int nghost, const
             InputNlist &inlist)
```

Evaluate the global tensor and component-wise force and virial.

#### Parameters

- **global\_tensor** – [out] The global tensor to evaluate.
- **force** – [out] The component-wise force of the global tensor, size odim x natoms x 3.
- **virial** – [out] The component-wise virial of the global tensor, size odim x 9.
- **atom\_tensor** – [out] The atomic tensor value of the model, size natoms x odim.
- **atom\_virial** – [out] The component-wise atomic virial of the global tensor, size odim x natoms x 9.
- **coord** – [in] The coordinates of atoms. The array should be of size natoms x 3.
- **atype** – [in] The atom types. The list should contain natoms ints.
- **box** – [in] The cell of the region. The array should be of size 9.
- **nghost** – [in] The number of ghost atoms.
- **inlist** – [in] The input neighbour list.

```
inline VALUETYPE cutoff() const
    Get the cutoff radius.
```

**Returns** The cutoff radius.

```
inline int numb_types() const
    Get the number of types.
```

**Returns** The number of types.

```
inline int output_dim() const
    Get the output dimension.
```

**Returns** The output dimension.

```
inline const std::vector<int> &sel_types() const
```

## Class DipoleChargeModifier

- Defined in file\_source\_api\_cc\_include\_DataModifier.h

## Class Documentation

class deepmd::DipoleChargeModifier

### Public Functions

DipoleChargeModifier()

DipoleChargeModifier(const std::string &model, const int &gpu\_rank = 0, const std::string &name\_scope = "")

inline ~DipoleChargeModifier()

void **init**(const std::string &model, const int &gpu\_rank = 0, const std::string &name\_scope = "")

void **print\_summary**(const std::string &pre) const

void **compute**(std::vector<VALUETYPE> &dfcorr\_, std::vector<VALUETYPE> &dvcorr\_, const std::vector<VALUETYPE> &dcoord\_, const std::vector<int> &dtype\_, const std::vector<VALUETYPE> &dbox, const std::vector<std::pair<int, int>> &pairs, const std::vector<VALUETYPE> &delef\_, const int nghost, const *InputNlist* &imp\_list)

inline VALUETYPE **cutoff**() const

inline int **numb\_types**() const

inline std::vector<int> **sel\_types**() const

## 15.3.3 Functions

### Function deepmd::check\_status

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

void deepmd::check\_status(const tensorflow::Status &status)  
Check TensorFlow status. Exit if not OK.

**Parameters** **status** – [in] TensorFlow status.

## Function deepmd::get\_env\_nthreads

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

void deepmd::get\_env\_nthreads(int &num\_intra\_nthreads, int &num\_inter\_nthreads)  
Get the number of threads from the environment variable.

**Parameters**

- **num\_intra\_nthreads** – [out] The number of intra threads. Read from TF\_INTRA\_OP\_PARALLELISM\_THREADS.
- **num\_inter\_nthreads** – [out] The number of inter threads. Read from TF\_INTER\_OP\_PARALLELISM\_THREADS.

## Function deepmd::load\_op\_library

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

void deepmd::load\_op\_library()  
Dynamically load OP library. This should be called before loading graphs.

## Function deepmd::model\_compatible

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

bool deepmd::model\_compatible(std::string &model\_version)  
Check if the model version is supported.

**Parameters** **model\_version** – [in] The model version.

**Returns** Whether the model is supported (true or false).



**Function `deepmd::name_prefix`**

- Defined in `file_source_api_cc_include_common.h`

**Function Documentation**

`std::string deepmd::name_prefix(const std::string &name_scope)`

**Function `deepmd::select_by_type`**

- Defined in `file_source_api_cc_include_common.h`

**Function Documentation**

`void deepmd::select_by_type(std::vector<int> &fwd_map, std::vector<int> &bkw_map, int &nghost_real, const std::vector<VALUE_TYPE> &dcoord_, const std::vector<int> &dtype_, const int &nghost, const std::vector<int> &sel_type_)`

**Template Function `deepmd::select_map(std::vector<VT>&, const std::vector<VT>&, const std::vector<int>&, const int&)`**

- Defined in `file_source_api_cc_include_common.h`

**Function Documentation**

`template<typename VT>  
void deepmd::select_map(std::vector<VT> &out, const std::vector<VT> &in, const std::vector<int> &fwd_map, const int &stride)`

**Template Function `deepmd::select_map(typename std::vector<VT>::iterator, const typename std::vector<VT>::const_iterator, const std::vector<int>&, const int&)`**

- Defined in `file_source_api_cc_include_common.h`

**Function Documentation**

`template<typename VT>  
void deepmd::select_map(typename std::vector<VT>::iterator out, const typename std::vector<VT>::const_iterator in, const std::vector<int> &fwd_map, const int &stride)`

**Template Function `deepmd::select_map_inv(std::vector<VT>&, const std::vector<VT>&, const std::vector<int>&, const int&)`**

- Defined in `file_source_api_cc_include_common.h`

### Function Documentation

```
template<typename VT>
void deepmd::select_map_inv(std::vector<VT> &out, const std::vector<VT> &in, const std::vector<int>
                           &fwd_map, const int &stride)
```

**Template Function `deepmd::select_map_inv(typename std::vector<VT>::iterator, const typename std::vector<VT>::const_iterator, const std::vector<int>&, const int&)`**

- Defined in `file_source_api_cc_include_common.h`

### Function Documentation

```
template<typename VT>
void deepmd::select_map_inv(typename std::vector<VT>::iterator out, const typename
                           std::vector<VT>::const_iterator in, const std::vector<int> &fwd_map, const int
                           &stride)
```

### Function `deepmd::select_real_atoms`

- Defined in `file_source_api_cc_include_common.h`

### Function Documentation

```
void deepmd::select_real_atoms(std::vector<int> &fwd_map, std::vector<int> &bkw_map, int &nghost_real,
                              const std::vector<VALUETYPE> &dcoord_, const std::vector<int> &dtype_,
                              const int &nghost, const int &ntypes)
```

### Template Function `deepmd::session_get_scalar`

- Defined in `file_source_api_cc_include_common.h`

## Function Documentation

```
template<typename VT>
VT deepmd::session_get_scalar(tensorflow::Session *session, const std::string name, const std::string scope =
    "")
```

## Template Function deepmd::session\_get\_vector

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

```
template<typename VT>
void deepmd::session_get_vector(std::vector<VT> &o_vec, tensorflow::Session *session, const std::string
    name_, const std::string scope = "")
```

**Function** `deepmd::session_input_tensors`(`std::vector<std::pair<std::string, tensorflow::Tensor>>&`, `const std::vector<VALUETYPE>&`, `const int&`, `const std::vector<int>&`, `const std::vector<VALUETYPE>&`, `const VALUETYPE&`, `const std::vector<VALUETYPE>&`, `const std::vector<VALUETYPE>&`, `const deepmd::AtomMap<VALUETYPE>&`, `const std::string`)

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

```
int deepmd::session_input_tensors(std::vector<std::pair<std::string, tensorflow::Tensor>> &input_tensors,
    const std::vector<VALUETYPE> &dcoord_, const int &ntypes, const
    std::vector<int> &dtype_, const std::vector<VALUETYPE> &dbox, const
    VALUETYPE &cell_size, const std::vector<VALUETYPE> &fparam_,
    const std::vector<VALUETYPE> &aparam_, const
    deepmd::AtomMap<VALUETYPE> &atommap, const std::string scope =
    "")
```

**Function** `deepmd::session_input_tensors`(`std::vector<std::pair<std::string, tensorflow::Tensor>>&`, `const std::vector<VALUETYPE>&`, `const int&`, `const std::vector<int>&`, `const std::vector<VALUETYPE>&`, `InputNlist&`, `const std::vector<VALUETYPE>&`, `const std::vector<VALUETYPE>&`, `const deepmd::AtomMap<VALUETYPE>&`, `const int`, `const int`, `const std::string`)

- Defined in file\_source\_api\_cc\_include\_common.h

## Function Documentation

```
int deepmd::session_input_tensors(std::vector<std::pair<std::string, tensorflow::Tensor>> &input_tensors,
                                   const std::vector<VALUETYPE> &dcoord_, const int &ntypes, const
                                   std::vector<int> &dtype_, const std::vector<VALUETYPE> &dbox,
                                   InputNlist &dlist, const std::vector<VALUETYPE> &fparam_, const
                                   std::vector<VALUETYPE> &aparam_, const
                                   deepmd::AtomMap<VALUETYPE> &atommap, const int nghost, const int
                                   ago, const std::string scope = "")
```

## 15.3.4 Typedefs

### Typedef deepmd::ENERGYTYPE

- Defined in file\_source\_api\_cc\_include\_common.h

#### Typedef Documentation

```
typedef double deepmd::ENERGYTYPE
```

### Typedef deepmd::STRINGTYPE

- Defined in file\_source\_api\_cc\_include\_common.h

#### Typedef Documentation

```
typedef std::string deepmd::STRINGTYPE
```

### Typedef deepmd::VALUETYPE

- Defined in file\_source\_api\_cc\_include\_common.h

#### Typedef Documentation

```
typedef float deepmd::VALUETYPE
```

## LICENSE

The project DeePMD-kit is licensed under [GNU LGPLv3.0](#).



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## 17.2 Other Credits

- Zhang ZiXuan for designing the Deepmodeling logo.
- Everyone on the *Deepmodeling mailing list* for contributing to many discussions and decisions!

(If you have contributed to the `deepmd-kit` core package and your name is missing, please send an email to the contributors, or open a pull request in the [deepmd-kit repository](#))

- `genindex`
- `modindex`
- `search`



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