

Example 2: Fingerprint atomic crystal structures and learning their energy

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The main objective of this example is to get a small dataset of atomic crystal structures and their energy, fingerprint them, and develop some ML models using different learning algorithms.

1. Download data

The dataset contains 329 equilibrium structures of 13 different stoichiometries of Mg and Si, whose energy was computed using DFT. This dataset was reported in [T. D. Huan, *Pressure-stabilized binary compounds of magnesium and silicon*, Phys. Rev. Materials 2, 023803 (2018)]. It will be obtained from www.matsml.org. More information on the available datasets can be found at www.matsml.org.

```
In [1]: from matsml.data import Datasets
import os
import pandas as pd

# Load data
ds_name='crystals_MgSi'
data=Datasets(ds_name)
data.load_dataset()

# have a look at the content
print(pd.read_csv(os.path.join(os.getcwd(),str(ds_name), 'summary.csv')))

matsml_v1.3.0
+-----+
| Load requested dataset(s) |
| Data saved in crystals_MgSi |
| File name: target |
+-----+
0  mgSi_struct_01.vasp  -8.034797
1  mgSi_struct_02.vasp  -34.985797
2  mgSi_struct_03.vasp  -17.246812
3  mgSi_struct_04.vasp  -34.062642
4  mgSi_struct_05.vasp  -34.035175
   ... .
324  mgSi_struct_30.vasp  -40.698471
325  mgSi_struct_31.vasp  -40.598719
326  mgSi_struct_32.vasp  -10.03077
327  mgSi_struct_33.vasp  -6.705934
328  mgSi_struct_34.vasp  -40.362384
[329 rows x 2 columns]
```

2. Fingerprint the obtained data

Two kinds of crystal fingerprints will be used in this example

1. Ewald sum matrix [F. Faber, A. Lindmaa, O. Anatole von Lilienfeld, and R. Armiento, *Crystal structure representations for machine learning models of formation energies* Int. J. Quantum Chem., 115, 1094 (2015)] is an analogy to the Coulomb matrix for molecules, and its size also depends on the number of atoms of the structure. We used a similar projection on a set of Gaussian. Keyword for this fingerprint is **pesm_crystals**.

2. Smooth Overlap of Atomic Positions (SOAP) [S. P. Bartok, G. Csanyi, and M. Ceriotti, *Comparing molecules and fingerprints: Different across the Ewald sum space*, Chem. Phys. Chem. 18, 13754 (2016)] is a more sophisticated fingerprint. Different from the Ewald sum matrix is defined for the whole system, SOAP is defined for each atom. Herein, for simplicity, the atomic fingerprints are added up to make the fingerprint for the whole system. In some ML potential, the SOAP fingerprints are used in a different way, involving the "atomic energy". The keyword for SOAP in matsML is **soap_crystals**.

```
In [2]: import os
import pandas as pd
from matsml.fingerprint import Fingerprint
summary=os.path.join(os.getcwd(), 'crystals_MgSi/summary.csv')
data_loc = os.path.join(os.getcwd(), 'crystals_MgSi')
fp_dim=26 # intended fingerprint dimensionality
verbosity=0 # verbosity, 0 or 1

# Ewald sum matrix
data_params_pesm = {
    'summary': summary,
    'data_loc': data_loc,
    'fp_file': 'fp_crystals_MgSi_pesm.csv',
    'fp_dim': fp_dim,
    'verbosity': verbosity,
}

fp_pesm = Fingerprint(data_params_pesm)
fp_pesm.get_fingerprint()

# SOAP
data_params_soap = {
    'summary': summary,
    'data_loc': data_loc,
    'fp_file': 'fp_crystals_MgSi_soap.csv',
    'fp_dim': fp_dim,
    'verbosity': verbosity,
}

fp_soap = Fingerprint(data_params_soap)
fp_soap.get_fingerprint()

Atomic structure fingerprinting
summary           /home/huantran/work_local/matsml/examples/ex3_crystals/crystals_MgSi/summary.csv
sv
data_loc          /home/huantran/work_local/matsml/examples/ex3_crystals/crystals_MgSi
fp_type           rbf
fp_file           fp_crystals_MgSi_pesm.csv
fp_dim            26
verbosity         0
Read input
num_structs      329
Computing Ewald sum Matrix
[=====] 100%
Projecting Ewald sum matrix to create fingerprints
[=====] 100%
Done fingerprinting, results saved in fp_crystals_MgSi_pesm.csv
Atomic structure fingerprinting
summary           /home/huantran/work_local/matsml/examples/ex3_crystals/crystals_MgSi/summary.csv
sv
data_loc          /home/huantran/work_local/matsml/examples/ex3_crystals/crystals_MgSi
fp_type           soap_crystals
fp_file           fp_crystals_MgSi_soap.csv
fp_dim            26
verbosity         0
Read input
num_structs      329
Computing SOAP fingerprint with Dscribe
[=====] 100%
Done fingerprinting, results saved in fp_crystals_MgSi_soap.csv
```

The fingerprinting step maybe a bit slow for a tutorial because we need to set **n_atoms_max=28**, which results in quite large Ewald sum matrices. A version of fingerprinted data can also be obtained in case you want to skip this step.

```
In [3]: from matsml.data import Datasets
import os
import pandas as pd

# Load data
data=Datasets(ds_name)
data.load_dataset()

print(os.path.isfile('fp_crystals_MgSi_soap.gz'), os.path.isfile('fp_crystals_MgSi_pesm.gz'))
Load requested dataset(s)
Data saved in fp_crystals_MgSi_soap.csv.gz
Data saved in fp_crystals_MgSi_pesm.csv.gz
True
```

3. Train several ML models with two fingerprint files just created

```
In [4]: # data parameters for learning
id_col = ['id'] # ID column in the fingerprint data
y_col = ['target'] # target (y) column(s)
comment_cols = [] # columns not used as id, x, or y
n_trains = 0.9 # % for training, 10% for validating
sampling = 'random' # method for train/test splitting
x_scaling = 'minmax'
y_scaling = 'minmax'

data_params_pesm = {
    'data_file': 'fp_crystals_MgSi_pesm.csv',
    'id_col': id_col,
    'y_col': y_col,
    'comment_cols': comment_cols,
    'x_scaling': x_scaling,
    'y_scaling': y_scaling,
    'sampling': sampling,
    'n_trains': n_trains,
}

data_params_soap = {
    'data_file': 'fp_crystals_MgSi_soap.csv',
    'id_col': id_col,
    'y_col': y_col,
    'comment_cols': comment_cols,
    'x_scaling': x_scaling,
    'y_scaling': x_scaling,
    'sampling': sampling,
    'n_trains': n_trains,
}
```

3a. Fully-connected NeuralNet

```
In [5]: from matsml.models import FCNN
# Model parameters
layers = [4, 4] # list of nodes in hidden layers
epochs = 2000 # Epochs
nfold_cv = 5 # Number of folds for cross validation
use_bias = True # Use bias term or not
model_file = 'model_nn.pkl' # Name of the model file to be created
verbosity = 0 # Verbosity, 0 or 1
batch_size = 32 # Default batch size
loss = 'mse' # Loss function
activ_func = 'selu' # Options: "tanh", "relu", and more
optimizer = 'adam' # Options: "Nadam", "Adam", and more

model_params = {
    'layers': layers,
    'activ_func': activ_func,
    'nfold_cv': nfold_cv,
    'optimizer': optimizer,
    'use_bias': use_bias,
    'model_file': model_file,
    'loss': loss,
    'batch_size': batch_size,
    'verbosity': verbosity,
    'mse_cv': False,
}
```

```
# PESM
model = FCNN(data_params=data_params_pesm, model_params=model_params)
model.train()
model.plot(pdf_output=False)

Checking parameters
model_file not ends with ".weights.h5", renamed
Learning fingerprinted/featured data
algorithm          fully connected NeuralNet w/ TensorFlow
layers             [4, 4]
activ_func         selu
epochs             2000
optimizer          nadam
nfold_cv           5
verbosity          0

Read data
data_file          fp_crystals_MgSi_pesm.csv
data_size          329
training_size     98.0 %
test_size          10.0 %
x_dimensionality  19
y_dimensionality  1
y_label(s)        ['target']

Scaling x
xscaler saved in xscaler.pkl
Scaling y
minmax
```

```
Prepare train/test sets
random
Building model
FCNN
Training model w/ cross validation
[=====] 100%
Training model w/ cross validation
[=====] 100%
Done training, now make predictions & invert scaling
uncalculating y: minmax
uncalculating y: target
rmse training: 0.000000
rmse test: 0.000000
predictions made & saved in "training.csv" & "test.csv"

Plot results in "training.csv" & "test.csv"
training, (rmse & R2) = ( 0.250 & 1.000 )
test, (rmse & R2) = ( 0.388 & 1.000 )
showing target
```

3b. KRR

```
In [6]: from matsml.data import KRR
# Model parameters
nfold_cv = 5 # Number of folds for cross validation
model_file = 'model_krr.pkl' # Name of the model file to be created
verbosity = 0
rmse_cv = False
n_restarts_optimizer = 200

model_params = {
    'nfold_cv': nfold_cv,
    'model_file': model_file,
    'alpha': alpha,
    'gamma': gamma,
    'n_grids': n_grids,
    'kernel': 'rbf'
}
```

```
# SOAP
model = KRR(data_params=data_params_soap, model_params=model_params)
model.train()
model.plot(pdf_output=False)

Checking parameters
model_file not ends with ".weights.h5", renamed
Learning fingerprinted/featured data
algorithm          kernel ridge regression w/ scikit-learn
kernel             rbf
nfold_cv           5
optimizer          nadam
alpha              [-2, 5]
gamma              [-2, 5]
number of alpha/gamma grids 10

Read data
data_file          fp_crystals_MgSi_soap.csv
data_size          329
training_size     98.0 %
test_size          10.0 %
x_dimensionality  19
y_dimensionality  1
y_label(s)        ['target']

Scaling x
xscaler saved in xscaler.pkl
Scaling y
minmax
```

```
Prepare train/test sets
random
Building model
KRR
Training model w/ cross validation
[=====] 100%
KRR model trained, now make predictions & invert scaling
uncalculating y: minmax
uncalculating y: target
rmse training: 0.000000
rmse test: 0.000000
predictions made & saved in "training.csv" & "test.csv"

Plot results in "training.csv" & "test.csv"
training, (rmse & R2) = ( 0.204 & 0.999 )
test, (rmse & R2) = ( 0.319 & 0.999 )
showing target
```

3c. GPR

```
In [7]: from matsml.models import GPR
# Model parameters
nfold_cv = 5 # Number of folds for cross validation
model_file = 'model_gpr.pkl' # Name of the model file to be created
verbosity = 0
rmse_cv = False
n_restarts_optimizer = 200

model_params = {
    'nfold_cv': nfold_cv,
    'model_file': model_file,
    'alpha_l': alpha_l,
    'alpha_u': alpha_u,
    'gamma': gamma,
    'n_grids': n_grids,
    'kernel': 'rbf'
}
```

```
# SOAP
model = GPR(data_params=data_params_soap, model_params=model_params)
model.train()
model.plot(pdf_output=False)

Checking parameters
model_file not ends with ".weights.h5", renamed
Learning fingerprinted/featured data
algorithm          gaussian process regression w/ scikit-learn
kernel             rbf
nfold_cv           5
optimizer          nadam
alpha_l             200
alpha_u             200
gamma              [-2, 5]
noise_lb            10
noise_ub            10
n_restarts_cv       20
rmse_cv              False

Read data
data_file          fp_crystals_MgSi_soap.csv
data_size          329
training_size     98.0 %
test_size          10.0 %
x_dimensionality  19
y_dimensionality  1
y_label(s)        ['target']

Scaling x
xscaler saved in xscaler.pkl
Scaling y
minmax
```

```
Prepare train/test sets
random
Building model
GPR
Training model w/ cross validation
[=====] 100%
GPR model trained, now make predictions & invert scaling
uncalculating y: minmax
uncalculating y: target
rmse training: 0.000000
rmse test: 0.000000
predictions made & saved in "training.csv" & "test.csv"

Plot results in "training.csv" & "test.csv"
training, (rmse & R2) = ( 0.228 & 0.999 )
test, (rmse & R2) = ( 0.324 & 0.999 )
showing target
```

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