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# **pyscal Documentation**

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## Contents

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<b>1</b>	<b>Highlights</b>	<b>3</b>
<b>2</b>	<b>Getting started</b>	<b>5</b>
2.1	Installation . . . . .	5
<b>3</b>	<b>Download</b>	<b>9</b>
3.1	Downloads . . . . .	9
<b>4</b>	<b>Examples</b>	<b>11</b>
4.1	Examples . . . . .	11
<b>5</b>	<b>Methods implemented in pyscal</b>	<b>37</b>
5.1	Methods implemented in pyscal . . . . .	37
<b>6</b>	<b>News and updates</b>	<b>45</b>
6.1	News and updates . . . . .	45
<b>7</b>	<b>pyscal reference</b>	<b>47</b>
7.1	pyscal reference . . . . .	47
<b>8</b>	<b>Support, contributing and extending</b>	<b>67</b>
8.1	Support, contributing and extending . . . . .	67
8.2	Help and support . . . . .	68
8.3	Common issues . . . . .	68
<b>9</b>	<b>Credits</b>	<b>69</b>
9.1	Citing the code . . . . .	69
9.2	Developers . . . . .	69
9.3	Contributers . . . . .	69
9.4	Acknowledgements . . . . .	69
<b>10</b>	<b>License</b>	<b>71</b>
10.1	pyscal License . . . . .	71
	<b>Python Module Index</b>	<b>75</b>
	<b>Index</b>	<b>77</b>



**pyscal** is a python module for the calculation of local atomic structural environments including Steinhardt's bond orientational order parameters<sup>1</sup> during post-processing of atomistic simulation data. The core functionality of pyscal is written in C++ with python wrappers using [pybind11](#) which allows for fast calculations and easy extensions in python.

Steinhardt's order parameters are widely used for the identification of crystal structures<sup>3</sup>. They are also used to distinguish if an atom is in a solid or liquid environment<sup>4</sup>. pyscal is inspired by the [BondOrderAnalysis](#) code, but has since incorporated many additional features and modifications. The pyscal module includes the following functionalities:

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<sup>1</sup> Steinhardt, P. J., Nelson, D. R., & Ronchetti, M. (1983). *Physical Review B*, 28.

<sup>3</sup> Mickel, W., Kapfer, S. C., Schröder-Turk, G. E., & Mecke, K. (2013). *The Journal of Chemical Physics*, 138.

<sup>4</sup> Auer, S., & Frenkel, D. (2005). *Advances in Polymer Science*, 173.



# CHAPTER 1

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## Highlights

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- calculation of Steinhardt's order parameters and their averaged version<sup>2</sup>.
- links with the `Voro++` code, for the calculation of Steinhardt parameters weighted using the face areas of Voronoi polyhedra<sup>3</sup>.
- classification of atoms as solid or liquid<sup>4</sup>.
- clustering of particles based on a user defined property.
- methods for calculating radial distribution functions, Voronoi volumes of particles, number of vertices and face area of Voronoi polyhedra, and coordination numbers.
- calculation of angular parameters to identify diamond structure<sup>5</sup>.

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<sup>2</sup> Lechner, W., & Dellago, C. (2008). *The Journal of Chemical Physics*, 129.

<sup>5</sup> Uttormark, M. J., Thompson, M. O., Clancy, P. (1993). *Physical Review B*, 47.





## 2.1 Installation

### 2.1.1 Trying pyscal

You can try some examples provided with pyscal using [Binder](#) without installing the package. Please use [this link](#) to try the package.

### 2.1.2 Supported operating systems

pyscal can be installed on both Linux and Mac OS based systems. For Windows systems, we recommend using Bash on Windows. Please check [this tutorial](#) on how to set up Bash on Windows.

### 2.1.3 Installation using conda

pyscal can be installed directly using [Conda](#) from the [conda-forge channel](#) by the following statement-

```
conda install -c conda-forge pyscal
```

This is the recommended way to install if you have an [Anaconda](#) distribution.

The above command installs the [latest release version](#) of pyscal.

pyscal is no longer maintained for Python 2.

### 2.1.4 Quick installation

pyscal can be installed using the following steps-

- Download an archive of the pyscal library from [here](#).
- Extract the downloaded version. From the extracted folder, run, `python setup.py install --user`

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**Tip:** Pyscal can be installed system-wide using `python setup.py install`.

---

## 2.1.5 Installation from the repository

pyscal can be built from the repository by-

```
git clone https://github.com/srmnitc/pyscal.git
cd pyscal
python setup.py install --user
```

## 2.1.6 Using a conda environment

pyscal can also be installed in a conda environment, making it easier to manage dependencies. A python3 Conda environment can be created by,

```
conda create -n myenv python=3
```

Once created, the environment can be activated using,

```
conda activate myenv
```

In case Cmake and C++11 are not available, these can be installed using,

```
(myenv) conda install -c anaconda gcc
(myenv) conda install -c anaconda cmake
```

Now the pyscal repository can be cloned and the module can be installed. Python dependencies are installed automatically.

```
(myenv) git clone https://github.com/srmnitc/pyscal.git
(myenv) cd pyscal
(myenv) python setup.py install
```

---

**Tip:** A good guide on managing Conda environments is available [here](#).

---

## 2.1.7 Dependencies

Dependencies for the C++ part

- [Cmake](#)
- [C++ 11](#)

Dependencies for the python part

- [numpy](#)

Optional dependencies

- [pytest](#)
- [matplotlib](#)

## 2.1.8 Tests

In order to see if the installation worked, the following commands can be tried-

```
import pyscal.core as pc
pc.test()
```

The above code does some minimal tests and gives a value of `True` if `pyscal` was installed successfully. However, `pyscal` also contains automated tests which use the `pytest` python library, which can be installed by `pip install pytest`. The tests can be run by executing the command `pytest tests/` from the main code directory.

It is good idea to run the tests to check if everything is installed properly.



## 3.1 Downloads

The source code is available in latest stable or release versions. We recommend using the latest stable version for all updated features.

### 3.1.1 Source code

- latest stable version of pysical (tar.gz)
- release version (zip)

### 3.1.2 Documentation

- PDF version
- Epub version

### 3.1.3 Publication

- Publication
- citation



## 4.1 Examples

Different examples illustrating the functionality of this module is provided in this section. Interactive versions of these examples can be launched [here](#).

Examples are designed to run on [jupyter notebooks](#). A good tutorial on jupyter notebooks can be found [here](#). All files used in the examples can be found in `examples/` folder of the main [repository](#). A copy of the repository can be downloaded from [here](#).

### 4.1.1 Using pyscal

#### Getting started with pyscal

This example illustrates basic functionality of pyscal python library by setting up a system and the atoms.

```
import pyscal.core as pc
import numpy as np
```

#### The `System` class

`System` is the basic class of pyscal and is required to be setup in order to perform any calculations. It can be set up as-

```
sys = pc.System()
```

`sys` is a `System` object. But at this point, it is completely empty. We have to provide the system with the following information-

- the simulation box dimensions

- the positions of individual atoms.

Let us try to set up a small system, which is the bcc unitcell of lattice constant 1. The simulation box dimensions of such a unit cell would be `[[0.0, 1.0], [0.0, 1.0], [0.0, 1.0]]` where the first set correspond to the x axis, second to y axis and so on. The unitcell has 2 atoms and their positions are `[0,0,0]` and `[0.5, 0.5, 0.5]`.

```
sys.box = [[0.0, 1.0], [0.0, 1.0], [0.0, 1.0]]
```

We can easily check if everything worked by getting the box dimensions

```
sys.box
```

```
[[0.0, 1.0], [0.0, 1.0], [0.0, 1.0]]
```

### The `Atom` class

The next part is assigning the atoms. This can be done using the `Atom` class. Here, we will only look at the basic properties of `Atom` class. For a more detailed description, check the [documentation](#). Now let us create two atoms.

```
atom1 = pc.Atom()  
atom2 = pc.Atom()
```

Now two empty atom objects are created. The basic properties of an atom are its positions and id. There are various other properties which can be set here. A detailed description can be found [here](#).

```
atom1.pos = [0., 0., 0.]  
atom1.id = 0  
atom2.pos = [0.5, 0.5, 0.5]  
atom2.id = 1
```

Alternatively, atom objects can also be set up as

```
atom1 = pc.Atom(pos=[0., 0., 0.], id=0)  
atom2 = pc.Atom(pos=[0.5, 0.5, 0.5], id=1)
```

We can check the details of the atom by querying it

```
atom1.pos
```

```
[0.0, 0.0, 0.0]
```

### Combining `System` and `Atom`

Now that we have created the atoms, we can assign them to the system. We can also assign the same box we created before.

```
sys = pc.System()  
sys.atoms = [atom1, atom2]  
sys.box = [[0.0, 1.0], [0.0, 1.0], [0.0, 1.0]]
```

That sets up the system completely. It has both of its constituents - atoms and the simulation box. We can check if everything works correctly.



```
sys.atoms
```

```
[<pyscal.catom.Atom at 0x7fb343025830>, <pyscal.catom.Atom at 0x7fb343025b30>]
```

This returns all the atoms of the system. Alternatively a single atom can be accessed by,

```
atom = sys.get_atom(1)
```

The above call will fetch the atom at position 1 in the list of all atoms in the system.

Once you have all the atoms, you can modify any one and add it back to the list of all atoms in the system. The following statement will set the type of the first atom to 2.

```
atom = sys.atoms[0]
atom.type = 2
```

Lets verify if it was done properly

```
atom.type
```

```
2
```

Now we can push the atom back to the system with the new type

```
sys.set_atom(atom)
```

**Warning:** Due to Atom being a completely C++ class, it is necessary to use `get_atom()` and `set_atom()` to access individual atoms and set them back into the system object after modification. A list of all atoms however can be accessed directly by `atoms`

## Reading in an input file

We are all set! The *System* is ready for calculations. However, in most realistic simulation situations, we have many atoms and it can be difficult to set each of them individually. In this situation we can read in input file directly. An example input file containing 500 atoms in a simulation box can be read in automatically. The file we use for this example is a file of the `lammps-dump` format. `pyscal` can also read in POSCAR files. In principle, `pyscal` only needs the atom positions and simulation box size, so you can write a python function to process the input file, extract the details and pass to `pyscal`.

```
sys = pc.System()
sys.read_inputfile('conf.dump')
```

Once again, lets check if the box dimensions are read in correctly

```
sys.box
```

```
[[-7.66608, 11.1901], [-7.66915, 11.1931], [-7.74357, 11.2676]]
```

Now we can get all atoms that belong to this system

```
len(sys.atoms)
```

```
500
```

We can see that all the atoms are read in correctly and there are 500 atoms in total. Once again, individual atom properties can be accessed as before.

```
sys.atoms[0].pos
```

```
[-5.66782, -6.06781, -6.58151]
```

That's it! Now we are ready for some calculations. You can find more in the examples section of the documentation.

## 4.1.2 Finding nearest neighbors

### Find neighbors of an atom and calculating coordination numbers

In this example, we will read in a configuration from an MD simulation and then calculate the coordination number distribution. This example assumes that you read the [basic example](#).

```
import pyscal.core as pc
import numpy as np
import matplotlib.pyplot as plt
```

#### Read in a file

The first step is setting up a system. We can create atoms and simulation box using the `crystal_structures` module. Let us start by importing the module.

```
import pyscal.crystal_structures as pcs
```

```
atoms, box = pcs.make_crystal('bcc', lattice_constant= 4.00, repetitions=[6,6,6])
```

The above function creates an bcc crystal of 6x6x6 unit cells with a lattice constant of 4.00 along with a simulation box that encloses the particles. We can then create a *System* and assign the atoms and box to it.

```
sys = pc.System()
sys.atoms = atoms
sys.box = box
```

#### Calculating neighbors

We start by calculating the neighbors of each atom in the system. There are two ways to do this, using a `cutoff` method and using a `voronoi` polyhedra method. We will try with both of them. First we try with `cutoff` system - which has three sub options. We will check each of them in detail.

#### Cutoff method

Cutoff method takes cutoff distance value and finds all atoms within the cutoff distance of the host atom.

```
sys.find_neighbors(method='cutoff', cutoff=4.1)
```

Now lets get all the atoms.

```
atoms = sys.atoms
```

let us try accessing the coordination number of an atom

```
atoms[0].coordination
```

```
14
```

As we would expect for a bcc type lattice, we see that the atom has 14 neighbors (8 in the first shell and 6 in the second). Lets try a more interesting example by reading in a bcc system with thermal vibrations. Thermal vibrations lead to distortion in atomic positions, and hence there will be a distribution of coordination numbers.

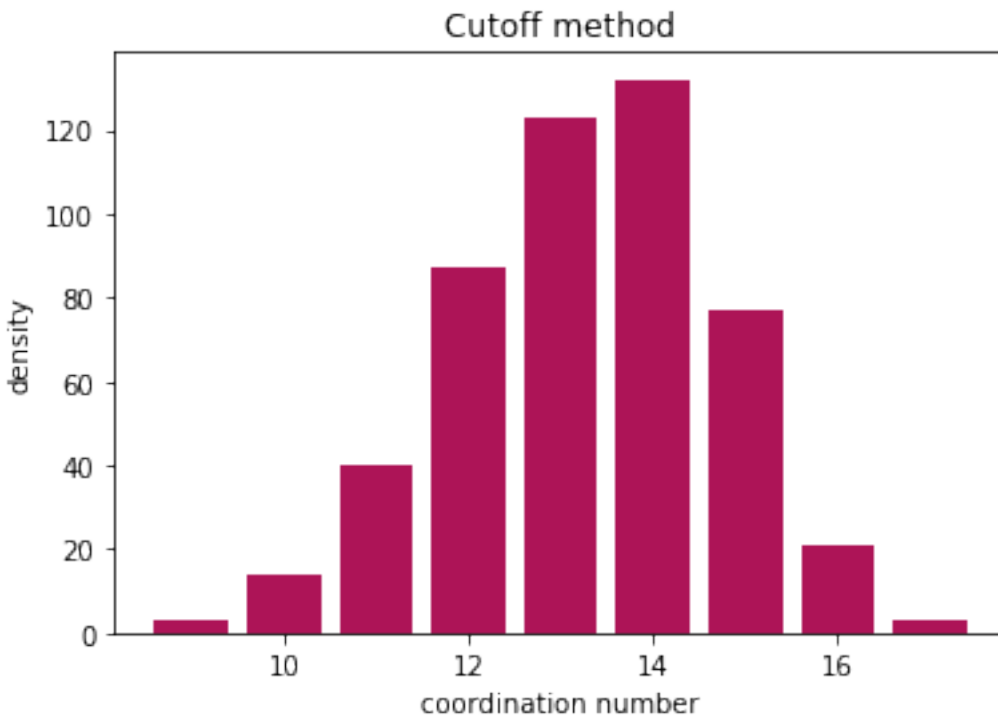
```
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff=3.6)
atoms = sys.atoms
```

We can loop over all atoms and create a histogram of the results

```
coord = [atom.coordination for atom in atoms]
```

Now lets plot and see the results

```
nos, counts = np.unique(coord, return_counts=True)
plt.bar(nos, counts, color="#AD1457")
plt.ylabel("density")
plt.xlabel("coordination number")
plt.title("Cutoff method")
```



## Adaptive cutoff methods

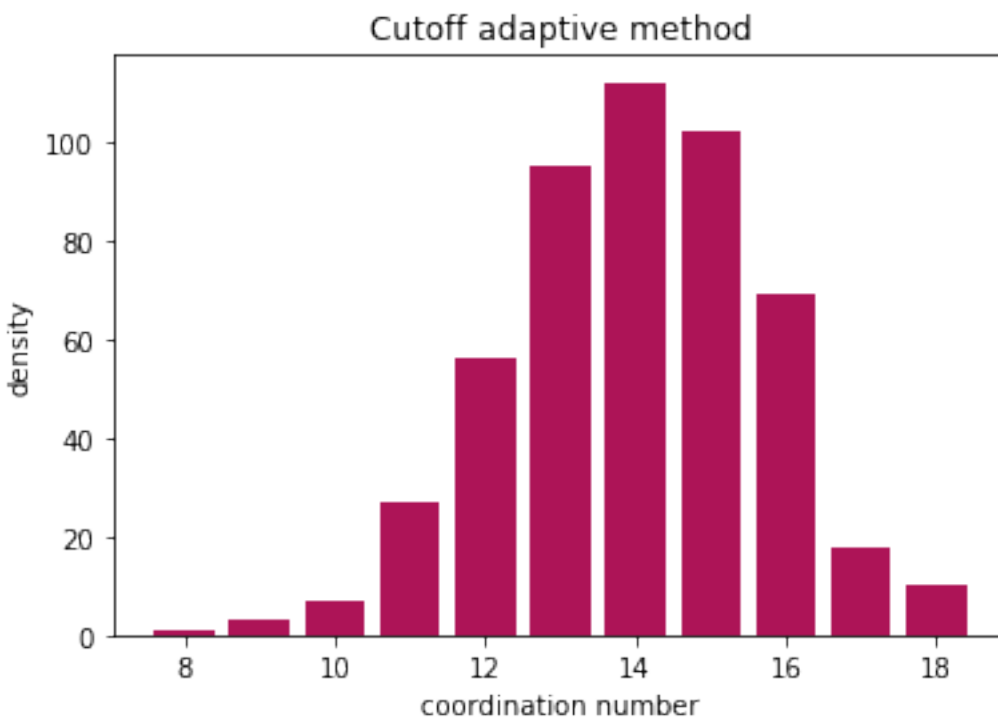
pyscal also has adaptive cutoff methods implemented. These methods remove the restriction on having a global cutoff. A distinct cutoff is selected for each atom during runtime. pyscal uses two distinct algorithms to do this - sann and adaptive. Please check the [documentation](#) for a explanation of these algorithms. For the purpose of this example, we will use the adaptive algorithm.

### adaptive algorithm

```
sys.find_neighbors(method='cutoff', cutoff='adaptive', padding=1.5)
atoms = sys.atoms
coord = [atom.coordination for atom in atoms]
```

Now let us plot

```
nos, counts = np.unique(coord, return_counts=True)
plt.bar(nos, counts, color="#AD1457")
plt.ylabel("density")
plt.xlabel("coordination number")
plt.title("Cutoff adaptive method")
```



The adaptive method also gives similar results!

### Voronoi method

Voronoi method calculates the voronoi polyhedra of all atoms. Any atom that shares a voronoi face area with the host atom are considered neighbors. Voronoi polyhedra is calculated using the [Voro++](#) code. However, you do not need to install this specifically as it is linked to pyscal.

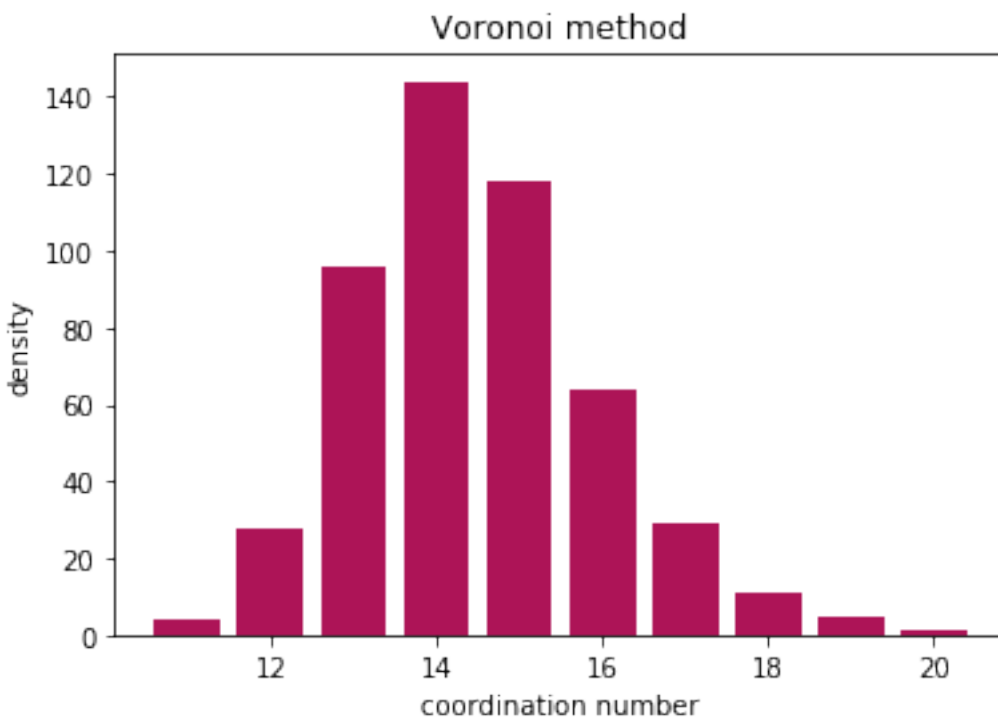
```
sys.find_neighbors(method='voronoi')
```

Once again, let us get all atoms and find their coordination

```
atoms = sys.atoms
coord = [atom.coordination for atom in atoms]
```

And visualise the results

```
nos, counts = np.unique(coord, return_counts=True)
plt.bar(nos, counts, color="#AD1457")
plt.ylabel("density")
plt.xlabel("coordination number")
plt.title("Voronoi method")
```



Finally..

All methods find the coordination number, and the results are comparable. Cutoff method is very sensitive to the choice of cutoff radius, but Voronoi method can slightly overestimate the neighbors due to thermal vibrations.

### 4.1.3 Steinhardt parameters

#### Calculating bond orientational order parameters

This example illustrates the calculation of bond orientational order parameters. Bond order parameters,  $q_l$  and their averaged versions,  $\bar{q}_l$  are widely used to identify atoms belong to different crystal structures. In this example, we will consider MD snapshots for bcc, fcc, hcp and liquid, and calculate the  $q_4$  and  $q_6$  parameters and their averaged versions which are widely used in literature. More details can be found [here](#).

```
import pyscal.core as pc
import pyscal.crystal_structures as pcs
import numpy as np
import matplotlib.pyplot as plt
```

In this example, we analyse MD configurations, first a set of perfect bcc, fcc and hcp structures and another set with thermal vibrations.

## Perfect structures

To create atoms and box for perfect structures, the `crystal_structures` module is used. The created atoms and boxes are then assigned to `System` objects.

```
bcc_atoms, bcc_box = pcs.make_crystal('bcc', lattice_constant=3.147, repetitions=[4,4,
↪4])
bcc = pc.System()
bcc.atoms = bcc_atoms
bcc.box = bcc_box
```

```
fcc_atoms, fcc_box = pcs.make_crystal('fcc', lattice_constant=3.147, repetitions=[4,4,
↪4])
fcc = pc.System()
fcc.atoms = fcc_atoms
fcc.box = fcc_box
```

```
hcp_atoms, hcp_box = pcs.make_crystal('hcp', lattice_constant=3.147, repetitions=[4,4,
↪4])
hcp = pc.System()
hcp.atoms = hcp_atoms
hcp.box = hcp_box
```

Next step is calculation of nearest neighbors. There are two ways to calculate neighbors, by using a cutoff distance or by using the voronoi cells. In this example, we will use the cutoff method and provide a cutoff distance for each structure.

## Finding the cutoff distance

The cutoff distance is normally calculated in a such a way that the atoms within the first shell is incorporated in this distance. The `calculate_rdf()` function can be used to find this cutoff distance.

```
bccrdf = bcc.calculate_rdf()
fccrdf = fcc.calculate_rdf()
hcprdf = hcp.calculate_rdf()
```

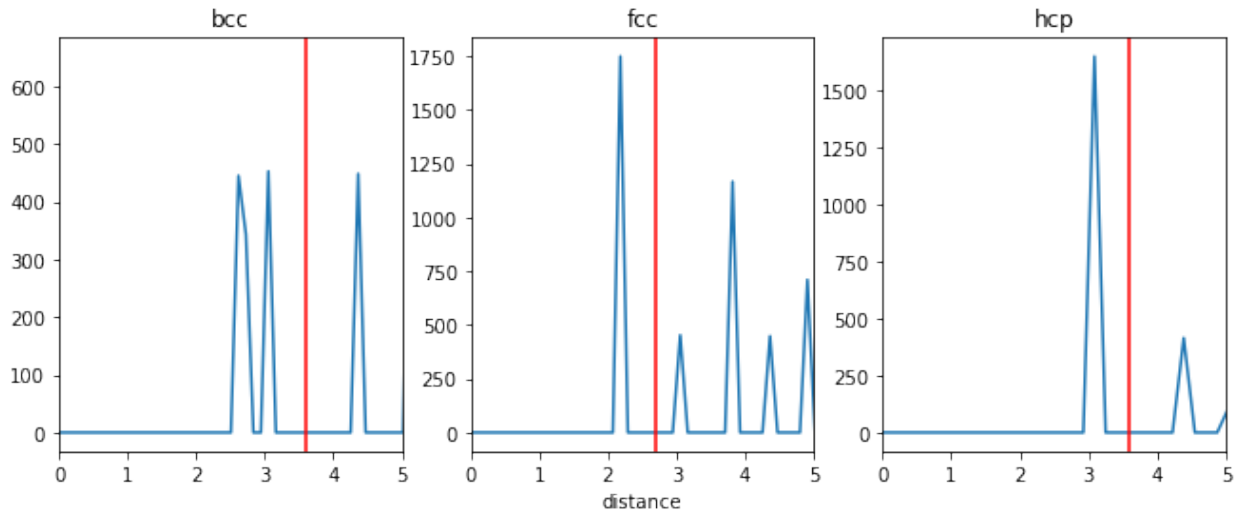
Now the calculated rdf is plotted

```
fig, (ax1, ax2, ax3) = plt.subplots(1, 3, figsize=(11,4))
ax1.plot(bccrdf[1], bccrdf[0])
ax2.plot(fccrdf[1], fccrdf[0])
ax3.plot(hcprdf[1], hcprdf[0])
ax1.set_xlim(0,5)
ax2.set_xlim(0,5)
ax3.set_xlim(0,5)
```

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```
ax1.set_title('bcc')
ax2.set_title('fcc')
ax3.set_title('hcp')
ax2.set_xlabel("distance")
ax1.axvline(3.6, color='red')
ax2.axvline(2.7, color='red')
ax3.axvline(3.6, color='red')
```



The selected cutoff distances are marked in red in the above plot. For bcc, since the first two shells are close to each other, for this example, we will take the cutoff in such a way that both shells are included.

### Steinhardt's parameters - cutoff neighbor method

```
bcc.find_neighbors(method='cutoff', cutoff=3.6)
fcc.find_neighbors(method='cutoff', cutoff=2.7)
hcp.find_neighbors(method='cutoff', cutoff=3.6)
```

We have used a cutoff of 3 here, but this is a parameter that has to be tuned. Using a different cutoff for each structure is possible, but it would complicate the method if the system has a mix of structures. Now we can calculate the  $q_4$  and  $q_6$  distributions

```
bcc.calculate_q([4, 6])
fcc.calculate_q([4, 6])
hcp.calculate_q([4, 6])
```

That's it! Now let's gather the results and plot them.

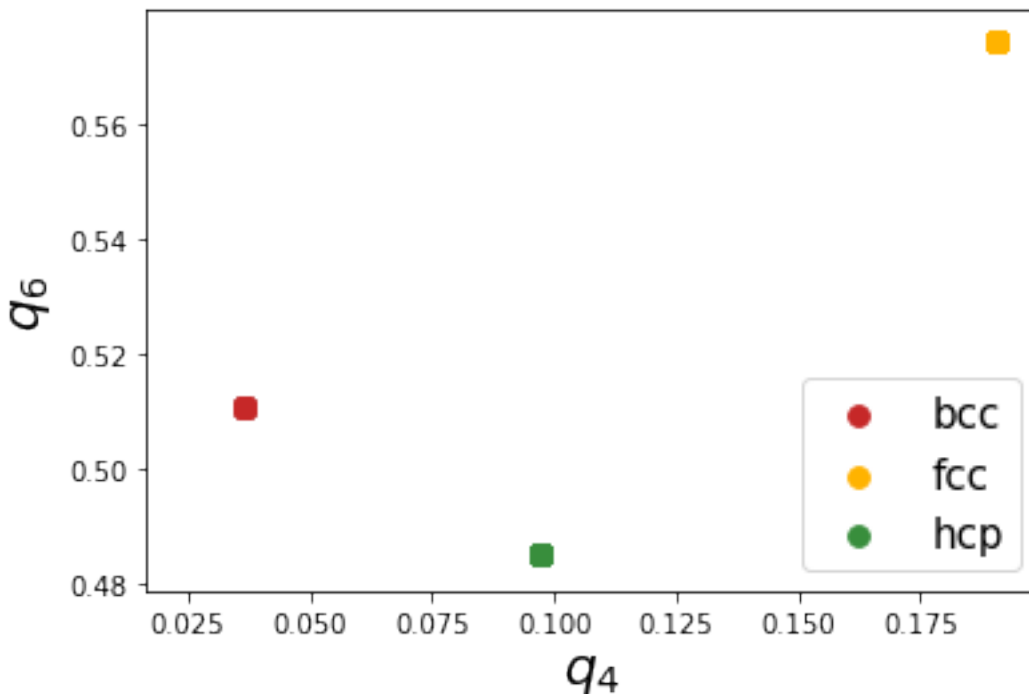
```
bccq = bcc.get_qvals([4, 6])
fccq = fcc.get_qvals([4, 6])
hcpq = hcp.get_qvals([4, 6])
```

```
plt.scatter(bccq[0], bccq[1], s=60, label='bcc', color='#C62828')
plt.scatter(fccq[0], fccq[1], s=60, label='fcc', color='#FFB300')
plt.scatter(hcpq[0], hcpq[1], s=60, label='hcp', color='#388E3C')
plt.xlabel("$q_4$", fontsize=20)
```

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```
plt.ylabel("$q_6$", fontsize=20)
plt.legend(loc=4, fontsize=15)
```



Firstly, we can see that Steinhardt parameter values of all the atoms fall on one specific point which is due to the absence of thermal vibrations. Next, all the points are well separated and show good distinction. However, at finite temperatures, the atomic positions are affected by thermal vibrations and hence show a spread in the distribution. We will show the effect of thermal vibrations in the next example.

### Structures with thermal vibrations

Once again, we create the reqd structures using the `crystal_structures` module. Noise can be applied to atomic positions using the `noise` keyword as shown below.

```
bcc_atoms, bcc_box = pcs.make_crystal('bcc', lattice_constant=3.147, repetitions=[10,
↪10,10], noise=0.01)
bcc = pc.System()
bcc.atoms = bcc_atoms
bcc.box = bcc_box
```

```
fcc_atoms, fcc_box = pcs.make_crystal('fcc', lattice_constant=3.147, repetitions=[10,
↪10,10], noise=0.01)
fcc = pc.System()
fcc.atoms = fcc_atoms
fcc.box = fcc_box
```

```
hcp_atoms, hcp_box = pcs.make_crystal('hcp', lattice_constant=3.147, repetitions=[10,
↪10,10], noise=0.01)
hcp = pc.System()
```

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```
hcp.atoms = hcp_atoms
hcp.box = hcp_box
```

### cutoff method

```
bcc.find_neighbors(method='cutoff', cutoff=3.6)
fcc.find_neighbors(method='cutoff', cutoff=2.7)
hcp.find_neighbors(method='cutoff', cutoff=3.6)
```

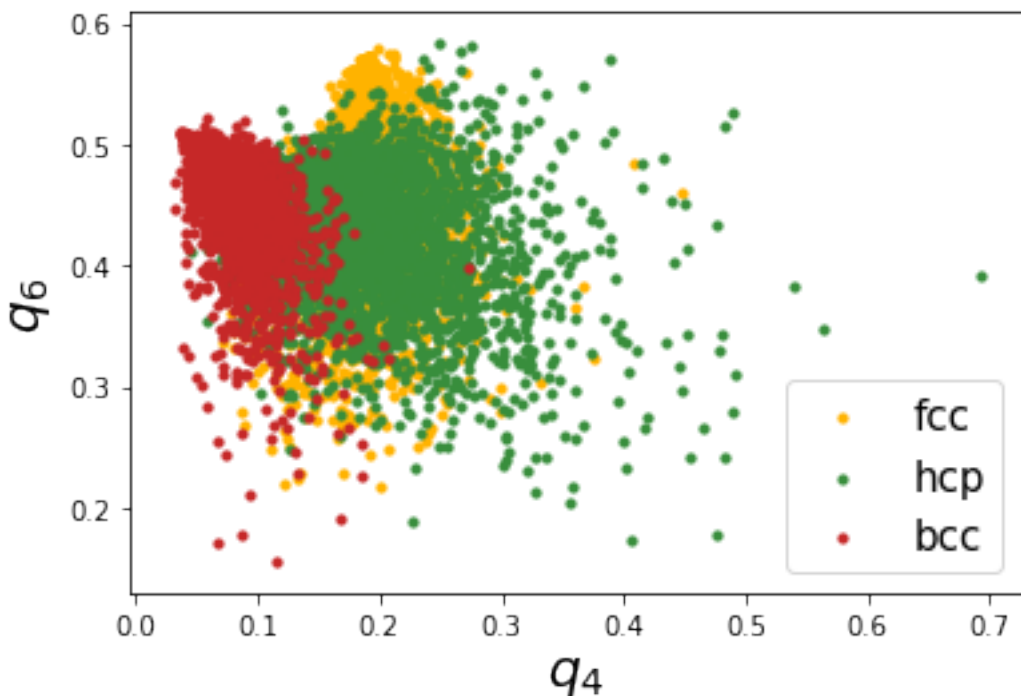
And now, calculate  $q_4$ ,  $q_6$  parameters

```
bcc.calculate_q([4,6])
fcc.calculate_q([4,6])
hcp.calculate_q([4,6])
```

Gather the q vales and plot them

```
bccq = bcc.get_qvals([4, 6])
fccq = fcc.get_qvals([4, 6])
hcpq = hcp.get_qvals([4, 6])
```

```
plt.scatter(fccq[0], fccq[1], s=10, label='fcc', color='#FFB300')
plt.scatter(hcpq[0], hcpq[1], s=10, label='hcp', color='#388E3C')
plt.scatter(bccq[0], bccq[1], s=10, label='bcc', color='#C62828')
plt.xlabel("$q_4$", fontsize=20)
plt.ylabel("$q_6$", fontsize=20)
plt.legend(loc=4, fontsize=15)
```



This is not so great as the first case, we can see that the thermal vibrations cause the distributions to spread a lot and

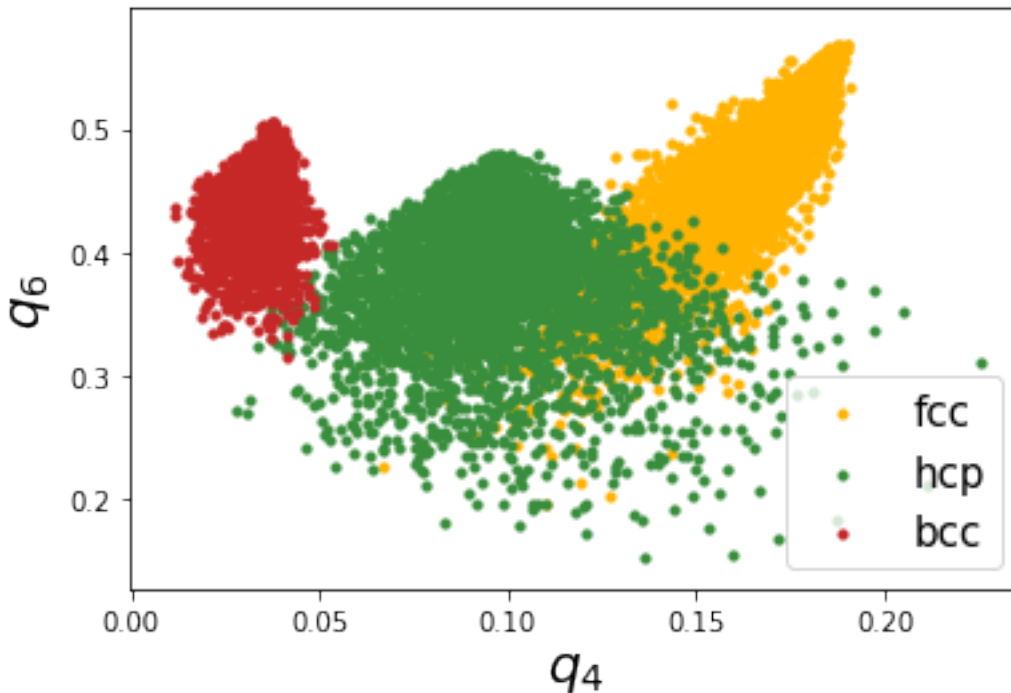
overlap with each other. Lechner and Dellago proposed using the averaged distributions,  $\bar{q}_4 - \bar{q}_6$  to better distinguish the distributions. Lets try that.

```
bcc.calculate_q([4,6], averaged=True)
fcc.calculate_q([4,6], averaged=True)
hcp.calculate_q([4,6], averaged=True)
```

```
bccaq = bcc.get_qvals([4, 6], averaged=True)
fccaq = fcc.get_qvals([4, 6], averaged=True)
hcpaq = hcp.get_qvals([4, 6], averaged=True)
```

Lets see if these distributions are better..

```
plt.scatter(fccaq[0], fccaq[1], s=10, label='fcc', color='#FFB300')
plt.scatter(hcpaq[0], hcpaq[1], s=10, label='hcp', color='#388E3C')
plt.scatter(bccaq[0], bccaq[1], s=10, label='bcc', color='#C62828')
plt.xlabel("$q_4$", fontsize=20)
plt.ylabel("$q_6$", fontsize=20)
plt.legend(loc=4, fontsize=15)
```



This looks much better! We can see that the resolution is much better than the non averaged versions.

There is also the possibility to calculate structures using Voronoi based neighbor identification too. Let's try that now.

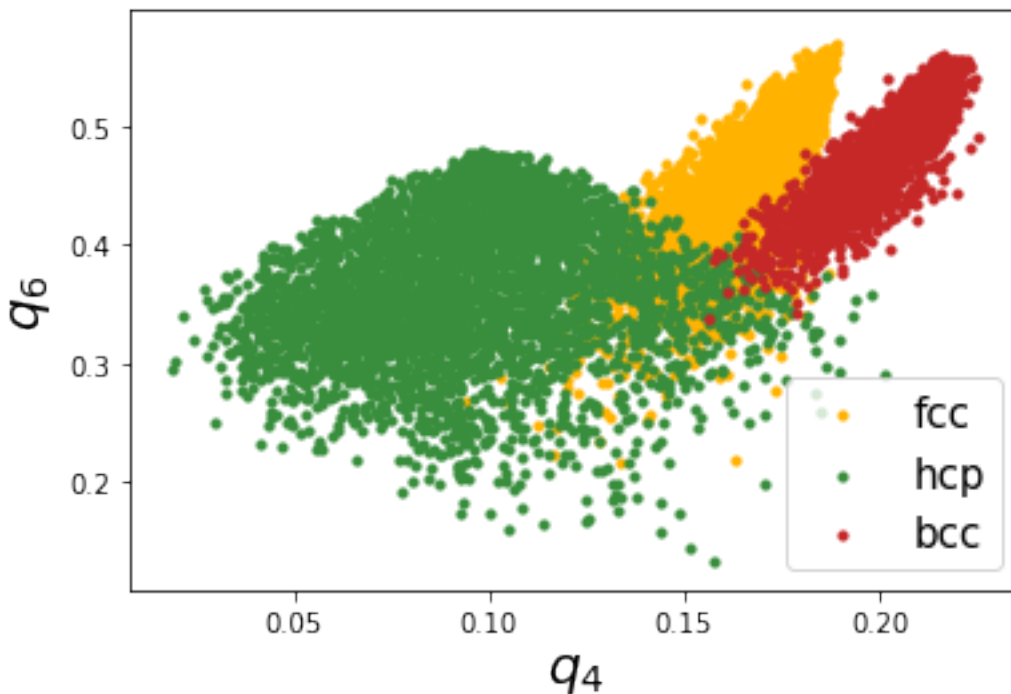
```
bcc.find_neighbors(method='voronoi')
fcc.find_neighbors(method='voronoi')
hcp.find_neighbors(method='voronoi')
```

```
bcc.calculate_q([4,6], averaged=True)
fcc.calculate_q([4,6], averaged=True)
hcp.calculate_q([4,6], averaged=True)
```

```
bccaq = bcc.get_qvals([4, 6], averaged=True)
fccaq = fcc.get_qvals([4, 6], averaged=True)
hcpaq = hcp.get_qvals([4, 6], averaged=True)
```

Plot the calculated points..

```
plt.scatter(fccaq[0], fccaq[1], s=10, label='fcc', color='#FFB300')
plt.scatter(hcpaq[0], hcpaq[1], s=10, label='hcp', color='#388E3C')
plt.scatter(bccaq[0], bccaq[1], s=10, label='bcc', color='#C62828')
plt.xlabel("$q_4$", fontsize=20)
plt.ylabel("$q_6$", fontsize=20)
plt.legend(loc=4, fontsize=15)
```



Voronoi based method also provides good resolution, the major difference being that the location of bcc distribution is different.

### Disorder variable

In this example, *disorder variable* which was introduced to measure the disorder of a system is explored. We start by importing the necessary modules. We will use *crystal\_structures* to create the necessary crystal structures.

```
import pyscal.core as pc
import pyscal.crystal_structures as pcs
import matplotlib.pyplot as plt
import numpy as np
```

First an fcc structure with a lattice constant of 4.00 is created.

```
fcc_atoms, fcc_box = pcs.make_crystal('fcc', lattice_constant=4, repetitions=[4,4,4])
```

The created atoms and box are assigned to a *System* object.

```
fcc = pc.System()
fcc.atoms = fcc_atoms
fcc.box = fcc_box
```

The next step is find the neighbors, and the calculate the Steinhardt parameter based on which we could calculate the disorder variable.

```
fcc.find_neighbors(method='cutoff', cutoff='adaptive')
```

Once the neighbors are found, we can calculate the Steinhardt parameter value. In this example  $q = 6$  will be used.

```
fcc.calculate_q(6)
```

Finally, disorder parameter can be calculated.

```
fcc.calculate_disorder()
```

The calculated disorder value can be accessed for each atom using the disorder variable.

```
atoms = fcc.atoms
```

```
disorder = [atom.disorder for atom in atoms]
```

```
np.mean(disorder)
```

```
-1.041556887034408e-16
```

As expected, for a perfect fcc structure, we can see that the disorder is zero. The variation of disorder variable on a distorted lattice can be explored now. We will once again use the noise keyword along with `make_crystal()` to create a distorted lattice.

```
fcc_atoms_d1, fcc_box_d1 = pcs.make_crystal('fcc', lattice_constant=4, repetitions=[4,
↪4, 4], noise=0.01)
fcc_d1 = pc.System()
fcc_d1.atoms = fcc_atoms_d1
fcc_d1.box = fcc_box_d1
```

Once again, find neighbors and then calculate disorder

```
fcc_d1.find_neighbors(method='cutoff', cutoff='adaptive')
fcc_d1.calculate_q(6)
fcc_d1.calculate_disorder()
```

Check the value of disorder

```
atoms_d1 = fcc_d1.atoms
```

```
disorder = [atom.disorder for atom in atoms_d1]
```

```
np.mean(disorder)
```

```
0.013889967380485688
```

The value of average disorder for the system has increased with noise. Finally trying with a high amount of noise.

```
fcc_atoms_d2, fcc_box_d2 = pcs.make_crystal('fcc', lattice_constant=4, repetitions=[4,
↪4,4], noise=0.1)
fcc_d2 = pc.System()
fcc_d2.atoms = fcc_atoms_d2
fcc_d2.box = fcc_box_d2
```

```
fcc_d2.find_neighbors(method='cutoff', cutoff='adaptive')
fcc_d2.calculate_q(6)
fcc_d2.calculate_disorder()
```

```
atoms_d2 = fcc_d2.atoms
```

```
disorder = [atom.disorder for atom in atoms_d2]
np.mean(disorder)
```

```
1.8469165876016702
```

The value of disorder parameter shows an increase with the amount of lattice distortion. An averaged version of disorder parameter, averaged over the neighbors for each atom can also be calculated as shown below.

```
fcc_d2.calculate_disorder(averaged=True)
```

```
atoms_d2 = fcc_d2.atoms
disorder = [atom.avg_disorder for atom in atoms_d2]
np.mean(disorder)
```

```
1.850630088115515
```

The disorder parameter can also be calculated for values of Steinhardt parameter other than 6. For example,

```
fcc_d2.find_neighbors(method='cutoff', cutoff='adaptive')
fcc_d2.calculate_q([4, 6])
fcc_d2.calculate_disorder(q=4, averaged=True)
```

```
atoms_d2 = fcc_d2.atoms
disorder = [atom.disorder for atom in atoms_d2]
np.mean(disorder)
```

```
1.880741277448693
```

$q = 4$ , for example, can be useful when measuring disorder in bcc crystals

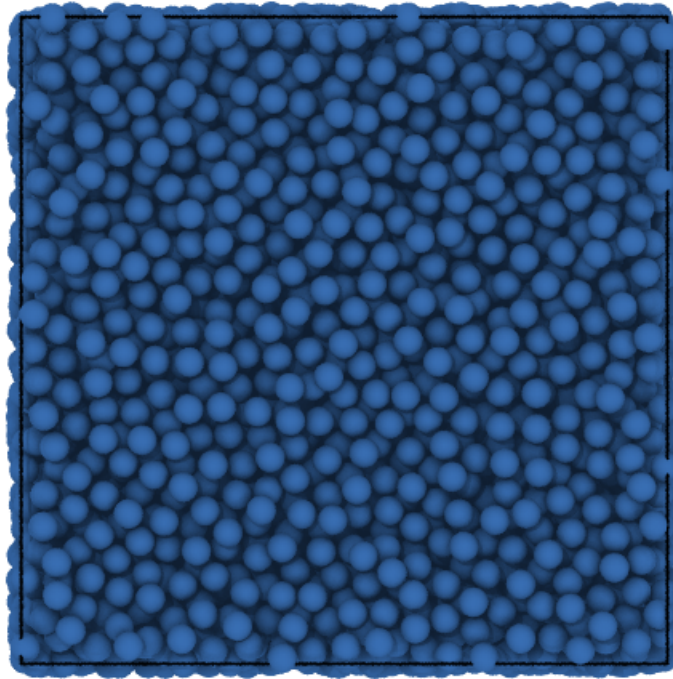
### Distinction of solid liquid atoms and clustering

In this example, we will take one configuration from a molecular dynamics simulation which has a solid cluster in liquid. The task is to identify solid atoms and cluster them. More details about the method can be found [here](#).

The first step is, of course, importing all the necessary module. For visualisation, we will use [Ovito](#).

The above image shows a visualization of the system using Ovito. Importing modules,

```
import pyscal.core as pc
```



Now we will set up a *System* with this input file, and calculate neighbors. Here we will use a cutoff method to find neighbors. More details about finding neighbors can be found [here](#).

```
sys = pc.System()
sys.read_inputfile('cluster.dump')
sys.find_neighbors(method='cutoff', cutoff=3.63)
```

Once we compute the neighbors, the next step is to find solid atoms. This can be done using *find\_solids()* method.

```
sys.find_solids(bonds=6, threshold=0.5, avgthreshold=0.6, cluster=False)
```

The above statement found all the solid atoms. Solid atoms can be identified by the value of the *solid* attribute. For that we first get the atom objects and select those with *solid* value as True.

```
atoms = sys.atoms
solids = [atom for atom in atoms if atom.solid]
len(solids)
```

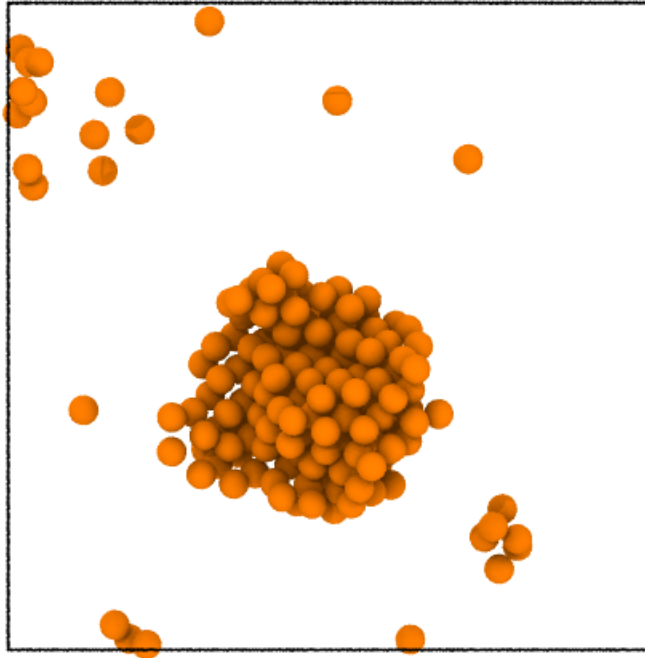
```
202
```

There are 202 solid atoms in the system. In order to visualise in Ovito, we need to first write it out to a trajectory file. This can be done with the help of *to\_file()* method of System. This method can help to save any attribute of the atom or any Steinhardt parameter value.

```
sys.to_file('sys.solid.dat', custom = ['solid'])
```

We can now visualize this file in Ovito. After opening the file in Ovito, the modifier *compute property* can be selected. The Output property should be selection and in the expression field, *solid==0* can be selected to select

all the non solid atoms. Applying a modifier `delete selected particles` can be applied to delete all the non solid particles. The system after removing all the liquid atoms is shown below.



### Clustering algorithm

You can see that there is a cluster of atom. The clustering functions that pyscal offers helps to select atoms that belong to this cluster. If you used `find_clusters()` with `cluster=True`, the clustering is carried out. Since we did used `cluster=False` above, we will rerun the function

```
sys.find_solids(bonds=6, threshold=0.5, avgthreshold=0.6, cluster=True)
```

```
176
```

You can see that the above function call returned the number of atoms belonging to the largest cluster as an output. In order to extract atoms that belong to the largest cluster, we can use the `largest_cluster` attribute of the atom.

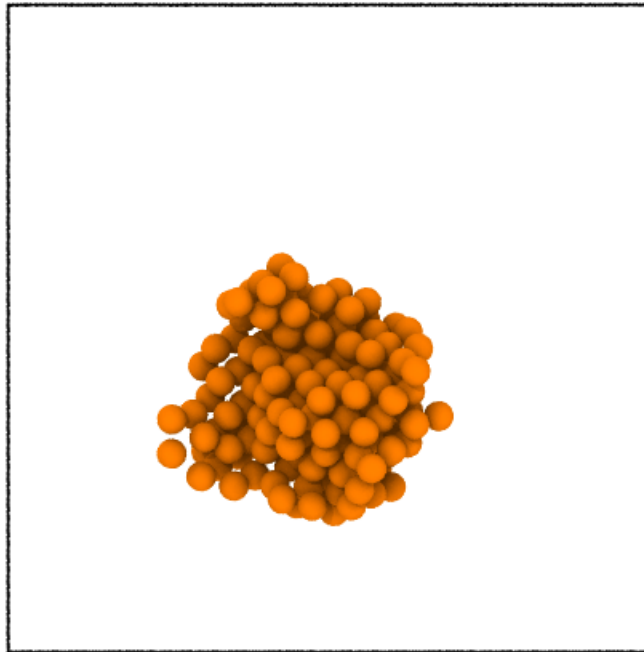
```
atoms = sys.atoms
largest_cluster = [atom for atom in atoms if atom.largest_cluster]
len(largest_cluster)
```

```
176
```

The value matches that given by the function. Once again we will save this information to a file and visualize it in Ovito.

```
sys.to_file('sys.cluster.dat', custom = ['solid', 'largest_cluster'])
```

The system visualized in Ovito following similar steps as above is shown below.



It is clear from the image that the largest cluster of solid atoms was successfully identified. Clustering can be done over any property. The following example with the same system will illustrate this.

### Clustering based on a custom property

In pyscal, clustering can be done based on any property. The following example illustrates this. To find the clusters based on a custom property, the `cluster_atoms()` method has to be used. The simulation box shown above has the centre roughly at (25, 25, 25). For the custom clustering, we will cluster all atoms within a distance of 10 from the the rough centre of the box at (25, 25, 25). Let us define a function that checks the above condition.

```
def check_distance(atom):  
    #get position of atom  
    pos = atom.pos  
    #calculate distance from (25, 25, 25)  
    dist = ((pos[0]-25)**2 + (pos[1]-25)**2 + (pos[2]-25)**2)**0.5  
    #check if dist < 10  
    return (dist <= 10)
```

The above function would return True or False depending on a condition and takes the Atom as an argument. These are the two important conditions to be satisfied. Now we can pass this function to cluster. First, set up the system and find the neighbors.

```
sys = pc.System()  
sys.read_inputfile('cluster.dump')  
sys.find_neighbors(method='cutoff', cutoff=3.63)
```

Now cluster



```
sys.cluster_atoms(check_distance)
```

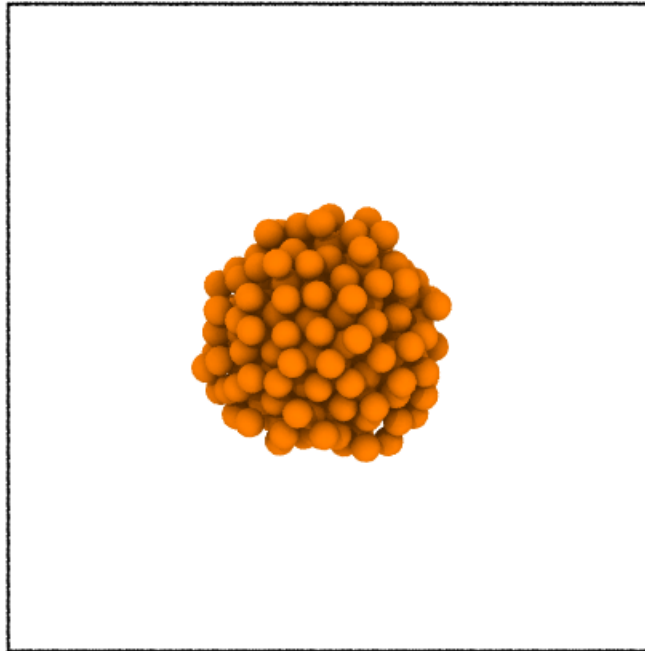
```
242
```

There are 242 atoms in the cluster! Once again we can check this, save to a file and visualize in ovito.

```
atoms = sys.atoms
largest_cluster = [atom for atom in atoms if atom.largest_cluster]
len(largest_cluster)
```

```
242
```

```
sys.to_file('sys.dist.dat', custom = ['solid', 'largest_cluster'])
```



This example illustrates that any property can be used to cluster the atoms!

#### 4.1.4 Angle based methods

##### Angular parameter

This illustrates the use of angular parameter to identify diamond structure. Angular parameter was introduced by [Uttormark et al.](#), and measures the tetrahedrality of the local atomic structure. An atom belonging to diamond structure has four nearest neighbors which gives rise to six three body angles around the atom. The angular parameter  $A$  is then defined as,

$$A = \sum_{i=1}^6 (\cos(\theta_i) + \frac{1}{3})^2$$

An atom belonging to diamond structure would show the value of angular params close to 0. The following example illustrates the use of this parameter.

```
import pyscal.core as pc
import pyscal.crystal_structures as pcs
import numpy as np
import matplotlib.pyplot as plt
```

## Create structures

The first step is to create some structures using the *crystal\_structures* module and assign it to a System. This can be done as follows-

```
atoms, box = pcs.make_crystal('diamond', lattice_constant=4, repetitions=[3,3,3])
sys = pc.System()
sys.atoms = atoms
sys.box = box
```

Now we can find the neighbors of all atoms. In this case we will use an adaptive method using the `find_neighbors()` which can find an individual cutoff for each atom.

```
sys.find_neighbors(method='cutoff', cutoff='adaptive')
```

Finally, the angular criteria can be calculated by,

```
sys.calculate_angularcriteria()
```

The above function assigns the angular value for each atom in the attribute `angular` which can be accessed using,

```
atoms = sys.atoms
angular = [atom.angular for atom in atoms]
```

The angular values are zero for atoms that belong to diamond structure.

## $\chi$ parameters

$\chi$  parameters introduced by Ackland and Jones measures the angles generated by pairs of neighbor atom around the host atom, and assigns it to a histogram to calculate a local structure. In this example, we will create different crystal structures and see how the  $\chi$  parameters change with respect to the local coordination.

```
import pyscal.core as pc
import pyscal.crystal_structures as pcs
import matplotlib.pyplot as plt
import numpy as np
```

The *crystal\_structures* module is used to create different perfect crystal structures. The created atoms and simulation box is then assigned to a *System* object. For this example, fcc, bcc, hcp and diamond structures are created.

```
fcc_atoms, fcc_box = pcs.make_crystal('fcc', lattice_constant=4, repetitions=[4,4,4])
fcc = pc.System()
fcc.atoms = fcc_atoms
fcc.box = fcc_box
```

```
bcc_atoms, bcc_box = pcs.make_crystal('bcc', lattice_constant=4, repetitions=[4,4,4])
bcc = pc.System()
bcc.atoms = bcc_atoms
bcc.box = bcc_box
```

```
hcp_atoms, hcp_box = pcs.make_crystal('hcp', lattice_constant=4, repetitions=[4,4,4])
hcp = pc.System()
hcp.atoms = hcp_atoms
hcp.box = hcp_box
```

```
dia_atoms, dia_box = pcs.make_crystal('diamond', lattice_constant=4, repetitions=[4,4,
→4])
dia = pc.System()
dia.atoms = dia_atoms
dia.box = dia_box
```

Before calculating  $\chi$  parameters, the neighbors for each atom need to be found.

```
fcc.find_neighbors(method='cutoff', cutoff='adaptive')
bcc.find_neighbors(method='cutoff', cutoff='adaptive')
hcp.find_neighbors(method='cutoff', cutoff='adaptive')
dia.find_neighbors(method='cutoff', cutoff='adaptive')
```

Now,  $\chi$  parameters can be calculated

```
fcc.calculate_chiparams()
bcc.calculate_chiparams()
hcp.calculate_chiparams()
dia.calculate_chiparams()
```

The calculated parameters for each atom can be accessed using the *chiparams* attribute.

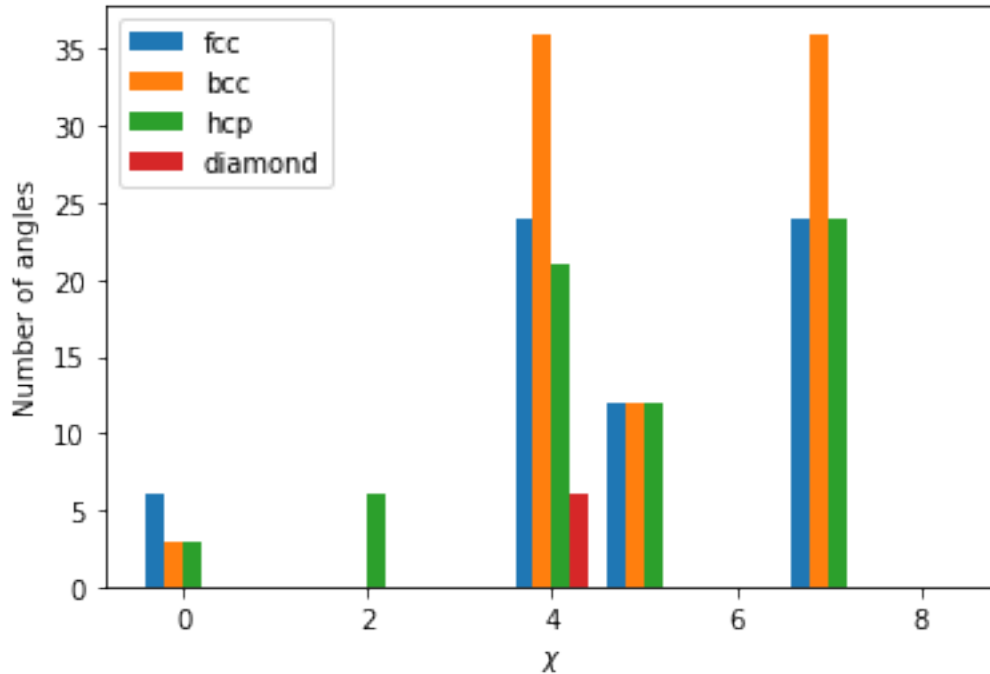
```
fcc_atoms = fcc.atoms
bcc_atoms = bcc.atoms
hcp_atoms = hcp.atoms
dia_atoms = dia.atoms
```

```
fcc_atoms[10].chiparams
```

```
[6, 0, 0, 0, 24, 12, 0, 24, 0]
```

The output is an array of length 9 which shows the number of neighbor angles found within specific bins as explained [here](#). The output for one atom from each structure is shown below.

```
plt.bar(np.array(range(9))-0.3, fcc_atoms[10].chiparams, width=0.2, label="fcc")
plt.bar(np.array(range(9))-0.1, bcc_atoms[10].chiparams, width=0.2, label="bcc")
plt.bar(np.array(range(9))+0.1, hcp_atoms[10].chiparams, width=0.2, label="hcp")
plt.bar(np.array(range(9))+0.3, dia_atoms[10].chiparams, width=0.2, label="diamond")
plt.xlabel("$\chi$")
plt.ylabel("Number of angles")
plt.legend()
```



The atoms exhibit a distinct fingerprint for each structure. Structural identification can be made up comparing the ratio of various  $\chi$  parameters as described in the [original publication](#).

## 4.1.5 Voronoi tessellation

### Voronoi parameters

Voronoi tessellation can be used to identify local structure by counting the number of faces of the Voronoi polyhedra of an atom. For each atom a vector  $\langle n_3 n_4 n_5 n_6 \rangle$  can be calculated where  $n_3$  is the number of Voronoi faces of the associated Voronoi polyhedron with three vertices,  $n_4$  is with four vertices and so on. Each perfect crystal structure such as a signature vector, for example, bcc can be identified by  $\langle 0 6 0 8 \rangle$  and fcc can be identified using  $\langle 0 12 0 0 \rangle$ . It is also a useful tool for identifying icosahedral structure which has the fingerprint  $\langle 0 0 12 0 \rangle$ .

```
import pyscal.core as pc
import pyscal.crystal_structures as pcs
import matplotlib.pyplot as plt
import numpy as np
```

The `crystal_structures` module is used to create different perfect crystal structures. The created atoms and simulation box is then assigned to a `System` object. For this example, fcc, bcc, hcp and diamond structures are created.

```
fcc_atoms, fcc_box = pcs.make_crystal('fcc', lattice_constant=4, repetitions=[4,4,4])
fcc = pc.System()
fcc.atoms = fcc_atoms
fcc.box = fcc_box
```

```
bcc_atoms, bcc_box = pcs.make_crystal('bcc', lattice_constant=4, repetitions=[4,4,4])
bcc = pc.System()
bcc.atoms = bcc_atoms
bcc.box = bcc_box
```

```
hcp_atoms, hcp_box = pcs.make_crystal('hcp', lattice_constant=4, repetitions=[4,4,4])
hcp = pc.System()
hcp.atoms = hcp_atoms
hcp.box = hcp_box
```

Before calculating the Voronoi polyhedron, the `neighbors` for each atom need to be found using Voronoi method.

```
fcc.find_neighbors(method='voronoi')
bcc.find_neighbors(method='voronoi')
hcp.find_neighbors(method='voronoi')
```

Now, Voronoi vector can be calculated

```
fcc.calculate_vorovector()
bcc.calculate_vorovector()
hcp.calculate_vorovector()
```

The calculated parameters for each atom can be accessed using the `vorovector` attribute.

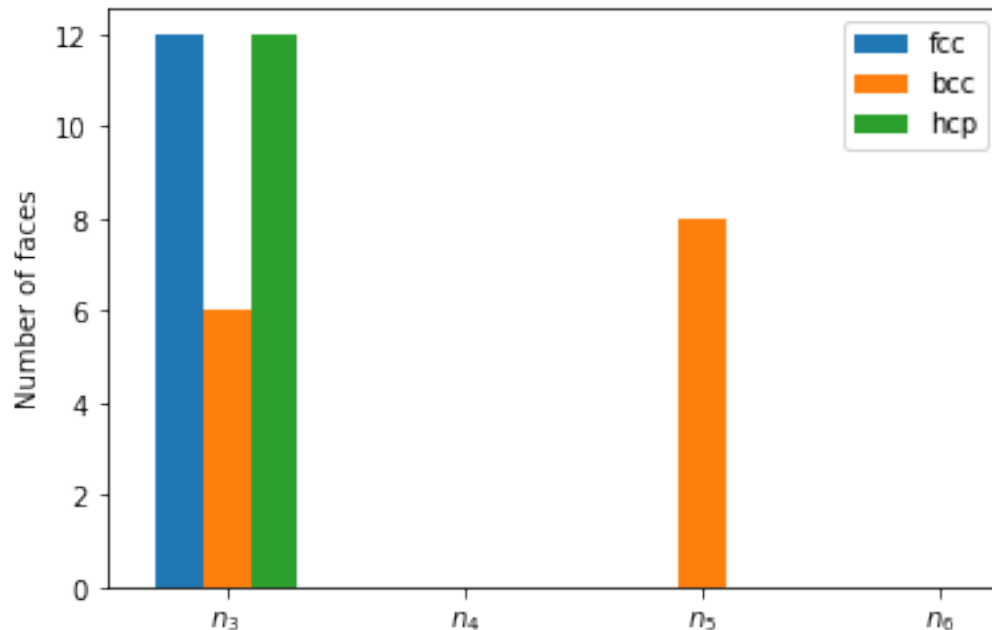
```
fcc_atoms = fcc.atoms
bcc_atoms = bcc.atoms
hcp_atoms = hcp.atoms
```

```
fcc_atoms[10].vorovector
```

```
[0, 12, 0, 0]
```

As expected, fcc structure exhibits 12 faces with four vertices each. For a single atom, the difference in the Voronoi fingerprint is shown below

```
fig, ax = plt.subplots()
ax.bar(np.array(range(4))-0.2, fcc_atoms[10].vorovector, width=0.2, label="fcc")
ax.bar(np.array(range(4)), bcc_atoms[10].vorovector, width=0.2, label="bcc")
ax.bar(np.array(range(4))+0.2, hcp_atoms[10].vorovector, width=0.2, label="hcp")
ax.set_xticks([1,2,3,4])
ax.set_xlim(0.5, 4.25)
ax.set_xticklabels(['$n_3$', '$n_4$', '$n_5$', '$n_6$'])
ax.set_ylabel("Number of faces")
ax.legend()
```



The difference in Voronoi fingerprint for bcc and the closed packed structures is clearly visible. Voronoi tessellation, however, is incapable of distinction between fcc and hcp structures.

### Voronoi volume

Voronoi volume, which is the volume of the Voronoi polyhedron is calculated when the neighbors are found. The volume can be accessed using the `volume` attribute.

```
fcc_atoms = fcc.atoms
```

```
fcc_vols = [atom.volume for atom in fcc_atoms]
```

```
np.mean(fcc_vols)
```

```
16.0
```

## 4.1.6 Other examples

### Saving System and Atom objects to file

pyscal offers tools to save `System` and `Atom` classes to file. There are two methods to do this. The `to_file()` method can save a trajectory file which contains all the atom positions and system box dimensions.

The second approach makes use of `numpy.save` and `numpy.load` methods to save the information. Information including calculated neighbors, q values, solidity, voronoi volume etc are all saved. Saving this information is beneficial in systems with a large number of atoms as it saves time which would otherwise be spent recalculating information. The `pickle_object` module provides the base functions for pickling support as is used internally in `System`.

```
import pyscal.core as pc
import pyscal.traj_process as ptp
```

First a system is set up using an input file

```
sys = pc.System()
sys.read_inputfile('conf.bcc')
```

In the next step, the neighbors are calculated, and  $\bar{q}_4$  and  $\bar{q}_6$  are also calculated.

```
sys.find_neighbors(method='cutoff', cutoff=3.6)
sys.calculate_q([4, 6], averaged=True)
```

In order to prevent recalculation of neighbors, for example if later we need to calculate  $\bar{q}_8$  and  $\bar{q}_{10}$ , we can save the set of systems to a file.

### Saving individual system

Single System instances can be saved without `pickle_object` module directly, similar to how pandas `DataFrames` are saved to file.

```
sys.to_pickle('test_system.npy')
```

Thats it! The information is saved in the file. Once again, `read_systems()` can be used to read the System instance. Alternatively, a new System can be created and the information can be read in from a file.

```
new_sys = pc.System()
new_sys.from_pickle('test_system.npy')
```

This system retains all the information and hence it can be used for further calculations

```
new_sys.calculate_q([8, 10], averaged=True)
```

Here  $\bar{q}_8$  and  $\bar{q}_{10}$  were calculated without having to find neighbors again.

**Warning:** pickling can be incompatible with different python versions. As python documentation also points out - pickling objects is not secure. You should only unpickle objects that you trust.





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## Methods implemented in pycsal

---

### 5.1 Methods implemented in pycsal

#### 5.1.1 Methods to calculate neighbors of a particle

pycsal includes different methods to explore the local environment of a particle that rely on the calculation of nearest neighbors. Various approaches to compute the neighbors of particles are discussed here.

##### Fixed cutoff method

The most common method to calculate the nearest neighbors of an atom is using a cutoff radius. The neighborhood of an atom for calculation of Steinhardt's parameters<sup>1</sup> is often carried out using this method. Commonly, a cutoff is selected as the first minimum of the radial distribution functions. Once a cutoff is selected, the neighbors of an atom are those that fall within this selected radius. The following code snippet will use the cutoff method to calculate neighbors. Please check the [examples section](#) for basic use of the module. In this example, `conf.dump` is assumed to be the input configuration of the system. A cutoff radius of 3 is assumed for calculation of neighbors.

```
import pycsal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff=3)
```

##### Adaptive cutoff methods

A fixed cutoff radius can introduce limitations to explore the local environment of the particle in some cases:

- At finite temperatures, when thermal fluctuations take place, the selection of a fixed cutoff may result in an inaccurate description of the local environment.

---

<sup>1</sup> Steinhardt, PJ, Nelson, DR, Ronchetti, M. Phys Rev B 28, 1983.

- If there is more than one structure present in the system, for example, bcc and fcc, the selection of cutoff such that it includes the first shell of both structures can be difficult.

In order to achieve a more accurate description of the local environment, various adaptive approaches have been proposed. Two of the methods implemented in the module are discussed below.

### Solid angle based nearest neighbor algorithm (SANN)

SANN algorithm<sup>1</sup> determines the cutoff radius by counting the solid angles around an atom and equating it to  $4\pi$ . The algorithm solves the following equation iteratively.

$$R_i^{(m)} = \frac{\sum_{j=1}^m r_{i,j}}{m-2} < r_{i,m+1}$$

where  $i$  is the host atom,  $j$  are its neighbors with  $r_{ij}$  is the distance between atoms  $i$  and  $j$ .  $R_i$  is the cutoff radius for each particle  $i$  which is found by increasing the neighbor of neighbors  $m$  iteratively. For a description of the algorithm and more details, please check the reference<sup>2</sup>. SANN algorithm can be used to find the neighbors by,

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff='sann')
```

Since SANN algorithm involves sorting, a sufficiently large cutoff is used in the beginning to reduce the number entries to be sorted. This parameter is calculated by,

$$r_{initial} = \text{threshold} \times \left( \frac{\text{Simulation box volume}}{\text{Number of particles}} \right)^{\frac{1}{3}}$$

a tunable `threshold` parameter can be set through function arguments.

### Adaptive cutoff method

An adaptive cutoff specific for each atom can also be found using an algorithm similar to adaptive common neighbor analysis<sup>2</sup>. This adaptive cutoff is calculated by first making a list of all neighbor distances for each atom similar to SANN method. Once this list is available, then the cutoff is calculated from,

$$r_{cut}(i) = \text{padding} \times \left( \frac{1}{nlimit} \sum_{j=1}^{nlimit} r_{ij} \right)$$

This method can be chosen by,

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff='adaptive')
```

The `padding` and `nlimit` parameters in the above equation can be tuned using the respective keywords.

Either of the adaptive method can be used to find neighbors, which can then be used to calculate Steinhardt's parameters or their averaged version.

<sup>1</sup> van Meel, JA, Fillion, L, Valeriani, C, Frenkel, D, J Chem Phys 234107, 2012.

<sup>2</sup> Stukowski, A, Model Simul Mater SC 20, 2012.

## Voronoi tessellation

Voronoi tessellation provides a completely parameter free geometric approach for calculation of neighbors. `Voro++` code is used for Voronoi tessellation. Neighbors can be calculated using this method by,

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='voronoi')
```

Finding neighbors using Voronoi tessellation also calculates a weight for each neighbor. The weight of a neighbor  $j$  towards a host atom  $i$  is given by,

$$W_{ij} = \frac{A_{ij}}{\sum_{j=1}^N A_{ij}}$$

where  $A_{ij}$  is the area of Voronoi facet between atom  $i$  and  $j$ ,  $N$  are all the neighbors identified through Voronoi tessellation. This weight can be used later for calculation of weighted Steinhardt's parameters. Optionally, it is possible to choose the exponent for this weight. Option `vorosexp` is used to set this option. For example if `vorosexp=2`, the weight would be calculated as,

$$W_{ij} = \frac{A_{ij}^2}{\sum_{j=1}^N A_{ij}^2}$$

### 5.1.2 Steinhardt's bond orientational order parameters

#### Steinhardt's parameters

Steinhardt's bond orientational order parameters<sup>1</sup> are a set of parameters based on [spherical harmonics](#) to explore the local atomic environment. These parameters have been used extensively for various uses such as distinction of crystal structures, identification of solid and liquid atoms and identification of defects<sup>2</sup>.

These parameters, which are rotationally and translationally invariant are defined by,

$$q_l(i) = \left( \frac{4\pi}{2l+1} \sum_{m=-l}^l |q_{lm}(i)|^2 \right)^{\frac{1}{2}}$$

where,

$$q_{lm}(i) = \frac{1}{N(i)} \sum_{j=1}^{N(i)} Y_{lm}(\mathbf{r}_{ij})$$

in which  $Y_{lm}$  are the spherical harmonics and  $N(i)$  is the number of neighbours of particle  $i$ ,  $\mathbf{r}_{ij}$  is the vector connecting particles  $i$  and  $j$ , and  $l$  and  $m$  are both integers with  $m \in [-l, +l]$ . Various parameters have found specific uses, such as  $q_2$  and  $q_6$  for identification of crystallinity,  $q_6$  for identification of solidity, and  $q_4$  and  $q_6$  for distinction of crystal structures<sup>2</sup>. Commonly this method uses a cutoff radius to identify the neighbors of an atom. The cutoff can be chosen based on [different methods available](#). Once the cutoff is chosen and neighbors are calculated, the calculation of Steinhardt's parameters is straightforward.

<sup>1</sup> Steinhardt, PJ, Nelson, DR, Ronchetti, M. Phys Rev B 28, 1983.

<sup>2</sup> Mickel, W, Kapfer, SC, Schroder-Turk, GE, Mecke, K, J Chem Phys 138, 2013.

```
sys.calculate_q([4, 6])
q = sys.get_qvals([4, 6])
```

**Note:** Associated methods

*find\_neighbors()* *calculate\_q()* *get\_qvals()* *get\_q()* Example

---

## Averaged Steinhardt's parameters

At high temperatures, thermal vibrations affect the atomic positions. This in turn leads to overlapping distributions of  $q_l$  parameters, which makes the identification of crystal structures difficult. To address this problem, the averaged version  $\bar{q}_l$  of Steinhardt's parameters was introduced by Lechner and Dellago<sup>1</sup>.  $\bar{q}_l$  is given by,

$$\bar{q}_l(i) = \left( \frac{4\pi}{2l+1} \sum_{m=-l}^l \left| \frac{1}{\tilde{N}(i)} \sum_{k=0}^{\tilde{N}(i)} q_{lm}(k) \right|^2 \right)^{\frac{1}{2}}$$

where the sum from  $k = 0$  to  $\tilde{N}(i)$  is over all the neighbors and the particle itself. The averaged parameters takes into account the first neighbor shell and also information from the neighboring atoms and thus reduces the overlap between the distributions. Commonly  $\bar{q}_4$  and  $\bar{q}_6$  are used in identification of crystal structures. Averaged versions can be calculated by setting the keyword `averaged=True` as follows.

```
sys.calculate_q([4, 6], averaged=True)
q = sys.get_qvals([4, 6], averaged=True)
```

**Note:** Associated methods

*find\_neighbors()* *calculate\_q()* *get\_qvals()* *get\_q()* Example

---

## Voronoi weighted Steinhardt's parameters

In order to improve the resolution of crystal structures Mickel et al<sup>1</sup> proposed weighting the contribution of each neighbor to the Steinhardt parameters by the ratio of the area of the Voronoi facet shared between the neighbor and host atom. The weighted parameters are given by,

$$q_{lm}(i) = \frac{1}{N(i)} \sum_{j=1}^{N(i)} \frac{A_{ij}}{A} Y_{lm}(\mathbf{r}_{ij})$$

where  $A_{ij}$  is the area of the Voronoi facet between atoms  $i$  and  $j$  and  $A$  is the sum of the face areas of atom  $i$ . In `pyscal`, the area weights are already assigned during the neighbor calculation phase when the Voronoi method is used to calculate neighbors in the `find_neighbors()`. The Voronoi weighted Steinhardt's parameters can be calculated as follows,

```
sys.find_neighbors(method='voronoi')
sys.calculate_q([4, 6])
q = sys.get_qvals([4, 6])
```

---

<sup>1</sup> Lechner, W, Dellago, C, J Chem Phys, 2013.

<sup>1</sup> Mickel, W, Kapfer, SC, Schroder-Turk, GE, Mecke, K, J Chem Phys 138, 2013.

The weighted Steinhardt's parameters can also be averaged as described above. Once again, the keyword `averaged=True` can be used for this purpose.

```
sys.find_neighbors(method='voronoi')
sys.calculate_q([4, 6], averaged=True)
q = sys.get_qvals([4, 6], averaged=True)
```

It was also proposed that higher powers of the weight<sup>2</sup>  $\frac{A_{ij}^\alpha}{A(\alpha)}$  where  $\alpha = 2, 3$  can also be used, where  $A(\alpha) = \sum_{j=1}^{N(i)} A_{ij}^\alpha$ . The value of this can be set using the keyword `voroexp` during the neighbor calculation phase.

```
sys.find_neighbors(method='voronoi', voroexp=2)
```

If the value of `voroexp` is set to 0, the neighbors would be found using Voronoi method, but the calculated Steinhardt's parameters will not be weighted.

---

**Note:** Associated methods

*find\_neighbors()* *calculate\_q()* *get\_qvals()* *get\_q()*

---

## Disorder parameter

Kawasaki and Onuki<sup>1</sup> proposed a disorder variable based on Steinhardt's order parameters which can be used to distinguish between ordered and disordered structures.

The disorder variable for an atom is defined as,

$$D_j = \frac{1}{n_b^j} \sum_{k \in neighbors} [S_{jj} + S_{kk} - 2S_{jk}]$$

where S is given by,

$$S_{jk} = \sum_{-l \leq m \leq l} q_{lm}^j (q_{lm}^k)^*$$

$l = 6$  was used in the original publication as it is a good indicator of crystallinity. However,  $l = 4$  can also be used for treating bcc structures. An averaged disorder parameter for each atom can also be calculated in pyscal,

$$\bar{D}_j = \frac{1}{n_b^j} \sum_{k \in neighbors} D_j$$

In pyscal, disorder parameter can be calculated by the following code-block,

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff=0)
sys.calculate_q(6)
sys.calculate_disorder(averaged=True, q=6)
```

The value of `q` can be replaced with whichever is required from 2-12. The calculated values can be accessed by, *disorder* and *avg\_disorder*.

---

**Note:** Associated methods

<sup>2</sup> Haerberle, J, Sperl, M, Born, P Arxiv 2019.

<sup>1</sup> Kawasaki .T, Onuki .A, JCP 135, 174109 (2011)

*calculate\_q() calculate\_disorder() disorder avg\_disorder* Example

---

## Classification of atoms as solid or liquid

pyscal can also be used to distinguish solid and liquid atoms. The classification is based on Steinhardt's parameters, specifically  $q_6$ . The method defines two neighboring atoms  $i$  and  $j$  as having solid bonds if a parameter  $s_{ij}$ <sup>1</sup>,

$$s_{ij} = \sum_{m=-6}^6 q_{6m}(i)q_{6m}^*(j) \geq \text{threshold}$$

Additionally, a second order parameter is used to improve the distinction in solid-liquid boundaries<sup>2</sup>. This is defined by the criteria,

$$\langle s_{ij} \rangle > \text{avgthreshold}$$

If a particle has  $n$  number of bonds with  $s_{ij} \geq \text{threshold}$  and the above condition is also satisfied, it is considered as a solid. The solid atoms can be clustered to find the largest solid cluster of atoms. Please check the [examples](#) on how to do this.

Finding solid atoms in liquid start with reading in a file and calculation of neighbors.

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff=4)
```

Once again, there are various methods for finding neighbors. Please check [here](#) for details on neighbor calculation methods. Once the neighbors are calculated, solid atoms can be found directly by,

```
sys.find_solids(bonds=6, threshold=0.5, avgthreshold=0.6, cluster=True)
```

bonds set the number of minimum bonds a particle should have (as defined above), threshold and avgthreshold are the same quantities that appear in the equations above. Setting the keyword cluster to True returns the size of the largest solid cluster. It is also possible to check if each atom is solid or not.

```
atoms = sys.atom
solids = [atom.solid for atom in atoms]
```

---

**Note:** Associated methods

*find\_neighbors() calculate\_q() find\_solids() solid()* Example

---

## 5.1.3 Angle based methods

### Angular criteria for identification of diamond structure

Angular parameter introduced by Uttormark et al<sup>1</sup> is used to measure the tetrahedrality of local atomic structure. An atom belonging to diamond structure has four nearest neighbors which gives rise to six three body angles around the atom. The angular parameter  $A$  is then defined as,

<sup>1</sup> Auer, S, Frenkel, D. Adv Polym Sci 173, 2005

<sup>2</sup> Bokeloh, J, Rozas, RE, Horbach, J, Wilde, G, Phys. Rev. Lett. 107, 2011

<sup>1</sup> Uttormark, MJ, Thompson, MO, Clancy, P, Phys. Rev. B 47, 1993

$$A = \sum_{i=1}^6 (\cos(\theta_i) + \frac{1}{3})^2$$

An atom belonging to diamond structure would show the value of angular params close to 0. Angular parameter can be calculated in pyscal using the following method -

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff='adaptive')
sys.calculate_angularcriteria()
```

The calculated angular criteria value can be accessed for each atom using *angular*.

**Note:** Associated methods

*calculate\_angularcriteria()* *angular* Example

## $\chi$ parameters for structural identification

$\chi$  parameters introduced by Ackland and Jones<sup>1</sup> measures all local angles created by an atom with its neighbors and creates a histogram of these angles to produce vector which can be used to identify structures. After finding the neighbors of an atom,  $\cos\theta_{ijk}$  for atoms j and k which are neighbors of i is calculated for all combinations of i, j and k. The set of all calculated cosine values are then added to a histogram with the following bins - [-1.0, -0.945, -0.915, -0.755, -0.705, -0.195, 0.195, 0.245, 0.795, 1.0]. Compared to  $\chi$  parameters from  $\chi_0$  to  $\chi_7$  in the associated publication, the vector calculated in pyscal contains values from  $\chi_0$  to  $\chi_8$  which is due to an additional  $\chi$  parameter which measures the number of neighbors between cosines -0.705 to -0.195. The  $\chi$  vector is characteristic of the local atomic environment and can be used to identify crystal structures, details of which can be found in the publication<sup>1</sup>.

$\chi$  parameters can be calculated in pyscal using,

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='cutoff', cutoff='adaptive')
sys.calculate_chiparams()
```

The calculated values for each atom can be accessed using *chiparams*.

**Note:** Associated methods

*calculate\_chiparams()* *chiparams* Example

## 5.1.4 Voronoi tessellation to identify local structures

Voronoi tessellation can be used for identification of local structure by counting the number of faces of the Voronoi polyhedra of an atom<sup>12</sup>. For each atom a vector  $\langle n_3 n_4 n_5 n_6 \rangle$  can be calculated where  $n_3$  is the number of Voronoi faces of the associated Voronoi polyhedron with three vertices,  $n_4$  is with four vertices and so on. Each perfect crystal structure such as a signature vector, for example, bcc can be identified by  $\langle 0 6 0 8 \rangle$  and fcc can be identified using  $\langle 0 12 0 0 \rangle$ . It is also a useful tool for identifying icosahedral structure which has the fingerprint  $\langle 0 0 12 0 \rangle$ . In pyscal, the voronoi vector can be calculated using,

<sup>1</sup> Ackland, Jones, Phys. Rev. B 73, 2006

<sup>1</sup> Finney, J. L. PRS 319 ,1970

<sup>2</sup> Tanemura et al., PTP 58, 1977

```
import pyscal.core as pc
sys = pc.System()
sys.read_inputfile('conf.dump')
sys.find_neighbors(method='voronoi')
sys.calculate_vorovector()
```

The vector for each atom can be accessed using *vorovector*. Furthermore, the associated Voronoi volume of the polyhedron, which may be indicative of the local structure, is also automatically calculated when finding neighbors using *find\_neighbors()*. This value for each atom can be accessed by *volume*. An averaged version of the volume, which is averaged over the neighbors of an atom can be accessed using *avg\_volume*.

---

**Note:** Associated methods

*find\_neighbors()* *calculate\_vorovector()* *vorovector* *volume* *avg\_volume* Example

---



### 6.1 News and updates

- November 30, 2019 : pysical reaches over 1500 downloads on conda-forge channel. Thanks for the support!
- November 21, 2019 : pysical is selected as the E-CAM module of the month. See the news [here](#).
- November 3, 2019 : [Version 2.1.1](#) of pysical is released. This release introduces cell lists to speed up calculations for large number of atoms.
- November 1, 2019 : pysical paper is accepted in the Journal of Open Source Software. See the paper [here](#).
- October 29, 2019 : [Version 2.0.1](#) of pysical is released.
- October 17, 2019 : Publication for pysical submitted to the Journal of Open Source Software. See the review [here](#).
- October 2, 2019 : [Version 2.0.0](#) of pysical is released. This version contains significant update to the code, increasing the speed and memory footprint.
- August 4, 2019 : [Version 1.0.3](#) of pysical is released.
- July 12, 2019 : [Version 1.0.1](#) of pysical is released.
- July 12, 2019 : [Version 1.0.0](#) of pysical is released.



## 7.1 pyscal reference

### 7.1.1 pyscal Reference

#### pyscal.core module

Main module of pyscal. This module contains definitions of the two major classes in pyscal - the *System* and *Atom*. *Atom* is a pure pybind11 class whereas *System* is a hybrid class with additional python definitions. For the ease of use, *Atom* class should be imported from the *core* module. The original pybind11 definitions of *Atom* and *System* can be found in *catom* and *csystem* respectively.

#### **class** `pyscal.core.System`

Bases: `pyscal.csystem.System`

A python/pybind11 hybrid class for holding the properties of a system.

#### **box**

A list containing the dimensions of the simulation box in the format `[[x_low, x_high], [y_low, y_high], [z_low, z_high]]`

**Type** list of list of floats

#### **atoms**

**Type** list of *Atom* objects

#### **Notes**

A *System* consists of two major components - the simulation box and the atoms. All the associated variables are then calculated using this class.

**Note:** atoms can be accessed or set as `atoms`. However, due to technical reasons individual atoms should be accessed using the `get_atom()` method. An atom can be assigned to the atom using the `set_atom()` method.

---

## Examples

```
>>> sys = System()
>>> sys.read_inputfile('atoms.dat')
```

### `calculate_angularcriteria()`

Calculate the angular criteria for each atom :param None:

**Returns**

**Return type** None

### Notes

Calculates the angular criteria for each atom as defined in [1]. Angular criteria is useful for identification of diamond cubic structures. Angular criteria is defined by,

$$A = \sum_{i=1}^6 \left( \cos(\theta_i) + \frac{1}{3} \right)^2$$

where  $\cos(\theta)$  is the angle size suspended by each pair of neighbors of the central atom. A will have a value close to 0 for structures if the angles are close to 109 degrees. The calculated A parameter for each atom is stored in `angular`.

### References

### `calculate_chiparams (angles=False)`

Calculate the chi param vector for each atom

**Parameters** `angles` (*bool, optional*) – If True, return the list of cosines of all neighbor pairs

**Returns** `angles` – list of all cosine values, returned only if `angles` is True.

**Return type** array of floats

### Notes

This method tries to distinguish between crystal structures by finding the cosines of angles formed by an atom with its neighbors. These cosines are then histogrammed with bins `[-1.0, -0.945, -0.915, -0.755, -0.705, -0.195, 0.195, 0.245, 0.795, 1.0]` to find a vector for each atom that is indicative of its local coordination. Compared to chi parameters from `chi_0` to `chi_7` in the associated publication, the vector here is from `chi_0` to `chi_8`. This is due to an additional chi parameter which measures the number of neighbors between cosines -0.705 to -0.195.

Parameter `nlimit` specifies the number of nearest neighbors to be included in the analysis to find the cutoff. If parameter `angles` is true, an array of all cosine values is returned. The publication further provides combinations of chi parameters for structural identification which is not implemented here. The calculated chi params can be accessed using `chiparams`.

## References

**calculate\_disorder** (*averaged=False, q=6*)

Calculate the disorder criteria for each atom

### Parameters

- **averaged** (*bool, optional*) – If True, calculate the averaged disorder. Default False.
- **q** (*int, optional*) – The Steinhardt parameter value over which the bonds have to be calculated. Default 6.

### Returns

**Return type** None

## Notes

Calculate the disorder criteria as introduced in [1]. The disorder criteria value for each atom is defined by,

$$D_j = \frac{1}{N_b^j} \sum_{i=1}^{N_b} [S_{jj} + S_{kk} - 2S_{jk}]$$

where .. math:: S\_{\{ij\}} = \sum\_{m=-6}^6 q\_{\{6m\}}(i) q\_{\{6m\}}^\*(i)

The keyword *averaged* is True, the disorder value is averaged over the atom and its neighbors. The disorder value can be accessed using `disorder` and the averaged version can be accessed using `avg_disorder`. For ordered systems, the value of disorder would be zero which would increase and reach one for disordered systems.

## References

**calculate\_q** (*q, averaged=False*)

Find the Steinhardt parameter `q_l` for all atoms.

### Parameters

- **q\_l** (*int or list of ints*) – A list of all Steinhardt parameters to be found from 2-12.
- **averaged** (*bool, optional*) – If True, return the averaged q values, default False

### Returns

**Return type** None

## Notes

Enables calculation of the Steinhardt parameters [1] q from 2-12. The type of q values depend on the method used to calculate neighbors. See the description `find_neighbors()` for more details. If the keyword *average* is set to True, the averaged versions of the bond order parameter [2] is returned.

## References

**calculate\_rdf** (*histobins=100, histomin=0.0, histomax=None*)

Calculate the radial distribution function.

### Parameters

- **histobins** (*int*) – number of bins in the histogram
- **histomin** (*float, optional*) – minimum value of the distance histogram. Default 0.0.
- **histomax** (*float, optional*) – maximum value of the distance histogram. Default, the maximum value in all pair distances is used.

### Returns

- **rdf** (*array of ints*) – Radial distribution function
- **r** (*array of floats*) – radius in distance units

**calculate\_solidneighbors** ()

Find Solid neighbors of all atoms in the system.

**Parameters** None –

**Returns**

**Return type** None

## Notes

A solid bond is considered between two atoms if the `connection` between them is greater than 0.6.

**calculate\_sro** (*reference\_type=1, average=True, shells=2*)

Calculate short range order

### Parameters

- **reference\_type** (*int, optional*) – type of the atom to be used a reference. default 1
- **average** (*bool, optional*) – if True, average over all atoms of the reference type in the system. default True.

**Returns** **vec** – The short range order averaged over the whole system for atom of the reference type. Only returned if *average* is True. First value is SRO of the first neighbor shell and the second value corresponds to the second nearest neighbor shell.

**Return type** list of float

## Notes

Calculates the short range order for an AB alloy using the approach by Cowley [1]. Short range order is calculated as,

$$\alpha_i = 1 - \frac{n_i}{m_A c_i}$$

where  $n_i$  is the number of atoms of the non reference type among the  $c_i$  atoms in the  $i$ th shell.  $m_A$  is the concentration of the non reference atom. Please note that the value is calculated for shells 1 and 2 by default. In order for this to be possible, neighbors have to be found first using the `find_neighbors()`

method. The selected neighbor method should include the second shell as well. For this purpose *method=cutoff* can be chosen with a cutoff long enough to include the second shell. In order to estimate this cutoff, one can use the *calculate\_rdf()* method.

## References

**calculate\_vorovector** (*edge\_cutoff=0.05, area\_cutoff=0.01, edge\_length=False*)

get the voronoi structure identification vector.

**Parameters** **edge\_cutoff** (*float, optional*) – cutoff for edge length. Default 0.05.

**area\_cutoff** [*float, optional*] cutoff for face area. Default 0.01.

**edge\_length** [*bool, optional*] if True, a list of unrefined edge lengths are returned. Default false.

**Returns** **vorovector** – array of the form (n3, n4, n5, n6)

**Return type** array like, int

## Notes

Returns a vector of the form (*n3, n4, n5, n6*), where *n3* is the number of faces with 3 vertices, *n4* is the number of faces with 4 vertices and so on. This can be used to identify structures [1] [2].

The keywords *edge\_cutoff* and *area\_cutoff* can be used to tune the values to minimise the effect of thermal distortions. Edges are only considered in the analysis if the *edge\_length/sum(edge\_lengths)* is at least *edge\_cutoff*. Similarly, faces are only considered in the analysis if the *face\_area/sum(face\_areas)* is at least *face\_cutoff*.

## References

**cluster\_atoms** (*condition, largest=True, new\_algo=False, cutoff=0*)

Cluster atoms based on a property

### Parameters

- **condition** (*callable*) – function which should take an Atom object, and give a True/False output
- **largest** (*bool, optional*) – If True returns the size of the largest cluster. Default False.

**Returns** **lc** – Size of the largest cluster. Returned only if *largest* is True.

**Return type** int

## Notes

This function helps to cluster atoms based on a defined property. This property is defined by the user through the function *condition* which is passed as a parameter. For each atom in the system, the *condition* should give a True/False values.

When clustering, the code loops over each atom and its neighbors. If the *condition* is true for both host atom and the neighbor, they are assigned to the same cluster. For example, a condition to cluster solid atoms would be,

```
def condition(atom):  
    #if both atom is solid  
    return (atom1.solid)
```

Check examples for more details.

**find\_clusters** (*recursive=True, largest=True*)

Find the clusters of all atoms in the system.

#### Parameters

- **recursive** (*Bool, optional*) – If True, use a recursive clustering algorithm, otherwise use an id based clustering. The difference in values between two methods can be upto 3 particles. Default True.
- **largest** (*Bool, optional*) – If True, return the number of particles in the largest cluster. Default True.

**Returns cluster** – The size of the largest cluster in the system. Only returned if *largest* is set to True.

**Return type** int

#### Notes

Go through all the atoms in the system and cluster them together based on the *issolid* parameter of the atom. To cluster based on any user defined criteria, you can use *set\_solid* method of *Atom* to explicitly set the *issolid* value.

**Warning:** This function is deprecated and will be removed in a future release. Please use *cluster\_atoms()* instead.

**find\_largestcluster** ()

Find the largest solid cluster of atoms in the system from all the clusters.

**Parameters** None –

**Returns cluster** – the size of the largest cluster

**Return type** int

#### Notes

*pyscal.core.System.find\_clusters()* has to be used before using this function.

**find\_neighbors** (*method='cutoff', cutoff=None, threshold=2, filter=None, voroexp=1, padding=1.2, nlimit=6, cells=False*)

Find neighbors of all atoms in the *System*.

#### Parameters

- **method** (*{'cutoff', 'voronoi'}*) – *cutoff* method finds neighbors of an atom within a specified or adaptive cutoff distance from the atom. *voronoi* method finds atoms that share a Voronoi polyhedra face with the atom. Default, *cutoff*
- **cutoff** (*{ float, 'sann', 'adaptive'}*) – the cutoff distance to be used for the *cutoff* based neighbor calculation method described above. If the value is specified as



0 or *adaptive*, adaptive method is used. If the value is specified as *sann*, sann algorithm is used.

- **threshold** (*float, optional*) – only used if *cutoff=adaptive*. A threshold which is used as safe limit for calculation of cutoff.
- **filter** (*{'None', 'type'}, optional*) – apply a filter to nearest neighbor calculation. If the *filter* keyword is set to *type*, only atoms of the same type would be included in the neighbor calculations. Default None.
- **voroexp** (*int, optional*) – only used if *method=voronoi*. Power of the neighbor weight used to weight the contribution of each atom towards Steinhardt parameter values. Default 1.
- **padding** (*double, optional*) – only used if *cutoff=adaptive*. A safe padding value used after an adaptive cutoff is found. Default 1.2.
- **nlimit** (*int, optional*) – only used if *cutoff=adaptive*. The number of particles to be considered for the calculation of adaptive cutoff. Default 6.

### Returns

**Return type** None

### Raises

- `RuntimeWarning` – raised when *threshold* value is too low. A low threshold value will lead to ‘sann’ algorithm not converging when finding a neighbor. This function will try to automatically increase *threshold* and check again.
- `RuntimeError` – raised when neighbor search was unsuccessful. This is due to a low *threshold* value.

### Notes

This function calculates the neighbors of each particle. There are several ways to do this. A complete description of the methods can be [found here](#).

Method *cutoff* and specifying a cutoff radius uses the traditional approach being the one in which the neighbors of an atom are the ones that lie in the cutoff distance around it.

In order to reduce time during the distance sorting during the adaptive methods, pyscal sets an initial guess for a cutoff distance. This is calculated as,

$$r_{initial} = threshold * (simulation\ box\ volume / number\ of\ particles)^{(1/3)}$$

*threshold* is a safe multiplier used for the guess value and can be set using the *threshold* keyword.

In Method *cutoff*, if *cutoff='adaptive'*, an adaptive cutoff is found during runtime for each atom [1]. Setting the cutoff radius to 0 also uses this algorithm. The cutoff for an atom *i* is found using,

$$r_c(i) = padding * ((1/nlimit) * \sum_{j=1}^{nlimit} (r_{ij}))$$

*padding* is a safe multiplier to the cutoff distance that can be set through the keyword *padding*. *nlimit* keyword sets the limit for the top *nlimit* atoms to be taken into account to calculate the cutoff radius.

In Method *cutoff*, if *cutoff='sann'*, sann algorithm is used [2]. There are no parameters to tune sann algorithm.

The second approach is using Voronoi polyhedra which also assigns a weight to each neighbor in the ratio of the face area between the two atoms. Higher powers of this weight can also be used [3]. The keyword *voroexp* can be used to set this weight.

**Warning:** Adaptive cutoff uses a padding over the initial guessed “neighbor distance”. By default it is 2. In case of a warning that *threshold* is inadequate, this parameter should be further increased. High/low value of this parameter will correspond to the time taken for finding neighbors.

## References

**find\_solid** (*bonds=0.5, threshold=0.5, avgthreshold=0.6, cluster=True, q=6, new\_algo=False, cutoff=0*)

Distinguish solid and liquid atoms in the system.

### Parameters

- **bonds** (*int or float, optional*) – Minimum number of solid bonds for an atom to be identified as a solid if the value is an integer. Minimum fraction of neighbors of an atom that should be solid for an atom to be solid if the value is float between 0-1. Default 0.5.
- **threshold** (*double, optional*) – Solid bond cutoff value. Default 0.5.
- **avgthreshold** (*double, optional*) – Value required for Averaged solid bond cutoff for an atom to be identified as solid. Default 0.6.
- **cluster** (*bool, optional*) – If True, cluster the solid atoms and return the number of atoms in the largest cluster.
- **q** (*int, optional*) – The Steinhardt parameter value over which the bonds have to be calculated. Default 6.

**Returns solid** – Size of the largest solid cluster. Returned only if *cluster=True*.

**Return type** int

## Notes

The neighbors should be calculated before running this function. Check *find\_neighbors()* method.

*bonds* define the number of solid bonds of an atom to be identified as solid. Two particles are said to be ‘bonded’ if [1],

$$s_{ij} = \sum_{m=-6}^6 q_{6m}(i)q_{6m}^*(i) \geq threshold$$

where *threshold* values is also an optional parameter.

If the value of *bonds* is a fraction between 0 and 1, at least that much of an atom’s neighbors should be solid for the atom to be solid.

An additional parameter *avgthreshold* is an additional parameter to improve solid-liquid distinction. In addition to having a the specified number of *bonds*,

$$\langle s_{ij} \rangle > avgthreshold$$

also needs to be satisfied. In case another q value has to be used for calculation of *S\_ij*, it can be set used the *q* attribute.

## References

### `from_pickle` (*file*)

Read the contents of *System* object from a pickle file.

**Parameters** `file` (*string*) – name of input file

**Returns**

**Return type** None

## Notes

This function can be used to set up a system from a file. A *System* object needs to be created first.

## Examples

```
>>> sys = System()
>>> sys.from_pickle(filename)
```

### `get_atom` (*index*)

Get the *Atom* object at the queried position in the list of all atoms in the *System*.

**Parameters** `index` (*int*) – index of required atom in the list of all atoms.

**Returns** `atom` – atom object at the queried position.

**Return type** Atom object

### `get_distance` (*atom1*, *atom2*, *vector=False*)

Get the distance between two atoms.

**Parameters**

- `atom1` (*Atom* object) – first atom
- `atom2` (*Atom* object) – second atom
- `vector` (*bool*, *optional*) – If True, the displacement vector connecting the atoms is also returned. default false.

**Returns** `distance` – distance between the first and second atom.

**Return type** double

## Notes

Periodic boundary conditions are assumed by default.

### `get_qvals` (*q*, *averaged=False*)

Get the required `q_l` (Steinhardt parameter) values of all atoms.

**Parameters**

- `q_l` (*int* or *list of ints*) – required `q_l` value with `l` from 2-12
- `averaged` (*bool*, *optional*) – If True, return the averaged `q` values, default False

**Returns** `qvals` – list of `q_l` of all atoms.

**Return type** list of floats

## Notes

The function returns a list of `q_l` values in the same order as the list of the atoms in the system.

### `prepare_pickle()`

Prepare the system for pickling and create a picklable system

**Parameters** None –

**Returns** `psys`

**Return type** picklable system object

## Notes

This function prepares the system object for pickling. From a user perspective, the `to_pickle()` method should be used directly.

**See also:**

`to_file()`

### `read_inputfile(filename, format='lammgs-dump', frame=-1, compressed=False, customkeys=None, is_triclinic=False)`

Read input file that contains the information of system configuration.

#### Parameters

- **filename** (*string*) – name of the input file.
- **format** (`{'lammgs-dump', 'poscar', 'ase', 'mdtraj'}`) – format of the input file, in case of *ase* the ASE Atoms object
- **compressed** (*bool, optional*) – If True, force to read a gz compressed format, default False.
- **frame** (*int*) – If the trajectory contains more than one time step, the slice can be specified using the *frame* option.

---

**Note:** works only with *lammgs-dump* format.

---

- **customkeys** (*list*) – A list containing names of headers of extra data that needs to be read in from the input file.
- **is\_triclinic** (*bool, optional*) – Only used in the case of *format='ase'*. If the read ase object is triclinic, this options should be set to True.

#### Returns

**Return type** None

## Notes

*format* keyword specifies the format of the input file. Currently only *lammgs-dump* and *poscar* files are supported. Additionally, the widely use Atomic Simulation environment (<https://wiki.fysik.dtu.dk/ase/ase/ase.html>). *mdtraj* objects (<http://mdtraj.org/1.9.3/>) are also supported by using the keyword '*mdtraj*' for format. Please note that triclinic boxes are not yet supported for *mdtraj* format. Atoms object can also be used directly. This function uses the `traj_process()` module to process a file which is then assigned to system.

*compressed* keyword is not required if a file ends with *.gz* extension, it is automatically treated as a compressed file.

*frame* keyword allows to read in a particular slice from a long trajectory. If all slices need to be analysed, this is a very inefficient way. For handling multiple time slices, the *traj\_process()* module offers a better set of tools.

Triclinic simulation boxes can also be read in for *lammps-dump*. No special keyword is necessary.

If *custom\_keys* are provided, this extra information is read in from input files if available. This information is not passed to the C++ instance of *atom*, and is stored as a dictionary. It can be accessed directly as *atom.custom['customval']*

#### **reset\_neighbors ()**

Reset the neighbors of all atoms in the system.

**Parameters** *None* –

**Returns**

**Return type** *None*

#### **Notes**

It is used automatically when neighbors are recalculated.

#### **set\_atom (atom)**

Return the atom to its original location after modification.

**Parameters** *atom (Atom)* – atom to be replaced

**Returns**

**Return type** *None*

#### **Notes**

For example, an *Atom* at location *i* in the list of all atoms in *System* can be queried by, *atom = System.get\_atom(i)*, then any kind of modification, for example, the position of the *Atom* can be done by, *atom.pos = [2.3, 4.5, 4.5]*. After modification, the *Atom* can be set back to its position in *System* by *set\_atom()*.

Although the complete list of atoms can be accessed or set using *atoms = sys.atoms*, *get\_atom* and *set\_atom* functions should be used for accessing individual atoms. If an atom already exists at that index in the list, it will be overwritten and will lead to loss of information.

#### **to\_file (outfile, format='lammps-dump', custom=None, compressed=False)**

Save the system instance to a trajectory file.

**Parameters**

- **outfile** (*string*) – name of the output file
- **format** (*string, optional*) – format of the output file, default *lammps-dump*. Currently only *lammps-dump* format is supported.
- **custom** (*list of strings, optional*) – a list of extra atom wise values to be written in the output file.
- **compressed** (*bool, optional*) – If true, the output is written as a compressed file.

**Returns**

**Return type** None

### Notes

`to_pickle` (*file*)

Save a system to pickle file

**Parameters** `file` (*string*) – name of output file

**Returns**

**Return type** None

### Notes

This function can be used to save a *System* object directly to file. This retains all the calculated quantities of the system, including the atoms and their properties. This can be useful to restart the calculation. The function uses *numpy.save* method to save the information. Hence pickling between different versions of python could lead to issues.

**Warning:** Pickling between different versions of numpy or python could be incompatible. Pickling is not secure. You should only unpickle objects that you trust.

`pyscal.core.test` ()

A simple function to test if the module works

**Parameters** None –

**Returns** `works` – True if the module works and could create a System and Atom object False otherwise.

**Return type** bool

**class** `pyscal.catom.Atom`

Bases: `pybind11_builtins.pybind11_object`

Class to store atom details.

**Parameters**

- `pos` (*list of floats of length 3*) – position of the *Atom*, default [0,0,0]
- `id` (*int*) – id of the *Atom*, default 0
- `type` (*int*) – type of the *Atom*, default 1

### Notes

A pybind11 class for holding the properties of a single atom. Various properties of the atom can be accessed through the attributes and member functions which are described below in detail. Atoms can be created individually or directly by reading a file. Check the examples for more details on how atoms are created. For creating atoms directly from an input file check the documentation of *System* class.

Although an *Atom* object can be created independently, *Atom* should be thought of inherently as members of the *System* class. All the properties that define an atom are relative to the parent class. *System* has a list of all atoms. All the properties of an atom, hence should be calculated through *System*.

## Examples

```

>>> #method 1 - individually
>>> atom = Atom()
>>> #now set positions of the atoms
>>> atom.pos = [23.0, 45.2, 34.2]
>>> #now set id
>>> atom.id = 23
>>> #now set type
>>> atom.type = 1
>>> #Setting through constructor
>>> atom = Atom([23.0, 45.2, 34.2], 23, 1)

```

## References

Creation of atoms.

### **allaq**

*list of floats.* list of all averaged q values of the atom.

### **allq**

*list of floats.* list of all q values of the atom.

### **angular**

*Float.* The value of angular parameter A of an atom. The angular parameter measures the tetrahedral coordination of an atom. Meaningful values are only returned if the property is calculated using `calculate_angularcriteria()`.

### **avg\_angular**

*Float.* The average angular parameter value. Not used currently.

### **avg\_disorder**

*Float.* The value of averaged disorder parameter.

### **avg\_sij**

*float.* Value of averaged  $s_{ij}$  which is used for identification of solid atoms.  $s_{ij}$  is defined by

$$s_{ij} = \sum_{m=-l}^l q_{lm}(i)q_{lm}^*(i)$$

### **avg\_volume**

*float.* Averaged version of the Voronoi volume which is calculated as an average over itself and its neighbors. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

### **bonds**

*Int.* The number of solid bonds of an atom.

### **chiparams**

*Float.* The value of chiparameter of an atom. The return value is a vector of length 8. Meaningful values are only returned if chi params are calculated using `calculate_chiparams()`.

### **cluster**

*int.* identification number of the cluster that the atom belongs to.

### **condition**

*int.* condition that specifies if an atom is included in the clustering algorithm or not. Only atoms with the value of `condition=1` will be used for clustering in `cluster_atoms()`.

**coordination**

*int.* coordination number of the atom. Coordination will only be updated after neighbors are calculated using `find_neighbors()`.

**custom**

*dict.* dictionary specifying custom values for an atom. The module only stores the id, type and position of the atom. If any extra values need to be stored, they can be stored in custom using `atom.custom = {"velocity":12}`. `read_inputfile()` can also read in extra atom information. By default, custom values are treated as string.

**cutoff**

*double.* cutoff used for finding neighbors for each atom.

**disorder**

*Float.* The value of disorder parameter.

**edge\_lengths**

*list of floats.* For each face, this vector contains the lengths of edges that make up the Voronoi polyhedra of the atom. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

**face\_perimeters**

*list of floats.* List consisting of the perimeters of each Voronoi face of an atom. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

**face\_vertices**

*list of floats.* A list of the number of vertices shared between an atom and its neighbors. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

**get\_q()**

Calculate the steinhardt parameter `q_l` value.

**Parameters**

- `q` (*int or list of ints*) – number of the required `q_l` - from 2-12
- `averaged` (*bool, optional*) – If True, return the averaged `q` values, If False, return the non averaged ones default False

**Returns** `q_l` – the value(s) of the queried Steinhardt parameter(s).

**Return type** float or list of floats

**Notes**

Please check this [link](#) for more details about Steinhardts parameters and the averaged versions.

Meaningful values are only returned if `calculate_q()` is used.

**id**

*int.* Id of the atom.

**largest\_cluster**

*bool.* True if the atom belongs to the largest cluster, False otherwise. Largest cluster is only identified after using the `cluster_atoms()` function.

**loc**

*int.* indicates the position of the atom in the list of all atoms.

**mask**

*bool.* Mask variable for atom. If mask is true, the atom is ignored from calculations.



**neighbor\_distance**

*List of floats.* List of neighbor distances of the atom.

**neighbor\_weights**

*List of floats.* Used to weight the contribution of each neighbor atom towards the value of Steinhardt's parameters. By default, each atom has a weight of 1 each. However, if `find_neighbors()` is used with `method='voronoi'`, each neighbor gets a weight proportional to the area shared between the neighboring atom and host atom.

**neighbors**

*List of ints.* List of neighbors of the atom. The list contains indices of neighbor atoms which indicate their position in the list of all atoms.

**pos**

*List of floats of the type [x, y, z], default [0, 0, 0].* Position of the atom.

**set\_q()**

Set the value of steinhardt parameter `q_l`.

**Parameters**

- **q** (*int or list of ints*) – number of the required `q_l` - from 2-12
- **val** (*float or list of floats*) – value(s) of Steinhardt parameter(s).
- **averaged** (*bool, optional*) – If True, return the averaged `q` values, If False, return the non averaged ones default False

**Returns**

**Return type** None

**sij**

*float.* Value of `s_ij` which is used for identification of solid atoms. `s_ij` is defined by

$$s_{ij} = \sum_{m=-l}^l q_{lm}(i) q_{lm}^*(i)$$

**solid**

*bool.* True if the atom is solid, False otherwise. Solid atoms are only identified after using the `find_solids()` function.

**sro**

*Float.* The value of short range order parameter.

**structure**

*int.* Indicates the structure of atom. Not used currently.

**surface**

*bool.* True if the atom has at least one liquid neighbor, False otherwise. Surface atoms are only identified after using the `find_solids()` function.

**type**

*int.* int specifying type of the atom.

**vertex\_numbers**

*list of floats.* For each Voronoi face of the atom, this values includes a List of vertices that constitute the face. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

**vertex\_vectors**

*list of floats.* A list of positions of each vertex of the Voronoi polyhedra of the atom. Only calculated when the `find_neighbors()` using the `method='voronoi'` option is used.

**volume**

*float*. Voronoi volume of the atom. The Voronoi volume is only calculated if neighbors are found using the `find_neighbors()` using the `method='voronoi'` option.

**vorovector**

*list of ints*. A vector of the form  $(n_3, n_4, n_5, n_6)$  where  $n_3$  is the number of faces with 3 vertices,  $n_4$  is the number of faces with 4 vertices and so on. This can be used to identify structures [1][2]. Vorovector is calculated if the `calculate_vorovector()` method is used.

**References**

**pyscal.crystal\_structures module**

pyscal module for creating crystal structures.

`pyscal.crystal_structures.make_crystal` (*structure*, *lattice\_constant=1.0*, *repetitions=None*, *ca\_ratio=1.633*, *noise=0*)

Create a basic crystal structure and return it as a list of *Atom* objects and box dimensions.

**Parameters**

- **structure** (`{'bcc', 'fcc', 'hcp', 'diamond' or '112'}`) – type of the crystal structure
- **lattice\_constant** (*float, optional*) – lattice constant of the crystal structure, default 1
- **repetitions** (*list of ints of len 3, optional*) – of type  $[n_x, n_y, n_z]$ , repetitions of the unit cell in x, y and z directions. default  $[1, 1, 1]$ .
- **ca\_ratio** (*float, optional*) – ratio of *c/a* for hcp structures, default 1.633
- **noise** (*float, optional*) – If provided add normally distributed noise with standard deviation *noise* to the atomic positions.

**Returns**

- **atoms** (list of *Atom* objects) – list of all atoms as created by user input
- **box** (*list of list of floats*) – list of the type  $[[x_{low}, x_{high}], [y_{low}, y_{high}], [z_{low}, z_{high}]]$  where each of them are the lower and upper limits of the simulation box in x, y and z directions respectively.

**Examples**

```

>>> atoms, box = make_crystal('bcc', lattice_constant=3.48, repetitions=[2,2,2])
>>> sys = System()
>>> sys.assign_atoms(atoms, box)
```

**pyscal.traj\_process module**

pyscal module containing methods for processing of a trajectory. Methods for reading of input files formats, writing of output files etc are provided in this module.

`pyscal.traj_process.read_ase` (*aseobject*, *check\_triclinic=False*, *box\_vectors=False*)

Function to read from a ASE atoms objects

**Parameters**

- **aseobject** (*ASE Atoms object*) – name of the ASE atoms object
- **triclinic** (*bool, optional*) – True if the configuration is triclinic
- **box\_vectors** (*bool, optional*) – If true, return the full box vectors along with *boxdims* which gives upper and lower bounds. default False.

```
pyscal.traj_process.read_lammps_dump(infile, compressed=False, check_triclinic=False,
                                     box_vectors=False, customkeys=None)
```

Function to read a lammps dump file format - single time slice.

#### Parameters

- **infile** (*string*) – name of the input file
- **compressed** (*bool, optional*) – force to read a gz zipped file. If the filename ends with *.gz*, use of this keyword is not necessary. Default True.
- **check\_triclinic** (*bool, optional*) – If true check if the sim box is triclinic. Default False.
- **box\_vectors** (*bool, optional*) – If true, return the full box vectors along with *boxdims* which gives upper and lower bounds. default False.
- **customkeys** (*list of strings, optional*) – A list of extra keywords to read from trajectory file.

#### Returns

- **atoms** (list of *Atom* objects) – list of all atoms as created by user input
- **boxdims** (*list of list of floats*) – The dimensions of the box. This is of the form  $[[x_{lo}, x_{hi}], [y_{lo}, y_{hi}], [z_{lo}, z_{hi}]]$  where *lo* and *hi* are the upper and lower bounds of the simulation box along each axes. For triclinic boxes, this is scaled to  $[0, \text{scalar length of the vector}]$ .
- **box** (*list of list of floats*) – list of the type  $[[x1, x2, x3], [y1, y2, y3], [z1, z2, z3]]$  which are the box vectors. Only returned if *box\_vectors* is set to True.
- **triclinic** (*bool*) – True if the box is triclinic. Only returned if *check\_triclinic* is set to True
- .. *note::* – Values are always returned in the order *atoms, boxdims, box, triclinic* if all return keywords are selected. For example, if *check\_triclinic* is not selected, the return values would still preserve the order and fall back to *atoms, boxdims, box*.

#### Notes

Read a lammps-dump style snapshot that can have variable headers, reads in type and so on. Zipped files which end with a *.gz* can also be read automatically. However, if the file does not end with a *.gz* extension, keyword *compressed = True* can also be used.

#### Examples

```
>>> atoms, box = read_lammps_dump('conf.dump')
>>> atoms, box = read_lammps_dump('conf.dump.gz')
>>> atoms, box = read_lammps_dump('conf.d', compressed=True)
```

```
pyscal.traj_process.read_mdtraj(mdobject, check_triclinic=False, box_vectors=False)
```

Function to read from an MDTraj atoms objects

#### Parameters

- **mobject** (*MDTraj Atoms object*) – name of the MDTraj atoms object
- **triclinic** (*bool, optional*) – True if the configuration is triclinic
- **box\_vectors** (*bool, optional*) – If true, return the full box vectors along with *boxdims* which gives upper and lower bounds. default False.

`pyscal.traj_process.read_poscar` (*infile, compressed=False, box\_vectors=False*)

Function to read a POSCAR format.

#### Parameters

- **infile** (*string*) – name of the input file
- **compressed** (*bool, optional*) – force to read a gz zipped file. If the filename ends with *.gz*, use of this keyword is not necessary, Default False

#### Returns

- **atoms** (list of *Atom* objects) – list of all atoms as created by user input
- **box** (*list of list of floats*) – list of the type *[[xlow, xhigh], [ylow, yhigh], [zlow, zhigh]]* where each of them are the lower and upper limits of the simulation box in x, y and z directions respectively.

#### Examples

```

>>> atoms, box = read_poscar('POSCAR')
>>> atoms, box = read_poscar('POSCAR.gz')
>>> atoms, box = read_poscar('POSCAR.dat', compressed=True)
```

`pyscal.traj_process.split_traj_lammps_dump` (*infile, compressed=False*)

Read in a LAMMPS dump trajectory file and convert it to individual time slices.

#### Parameters

- **filename** (*string*) – name of input file
- **compressed** (*bool, optional*) – force to read a gz zipped file. If the filename ends with *.gz*, use of this keyword is not necessary, Default False.

**Returns** *snaps* – a list of filenames which contain individual frames from the main trajectory.

**Return type** list of strings

`pyscal.traj_process.split_trajectory` (*infile, format='lammps-dump', compressed=False*)

Read in a trajectory file and convert it to individual time slices.

#### Parameters

- **filename** (*string*) – name of input file
- **format** (*format of the input file*) – only *lammps-dump* is supported now.
- **compressed** (*bool, optional*) – force to read a gz zipped file. If the filename ends with *.gz*, use of this keyword is not necessary.

**Returns** *snaps* – a list of filenames which contain individual frames from the main trajectory.

**Return type** list of strings

## Notes

This is a wrapper function around `split_traj_lammps_dump` function.

`pyscal.traj_process.write_structure` (*sys*, *outfile*, *format='lammps-dump'*, *compressed=False*,  
*customkey=None*, *customvals=None*)

Write the state of the system to a trajectory file.

### Parameters

- **sys** (*System* object) – the system object to be written out
- **outfile** (*string*) – name of the output file
- **format** (*string*, *optional*) – the format of the output file, as of now only *lammps-dump* format is supported.
- **compressed** (*bool*, *default false*) – write a .gz format
- **customkey** (*string or list of strings*, *optional*) – If specified, it adds this custom column to the dump file. Default None.
- **customvals** (*list or list of lists*, *optional*) – If *customkey* is specified, *customvals* take an array of the same length as number of atoms, which contains the values to be written out.

### Returns

**Return type** None

## pyscal.pickle module



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## Support, contributing and extending

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### 8.1 Support, contributing and extending

pyscal welcomes and appreciates contribution and extension to the module. Rather than local modifications, we request that the modifications be submitted through a pull request, so that the module can be continuously improved.

The following links will help you get started with contributing to pyscal.

#### 8.1.1 Contributions to existing features

##### Reporting and fixing bugs

In case a bug is found in the module, it can be reported on the [issues page of the repository](#). After clicking on the new issue button, there is template already provided for Bug report. Please choose this and make sure the necessary fields are filled. Once a bug is reported, the status can once again monitored on the issues page. Additionally, you are of course very welcome to fix any existing bugs.

#### 8.1.2 New features

If you have an idea for new feature, you can submit a feature idea through the [issues page of the repository](#). After choosing new issue, please choose the template for feature request. As much as information as you can provide about the new feature would be greatly helpful. Additionally, you could also work on feature requests already on the issues page. The following instructions will help you get started with local feature development.

##### Setting up local environment

1. The first step is to fork pyscal. A detailed tutorial on forking can be found [here](#). After forking, clone the repository to your local machine.
2. We recommend creating a virtual environment to test new features or improvements to features. See this [link](#) for help on managing environments.

3. Once the environment is set up, you can create a new branch for your feature by `git checkout -b new_feaature`.
4. Now implement the necessary feature.
5. Once done, you can reinstall `pyscal` by `python setup.py install`. After that please make sure that the existing tests work by running `pytest tests/` from the main module folder.
6. If the tests work, you are almost done! If the new feature is not covered in existing tests, you can to write a new test in the tests folder. `pyscal` uses `pytest` for tests. [This link](#) will help you get started.
7. Add the necessary docstrings for the new functions implemented. `pyscal` uses the [numpy docstring format](#) for documentation.
8. Bonus task: Set up few examples that document how the feature works in the `docs/source/` folder and link it to the examples section.
9. Final step - Submit a pull request through github. Before you submit, please make sure that the new feature is documented and has tests. Once the request is submitted, automated tests would be done. Your pull request will fail the tests if - the unit tests fail, or if the test coverage falls below 80%. If all tests are successful, your feaature will be incorporated to `pyscal` and your contributions will be credited.

If you have trouble with any of the steps, or you need help, please [send an email](#) and we will be happy to help! All of the contributions are greatly appreciated and will be credited in Developers/Acknowledgements page.

## 8.2 Help and support

In case of bugs and feature improvements, you are welcome to create a new issue on the [github repo](#). You are also welcome to fix a bug or implement a feature. Please see the [extending and contributing](#) section for more details.

Any other questions or suggestions are welcome, please contact us.

## 8.3 Common issues

- **Installation of the package without administrator privileges**

In case of any problems with installation, we recommend that you install the package in a conda environment. Details on managing and creating environments can be found [here](#) .

- **C++11 is not available**

`pyscal` needs C++11 to install and run. In case you do not have c++11, it can be installed in a conda environment by following [this link](#) . After installing `gcc`, once the conda environment is reactivated, the environment variables are set. The installation should proceed now without problems.

- **cmake is not available**

`cmake` can be installed in a conda environment. Details on managing and creating environments can be found [here](#) . The `cmake` package can be installed from conda following [this link](#).



### 9.1 Citing the code

If you use `pyscal` in your work, the citation of the [following article](#) will be greatly appreciated:

Sarath Menon, Grisell Díaz Leines and Jutta Rogal (2019). `pyscal`: A python module for structural analysis of atomic environments. *Journal of Open Source Software*, 4(43), 1824, <https://doi.org/10.21105/joss.01824>

Citation in bib format can be downloaded [here](#).

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- Jan Janßen - developing and maintaining a [conda-forge](#) recipe.

### 9.4 Acknowledgements

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**p**

`pyscal.catom`, 58

`pyscal.core`, 47

`pyscal.crystal_structures`, 62

`pyscal.traj_process`, 62





**A**

allaq (*pyscal.catom.Atom attribute*), 59  
 allq (*pyscal.catom.Atom attribute*), 59  
 angular (*pyscal.catom.Atom attribute*), 59  
 Atom (*class in pyscal.catom*), 58  
 atoms (*pyscal.core.System attribute*), 47  
 avg\_angular (*pyscal.catom.Atom attribute*), 59  
 avg\_disorder (*pyscal.catom.Atom attribute*), 59  
 avg\_sij (*pyscal.catom.Atom attribute*), 59  
 avg\_volume (*pyscal.catom.Atom attribute*), 59

**B**

bonds (*pyscal.catom.Atom attribute*), 59  
 box (*pyscal.core.System attribute*), 47

**C**

calculate\_angularcriteria() (*pyscal.core.System method*), 48  
 calculate\_chiparams() (*pyscal.core.System method*), 48  
 calculate\_disorder() (*pyscal.core.System method*), 49  
 calculate\_q() (*pyscal.core.System method*), 49  
 calculate\_rdf() (*pyscal.core.System method*), 50  
 calculate\_solidneighbors() (*pyscal.core.System method*), 50  
 calculate\_sro() (*pyscal.core.System method*), 50  
 calculate\_vorovector() (*pyscal.core.System method*), 51  
 chiparams (*pyscal.catom.Atom attribute*), 59  
 cluster (*pyscal.catom.Atom attribute*), 59  
 cluster\_atoms() (*pyscal.core.System method*), 51  
 condition (*pyscal.catom.Atom attribute*), 59  
 coordination (*pyscal.catom.Atom attribute*), 59  
 custom (*pyscal.catom.Atom attribute*), 60  
 cutoff (*pyscal.catom.Atom attribute*), 60

**D**

disorder (*pyscal.catom.Atom attribute*), 60

**E**

edge\_lengths (*pyscal.catom.Atom attribute*), 60

**F**

face\_perimeters (*pyscal.catom.Atom attribute*), 60  
 face\_vertices (*pyscal.catom.Atom attribute*), 60  
 find\_clusters() (*pyscal.core.System method*), 52  
 find\_largestcluster() (*pyscal.core.System method*), 52  
 find\_neighbors() (*pyscal.core.System method*), 52  
 find\_solids() (*pyscal.core.System method*), 54  
 from\_pickle() (*pyscal.core.System method*), 55

**G**

get\_atom() (*pyscal.core.System method*), 55  
 get\_distance() (*pyscal.core.System method*), 55  
 get\_q() (*pyscal.catom.Atom method*), 60  
 get\_qvals() (*pyscal.core.System method*), 55

**I**

id (*pyscal.catom.Atom attribute*), 60

**L**

largest\_cluster (*pyscal.catom.Atom attribute*), 60  
 loc (*pyscal.catom.Atom attribute*), 60

**M**

make\_crystal() (*in module pyscal.crystal\_structures*), 62  
 mask (*pyscal.catom.Atom attribute*), 60

**N**

neighbor\_distance (*pyscal.catom.Atom attribute*), 60  
 neighbor\_weights (*pyscal.catom.Atom attribute*), 61  
 neighbors (*pyscal.catom.Atom attribute*), 61

## P

pos (*pyscal.catom.Atom attribute*), 61  
prepare\_pickle() (*pyscal.core.System method*), 56  
pyscal.catom (*module*), 58  
pyscal.core (*module*), 47  
pyscal.crystal\_structures (*module*), 62  
pyscal.traj\_process (*module*), 62

## R

read\_ase() (*in module pyscal.traj\_process*), 62  
read\_inputfile() (*pyscal.core.System method*), 56  
read\_lammps\_dump() (*in module  
pyscal.traj\_process*), 63  
read\_mdtraj() (*in module pyscal.traj\_process*), 63  
read\_poscar() (*in module pyscal.traj\_process*), 64  
reset\_neighbors() (*pyscal.core.System method*),  
57

## S

set\_atom() (*pyscal.core.System method*), 57  
set\_q() (*pyscal.catom.Atom method*), 61  
sij (*pyscal.catom.Atom attribute*), 61  
solid (*pyscal.catom.Atom attribute*), 61  
split\_traj\_lammps\_dump() (*in module  
pyscal.traj\_process*), 64  
split\_trajectory() (*in module  
pyscal.traj\_process*), 64  
sro (*pyscal.catom.Atom attribute*), 61  
structure (*pyscal.catom.Atom attribute*), 61  
surface (*pyscal.catom.Atom attribute*), 61  
System (*class in pyscal.core*), 47

## T

test() (*in module pyscal.core*), 58  
to\_file() (*pyscal.core.System method*), 57  
to\_pickle() (*pyscal.core.System method*), 58  
type (*pyscal.catom.Atom attribute*), 61

## V

vertex\_numbers (*pyscal.catom.Atom attribute*), 61  
vertex\_vectors (*pyscal.catom.Atom attribute*), 61  
volume (*pyscal.catom.Atom attribute*), 61  
vorovector (*pyscal.catom.Atom attribute*), 62

## W

write\_structure() (*in module  
pyscal.traj\_process*), 65