

## COOP Utility how to use ?

Dr Mohan L Verma

Computational Nanoionics Research Lab, Department of Applied Physics,

FETSSGI, Shri Shankaracharya Technical Campus Junwani

Bhilai (Chhattisgarh ) INDIA 490020

22 NOVEMBER 2014

---

This utility is available in `~/siesta/Util/COOP`.

If your siesta has been successfully compiled, then using simple “make” command in this directory, one can get required *mprop* binary file. Copy this binary file in your working directory for coop/cohp/pdos analysis of your system under study.

In order to start using coop utility first of all you have to add :

*COOP*.Write `.true`.

In your input `*.fdf` file.

After a successful siesta run, this will generate all required files i.e. `*.HSX` and `*.WFSX` in working directory. For further coop analysis, make a directory `COOP` and copy `*.HSX`, `*.WFSX` file and *mprop* compiled in `~/siesta/Util/COOP` in this directory.

Now let us create two different input files for coop/cohp as well as PDOS study.

Here I am giving you one example of BATIO3 taken from siesta-L.

(a) For COOP/COHP study

make a text file entitled as *coo.mpr* containing following :

```

BaTiO3 # Name of the siesta output files (as in SystemLabel)
COOP # calculation is a COOP analysis (could be DOS)
Ti-O # (line(2)) Name of the current curve: Coop/cohp for Ti-O which
      include Ti(3d, 4s,6p) and O(2s,2p)
Ti # (lines(3,20)) Reference atom, for which you could have
included a list of atomic orbitals. Since there's none, all the orbitals of
the Ti will be included in the analysis.
2.0 3.0 # (line(4)) Bond distance range in calculating COOP/COHP
O # (line(5)) Neighboring atoms, for which you could have
included a list of atomic orbitals. Since there's none, all the orbitals of
the O atoms in the range 2-3 Bohr will be included in the analysis.
Ti3d-O2s # Coop/Cohp for Ti(3d)-O(2s)
Ti_3d
2.0 3.0 # Bond distance range in calculating COOP/COHP
O_2s
Ti3d-O2p # Coop/Cohp for Ti(3d)-O(2p)
Ti_3d
2.0 3.0 # Bond distance range in calculating COOP/COHP
O_2p
.
.

```

---

Then for COHP/COOP run the command in working directory :

```
./mprop -s 0.1 -n 500 -m -25 -M 25 coo
```

Here -s parameter for energy smearing in calculate coop/cohp/pdos. It should be approximately equal to  $(M-m)/n$ , -n parameter is number of points in coop/cohp/pdos data -m and -M parameters is the lowest and highest energy

point for coop/cohp/pdos calculation. Remember there is no empty line in coo.mpr.

(b) For DOS/PDOS

make another text file entitled as *pdos.mpr* containing following :

BaTiO3 #outputname

DOS

Ti\_dos

Ti

Ti3d

Ti\_3d

Ti4s

Ti\_4s

O2p

O\_2p

.

.

---

and use the command in working directory as :

```
./mprop -s 0.01 -n 500 -m -15 -M 15 pdos
```

For details of this utility simply type `./mprop -h` in the COOP utility folder of SIESTA. It will give you the manual. Some test files are also given in `~/siesta/Util/COOP/Tests`.

Now using a suitable plotting tool you can plot

\*.PDOS, \*.COOP or \*.COHP files for different bonds.

All the best.

Please give the feedback in [drmohanlv@gmail.com](mailto:drmohanlv@gmail.com)