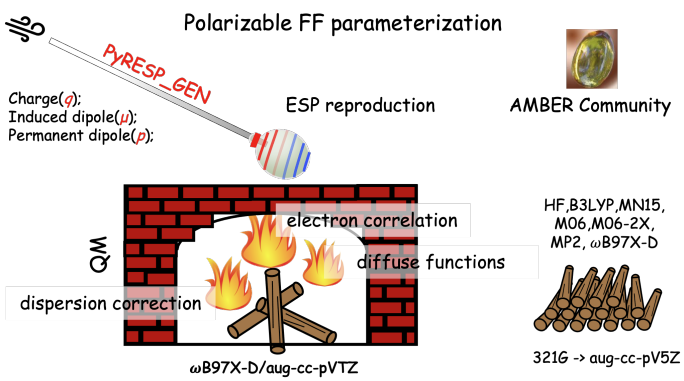
Parameterization of Polarizable Gaussian Multipole (pGM) models with the help of PyRESP_GEN

Feb 16, 2023 • Qiang Zhu, Yongxian Wu

1. Introduction

Accurate description of the electrostatic interactions plays significant role in the molecular simulations. For well characterizing the electrostatic interactions, various polarizable methods have been proposed,[1] such as fluctuating charge (FQ), inducible dipole (ID), and Drude oscillator and so on. Among these methods, polarization catastrophe was observed. An alternative was polarizable Gaussian Multipole (pGM) Model which utilizing the Gaussian functions with the point charges and dipoles replaced by s-orbital functions and p-orbital functions. This method could bypass the catastrophe automatically given the Gaussian functions are sufficiently diffuse. Recently, the robustness of pGM model has been validated on the interaction energies,[2] many-body interaction energies together with the non-additive and additive contribution,[2] and polarizability anisotropy.[3] However, the input file preparation for the pGM model parameter determination is error-prone and laborious. As a consequence, we developed a program, PyRESP_GEN , which is easy-to-use and flexible.[4] This program only requires ESP data file generated by espgen and could dumps 1st stage and 2nd stage file for pGM model parameterization, automatically.

In this tutorial, we will give a detailed instruction on how to make use of PyRESP_GEN[4] for generating input files for `pGM-ind` and `pGM-perm` model. Then, we will show examples on the parameterization derivation using PyRESP[2].



This tutorial is organized in the following order:

- Program Installation
  - PyRESP_GEN
  - PyRESP
- Arguments explanation of PyRESP_GEN
- Examples
  - CH3SCH3
  - NH4+ (charged molecule)
  - CH3NH2
- References

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2. Installation

2.1 Installation of PyRESP_GEN

- From source

```
$ git clone git@github.com:csu1505110121/pyresp_gen.git
$ cd pyresp_gen
$ conda env create -n ENV_NAME -f pyresp_gen_env.yml
$ conda activate ENV_NAME
$ export PATH=/path/to/pyresp_gen:$PATH
    Setting the environment path:
      - For `Zsh` Shell: Editing the ~/.zshrc and adding the following l
         export PATH=/your/path/to/pyresp_gen:$PATH
      - For `Bash` User: Editing the ~/.bashrc file and adding the same
         export PATH=/your/path/to/pyresp_gen:$PATH
$ source ~/.zshrc or source ~/.bashrc (effective immediately)
```

The whole package contains the following files and arranged in such hierarchical structure

```
$ tree
```

```
.
├── README.md
├── __init__.py
├── __pycache__
│   ├── constant.cpython-38.pyc
│   ├── constant_radii.cpython-38.pyc
│   ├── prepin.cpython-38.pyc
│   └── zmatrix.cpython-38.pyc
├── constant.py
├── constant_radii.py
├── example
│   ├── C2H6_b3lyp_321g_esp.dat
│   ├── C3H8_mp2_a4z_esp.dat
│   ├── C6H6_b3lyp_321g_esp.dat
│   ├── CH3F_ccsd_a4z_esp.dat
│   ├── CH3NH2_mp2_a4z_esp.dat
│   ├── CH3S2CH3_b3lyp_321g_esp.dat
│   ├── CH3SO2CH3_mp2_a4z_esp.dat
│   ├── CHNHOH_mp2_a4z_esp.dat
│   ├── H2_ccsd_a5z_esp.dat
│   ├── esp.dat
│   └── qiang_test_case_esp_b321.dat
├── prepin.py
├── pyresp_gen.py
├── pyresp_gen_env.yml
└── zmatrix.py
```

The necessary files are `constant.py`, `constant_radii.py`, `prepin.py`, `pyresp_gen.py`,and `zmatrix.py`.

Core functions are all stored in the file `zmatrix.py`. Some test examples could be found in directory `example`.

2.2 Installation of PyRESP

- From source

```
$ git clone git@github.com:ShijiZ/PyRESP.git
$ export PATH=/path/to/PyRESP:$PATH
  Setting the environment path:
    - For `Zsh` User: Editing the ~/.zshrc and adding the following
       export PATH=/your/path/to/PyRESP:$PATH
    - For `Bash` User: Editing the ~/.bashrc file and adding the same
```

```
        export PATH=/your/path/to/PyRESP:$PATH
$ export HOME_PYRESP=/your/path/to/PyRESP/polarizability
$ source ~/.zshrc or source ~/.bashrc (effective immediately)
```

The whole package contains the following files

```
$ tree
.
├── polarizability
│   └── pGM-pol-2016-09-01
├── py_resp.py
```

`py_resp.py` is the main script, and `pGM-pol-2016-09-01` stores the polarizability parameters derived by Wang et al.[3]

---

3. Arguments explanation

3.1 PyRESP_GEN

```
  Usage: pyresp_gen.py [-h] --espdat ESPDAT [--Istage ISTAGE] [--IIstage
                       [--charge CHARGE] [--QWT1 QWT1] [--QWT2 QWT2] [--PW
                       [--DEPTH DEPTH] [--verbose VERBOSE] [--strategy STR
```

Necessary arguments:

`--espdat` or `-i` ESPDAT: Input file of esp data

Optional arguments:

1. `-h` or `--help` : Show help message and exit
2. `--Istage` or `-f1` ISTAGE: Output filename of 1st stage (default: `pyrespgen.1st`)
3. `--IIstage` or `-f2` IISTAGE: Output filename of 2nd stage (default: `pyrespgen.2nd`)
4. `--ptype` or `-p` PTYPE: Polarization type: x `chg` | x `ind` |x `perm` | x `perm-v` (default: `chg`)
5. `--dtype` or `-d` DTYPE: Damping function type: x `additive` | x `applequist` | x `tinker` | x `exp` | x `linear` (default: `additive`)
6. `--nmol` or `-n` NMOL: Number of conformations (default: `1`)

7. `--charge` or `-q` CHARGE: Total charge for this structure or conformer (default: `0`)
8. `--QWT1` or `-qwt1` QWT1: charge constraint (a_q) for 1st stage; (default: `0.0005`)
9. `--QWT2` or `-qwt2` QWT2: charge constraint (a_q) for 2nd stage; (default: `0.001`)
10. `--PWT1` or `-pwt1` PWT1: permanent dipoles (a_p) for 1st stage; (default: `0.0001`)
11. `--PWT2` or `-pwt2` PWT2: permanent dipoles (a_p) for 2nd stage; (default: `0.0005`)
12. `--EXC12` or `-exc12` EXC12: include (0) or exclude (1) 1-2 interaction (default: `0`)
13. `--EXC13` or `-exc13` EXC13: include (0) or exclude (1) 1-3 interaction (default: `0`)
14. `--DEPTH` or `-depth` DEPTH: Maximum depth for searching equivalent atoms (default: `3`)
15. `--verbose` or `-v` VERBOSE: Print verbose information (default: `0`)
16. `--strategy` or `-strategy` STRATEGY: Strategy for pGM-perm, only for debugging (default: `2`)

3.2 PyRESP

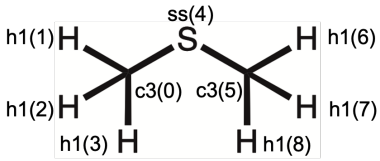
```
Usage: py_resp.py [-O] -i input -o output [-q qin] [-ip polariz] -t qout
```

Optional arguments:

1. `-h`, `--help`: Show this help message and exit
2. `-O`: Overwrite output files if they exist
3. `-i`, `--input` INPUT type: input, required; description: input of general information
4. `-e`, `--espot` ESPOT type: input, required; description: input of ESP and coordinates
5. `-q`, `--qin` QIN type: input, optional; description: replacement parameters
6. `-o`, `--output` OUTPUT type: output, always produced; description: output of results
7. `-t`, `--qout` QOUT type: output, always produced; description: output of parameters
8. `-s`, `--esout` ESOUT type: output, optional; description: generated ESP values for new parameters
9. `-ip` POLARIZ, –polariz POLARIZ type: input, optional; description: atomic polarizabilities

4. Examples

4.1 Case 1: CH3SCH3



4.1.1 Generation of electrostatic potentials with Gaussian

Step 1: input file generation

```
(filename: CH3SCH3.com)
%chk=CH3SCH3_a2z                          (specify the chk file name)
%nproc=28                                 (specify the num. of process )
%mem=28GB                                 (specify the memory)
#b3lyp/aug-cc-pvdz                        (methods/basis sets)
#SCF=tight
#maxdisk=200GB
#Pop=MK iop(6/33=2) iop(6/42=6) iop(6/43=20)
#IOP(5/87=12)
#density=current

   C3 MP2/6-311++G(d,p) coordinates     (optional)

  0  (charge)                    1. (multiplicity)
  C (elem) -1.361796871769 (x coor) -0.515789669798  (y coor) -0.0000578
  H (elem) -2.293815474604 (x coor)  0.053063245903  (y coor) -0.0001009
  H (elem) -1.338738381082 (x coor) -1.144434093987  (y coor) -0.8939501
  H (elem) -1.338815515689 (x coor) -1.144425446053  (y coor)  0.8938425
  S (elem)  0.000000000000 (x coor)  0.666316788502  (y coor) -0.0000057
  C (elem)  1.361796871989 (x coor) -0.515789668820  (y coor)  0.0000668
  H (elem)  2.293815474803 (x coor)  0.053063247384  (y coor)  0.0001089
  H (elem)  1.338733743617 (x coor) -1.144425283672  (y coor)  0.8939653
  H (elem)  1.338820151777 (x coor) -1.144434253910  (y coor) -0.8938274
(blank is needed here)
(blank is needed here)
```

Input file: CH3SCH3.com

Step 2: Execute Gaussian

```
# Make sure you have install Gaussian 16 or 09 correctly.
$ g16 CH3SCH3.com &
```

Output file: CH3SCH3.log

Step 3: Convert the log file into ESP file

```
$ espgen_junmei -i CH3SCH3.gout -o CH3SCH3.dat -p 1
## You will see following files:
## ESPGEN.TMP and CH3SCH3.dat
```

Esp data file: CH3SCH3.dat

The `dat` file head is shown as below:

```
   1     9 (num. of atoms) 3780 (num. of grids)    0 MOL        9   3780
   2                  -2.5734232E+00 (x coor) -9.7470177E-01 (y coor) -
   3                  -4.3346818E+00 (x coor)  1.0027453E-01 (y coor) -
   4                  -2.5298480E+00 (x coor) -2.1626667E+00 (y coor) -
   5                  -2.5299954E+00 (x coor) -2.1626497E+00 (y coor)
   6                   0.0000000E+00 (x coor)  1.2591566E+00 (y coor) -
   7                   2.5734232E+00 (x coor) -9.7470177E-01 (y coor)
   8                   4.3346818E+00 (x coor)  1.0027453E-01 (y coor)
   9                   2.5298404E+00  -2.1626497E+00   1.6893489E+00
  10                   2.5300029E+00  -2.1626667E+00  -1.6890881E+00
  11   -1.2030000E-03 (esp value)  -3.3327472E+00 (esp x coor)  3.404889
```

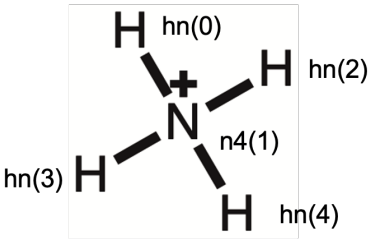
4.1.2 PyRESP_GEN generation

Step 1: Input file generation

```
# generating input file for RESP
$ cd 3-resp
$ pyresp_gen.py -i CH3SCH3.dat -p chg
# cd 4-ind
$ pyresp_gen.py -i CH3SCH3.dat -p ind
# cd 5-perm
$ pyresp_gen.py -i CH3SCH3.dat -p perm
```

3-resp; 4-ind; 5-perm

4.2 Case 2: NH4+



4.2.1 Generation of electrostatic potentials with Gaussian

Step 1: Input file generation

```
%chk=NH4+_b3lyp_a2z_esp
%nproc=28
%mem=28GB
#b3lyp/aug-cc-pvdz
#SCF=tight
#maxdisk=200GB
#Pop=MK iop(6/33=2) iop(6/42=6) iop(6/43=20)
#IOP(5/87=12)
#density=current

    Coordinates from nh4_m6311_opt.chk

    1    1
H   -0.951190136213    0.348537851523    0.152959323805
N   -0.000052158259    0.000090031932    0.000048013550
H    0.142159883375   -0.855519120874    0.545365091572
H    0.133112562719   -0.203821543598   -0.995003830076
H    0.676282797933    0.710172589425    0.296343319850
```

NH4+.com

Step 2: Execute Gaussian

```
$ g16 NH4+.com &
```

NH4+.log

Step 3: Convert the log file into ESP file

```
$ espgen_junmei -i NH4+.gout -o NH4+.dat -p 1
## You will see following files:
## ESPGEN.TMP and NH4+.dat
```

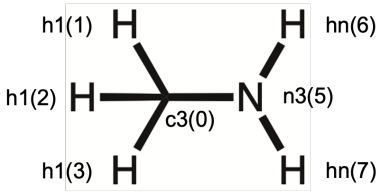
NH4+.dat

4.2.2 PyRESP_GEN generation

Step 1: Input file generation

```
***  Caution                                                 ***
***  for charged species                                     ***
***  you need arg `-q` to specify the charge manually ***
# generating input file for RESP
$ cd 3-resp
$ pyresp_gen.py -i CH3SCH3.dat -p chg -q 1
# cd 4-ind
$ pyresp_gen.py -i CH3SCH3.dat -p ind -q 1
# cd 5-perm
$ pyresp_gen.py -i CH3SCH3.dat -p perm -q 1
```

4.3 Case 3: CH3NH2



4.3.1 Generation of electrostatic potentials with Gaussian

Step 1: Input file generation

```
%chk=CH3NH2_b3lyp_a2z_esp
%nproc=28
%mem=28GB
#b3lyp/aug-cc-pvdz
#SCF=tight
#maxdisk=200GB
#Pop=MK iop(6/33=2) iop(6/42=6) iop(6/43=20)
#IOP(5/87=12)
#density=current
```

```
 B2 MP2/6-311++G(d,p) coordinates

0                     1
C       -0.708095503398       -0.000000893539        0.017712823484
H       -1.112963870065       -0.880513863166       -0.486271271246
H       -1.074379816824       -0.000087389127        1.053630363354
H       -1.112943454187        0.880611141673       -0.486114099690
N        0.750287956697       -0.000000780330       -0.122136797163
H        1.148419546341        0.813654667261        0.333717877871
H        1.148424918244       -0.813653733099        0.333717768949
```

CH3NH2.com

Step 2: Execute Gaussian

```
$ g16 CH3NH2.com &
```

CH3NH2.log

Step 3: Convert the log file into ESP file

```
$ espgen_junmei -i CH3NH2.gout -o CH3NH2.dat -p 1
## You will see following files:
## ESPGEN.TMP and CH3NH2.dat
```

CH3NH2.dat

4.3.2 PyRESP_GEN generation

Step 1: Input file generation

```
# generating input file for RESP
$ cd 3-resp
$ pyresp_gen.py -i CH3NH2.dat -p chg -q 0 -v 1
# cd 4-ind
$ pyresp_gen.py -i CH3NH2.dat -p ind -q 0 -v 1
# cd 5-perm
$ pyresp_gen.py -i CH3NH2.dat -p perm -q 0 -v 1
```

Since argment `-v` is activated, you will see verbose output information on the screen as below

```
Distance Map in the unit of angstrom (A)
      c3     h1     h1     h1     n3     hn     hn
6  0.000  1.092  1.099  1.092  1.465  2.051  2.051
1  1.092  0.000  1.774  1.761  2.093  2.942  2.406
1  1.099  1.774  0.000  1.774  2.171  2.474  2.474
1  1.092  1.761  1.774  0.000  2.093  2.406  2.942
7  1.465  2.093  2.171  2.093  0.000  1.014  1.014
1  2.051  2.942  2.474  2.406  1.014  0.000  1.627
1  2.051  2.406  2.474  2.942  1.014  1.627  0.000
Equivalent Atom Map:
 +   1 denotes equil
 +   0 denotes not equil
     6    1    1    1    7    1    1
6  1.0  0.0  0.0  0.0  0.0  0.0  0.0
1  0.0  1.0  1.0  1.0  0.0  0.0  0.0
1  0.0  1.0  1.0  1.0  0.0  0.0  0.0
1  0.0  1.0  1.0  1.0  0.0  0.0  0.0
7  0.0  0.0  0.0  0.0  1.0  0.0  0.0
1  0.0  0.0  0.0  0.0  0.0  1.0  1.0
1  0.0  0.0  0.0  0.0  0.0  1.0  1.0
#------------------------------------------------------------#
Detailed Info. derived from the *Distance Map*:
Idx. Center    Idx. Bonded (Atm. Type Bonded)
    0     1 (   h1)    2 (   h1)    3 (   h1)    4 (   n3)
    1     0 (   c3)
    2     0 (   c3)
    3     0 (   c3)
    4     0 (   c3)    5 (   hn)    6 (   hn)
    5     4 (   n3)
    6     4 (   n3)
Detailed Info. for -CH2-:
    NO -CH2- FRAGMENT WAS DETECTED *PLEASE CHECK STRUCTURE*
Detailed Info. for -CH3:
     Index for Carbon was listed below:
     o    0
Equivalent HEAVY atom index:
    NO EQUIVALENT HEAVY ATOM WAS DETECTED!
Equivalent HYDROGEN atom index for -CH2-:
    NO -CH2- FRAGMENT WAS DETECTED!
Equivalent HYDROGEN atom index for -CH3-:
EQUIVALENT HYDROGEN INDEX (-CH3):
 Idx.     Idx.
```

```
    1     2
    1     3
Equivalent HYDROGEN atom index exclude -CH2- and -CH3
EQUILVALENT HYDROGEN INDEX (EXCLUDING -CH2-, -CH3)
 Idx.     Idx.
    5     6
#-----------------------------END-----------------------------#
```

The **first matrix** is `distance map` in the unit of angstrom, it defines the distance formed between any two paired atoms;

The **second matrix** is `equivalent atom map` which defines the equivalence between two atom, `1` for equivalent and `0` for inequivalent;

Following message is detailed information derived from Distance Map ;

Taking molecule `CH3NH2` as an example:

The first atom with index `0` is bonded with four atoms, namely, `1(h1)` , `2(h1)` , `3(h1)` , and `4(n3)` , the str in the parentheses is the atom type derived from `espgen` ;

Then, message shows the information of function group `-CH2-` and `-CH3` .

In this molecule, only one `-CH3` group was found, and index of atom Carbon is `0` ;

Additional information is the equivalence information for `heavy atoms (excluding -CH2-, -CH3)` , `-CH2-` , `-CH3` , and `hydrogen atoms (excluding -CH2-,-CH3)` , `-CH2-` , `-CH3` .

For example, in `CH3NH2` molecule, equivalent `H` atoms of `-CH3` is as below:

```
1(h1) == 2(h1)
1(h1) == 3(h1)
```

Since no `-CH2-` was found in `CH3NH2` , no equivalent H atom index of `-CH2-` was detected.

Equivalent hydrogen index (excluding `-CH2-` , `-CH3`) was found

```
5(hn) == 6(hn)
```

4.4 PyRESP execution

4.4.1 For `RESP` model

```
# Stage one
$ py_resp.py -O\
$            -i pyrespgen.1st\ (1st file generated by PyRESP_GEN)
$            -o pyrespgen.1st.out\ (output filename specified by yoursel
$            -e ESPDATA.dat\ (esp data file generated by ESPGEN)
$            -s FITTED_ESPDATA.1st.esp\ (filename of fitted esp data)
$            -t FITTED_CHG.1st.chg\ (filename of fitted chg data)

# Stage two
$ py_resp.py -O \
$            -i pyrespgen.2nd\ (2nd file generated by PyRESP_GEN)
$            -o pyrespgen.2nd.out\
$            -e ESPDATA.dat\ (esp data file generated by ESPGEN)
$            -s FITTED_ESPDATA.2nd.esp\ (filename of fitted esp data)
$            -t FITTED_ESPDATA.2nd.chg\ (filename of fitted chg data)
$            -q FITTED_CHG.1st.chg (1st fitted chg data)
```

4.4.2 For `pGM-ind` and `pGM-perm` model

```
# Stage one
$ py_resp.py -O\
$            -i pyrespgen.1st\ (1st file generated by PyRESP_GEN)
$            -o pyrespgen.1st.out\ (output filename specified by yoursel
$            -e ESPDATA.dat\ (esp data file generated by ESPGEN)
$            -ip ${HOME_PYRESP}/pGM-pol-2016-09-01\ (polarizability para
$            -s FITTED_ESPDATA.1st.esp\ (filename of fitted esp data)
$            -t FITTED_CHG.1st.chg\ (filename of fitted chg data)

# Stage two
$ py_resp.py -O \
$            -i pyrespgen.2nd\ (2nd file generated by PyRESP_GEN)
$            -o pyrespgen.2nd.out\
$            -e ESPDATA.dat\ (esp data file generated by ESPGEN)
$            -ip ${HOME_PYRESP}/pGM-pol-2016-09-01\ (polarizability para
$            -s FITTED_ESPDATA.2nd.esp\ (filename of fitted esp data)
$            -t FITTED_ESPDATA.2nd.chg\ (filename of fitted chg data)
$            -q FITTED_CHG.1st.chg (1st fitted chg data)
```

References

[1] Qiang Zhu, Yang Ge, Wei Li,* and Jing Ma*. Treating Polarization Effects in Charged and Polar Bio-Molecules Through Variable Electrostatic Parameters. *J. Chem. Theory Comput.* **2023**, 19, 2, 396–411;

[2] Shiji Zhao, Haixin Wei, Piotr Cieplak, Yong Duan,* and Ray Luo.* PyRESP: A Program for Electrostatic Parameterizations of Additive and Induced Dipole Polarizable Force Fields. *J. Chem. Theory Comput.* **2022**, 18, 6, 3654–3670;

[3] Junmei Wang*, Piotr Cieplak, Ray Luo, and Yong Duan*. Development of Polarizable Gaussian Model for Molecular Mechanical Calculations I: Atomic Polarizability Parameterization To Reproduce ab Initio Anisotropy. *J. Chem. Theory Comput.* **2019**, 15, 2, 1146–1158;

[4] Qiang Zhu, Yongxian Wu, Shiji Zhao, Piotr Cieplak, Yong Duan,* Ray Luo.* Streamlining and Optimizing Strategies of Electrostatic Parameterization *J. Chem. Theory Comput.* **2023**, 19,18, 6353-6365.

Qiang's Blog

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时时勤拂拭，勿使惹尘埃