GEOMETRY OPTIMIZATION

In this tutorial, you will learn how to perform a geometry optimization with FHI-vibes for fcc Silicon. At the same time, you will also learn a little bit about the internal settings in FHI-aims. Note that you can find the full manual for FHI-aims as PDF in /home/triqs/FHI_local/FHI-aims/.

Define Inputs

FHI-vibes workflows typically rely on two input files:

- 1) a **geometry file**, which specifies the atomic positions and cell vectors.
- 2) a **control file**, which contains the calculator section and defines the computational tasks and all the numerical parameters.

To kick off our first relaxation, we'll use the geometry.in file for bulk Silicon in the primitive cell.

The calculator section is contained in the file calculator.in. Let's firstly walk through these settings once:

- [files]
 - geometry: geometry.in : read the input geometry from geometry.in .
- [calculator]
 - o name: aims means that FHI-aims will be used.
 - socketio: true means that the socketIO communication will be used. This
 will speed up the computation by reusing some information from one evaluation to
 the next.
- [calculator.parameters]
 - xc: pw-lda means that the pw-LDA exchange-correlation functional will be used.
 - compute forces: true means that forces will be computed.

- [calculator.kpoints]
 - \circ density: 2 use a k-point density of at least 2 per \mathring{A}^{-1}
- [calculator.basissets]
 - o default: light: use light default basis sets and numerical settings for silicon. By default, FHI-aims provides a series of different pre-configured numerical sets and basis sets for all elements of the periodic table. The here chosen light settings are ideal to obtain qualitatively correct results in a short time. Fully converged and more accurate results can be obtained by using intermediate, tight, or even really_tight settings. In addition, it is always possible to customize the basis sets for the actual system of interest to better balance speed and accuracy.

We will use these settings defined in calculator.in for most of the rest of these tutorials. Let's first make a copy for the relaxation step:

```
cp calculator.in relaxation.in
```

Next, use the command line interface (CLI) of FHI-vibes to obtain default settings for performing the relaxation and appending them to the input file:

```
vibes template relaxation >> relaxation.in
```

This has now added an additional section for the relaxation settings to your **control file**. Accordingly, the updated input file relaxation in should look like this:

[files] geometry: geometry.in [calculator] name: aims socketio: True [calculator.parameters] pw-lda xc: compute_forces: true [calculator.kpoints] 2 density: [calculator.basissets] default: light [relaxation] driver: **BFGS** fmax: 0.001 unit cell: True fix_symmetry: False hydrostatic_strain: False constant volume: False 0.0 scalar pressure: decimals: 12 1e-05 symprec: workdir: relaxation [relaxation.kwargs] maxstep: 0.2 logfile: relaxation.log restart: bfgs.restart

The settings file template you just generated contains all the necessary settings to set up and run a geometry optimization with <code>FHI-vibes</code> using <code>FHI-aims</code> as the force/stress calculator. <code>FHI-vibes</code> will perform a BFGS optimization of the structure as implemented in <code>Atomic Simulation Environment</code> (ASE). As the keywords suggest, a full unit cell relaxation will be performed, no symmetry constraints will be applied, and the relaxation will stop once the maximum force acting on the atoms is smaller than 0.001 eV/Å. More details on these keywords can be found in <code>the documentation</code>.

Run calculation

```
pipe the output, e.g., like this:
```

```
vibes run relaxation | tee log.relaxation
```

FHI-vibes will create a working directory with the default name relaxation and will handle running the FHI-aims calculations necessary to perform the geometry optimization. The log file relaxation.log should read like that:

```
[vibes.run]
              run relaxation workflow with settings from relaxation.in
                ** /draco/u/christia/Codes/vibes v2/tutorials/GR/relaxate
 [relaxation]
 [calculator] Update aims k grid with kpt density of 3 to [8, 8, 8]
 [calculator] .. add `sc accuracy rho: 1e-06` to parameters (default)
 [calculator] .. add `relativistic: atomic_zora scalar` to parameters
                .. add `compensate_multipole_errors: False` to paramete:
 [calculator]
                .. add `output_level: MD_light` to parameters (default)
 [calculator]
 [calculator]
                Add basisset `light` for atom `Si` to basissets folder.
               Calculator: aims
 [calculator]
 [calculator] settings:
 [calculator]
                 xc: pw-lda
 [calculator]
                  compute forces: True
 [calculator]
                 k_grid: [8, 8, 8]
                  sc_accuracy_rho: 1e-06
 [calculator]
 [calculator]
                  relativistic: atomic_zora scalar
                  compensate_multipole_errors: False
 [calculator]
                  output_level: MD_light
 [calculator]
                  compute analytical stress: True
 [calculator]
                  use pimd wrapper: ('localhost', 10011)
 [calculator]
                  aims_command: /u/christia/Codes/vibes_v2/run_aims.sh
 [calculator]
                  species dir: /draco/u/christia/Codes/vibes v2/tutoria
 [calculator]
 [relaxation]
                filter settings:
                 hydrostatic_strain: False
 [relaxation]
 [relaxation]
                  constant_volume: False
 [relaxation]
                  scalar pressure: 0.0
 [relaxation]
                driver: BFGS
 [relaxation]
               settings:
 [relaxation]
                 type: optimization
                  optimizer: BFGS
 [relaxation]
 [relaxation]
                  maxstep: 0.2
 [socketio]
                Use SocketIO with host localhost and port 10011
 [relaxation] filter settings:
 [relaxation]
                  hydrostatic strain: False
 [relaxation]
                 constant_volume: False
                 scalar pressure: 0.0
 [relaxation]
 [relaxation] Start step 0
 [relaxation] Step 0 finished.
 [relaxation]
                .. residual force: 0.000 meV/AA
 [relaxation] .. residual stress: 289.641 meV/AA**3
```

```
[vibes] .. Space group: Fd-3m (227)
[relaxation]
             clean atoms before logging
[relaxation] .. log
[relaxation] Step 1 finished.
[relaxation] .. residual force: 0.000 meV/AA
[relaxation]
             .. residual stress: 3.463 meV/AA**3
            .. Space group: Fd-3m (227)
[vibes]
[relaxation] clean atoms before logging
[relaxation] .. log
[relaxation] Step 2 finished.
[relaxation] .. residual force: 0.000 meV/AA
[relaxation] .. residual stress: 0.039 meV/AA**3
              .. Space group: Fd-3m (227)
[vibes]
[relaxation] clean atoms before logging
[relaxation] .. log
[relaxation]
             Relaxation converged.
[relaxation] done.
```

You will find the FHI-aims in- and output in relaxation/calculation/, the final converged structure in relaxation/geometry.in.next_step, and a summary of the relaxation path in relaxation/relaxation.log.

For a detailed summary of the relaxation path, you may run

```
vibes info relaxation relaxation/trajectory.son
```

and obtain an output like:

```
Relaxation info for relaxation/trajectory.son:
               1.000e+00 meV/AA
fmax:
# Step | Free energy | F-F(1)
                                 max. force max. stress
                                                             Vol
             [eV]
                         [meV] [meV/AA] [meV/AA^3]
                                                             [AA
   1
       -15748.26920828
                         -3.914683
                                       0.0000
                                                     5.0815
                                                              3
   2
       -15748.26921491
                         -3.921313
                                       0.0000
                                                     0.1132
                                                              3
--> converged.
```

It shows how energy, forces, and stresses have decreased during the relaxation, until convergence was reached.

OPTIONAL: You can also look at the relaxed structure in

relaxation/geometry.in.next_step in an editor. Do you notice something? Try removing the old relaxation via

```
mv relaxation relaxation.old
```

and restarting the relaxation with the setting

fix_symmetry: True

What changed?