# **DFT-toolkit**

**DFT-toolkit** is a Python package for automating DFT calculations across multiple DFT software packages. It allows users to create, submit, and monitor jobs in the SLURM queue, as well as build multi-step calculation pipelines with defined dependencies between steps. DFT-toolkit is designed to work with any DFT software and can be run on any HPC cluster using SLURM.

### Installation

To use DFT-toolkit you need to clone its repository:

git clone https://github.com/mszyszko-uw/vasp-processing.git and install requirements:

- Python >= 3.6
- pip ≥ 19.0
- simple\_slurm-0.3.6
- PyYAML==6.0.2

#### by

pip install -r .\requirements.txt

We strongly recommend using a separate Python environment for this installation. Use a virtual environment or any conda environment.

# Quickstart

```
DTF toolkit can be run with Python by:
```

```
python dft_toolkit.py [options] action
```

a list of available options and parameters can be obtained by:

```
python dft toolkit.py --help
```

#### Available actions

- freenodes list all available node on a machine witch free CPUs and memory,
- waiting create a rapport about waiting time in SLURM queue,
- print- print SLURM scripts,
- create create SLURM scripts,
- submit create and submit SLURM scripts,
- array run job array from all subdirectories,
- checkqueue list all user jobs,
- canceljob cancel a job,
- jobinfo print a job details from SLURM,
- print\_avalable\_steps print defined jobs.

## Available options

• -h, --help show this help message and exit

```
• --path PATH set a path to the working directory or resource,
```

- --config CONFIGURE FILE set a configuration file,
- --id JOB ID define a SLURM Job ID (for details or cancellation),
- --steps STEPS set up a list of jobs to run,
- --array run job array based on step and path
- --dependency step DEPENDENCY STEP A step that blocks rest of steps

### Configurations files

DFT-Toolkit uses two configuration files:

- 1. Machine file for definite a cluster details in yaml or json format,
- 2. step file (steps.yaml) where pipeline's steps are defined.

#### Machine file

The machine file is used for defining computer cluster details like SLURM partitions, module names and python environment details. It has 3 sections:

- slurm where you can define a cluster details using SLURM keywords (like, nodes, partitions)
- script where you can set up exact module name. All modules listed in this section will be loaded in queue job,
- env where you can specify what type (type) of python environment you are using (virtual environment or conda) and path (path) to your environment.

You should have a separate machine file for each computer cluster you use and select the right one with --config options.

### Steps definition

steps.yaml is used for the definition of pipeline's steps. The file has a separate section for each step. Each step has two parts: slurm and cmd. In the slurm section you can define SLURM job parameters with SLURM keywords. The cmd section is a body of SLURM script and all calculations, preprocessing and postprocessing commands are listed (Use cmd: | for multiline script).

```
#number of nodes
   nodes: 1
                               #total number of CPUs
   ntasks: 28
   mem_per_cpu: "2GB"
                               #memory per CPU - 56G in total
 cmd: | #commands to run at step: scf
   ulimit -s unlimited
   START DIR="$ (pwd) "
   cd "$output"
   mpiexec vasp std > log
postprocessing: #step 2
 slurm:
   time: "0:20:00"
   nodes: 1
   ntasks: 1
   mem per cpu: "1GB"
 cmd: |
   cd OUTPUTS
   python ../postprocessing plot.py
```

# **Examples**

In this example you're going to learn how to create a working pipeline based on an existing SLURM script. Let's assume that you have a SLURM script:

```
#!/bin/bash -l
#SBATCH --job-name=s01e01scf
#SBATCH --time=0:05:00
#SBATCH --account=plg2dmagsem-cpu
#SBATCH --partition=plgrid
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=28
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1GB
#SBATCH --output=out step01
#SBATCH --error=err step01
ulimit -s unlimited
module load intel-compilers/2023.2.1 impi/2021.10.0
VASP/6.5.1-Dsingle prec bse
module load Python/3.11.5 matplotlib/3.8.2 h5py/3.11.0
START DIR="$ (pwd)"
output=$(python3 toolkit.py --step step01 --part dry)
cd "$output"
mpiexec vasp std > log
cd "$START DIR"
output=$(python3 toolkit.py --step step01 --part scf)
```

```
cd "$output"
mpiexec vasp std > log
You need to follow steps:
  1. create virtual environment
     python -m venv ./tollbox env
  2. clone repository
     git clone https://github.com/mszyszko-uw/vasp-processing.git
  3. install all dependences
     ./tollbox_env/bin/activate
     cd vasp-processing
     pip install -r requirements.txt
  4. create machine file and fill PARTITION _ and PATH
     #config.yaml
     slurm:
             nodes: 1
              partition: PARTITION
              time: "1:00:00"
     script:
             module: vasp/22
     env:
             type: venv #venv or conda
              path: PATH /tollbox env
  5. create steps file
     #steps.yaml
     scf:
       slurm:
         time: "0:05:00"
         nodes: 1
         ntasks: 28
         mem per cpu: "1GB"
       cmd: |
         ulimit -s unlimited
         module load intel-compilers/2023.2.1 impi/2021.10.0
     VASP/6.5.1-Dsingle prec bse
         module load Python/3.11.5 matplotlib/3.8.2 h5py/3.11.0
         START DIR="$ (pwd) "
         output=$(python3 toolkit.py --step step01 --part dry)
         cd "$output"
         mpiexec vasp std > log
         cd "$START DIR"
         output=$(python3 toolkit.py --step step01 --part scf)
         cd "$output"
         mpiexec vasp std > log
  6. examin SLURM script
```

python dft toolkit.py --steps scf print

## 7. run calculations

python dft\_toolkit.py --steps scf submit