MAGUS:

Machine learning And Graph theory assisted Universal structure Searcher

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Manual

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https://gitlab.com/bigd4/magus

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Chapter 1

Installation

1.1 Dependency

MAGUS needs python>=3.6 and gcc>=4.8. You should install pip before using it to install other packages. The following python packages are required:

```
numpy
scipy
scikit-learn
pyyaml>=6.0
ase>=3.18
networkx
spglib
pandas
prettytable
packaging
```

The following python packages are optional:

```
beautifulreport
plotly
dscribe
networkx
pymatgen
```

If you want to use MTP, you need to install mlip.

1.2 Preparation

1.2.1 Set up the ASE API with Vasp

MAGUS does VASP calculation based on ASE API. Hence, you need to do the following preparations first.

1) Make a new file run_vasp.py:

```
import subprocess
exitcode = subprocess.call("mpiexec.hydra vasp_std",
shell=True)
```

ase manual.

2) Make a new mypps dir to store vasp pseudopotentials. You can also use soft links:

```
mypps/
|--- potpaw
|--- potpaw_GGA
|--- potpaw_PBE
```

```
$ ln -s /your/path/PBE-5.4 mypps/potpaw_PBE
```

Three sub directories correspond to LDA, PW91 and PBE, respectively. It is allowed to leave some of them nonexistent if you do use these potentials. It is also allowed to add other pseudopotentials.

3) Set environment variables:

```
$ export VASP_SCRIPT=/your/path/run_vasp.py
$ export VASP_PP_PATH=/your/path/mypps
```

More information in: ase manual for vasp calculator.

Notice: run_vasp.py and mypps should not be under magus dir.

1.2.2 Set up Job System

MAGUS is developed under LSF job system, which is the default setting. But we also add support to SLURM and PBS job systems. You need to set an environment variable if you are not using the default LSF job system:

\$ export JOB_SYSTEM=<your-job-system>

Add this line into your **bashrc** to make the setting work every time you log in.

1.2.3 Machine Learning Package Installation (Optional)

MLIP is a software for Machine Learning Interatomic Potentials. It has been developed at Skoltech (Moscow) by Alexander Shapeev, Evgeny Podryabinkin, Konstantin Gubaev, and Ivan Novikov.* According to the license, MLIP is not allowed to be published and otherwise distributed. You need to register in https://mlip.skoltech.ru/download/ and follow the instructions.

1.2.4 Build a Virtual Environment (Optional)

And we highly recommend that you use Anaconda to build a virtual environment and install MAGUS in an isolated environment to avoid conflicts. After installing anaconda, it will automatically write several lines in your <code>bashrc</code> which is used to initialize anaconda environment. You should source <code>bashrc</code> or re-login to make anaconda activated. If you do the jobs correctly, your shell prompt should be modified to be started as <code>(base)</code>, which means you are now in base environment of anaconda. Then, create a new virtual environment with

\$ conda create -n <your-env-name> python=<python-version>

<your-env-name> is the name of the environment that you can define as you will, and <python-version> should be not less than 3.6. When you want to activate this environment, use

\$ conda activate <your-env-name>

1.3 Install with pip

It is convenient to install with pip. It will automatically download the source code and install the required python packages. The install command is

^{*}Novikov, Ivan S., et al. "The MLIP package: moment tensor potentials with MPI and active learning." Machine Learning: Science and Technology 2.2 (2020): 025002.

\$ pip install git+https://gitlab.com/bigd4/magus.git

You may need to type in your username and password of your gitlab account because the project is not public. If you want to install in a virtual environment, do not forget to activate the environment first. If you works in a cluster and do not have permission to install in the default location, you may add **--user** parameter.

1.4 Install with Source Code

1.4.1 Download Code

1.4.1.1 Use git

Clone the project and submodules to local file system:

\$ git clone --recursive https://gitlab.com:bigd4/magus.git

1.4.1.2 From Website

If you have problem downloading with git, you have the alternative choose to download the zipped package on our gitlab website. Notice that the submodules such as pybind11 will not be downloaded at the same time. You should download and extract them and replace the empty folders in the source code, respectively.

1.4.2 Use pip to Install the Source Code

After downloading the code, go into the directory and install with:

\$ pip install -e .

pip will read **setup.py** in your current directory and install. The **-e** option means python will import the module from the current path, but not copy the codes to the default lib path and import the module there, which is convenient for modifying in the future. If you do not have the need, you can remove the option.

1.5 Install Offline

If you have no access to Internet and your cluster does not have a python pypi mirror, which means you cannot use pip to install packages. You have the alternative choose to download with our pre-built offline installation package. You can download it from here. Install with

```
$ ./magus-<version-number>.sh
```

Follow the instructions. It will build an isolated conda environment with all required packages. You should go into your install path. Then, add **bin** into PATH and add condalib into PYTHONPATH. Notice that this method will build a new conda. If have already installed a conda in your system, the new one will not merge into the old one, which may cause difficulties to switch conda environments. As a result, it is not recommended to install with this method if your pip works normally.

1.6 Other Settings

1.6.1 Set up Environment Variables

To run MAGUS in your console, you need to add PATH in bashrc.

```
$ export PATH=$PATH:/your_path_to_magus
$ export PYTHONPATH=$PYTHONPATH:/your_path_to_magus
```

1.6.2 Set up Auto Completion (Optional)

We have prepared a shell completion script for MAGUS. Add the following line into **bashrc**:

```
$ source your_path_to_magus/auto_complete.sh
```

1.7 Check Installation

If MAGUS is properly installed, you can see the version number by the following command in console:

\$ magus -v

1.0.5

If you have installed other optional packages, you can check if they are properly installed using:

\$ magus checkpack

Chapter 2

Examples

2.1 Example List

number	target
01	Generate structures
02	Relax structures
03	3D bulk search
04	Molecule crystal search
05	Cluster search
06	Surface reconstruct
07	Machine learning search
08	2D bulk search

2.2 Example Introductions

2.2.1 Generate structures

- **01--1-B12**: Generate 3d periodic crystal structures of boron with 12 atoms per unit cell by symmetry.
- **01--2-NH4NO3**: Generate 3d periodic crystal structures of molecule crystal with 8 NH4 and NO3 molecules per unit cell by symmetry Pccn (56).

2.2.2 Relax structures

- **02--1-C8-VASP**: Structure relaxation of diamond by vasp interface.
- **02--2-B12-MTP**: Relax 2000 structures with MTP and VASP.

2.2.3 3D bulk search

- **03--1-Al-fix-EMT**: GAsearch of fixed composition Al (12 atoms per cell) by EMT.
- **03--2-Al-fix-VASP**: GAsearch of fixed composition Al (12 atoms per cell) by VASP.
- 03--3-Ti02-fix-VASP: GAsearch of fixed composition TiO_2 (12 atoms per cell).
- **03--4-MgAlO-fix-GULP**: GAsearch of fixed composition MgAlO under high pressure by GULP.
- 03--5-Si-fix-Castep: GAsearch of fixed composition Si by Castep.
- 03--6-ZnOH-var-GULP: GAsearch of variable composition $Zn_x(OH)_y$.

2.2.4 Molecule crystal search

• **04--1-CH4-fix-VASP**: GAsearch of molecule crystal CH4 with 4 molecules per unit cell.

2.2.5 Cluster search

• **05--1-LJ26**: Ground state of Lennard-Jones cluster of 26 atoms.

2.2.6 Surface reconstruct

- $06--1-C_2x1_100$: Surface reconstruction of diamond $(100)-2\times1$.
- **06--2-Sn02_4x1_110**: Surface reconstruction of SnO_2 (110)-4×1.

2.2.7 Machine learning search

- $07-1-MgSiO_3-MTP$: Use mtp to search MgSiO₃ under high pressure.
- **07--2-Na-NEP**: A toy example for use NEP to search sodium.

2.2.8 2D bulk search

• **08--1-graphene**: GAsearch of 2D carbon (graphene) by VASP.

Chapter 3

Parameters

3.1 HELP FOR INPUTS

In magus we use inputs including command lines and parameter input file (in yaml format) to control programs.

If you are a new user of MAGUS (AND SINCERELY THANKS VERY MUCH FOR USING OUR PROGRAM!), before you read the full description about all inputs below, we recommand first taking a look at examples which are easier to follow.

3.1.1 Command lines

You can simply type

```
$ magus -h
```

to see which commands are supported for magus. You will see

```
show this help message and exit
  -h, --help
                        print version
  -v, --version
Valid subcommands:
  {search, summary, clean, prepare, calculate, generate,
  checkpack,test,update,getslabtool,mutate,parmhelp}
                        search structures
    search
                        summary the results
    summary
                        clean the path
    clean
                        generate InputFold etc to prepare
    prepare
    for the search
    calculate
                        calculate many structures
    generate
                        generate many structures
                        check full
    checkpack
                        do unit test of magus
    test
    update
                        update magus
                        tools to getslab in surface search
    getslabtool
    mode
                        mutation test
    mutate
```

which prints valid subcommands. You can also helps for each command line:

3.1.2 search

```
log.txt)
-i INPUT_FILE, --input-file INPUT_FILE
the input parameter file in yaml
format (default:
input.yaml)
-m, --use-ml use ml to accelerate(?) the search
(default: False)
-r, --restart Restart the searching. (default:
False)
```

3.1.3 summary

```
$ magus summary -h
usage: magus summary [-h] [-p PREC] [-r] [-s]
[--need-sort] [-o OUTDIR]
                     [-n SHOW_NUMBER] [-sb SORTED_BY
                     [SORTED_BY ...]]
                     [-rm REMOVE_FEATURES [REMOVE_FEATURES
                     [-a ADD_FEATURES [ADD_FEATURES ...]]
                     [-b BOUNDARY [BOUNDARY ...]] [-t
                     {bulk,cluster}]
                     filenames [filenames ...]
positional arguments:
  filenames
                        file (or files) to summary
optional arguments:
  -h, --help
                        show this help message and exit
  -p PREC, --prec PREC tolerance for symmetry finding
  (default: 0.1)
  -r, --reverse
                        whether to reverse sort (default:
  False)
  -s, --save
                        whether to save POSCARS (default:
  False)
                        whether to sort (default: False)
  --need-sort
  -o OUTDIR, --outdir OUTDIR
```

```
where to save POSCARS (default: .)
-n SHOW_NUMBER, --show-number SHOW_NUMBER
                      number of show in screen (default:
                      100)
-sb SORTED_BY [SORTED_BY ...], --sorted-by SORTED_BY
[SORTED_BY ...]
                      sorted by which arg (default:
                      Default)
-rm REMOVE_FEATURES [REMOVE_FEATURES ...],
--remove-features REMOVE_FEATURES [REMOVE_FEATURES ...]
                      the features to be removed from
                      the show features
                      (default: [])
-a ADD_FEATURES [ADD_FEATURES ...], --add-features
ADD_FEATURES [ADD_FEATURES ...]
                      the features to be added to the
                      show features
                      (default: [])
                      use variable composition mode
-v, --var
(default: False)
-b BOUNDARY [BOUNDARY ...], --boundary BOUNDARY
[BOUNDARY ...]
                      in variable composition mode: add
                      boundary (default:
                      [])
-t {bulk,cluster}, --atoms-type {bulk,cluster}
```

3.1.4 clean

```
$ magus clean -h

usage: magus clean [-h] [-f]

optional arguments:
   -h, --help show this help message and exit
   -f, --force rua!!!! (default: False)
```

3.1.5 prepare

```
$ magus prepare -h
usage: magus prepare [-h] [-v] [-m]

optional arguments:
  -h, --help show this help message and exit
  -v, --var variable composition search (default: False)
  -m, --mol molecule crystal search (default: False)
```

3.1.6 calculate

```
$ magus calculate -h
usage: magus calculate [-h] [-ll
{DEBUG, INFO, WARNING, ERROR}] [-lp LOG_PATH]
                        [-m {scf,relax}] [-i INPUT_FILE]
                        [-o OUTPUT_FILE]
                        [-p PRESSURE]
                        filename
positional arguments:
  filename
                        structures to relax
optional arguments:
                         show this help message and exit
  -h, --help
  -ll {DEBUG, INFO, WARNING, ERROR}, --log-level
  {DEBUG, INFO, WARNING, ERROR}
                         set verbosity level by strings:
                         ERROR, WARNING, INFO
                         and DEBUG (default: INFO)
  -lp LOG_PATH, --log-path LOG_PATH
                         set log file to log messages to
                         disk (default:
                         log.txt)
  -m {scf,relax}, --mode {scf,relax}
                         scf or relax (default: relax)
  -i INPUT_FILE, --input-file INPUT_FILE
```

```
the input parameter file in yaml
format (default:
input.yaml)
-o OUTPUT_FILE, --output-file OUTPUT_FILE
output traj file (default:
out.traj)
-p PRESSURE, --pressure PRESSURE
add pressure (default: None)
```

3.1.7 generate

```
$ magus generate -h
usage: magus generate [-h] [-ll
{DEBUG, INFO, WARNING, ERROR}] [-lp LOG_PATH]
                      [-i INPUT_FILE] [-o OUTPUT_FILE] [-n
                      NUMBER 1
optional arguments:
  -h, --help
                        show this help message and exit
 -ll {DEBUG, INFO, WARNING, ERROR}, --log-level
  {DEBUG, INFO, WARNING, ERROR}
                         set verbosity level by strings:
                        ERROR, WARNING, INFO
                        and DEBUG (default: INFO)
  -lp LOG_PATH, --log-path LOG_PATH
                         set log file to log messages to
                        disk (default:
                        log.txt)
  -i INPUT_FILE, --input-file INPUT_FILE
                        the input parameter file in yaml
                        format (default:
                        input.yaml)
  -o OUTPUT_FILE, --output-file OUTPUT_FILE
                        where to save generated traj
                         (default: gen.traj)
  -n NUMBER, --number NUMBER
                        generate number (default: 10)
```

3.1.8 checkpack

```
$ magus checkpack -h
usage: magus checkpack [-h] [-ll
{DEBUG, INFO, WARNING, ERROR}] [-lp LOG_PATH]
                        [{all,calculators,comparators,fingerprints}]
positional arguments:
  {all, calculators, comparators, fingerprints}
                         the package to check (default:
                         all)
optional arguments:
 -h, --help
                        show this help message and exit
 -ll {DEBUG, INFO, WARNING, ERROR}, --log-level
  {DEBUG, INFO, WARNING, ERROR}
                         set verbosity level by strings:
                         ERROR, WARNING, INFO
                         and DEBUG (default: INFO)
  -lp LOG_PATH, --log-path LOG_PATH
                         set log file to log messages to
                         disk (default:
                         log.txt)
```

3.1.9 test

3.1.10 update

```
$ magus update -h

usage: magus update [-h] [-u] [-f]
optional arguments:
  -h, --help show this help message and exit
  -u, --user add --user to pip install (default: False)
  -f, --force add --force-reinstall to pip install
  (default: False)
```

3.1.11 getslabtool

3.1.12 mutate

```
$ magus mutate -h

usage: magus mutate [-h] [-i INPUT_FILE] [-s SEED_FILE]

[-o OUTPUT_FILE]

[--cutandsplice] [--replaceball]

[--soft] [--perm]
```

```
[--lattice] [--ripple] [--slip]
                    [--rotate] [--rattle]
                    [--formula] [--lyrslip] [--shell]
                    [--lyrsym] [--clusym]
optional arguments:
  -h, --help
                        show this help message and exit
  -i INPUT_FILE, --input_file INPUT_FILE
                        input_file (default: input.yaml)
  -s SEED_FILE, --seed_file SEED_FILE
                        seed_file (default: seed.traj)
  -o OUTPUT_FILE, --output_file OUTPUT_FILE
                        output_file (default: result)
  --cutandsplice
                        add option to use operation!
  (default: False)
  --replaceball
                        add option to use operation!
  (default: False)
  --soft
                        add option to use operation!
  (default: False)
                        add option to use operation!
  --perm
  (default: False)
  --lattice
                        add option to use operation!
  (default: False)
  --ripple
                        add option to use operation!
  (default: False)
  --slip
                        add option to use operation!
  (default: False)
                        add option to use operation!
  --rotate
  (default: False)
                        add option to use operation!
  --rattle
  (default: False)
  --formula
                        add option to use operation!
  (default: False)
  --lyrslip
                        add option to use operation!
  (default: False)
  --shell
                        add option to use operation!
  (default: False)
  --lyrsym
                        add option to use operation!
  (default: False)
                        add option to use operation!
  --clusym
  (default: False)
```

```
\end{tcolorbox}
\section{parameter input files}
A yaml format parameter file is also necessary. By default is 'input.yaml'. IN THE FUTURE we will add command line to easily export notes and default values by \begin{tcolorbox}[breakable, enhanced]     \begin{minted}[breaklines, breaksymbolleft={},]{bash} $ magus parmhelp
```

to see help for which parameters you can set in 'input.yaml'. For current version they are:

```
parameter information for <class
'magus.parameters.magusParameters'>
+++++^^IDefault parameters^^I++++
               : type of formula, choose from fix or var
formulaType
                  default value: fix
structureType : structure type, choose from bulk, layer,
confined_bulk, cluster, surface
                  default value: bulk
               : spacegroup to generate random structures
spacegroup
                  default value: [1-230]
               : DFTRelax
DFTRelax
                  default value: False
initSize
               : size of first population
                  default value: =popSize
               : number of good indivials per generation
goodSize
                  default value: =popSize
               : search molecule clusters
molMode
                  default value: False
               : use Machine learning relaxation
mlRelax
                  default value: False
symprec
               : tolerance for symmetry finding
                  default value: 0.1
               : limitation to detect clusters
bondRatio
                  default value: 1.15
eleSize
               : used in variable composition mode,
control how many boundary structures are generated
                  default value: 0
```

volRatio : cell_volume/SUM(atom_ball_volume) when generating structures (around this number) default value: 2 dRatio : distance between each pair of two atoms in the structure is not less than (radius1+radius2)*d_ratio default value: 0.7 : methods to detect mol, choose from 1 and molDetector 2. See Hao Gao, Junjie Wang, Zhaopeng Guo, Jian Sun, "Determining dimensionalities and multiplicities of crystal nets" npj Comput. Mater. 6, 143 (2020) [doi.org/10.1016/j.fmre.2021.06.005] for more details. default value: 0 addSym : whether to add symmetry before crossover and mutation default value: True : ratio of new generated random structures randRatio in next generation default value: 0.2 chkMol : use mol dectector default value: False : check seeds chkSeed default value: True diffE : energy difference to determin structure duplicates default value: 0.01 : volume difference to determin structure diffV duplicates default value: 0.05 comparator : comparator, type magus checkpack to see which comparators you have. default value: nepdes fp_calc : fingerprints, type magus checkpack to see which fingerprint method you have. default value: nepdes : number of good individuals per generation n_cluster

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default value: =saveGood

autoOpRatio : automantic GA operation ratio default value: False autoRandomRatio: automantic random structure generation ratio default value: False parameter information for <class 'magus.generators.random.MoleculeSPGGenerator'> +++++^^IRequirement parameters^^I++++ input mols : input molecules formula_type : type of formula, choose from fix or var symbols : atom symbols : formula formula min_n_atoms : minimum number of atoms per unit cell
max_n_atoms : maximum number of atoms per unit cell +++++^^IDefault parameters^^I++++ : tolerance for symmetry finding for symprec molucule default value: 0.1 threshold_mol : distance between each pair of two molecules in the structure is not less than (mol_radius1+mol_radius2)*threshold_mol default value: 1.0 max_attempts : max attempts to generate a random structure default value: 50 : probability of generate primitive cell p_pri default value: 0.0 volume_ratio : cell_volume/SUM(atom_ball_volume) when generating structures (around this number) default value: 1.5 n_split : split cell into n_split parts default value: [1] dimension : dimension default value: 3 ele_size : number of single compontent structures to generate to decide hull boundarys in variable composition mode default value: 0 min_lattice : min lattice

```
default value: [-1, -1, -1, -1, -1]
               : max lattice
max_lattice
                  default value: [-1, -1, -1, -1, -1]
min_volume
               : min volume
                  default value: -1
               : max volume
max_volume
                  default value: -1
               : minimum formula
min_n_formula
                  default value: None
max_n_formula
               : maximum formula
                  default value: None
d_ratio
               : distance between each pair of two atoms
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
               : spacegroup to generate random structures
spacegroup
                  default value: [1-230]
               : max formula ratio in variable
max_ratio
composition mode, for example set 10 and Zn11(OH) is not
allowed
                  default value: 1000
full_ele
               : only generate structures with full
elements
                  default value: True
parameter information for <class
'magus.generators.random.LayerSPGGenerator'>
+++++^^IRequirement parameters^^I++++
min_thickness : minimum thickness
max_thickness : maximum thickness
formula_type
               : type of formula, choose from fix or var
symbols
               : atom symbols
formula
              : formula
min_n_atoms
               : minimum number of atoms per unit cell
              : maximum number of atoms per unit cell
max_n_atoms
+++++^^IDefault parameters^^I++++
```

symprec : symprec

default value: 0.1

threshold_mol : threshold_mol

default value: 1.0

spg_type : spg_type

default value: layer

vacuum_thickness: vacuum_thickness

default value: 10

max_attempts : max attempts to generate a random

structure

default value: 50

p_pri : probability of generate primitive cell

default value: 0.0

volume_ratio : cell_volume/SUM(atom_ball_volume) when

generating structures (around this number)

default value: 1.5

n_split : split cell into n_split parts

default value: [1]

dimension : dimension

default value: 3

ele_size : number of single compontent structures to

generate to decide hull boundarys in

variable composition mode

default value: 0

min_lattice : min lattice

default value: [-1, -1, -1, -1, -1]

max_lattice : max lattice

default value: [-1, -1, -1, -1, -1]

min_volume : min volume

default value: -1

default value: -1

min_n_formula : minimum formula

default value: None

max_n_formula : maximum formula

default value: None

d_ratio : distance between each pair of two atoms

in the structure is

not less than (radius1+radius2)*d_ratio

default value: 1.0

```
distance_matrix: distance between each pair of two atoms
in the structure is
                  not less than
                  (radius1+radius2)*distance_matrix[1][2]
                   default value: None
                : spacegroup to generate random structures
spacegroup
                   default value: [1-230]
                : max formula ratio in variable
max_ratio
composition mode, for example set 10 and Zn11(OH) is not
allowed
                   default value: 1000
full_ele
                : only generate structures with full
elements
                   default value: True
parameter information for <class
'magus.reconstruct.generator.ClusterSPGGenerator'>
+++++^^IRequirement parameters^^I++++
formula_type : type of formula, choose from fix or var
symbols : atom symbols
          : formula
formula
min_n_atoms : minimum number of atoms per unit cell
max_n_atoms : maximum number of atoms per unit cell
+++++^^IDefault parameters^^I++++
vacuum_thickness: vacuum thickness
                   default value: 10
parameter information for <class
'magus.generators.random.SPGGenerator'>
+++++^^IRequirement parameters^^I++++
formula_type : type of formula, choose from fix or var
symbols : atom symbols
formula : formula
min_n_atoms : minimum number of atoms per unit cell
max_n_atoms : maximum number of atoms per unit cell
+++++^^IDefault parameters^^I++++
max_attempts : max attempts to generate a random
structure
                   default value: 50
                : probability of generate primitive cell
p_pri
                   default value: 0.0
```

```
volume ratio
               : cell_volume/SUM(atom_ball_volume) when
generating structures (around this number)
                  default value: 1.5
n_split
               : split cell into n_split parts
                  default value: [1]
dimension
               : dimension
                  default value: 3
               : number of single compontent structures to
ele_size
                 generate to decide hull boundarys in
                 variable composition mode
                  default value: 0
               : min lattice
min_lattice
                  default value: [-1, -1, -1, -1, -1]
max_lattice
               : max lattice
                  default value: [-1, -1, -1, -1, -1]
min_volume
               : min volume
                  default value: -1
max_volume
               : max volume
                  default value: -1
               : minimum formula
min_n_formula
                  default value: None
               : maximum formula
max_n_formula
                  default value: None
d_ratio
               : distance between each pair of two atoms
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
               : spacegroup to generate random structures
spacegroup
                  default value: [1-230]
                  max formula ratio in variable
max_ratio
composition mode, for example set 10 and Zn11(OH) is not
allowed
                  default value: 1000
full_ele
               : only generate structures with full
elements
                  default value: True
```

```
parameter information for <class
'magus.reconstruct.generator.SurfaceGenerator'>
+++++^*IRequirement parameters^*I++++
              : type of formula, choose from fix or var
formula_type
symbols
               : atom symbols
formula
               : formula
               : minimum number of atoms per unit cell
min_n_atoms
max_n_atoms
               : maximum number of atoms per unit cell
+++++^^IDefault parameters^^I++++
randwalk_range : maximum range of random walk
                  default value: 0.5
randwalk_ratio : ratio of random walk atoms
                  default value: 0.3
               : size[x] of reconstruction
rcs_x
                  default value: [1]
               : size[y] of reconstruction
rcs_y
                  default value: [1]
buffer
               : use buffer layer
                  default value: True
               : formula of surface region
rcs_formula
                  default value: None
               : generate with planegroup/layergroup
spg_type
                  default value: plane
+++++^^Islabinfo parameters^^I++++
bulk_file
               : file of bulk structure
                  default value: None
cutslices
               : bulk_file contains how many atom layers
                  default value: 2
bulk_layernum
               : number of atom layers in substrate region
                  default value: 3
buffer_layernum: number of atom layers in buffer region
                  default value: 3
               : number of atom layers in top surface
rcs_layernum
region
                  default value: 2
               : Miller indices of surface direction,
direction
i.e.[1,0,0]
                  default value: None
               : R
rotate
                  default value: 0
```

```
: matrix notation
matrix
                  default value: None
addH
               : passivate bottom surface with H
                  default value: False
               : use primitive cell
pcell
                  default value: True
+++++^^Imodification parameters^^I++++
               : adsorb atoms to cleaved surface
adsorb
                  default value: {}
               : clean cleaved surface
clean
                  default value: {}
defect
               : add defect to cleaved surface
                  default value: {}
parameter information for <class
'magus.populations.individuals.Bulk'>
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
symprec
+++++^^IDefault parameters^^I++++
mol_detector
               : methods to detect mol, choose from 1 and
2. See
                 Hao Gao, Junjie Wang, Zhaopeng Guo, Jian
                 Sun, "Determining dimensionalities and
                 multiplicities
                 of crystal nets" npj Comput. Mater. 6,
                 143 (2020)
                 [doi.org/10.1016/j.fmre.2021.06.005]
                 for more details.
                  default value: 0
               : attempts to repair structures when doing
n_repair_try
GA operation
                  default value: 5
               : maximum attempts
max_attempts
                  default value: 50
               : if check seeds
check_seed
                  default value: False
min_lattice
               : min lattice
                  default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
               : max_lattice
max_lattice
```

```
default value: [99, 99, 99, 135, 135,
                  135]
d_ratio
               : distance between each pair of two atoms
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
radius
               : radius
                  default value: None
max_forces
               : if forces of a structure larger is than
this number it will be deleted.
                  default value: 50.0
               : if enthalpy of a structure is larger than
max_enthalpy
this number it will be deleted.
                  default value: 100.0
full_ele
               : full ele
                  default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                  default value: 8
parameter information for <class
'magus.populations.individuals.Layer'>
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
symprec
+++++^^IDefault parameters^^I++++
vacuum_thickness: vacuum_thickness
                  default value: 10
bond_ratio
               : bond ratio
                  default value: 1.1
n_repair_try
               : attempts to repair structures when doing
GA operation
                  default value: 5
max_attempts
              : maximum attempts
                  default value: 50
               : if check seeds
check_seed
                  default value: False
```

```
min_lattice
               : min_lattice
                  default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
max_lattice
               : max_lattice
                  default value: [99, 99, 99, 135, 135,
                  135]
               : distance between each pair of two atoms
d_ratio
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
radius
               : radius
                  default value: None
max_forces
               : if forces of a structure larger is than
this number it will be deleted.
                  default value: 50.0
max enthalpy
              : if enthalpy of a structure is larger than
this number it will be deleted.
                  default value: 100.0
               : full_ele
full_ele
                  default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                  default value: 8
parameter information for <class
'magus.populations.individuals.ConfinedBulk'>
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
symprec
+++++^^IDefault parameters^^I++++
vacuum_thickness: vacuum thickness
                  default value: 10
n_repair_try
               : attempts to repair structures when doing
GA operation
                  default value: 5
               : maximum attempts
max_attempts
                  default value: 50
```

```
check_seed
               : if check seeds
                  default value: False
min_lattice
               : min_lattice
                 default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
               : max_lattice
max_lattice
                  default value: [99, 99, 99, 135, 135,
d_ratio
               : distance between each pair of two atoms
in the structure is
                 not less than (radius1+radius2)*d_ratio
                 default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                 default value: None
               : radius
radius
                 default value: None
max_forces
               : if forces of a structure larger is than
this number it will be deleted.
                  default value: 50.0
               : if enthalpy of a structure is larger than
max_enthalpy
this number it will be deleted.
                  default value: 100.0
               : full_ele
full_ele
                 default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                 default value: 8
parameter information for <class
'magus.reconstruct.individuals.Surface'>
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
symprec
+++++^^IDefault parameters^^I++++
vacuum_thickness: vacuum thickness
                 default value: 10
buffer
               : use buffer region
                 default value: True
               : fix atom positions in substrate
fixbulk
```

```
default value: True
               : file name for slices file
slices_file
                  default value: Ref/layerslices.traj
n_repair_try
               : attempts to repair structures when doing
GA operation
                  default value: 5
               : maximum attempts
max_attempts
                  default value: 50
               : if check seeds
check_seed
                  default value: False
min_lattice
               : min_lattice
                  default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
               : max_lattice
max_lattice
                  default value: [99, 99, 99, 135, 135,
                  135]
               : distance between each pair of two atoms
d_ratio
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
radius
               : radius
                  default value: None
max_forces
               : if forces of a structure larger is than
this number it will be deleted.
                  default value: 50.0
max_enthalpy
               : if enthalpy of a structure is larger than
this number it will be deleted.
                  default value: 100.0
full_ele
               : full ele
                  default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                  default value: 8
parameter information for <class
'magus.reconstruct.individuals.Cluster'>
```

```
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
symprec
+++++^^IDefault parameters^^I++++
vacuum_thickness: vacuum thickness surrounding cluster to
break pbc when runing calculation
                  default value: 10
               : two atoms are "connected" if their
cutoff
distance < cutoff*radius.
                  default value: 1.0
weighten
               : use weighten atoms when appending or
removing atoms
                  default value: True
n_repair_try
               : attempts to repair structures when doing
GA operation
                  default value: 5
               : maximum attempts
max_attempts
                  default value: 50
               : if check seeds
check_seed
                  default value: False
min_lattice
               : min lattice
                  default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
               : max_lattice
max_lattice
                  default value: [99, 99, 99, 135, 135,
                  135]
               : distance between each pair of two atoms
d_ratio
in the structure is
                 not less than (radius1+radius2)*d_ratio
                  default value: 1.0
distance_matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                  default value: None
radius
               : radius
                  default value: None
max_forces
               : if forces of a structure larger is than
this number it will be deleted.
                  default value: 50.0
max_enthalpy : if enthalpy of a structure is larger than
this number it will be deleted.
```

```
default value: 100.0
               : full ele
full_ele
                  default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                  default value: 8
parameter information for <class
'magus.reconstruct.individuals.AdClus'>
+++++^^IRequirement parameters^^I++++
               : tolerance for symmetry finding
+++++^^IDefault parameters^^I++++
               : substrate file name
substrate
                  default value: substrate.vasp
dist_clus2surface: distance from cluster to surface
                  default value: 2
               : size
size
                  default value: [1, 1]
vacuum_thickness: vacuum thickness surrounding cluster to
break pbc when runing calculation
                  default value: 10
               : two atoms are "connected" if their
cutoff
distance < cutoff*radius.
                  default value: 1.0
weighten
               : use weighten atoms when appending or
removing atoms
                  default value: True
               : attempts to repair structures when doing
n_repair_try
GA operation
                  default value: 5
               : maximum attempts
max_attempts
                  default value: 50
               : if check seeds
check_seed
                  default value: False
min_lattice
               : min_lattice
                  default value: [0.0, 0.0, 0.0, 45.0,
                  45.0, 45.0]
max_lattice
               : max_lattice
                  default value: [99, 99, 99, 135, 135,
```

```
d ratio
              : distance between each pair of two atoms
in the structure is
                not less than (radius1+radius2)*d_ratio
                 default value: 1.0
distance matrix: distance between each pair of two atoms
in the structure is
                 not less than
                 (radius1+radius2)*distance_matrix[1][2]
                 default value: None
radius
               : radius
                 default value: None
max_forces : if forces of a structure larger is than
this number it will be deleted.
                 default value: 50.0
max_enthalpy : if enthalpy of a structure is larger than
this number it will be deleted.
                 default value: 100.0
full_ele
              : full ele
                 default value: True
max_length_ratio: if max-cell-length/min-cell-length of a
structure is larger than this number it will be deleted.
                 default value: 8
parameter information for <class
'magus.populations.populations.FixPopulation'>
+++++^^IRequirement parameters^^I++++
results_dir : path for results
pop_size
              : population size
symbols
             : symbols
              : formula
formula
+++++^^IDefault parameters^^I++++
check_seed : if check seed is turned on, we will check
your seeds and delete those donot meet requirements
                 default value: False
parameter information for <class
'magus.populations.populations.VarPopulation'>
+++++^^IRequirement parameters^^I++++
results_dir : path for results
              : population size
pop_size
symbols
              : symbols
```

```
: formula
formula
+++++^^IDefault parameters^^I++++
check_seed : if check seed is turned on, we will check
your seeds and delete those donot meet requirements
                 default value: False
parameter information for <class
'magus.reconstruct.individuals.RcsPopulation'>
+++++^^IRequirement parameters^^I++++
results_dir : path for results
: formula
formula
+++++^^IDefault parameters^^I++++
check_seed : if check seed is turned on, we will check
your seeds and delete those donot meet requirements
                 default value: False
parameter information for <class
'magus.operations.crossovers.CutAndSplicePairing'>
+++++^^IDefault parameters^^I++++
tryNum
             : try attempts
                default value: 50
cut_disp : cut displacement
                 default value: 0
best_match : choose best match
                 default value: False
parameter information for <class
'magus.operations.crossovers.ReplaceBallPairing'>
+++++^^IDefault parameters^^I++++
tryNum
             : try attempts
                 default value: 50
cut_range : cut range
                 default value: [1, 2]
parameter information for <class
'magus.operations.mutations.SoftMutation'>
+++++^^IDefault parameters^^I++++
              : tryNum
tryNum
                 default value: 50
```

```
parameter information for <class
'magus.operations.mutations.PermMutation'>
+++++^^IDefault parameters^^I++++
              : try attempts
tryNum
                 default value: 50
frac_swaps : possibility to swap
                 default value: 0.5
parameter information for <class
'magus.operations.mutations.LatticeMutation'>
+++++^^IDefault parameters^^I++++
tryNum
               : try attempts
                 default value: 50
              : Gauss distribution standard deviation
sigma
                 default value: 0.1
cell_cut
               : coefficient of gauss distribution in cell
mutation
                 default value: 1
keep_volume
               : whether to keep the volume unchange
                 default value: True
parameter information for <class
'magus.operations.mutations.RippleMutation'>
+++++^^IDefault parameters^^I++++
               : try attempts
tryNum
                  default value: 50
               : rho
rho
                  default value: 0.3
mu
                 default value: 2
eta
               : eta
                 default value: 1
parameter information for <class
'magus.operations.mutations.SlipMutation'>
+++++^^IDefault parameters^^I++++
tryNum
              : try attempts
                 default value: 50
               : cut position
cut
                 default value: 0.5
```

```
randRange : range of movement
             default value: [0.5, 2]
parameter information for <class
'magus.operations.mutations.RotateMutation'>
+++++^^IDefault parameters^^I++++
              : try attempts
tryNum
                 default value: 50
              : possibility
р
                 default value: 1
parameter information for <class
'magus.operations.mutations.RattleMutation'>
+++++^^IDefault parameters^^I++++
              : try attempts
tryNum
                 default value: 50
              : possibility
р
                default value: 0.25
rattle_range : range of rattle
                default value: 4
d_ratio
             : d ratio
                 default value: 0.7
keep_sym : if keeps symmetry when rattles
                 default value: None
symprec
              : tolerance for symmetry finding
                 default value: 0.1
parameter information for <class
'magus.operations.mutations.FormulaMutation'>
+++++^^IDefault parameters^^I++++
tryNum
             : try attempts
                 default value: 10
n_candidate : number of candidates
                 default value: 5
parameter information for <class
'magus.reconstruct.ga.LyrSlipMutation'>
+++++^^IDefault parameters^^I++++
tryNum
              : tryNum
                 default value: 10
cut
              : cut
```

```
default value: 0.2
randRange
              : randRange
                 default value: [0, 1]
parameter information for <class
'magus.reconstruct.ga.ShellMutation'>
+++++^^IDefault parameters^^I++++
              : tryNum
tryNum
                 default value: 10
d
               : d
                 default value: 0.23
parameter information for <class
'magus.reconstruct.ga.LyrSymMutation'>
+++++^^IDefault parameters^^I++++
              : tryNum
tryNum
                 default value: 10
symprec
              : symprec
                 default value: 0.0001
parameter information for <class
'magus.reconstruct.ga.CluSymMutation'>
+++++^^IDefault parameters^^I++++
tryNum
              : tryNum
                 default value: 10
symprec
              : symprec
                 default value: 0.0001
parameter information for <class
'magus.calculators.emt.EMTCalculator'>
+++++^^IRequirement parameters^^I++++
              : work dictionary
work_dir
job_prefix : calculation dictionary
+++++^^IDefault parameters^^I++++
               : convergence energy
eps
                 default value: 0.05
              : maximum number of relax steps
max_step
                 default value: 100
optimizer
               : optimizer method, choose from bfgs, fire,
lbfgs
                 default value: bfgs
```

max_move : max range of movement

default value: 0.1

relax_lattice : if to relax lattice

default value: True

pressure : pressure

default value: 0.0

parameter information for <class

'magus.calculators.lammps.LammpsCalculator'>

+++++^^IDefault parameters^^I++++

mode : choose from parallel or serial

default value: parallel

pressure : pressure

default value: 0.0

exe_cmd : command line to run lammps

default value:

save_traj : save_traj

default value: False

atomStyle : atomStyle

default value: atomic

job_prefix : job_prefix

default value: Lammps

+++++^^IRequirement_parallel parameters^^I++++

queue_name
num_core
: quene name
num_core

work_dir : work dictionary

job_prefix : calculation dictionary

+++++^^IDefault_parallel parameters^^I++++

pre_processing : serves to add any sentence you wish when submiting the job to change system variables, load modules

etc.

default value:

wait_time : wait_time

default value: 200

verbose : verbose

default value: False

kill_time : kill_time

default value: 100000

num_parallel : num_parallel

default value: 1

pressure : pressure

```
default value: 0.0
parameter information for <class
'magus.calculators.mtp.MTPNoSelectCalculator'>
+++++^^IDefault parameters^^I++++
               : choose from parallel or serial
mode
                  default value: parallel
               : pressure
pressure
                  default value: 0.0
force_tolerance: force_tolerance
                  default value: 0.05
stress_tolerance: stress_tolerance
                  default value: 1.0
               : min dist
min_dist
                  default value: 0.5
               : n_epoch
n_epoch
                  default value: 200
job_prefix
               : job_prefix
                  default value: MTP
+++++^^IRequirement_parallel parameters^^I++++
               : quene name
queue_name
num_core
               : num_core
work_dir
              : work dictionary
job_prefix
              : calculation dictionary
+++++^^IDefault_parallel parameters^^I++++
pre_processing : serves to add any sentence you wish when
submiting the job to change system variables, load modules
etc.
                  default value:
               : wait_time
wait_time
                  default value: 200
verbose
               : verbose
                  default value: False
kill_time
              : kill_time
                  default value: 100000
               : num_parallel
num_parallel
                  default value: 1
pressure
               : pressure
                  default value: 0.0
```

```
parameter information for <class
'magus.calculators.mtp.MTPSelectCalculator'>
+++++^^IDefault parameters^^I++++
mode
               : choose from parallel or serial
                  default value: parallel
               : pressure
pressure
                  default value: 0.0
               : xc
ХC
                  default value: PBE
weights
               : weights
                  default value: [1.0, 0.01, 0.001]
scaled_by_force: scaled_by_force
                  default value: 0.0
force_tolerance: force_tolerance
                  default value: 0.05
stress_tolerance: stress_tolerance
                  default value: 1.0
min_dist
               : min dist
                  default value: 0.5
n_epoch
               : n epoch
                  default value: 200
ignore_weights : ignore_weights
                  default value: True
job_prefix
               : job_prefix
                  default value: MTP
               : n_fail
n_fail
                  default value: 0
+++++^^IRequirement_parallel parameters^^I++++
queue_name
               : quene name
num_core
               : num_core
work_dir
               : work dictionary
job_prefix
               : calculation dictionary
+++++^^IDefault_parallel parameters^^I++++
pre_processing : serves to add any sentence you wish when
submiting the job to change system variables, load modules
etc.
                  default value:
wait_time
               : wait_time
                  default value: 200
               : verbose
verbose
                  default value: False
```

queue_name

job_prefix

num_core
work_dir

kill_time : kill time default value: 100000 num_parallel : num_parallel default value: 1 pressure : pressure default value: 0.0 parameter information for <class 'magus.calculators.mtp.MTPLammpsCalculator'> +++++^^IDefault parameters^^I++++ mode : choose from parallel or serial default value: parallel : pressure pressure default value: 0.0 : xc ХC default value: PBE weights : weights default value: [1.0, 0.01, 0.001] scaled_by_force: scaled_by_force default value: 0.0 force_tolerance: force_tolerance default value: 0.05 stress_tolerance: stress_tolerance default value: 1.0 min_dist : min dist default value: 0.5 n_epoch : n_epoch default value: 200 ignore_weights : ignore_weights default value: True : job_prefix job_prefix default value: MTP n_fail : n fail default value: 0

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: calculation dictionary

+++++^^IRequirement_parallel parameters^^I++++

: work dictionary

: quene name
: num_core

+++++^^IDefault_parallel parameters^^I++++

```
pre_processing : serves to add any sentence you wish when
submiting the job to change system variables, load modules
etc.
                 default value:
              : wait time
wait_time
                 default value: 200
              : verbose
verbose
                 default value: False
kill_time
              : kill_time
                 default value: 100000
num_parallel
              : num_parallel
                 default value: 1
pressure
               : pressure
                 default value: 0.0
parameter information for <class
'magus.calculators.quip.QUIPCalculator'>
+++++^^IRequirement parameters^^I++++
work_dir
             : work dictionary
job_prefix
              : calculation dictionary
+++++^^IDefault parameters^^I++++
               : convergence energy
eps
                 default value: 0.05
              : maximum number of relax steps
max_step
                 default value: 100
optimizer
               : optimizer method, choose from bfgs, fire,
lbfgs
                 default value: bfgs
              : max range of movement
max_move
                 default value: 0.1
relax_lattice : if to relax lattice
                 default value: True
pressure
               : pressure
                 default value: 0.0
parameter information for <class
'magus.calculators.vasp.VaspCalculator'>
+++++^^IDefault parameters^^I++++
mode
               : choose from parallel or serial
                 default value: parallel
               : pressure
pressure
```

```
default value: 0.0
               : xc
хс
                  default value: PBE
             : pp_label
pp_label
                  default value: None
job_prefix
               : job_prefix
                  default value: Vasp
+++++^^IRequirement_parallel parameters^^I++++
queue_name
               : quene name
num_core
work_dir
job_prefix
: num_core
: work dictionary
: calculation dictionary
+++++^^IDefault_parallel parameters^^I++++
pre_processing : serves to add any sentence you wish when
submiting the job to change system variables, load modules
etc.
                  default value:
wait_time
               : wait_time
                  default value: 200
               : verbose
verbose
                  default value: False
kill_time
               : kill_time
                  default value: 100000
num_parallel
               : num_parallel
                  default value: 1
pressure
               : pressure
                  default value: 0.0
parameter information for <class
'magus.calculators.castep.CastepCalculator'>
+++++^^IDefault parameters^^I++++
               : choose from parallel or serial
mode
                  default value: parallel
               : pressure
pressure
                  default value: 0.0
xc_functional : xc_functional
                  default value: PBE
pspot
               : pspot
                  default value: 00PBE
               : suffix
suffix
                  default value: usp
```

```
job_prefix
               : job_prefix
                 default value: Castep
kpts
               : kpts
                 default value: {'density': 10, 'gamma':
                 True, 'even': False}
castep_command : castep_command
                 default value: castep
castep_pp_path : castep_pp_path
                  default value: None
+++++^^IRequirement_parallel parameters^^I++++
queue_name
               : quene name
num_core
               : num_core
work_dir
               : work dictionary
job_prefix : calculation dictionary
+++++^^IDefault_parallel parameters^^I++++
pre_processing : serves to add any sentence you wish when
submiting the job to change system variables, load modules
etc.
                 default value:
wait_time
               : wait_time
                  default value: 200
               : verbose
verbose
                 default value: False
kill_time
               : kill_time
                  default value: 100000
               : num_parallel
num_parallel
                  default value: 1
               : pressure
pressure
                  default value: 0.0
parameter information for <class
'magus.calculators.lj.LJCalculator'>
+++++^^IRequirement parameters^^I++++
              : work dictionary
work_dir
job_prefix
              : calculation dictionary
+++++^^IDefault parameters^^I++++
              : convergence energy
eps
                  default value: 0.05
               : maximum number of relax steps
max_step
                  default value: 100
```

optimizer : optimizer method, choose from bfgs, fire,

lbfgs

default value: bfgs

max_move : max range of movement

default value: 0.1

relax_lattice : if to relax lattice

default value: True

pressure : pressure

default value: 0.0

parameter information for <class

'magus.calculators.gulp.GulpCalculator'>

+++++^^IDefault parameters^^I++++

mode : choose from parallel or serial

default value: parallel

pressure : pressure

default value: 0.0

exe_cmd : command line to run gulp

default value: gulp < input > output

job_prefix : job_prefix

default value: Gulp

+++++^^IRequirement_parallel parameters^^I++++

queue_name
num_core
: quene name
num_core

work_dir : work dictionary

job_prefix : calculation dictionary
+++++^^IDefault_parallel parameters^^I+++++

pre_processing : serves to add any sentence you wish when submiting the job to change system variables, load modules

etc.

default value:

wait_time : wait_time

default value: 200

verbose : verbose

default value: False

kill_time : kill_time

default value: 100000

num_parallel : num_parallel

default value: 1

pressure : pressure

default value: 0.0

```
parameter information for <class
'magus.calculators.base.AdjointCalculator'>
+++++^^IRequirement parameters^^I++++
work dir
              : work dictionary
job_prefix : calculation dictionary
+++++^^IDefault parameters^^I++++
               : pressure
                  default value: 0.0
parameter information for <class
'magus.calculators.mtp.TwoShareMTPCalculator'>
+++++^^IRequirement parameters^^I++++
               : work dictionary
work_dir
              : calculation dictionary
job_prefix
+++++^^IDefault parameters^^I++++
               : pressure
pressure
                  default value: 0.0
```