#### ASE 简明介绍

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ASE is an Atomic Simulation Environment written in the Python programming language with the aim of setting up, manipulating, manipulating, running, visualizing, and analyzing atomistic simulations.

Supported Calculators:



#### 设计目标

- Easy to use & Flexible
  - graphical user interface, Command line tool, "for-loop" constructions
- Customizable
  - Python code in ASE is structured in modules
  - ase.calculators for calculating energies, forces and stresses
  - ase.md and ase.optimize modules for controlling the motion of atoms
  - constraints objects and filters for performing nudged-elastic-band calculations etc.
- Pythonic
  - interactively, popular NumPy package, analyse & plot
- Open
  - CAMPOS Atomic Simulation Environment is released under the GNU LGPL 2.1 or any later version.

```
wszhang@node450 test mpi]$ls /opt/ase/3.13.0/ase/
atom.pv
                                                               phonons.py
                                                                                   units.py
atom.pyc
                                            neb.pv
                                                               quaternions.py
                                                                                   units.pvc
                                            neighborlist.py
atoms.py
             constraints.py
                                            neighborlist.pyc
atoms.pyc
                              infrared.py
autoneb.py
                                init .py
                                                               structure.py
                                init .pyc
                                            parallel.py
                                                                                   xrdebye.py
             dimer.py
                                            parallel.pvc
                                                               thermochemistry.pv
             eos.pv
                                            phasediagram.py
wszhang@node450 test mpil$ls /opt/ase/3.13.0/ase/calculators/
abinit.py
                    dacapo.py
                                                       lj.py
                                 gaussian.py
aims.py
                                  general.py
                                                       loggingcalc.py
                                                                         singlepoint.py
amber.py
                    dftb.py
                                  gromacs.py
                                                                         test.pv
                                                       mopac.py
                                    init_.py
                    eam.pv
                                                                         tip3p.pv
                                                       morse.pv
                    elk.py
calculator.pv
                                    init .pyc
                                                       neighborlist.py
                                                                         turbomole.pv
calculator.pvc
                    emt.py
                                  interfacechecker.pv
                                                       nwchem.pv
                                                                         vasp.pv
castep.pv
                    exciting.py
                                  interface.py
                                                                         vdwcorrection.pv
                                                       octopus.py
checkpoint.py
                    ff.py
                                                       onetep.py
cp2k.py
                    fleur.py
                                  lammpsrun.py
                                                       qmmm.py
wszhang@node450 test mpi]$ls /opt/ase/3.13.0/ase/optimize/
                                        init .py
                                                    minimahopping.py
basin.pv
                        bfgs.py
                        fire.py
bfgslinesearch.py
                                       lbfgs.py
                                                    oldqn.py
                                                                       sciopt.py
bfgslinesearch.py~yuan fmin bfgs.py
                                      mdmin.py
                                                    optimize.py
```

### 模块与功能

#### https://wiki.fysik.dtu.dk/ase/ase/ase.html

The Atomorphism	Genetic Algorithm		
The Atoms object	ASE's GUI		
Units	General crystal structures and surfaces		
File input and output			
Building things	Nanoparticles and clusters		
	Visualization		
Equation of state	Calculators		
Collections	Density Functional Theory		
The data module	Vibration analysis		
Structure optimization	Phonon calculations		
Molecular dynamics	Phase diagrams and Pourbaix diagrams		
Constraints	Thermochemistry		
Using the spacegroup subpackage	Utillity functions and classes		
Building neighbor-lists	Parallel calculations		
Geometry tools	Dimer method		
A database for atoms	The Atom object		
Nudged elastic band	Electron transport		

```
1>>> # Example: structure optimization of hydrogen molecule
 2>>> from ase import Atoms
 3>>> from ase.optimize import BFGS
 4>>> from ase.calculators.nwchem import NWChem
 5>>> from ase.io import write
 6>>> h2 = Atoms('H2'.
                   positions=[[0, 0, 0], [0, 0, 0.7]])
 7...
 8>>> h2.calc = NWChem(xc='PBE')
 9>>> opt = BFGS(h2)
10>>> opt.run(fmax=0.02)
11BFGS: 0 19:10:49 -31.435229 2.2691
12BFGS: 1 19:10:50 -31.490773 0.3740

    13BFGS:
    2
    19:10:50
    -31.492791
    0.0630

    14BFGS:
    3
    19:10:51
    -31.492848
    0.0023

15>>> write('H2.xyz', h2)
16>>> h2.get potential energy()
17-31.492847800329216
```



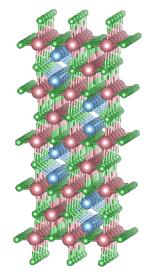
Finally: Add ~/ase to your PYTHONPATH environment variable.

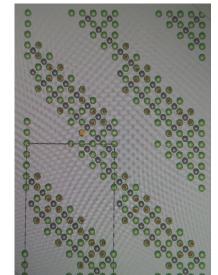
ASE 简明介绍 安装运行 [8 / 33]

#### Parallel calculation: Abinit

```
1from ase import Atoms
2from ase.units import Ry
 sfrom ase.calculators.abinit import Abinit
5a0 = 5.43
6bulk = Atoms('Si2', [(0, 0, 0),
                       (0.25, 0.25, 0.25)].
              pbc=True)
9b = a0 / 2
10bulk.set_cell([(0, b, b),
                 (b, 0, b),
                 (b, b, 0)], scale atoms=True)
| 14calc = Abinit(
                command = "mpirun, _n, 24, _machinefile, ,%s, abinit, <, PREFIX.files, >,,
15
                     PREFIX.log"%hostfile, # 关键的设置!!!
               label='Si',
               nbands=8, # one can specify any abinit keywords
                ecut=10 * Ry, # warning — used to speedup the test
                kpts=[4, 4, 4], # warning - used to speedup the test
                chksvmbreak=0.
23# one can specify abinit keywords also using set
24calc.set(toldfe=1.0e-2) # warning - used to speedup the test
25bulk.set calculator(calc)
26e = bulk.get potential energy()
```

### 手工沿着非晶格矢量方向切片很麻烦, 容易出错





希望:

错误:

6import time 7import subprocess simport string 9import copy 10 import numpy as np 11import math 12from io import StringIO 13from string import ljust 14from \_elementtree import Element 15import ase 16import ase.io as aio 17import ase, build as abd 18import ase.optimize as aopt 19import ase.visualize as av 20 import ase.constraints as ac 21from ase import Atoms 22from ase.units import Ry 24pname = "ZnGaO\_5layers\_CO2" |25#读取原子结构对象: 26zngao = aio.read('zngao.cif',format='cif') 调整输入文件: 结构 & KPOINT

切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 I

#!/usr/bin/python 2# -\*- coding: utf-8 -\*-

simport os 4import re 5import sys

29# 创建超胞 30# Make SuperCell  $_{31}$ #P = np.array([[ 3, 0, 0], |32# [ 0, 2, 0], |33# [ 0, 0, 2]]) 34#zngaos = abd.make supercell(zngao, P) 37# Cut layers |ss# 对ZnGaO进行切片,切出5个layer,每个layer面的边矢量为 (2,0,0), (0,2,-2), 同时容 许些许误差: tolerance。 silvers = abd.cut(zngao, (2,0,0), (0,2,-2), nlayers=5, origo=(0,0,-0.02),tolerance=0.015, extend=1.0) 40# 对切片后的slab进行旋转,晶格矢量也一起旋转: 41 layers.rotate( (0,1,1), (0,0,1), rotate\_cell=True) 42 layers.set\_positions( layers.positions.round(decimals=6,) ) 43layers.set\_cell( layers.cell.round(decimals=6,) ) |44# 增加第三个晶格矢量z方向的长度,建立真空层: 45layers.cell[2][2] = 20. 46# 重新对原子结构对象中的原子进行排序,重分配原子序号: 47slab = abd.sort(layers) 48# 将原子结构平移, 置于晶格中央: 49slab.center(axis=(0,1,2),) 4axis=(0,1,2),) 4vacuum=10.0,about=(1., 1., 1.)) 51 Γ12 / 331 ASE 简明介绍 调整输入文件: 结构 & KPOINT

切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 II

152#设定需要添加的分子结构与旋转取向: 53h CO2 = 2.054CO2 = abd.molecule('CO2') 55C02.rotate( (0,1,0), (0,0,1), rotate cell=False) 56CO2.rotate((0,0,1), math.pi/4, rotate\_cell=False) 58h CO2H = 2.059CO2H = abd.molecule('CO2') 60CO2H.rotate( (0,1,0), (0,0,1), rotate cell=False) 61CO2H.rotate((0,0,1), math.pi/4, rotate cell=False) 62CO2H.append(ase.Atom('H')) 63CO2H.positions[3] = np.array([-1.2, 1.2, 0.])65a = 15.066CO2.set cell([ (a, 0, 0), (0. a. 0).(0, 0, a) ], )#scale\_atoms=True) 69CO2.set pbc(pbc=True) 70C02.center(axis=(0,1,2), )#vacuum=10.0,about=(1., 1., 1.)) 173# 改变特定条件的原子的元素号: 74for i in range(len(slab)): if slab[i].symbol == Ga' and abs(slab[i].position[2]-12.947) < 0.1: slab[i].symbol = 'Ce' 77slab[7].symbol='Ga' 178# 删除某序号的原子: 79del slab[21] Γ13 / 331 ASE 简明介绍 调整输入文件: 结构 & KPOINT

切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 III

```
84print slab[-1]
187# 添加分子预定吸附位置 add adsorbate
|ssabd.add_adsorbate(slab, CO2, h_CO2, position=(8.380,14.062) )
89stru = slab
92# setting PROPERTY
sstru.set pbc((True, True, True)) # a.pbc = (True, True, False)
196# 设定结构中的移动受限的原子 Constraints
97#constraintlist = []
98#constraintlist.append(fix1layer)
| se#constraintlist.append( ac.FixAtoms(mask=[True for atom in slab ]) )
#constraintlist.append( ac.FixAtoms(indices=[4]) )
101#for i in [5,15,16]:
      constraintlist.append( ac.FixedLine( i, [0,1,0]) )
offix1layer = ac.FixAtoms(indices=[atom.index for atom in stru
ASE 简明介绍
                                                                                Γ14 / 331
                              调整输入文件: 结构 & KPOINT
```

切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 IV

statom add = ase.Atom('Ga', [8.380396500000016, 14.062033500000002,

l∞**#** 添加新原子

82print atom\_add 83slab = slab + atom add

15.9471504999999991)

```
if (atom.position[2] < 7.5 and atom.position[2] > 6.5 and atom.symbol
                   == 'Ga' ) ] )
too#fix1layer = ac.FixAtoms(indices=[0] )
107#constraintlist = [fix1layer]
losstru.set constraint([fix1layer,])
109
m# Filters 对晶格进行限制
12#from ase.constraints import StrainFilter
#fixed = StrainFilter(stru)
14#optobj = ac.UnitCellFilter( stru ) #hydrostatic strain=True ) #mask=[True,True,
      False.False.False] )
17# 打开/读取/准备 历史轨迹文件:
118# open & read & save traj
#stru_final = aio.read(pname+'.traj',)
20#av.view(stru_final) #:图形化查看原子轨迹,可动画播放
121#
|22traj_hist = aio.Trajectory(pname+'.traj',) #mode='r')
\lfloor 23 \# stru = traj_hist[-1]
124#av.view(traj hist)
125#
straj = aio.Trajectory(pname+'.traj', 'w', stru) #(pname+'.traj', 'a'/'w', stru)
127#traj.write()
129
```

调整输入文件: 结构 & KPOINT

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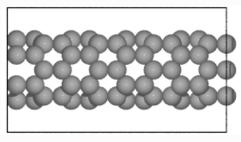
切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 V

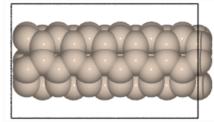
```
30# View & Print & Save Structure
|siprint "\n⊔stru.get_chemical_symbols():\n", stru.get_chemical_symbols()
32#print "\n stru.arrays:\n",
                                  stru.arrays #CO2.positions #CO2.
      get_scaled_positions()
                                             #CO2.get_cell() CO2.numbers
stru.cell
34print "\n⊔stru.pbc:\n",
                                 stru.pbc
35print "\n_stru.constraints:\n", stru.constraints
|se#aio.write(pname+'.ini.pov', stru, rotation='0x', run_povray=True)
37aio.write(pname+'.ini.png', stru, rotation='-80x')
 aio.write(pname+'.ini.vasp', stru, format='vasp')
139aio.write(pname+'.ini.xyz', stru, format='xyz')
40aio.write(pname+'.ini.cif', stru, format='cif')
41print "\nusaveduinitialuatomsustructureu"
45#av.view(stru)
```

切片、扩胞、旋转、替换删除添加、吸附、固定、轨迹 VI

#### 内置常用结构

```
1>>> from ase.build import molecule
2>>> atoms = molecule('H2O')
3
4>>> from ase.build import nanotube
5>>> cnt1 = nanotube(6, 0, length=4)
5>>> cnt2 = nanotube(3, 3, length=6, bond=1.4, symbol='Si')
```





# 生成 kpoints I

```
ase.dft.kpoints.monkhorst_pack,
ase.dft.kpoints.special_points
```

```
1>>> from ase.dft.kpoints import *
 2>>> monkhorst_pack((4, 1, 1))
 array([[-0.375, 0., 0.],
[-0.125, 0., 0.],
5 [ 0.125, 0. , 0. ],
6 [ 0.375, 0. , 0. ]])
>>> get_monkhorst_pack_size_and_offset([[0, 0, 0]])
8(array([1, 1, 1]), array([ 0., 0., 0.]))
10>>> from ase.dft.kpoints(import special_paths, special_points, parse_path_string)
11>>> paths = special paths['bcc']
12>>> paths
13[['G', 'H', 'N', 'G', 'P', 'H'], ['P', 'N']]
14>>> points = special_points['bcc']
15>>> points
_{16}{'H': [0.5, -0.5, 0.5], 'N': [0, 0, 0.5], 'P': [0.25, 0.25, 0.25],
17 'G': [0. 0. 0]}
18>>> kpts = [points[k] for k in paths[0]] # G H N G P H
19>>> kpts
20[[0, 0, 0], [0.5, -0.5, 0.5], [0, 0, 0.5], [0, 0, 0], [0.25, 0.25, 0.25], [0.5, 0.5]
      -0.5, 0.5]
```

# 生成 kpoints II

#### ase.dft.kpoints.special\_points

Special points from [Setyawana-Curtarolo]:			
Cubic	GXMGRX,MR		
FCC	GXWKGLUWLK,UX		
BCC	GHNGPH,PN		
Tetragonal	GXMGZRAZ,XR,MA	//_images/tetragonal.svg	
Orthorhombic	GXSYGZURTZ,YT,UX,SR	₩	
Hexagonal	GMKGALHA,LM,KH	•	
Monoclinic	GYHCEM1AXH1,MDZ,YD	<b>®</b>	

#### Run CP2k Structure Optimization I

https://wiki.fysik.dtu.dk/ase/gallery/gallery.html

```
# 此处省略结构构建
 2# CP2K
 sfrom ase.calculators.cp2k import CP2K
 4#CP2K.command = "mpijob cp2k_shell.popt"
 s#os.environ['ASE_CP2K_COMMAND'] = "mpijob cp2k_shell.popt"
            ASE CP2K COMMAND: \n",os.environ['ASE CP2K COMMAND'],"\n"
 6#print
 7inp_str = '''
 ∘&GĪ.ΩBAT.
    PRINT LEVEL MEDIUM !MEDIUM LOW
11&FND GLOBAL
12&FORCE EVAL
    !METHOD Quickstep
    !STRESS TENSOR ANALYTICAL
    &DFT
       &QS
          EPS DEFAULT 1.0E-10
       &END QS
       &SCF
          SCF GUESS ATOMIC !RESTART !ATOMIC
          EPS_SCF 1.0E-6
          ADDED MOS 200
          CHOLESKY INVERSE
          &DIAGONALIZATION
             ALGORITHM STANDARD
26
```

## Run CP2k Structure Optimization II

53!&MOTION

```
&FND DTAGONALTZATTON
27
         &MIXING ON
            METHOD BROYDEN MIXING
                                 ! NEW
                                         ! BROYDEN MIXING NEW BROYDEN MIXING
                MULTISECANT MIXING
            ALPHA 0.1
            BETA 1.5
            INBROYDEN 8
         &END MIXING
         &SMEAR ON
            !ELECTRONIC TEMPERATURE [K] 600
            METHOD ENERGY WINDOW
            WINDOW_SIZE [eV] 0.2
         &FND SMEAR
      &END SCF
      &MGR.TD
         NGRIDS 4
         CUTOFF %s
         REL CUTOFF %s
      &END MGRID
       !&FORCES ON
       !&END FORCES
    &FND DFT
51&END FORCE EVAL
```

### Run CP2k Structure Optimization III

```
&CELL OPT
54
         KEEP_ANGLES
55
56
         !KEEP_SYMMETRY
57
         !EXTERNAL PRESSURE [GPa] 0
58
         OPTIMIZER CG
59
         &CG
60
           &LINE SEARCH
61
             TYPE 2PNT
62
           &END LINE_SEARCH
63
         &END CG
         TYPE DIRECT CELL OPT
64
                                !GEO OPT
      &END CELL_OPT
65
      !&GEO OPT
66
67
          TYPE MINIMIZATION
68
          MAX_DR 1.0E-03
69
         MAX_FORCE 1.0E-03
70
          RMS_DR 1.0E-03
71
          RMS_FORCE 1.0E-03
72
          MAX ITER 200
73
          OPTIMIZER BFGS
74
         !&BFGS
75
         ! MAX STEEP STEPS 0
         ! RESTART_LIMIT 9.0E-01
76
         !&END BFGS
77
78
      !&END GEO OPT
79
      !&CONSTRAINT
80
          &FIXED ATOMS
81
            COMPONENTS TO FIX XYZ
```

[22 / 33]

#### Run CP2k Structure Optimization IV

```
LIST 2
82
83
         &END FIXED ATOMS
84
    !&END CONSTRAINT
85! &END MOTION
87calc = CP2K(#
              command = 'mpijobucp2k_shell.popt',
              label = pname,
89
              #inp = inp_str%cutoff ,
              potential_file = 'GTH_POTENTIALS', # POTENTIAL
91
              pseudo potential = 'auto',
              basis_set_file = 'BASIS_MOLOPT_addUCL', # 'BASIS MOLOPT UCL', #'
                  BASIS MOLOPT',
              basis set
                               = 'DZVP-MOLOPT-SR-GTH',
94
              xc = 'PBE', # B3LYP, PADE
             #uks = True,
             \#charge = 0,
              cutoff = None, #400 * Ry, #default:400*
              \max scf = 300,
99
              #debug = True.
100
              #PRINT_LEVEL
101
103cutoff = 1000
104rel cutoff = 60
los#for cutoff in [1400]: #600, 800, 1000, 1200]:
      #[200,300,400,500,600,700,800,900,1000]:
loc# for rel_cutoff in [40,60,80,100]:
or## one can specify abinit keywords also using set :
```

[23 / 33]

#### Run CP2k Structure Optimization V

```
hos##calc.set( toldfe = 1.0e-5)
ogcalc.set( inp = inp str%(cutoff, rel cutoff) )
110slab.set calculator(calc)
#e0_slab = slab.get_potential_energy()
#print "\n cutoff = %s, rel_cutoff = %s, e0_slab = %s "%(cutoff, rel_cutoff,
      e0 slab)
"# os.system( " grep -E -6 \"MULTIGRID INFO\" %s | tail -n 8 "%(pname+".out")
116# Dynamics
http://dyn = aopt.BFGSLineSearch(fixed,trajectory=pname+'.traj') #, restart='***.pckl')
| lasdyn = aopt.BFGSLineSearch(slab )#, restart='layers COPT.traj')
120#dyn.attach(traj.write)
121dyn.attach(traj)
22#dyn.replay_trajectory('layers_COPT.traj')
24#dyn.run(fmax=0.002,steps=150)
125dyn.run(fmax=0.02)
28e slab = slab.get potential energy()
129print "\nue_slab_uuuu=u", e_slab
```

#### Outputs I

```
ncpus tot = 72, hostdict = {'node109': 24, 'node111': 24, 'node110': 24}
3 slab.cell:
4[[ 16.6716
             0.
                  0.
5 [ 0.
              23.577203 0.
                                 11
6 Γ −0.
             0.
                        20.
8 slab.pbc:
[ True True True]
11 slab.constraints:
12[FixAtoms(indices=[0, 4, 5, 11, 15, 16, 27, 37, 40, 44, 45, 51, 55, 56, 67, 77])]
14 saved initial atoms structure
                Step[FC]
                             Time Energy
                                                       fmax
16BFGSLineSearch: 0[ 0] 12:08:45 -285534.437492
                                                    2.6137
| 17BFGSLineSearch: 1[ 2] 12:29:12 -285545.964819
                                                    10.2057
18BFGSLineSearch: 2[ 4] 13:14:37 -285549.406292
                                                       1.1386
19 . . .
20BFGSLineSearch: 206[268] 15:34:38 -285556.418339
                                                       0.0255
21BFGSLineSearch: 207[269] 15:38:29 -285556.418555
                                                       0.0841
22BFGSLineSearch: 208[273] 15:59:44 -285556.418613
                                                       0.0420
23BFGSLineSearch: 209[274] 16:04:11 -285556.418761
                                                       0.0751
24BFGSLineSearch: 210[275] 16:08:49 -285556.418875
                                                       0.0209
25BFGSLineSearch: 211[276] 16:13:11 -285556.418995
                                                       0.0123
_{27} e_{slab} = -285556.418995
```

#### Structure Optimization Banchmark

#### C5H12

Geometry optimization of gas-phase molecule.

Calculator used: GPAW (Icao)

Optimizer	Optimizer Steps	Force evaluations	Energy	Time [sec]	Note
BFGS	10	10	-85.26102	32	
LBFGS	10	10	-85.26102	32	
LBFGSLineSearch	11	26	-85.26267	69	
FIRE	38	38	-85.26096	80	
MDMin	21	21	-85.26111	66	
SciPyFminCG	9	18	-85.26218	46	
SciPyFminBFGS	11	21	-85.26165	46	
BFGSLineSearch	8	15	-85.26182	58	
GoodOldQuasiNewton	13	13	-85.26216	36	

#### nanoparticle

Adsorption of a NH on a Pd nanoparticle.

Calculator used: GPAW (Icao)

Optimizer	Optimizer Steps	Force evaluations	Energy	Time [sec]	Note
BFGS	28	28	-16.23916	109	
LBFGS	57	57	-16.25660	185	
LBFGSLineSearch	16	60	nan	158	An exception occurred
FIRE	73	73	-16.25149	191	
MDMin	47	47	-16.25064	158	
SciPyFminCG	17	48	nan	153	An exception occurred
SciPyFminBFGS	17	18	-16.24096	75	

ASE 简明介绍

计算功能

#### Molecular dynamics

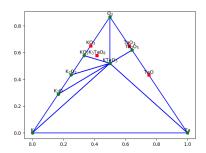
#### Nudged Elastic Band I

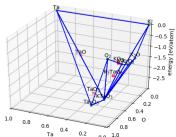
```
1from ase import io
 2from ase.neb import NEB
 3from ase.optimize import MDMin
 # Read initial and final states:
 5initial = io.read('A.trai')
6final = io.read('B.traj')
# Make a band consisting of 5 images:
 simages = [initial]
 simages += [initial.copy() for i in range(3)]
10 images += [final]
neb = NEB(images)
12# Interpolate linearly the potisions of the three middle images:
13neb.interpolate()
4# Set calculators:
15for image in images[1:4]:
      image.set_calculator(MyCalculator(...))
17# Optimize:
18 optimizer = MDMin(neb, trajectory='A2B.traj')
19 optimizer.run(fmax=0.04)
23#Parallelization over images
24from ase.parallel import rank, size
25from ase.calculators.emt import EMT
26# Number of internal images:
|_{27n} = len(images) - 2
28j = rank * n // size
```

# Nudged Elastic Band II

```
29for i, image in enumerate(images[1:-1]):
30    if i == j:
31        image.set_calculator(EMT())
```

#### Phase Diagrams





## 计算声子: phonons.py

```
calculated with the so-called finite-displacement method where the
def init (self, atoms, calc=None, supercell=(1, 1, 1), name=None,
            delta=0.01. refcell=None):
```

计算功能

#### Calculator: abinit.py I

```
1 58 class Abinit(FileIOCalculator):
         """Class for doing ABINIT calculations.
2 59
3 61
         The default parameters are very close to those that the ABINIT
4 62
         Fortran code would use. These are the exceptions::
           calc = Abinit(label='abinit', xc='LDA', ecut=400, toldfe=1e-5)
5 64
6 65
7 67
         implemented_properties = ['energy', 'forces', 'stress', 'magmom']
9 78
         def init (self, restart=None, ignore_bad_restart_file=False,
10 79
                       label='abinit', atoms=None, scratch=None, **kwargs):
12118
         def write_input(self, atoms, properties=None, system_changes=None):
         def read(self. label):
 263
             """Read results from ABINIT's text-output file."""
15264
17276
         def read_results(self):
             # Forces:
19335
20336
             for line in lines:
21337
                  if line.rfind('cartesian, forces, (ev/angstrom), at, end:') > -1:
 338
                      forces = []
 339
                      for i in range(natoms):
 340
                          forces.append(np.array(
25341
                                   [float(f) for f in next(lines).split()[1:]]))
26342
                      self.results['forces'] = np.arrav(forces)
27343
                      break
28344
             else:
```

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#### Calculator: abinit.py II

```
29345
                  raise RuntimeError
 346
31347
              self.width = self.read electronic temperature()
 348
              self.nband = self.read number of bands()
 349
              self.niter = self.read number of iterations()
34350
              self.nelect = self.read number of electrons()
35351
              self.results['magmom'] = self.read magnetic moment()
37457
          def read number of iterations(self):
39467
          def read_electronic_temperature(self):
41478
          def read number of electrons(self):
43496
          def get kpts info(self, kpt=0, spin=0, mode='eigenvalues'):
45514
          def read magnetic moment(self):
47524
          def get_fermi_level(self):
49527
          def get eigenvalues(self, kpt=0, spin=0):
51530
          def get occupations(self, kpt=0, spin=0):
```