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ATOMIC SIMULATION RECIPES

Proposal

We should have some standardized form for scripts.

Outline

- What is the problem
- Our suggestion
 - How should it work in practice?
 - Examples
 - Design choices

Normal ASE workflow

To relax a structure I would probably start with a script like this.

I would gradually expand my script:

- Save each relaxation step
- Relax cell: `UnitCellFilter()`
- Etc...

In time the script would have grown significantly.

```
File Edit Options Buffers Tools Python Help
dataset = spglib.get_symmetry_dataset(ats(atoms),
                                     symprec=1e-4,
                                     angle_tolerance=0.1)

atoms = SpgAtoms.from_atoms(atoms)
atoms.set_symmetries(symmetries=dataset['rotations'],
                    translations=dataset['translations'])

if dftd3:
    calc = DFTD3(dft=dft)
else:
    calc = dft
atoms.calc = calc

spgname, number = spglib.get_spacegroup(ats(read('unrelaxed.json',
                                             parallel=False)),
                                       symprec=1e-4,
                                       angle_tolerance=0.1).split())

# We are fixing atom=0 to reduce computational effort
from ase.constraints import ExpCellFilter
filter = ExpCellFilter(atoms, mask=smask)
opt = myBFGS(filter,
            logfile=name + '.log',
            trajectory=Trajectory(name + '.traj', 'a', atoms))

# fmax=0 here because we have implemented our own convergence criteria
runner = opt.irun(fmax=0)
for _ in runner:
    # Check that the symmetry has not been broken
    spgname2, number2 = spglib.get_spacegroup(ats(atoms),
                                              symprec=1e-4,
                                              angle_tolerance=0.1).split()

    if not (allow_symmetry_breaking or number == number2):
        # Log the last step
        opt.log()
        opt.call_observers()
        msg = ('The symmetry was broken during the relaxation! '
              f'The initial spacegroup was {spgname} {number} '
              f'but it changed to {spgname2} {number2} during '
              'the relaxation.')
        raise AssertionError(msg)

    if is_relax_done(atoms, fmax=0.01, smax=0.002, smask=smask):
        opt.log()
        opt.call_observers()
        break

return atoms

def BN_check():
```

Relax



Phonons



Bandstructure

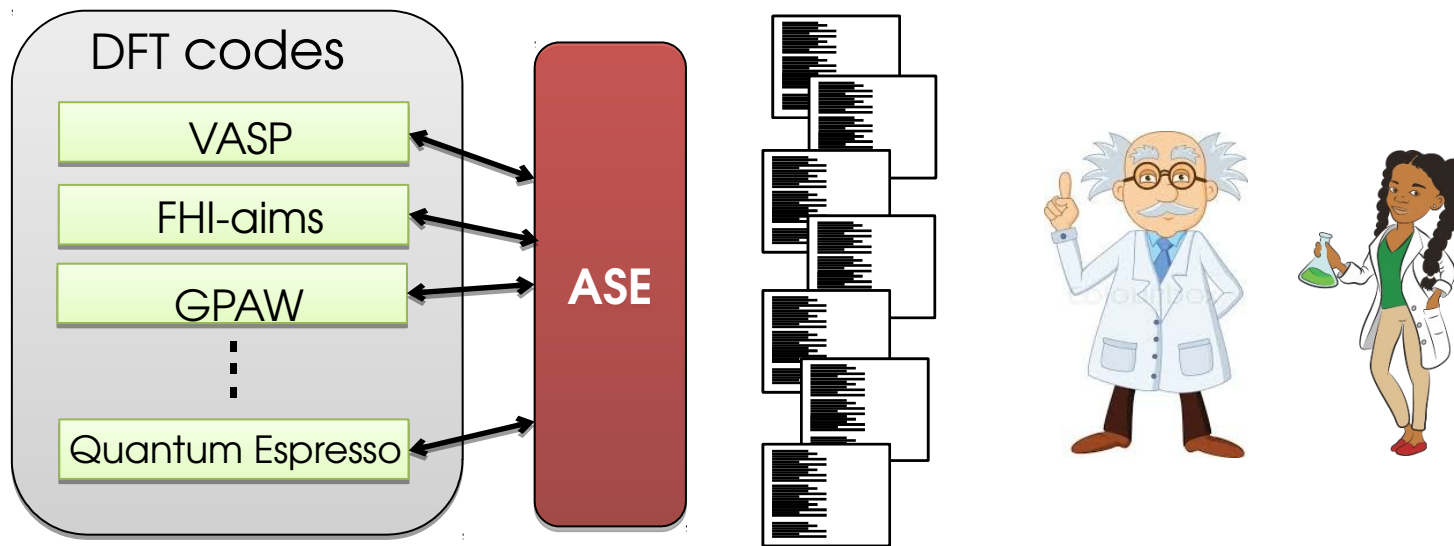


...



These scripts become my recipes to
calculate properties

The big picture



"Pile of scripts"
- Adam Jackson

Waste of student time?

- Many (most, all?) students go through this process
 - Writing a script, improving on it
 - Doing the same mistakes
 - Implementing variants the same good ideas
 - Converge to (mostly) the same script
- Learning experience?
 - Some important lessons in this process
 - Some not so important
 - Some definitely a waste of time

Using new modules



Developer



Module



Student



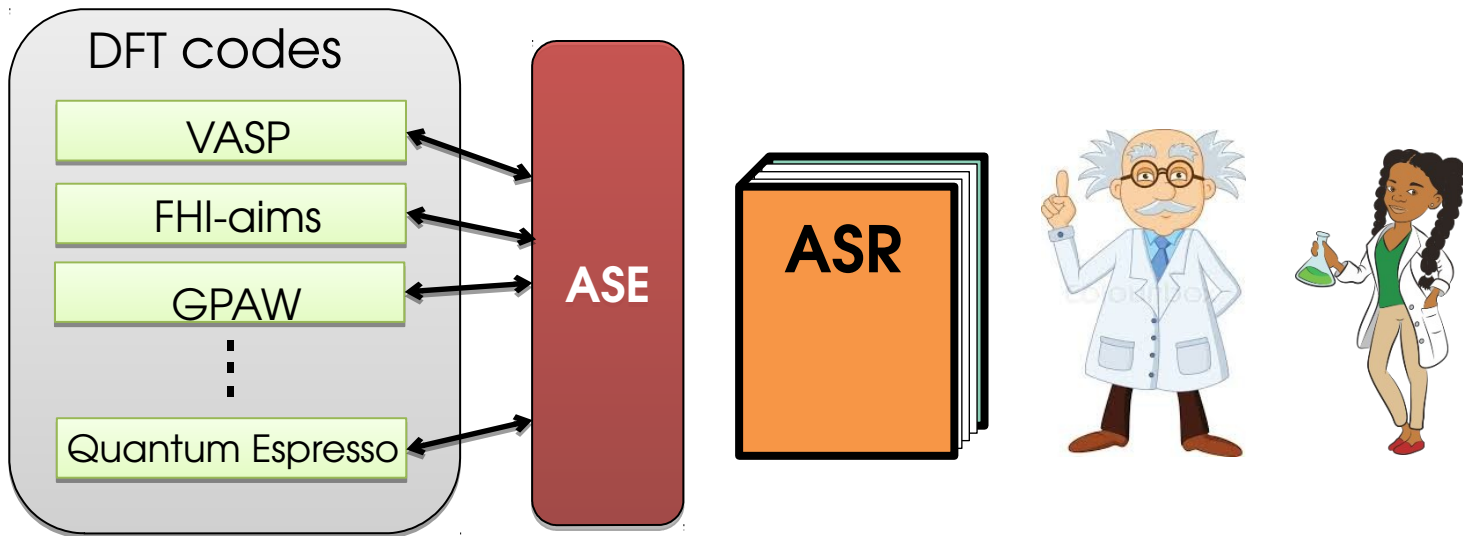
Script

Tutorials are often solving an artificial problem, scripts solve a real world problem.
Do we need a place for those?

Anecdote

- AIMS workshop, ASE tutorial Barcelona 2019
- “Are there any predefined scripts for relaxing a structure?”
- Do we need a repository and some standardized form for scripts? Could we even agree on something?

The big picture



What should such a package be/do/not do?

**OUR SUGGESTION
(BASED ON OUR NEEDS,
UP FOR DISCUSSION)**

What is a recipe?

- **A annotated function that returns its results as a dictionary.**
- Results are saved to a json file.
- The `@command` decorator takes care of everything.
- In particular, gives the function a command line interface.
- The ASR package is just a collection of scripts containing recipes.

```
File Edit View Search Terminal Help
File Edit Options Buffers Tools Python Virtual Envs Elp
from asr.core import command, option

@command()
@option('--fmax', help='Minimum force tolerance.')
def relax(fmax=0.01):
    """This function relaxes a structure"""
    from ase.optimize.bfgs import BFGS
    BFGS(...).run(fmax)
    results = {'energy': ...}
    return results

if __name__ == '__main__':
    relax.cli()
```

Command line interface

```
$ python3 -m asr.relax --help
```

```
Usage: python -m asr.relax [OPTIONS]
```

```
    This function relaxes a structure
```

```
Options:
```

```
--fmax FLOAT    Minimum force tolerance.  [default: 0.01]
```

```
-h, --help      Show this message and exit.
```

Full disclosure:

The actual relax recipe

```
@command('asr.relax',
        requires=['unrelaxed.json'],
        creates=['structure.json'])
@option('-c', '--calculator', help='Calculator and its parameters.')
@option('--d3/--nod3', help='Relax with vdW D3')
@option('--fixcell', is_flag=True, help='Don\'t relax stresses')
@option('--allow-symmetry-breaking', is_flag=True,
        help='Allow symmetries to be broken during relaxation')
def main(calculator={'name': 'gpaw',
                     'mode': {'name': 'pw', 'ecut': 800},
                     'xc': 'PBE',
                     'kpts': {'density': 6.0, 'gamma': True},
                     'basis': 'dzp',
                     'symmetry': {'symmorphic': False},
                     'convergence': {'forces': 1e-4},
                     'txt': 'relax.txt'}
```

Example: Relax silver

```
$ ase build Ag unrelaxed.json --crystal-structure fcc
```

```
$ python3 -m asr.relax --calculator '{"name': 'emt'}"
```

```
Running asr.relax(calculator={'name': 'emt'}, d3=False,  
fixcell=False, allow_symmetry_breaking=False)
```

```
$ ls
```

```
relax.log  relax.traj  results-asr.relax.json  
structure.json  unrelaxed.json
```

Result files

```
$ cat results-asr.relax.json
{
  "energy": -0.0003663968564069364,
  "__params__": {
    "calculator": {"name": "emt"},
    "d3": false,
    "fixcell": false,
    "allow_symmetry_breaking": false
  },
  "__versions__": {
    "asr": "19.8.20-8ad12500add3f21047dc2b5a91cecbd3daa07d39",
    "ase": "3.19.0b1-da3288338c6896a9a5b15322d303471d826f7486",
  }
}
```


Result files

```
$ cat results-asr.relax.json
{
  "energy": -0.0003663968564069364,
  ...

  "__creates__": {
    "structure.json": "1bb6cf42c49864c81d7f3a394918b71a"
  },
  "__requires__": {
    "unrelaxed.json": "be8cc1a545f45522e9880635bfe955c5"
  },
}
```

Important: Direct relation between scripts and CLI

```
$ python3 -m asr.relax --calculator '{"name': 'emt'}"  
Running asr.relax(calculator={'name': 'emt'}, d3=False,  
fixcell=False, allow_symmetry_breaking=False)
```

=

```
from asr.relax import main as relax  
  
relax(calculator={'name': 'emt'}, d3=False,  
      fixcell=False, allow_symmetry_breaking=False)
```

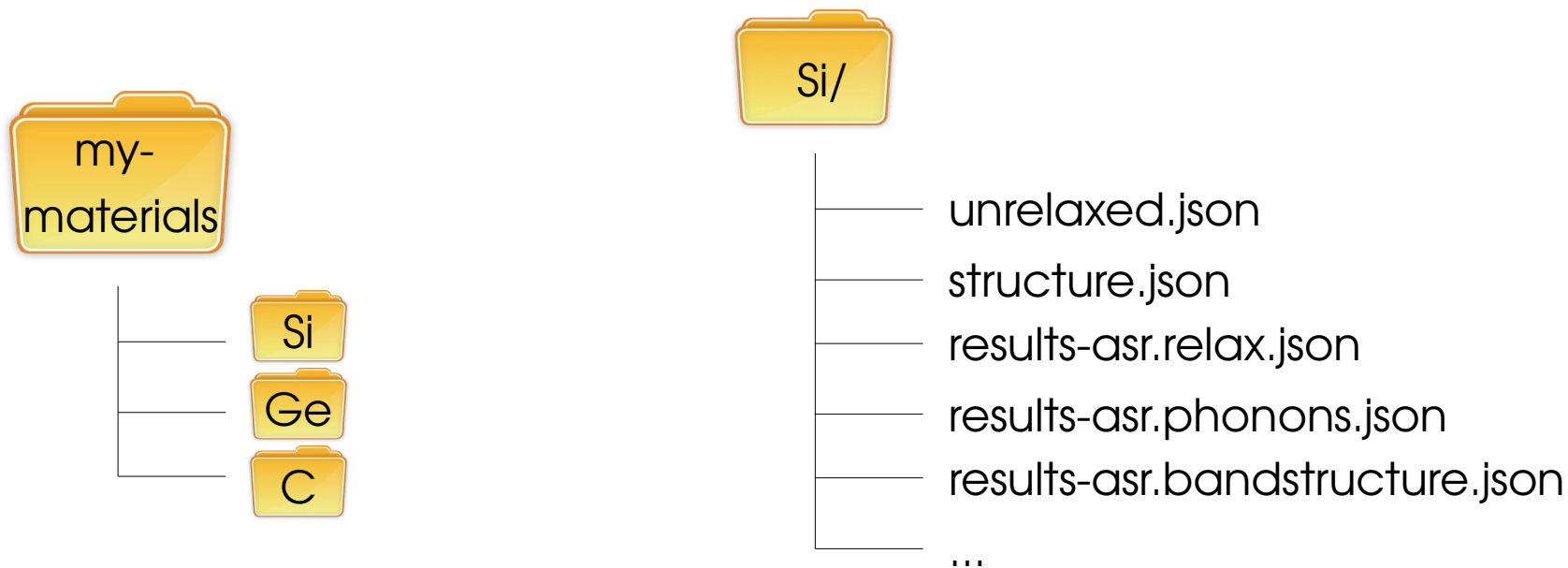
Parameter files

```
$ p -m asr.setup.params asr.relax:calculator '{"name':'emt'}"
```

```
$ cat params.json
```

```
{  
  "asr.relax": {  
    "calculator": {  
      "name": "emt"  
    }  
  }  
}
```

One folder contains one material



Collecting to a database becomes easy

Recipes so far

Recipes that would work for all calculators

- `asr.relax`
- `(asr.phonons)`
- `asr.stiffness`
- `asr.structureinfo`
- `(asr.convex_hull)`
- `((asr.bandstructure))`

Recipes that work only for GPAW

- `asr.gs@calculate`
- `asr.bandstructure@calculate`
- `asr.berry`
- `asr.polarizability`
- `asr.effective_masses`
- `asr.fermi_surface`
- `...`

Summary of design choices

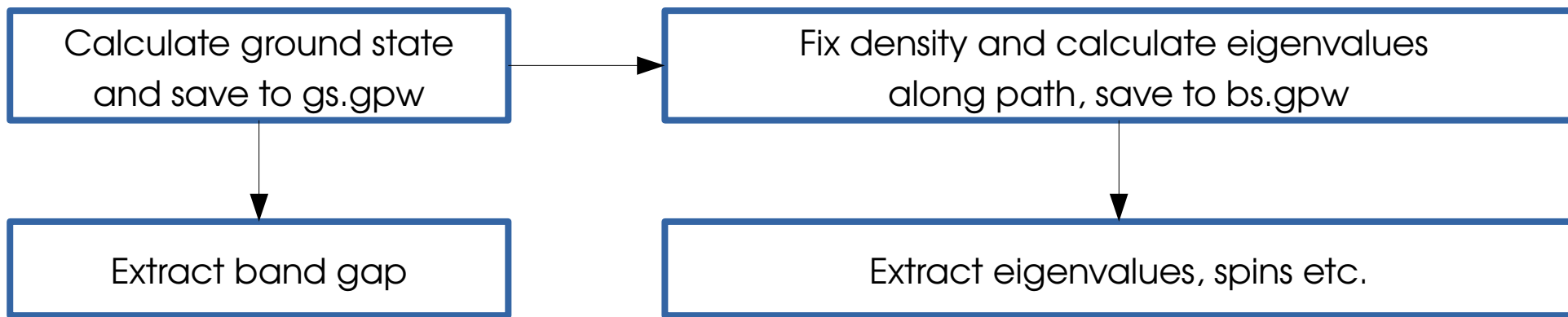
- Recipe = Decorated, annotated Python function
- ASR = A collection of recipes
- Results saved in json files
 - Contains parameters, versions, file hashes
- One-to-one correspondence between CLI and scripts.
- One folder = one material, only have to run a recipe in a folder once.
- Put parameters in a parameter file.
- ASR is available on PyPI
 - `$ pip install asr`

Discussion

- Should we have some standardized script format?
- Data provenance: *“Data provenance provides a historical record of the data and its origins.”*
 - Checksums, git-hashes = reasonably data provenant?
- Issues: design choices, generality, file formats, documentation.
- ASR is available on PyPI
 - `$ pip install asr`
- Thank you for your attention.

Advanced properties

- Many properties are difficult to generalize to other calculators because they depend on the detailed workings of each calculator
- Many properties constitute small workflows in themselves that might be different for every calculator.
- For example, to calculate a bandstructure in GPAW



Workflow

```
$ asr run asr.gs@calculate  
$ asr run asr.bandstructure@calculate  
$ asr run asr.bandstructure  
  
# I also want the band gap  
  
$ asr run asr.gs
```

asr.gs

```
from asr.core import command
```

```
@command()
def calculate():
    """Calculate ground state and save to gs.gpw"""
    ...
```



```
@command(dependencies=['asr.gs@calculate'])
def main():
    """Extract data (band gap etc.) from gs.gpw"""
    ...
```

```
if __name__ == '__main__':
    main.cli()
```

```
$ python3 -m asr.bandstructure
$ python3 -m asr.gs
```

Dependencies

asr.bandstructure

```
from asr.core import command
```

```
@command(dependencies=['asr.gs'])
def calculate():
    """Fix density and save raw data in bs.gpw"""
    ...
```



```
@command(dependencies=['asr.bandstructure@calculate'])
def main():
    """Extract eigenvalues and save bandstructure"""
    ...
```

```
if __name__ == '__main__':
    main.cli()
```