

How to run a small example with STRUPHY_April2020.py – a very short overview

1. It is recommended to use Pyccl <https://github.com/pyccl/pyccl> for code acceleration. After cloning the repository and making sure that all dependencies are there, one can install pyccl with “`python3 -m pip install --user -e .`”. If one wants to work with pure Python, this step can be skipped.
2. All inputs for a simulation are e.g. in “*simulation_06042020_2*”: *initial_conditions_MHD.py*, *initial_conditions_PIC.py*, *equilibrium_MHD.py*, *equilibrium_PIC.py* and *parameters.py*.
3. The file *interface.py* collects all input files and distributes them to all subroutines. This means that you have to make sure that the link to the input files is correct. E.g.

```
import hylife.simulation_06042020_2.equilibrium_MHD as eq_mhd
import hylife.simulation_06042020_2.equilibrium_PIC as eq_pic
import hylife.simulation_06042020_2.initial_conditions_MHD as ini_mhd
import hylife.simulation_06042020_2.initial_conditions_PIC as ini_pic
```

in lines 11-14.

4. If you use pyccl, now is the time to apply it! For this you have to make sure that in the makefile that the link to the input files is correct. E.g.

```
EQM := hylife/simulation_06042020_2/equilibrium_MHD
EQP := hylife/simulation_06042020_2/equilibrium_PIC
ICM := hylife/simulation_06042020_2/initial_conditions_MHD
ICP := hylife/simulation_06042020_2/initial_conditions_PIC
```

in lines 14-17. You can then generate the Fortran files just by typing “*make*”. This may take a couple of minutes.

5. Now everything is there to run the main code “STRUPHY_April2020.py”. Again you have to make sure that the link to the input files is correct, i.e.

```
import hylife.simulation_06042020_2.parameters as pa # name input folder here!
identifier = 'simulation_06042020_2' # name input folder here!
```

in lines 29 and 30. You can then run the code with “`python3 STRUPHY_April2020.py`”. This will output some data in the folder “*simulation_06042020_2*”.