

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

in lines 6-9.

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

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

in lines 14-17. You can then generate the Fortran and .so files just by typing “*make*”. This may take a couple of minutes (10-15 minutes for the first time).

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 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 into the folder “*simulation_06042020_2*”.