

How to run a small example with STRUPHY.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 (e.g. a working Fortran compiler) 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 “`simulations/example_analytical`”: `initial_conditions_MHD.py`, `initial_conditions_PIC.py`, `equilibrium_MHD.py`, `equilibrium_PIC.py` and `parameters_example_analytical.py`.
3. The file `interface_analytical.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 example_analytical.equilibrium_MHD as eq_mhd
import example_analytical.equilibrium_PIC as eq_pic
import example_analytical.initial_conditions_MHD as ini_mhd
import example_analytical.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, i.e.

```
run = example_analytical
```

in line 13. You can then generate the Fortran and .so files just by typing “`make`”. This takes about 1 minute.

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

```
import simulations.example_analytical.parameters_example_analytical as pa # name
input folder here!
identifier = 'example_analytical' # name input folder here!
```

in lines 32 and 33. You can then run the code with “`python3 STRUPHY.py`”. This will create the file “`results_example_analytical.hdf5`” with some output data into the folder “`simulations/example_analytical`”.