Interface, outputs, post-processing

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The minimum knowledge to use Smilei

if you want to keep away from the code

1. Compile
2. Write an input file (a.k.a. *namelist*)
3. Run the program
4. Read & post-process the outputs

Smilei already does much of the work for you

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Requirements to compile & run

- C++11 compiler (with openMP)
- MPI, supporting `MPI_THREAD_MULTIPLE` if openMP
- Compatible HDF5
- Python 2.7+

Help is given on our website

Compiling Smilei

```
$ make
```

```
$ make -j 8       # compile with 8 processors
```

```
$ make clean      # reset compilation
```

```
$ make doc        # compile documentation
```

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The input file is written in *python*

- While the code is *C++*, the input is *python*
- Units are all normalized ($c, m_e, q_e, m_e c, m_e c^2, n_c$, etc.)
- Instructions interpreted by Smilei only inside *blocks*

```
Main(
  timestep = 0.01,
  grid_length = [10., 20.],
  ...
)

LoadBalancing(
  every = 200
)
```

```
Species(
  name = "electrons1",
  particles_per_cell = 1000,
  ...
)

DiagFields(
  every = 1000,
)
```

The *python* input provides flexibility

- Calculate simulation parameters at runtime

```
omega0_SI    = 2. * math.pi * 3e8 / 1.06e-6
duration_SI = 300.e-15
Main( simulation_time = duration_SI * omega0_SI, ... )
```

Change units

```
for s in [“ion1”, “ion2”, “ion3”, “ion4”]:
    DiagParticleBinning( species = [s], ... )
```

Loops

- Plasma & laser profiles are given as *functions*

```
def f(x,y): return x*math.exp(-(y-y0)**2)
Species( number_density = f, ... )
```

User’s profile

```
Species( number_density = gaussian(fwhm=3), ... )
```

Built-in profile

- Any python code accepted

Import modules, read external files, run other scripts, etc.

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A *test mode* to check input consistency

```
$ smilei_test myinput.py
```

Runs through code initialization only.

Only loads one patch.

Fast & convenient

A basic example to run a simulation

```
$ mkdir mysimulation
$ cp myinput.py mysimulation
$ cp smilei mysimulation
$ cd mysimulation
$ mpirun -n 4 smilei myinput.py
```

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Outputs

- Standard output: *lots of info, warnings, errors, etc.*
- Diagnostics

`Scalar`	TXT	global simulation quantities
`Fields`	HDF5	direct output of the fields arrays
`Probe`	HDF5	fields interpolated on regular grids
`ParticleBinning`	HDF5	versatile averaged particle data
`Screen`	HDF5	time-integrated particles passing through surface
`TrackParticles`	HDF5	particle trajectories

- Migration towards openPMD (standard for particle/mesh data)

  Operational for `Fields` & `TrackParticles`

- Checkpoints (≡ dumps and restarts)

  HDF5 files in the `checkpoints` folder for restarting the simulation

Included *python* post-processing

- The repository includes a *python* module happi

```
$ make happi
$ ipython
In [1]: import happi
```

Limitations: no parallel processing; limited in memory

- Get simulation parameters

```
In [2]: S = happi.Open(“path/to/my/simulation/”)
In [3]: timestep = S.namelist.Main.timestep
```

- Data manipulation

basic operations, change units, slicing, etc.

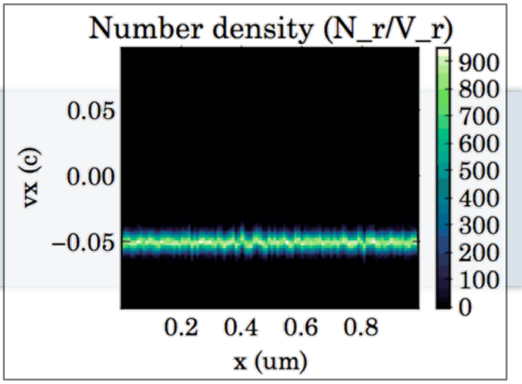
- Obtain raw or processed data

```
In [7]: S.ParticleBinning(0).getData()
```

Easy visualization

- Plot simulation results

```
In [4]: S.ParticleBinning(0).plot()
In [5]: S.ParticleBinning(0).streak()
In [6]: S.ParticleBinning(0).animate()
```



- Convert to VTK format (for VisIt or Paraview)

```
In [7]: S.ParticleBinning(0, timesteps=1000).toVTK()
```

- The openPMD-compliant diagnostics can be opened in VisIt

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Questions ?