Profiles in SMILEI

F. Pérez

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Several quantities require the input of a spatial and/or temporal profile:

- Species density: to define either charge or number density of a species at each point.
- Species average velocity: to define an offset of the velocity distribution at each point.
- Species temperature: to define the width of the velocity distribution at each point (valid only for distributions which require a temperature value).
- External field: to define an initial external field at each point.
- Laser: to define a temporal and/or spatial laser enveloppe.

Contents

1	Species profiles		
	1.1	First technique: no profile	
	1.2	Second technique: python profile	
	1.3	Third technique: built-in <i>python</i> functions	
	1.4	Fourth technique: old-style built-in c++ profiles (not recommended)	
		xternal field profiles	
	2.1	First technique: no profile	
	2.2	Second technique: python function or python built-in profile	
	2.3	Last technique: old-style built-in c++ profiles (not recommended)	
3	Las	er profiles	

1 Species profiles

For each species, it is possible to define spatial profiles that will determine the initial distribution of the particles. There are many ways to define a profile.

1.1 First technique: no profile

You may decide to have a constant profile: a constant value over the whole box. In this case, it is very easy: you do not need to define a profile.

For the density, you only need to define the keyword **density**. For example:

defines a species with density $10 n_c$ over the whole box (n_c is the critical density of light which wavelength is equal to the normalization length).

For the drift velocity, you only need to define the keyword mean_velocity. For example:

```
Species( ... ,
    mean_velocity = [0.05, 0., 0.],
    ... )
```

defines a species with drift velocity $v_x = 0.05 c$ over the whole box (c is the speed of light).

For the temperature, you only need to define the keyword **temperature**. For example:

```
Species( ... ,
    initMomentum_type = "maxwell-juettner",
    temperature = [1e-5],
    ... )
```

defines a species with a Maxwell-Jüttner distribution of temperature $T = 10^{-5} m_e c^2$ over the whole box. Note that the temperature may be anisotropic: temperature=[1e-5, 2e-5].

1.2 Second technique: python profile

Any *python* function can be a profile. You must have basic *python* knowledge to build these functions. Examples:

```
def f(x):
    if x<1.: return 0.
    if x>1.: return 1.

def f(x,y):  # two variables for 2D simulation
    import math
    twoPI = 2.* math.pi
    return math.cos( twoPI * x/3.2 )
f = lambda x: x**2 - 1
```

Once the function is created, you have to include it in the species definition, using the keywords dens_profile, mvel_x_profile, mvel_y_profile, mvel_z_profile, temp_x_profile, temp_y_profile or temp_z_profile:

```
Species( ... ,
    density = 10.,
    dens_profile = f,
    ... )
```

```
Species( ... ,
    temperature = [1e-5],
    temp_x_profile = f,
    temp_y_profile = f,
    temp_z_profile = f,
    ... )
```

and so on \dots

Important note:

The density, mean_velocity and temperature are always required. They define a factor by which the profile is multiplied.

1.3 Third technique: built-in python functions

SMILEI provides some python functions to help you build your profiles.

The same keywords from the previous sections apply. We use the notation ****_profile, where **** is one of dens, mvel_x, mvel_y, mvel_z, temp_x, temp_y or temp_z, depending on what profile you want to define.

Do not forget the density, mean_velocity and temperature keywords in any case!

To define a constant profile:

```
****_profile = constant(value=1., xvacuum=0., yvacuum=0.)
```

The argument value can be used to change the magnitude, but typically constant() is used. xvacuum and yvacuum are empty lengths before starting the profile.

To define a trapezoidal profile:

where max is the maximum value, xvacuum is the empty length before the ramp up, xplateau is the length of the plateau (default is sim_length - xvacuum), xslope1 is the length of the ramp up and xslope2 is the length of the ramp down. The other arguments are the same, but for a 2D simulation. All arguments are optional.

To define a gaussian profile:

where max is the maximum value, xvacuum is the empty length before starting the profile, xlength is the length of the profile (default is $sim_length - xvacuum$), xfwhm is the gaussian FWHM (default is xlength/3.), xcenter is the gaussian center position (default is in the middle of xlength and xorder is the order of the gaussian. The other arguments are the same, but for a 2D simulation. If yorder==0, then the profile is constant over y.

All arguments are optional.

To define a polygonal profile:

```
****_profile = polygonal( xpoints=[], xvalues=[] )
```

where **xpoints** is a list defining the position of points, and **xvalues** is a list defining the values of the profile at each point.

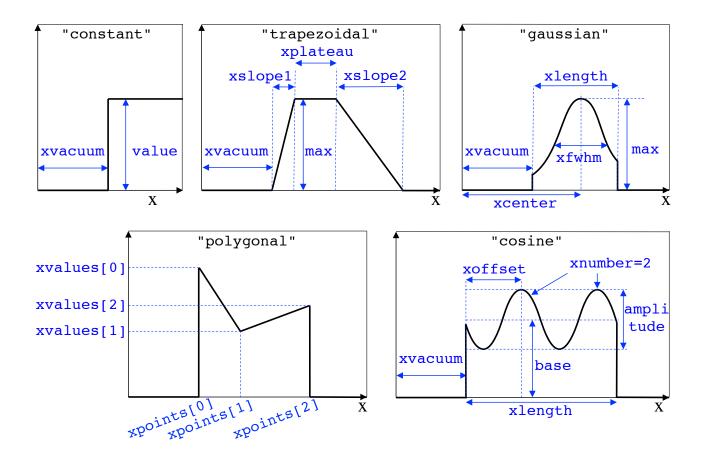
All arguments are optional.

To define a cosine profile:

```
****_profile = cosine( base=1., amplitude=1., xvacuum=0., xlength=None, xoffset=0., xnumber=1 )
```

where base is an offset of the profile value, amplitude is the amplitude of the cosine, xvacuum is the empty length before starting the profile, xlength is the length of the profile (default is sim_length - xvacuum), xoffset is the offset of the first peak and xnumber is the number of periods within xlength. All arguments are optional.

Example:



1.4 Fourth technique: old-style built-in c++ profiles (not recommended)

SMILEI still has hard-coded profiles that will be deprecated. They are mostly used for backwards-compatibility.

```
In this situation, several keywords may be needed: ****_profile, vacuum_length, ****_length_x, ****_length_y, ****_length_z, ****_dbl_params and ****_int_params.
```

The use of these keywords depends on the type of profile.

```
Species( ... ,
          ****_profile = "constant",
          vacuum_length = [x, y],
          ... )
```

```
Species( ... ,
    ****_profile = "trapezoidal",
    vacuum_length = [x, y],
    ****_length_x = [xplateau, xslope1, xslope2],
    ****_length_y = [yplateau, yslope1, yslope2],
    ... )
```

```
Species( ... ,
          ****_profile = "gaussian",
          vacuum_length = [x, y],
          ****_length_x = [xlength, xfwhm, xcenter],
          ****_length_y = [ylength, yfwhm, ycenter],
          ****_int_params = [xorder, yorder],
          ... )
```

```
Species( ... ,
          ****_profile = "polygonal",
          vacuum_length = [x, y],
          ****_length_x = [xpoints],
          ****_dbl_params = [xvalues],
          ... )
```

2 External field profiles

External field profiles work almost the same way as species profiles.

2.1 First technique: no profile

```
ExtField(
          field = "any_field",
          magnitude = magnitude
)
```

The magnitude keyword determines a constant value of the chosen external field.

2.2 Second technique: python function or python built-in profile

where *myProfile* is a *python* function or a built-in *python* profile. All the built-in profiles from section 1.3 are available here.

2.3 Last technique: old-style built-in c++ profiles (not recommended)

The built-in profiles are the same as the species profiles (see section 1.4). However, the keywords are different: profile, length_params_x, length_params_y, length_params_z, double_params and int_params.

3 Laser profiles

Anybody?