The particle diagnostic in SMILEI

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The *particle diagnostic* collects data from the macro-particles and processes them during runtime. It does not provide information on individual particles: instead, it produces averaged quantities like the particle density, currents, etc.

The data may be collected from one or several particle species.

The data is discretized inside a "grid" chosen by the user. This grid may be of any dimension.
Examples:

- 1-dimensional grid along the position x (gives density variation along x)
- 2-dimensional grid along positions x and y (gives density map)
- 1-dimensional grid along the velocity v_x (gives the velocity distribution)
- 2-dimensional grid along position x and momentum p_x (gives the phase-space)
- 1-dimensional grid along the kinetic energy E_{kin} (gives the energy distribution)
- 3-dimensional grid along x, y and E_{kin} (gives the density map for several energies)
- 1-dimensional grid along the charge $Z^\star$ (gives the charge distribution)

Each dimension of the grid is called "axis".

The user may choose to average the data over several time-steps.

1 How to add a particle diagnostic in the input file

In the input file, you can add a particle diagnostic with the following syntax.

```
diagnostic particles
        output = output
        every = every
        time_average = time_average
        species = species1 species2 ...
        axis = type min max nsteps [logscale] [edge_inclusive]
        axis = type min max nsteps [logscale] [edge_inclusive]
        ...
end
```

- *output* must be set to `density`, `current_density_x`, `current_density_y`, `current_density_z`. It determines the data that is summed in each cell of the grid. In the case of `density`, the *weights* are summed. In the case of `current_density_x`, the $weights \times v_x$ are summed (etc.)

- *every* must be a positive integer. It is the number of time-steps between each output.

- *time_average* must be a positive integer. It is the number of time-steps during which the data is averaged before output.

- *species1 species2 ...* must be one or several species. Species are recognized by their parameter `species_type` that is included in each group `species ... end`

- `axis` is an argument that describes one axis of the grid.
  Syntax: `axis = type min max nsteps [logscale] [edge_inclusive]`
  type can be `x`, `y`, `z`, `px`, `py`, `pz`, `gamma`, `ekin`, `vx`, `vy`, `vz` or `charge`.
  The axis is discretized for *type* from *min* to *max* in *nsteps* bins.
  The optional keyword `logscale` sets the axis scale to logarithmic instead of linear.
  The optional keyword `edge_inclusive` includes the particles outside the range [*min*, *max*] into the extrema bins.

There may be as many `axis` arguments as wanted in one `diagnostic particles` block.

There may be as many `diagnostic particles` blocks as wanted in the input file.

In the input file, you may add the following block as a reminder.

```
# DIAGNOSTICS ON PARTICLES - project the particles on a N-D arbitrary grid
# ----------------------------------------------------------------------
# output = density or current_density_[xyz]
#              => parameter that describes what quantity is obtained
# every        => integer > 0 : number of time-steps between each output
# time_average => integer > 0 : number of time-steps to average
# species      => list of one or several species whose data will be used
# axis   = _type_ _min_ _max_ _nsteps_ [logscale] [edge_inclusive]
#              => _type_ can be one of the following:
#                  x, y, z, px, py, pz, gamma, ekin, vx, vy, vz or charge
#              => the data is discretized for _type_ between _min_ and
#                  _max_, in _nsteps_ bins
#              => the optional [logscale] sets the scale to logarithmic
#              => the optional [edge_inclusive] forces the particles
#                  outside (_min_,_max_) to be counted in the extrema bins
#   example : axis = x 0 1 30
#   example : axis = px -1 1 100
# >>>> MANY AXES CAN BE ADDED IN A SINGLE DIAGNOSTIC <<<<
```

2 Examples

Variation of the density of species `electron1` from $x = 0$ to 1, every 5 time-steps, without time-averaging.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = x    0    1    30
end
```

Density map from $x = 0$ to 1, $y = 0$ to 1.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = x    0    1    30
        axis = y    0    1    30
end
```

Velocity distribution from $v_x = -0.1$ to 0.1.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = vx    -0.1    0.1    100
end
```

Phase space from $x = 0$ to 1 and from $px = -1$ to 1.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = x    0    1    30
        axis = px    -1    1    100
end
```

Energy distribution from 0.01 to 1 MeV in logarithmic scale. Note that the input units are $m_e c^2 \sim 0.5$ MeV.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = ekin    0.02    2   100  logscale
end
```

x-y density maps for three bands of energy: $[0, 1]$, $[1, 2]$, $[2, \infty]$. Note the use of `edge_inclusive` to reach energies up to ∞.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = x    0    1    30
        axis = y    0    1    30
        axis = ekin    0   6   3  edge_inclusive
end
```

Charge distribution from $Z^\star = 0$ to 10.

```
diagnostic particles
        output = density
        every = 5
        time_average = 1
        species = electron1
        axis = charge    -0.5   10.5   11
end
```

3 How to view and post-process a particle diagnostic

Each diagnostic produces one file like *ParticleDiagnostic0.h5*, *ParticleDiagnostic1.h5*, etc. They are numbered the same way as the order of appearance in the input file.

A python script *ParticleDiagnostic.py* is provided to view or extract data from these files. To run this script, you will need *python2.7* with the following packages: numpy, matplotlib, pylab, h5py.

First, run python and include the script:

```
python -i ParticleDiagnostic.py
```

(Alternately, you can include this file into your own script using, for example, `execfile("scripts/ParticleDiagnostic.py")`)

From the python prompt, you can run the function *ParticleDiagnostic* which can extract the diagnostic data and optionally display it in a graph window.

Syntax of the function *ParticleDiagnostic*:

```
ParticleDiagnostic(results_path, diagNumber=None, timesteps=None, slice=None,
                   units="code", data_log=False, data_min=None, data_max=None,
                   xmin=None, xmax=None, ymin=None, ymax=None,
                   figure=None)
```

- `results_path` = `_string_`
  Path to the directory where the outputs are stored.
  (Also, this has to contain one and only one input file *.in)

- `diagNumber` = `_int_` (optional)
  Number of the diagnostic. The first diagnostic has number 0.
  If not given, then a list of available diagnostics is printed.

- `timesteps` = `_int_` (optional)
  `timesteps` = `[_int_, _int_]` (optional)
  If omitted, all timesteps are used.
  If one number given, the nearest timestep available is used.
  If two numbers given, all the timesteps in between are used.

- `slice` = { *axis* : `"all", ...` } (optional)
  `slice` = { *axis* : `_double_, ...` } (optional)
  `slice` = { *axis* : `[_double_, _double_], ...` } (optional)
  This parameter is used to reduce the number of dimensions of the array.
  axis must be `"x"`, `"y"`, `"z"`, `"px"`, `"py"`, `"pz"`, `"p"`, `"gamma"`, `"ekin"`, `"vx"`, `"vy"`, `"vz"`, `"v"` or `"charge"`.
  Any axis of the same name will be removed with the following technique:
  - If the value is `"all"`, then a sum is performed over all the axis.
  - If the value is `_double_`, then only the bin closest to the value is kept.
  - If the value is `[_double_,_double_]`, then a sum is performed between the two values.
  Example: `{"x":[4,5]}` will sum all the data for x in the range [4,5].

- `units` = `"nice"` (optional)
  If `"nice"` is chosen, then units are converted into usual units.
  Distances in microns, density in cm^{-3}, energy in MeV.

- `data_log` = `True` or (`False`) (optional)
  If True, then $\log 10$ is applied to the output array before plotting.

- `data_min` = `_double_` (optional)
  `data_max` = `_double_` (optional)
  If present, output is rescaled before plotting.

- `xmin` = `_double_` (optional)
  `xmax` = `_double_` (optional)
  `ymin` = `_double_` (optional)
  `ymax` = `_double_` (optional)
  If present, axes are rescaled before plotting.

- `figure` = `None` (default)
  `figure` = `_int_` (optional)
  Choses the figure number that is passed to matplotlib.
  If absent or None, returns the first data without plotting.

Example of usage from the python prompt:

```
>>> ParticleDiagnostic("path/to/my/results", diagNumber=1, slice={"y":"all"},
   units="nice",data_min=0, data_max=3e14, figure=1)
```

This will take the diagnostic #1, and sum the grid over all the y axis. Then it will plot the resulting array in figure 1 from 0 to 3e14.