

# User Guide - LBM with Multiphase

Daniel Lehmberg, Tord Kriznik Srensen, Vishal Sontakke

Open a terminal at the source folder and type in `make` to build the project with assertion checks enabled (recommended). These checks are done for negative distribution values. Alternatively one can also use `make speed` to build the project without assertion checks (not recommended if randomly chosen values for the parameter  $G$  are chosen).

Once the project is built, the scenario file needs to be set up. Open the `project.dat` file inside the `scenarios` folder with any text editor. This file already consists default values of the input parameters to the code. Following is a description of all the parameters:

- **xlength**: This is the size of the cubic domain. Each cell in the domain is a cube of length 1 and thus the parameter **xlength** gives the number of cells in each direction. The total number of cells would thus be **xlength**<sup>3</sup>.
- **rhoRef0**, **rhoRef1**: The reference density for the component(s).
- **rhoFluct**: When initializing a single component its density is initialized with a random perturbation of size **rhoFluct** around **rhoRef**.
- **numComp**: The number of components can be specified with this parameter. Currently initialization for **numComp** = 1 and 2 is supported<sup>1</sup>. In case of a single component we have a density initialization with random perturbations. In case of 2 components, the initialization is based on randomly selecting a cell and putting density of one component to **rhoRef** of that component and the other to 0.0 in this cell, thus creating a random distribution of the 2 components.
- **tau0**, **tau1**: Based on the number of components one can provide a value for the relaxation time for the component(s). The components are numbered starting with a zero index and thus component 1 has relaxation time **tau0** and component 2 has relaxation time **tau1**.
- **m0**, **m1**: This is the molecular mass of the component(s).
- **G00**, **G01**, **G10**, **G11**: This is the interaction matrix giving the value for the Green's function based on nearest neighbor interaction. The value of **G<sub>ij</sub>** gives the strength of the interacting potential between components **i+1** and **j+1** since the components are numbered with index 0.

---

<sup>1</sup>Note: Multicomponent simulation is not fully supported without code adaptations

- **psi0, psi1:** This takes in integer values and uses the equation corresponding to that integer as the effective number density for that component as given below:
  - 0:  $\psi(x) = 1 - \exp(x)$
  - 1:  $\psi(x) = x$
- **timesteps:** This gives the number of time steps the simulation should run for.
- **timestepsPerPlotting:** This gives the number of time steps after which an output file must be written for visualization.
- **timestepDouble:** Double the timestep between plot after each timestep where a plot happened if this does not equal 0.
- **timestepMax:** This gives the maximum number of timesteps between plots.
- **iProc, jProc, kProc:** These parameters specify the number of sub-domains in each direction for parallel computation. In the **x** direction the domain will be divided into **iProc** sub-domains, in the **y** direction **jProc** sub-domains, and in the **z** direction **kProc** sub-domains. Thus we have **iProc\*jProc\*kProc** number of processes, each working on a cuboid.

Once the parameters are set up, one can open the terminal in the source folder and type in

```
mpirun -np <iProc*jProc*kProc> ./lbsim scenarios/project.dat
```

where **<iProc\*jProc\*kProc>** is the product of the number of sub-domains in each direction, which equals the total number of processes that are to be used by MPI.

If the program runs successfully, one can use **Paraview** to visualize the result. In **Paraview**, the files with the extension **\*.pvts** should be opened to view the entire domain at once. It is recommended to use the **CelldataToPointdata** filter to view a more smoother interpolated result.