Run a SimpleMD simulation starting from a system of at least 1000 atoms. Use settings for both the solid and liquid phases. You can find the SimpleMD standard code in the material for day 3:

## https://github.com/cecamschool2019/materials/tree/master/day3

- Write a C++ code to read the coordinate file (.xyz file) and compute the pair distances between all the particles in the system for each frame of the trajectory. Apply the periodic boundary conditions using the simulation box size that you can extract from the trajectory file
- Make a histogram of pair distances and use it to compute the radial distribution function g(r). Remember that it has to be normalized correctly so as to ensure that the g(r) is constant for large values of r
- Compare the *g*(*r*) obtained for the liquid and solid phases