

# Exercise Session 4

## MDMC Spring 2025

Salomé Guilbert, Qihao Zhang, Thibault Kläy, Evan Vasey, Sophia Johnson, Andrea Levy

April 08, 2025

## Reports Reminder

- We encourage you to work together, but the content in your report should be original
- If you use an image or wording from an external source please cite it correctly
- Please upload the recognizable pictures with good enough quality and a size large enough
- theoretical background & concepts for illustrating the exercises
- Mock exam will be provided

## Exercise 4 Structure

- Learning goals
  - Derive a time evolution integrator (e.g. Verlet)
  - Understand importance of periodic boundary conditions
  - Run a molecular dynamics simulation for a small molecule ( $\text{CO}_2$ )
- Chapter in script
  - Chapter 4 - Molecular Dynamics Simulations
- Resources
  - Understanding Molecular Simulation, Frenkel & Smit, 2nd Edition - Chapter 3 & Chapter 5 (extra)
  - Computer Simulation of Liquids, Allen & Tildesley, 2nd Edition - Chapter 4

## Exercise 4 - Intro & Tips

Today we will provide you a simple Molecular Dynamics (**Toy MD**) code in python and you will extend it to run a MD simulation.

- The theoretical part introduces you to MD

Be sure to understand what we mean by:

- ergodicity
  - phase space sampling
  - MD propagation algorithm
  - periodic boundary conditions
- In the practical part you will implement:
    - Velocity verlet algorithm
    - Periodic boundary conditions (PBC)

## Exercise 4 - ToyMD structure

ToyMD code structure:

- main code (propagation of MD steps) in `toy_md.py` script
- additional code for specific tasks, i.e. `toy_forces.py`
- parameters for the system in separate files (carbon-dioxide folder)



## Exercise 4 - Run ToyMD

ToyMD is a python script, which can be run

1. via terminal
2. via jupyter notebook

(see instructions in the exercise). In both cases, you will execute a bash command, passing files as arguments to the `toy_md.py` script with the following structure (paths may change):

```
python3 toy_md.py -c co2.pdb -p params.txt -ff  
force_field.txt -o traj.pdb -w co2-output.pdb
```

If you'd like to re-run the code with different parameters, please delete the previous `traj.pdb` file or rename it

## Exercises 4 & 5 - Additional Notes

Due to the Easter Break, report 4 won't be due until Tuesday April 29th when we hold the session for Exercise 5.

- 15 April: Course
- 18 - 27 April: Easter Break
- 29 April: Exercise 5 (and due date Ex4 @ 11am)
- 6 May: Course