

# User Guide

Classical Molecular Dynamics & Friction Tensor Calculation

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# Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
<b>2</b>	<b>Usage</b>	<b>4</b>
2.1	Prerequisites . . . . .	4
2.2	Compilation and Running . . . . .	4
<b>3</b>	<b>Code Structure and Features</b>	<b>5</b>
3.1	Main Program . . . . .	5
3.2	Modules . . . . .	5
3.3	Dependencies . . . . .	5
<b>4</b>	<b>Input Files Structure</b>	<b>6</b>
4.1	Simulation Parameters: <code>input.txt</code> . . . . .	6
4.2	Initial Configuration: <code>system.xyz</code> . . . . .	6
<b>5</b>	<b>Output Files</b>	<b>7</b>

## 1 Introduction

This Fortran program simulates the classical molecular dynamics of a solute consisting of four spheres immersed in a viscous solvent. The simulation uses Lennard-Jones potentials and integrates numerically the equations of motion using the Velocity Verlet algorithm.

The goal is to compute the friction tensor of the solute as a function of time through the time-autocorrelation function of the forces experienced by the solute particles.

## 2 Usage

### 2.1 Prerequisites

To compile and run this software, the following tools and libraries are required:

- GFortran: The GNU Fortran compiler.
- FFTW3: The "Fastest Fourier Transform in the West" library.
- Make: The GNU Make build tool.

### 2.2 Compilation and Running

A **Makefile** is provided in the source directory. To compile and run the program:

1. Navigate to the directory containing the source code (**verlet-LJ/**).
2. Run the command:

```
make
```

This will generate an executable named **simulation**.

Ensure that the linker flags in the Makefile (**-lfftw3 -lm**) match your system's configuration.

3. Once compiled, the simulation requires the input files (**input.txt** and **system.xyz**) to be present in the directory **input**. Run the executable from the terminal:

```
./simulation
```

### 3 Code Structure and Features

The source code is modular, with distinct responsibilities assigned to separate Fortran modules.

#### 3.1 Main Program

The driver of the molecular dynamics simulation is the `main.f90`. Its primary responsibility is the time-evolution of the system through Velocity Verlet integration scheme. Additionally it handles memory allocation, input reading and calls to other modules for initialization, minimization, and analysis.

#### 3.2 Modules

##### `force_module.f90`

Responsible for the evaluation of the forces and the potential energy. It models inter-atomic interactions via the Lennard-Jones potential. The module implements Periodic Boundary Conditions (PBC) utilizing the Minimum Image Convention, and applies a cutoff to optimize the computational cost of the  $O(N^2)$  pair-wise interactions.

##### `minimization_module.f90`

Performs an initial geometric optimization of the solvent structure, utilizing the conjugate gradient method (Polak-Ribière variant) to drive the system towards a local energy minimum. This procedure is critical for resolving high-energy overlaps in the initial configuration, thereby preventing numerical divergence.

##### `velocity_init_module.f90`

Initializes the solvent velocities from the Maxwell distribution corresponding to the target thermodynamic temperature. To ensure the reference frame remains inertial, the module explicitly removes any net center-of-mass drift resulting from the stochastic sampling.

##### `fft_correlation_module.f90`

A module acting as an interface to the FFTW3 library. It computes time-correlation functions through FFT, reducing the algorithmic complexity of correlation calculations from  $O(N^2)$  to  $O(N \log N)$ .

##### `friction_module.f90`

It computes the time-dependent memory kernel (friction tensor) via the autocorrelation function of the instantaneous random forces exerted by the solvent on the solute.

##### `kinds.f90`

Defines numerical precision parameters (single and double precision) used throughout the simulation for consistency.

#### 3.3 Dependencies

The program handles the compilation hierarchy:

- all modules depend on `kinds`.
- `minimization_module` depends on `force_module`.
- `friction_module` depends on `fft_correlation_module`.
- `main` depends on all modules.

## 4 Input Files Structure

### 4.1 Simulation Parameters: `input.txt`

The program reads simulation parameters from `input.txt`. The file format is rigid: parameters must be provided in the exact order shown below.

Line	Parameters	Description
1	<code>n, dt</code>	total number of steps and time step in picosecond
2	<code>mass, epsilon_ss, sigma_ss</code>	solvent mass, solvent-solvent LJ parameters
3	<code>epsilon_int, sigma_int</code>	solute-solvent LJ parameters
4	<code>temp, k_B</code>	temperature and Boltzmann constant
5	<code>box_L</code>	length of the cubic simulation box

Table 1: Structure of `input.txt`

Example of a `input.txt` file:

```
1 50000 0.001
2 18.015 63.597 3.1507
3 43.472 3.338
4 298.15 0.831
5 20.0
```

where the units of measurement used are picoseconds, Daltons, Kelvin, and angstroms.

### 4.2 Initial Configuration: `system.xyz`

The initial configuration must be provided in standard XYZ format; in this example it is generated by the Packmol software. The program assumes a specific order of lines:

1. Header: total number of atoms  $N$ .
2. Solute Block (indices 1 – 4): the first four entries must correspond to the solute particles.
3. Solvent Block (indices 5 –  $N$ ): the remaining entries correspond to the solvent particles.

## 5 Output Files

The simulation produces three output files:

- **trajectory.xyz**: contains the atomic coordinates of the system at regular intervals (every 100 steps). This file is compatible with visualization software such as VMD.
- **equilibration\_stats.dat**: records the system properties during the equilibration phase
  - Column 1: time
  - Column 2: potential energy
  - Column 3: mean squared displacement
- **friction\_tensor.dat**: contains the elements of the friction tensor, calculated as the time-autocorrelation of the forces acting on the solute.
  - Column 1: time
  - Columns 2-13: friction tensor diagonal components for each of the 4 solute particles.

A supplementary jupyter notebook (`Plot_Friction_Tensor.ipynb`) is provided in the `python_tool` directory. It allows to visualize the output data and graphically inspect the decay of the friction memory kernel.