# Simulations of Molecular Dynamics in AlmaLinux v.s. Debian-12 OS

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https://github.com/Mtanaka77/

### Settings and tests of simulations

Installation of AlmaLinux-9, May 2024, and Debian 12, Nov. 2024

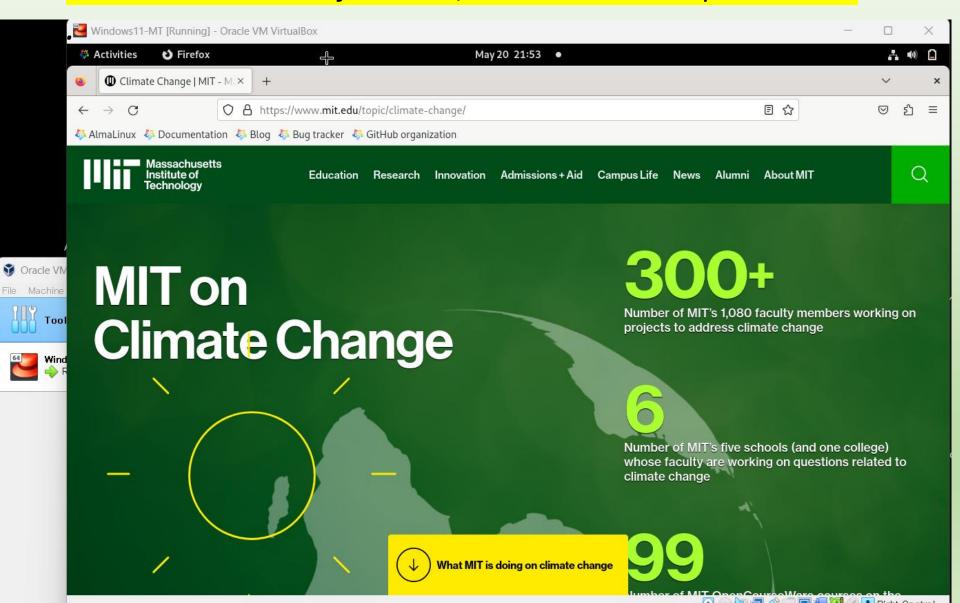
Use Windows 11, VirtualBox 7 to login Linux Linux gfortran and pip packages

Simulations, cf. https://github.com/Mtanaka77/

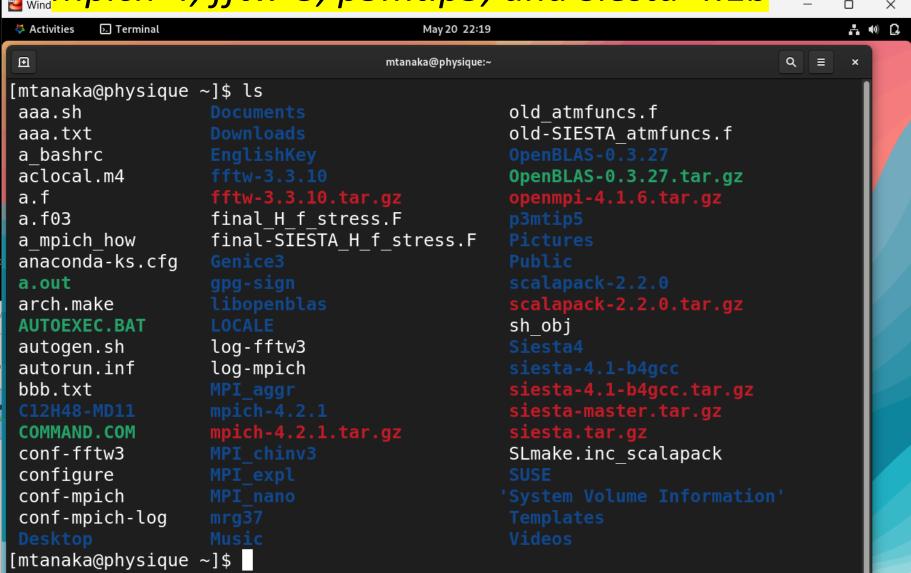
- >> Three-dimensional electrostatic p3mtip5 code, with tip5p and Ewald sums
- >> Siesta-4.1b, with mpich4 fft3w, OpenBLAS, and Scalapack

### Firefox works for AlmaLinux and Debian

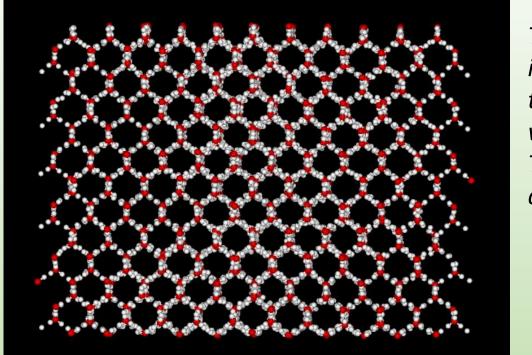
Debian can view all of internet, but AlmaLinux is quite limited



## Windows to Linux terminal shows installation of mpich-4, fftw-3, p3mtip5, and Siesta-4.1b————



#### Test of MD @p3mtip5p07a.f03, by 5-points water model



5.607D-01

95D-01

3.855D-04

This simulation run is OK, but timing is highly variable in time because the simulation in VirtualBox competes with many tasks of Windows 11.

The cpu2 which should be 0.6 sec at least is different with the time steps.

```
time:
            e kin.W
                    e img.W
                                e kin(M)
                                                                        e p3m
                  walltm
    e tot
                             VM
                                                   <ekin>
                                                              <eimg>
                                        exc
                                                                            cpu
        cpu1
                    cpu2
                                cpu3
            1.7095E+00
                        1.9537E-01
                                   0.0000E+00 - 1.6974E+02 3.0997E+01
                                                                        5.1888E
-04 -1.3684E+02
                  8.656D+02
                            1.353D-01
                                                   9.893D-04 1.131D-04
                                        0.000D+00
                                                                            1.1
        4.028D-04
                    1.106D+00
                                8.584D-03
15D+00
      25.0 1.7269E+00 1.9599E-01 0.0000E+00 -1.6972E+02 3.0949E+01
-04 -1.3685E+02
                  1.076D+03
                             1.095D-01
                                        0.000D+00
                                                   9.993D-04
                                                              1.134D-04
                                                                            1.7
43D+00
                    1.734D+00
                                8.680D-03
        3.641D-04
                                    0.0000E+00 -1.6976E+02 3.0940E+01
                                                                        5.4725E
            1.7385E+00
                        2.0207E-01
-04 -1.3688E+02
                  1.295D+03
                             1.117D-01 0.000D+00 1.006D-03 1.169D-04
                                                                            5.6
```

8.385D-03

#### Related pip3 packages

Compilation goes OK in genice2 software of CentOS 7. However, it goes errors in the pairlist package and thus not go forward in AlmaLinux-9.

#### **Debian 12**

The Debian OS has been installed, and is tested by "mrg37" which is quite OK. The pip3 packages and 'pip3 install genice2' is successfully installed. The initial water configuration turns to be perfect.

### To compile Scalapack Version 2

"This is the inside story of Scalapack's make."

One downloads scalapack-2.2.0.tgz and expands it. In BLACS, PBLAS, SRC, TOOLS, do \$ make (no option), except one difference in SRC.

Give -fallow-argument-mismatch at Makefile's \$(FC) line in SRC, then type \$ make -k when one meets errors. Scalapack is 10.7 MB for libscalapack.a

#### Test of ab-initio Siesta-4.1b code

A keyword -fallow-argument-mismatch is added in the arch.make file of Siesta-4.1b for AlmaLinux-9 and Debian-12

```
Architecture
               : gfortran-MPI
Compiler version: GNU Fortran (GCC) 11.4.1 20231218 (Red Hat 11.4.1-3)
Compiler flags : mpifort -02 -fPIC -ftree-vectorize -march=native -fallow-argu
ment-mismatch
PP flags : -DMPI -DFC_HAVE_ABORT
Libraries : -lgomp -L/opt/openbl
               : -lgomp -L/opt/openblas/lib -lopenblas -L/opt/scalapack/lib -l
scalapack
PARALLEL version
* Running on 6 nodes in parallel
>> Start of run: 2-JUN-2024 10:09:19
                          ********
                             WELCOME TO SIESTA
                          *********
reinit: Reading from c12h48.fdf
                                                          פאסטכאט.ט ev/Ang<sup>*</sup>*3
                                       ∪.∪∠0ŏ3∪U/
                       stesta:
                                       42.98698226 45.67350102
                                                                       kBar
                       siesta:
                       (Free)E+ p basis*V orbitals =
                                                          -2615.811579
                       (Free)Eharris+ p basis*V orbitals =
                                                                -2615.811579
                       dhscf: Vacuum level (max, mean) = -0.569553 -0.682007 eV
                       >> Start of run: 2-JUN-2024 10:09:19
                       >> End of run:
                                        2-JUN-2024 10:11:55
                       Job completed
```

#### Overall Points of AlmaLinux and Debian OS

The tests of classic and ab-initio molecular dynamics on AlmaLinux-9 OS are successful. Some alterations must be necessary on this specific operating system.

However, internet sites including FFTW3 fail by busy signal. The pip3 compilation of pairlist is wrong in AlmaLinux-9.

Debian 12 OS is installed, and gcc, make, mpich, fftw3 are set up on top. It is tested with MD and water initial cof pip3 (by Dr. Matsumoto) and Siesta-4.1b, all of which are quite fine on Debian.