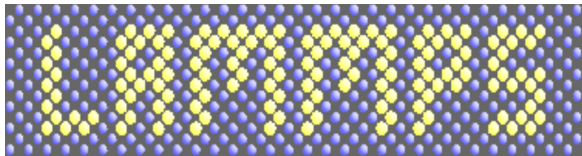


Performing density-functional tight-binding calculations with LAMMPS and the LATTE library

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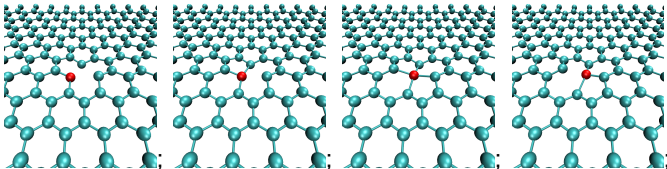
August 4, 2017

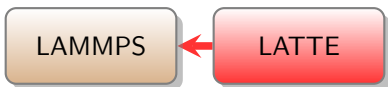


- 1 Introduction
 - Quantum-based Molecular Dynamics
- 2 Computational framework
- 3 Latte scf-dftb physical model
 - Latte library
- 4 Linear scaling
- 5 Applications at LANL

Quantum based MD

- Takes the quantum nature of the chemical bond explicitly into account.
- Free from the arbitrariness of choosing a particular force field.
- Allows for formation and rupture of bonds (chemical reactions).
- Electronic properties can be monitored along the simulation.
- **Computationally more demanding than classical MD.**





- **LAMMPS**: We benefit from most of the LAMMPS functionalities.
 - Integration of the nuclear degrees of freedom (Verlet)
 - Provides thermostats and barostats to perform NVT and NVP simulations.
 - Provides all the infrastructure to do geometry optimization using different algorithms.
 - We can compute transition barriers with the NEB method.
- **LATTE (M. Cawkwell)**: Forces computed at the SCC-DFTB level.
 - Provides forces and the potential component of the total energy.
 - Integrates the electronic degrees of freedom (XL) (provides charges)
 - Solves the electronic structure of the system.
 - Several solvers such as SP2, Truncated SP2, Chebyshev polynomial expansion, etc.

Our computational framework:



Capabilities in the format of a library.

- **LATTE**: A molecular dynamics package based around self-consistent-charge density functional tight binding theory (DFTB). We have also used this libraries in DFTB+.
- **PROGRESS**: This is a set of new capabilities offered as modules that rely entirely on BML. Several $\mathcal{O}(N)$ solvers for ρ are available.
- **BML**: Only linear algebra or mathematically related operations are performed. We have a fast sparse matrix-matrix multiplication.

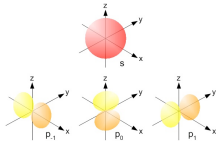
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- <https://github.com/qmmd/bml>
 - <https://github.com/lanl/qmd-progress>
 - <https://github.com/lanl/LATTE>

$$H_{i\alpha,j\beta}^0(r_{ij}) = A_0 \exp(A_1 r_{ij} + A_2 (r_{ij})^2 + A_3 (r_{ij})^3 + A_4 (r_{ij})^4)$$

$$S_{i\alpha,j\beta}(r_{ij}) = B_0 \exp(B_1 r_{ij} + B_2 (r_{ij})^2 + B_3 (r_{ij})^3 + B_4 (r_{ij})^4)$$

$$H_{i\alpha,j\beta} = H_{i\alpha,j\beta}^0 + \frac{1}{2} S_{i\alpha,j\beta} (V_i + V_j)$$

$$\mathbf{P} = [f(\mathbf{H})]_{\text{SCF}}$$



$$q_i = \frac{1}{2} \sum_{\alpha \in i} (P_{j\beta,i\alpha} S_{i\alpha,j\beta} + P_{i\alpha,j\beta} S_{j\beta,i\alpha}) - n_i^e$$

$$E = 2\text{Tr}(\mathbf{P}\mathbf{H}) + \frac{1}{2} \sum_{i,j \neq i} \gamma_{ij} q_i q_j + E_{\text{pair}}$$

$$F_{ij} = -\text{Tr} \left[\mathbf{P} \frac{\partial \mathbf{H}}{\partial r_{ij}} \right] - \frac{1}{2} \sum_i \sum_{j \neq i} q_i q_j \frac{\partial \gamma_{ij}}{\partial r_k} - \frac{\partial E_{\text{pair}}}{\partial r_{ij}}$$

Why LATTE?

- Fast analytical physical model based on product of exponentials.
- Improves transferability.
- Provides linear scaling solvers for the density matrix.
- Provides linear scaling solvers for the inverse overlap.
- Provides the Extended Lagrangian method.
- Efforts in obtaining highly accurate parametrizations are ongoing (EPO code developed by **N. Aguirre**)
- Solvers will be ported to Exascale computing through ongoing projects.

Compiling latte as a library

- The standalone LATTE code can be easily compiled as a library (lattelib.a).

```
$ cd; git clone git@github.com:lanl/LATTE.git  
$ cd ~/LATTE; make
```

- Both ifort (Intel) and gfortan (GNU) fortran compilers have been tested.
- LATTE can be easily linked to LAMMPS.

```
$ cd ~/lammeps/src  
$ make yes-latte  
$ make yes-molecule  
$ make serial
```


What do we need to run?

- LAMMPS usual input files (`data.system` and `in.system`)
- Add a “fix latte” to the input file:

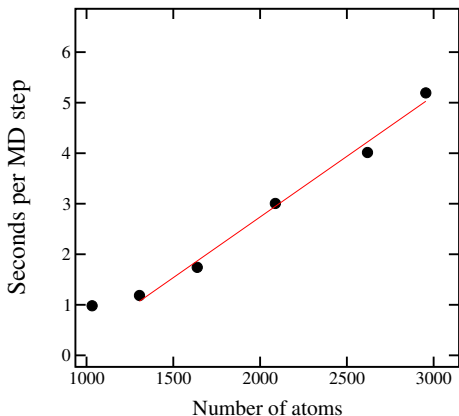
```
fix      2 all latte NULL
```

- LATTE control file (`latte.in`) and parameters folder (`TBparams`)
- Everything should be inside the same folder we are running.
- And we will run as:

```
$ ~/lammeps/src/lmp_serial < in.system
```

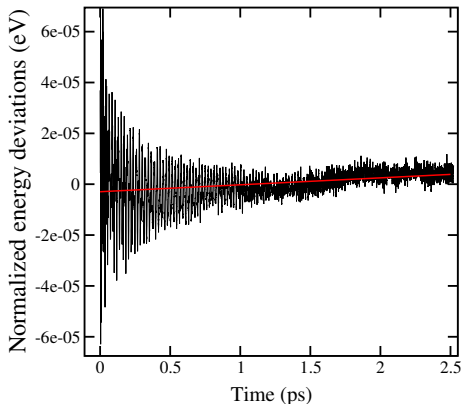
That's all!

Linear scaling using SP2 and XL methods



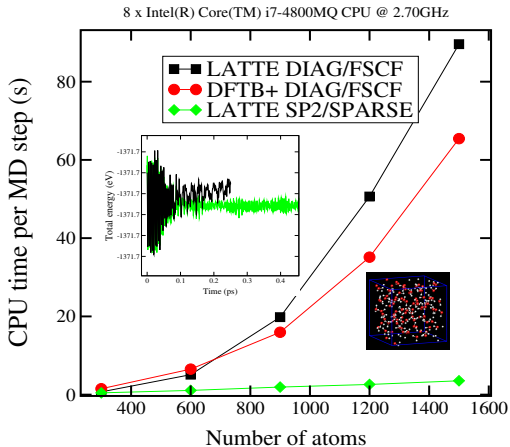
Linear scaling up to 3000 atoms system. Water boxes of different sizes. Calculations were performed on a 18-core 2.10 GHz Intel Xeon E5-2695 v4 processors.

Energy stability



Energy deviations for a 2955 atoms water box showing small energy fluctuations and energy drift. For this case the average fluctuation is no larger than $5 \mu\text{eV}/\text{atom}$ and the drift is about $3 \mu\text{eV}/\text{ps-atom}$

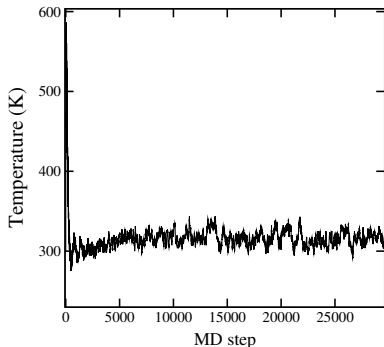
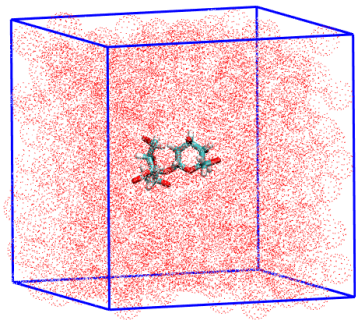
Linear scaling XLBO MD



- Linear scaling with low prefactor (green curve in graph)
- Full accuracy control.
- Perfect energy stability (green curve in the inset)

Sucrose conformers in water (A. Redondo)

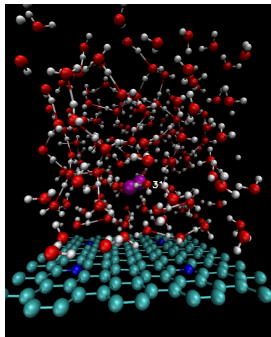
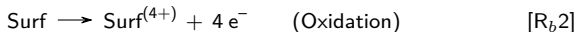
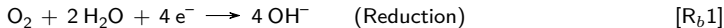
Linear scaling XLBO NVT QMD.



Left: Sucrose molecule solvated in 535 water molecules. Right: Temperature as a function of the molecular dynamics time step for an simulation with constant number of particles, temperature and pressure (NTP).

Next generation fuel cells (I. Matanovic)

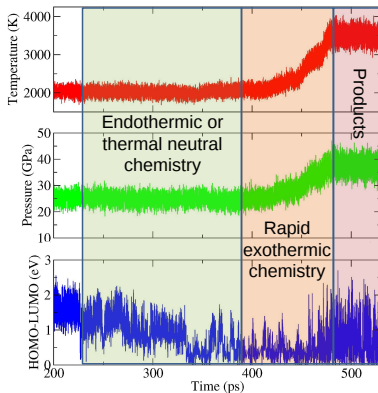
Full SCF NVT QMD with low electronic temperature.



Hugoniot shock compression (R. Perriot)

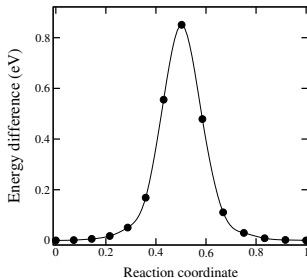
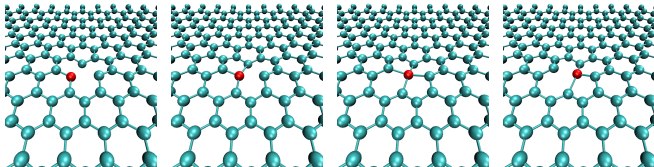
XL with limited SCF NVP QMD with high electronic and ionic temperature.

- 30 nitromethane molecules
- $P=24$ GPa, $T \sim 2000$ K
- NVE for 500 + ps
- Monitor T, P, HOMO-LUMO
- Reaction starts at ~ 230 ps
- ~ 15 ps/day on 16 threads



C vacancy movements in graphene (E. Martinez)

NEB (CG geometry optimization) with high-accuracy SCF convergence and moderate electronic temperature.



... We have extended the capabilities of LAMMPS to do fast quantum-based molecular dynamics simulations. The interface to LATTE will be available in the next LAMMPS release.

Thanks!

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