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# Path Integral Molecular Dynamics

Grégory GENESTE CEA, DAM, DIF, F-91297 Arpajon, France



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#### Coworkers:

Marc Torrent (parallelization over images)

François Bottin

Jessica Hermet (proton transport in oxides)

Hichem Dammak, Iabo SPMS, Ecole Centrale Paris Marc Hayoun, LSI, Ecole Polytechnique



### **Outline**

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Introduction: why studying quantum effects associated to atomic motions?

- I Path Integral (PI) methods
- II Technical points related to Path Integral Molecular Dynamics (PIMD)
- III Implementation of PIMD in ABINIT, keywords, etc
- IV Langevin PIMD, choice of random number generator, friction coefficient
- V Conclusion: in progress and future work



### Why studying quantum effects of atomic motions?

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Quantum effects of atomic motions are important Below the *Debye temperature* 

- CRUCIAL in the case of LIGHT elements, up to very high temperatures:

 $H_2$ , Debye T ~ 6000 K (vibration)

He: liquid down to zero K (under 1 atm) because of quantum effects

 IMPORTANT for « ordinary solids » with Debye temperature ~ RT or above



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One way to account for quantum effects = Path Integral (PI) methods

Based on the discretized version of Feynman's path Integral applied to the density operator.

Path integral for time evolution operator:

$$\langle x|e^{-iHt/\hbar}|x'\rangle = \int_{x}^{x'} Dx(s)e^{\frac{i}{\hbar}\int_{0}^{t} ds L(x(s),\frac{dx}{ds}(s))} = \int_{x}^{x'} Dx(s)e^{\frac{i}{\hbar}A(x(s))}$$

... and for the canonical density operator:  $t = -i \beta \hbar$ 

$$\langle x|e^{-\beta H}|x'\rangle = \int_{x}^{x'} Dx(s)e^{-\frac{1}{\hbar}\int_{0}^{\beta\hbar} ds \left[\frac{m}{2}\left(\frac{dx}{ds}\right)^{2} + V(x(s))\right]}$$



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### Canonical partition function:

$$Z = \int dx \int_{x}^{x} Dx(s) e^{-\frac{1}{\hbar} \int_{0}^{\beta \hbar} ds \left[ \frac{m}{2} \left( \frac{dx}{ds} \right)^{2} + V(x(s)) \right]} = \oint Dx(s) e^{-\frac{1}{\hbar} \int_{0}^{\beta \hbar} ds \left[ \frac{m}{2} \left( \frac{dx}{ds} \right)^{2} + V(x(s)) \right]}$$

$$x(0) = x(\beta \hbar) = x \qquad x(0) = x(\beta \hbar)$$

#### Discretized version:

$$Z = \lim_{P \to \infty} \left[ \frac{2\pi m P k_B T}{h^2} \right]^{3NP/2} \int_{\vec{R}_0} ... \int_{\vec{R}_{P-1}} e^{-\beta V_{eff}(\vec{R}_0...\vec{R}_{P-1})} d\vec{R}_0...d\vec{R}_{P-1}$$

#### with

$$\begin{split} \vec{R}_{s} &= (\vec{r_{1}}^{(s)}...\vec{r_{N}}^{(s)}) \quad 3N - vector \\ V_{eff}(\vec{R}_{0}...\vec{R}_{P-1}) &= V_{eff}(\vec{r_{1}}^{(0)}...\vec{r_{N}}^{(0)}...\vec{r_{1}}^{(P-1)}...\vec{r_{N}}^{(P-1)}) \\ V_{eff}(\vec{R}_{0}...\vec{R}_{P-1}) &= \sum_{s=0}^{P-1} \big[ \sum_{i=1}^{N} \frac{1}{2} k(P,\beta) (\vec{r_{i}}^{(s)} - \vec{r_{i}}^{(s+1)})^{2} + \frac{1}{P} V(\vec{r_{1}}^{(s)}...\vec{r_{N}}^{(s)}) \big] \end{split}$$



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Spring constant 
$$k(P,\beta) = \frac{mP}{\hbar^2 \beta^2} = \frac{mPk_B^2 T^2}{\hbar^2}$$

P = « Trotter » number

with cyclic boundary condition:

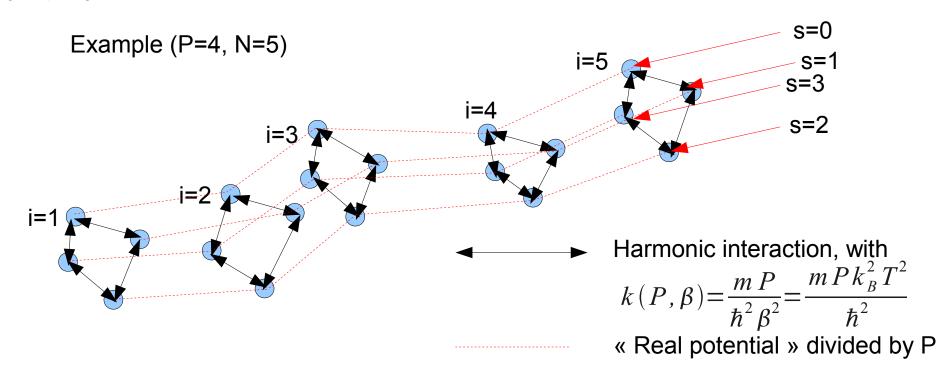
$$\vec{r}_i^{(P)} = \vec{r}_i^{(0)}$$

$$Z = \lim_{P \to \infty} \left[ \frac{2\pi m P k_B T}{h^2} \right]^{3\text{NP/2}} \int_{\vec{R}_0} \dots \int_{\vec{R}_{P-1}} e^{-\beta V_{\text{eff}}(\vec{R}_0 \dots \vec{R}_{P-1})} d\vec{R}_0 \dots d\vec{R}_{P-1}$$

The right member is the CLASSICAL partition function (for fixed Trotter number P) of the following CLASSICAL system (of NxP particles): (up to a multiplicative constant)



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s = « imaginary time »
Ensemble of « quasi-particles » for fixed s = « imaginary time slice »



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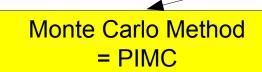
Each quantum system has, for fixed P, a classical equivalent = « CLASSICAL ISOMORPHISM »

In the limit of **infinite Trotter numbers**, the physical EQUILIBRIUM properties of the quantum system are the same as those of the classical equivalent.

One gets directly the observables in the CANONICAL ensemble.

Can be extended easily to the isothermal-isobaric (NPT) ensemble. Ex: Barrat, Loubeyre, Klein, J. Chem. Phys. 90, 5644 (1989)

Thus, the EQUILIBRIUM properties of the classical equivalent system can be reached by any CLASSICAL simulation technique



Molecular Dynamics Method =PIMD



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Path Integral is an elegant way to do Quantum Mechanics ...

... without wave function !!!

NB: at low temperature, the Trotter number should be chosen very high

=> one recovers the complexity of QM!



# Comique • energies alternatives Limitations

$$Z = \lim_{P \to \infty} \left[ \frac{2\pi m P k_B T}{h^2} \right]^{3\text{NP/2}} \int_{\vec{R}_0} ... \int_{\vec{R}_{P-1}} e^{-\beta V_{\text{eff}}(\vec{R}_0 ... \vec{R}_{P-1})} d\vec{R}_0 ... d\vec{R}_{P-1}$$

Is obtained from

$$Z = \int_{\vec{R}} \rho(\vec{R}, \vec{R}; \beta) d\vec{R}$$

where  $\rho(\vec{R}, \vec{R}'; \beta)$  is the density matrix in the position representation:

$$\rho(\vec{R}, \vec{R}'; \beta) = \langle \vec{R} | e^{-\beta H} | \vec{R}' \rangle$$

Such a formulation implicitely assumes DISCERNABLE particles.

In the case of INDISTINGUISHABLE particles, Z writes:

1) for BOSONS:

$$Z^{B} = \frac{1}{N!} \sum_{p \in S(n)} \int_{\vec{R}} \rho(\vec{R}, p\vec{R}; \beta) d\vec{R}$$

2) for FERMIONS:

Permutation signature

S: Permutation signal 
$$Z^F = \frac{1}{N!} \sum_{p \in S(n)} \epsilon(p) \int_{\vec{R}} \rho(\vec{R}, p \vec{R}; \beta) d\vec{R}$$



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### **IN PRACTISE: Primitive Approximation (PA)**

For fixed P: 
$$Z \approx \left[\frac{2\pi m P k_B T}{h^2}\right]^{3\text{NP/2}} \int_{\vec{R}_0} ... \int_{\vec{R}_{P-1}} e^{-\beta V_{\text{eff}}(\vec{R}_0...\vec{R}_{P-1})} d\vec{R}_0 ... d\vec{R}_{P-1}$$
 
$$Z = \lim_{P \to \infty} Z_P$$
 
$$Z_P = \left[\frac{2\pi m P k_B T}{h^2}\right]^{3\text{NP/2}} \int_{\vec{R}_0} ... \int_{\vec{R}_{P-1}} e^{-\beta V_{\text{eff}}(\vec{R}_0...\vec{R}_{P-1})} d\vec{R}_0 ... d\vec{R}_{P-1}$$

Calculations are performed for fixed P Observables are computed using  $Z_P$ , i.e. in the PA. Quantities must be CONVERGED with P

<A> computed from  $Z_p$  = **Primitive Estimator of A** 



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# **Example:** Energy Primitive Estimator: $\langle E \rangle_P = -\frac{\partial \ln Z_P}{\partial \beta}$

Using

$$Z_{P} = \left[\frac{2\pi m P k_{B} T}{h^{2}}\right]^{3\text{NP}/2} \int_{\vec{R}_{0}} ... \int_{\vec{R}_{P-1}} e^{-\beta V_{eff}(\vec{R}_{0}...\vec{R}_{P-1})} d\vec{R}_{0}...d\vec{R}_{P-1}$$

one gets:

Kinetic Energy Estimator

Potential Energy Estimator



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$$Z = \lim_{P \to \infty} \left[ \frac{2 \pi m P k_B T}{h^2} \right]^{3NP/2} \int_{\vec{R}_0} \dots \int_{\vec{R}_{P-1}} e^{-\beta V_{eff}(\vec{R}_0 \dots \vec{R}_{P-1})} d \vec{R}_0 \dots d \vec{R}_{P-1}$$

$$V_{eff}(\vec{R}_0 \dots \vec{R}_{P-1}) = \sum_{s=0}^{P-1} \left[ \sum_{i=1}^{N} \frac{1}{2} k(P, \beta) (\vec{r}_i^{(s)} - \vec{r}_i^{(s+1)})^2 + \frac{1}{P} V(\vec{r}_1^{(s)} \dots \vec{r}_N^{(s)}) \right]$$

$$k(P, \beta) = \frac{m P}{\hbar^2 \beta^2} = \frac{m P k_B^2 T^2}{\hbar^2}$$

This term grows to infinity as P tends to infinity

tends to ZERO as P tends to infinity!

In the limit of large P, the classical system is mainly HARMONIC

Standard MD algorithms such as Nose-Hoover thermostat fail to correctly sample the phase space => non ergodic trajectory



How to recover ergodicity in PIMD?

Marx, Parrinello, J. Chem. Phys. 104, 4080 (1996)
Tuckerman, Marx, Klein, Parrinello, J. Chem. Phys. 104, 5579 (1996)

- 1) Thermostat chains (Martyna, Tobias, Klein, J. Chem. Phys. 101, 4177 (1994)) + coordinate transformations (staging or normal mode)
- => the corresponding scheme has been extended to the NPT ensemble Equations of PIMD in the NPT ensemble:

  Martyna, Hugghes, Tuckerman, J. Chem. Phys. 110, 3275 (1999)
- 2) Alternative way: Langevin dynamics Uses random numbers



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### **LANGEVIN DYNAMICS**

NVT: « Langevin thermostat »  $m \frac{d^2 \vec{r}_i^{(s)}}{dt^2} = \vec{f}_i^{(s)} - \gamma m \frac{d \vec{r}_i^{(s)}}{dt} + \vec{R}_i^{(s)}$  with  $\vec{f}_i^{(s)} = -\frac{1}{P} \vec{\nabla} V_{\vec{r}_i} (\vec{r}_1^{(s)} ... \vec{r}_N^{(s)}) - k(P, \beta) (2 \vec{r}_i^{(s)} - \vec{r}_i^{(s+1)} - \vec{r}_i^{(s-1)})$ 

$$-\gamma m \frac{d\vec{r_i^{(s)}}}{dt}$$
 = friction force  
+ $\vec{R_i^{(s)}}$  = random « Langevin » force (white noise)

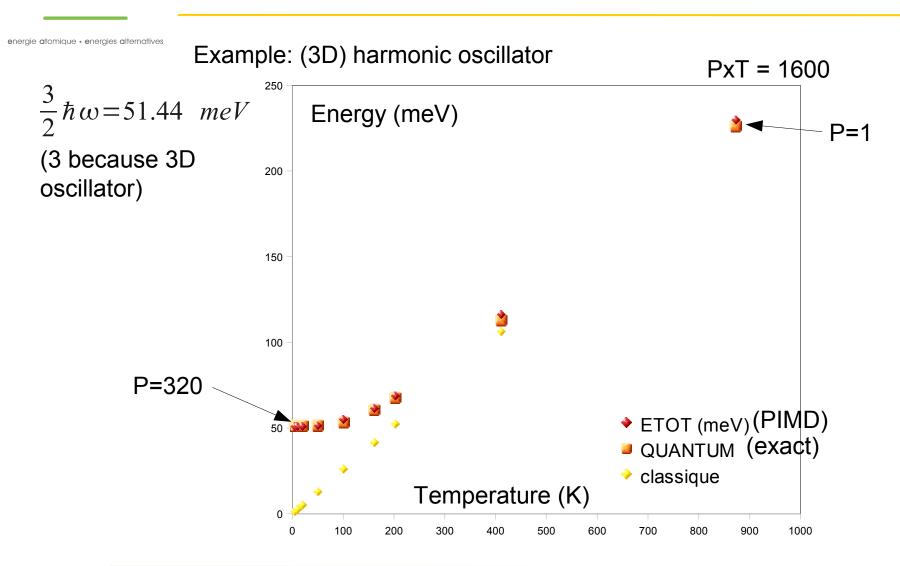
Langevin force: Quigley, Probert, Comput. Phys. Comm. 169, 322 (2005)

Gaussian with variance

$$\sqrt{\frac{2 \gamma m k_B T}{\delta t}}$$
Time

Time step







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How to implement the Langevin method in the NPT ensemble? This has been formulated by Quigley and Probert

J. Chem. Phys. 120, 11432 (2004); Comput. Phys. Comm. 169, 322 (2005)

$$\frac{d\vec{p}_{i}^{(s)}}{dt} = \vec{f}_{i}^{(s)} - \gamma \frac{d\vec{p}_{i}^{(s)}}{dt} + \vec{R}_{i}^{(s)} - \frac{p_{G}}{W_{g}} \vec{p}_{i}^{(s)} - (\frac{1}{N_{f}}) \frac{Tr[p_{G}]}{W_{g}} \vec{p}_{i}^{(s)}$$

$$\frac{d\vec{r}_{i}^{(s)}}{dt} = \frac{\vec{p}_{i}^{(s)}}{m} + \frac{p_{G}}{W_{g}} \vec{r}_{i}^{(s)}$$

$$\frac{dh}{dt} = \frac{p_{G}h}{W_{g}} \frac{dp_{G}}{dt} = V(X - P_{\exp}Id) + \frac{1}{N_{f}} \sum_{i,s} \frac{\vec{p}_{i}^{(s)2}}{m} Id - \gamma_{G} p_{G} + R_{p}$$

in which X is an « internal pressure » defined by

$$\begin{split} VX_{\alpha\beta} &= \sum_{i,\,s} p_{i,\,\alpha}^{(s)} \frac{p_{i,\,\beta}^{(s)}}{m} + r_{i,\,\alpha}^{(s)} f_{i,\,\beta}^{(s)} - (\phi'h^T)_{\alpha\beta} \\ (\phi')_{\alpha\beta} &= \frac{\partial\,\phi}{\partial\,h_{\alpha\beta}} & \text{Combines Langevin dynamics and } \\ &\text{Martyna $\it{et al}$ barostat} \end{split}$$



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- ABINIT already contains a structure adapted to PIMD
- this structure is devoted to algorithms using different IMAGES of the system
- these images are propagated at the same time, according to the chosen algorithm
- well adapted to NEB, string method, etc
- the two subroutines contained in ABINIT that control these algorithms:

gstateimg.F90 predictimg.F90

### First, let us have a look at these two existing routines:



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### Subroutine gstateimg.F90, general structure :

Loop on itimimage (propagation of images)

do itimimage=1,ntimimage

1) loop on the images (that evolve) to compute energy, forces...

do idynimage=1,ndynimage

Call **gstate**: computed total energy, forces, stress for each image

end do

2) Evolution of images
Call **predictimg**end do



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#### Subroutine predictimg

=> chooses the algorithm to propagate the images (according to the value of imgmov)

### Other Algorithms (string, etc)

#### select case(imgmov)

case(0)

call predict\_copy(acell\_timimage,itimimage,list\_dynimage,natom,ndynimage,nimage,ntimimage,&

& rprim\_timimage,vel\_timimage,xred\_timimage)

case(1)

call predict\_steepest(acell\_timimage,fxcartfactor,itimimage,list\_dynimage,natom,ndynimage,nimage,ntimimage,& results gs timimage,rprim timimage,vel timimage,xred timimage)

# Here comes PIMD!

case(2)

call predict\_string(acell\_timimage,fxcartfactor,iatfix,itimimage,list\_dynimage,natom.ndynimage,nimage,nimage,ntimimage,& results\_gs\_timimage\_rerm\_timimage,ver\_ummage,xreg\_timimage;

case(9, 13)

- ! Path Integral Molecular Dynamics
- call predict\_pimd(acell\_timimage,fxcartfactor,itimimage,list\_dynimage,natom,ndynimage,nimage,ntimimage,& results\_gs\_timimage,rprim\_timimage,vel\_timimage,xred\_timimage,mdparam)

case defauit

end select



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PIMD implemented in: SUBROUTINE predict\_pimd.F90

### Two algorithms:

- Langevin dynamics
- Nose Hoover chains + coordinate transformation

#### In two ensembles:

- NVT
- NPT

Rq: Langevin NPT uses Quigley-Probert algorithm



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#### Associated keywords:

#### **Choice of algorithm:**

imgmov=9 (Langevin) or 13 (Nose-Hoover chains)

#### **Choice of statistical ensemble:**

optcell = 0 if NVT, 2 if NPT

nimage = TROTTER number ntimimage = number of time steps

mditemp = initial temperature mdftemp = thermostat temperature dtion = time step

Langevin thermostat:

vis= friction coeff in the case of Langevin dynamics



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Langevin dynamics is a powerfool way to recover ergodicity, ...

- ... but special care should be paid to:
- 1) Choice of random number generator
- 2) Choice of friction coefficient



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### 1) Random number generator:

Langevin dynamics requires random numbers
The quality of the random number generator is crucial!

#### Possible choices:

- (1) in ABINIT: subroutine uniformrandom.f90
- (2) intrinsic function of fortran = random\_number
- (3) random number generator: ZBQ (R.Chandler, generator from G. Marsaglia and A. Zaman, Annals of Appl. Probability 1 (1991), 462-480)

Test of algorithm on a long trajectory => (2) and (3) give better result than (1)



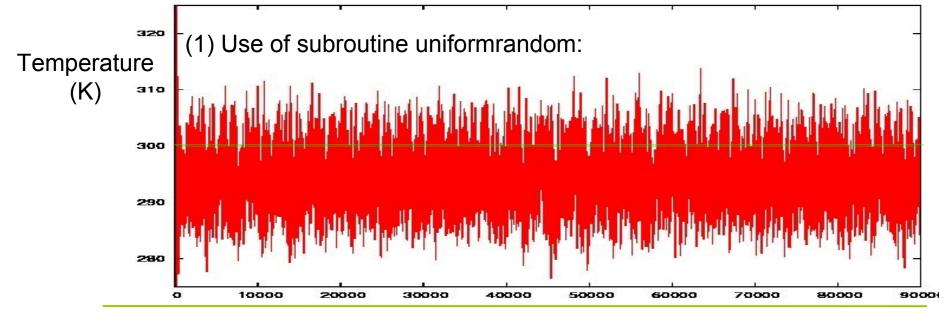
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Best way to test MD algorithm is to perform A LONG trajectory on a BIG system, but

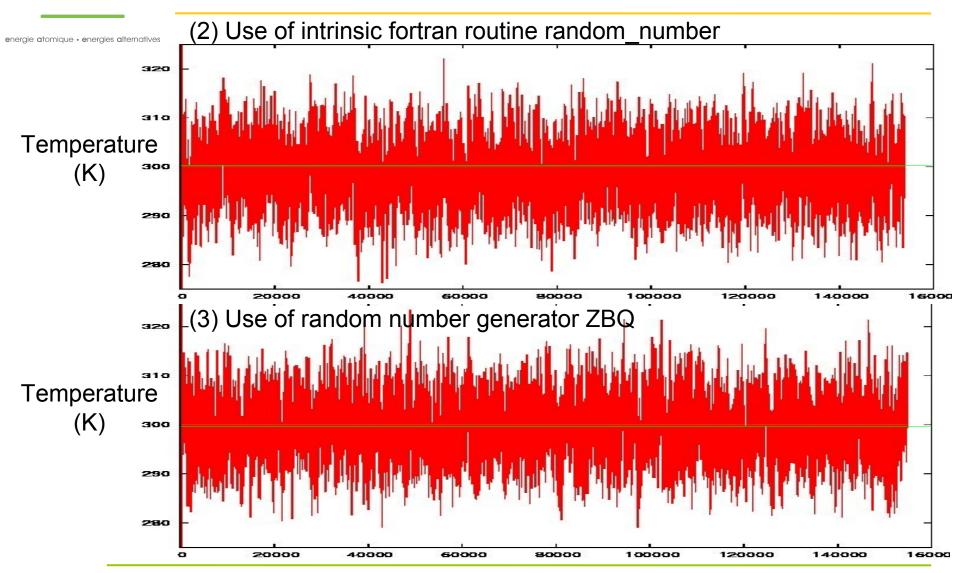
... difficult in ab initio!

=> remove (temporary) the ab initio part of ABINIT !!!!!
and replace it by a phenomenological potential

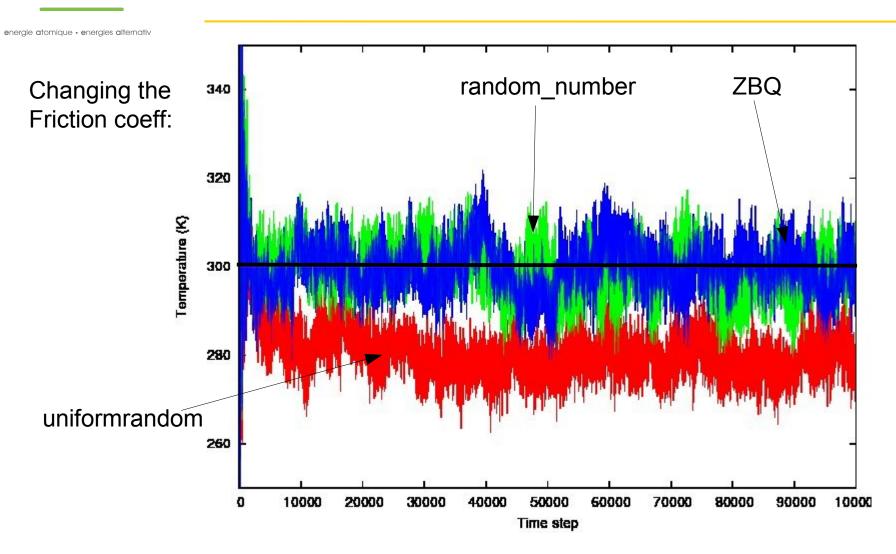
=> 100 000 time steps on 1728 particles, T=300 K













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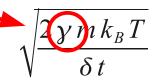
# **Langevin PIMD**

### 2) Friction coefficient

- Langevin thermostat requires special attention to the choice of the friction coefficient

$$m\frac{d^{2}\vec{r}_{i}^{(s)}}{dt^{2}} = \vec{f}_{i}^{(s)} - (y)n\frac{d\vec{r}_{i}^{(s)}}{dt} + \vec{R}_{i}^{(s)}$$

Random (Langevin) force randomly chosen at each step according to a normal law with variance



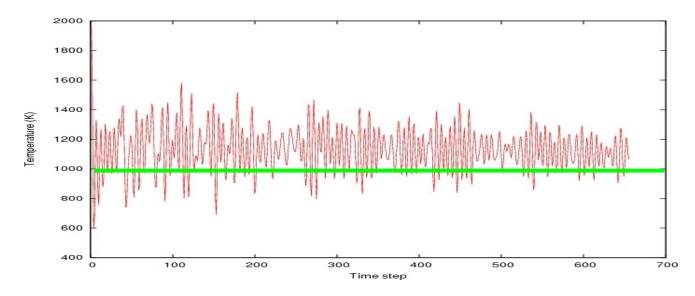
- $1/\gamma$  roughly corresponds to the time needed to equilibrate the system The higher  $\gamma$ , the faster your system is equilibrated... but
- γ (homogeneous to a frequency) should be chosen smaller than the characteristic phonon frequencies of the system
   a compromise must be found!



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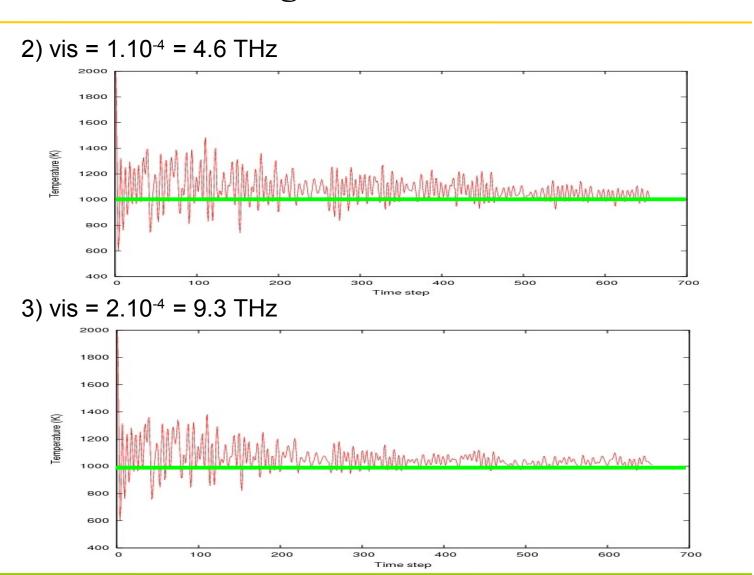
**Example**: PIMD with ABINIT, NVT Langevin Box of 20 H<sub>2</sub> molecules, P=20, 100 processors (// band-FFT) Several tests with Vis = 2.10<sup>-5</sup>, 1.10<sup>-4</sup>, 2.10<sup>-4</sup>, 5.10<sup>-4</sup> (given in inverse atomic time units) mditemp= 2000 K; mdftemp = 1000 K, dtion=20

1) vis = 
$$2.10^{-5}$$
 =  $0.9$  THz



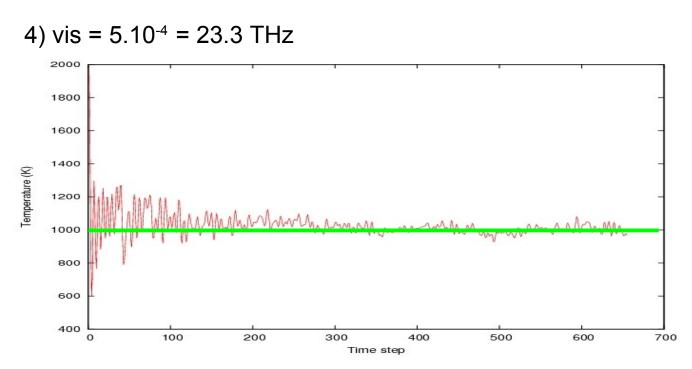


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Rq: stretching vibration of  $H_2$  molecule = 4160 cm<sup>-1</sup> = 125 THz



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#### Be careful to the TIME STEP!

- usually, systems interesting for PIMD contain LIGHT atoms(H, He, etc) => high phonon frequencies
- The DEFAULT value of DTION is TOO high in such cases Default value: dtion=100 (~ 2.10<sup>-15</sup> s)



### **CONCLUSION**

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- PIMD works in NVT and NPT in the case of Langevin Dynamics, in // (k-point, band, fft)
- Nose-Hoover chains implementation in progress (NVT and NPT)
- with P=1, one recovers classical dynamics => PIMD also involves classical MD (=> new algorighms in ABINIT)
- systems of interest:
   H<sub>2</sub>, LiH
   proton transport in oxides



### **CONCLUSION**

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#### **PARALLELIZATION:**

- Loop over images : highly parallelizable !
- currently IMPLEMENTED by M. TORRENT (for all image algorithms)
- => will provide a 4<sup>th</sup> level of // in ABINIT