

GLE Principle
 The 3-step procedu
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 Tutorial T Final



# Generalised Langevin Equation GLE (1 & 2 baths) Manual and Tutorials for LAMMPS

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1. GLE Principles









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## 1.1. GLE Principles

• Solving GLE for central region connected to  $\nu=1,2,...$  bath(s):

$$\frac{dr_{i\alpha}}{dt} = \frac{p_{i\alpha}}{m_i} 
\frac{dp_{i\alpha}}{dt} = F_{i\alpha}(\mathbf{r}) - \int_{-\infty}^{t} dt' \sum_{\nu,i'\alpha'} K_{i\alpha,i'\alpha'}^{(\nu)}(t,t';\mathbf{r}) \dot{r}_{i'\alpha'}(t') + \sum_{\nu} \eta_{i\alpha}^{(\nu)}(t;\mathbf{r}),$$

• where  $F_{i\alpha}$  is the total force (including polarisation effects of the atoms of the baths) acting on atom i, of the central region, in the direction  $\alpha=x,y,z$ , the stochastic forces (colored noise  $\eta_{i\alpha}^{(\nu)}(t;\mathbf{r})$ ) are associated with each independent bath  $\nu$  and  $K_{i\alpha,i'\alpha'}^{(\nu)}(t,t';\mathbf{r})$  is the friction (memory) Kernel.









## 1.2. GLE Principles

- The latter is related to the vibrational properties of the baths, described by their respective polarisation matrix  $\Pi_{b_{\nu},b'_{\nu}}(t-t')$  where the baths degrees of freedom (DOF)  $b_{\nu} \equiv l_{\nu} \gamma$  correspond to bath atom  $l_{\nu}$  and Cartesian coordinate  $\gamma$ .
- To solve the GLE, each degree of freedom  $i\alpha$  in the thermostatted group (id-group) is supplemented with two sets of auxiliary degrees of freedom (aDOF) associated with the sets of parameters  $\{c_{b_{\nu}}^{(k_{\nu})}, \tau_{k_{\nu}}, \omega_{k_{\nu}}\}$ . These parameters are determined from the mapping of the polarisation matrix  $\Pi_{b_{\nu},b'_{\nu}}(t-t')$  onto the following specific analytic form.







## 1.3. GLE Principles

• After Fourier transformation, the mapping is given by:

$$\Pi_{b_{\nu},b'_{\nu}}(\omega) \to \sum_{k_{\nu}} c_{b_{\nu}}^{(k_{\nu})} c_{b'_{\nu}}^{(k_{\nu})} \left[ \frac{\tau_{k_{\nu}}}{1 + (\omega - \omega_{k_{\nu}})^{2} \tau_{k_{\nu}}^{2}} + \frac{\tau_{k_{\nu}}}{1 + (\omega + \omega_{k_{\nu}})^{2} \tau_{k_{\nu}}^{2}} \right].$$

- Before being able to run the LAMMPS fix gle1bath or gle2baths, one has to determine the sets of coefficients  $\{c_{b_{\nu}}^{(k_{\nu})}, \tau_{k_{\nu}}, \omega_{k_{\nu}}\}$ .
- For this, a 3-step procedure should be followed.









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## 2. The 3-step procedure

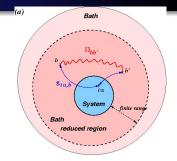
- We now summarise the 3-step procedure of the case of an open system connected to a single thermal bath.
- Similar principles hold when working with the 2 baths situations





## 2.1. Step 1

- Build the entire system, consisting of 3 regions:
  - the central system region
  - the bath region
  - the bath reduced region,
     a smaller part of the bath itself



• Calculate the dynamical matrix  $D_{b,b'}$  of the entire bath region from the derivatives of the forces

$$D_{b,b'} = 1/\sqrt{\mu_l \mu_{l'}} \ \partial f_{b'}/\partial r_b$$

Step 1 is usually performed by using the LAMMPS code and the appropriate script (see below, and the
example given in the Tutorial - 1)







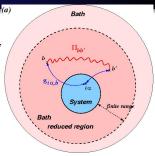
## 2.2. Step 2

- ullet Perform the mapping of the polarisation  $\Pi_{b_
  u,}$
- Fit the exact result

$$\Pi_{b,b'}(\omega) = -\frac{2}{|\omega|} \ \text{Im} \ \big[\omega^2 \mathbf{1} - \mathbf{D} + i\varepsilon\big]_{b,b'}^{-1}$$

onto

$$\begin{split} \sum_{k_{\nu}} c_{b_{\nu}}^{(k_{\nu})} c_{b_{\nu}'}^{(k_{\nu})} \left[ \frac{\tau_{k_{\nu}}}{1 + (\omega - \omega_{k_{\nu}})^2 \tau_{k_{\nu}}^2} \right] \\ \text{for } \omega \geq 0. \end{split}$$



- The mapping is done **only** for the bath DOF b, b' located inside the bath reduced region (because of the finite range of the interaction).
- Step 2 is performed with our home-built codes (see below, and the example given in the Tutorial 1)









## 2.3. Step 3

Step 2 has generated all the necessary output files containing the parameters  $\{c_{b_{\nu}}^{(k_{\nu})},\tau_{k_{\nu}},\omega_{k_{\nu}}\} \text{ necessary for}$  the GLE LAMMPS runs



(a)

- Run the LAMMPS fix gle1bath
- The system consists now of only 2 regions:
   the central system region and the bath reduced region,
- The GLE MD runs are performed on the atom in the central system region (The atoms of the bath reduced region are kept at fixed position during the gle runs)



Bath

System

reduced region







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## 3.1. Download code for LAMMPS

Go to the following url:

https://github.com/HerveNess/gleKCL/tree/master

to download the files









## 3.2. Download code for LAMMPS

- In branch master
  - README file README.md
  - the present document GLE1or2B\_kcl.pdf
- In branch source code
  - LAMMPS codes: fix\_glekcl.cpp and fix\_glekcl.h fix\_gle2baths.cpp and fix\_gle2baths.h
  - and all the other codes for pre/post-treatment as listed in the README file
- In branch tutorials
  - the LAMMPS scripts \*.Imp for the tutorial described from Slide 27









## 3.3. Download code for LAMMPS

#### IMPORTANT REMARK:

- It is assumed that the reader has some knowledge about using Unix-based computers.
- It is assumed that the reader has some knowledge about the LAMMPS code
- i.e. how to download, compile, run LAMMPS and how to use and build elementary LAMMPS scripts.
- For simplicity of use, the GLE source codes for LAMMPS for the following tutorials are available only for serial calculations,
   i.e. use make serial to compile the LAMMPS code.









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## 4.1. Code - description

- file name: DynMat\_from\_forces\_eVAng\_readmass.f90
- short description: calculate the symmetric dynamical matrix from the forces  $f_{j\beta}^{(\pm,i\alpha)}$  of the displaced atoms  $r_{i\alpha} \to r_{i\alpha} \pm \Delta$
- operation: compile file gfortran DynMat\_from\_forces\_eVAng\_readmass.f90 -o DynMat\_from\_forces\_eVAng\_readmass









## 4.2. Code - description

- files name: polar\_matrix\_Plbb\_readdynmat\_v5\_fit\_newinput.f90 parameters\_and\_co\_readdynmat\_v5\_fit\_eVAng.f90 makefile\_readdynmat\_v5\_fit\_newinput
- ullet short description: perform mapping of polarisation matrix  $\Pi_{ij}$  for only 2 indexes i and j, need input file  $input\_new\_rdynmat.in$
- operation: *cp makefile\_readdynmat\_v5\_fit\_newinput makefile*  then *make* compiles the fortran codes into *polar\_matrix\_Plbb\_readdynmat\_v5\_fit\_newinput*









## 4.3. Code - description

- files name: polar\_matrix\_PIbb\_readdynmat\_v13\_fit\_withCregion\_newinput.f90 parameters\_and\_co\_readdynmat\_v13\_fit\_withCregion\_newinput.f90 makefile\_v13\_fit\_withCregion\_newinput
- short description: perform mapping of polarisation matrix  $\Pi_{ij}$  all indices i and j corresponding to the atoms in the bath reduced region, need input file  $input\_new\_rdynmat.in$ , and files  $coord\_bath\_at.dat$  and  $coord\_bathreduced\_at.dat$
- operation: *cp makefile\_v13\_fit\_withCregion\_newinput makefile*  then *make* compiles the fortran codes into *polar\_matrix\_PIbb\_readdynmat\_v5\_fit\_newinput*









## 4.4. Code - description

- file name: swapIDbathXred\_old2new\_v1.f90
- short description:
   check atom coordinates and identify the LAMMPS ID index of the
   atoms contained in the two input files named
   old\_coord\_bathXred\_at\_sort.dat and new\_coord\_bathXred\_at\_sort.dat
- operation: gfortran swapIDbathXred\_old2new\_v1.f90 -o swapIDbathXred\_old2new\_v1









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#### 5.1. What is needed:

- a LAMMPS script to

   (an example is given by file
   get\_all\_forces\_model\_small\_sys\_C\_withCregion.lmp in the Tutorial):
  - build the system and bath (including the bath reduced region)
  - calculate and print out the forces  $f_{j\beta}^{(\pm,i\alpha)} = f_{j\beta}[r_{i\alpha} \to r_{i\alpha} \pm \Delta]$  on each atom j (direction  $\beta$ ) of the bath, when the atoms i in the system are moved  $\to r_{i\alpha} \pm \Delta$  in the direction  $\alpha$
  - the forces are saved in file forces.dat









#### 5.2. What is needed:

• code  $DynMat\_from\_forces\_eVAng\_readmass$  calculates the dynamical matrix  $D_{b,b'}$  from the forces  $f_{j\beta}^{(\pm,i\alpha)}$ 

o input file: forces.dat

output file: dynmat\_coeff.dat







#### 5.3. What is needed:

- code  $polar\_matrix\_Plbb\_readdynmat\_v5\_fit\_newinput$  calculates the mapping of the polarisation matrix elements (diagonal)  $\Pi_{ip,ip}(\omega)$ ,  $\Pi_{jp,jp}(\omega)$  and (off-diagonal)  $\Pi_{ip,jp}(\omega)$  for **only** 2 indexes ip,jp
- input files: dynmat\_coeff.dat and input\_new\_rdynmat.in
- output files (x-y format): *imDbbrecur\_ovw.xxxx.dat* to be compared with *fit\_imDbbrecur\_ovw\_modCavtauk.xxxx.dat* and

imDbbrecur\_ovw\_IJ.xxxxyyyy.dat to be compared with fit\_imDbbrecur\_ovw\_IJ\_avtauk.xxxxyyyy.dat

xxxx and yyyy are strings of characters of the integers ip and jp









#### 5.4. What is needed:

- code  $polar\_matrix\_Plbb\_readdynmat\_v13\_fit\_newinput$  calculates the mapping of all the polarisation matrix elements  $\Pi_{ip,jp}(\omega)$  for the indexes ip,jp corresponding to atoms located within the bath reduced region
- input files dynmat\_coeff.dat and input\_new\_rdynmat.in
- output files (x-y format) same as for Section 5.3.
- output files:  $\begin{array}{l} \text{fit\_coef\_taukomegak\_lmp.dat} \text{ for the } \tau_{k_{\nu}}, \omega_{k_{\nu}} \text{ parameters,} \\ \text{and } \textit{fit\_coef\_cbk\_lmp.dat} \text{ for the } c_{b_{\nu}}^{(k_{\nu})} \text{ parameters.} \end{array}$









#### 5.5. What is needed:

- Finally, a LAMMPS script to perform the GLE runs
- an example is given by file gle\_test\_small\_sys\_C\_T100\_mubar32\_52kts\_seed2.lmp in the Tutorial
- other input files: fit\_coef\_taukomegak\_lmp.dat and fit\_coef\_cbk\_lmp.dat
- output files are specified in the LAMMPS script gle\_test\_small\_sys\_C\_T100\_mubar32\_52kts\_seed2.lmp
- further intermediate steps are actually needed, they are clearly detailed in the Tutorial Section.









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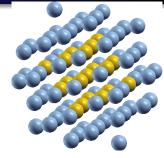








#### 6.1. Tutorial - 1



- GLE with 1 bath for Lennard-Jones clusters
- from our paper Physical Review B 91, 014301 (2015)
   here









#### 6.2. Tutorial - 1

- First of all, to make things clear and neat, in your local directory,
- create 3 new sub-directories:

```
calcforce
fitPlbb
rungle
```









## 6.3.1. Tutorial - 1 / In sub-directory calcforce

#### In sub-directory calcforce

- run LAMMPS code with script file get\_all\_forces\_model\_small\_sys\_C\_withCregion.lmp
- that will create a cluster of 19 atoms for the central system (cutting out a sphere of a fcc crystal lattice) a spherical region around the central system representing the bath region (116 atoms), and another spherical region around the central system, with a small radius, representing the bath reduced region (68 atoms).









## 6.3.2. In sub-directory calcforce

- the LAMMPS script file get\_all\_forces\_model\_small\_sys\_C\_withCregion.lmp
- generates the central system (group system\_atoms), the bath region (group bath\_atoms), the bath reduced region (group bath\_reduced)
- generates the necessary files for post-treatment
- calculates all the forces (stored in file named forces.dat) for/with the displaced atoms in order to obtain the dynamical matrix for the central region.









#### 6.3.2. In sub-directory calcforce

- run code DynMat\_from\_forces\_eVAng\_readmass
- it calculates the dynamical matrix of the central region rom the forces in file forces.dat
- the results are stored in file named dynmat\_coeff.dat
- the file dynmat\_coeff\_unsym.dat can be removed, as it is now obsolete









#### 6.3.3. In sub-directory calcforce

edit the files
 coord\_bath\_at\_sort.dat and coord\_bathreduced\_at\_sort.dat
 in such a way that only the last TIMESTEP group of coordinates
 are kept,

```
i.e.
   ITEM: TIMESTEP
   810
   ITEM: NUMBER OF ATOMS
   68
   ITEM: BOX BOUNDS DD DD DD
   0 96.6
   0.96.6
   0.96.6
   ITEM: ATOMS id x y z mass
   1 52 325 52 325 52 325 63 55
   4 48.3 52.325 52.325 63.55
   7 44.275 52.325 52.325 63.55
   10 52.325 48.3 52.325 63.55
   11 48.3 50.3125 54.3375 63.55
   12 50.3125 48.3 54.3375 63.55
   13 50.3125 50.3125 52.325 63.55
```







## 6.4.1. Tutorial - 1 / In sub-directory fitPlbb

#### In sub-directory fitPIbb

- copy the file dynmat\_coeff.dat from sub-directory calcforce, or use symbolic link
- from the file  $dynmat\_coeff.dat$ , we can start the mapping of the polarisation matrix  $\Pi_{b,b'}(\omega)$
- run code polar\_matrix\_Plbb\_readdynmat\_v5\_fit\_newinput
- input file input\_new\_rdynmat.in





# 0.0540 6.4.2. In sub-directory fit!

# input file input\_new\_rdynmat.in

- 1st line: Units used in the LAMMPS run
- 2nd line: Number of levels in the continued fraction used in the Lanczos algoritm (max value  $3N_{\rm atoms}$ ).

# Mb coef Lanczos recursion method

# continued fraction termination 0: finite In. 1: (a.b) infty # Im part Lorentzian and option 0 for cont\_frac Nb w-points for DOS plot

# extra w k peak : type and extra, neig <- neig \* (1 + extra)
# initial scaling for amplitude [in %] for init fit, between 5% to 200%
# initial scaling for taw k for init fit, between 10 to 200

# segment length - for eigen/v\_k freq search & refine

- 3rd line: termination of the continued fraction.
- 4th line: value of the tiny imaginary part for the termination 0 of the continued fraction.
- 5th line: Number of energy grid points.
- 6th line: length of the segment (number of points) for some averages within the automatic search of the peaks  $\omega_k$  in the  $\Pi_{hh'}$  matrix (max value Number of energy grid points). Typical value between 5 and 20. The larger the value, the lesser number of peaks is obtained.
- ullet 7th line: when needed, the user can add extra peaks around the origin  $\omega\sim 0$ . The grid spacing for these extra peaks is linear or quadratic (1.2). The value of extra represent the percentage of extra peaks needed.
- 8th line: initial scaling for the amplitude  $c_h^{(k)}$  for starting point of the fitting procedure (typically between 5 to 20%).
- 9th line: initial scaling for  $\tau_k$  for starting point of the fitting procedure (typically between 10 to 200%).





# 6.4.3. In sub-directory fit!

FOR FIT: Site/coord (ilat/xyz) indices ip, jp = ?

- enter value of 2 integers i and j, they represent the indexes of 2 different bath DOFs  $i\alpha$  (ip) and  $j\beta$  (ip).
- ullet integer values between 1 and  $3N_{
  m atoms}^{
  m bath}$  correspond to the atoms in the bath region, indexed by the LAMMPS code.
- the code calculates the fitting of the matrix elements (diagonal)  $\Pi_{in,in}(\omega)$ ,  $\Pi_{in,in}(\omega)$  and (off-diagonal)  $\Pi_{in,in}(\omega)$ .





# 6.4.4. In sub-directory fith peaks: quadratic space / more points close to 0 IT: Site/coord (ilat/xvz) indices ip, ip = ?

output files named:

fit\_imDbbrecur\_ovw\_modCavtauk.xxxx.dat fit\_imDbbrecur\_IJ\_ovw\_min2.xxxxyyyy.dat or fit\_imDbbrecur\_IJ\_ovw\_min3.xxxxyyyy.dat to be compared againts the exact results in files named imDbbrecur ovw.xxxx.dat and imDbbrecur\_ovw\_IJ.xxxxyyyy.dat

- xxxx and yyyy are strings of characters of the integers ip and ip
- change the different parameters in input file input\_new\_rdynmat.in, i.e. number of peaks, type of grid, imaginary part, numbers of levels in the continued fraction, ...
- until the fitting is considered to be sufficiently good.







#### 6.4.5. In sub-directory fitPlbb

- Once the parameters in input file input\_new\_rdynmat.in are considered good enough for the fitting, we can start the whole mapping procedure of the polarisation matrix for all atoms in the bath reduced region for that
- run code
   polar\_matrix\_Plbb\_readdynmat\_v13\_fit\_withCregion\_newinput
   with the same input file input\_new\_rdynmat.in









#### 6.4.6. In sub-directory fitPlbb

- in the local directory where the code is launched,
   one also needs two supplementary files, giving information of the atoms in the bath region, and atoms in the bath reduced region.
- they were already generated by the LAMMPS script for the calculation of the forces in sub-directory calcforce
- copy (link) files
   coord\_bath\_at\_sort.dat and coord\_bathreduced\_at\_sort.dat from
   ../calcforce/ into ./fitPlbb









#### 6.4.7. In sub-directory fitPlbb

#### Then

- run code polar\_matrix\_Plbb\_readdynmat\_v13\_fit\_newinput
   with the same input file input\_new\_rdynmat.in
- the mapping (fitting) procedure is then performed for all atoms  $(N_{\text{atoms}}^{\text{bath reduced}})$  contained in the **bath reduced region**
- The fitting procedure may run for a "long" time
- the output files for the mapping coefficients are named: fit\_coef\_taukomegak\_lmp.dat and

fit\_coef\_cbk\_lmp.dat









#### 6.4.8. In sub-directory fitPlbb

- The file fit\_coef\_taukomegak\_lmp.dat contains
  - 3 columns (of length  $N^{\rm aDOF}$ ) representing the parameters  $k, \tau_k, \omega_k$  (with k=0 to  $N^{\rm aDOF}-1$ )

where  $N^{\mathrm{aDOF}}$  is the number of auxilliary DOFs, i.e. the number of peaks in the fitting.

- The file fit\_coef\_cbk\_lmp.dat has the following structure
  - first line: number of columns  $3N_{\rm atoms}^{\rm bath\ reduced} + 3$
  - ullet each of the following  $N_{
    m atoms}^{
    m bath\ reduced}$  line contains index i, LAMMPS ID index of the atom i, mass of atom i, vector of the coefficients  $c_b^{(k)}$
- These 2 files will be input files for running the subsequent GLE-LAMMPS scripts









## 6.4.9. In sub-directory fitPlbb

- The mapping procedure also generate 3 huge files (only needed in case of failure of the fitting process).
- These 3 files (SignMixedCoef.dat, SignEachCoef.dat and SignPMONE\_EachCoef.dat) can be removed to save disk-space









- Before being able to run the subsequent GLE LAMMPS scripts one needs to edit the content of the file fit\_coef\_cbk\_Imp.dat to modify the list of LAMMPS ID index of the atom i
- Why?
- In the GLE LAMMPS runs, we need to have ONLY the atoms in the bath reduced region,
   while in the calculations of the dynamical matrix, we were using all the atom in the bath region
- In the GLE LAMMPS runs, the atoms in the bath region outside the bath reduced region will be removed, and consequently there might be a modification of the LAMMPS ID index for some of the atoms present in the bath reduced region.









# 6.5.1. Tutorial - 1 / In sub-directory rungle

#### In sub-directory rungle

- copy (or symbolic link) the files fit\_coef\_taukomegak\_lmp.dat and fit\_coef\_cbk\_lmp.dat from sub-directory fitPlbb,
- run LAMMPS with the script gle\_test\_small\_sys\_C\_T100\_mubar32\_52kts\_seed2.lmp for 0 timestep
- Then compared the LAMMPS ID index of the atoms in the generated file coord\_bathreduced\_at\_sort.dat against the LAMMPS ID index in the file with the same name in the sub-directory calcforce









#### 6.5.2. In sub-directory rungle

- The one-to-one correspondence between the "old" and "new" LAMMPS ID indexes can be done automatically by using the code swapIDbathXred\_old2new\_v1.f90
- cp ../calcforce/coord\_bathreduced\_at\_sort.dat
   ./old\_coord\_bathXred\_at\_sort.dat
   cp ./coord\_bathreduced\_at\_sort.dat
   ./new\_coord\_bathXred\_at\_sort.dat
- edit file new\_coord\_bathXred\_at\_sort.dat such that it has the same format as file old\_coord\_bathXred\_at\_sort.dat
- run code swapIDbathXred\_old2new\_v1
- Then simply edit the file fit\_coef\_cbk\_lmp.dat and use the "new" indexes for the atoms in the bath reduced region









# 6.5.3. In sub-directory rungle

- Once this is done, the GLE LAMMPS is fully ready
- You can run the GLE LAMMPS script .Imp for as many timesteps needed
- and do GLE MD runs and extract forces, velocities, autocorrelation, thermodynamical properties, ...
   as usual done for any other LAMMPS calculation.









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#### 7.1. Contacts & Support

• For further information and/or help, contact us at

#### gle.at.kcl@gmail.com

- We are welcoming any suggestions for further development of our codes,
- We are open to develop fruitful collaborations on research projects using our GLE codes









#### 7.2. Papers

- L. Kantorovich, Phys. Rev. B 78 094304 (2008).
- L. Stella, C. D. Lorenz and L. Kantorovich, Phys. Rev. B 89, 134303 (2014).
- H. Ness, L. Stella, C. D. Lorenz and L. Kantorovich, Phys. Rev. B 91, 014301 (2015).
- H. Ness, A. Genina, L. Stella, C. D. Lorenz and L. Kantorovich, Phys. Rev. B 93, 174303 (2016).
- H. Ness, L. Stella, C. D. Lorenz and L. Kantorovich, arXiv:1612.00990









#### 7.3. Miscellaneous

- The GLE source codes for LAMMPS for the present tutorials are available only for serial calculations,
  - i.e. use make serial to compile the LAMMPS code
- The full MPI versions are under last optimisation steps.
- They are available upon request and within the frame of developing new collaborations (at least, at the present stage of the development of our GLE codes).

