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Journal of Physics: Condensed Matter PAPER Related content Temperature dependence of the Young's modulus - Atomistic modeling at experimental strain rates and timescales of polymers calculated using a hybrid molecular Xian Yan, Penghui Cao, Weiwei Tao et al. - Effects of temperature and strain rate on mechanics-molecular dynamics method the deformation of amorphous polyethylene: a comparison between molecular dynamics simulations and experimental results To cite this article: Iwan H Sahputra et al 2018 J. Phys.: Condens. Matter 30 355901 I H Sahputra and A T Echtermeyer - An investigation of the tensile deformation and failure of an epoxy/Cu interface using coarse-grained molecular dynamics View the article online for updates and enhancements. simulations Shaorui Yang and Jianmin Qu This content was downloaded from IP address 147.188.98.222 on 26/03/2019 at 13:29 Journal of Physics: Condensed Matter J. Phys.: Condens. Matter 30 (2018) 355901 (6pp) <https://doi.org/10.1088/1361-648X/aad588> Temperature dependence of the Young's modulus of polymers calculated using a hybrid molecular

mechanics–molecular dynamics method Iwan H Sahputra , Alessio Alexiadis and Michael J Adams [School of Chemical Engineering, University of Birmingham, Birmingham, United Kingdom](#) E-mail: [I.H.Sahputra@bham.ac.uk](mailto:I.H.Sahputra@bham.ac.uk) Received 19 June 2018, revised 19 July 2018 Accepted for publication 24 July 2018 Published 7 August 2018 Abstract A hybrid molecular mechanics–molecular dynamics (MM–MD) method is proposed to calculate the Young’s modulus of polymers at various temperature. It overcomes the limitation that MD is restricted to extremely high strain rates. A case study based on poly-methyl- methacrylate demonstrates that, contrary to previous MD studies, the method is able to accurately reproduce the effect of temperature on the Young’s modulus in close agreement with experimental data. The method can also predict a more clear transition between the glassy and rubbery states than previous MD studies. Keywords: Young’s modulus, molecular mechanics, molecular dynamics, glass transition, poly-methyl- methacrylate (Some figures may appear in colour only in the online journal) 1. Introduction Molecular [dynamics \(MD\) simulations have been](#) increasingly utilised [to study the](#) behaviour [of](#) polymers [and](#), in particular, to calculate their physical, chemical and mechanical properties. However, to study structural deformation under the influence of applied strain or stress (e.g. to calculate the Young’s modulus) there are challenges in tracking the detailed evolution of the system over an experimental time-scale. The polymer chains are trapped in local energy minima and, hence, relatively long times are required to achieve the global minimum. This cannot be addressed by MD since the time-steps are of the order of femtoseconds. In MD, the integration of the equation of motion is performed sequentially and thus parallelization of processors does not reduce the computational time required. Several methods have been proposed to accelerate MD simulations for such applications, e.g. by using higher temperatures, strain rates or stresses. However, greater values of these parameters affect the physical properties of organic polymers 1361-648X/18/355901+6\$33.00 particularly during deformation, for example, higher strain rates increase the Young’s modulus while higher temperatures lead to a reduction [1–3]. Moreover, the lowest strain rates that can be applied even with high performance computing is of the order of  $10^7$ – $10^9$  s<sup>-1</sup> so that even by increasing the temperature it is only possible to access mechanical properties in the glassy or near-glassy state. Thus, thermally induced transitions to the rubbery or melt states cannot be studied nor those induced by plasticisation. The current lowest strain rates that are accessible by MD are still much higher than experimental quasi-static loading rates, which are typically less than  $10$ – $1$  s<sup>-1</sup>. Other approaches have been proposed to address the time-scale limitation of MD, for example, temperature-accelerated dynamics [4], parallel-replica dynamics [5], metadynamics [6] and hyperdynamics [7]. These methods have been developed primarily to investigate the behaviour of systems in the absence of externally applied stresses or strains, such as diffusion and chemical reactions. However, the computation of the Young’s moduli depends normally on applying a small © 2018 IOP Publishing Ltd Printed in the UK external strain and, consequently, these methods are unsuitable for this application. An alternative strategy is the application of small incremental strains at a constant strain rate and subsequent relaxation of the system after each increment [8, 9]. However, in practice even the lower limit of the accessible strain rates is extremely high; therefore the system has only a very limited time to explore its potential energy surface (PES). As a result, there is a limit to the magnitude of the energy barriers that can be crossed and thus the system will adopt a meta-stable state corresponding to a local but not a global energy minimum. Other methods have been developed to mitigate this effect. The ABC (autonomous basin climbing) method [10, 11] is probably the most widely applied in which penalty functions are incorporated to the PES in order to drive the system out of the current energy level. The ABC approach is mainly used for metals [12–14], and has a number of disadvantages [15], e.g. (i) it is computationally expensive because of the penalty functions, (ii) there is not a rigorous approach for selecting the appropriate penalty functions and (iii) the method is more suitable at low temperatures when the entropic effects are not dominant, i.e. when the energy barriers are high such that the entropy can be neglected. In the current work, a combination of molecular

mechanics (MM), energy minimization and MD simulation is proposed to study [the effect of temperature on the Young's modulus of](#) polymers. MM is based on a model of atomic interactions within a system by considering related processes such stretching, deviations and rotations about single bonds. The arrangement of the atoms in the stable state corresponds to the minimum energy, which commonly is computed by the application of a minimization algorithm. The macroscopic properties then can be calculated from the stable configuration. However, the contribution of the kinetic energy to the dynamics of the system is ignored in MM, and consequently the effects of temperature are not considered. MD accounts for the dynamics in terms of both the potential and kinetic energies. Therefore, combining MM, energy minimization and MD will drive the system to the stable state at the specified temperature and then the macroscopic properties may be calculated much more accurately. Thus, this hybrid approach does not require penalty functions as is the case for the ABC method and is applicable to any temperature.

2. Methods The procedure employed for combining MM and MD, as illustrated in figure 1, is listed below.

1. NVT step: initially the system is equilibrated at a specified temperature (NVT ensemble) by means of MD simulations.
2. MM step: a small strain increment is applied instantaneously in one orthogonal direction of the simulation box by changing the length of the box in that direction and re-mapping the atomic coordinates to the new box dimension. This will cause a deviation from the previous stable configuration to a new configuration with a greater potential energy level. In this MM step, only the potential energy is perturbed due to changes in the position of the atoms.
3. Minimization step: energy is minimized using a conjugate gradient algorithm while maintaining the value of the imposed strain. During minimization, the box size is changed in the transversal direction to maintain a constant external pressure of 1 atm. This is important for compressible materials, such as polymers, with Poisson's ratio  $< 0.5$ . To control the external pressure during energy minimization, a method proposed by Parrinello and Rahman [16] is employed, based on the objective function:  $E = U + P_t (V - V_0) + E_{\text{strain}}$  (1) where  $U$  is the potential energy of the system,  $P_t$  is the target pressure,  $V$  and  $V_0$  are the system and reference volumes, and  $E_{\text{strain}}$  is the strain energy expression proposed by Parrinello and Rahman.
4. NPT step: the minimization step minimizes the potential energy, but it does not control the temperature of the system. This is achieved in the current step, when the system is further evolved by means of MD simulation at Figure 2. Step 3 may be combined with additional energy minimization processes and repeated several times in order to gradually change the pressure to the specified value. the specified temperature and also 1 atm pressure in the transversal directions. This step will drive the system to the stable state such that it accounts for the contribution from both potential and kinetic energies.
5. Stress calculation step: finally, the stress,  $\sigma$ , is calculated taking account of the contribution from both the potential and kinetic energies by using the following expression:  $\sigma = \frac{1}{V} \left( \sum_i m_i v_i^2 + \sum_i r_i \cdot f_i \right)$  (2) where  $N$  is the number of atoms in the system,  $m_i$  the mass of atom  $i$ ,  $v_i$  the velocity of atom  $i$ ,  $V$  the system volume,  $r_i$  the position of atom  $i$ , and  $f_i$  the force acting on atom  $i$ . Steps 2–5 are repeated to calculate the stress for the range of imposed strain values.
6. Calculation of the Young's modulus: The Young's modulus is calculated from the linear gradient of the stress as a function of strain using the least squares best fit. In step 3, the pressure defined by equation (1) is a sensitive function of the volume and, in order to achieve the objective pressure, the minimization algorithm changes the volume; thus it can be difficult for the algorithm to minimize the energy of the system at the specified pressure with high precision. Therefore, in some cases, it is required that step 3 in combination with additional minimization energy processes, is repeated several times in order to gradually change the pressure to the specified value (figure 2).

Figure 3. An energy minimization process may be performed in between two MD simulations in step 4 to accelerate the rate at which the equilibrium state is achieved. In step 4, to increase the rate at which the stable state is achieved, an additional energy minimization process may be performed between MD simulations (figure 3). The fluctuation of the properties of the system, such as energy,

temperature and pressure, are monitored until the values become stable. When equilibrium has been reached, the fluctuations are proportional to  $1/\sqrt{N}$  where  $N$  is the size of the system.

3. Application of the MM-MD method: a case study for poly-methyl-methacrylate In this section, the method is applied to the specific case of poly-methyl-methacrylate (PMMA). It is well established [that increasing the temperature](#) of a polymer [reduces the](#) elastic modulus e.g. the tensile storage modulus of PMMA [17, 18] ([the storage modulus is approximately equal to the elastic modulus for a single, rapid stress at a small strain in the linear viscoelastic region](#) [19]). The current case study involves an isotactic-PMMA model containing 5 chains, each with 400 monomers, and the DREIDING force field [20] was employed. The details on how to prepare and equilibrate the model are described in a previous publication [21], where the validity of the DREIDING force field was evaluated and compared to other force fields. For each equilibrated model at a range of temperatures (200–400 K), the hybrid MM-MD method was applied to calculate the Young's modulus using LAMMPS [22]. The maximum strain was set to 1% for which a linear relationship between stress and strain is typically observed experimentally. The strain was applied by ten successive small strain increments (i.e. 0.1% strain increments each for step 2 in figure 1) in order to obtain sufficient data points for calculating the gradient. The [Polak-Ribiere version](#) [23] [of the conjugate gradient algorithm was used for the energy](#) minimization processes [with a force stopping criteria of 10<sup>-9</sup>](#). Steps 3 and 4 Figure 4. Evolution of the kinetic energy (a) and potential energy (b) during the first 5000 MD simulation time-steps (step 4). The temperature decreases after the energy minimization in step 3 and the thermostat in the MD simulations of step 4 increases the temperature, and thus the kinetic energy. were performed as those described in figures 2 and 3. The MD simulations were done with a time step of 1 fs. Figure 4 shows an example of the implementation of the method using the model equilibrated at 200 K, during step 4—MD simulations. The [temperature and pressure were controlled using](#) the [Nosé-Hoover](#) thermostat [and](#) barostat. Initially, [the temperature was](#) calculated [to](#) be about 100 K. The lower temperature here is due to the previous energy minimization (step 3), where the temperature was not maintained at 200 K. After about 3000 time-steps of the simulations, the temperature increases to the specified value of 200 K. There was a corresponding increase in the kinetic energy (figure 4(a)) and a reduction (i.e. less negative value) in the potential energy (figure 4(b)). There is a linear relationship between the calculated stress and strain as shown in figure 5 and the Young's modulus was calculated from the gradient. The computed [effect of temperature on the Young's](#) modulus is plotted in figure 6 together with the DMA experimental tensile storage modulus data [17] and previous MD simulation results [21, 24]. The DMA measurements were performed at a frequency of 1 Hz, which corresponds to a strain rate of  $2.1 \times 10^{-3} \text{ s}^{-1}$ . The previous MD simulations were carried out with a full atom model [at a constant strain rate of 109 s<sup>-1</sup>](#) and [the Young's moduli were calculated from the gradients of the stress-strain curves](#) [21], [and](#) also with a united atom model at a small deformation with the Young's moduli calculated from the stiffness matrix constants [24]. Figure 6 shows that MD alone (MD-1 and MD-2) does not result in a close fit to the experimental data, while the MM-MD technique proposed here achieves a very close agreement. The moduli calculated by simulations MD-1 [are in a good agreement with the experimental values](#) at temperatures in the range 200–300 K. However, the results are much greater than experimental values at temperatures > 300 K. On the other hand, the modulus calculated by simulations MD-2 is smaller at temperature 300 K, and the moduli are greater at temperatures > 375 K compared to the experimental values. The high strain rates associated with MD simulations (MD-1 Figure 5. A plot of the stress as a function of strain calculated for the PMMA model at 200 K; the Young's modulus is calculated from the gradient of the best linear fit (dashed line). Figure 6. A comparison of the measured (DMA experiments [17]) and computed values of the Young's moduli as a function of temperature. The computed values correspond to those obtained in the current work (MM-MD) and previous MD results (MD-1 (previous work) [21] and MD-2 (previous work) [24]). Figure 7. Normalised dihedral, improper and van der Waals (vdW) energies as

a function of temperature. There is a change in the gradient at the temperature about 350 K, which is related to the T<sub>g</sub> and MD-2) restrict the mobility of the polymer chains under uniaxial tension and the polymer has a glassy response even at temperatures greater than the glass transition value (T<sub>g</sub>). Thus, it is not possible to study thermally induced transitions to the rubbery or melt states using the conventional MD simulations. However, the moduli calculated using the proposed method at various temperatures are in a close agreement with the experimental values, even at high temperatures. Thus, this method can be developed further to examine other temperature and rate dependent behaviour of viscoelastic materials, such as creep and stress relaxation. For example, it could be applied to examine the plasticisation of organic polymers that result in a transition from the glassy to the rubbery state. The relatively close agreement between the calculated and the DMA measurement values shown in figure 6 suggests that the MM-MD method can achieve stable states of the system deformed with a strain rate equivalent to an experimental value of order  $10^{-3} \text{ s}^{-1}$ . Thus this method can be used to calculate the Young's modulus of polymers at a strain rate that is comparable to typical experimental quasi-static loading rates. With the current computation technology, the smallest strain rates that are accessible by conventional MD simulations are still much greater than those that can be achieved by the proposed method. Figure 6 also demonstrates that the hybrid MM-MD method can be used to calculate, within a close approximation, the T<sub>g</sub> of the polymer. It may be observed that there is a sharp decrease in the calculated and experimental Young's modulus for the temperature range of 350–400 K. This indicates a transition between the glassy and rubbery regions of PMMA. Previous MD studies (MD-1 and MD-2) could not effectively reproduce this transition. Simulations MD-1 produce only a slow decrease in the modulus in the temperature of range 400–500 K. Moreover, simulations MD-2 indicate only a small change in modulus at high temperatures. Therefore, it is difficult to predict the T<sub>g</sub> by using conventional MD simulations. Small discrepancies between the calculated T<sub>g</sub> by using the proposed method and the experimental value may be caused by several factors, such as the differences in the tacticity, number of monomers, number of chains, and thermal history of the experimental samples and the simulation model. The T<sub>g</sub> of PMMA has been shown experimentally to depend on the degree of polymerisation and tacticity [25] but is in the range 328–397 K. Additionally, the molecular weight of the current simulated PMMA is 40 kDa, which is greater than the critical entanglement value; it is considerably less than that of typical commercial PMMAs, which are in the range 130–2200 kDa [26]. The computational time required by the method is approximately a factor of 10 longer than previous work (MD-1) when performed using the same number of processors and the same high performance computing machine. Considering that the strain rate applied in the previous method (MD-1) is much faster ( $10^9 \text{ s}^{-1}$ ) compared with the proposed method ( $\sim 10^{-3} \text{ s}^{-1}$ ), the computational time required by the method is still reasonable. The glass transition behaviour is also shown in the other temperature dependence properties, such as specific volume or enthalpy, measured experimentally. Theoretically, the volume change and glass transition when polymers are cooled may be explained by the free volume concept; at the same temperature, a polymer with higher T<sub>g</sub> has a lower percentage free volume than one with lower T<sub>g</sub> [27]. The free volume is the volume which is not 'occupied' by polymers' molecules. The volume occupied by polymers' molecules depends on the arrangement of the polymer chains. In MD, some properties at atomistic level can be accessed and calculated to provide additional insights about the nature of the glass transition. Figure 7 presents the normalised dihedral, improper and van der Waals (vdW) energies as a function of temperature calculated in step 4 (see figure 1). It may be observed that there is a transition in the gradient of the energies at a temperature of  $\sim 350 \text{ K}$ , which is related to the T<sub>g</sub>. The dihedral and improper energies are those required for rotation about a chemical bond and out-of-plane bending motions respectively, thus they affect the change in structure of individual polymer chains. These motions require less energy than stretching or bending bonds and therefore most variation in polymer structure arises from these motions.

Higher dihedral and improper energies at a high temperature indicate that the structure has a larger free volume, providing more space for molecular vibrations. On other hand, the vdW energy depends on the interactions between different polymer chains, which is affected by the structure of individual chains and their neighbours. A greater vdW energy at a low temperature indicates a more compact structure of the polymer chains and thus less free volume, which restricts the movement of the chains sliding against each other.

4. Conclusion A hybrid MM-MD method for calculating the temperature dependence of the Young's modulus for organic polymers has been developed. It overcomes the limitation of MD of being restricted to extremely high strain rates and thus not able to accurately account for thermal softening, which is observed at experimental accessible strain rates. Additionally, the method can be used to calculate the temperature of the glass-rubber transition within a close approximation. [Acknowledgments](#) [This work was supported by the Engineering and Physical Sciences Research Council \(grant number: EP/M02959X/1\).](#) [The computations using the hybrid MM-MD method have been performed on the supercomputing system of the Institute of Process Engineering, Chinese Academy of Sciences.](#) ORCID iDs Iwan H Sahputra <https://orcid.org/0000-0001-9851-7646>

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