

Improvements and limitations of Mie n-6 force fields for predicting liquid shear viscosity at saturation and elevated pressures

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Abstract

While many common force fields are developed based only liquid density and heat of vaporization at room temperature, several more recent force fields have taken into account saturated vapor pressure and saturated liquid density over substantial portions of the vapor-liquid coexistence curve for multiple compounds simultaneously, enhancing transferability. This manuscript explores the hypothesis that greater accuracy in characterizing the coexistence properties may lead to greater accuracy for viscosity predictions. Three united atom force fields are considered in detail: the TraPPE-UA model of Siepmann and coworkers, the TAMie model of Gross and coworkers, the AUA4 model of Ungerer and coworkers, and the TraMie model of Potoff and coworkers. Equilibrium molecular dynamics simulations are performed in the NVT ensemble using the Green-Kubo method for viscosity characterization. Simulations are performed for linear alkanes with two to sixteen carbons and branched

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alkanes with four to nine carbons. Simulation conditions follow the saturated liquid from reduced temperatures of 0.5 to 0.9 and along the 293 K isotherm in the dense liquid region.

In general, the more accurate force fields for coexistence properties do indeed predict viscosity more accurately. For saturated liquids, both the TraMie and TAMie models provide roughly 10 % accuracy for linear alkanes, while deviations are closer to 20 to 50 % for AUA4 and TraPPE-UA models. For branched alkanes, the behavior is more complicated but TraMie still provides roughly 15 to 20 % accuracy, while the TAMie force field results in deviations of 20 to 40 %, and the TraPPE-UA and AUA4 force fields have deviations of approximately 25 to 60 %. The deviations tend to increase with decreasing temperature, with the exception of the TraMie deviations for propane, which are nearly constant to the triple point temperature.

For compressed liquids, the Mie potential models perform better once again, but tend to overestimate the viscosity at very high densities. Coincidentally, these models also tend to overestimate the pressure at high densities, such that plots of viscosity with respect to pressure are accurate to within about 10 % up to 200 MPa. Experimental viscosity data tend to be sparse above 200 MPa, but accurate predictions are obtained for propane to 1 GPa. Uncertainty estimates increase substantially for high pressures at low reduced temperatures. Nevertheless, a prediction is made for the viscosity of 2,2,4-trimethylpentane at 293K and 1 GPa.

Keywords:

Thermophysical Properties, Molecular Simulation

1. Introduction

The design of efficient and reliable technical processes requires accurate estimates of thermophysical properties. Shear viscosity (η) is an important property for characterizing flow, e.g. sizing pumps. There are primarily three different means by which shear viscosity estimates are obtained: experimental measurement, semi-empirical model prediction, and molecular simulation (molecular dynamics, MD). Significant limitations exist for each of these methods. For example, experimental measurements can be expensive, time-consuming, and challenging at extreme temperatures (T) and pressures (P). Semi-empirical models often

struggle from poor extrapolation due to model deficiencies, over-fitting, and the scarcity of *reliable* experimental data over a wide range of $P\rho T$ state space. Molecular dynamics requires extremely reliable force fields and robust simulation methods.

There are two fundamental challenges for utilizing molecular simulation to estimate viscosity. First, obtaining reproducible results is more difficult for transport properties, such as viscosity, than for static properties. Second, viscosity is extremely sensitive to the force field. In addition to the strong dependence on the non-bonded interactions, the bonded potential plays a much greater role for viscosity than for static properties. For example, varying the torsional potential has a significant impact on viscosity while vapor-liquid coexistence is relatively unaffected. Therefore, the ability to predict viscosities with molecular simulation requires both robust methods and adequate force fields.

Recently, a “Best Practices Guide” was developed to address the first challenge, namely, to improve reproducibility [1]. While we apply the “Best Practices”, the focus of this study is the second challenge. Specifically, we investigate the accuracy of united-atom Mie n-6 force fields, a popular class designed for the engineering purpose of predicting thermophysical properties. The suitability of these force fields for quantitative viscosity prediction has been widely debated in the literature. For example, some studies have suggested that united-atom models are inadequate for this purpose and recommended the use of all-atom models [2, 3, 4]. By contrast, Reference 5 suggests that great improvement is obtained by utilizing a Mie n-6 potential over the traditional Lennard-Jones 12-6 potential. Recently, it was shown that Mie n-6 potentials are overly repulsive at high densities/pressures. For these reasons, we study how well the united-atom Mie n-6 potentials perform both at saturation and elevated pressures.

Some studies have suggested that united-atom models are not capable of accurately reproducing viscosity and, therefore, anisotropic-united-atom or all-atom models are needed [2, 3, 4]. However, other studies have shown that with the appropriate tuning of the united-atom Mie n-6 parameters viscosity can be accurately predicted without significant deprecation of other properties [5]. [6] discusses different test cases (i.e. state points, compound

structures) where united-atom or anisotropic-united-atom models are adequate and inadequate for predicting viscosity.

Furthermore, Reference 7 demonstrated that it is important to include viscosity data when parameterizing a Mie n-6 force field to obtain a unique set of transferable parameters. The force fields compared in this study were optimized solely with static vapor-liquid coexistence data, e.g., saturated liquid densities and saturated vapor pressures. Therefore, an additional purpose of this study is to determine the transferability of these force fields that were not parameterized without viscosity data.

While the Potoff and TAMie force fields have shown considerable promise in predicting vapor-liquid equilibria and other static properties, their ability to predict dynamic properties, such as viscosity, has not been investigated previously.

Previously, AUA4 developed a modified torsional potential to improve prediction of viscosity. One purpose of this study is to determine if the state-of-the-art Mie potentials are adequate of predicting viscosity without modifying the torsional potential.

The outline for the present work is the following. Section 2 explains the force fields, simulation methodology, and data analysis. Section 3 presents the simulation results for each force field, compound, and state point studied. Section 4 discusses some important observations and limitations. Section 5 recaps the primary conclusions from this work.

2. Methods

2.1. Force field

A united-atom (UA) or anisotropic-united-atom (AUA) representation is used for each compound studied, i.e., normal and branched alkanes are represented with CH₃, CH₂, CH, and C sites. UA models assume that the UA interaction site is that of the carbon atom, while AUA models assume that the AUA interaction site is shifted away from the carbon atom and towards the hydrogen atom(s). Note that TraPPE and Potoff are UA force fields while TraPPE-2, AUA4, and TAMie are AUA force fields.

Note that only the terminal CH₃ sites are shifted in the TAMie force field. By contrast, AUA4 displaces the interaction location of non-terminal CH₂ and CH sites as well. For

simplicity, we only utilize the AUA4 force field with compounds that are composed exclusively of CH₃ and C interaction sites, i.e., ethane and 2,2-dimethylpropane. Table 1 provides the effective bond-lengths for terminal CH₃ sites. The bond-length for all non-terminal sites is 0.154 nm.

Table 1: Effective bond-lengths in units of nm for terminal (CH₃) UA or AUA interaction sites. Empty table entries for TraPPE-2 denote that the force field does not contain the corresponding interaction site type. Empty table entries in AUA4 arise because this force field uses a more complicated construction than the simple effective bond-length approach. Specifically, AUA4 requires CH₂ and CH interaction sites that are not along the C-C bond axis.

Bond	TraPPE, Potoff	TAMie	AUA4	TraPPE-2
CH ₃ -CH ₃	0.154	0.194	0.1967	0.230
CH ₃ -CH ₂	0.154	0.174	—	—
CH ₃ -CH	0.154	0.174	—	—
CH ₃ -C	0.154	0.174	0.1751	—

Although static thermodynamic properties (e.g., $\rho_{\text{liq}}^{\text{sat}}$) are generally insensitive to the choice of fixed or flexible bonds, dynamic properties (e.g., η) are much more sensitive. For this reason, we test the degree of variability that arises by implementing a harmonic oscillator model. The results are provided as Supporting Information.

The results presented in this work utilize fixed bond-lengths. The same angle and dihedral potentials are used for each force field. Angular bending interactions are evaluated using a harmonic potential:

$$u^{\text{bend}} = \frac{k_{\theta}}{2} (\theta - \theta_0)^2 \quad (1)$$

where u^{bend} is the bending energy, θ is the instantaneous bond angle, θ_0 is the equilibrium bond angle, and k_{θ} is the harmonic force constant which is equal to 62500 K/rad² for all bonding angles. Dihedral torsional interactions are determined using a cosine series:

$$u^{\text{tors}} = c_0 + c_1[1 + \cos \phi] + c_2[1 - \cos 2\phi] + c_3[1 + \cos 3\phi] \quad (2)$$

where u^{tors} is the torsional energy, ϕ is the dihedral angle and c_i are the Fourier constants. The equilibrium bond angles and torsional parameters are found in Tables 2 and 3, respectively.

Table 2: Equilibrium bond angles (θ_0). x and y are values between 0 and 3.

Bending sites	θ_0 (degrees)
$\text{CH}_x\text{-CH}_2\text{-CH}_y$	114.0
$\text{CH}_x\text{-CH-CH}_y$	112.0
$\text{CH}_x\text{-C-CH}_y$	109.5

Table 3: Fourier constants (c_i) in units of K. x and y are values between 0 and 3.

Torsion sites	c_0	c_1	c_2	c_3
$\text{CH}_x\text{-CH}_2\text{-CH}_2\text{-CH}_y$	0.0	355.03	-68.19	791.32
$\text{CH}_x\text{-CH}_2\text{-CH-CH}_y$	-251.06	428.73	-111.85	441.27
$\text{CH}_x\text{-CH}_2\text{-C-CH}_y$	0.0	0.0	0.0	461.29
$\text{CH}_x\text{-CH-CH-CH}_y$	-251.06	428.73	-111.85	441.27

Non-bonded interaction energies and forces between sites located in two different molecules or separated by more than three bonds are calculated using a Mie n-6 potential (of which the Lennard-Jones, LJ, 12-6 is a subclass) [8]:

$$u^{\text{vdw}}(\epsilon, \sigma, n; r) = \left(\frac{n}{n-6} \right) \left(\frac{n}{6} \right)^{\frac{6}{n-6}} \epsilon \left[\left(\frac{\sigma}{r} \right)^n - \left(\frac{\sigma}{r} \right)^6 \right] \quad (3)$$

where u^{vdw} is the van der Waals interaction, σ is the distance (r) where $u^{\text{vdw}} = 0$, $-\epsilon$ is the energy of the potential at the minimum (i.e. $u^{\text{vdw}} = -\epsilon$ and $\frac{\partial u^{\text{vdw}}}{\partial r} = 0$ for $r = r_{\text{min}}$), and n is the repulsive exponent. The non-bonded Mie n-6 force field parameters for TraPPE, TraPPE-2, Potoff, AUA4, and TAMie are provided in Table 4.

Table 4: Non-bonded (intermolecular) parameters for TraPPE [9, 10] (and TraPPE-2 [11]), Potoff [12, 13], AUA4 [14, 15], and TAMie [16, 17] force fields. The “short/long” Potoff CH and C parameters are included in parentheses. The ethane specific parameters for TAMie are included in parentheses.

	TraPPE (TraPPE-2)			Potoff (S/L)		
United-atom	ϵ (K)	σ (nm)	n	ϵ (K)	σ (nm)	n
CH ₃	98 (134.5)	0.375 (0.352)	12	121.25	0.3783	16
CH ₂	46	0.395	12	61	0.399	16
CH	10	0.468	12	15 (15/14)	0.46 (0.47/0.47)	16
C	0.5	0.640	12	1.2 (1.45/1.2)	0.61 (0.61/0.62)	16
	AUA4			TAMie		
CH ₃	120.15	0.3607	12	136.318 (130.780)	0.36034 (0.36463)	14
CH ₂	86.29	0.3461	12	52.9133	0.40400	14
CH	50.98	0.3363	12	14.5392	0.43656	14
C	15.04	0.244	12	—	—	—

Note that TraPPE (TraPPE-2) and TAMie implement a different set of CH₃ parameters for ethane. Also, Potoff reports a “generalized” and “short/long” (S/L) CH and C parameter set. The Potoff “generalized” CH and C parameter set is an attempt at a completely transferable set. However, since the “generalized” parameters performed poorly for some compounds, the S/L parameter set was proposed, where the “short” and “long” parameters are implemented when the number of carbons in the backbone is ≤ 4 and > 4 , respectively.

Non-bonded interactions between two different site types (i.e. cross-interactions) are determined using Lorentz-Berthelot combining rules [18] for ϵ and σ , respectively, and an arithmetic mean for the repulsive exponent n (as recommended in Reference 12):

$$\epsilon_{ij} = \sqrt{\epsilon_{ii}\epsilon_{jj}} \quad (4)$$

$$\sigma_{ij} = \frac{\sigma_{ii} + \sigma_{jj}}{2} \quad (5)$$

$$n_{ij} = \frac{n_{ii} + n_{jj}}{2} \quad (6)$$

where the ij subscript refers to cross-interactions and the subscripts ii and jj refer to same-site interactions.

2.2. Simulation set-up

Viscosity estimates can be obtained from both equilibrium molecular dynamics (EMD) and non-equilibrium molecular dynamics (NEMD) simulations. The “Best Practices Guide” is currently limited to EMD methods and purports that NEMD might be necessary for high viscosities (greater than 0.02 Pa-s). One purpose of the present work is to demonstrate that, by applying these guidelines, EMD can also provide meaningful estimates for highly viscous systems.

Equilibrium molecular dynamics simulations are performed using GROMACS version 2018 [19]. GROMACS was compiled using the BLANK compiler. Example GROMACS input files (.top, .gro. and .mdp) are provided as Supporting Information. In addition, the shell and python scripts used for preparing and analyzing simulations are available on GitHub. The simulation specifications are provided in Tables 5 and 6.

Table 5: General simulation specifications.

Time-step (fs)	2
Equilibration time (ns)	1
Production time (ns)	1, 2, 4, or 8
Cut-off length (nm)	1.4 (1.0 Potoff)
Tail-corrections [20]	U and P
Constrained bonds	LINCS
LINCS-order	8
Number of molecules	400

Note that the non-bonded cut-off distance is 1.4 nm for each force field except Potoff, which employs a 1.0 nm cut-off (as recommended by the authors). Also, notice that the

Table 6: Integrator, thermostat and barostat specifications.

	<i>NPT</i> Equil.	<i>NPT</i> Prod.	<i>NVT</i> Equil.	<i>NVT</i> Prod.
Integrator	Velocity Verlet	Leap frog	Velocity Verlet	Velocity Verlet
Thermostat	Velocity rescale	Nosé-Hoover	Nosé-Hoover	Nosé-Hoover
Thermostat time-constant (ps)	1.0	1.0	1.0	1.0
Barostat	Berendsen	Parrinello-Rahman	N/A	N/A
Barostat time-constant (ps)	1.0	5.0	N/A	N/A
Barostat compressibility	4.5e-5	4.5e-5	N/A	N/A

production time depends on the system, i.e., the compound and state point, where larger compounds, lower temperatures, and higher densities necessitate longer simulations. For most systems, 1 ns is a sufficient production time, while an 8 ns production time is required for the most viscous systems, e.g., 2,2,4-trimethylpentane at elevated pressures. Following “Best Practices”, we compute η with several different production times (1, 2, 4, and 8 ns) for select systems to verify that the results are indistinguishable (see Supporting Information). Furthermore, we investigate system size effects by comparing results with 100, 200, 400, and 800 molecules (see Supporting Information). In addition, we compare fixed and flexible bonds in the Supporting Information.

As recommended by “Best Practices,” we utilize 30 to 60 independent replicates to improve the precision and to provide more rigorous estimates of uncertainty. To ensure independence between replicates, a series of MD simulations are performed for each replicate. When the viscosity is desired at a prescribed temperature and density ($\eta(\rho, T)$), three stages are required: energy minimization, *NVT* equilibration, and *NVT* production. When the viscosity is desired at a prescribed temperature and pressure ($\eta(P, T)$), five stages are required: energy minimization, *NPT* equilibration, *NPT* production, *NVT* equilibration, and *NVT* production. Note that, according to “Best Practices”, the final production stage simulations

are always performed using the NVT ensemble.

Two different classes of viscosity are investigated in this study, namely, saturated liquid viscosity ($\eta_{\text{liq}}^{\text{sat}}$) and compressed liquid viscosities at $T = 293$ K ($\eta_{\text{liq}}^{\text{comp}}$).

Saturated liquid viscosities are estimated by performing NVT ensemble simulations at various temperatures (T^{sat}) and densities ($\rho_{\text{liq}}^{\text{sat}}$). The simulation densities correspond to the REFPROP $\rho_{\text{liq}}^{\text{sat}}$, which is admittedly not equivalent to the force field $\rho_{\text{liq}}^{\text{sat}}$. This point is discussed in greater detail in Section 4.

Two different simulation protocols are implemented for estimating compressed liquid viscosities ($\eta_{\text{liq}}^{\text{comp}}$). Specifically, we perform simulations with each force field either at the same ρ or the same P . For the purpose of comparing trends between force fields and REFPROP, these two methods are essentially equivalent. From a practical standpoint, estimating η at a given P requires performing preliminary NPT ensemble simulations to determine the corresponding box size.

2.3. Data analysis

Following the “Best Practices” recommendation, we implement the Green-Kubo “time-decomposition” analysis to extract viscosity from EMD simulations. We refer the interested reader to References 1 and 21 for further details. In brief, the Green-Kubo integral is computed with respect to time according to

$$\eta(t) = \frac{V}{3k_{\text{B}}TN_{\text{reps}}} \sum_{n=1}^{N_{\text{reps}}} \sum_{\alpha \neq \beta} \int_0^t dt' \langle \tau_{\alpha\beta,n}(t') \tau_{\alpha\beta,n}(0) \rangle_{t_0} \quad (7)$$

where V is the volume, k_{B} is the Boltzmann constant, $\langle \cdots \rangle_{t_0}$ denotes an average over time origins, α and $\beta = x, y$, or z Cartesian coordinates, and $\tau_{\alpha\beta,n}$ is the α - β off-diagonal stress tensor element for the n^{th} replicate.

$\tau_{\alpha\beta,n}$ is recorded every 6 fs (3 time-steps) to adequately integrate the initial rapid decay of the autocorrelation function. To improve precision, Equation 7 is an average over 30 to 60 independent replicate simulations (N_{reps}), twelve different time-origins (t_0), and all three unique off-diagonal components of the stress tensor (hence the factor of 3 in the denominator).

Obtaining the “true” infinite time limit viscosity (η^∞) requires evaluating Equation 7 as $t \rightarrow \infty$. Following “Best Practices”, we fit a double-exponential function to the “running integral”

$$\eta(t) = A\alpha\tau_1(1 - \exp(-t/\tau_1)) + A(1 - \alpha)\tau_2(1 - \exp(-t/\tau_2)) \quad (8)$$

where A , α , τ_1 , and τ_2 are fitting parameters and $\eta^\infty = A\alpha\tau_1 + A(1 - \alpha)\tau_2$.

Since the Green-Kubo “running integral” suffers from extreme fluctuations at long times, Equation 8 is fit to Equation 7 by minimizing a weighted sum-squared error objective function. Weights are equal to the inverse of the standard deviation (σ_η) of the replicate simulations. The model At^b is used to represent σ_η with respect to time.

Following a heuristic proposed in Reference 21, data are excluded where $\sigma_\eta > 40\%$ η^∞ . Occasionally this heuristic resulted in a long-time cut-off that was too short, which lead to very poor fits. In such cases, it was necessary to manually increase the cut-off time to 80 % η^∞ . Erroneously large fluctuations also exist at very short times. Following “Best Practices,” only data for $t > 3$ ps are included in the fitting of Equation 8.

As recommend by “Best Practices”, uncertainties are obtained by bootstrap re-sampling. Specifically, the fitting process described previously is repeated hundreds of times using randomly selected subsets of replicate simulations. Furthermore, each repetition uses a randomly selected long-time cut-off between 30 % η^∞ and 50 % η^∞ to account for the uncertainty in the 40 % heuristic. A 95 % confidence interval is obtained from the distribution of bootstrap estimates for η_∞ . An example of this process is provided as Supporting Information.

3. Results

Six normal and seven branched alkanes of varying chain-length and degree of branching are simulated in this study. We only consider compounds with available REFPROP equations-of-state and viscosity correlations [22]. Specifically, we simulate ethane [23, 24], propane [25, 26], *n*-butane [27, 28], *n*-octane [29, 30], *n*-dodecane [31, 32], *n*-hexadecane [33, 34], 2-methylpropane [35, 36], 2-methylbutane [35, 37], 2-methylpentane [35, 37], 3-methylpentane [38, 37], 2,2-dimethylpropane [35, 37], 2,3-dimethylbutane [38, 37], and 2,2,4-

trimethylpentane [39, 37].

Each compound was simulated using the TraPPE (UA LJ 12-6) and Potoff S/L (UA Mie 16-6) force fields. Potoff “short” parameters are used for 2-methylpropane, 2-methylbutane, 2,2-dimethylpropane, and 2,3-dimethylbutane while Potoff “long” parameters are utilized for 2-methylpentane, 3-methylpentane, and 2,2,4-trimethylpentane. Only 2,2-dimethylpropane was simulated with AUA4 (AUA LJ 12-6) while 2,2-dimethylpropane and 2,2,4-trimethylpentane were not simulated using the TAMie (AUA Mie 14-6) force field.

Table 7 demonstrates which compounds, force fields, and viscosity types were simulated in this study.

Table 7: Compounds, force fields, and state points. “X”: simulated, “O”: not simulated, “S” simulated with “Short” parameters, “L” simulated with “Long” parameters.

	TraPPE (TraPPE-2)		Potoff (S/L)		AUA4		TAMie	
Compound	$\eta_{\text{liq}}^{\text{sat}}$	$\eta_{\text{liq}}^{\text{comp}}$	$\eta_{\text{liq}}^{\text{sat}}$	$\eta_{\text{liq}}^{\text{comp}}$	$\eta_{\text{liq}}^{\text{sat}}$	$\eta_{\text{liq}}^{\text{comp}}$	$\eta_{\text{liq}}^{\text{sat}}$	$\eta_{\text{liq}}^{\text{comp}}$
ethane	X	X	X	X	X	X	X	X
propane	X	X	X	X	O	O	X	X
<i>n</i> -butane	X	X	X	X	O	O	X	X
<i>n</i> -octane	X	X	X	X	O	O	X	X
<i>n</i> -dodecane	X	O	X	O	O	O	X	O
<i>n</i> -hexadecane	X	O	X	O	O	O	X	O
2-methylpropane	X	X	S	S	O	O	X	X
2-methylbutane	X	X	S	S	O	O	X	X
2,2-dimethylpropane	X	X	S	S	X	X	O	O
2,3-dimethylbutane	X	X	S	S	O	O	X	X
2-methylpentane	X	X	L	L	O	O	X	X
3-methylpentane	X	X	L	L	O	O	X	X
2,2,4-trimethylpentane	X	X	L	L	O	O	O	O

Sections 3.1 and 3.2 present results for saturated liquid viscosities and compressed liquid viscosities, respectively. In both sections, the n -alkane results are followed by the branched alkane results. Simulation results are compared with the REFPROP viscosity correlations and experimental data from the ThermoData Engine (TDE) database [40].

3.1. Saturated Liquid

3.1.1. n -Alkanes

Figure 1 compares the TraPPE (UA LJ 12-6), TraPPE-2 (AUA LJ 12-6), TAMie (AUA Mie 14-6), Potoff (UA Mie 16-6), and the Bayesian parameter sets for $n = 13, 14, 15$, and 16.

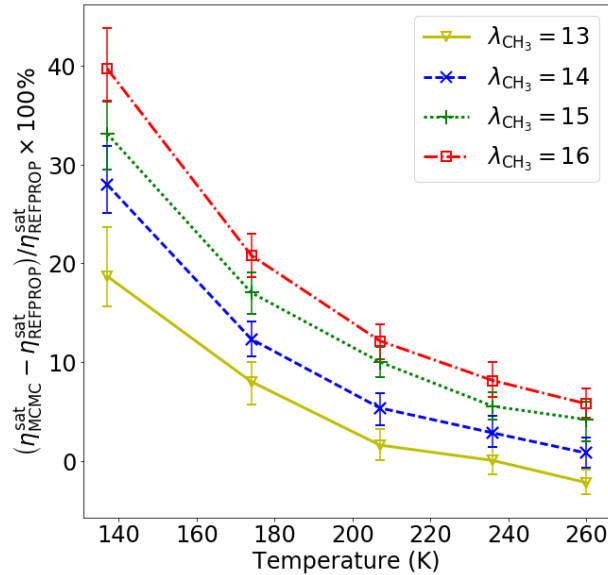


Figure 1: Saturated liquid viscosities for ethane. Colors/symbols denote different force fields.

Figure 2 compares the TraPPE (UA LJ 12-6), Potoff (UA Mie 16-6), and TAMie (AUA Mie 14-6) saturated liquid viscosities for propane, n -butane, and n -octane. Similar to what has been demonstrated in previous studies, the TraPPE force field significantly under predicts η_{liq}^{sat} (between 30 and 80 %) with the deviation increasing towards the triple point temperature. By contrast, the Potoff and TAMie force fields agree with the REFPROP values for these compounds to within 10 % over the entire temperature range studied (which includes the triple point for propane), and do not demonstrate a strong temperature dependence.

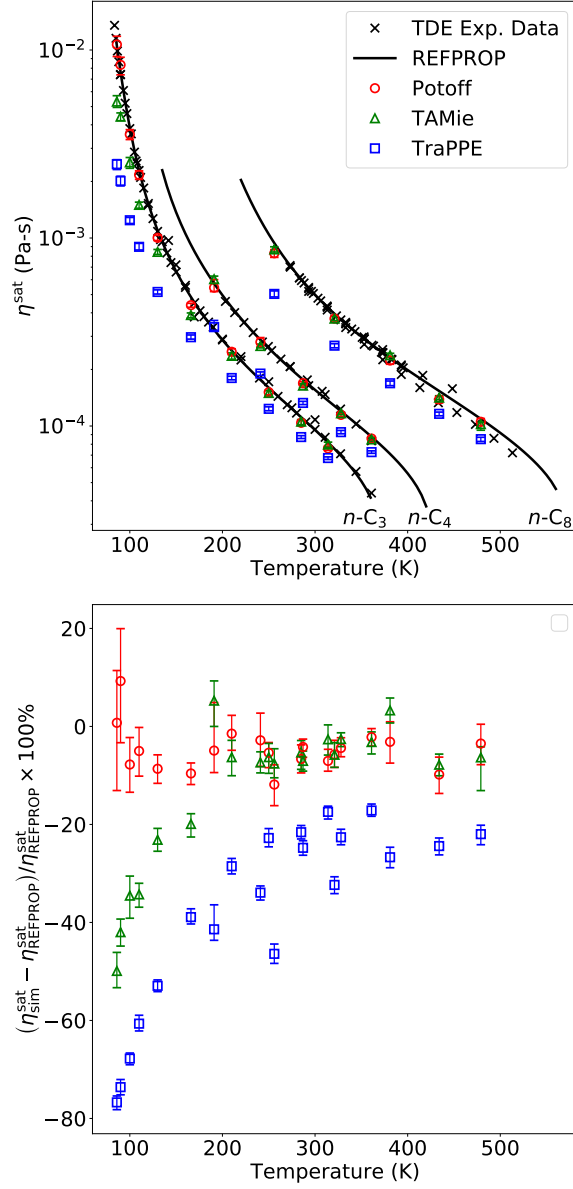


Figure 2: Saturated liquid viscosities for propane, n -butane, and n -octane. Colors/symbols denote different force fields.

Figure 3 compares the TraPPE, Potoff, and TAMie saturated liquid viscosities for n -dodecane and n -hexadecane. Although the TAMie and TraPPE results for these compounds are similar to those observed in Figure 2, it is quite curious that the Potoff results are nearly identical to the TraPPE results for n -dodecane (which significantly under predict η^{sat}).

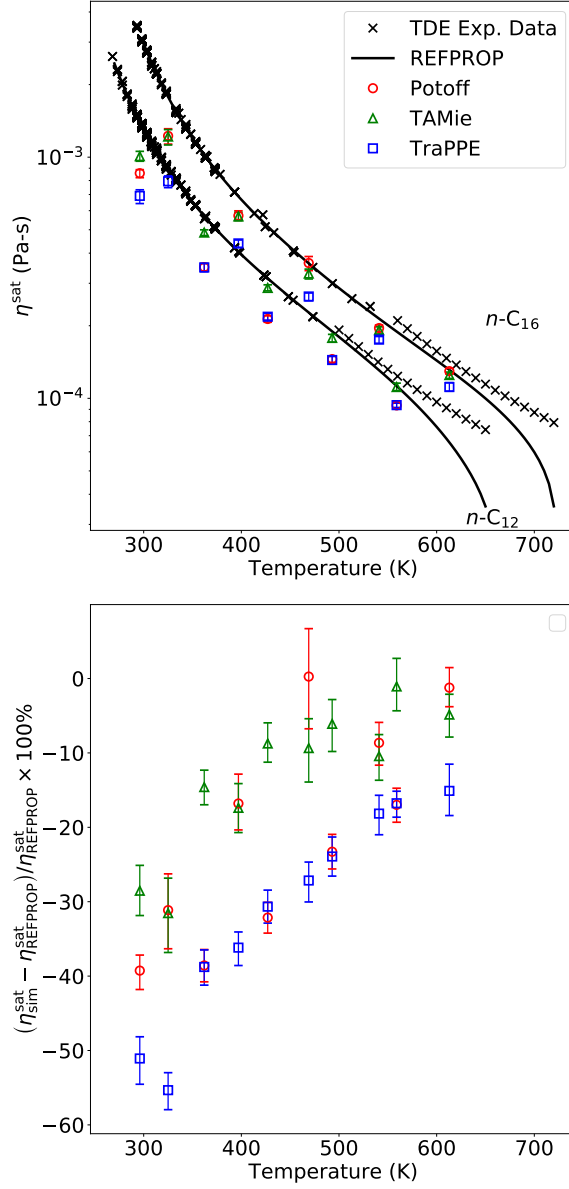


Figure 3: Saturated liquid viscosities for n -dodecane and n -hexadecane. Colors/symbols denote different force fields.

3.1.2. Branched alkanes

Figures 4 and 5 compare the saturated liquid viscosities for each force field and branched alkane studied. Figures 4 and 5 present results for the compounds classified by Potoff as “short” and “long”, respectively. Specifically, Figure 4 depicts 2-methylpropane, 2,2-

dimethylpropane, 2-methylbutane, and 2,3-dimethylbutane, while Figure 5 contains 2-methylpentane, 3-methylpentane, and 2,2,4-trimethylpentane. Each compound was simulated using the TraPPE (UA LJ 12-6) and Potoff (UA Mie 16-6) force fields. However, only 2,2-dimethylpropane was simulated with AUA4 (AUA LJ 12-6) while 2,2-dimethylpropane and 2,2,4-trimethylpentane were not simulated using the TAMie (AUA Mie 14-6) force field.

From Figures 4 and 5, we see that the Potoff S/L and TAMie force fields are not as accurate for these branched alkanes as for the normal alkanes. In particular, Potoff and TAMie demonstrates the same temperature dependence observed for other force fields, where the deviations are largest at lower temperatures. However, Potoff still provides considerable improvement compared to the LJ 12-6 based models, i.e., TraPPE and AUA4. Note that the performance is similar for the Potoff “short” and “long” parameters in Figures 4 and 5, respectively.

The deviations for each force field are largest for 2-methylpropane and 2,2-dimethylpropane. Since these compounds are primarily composed of CH₃ UA sites, this poor performance is likely due to the assumption that the CH₃ non-bonded parameters are transferable from *n*-alkanes to branched alkanes. Improvement might be possible if the CH₃ parameters were different depending on the neighboring UA site type. However, we emphasize that REFPROP states that the viscosity correlation for 2,2-dimethylpropane is not of “reference quality.”

3.2. Compressed liquid

Section 3.1 demonstrated that Mie *n*-6 based force fields (Potoff and TAMie) are considerably more reliable for predicting saturated liquid viscosities than LJ 12-6 based force fields (TraPPE and AUA4). However, both the Potoff and TAMie non-bonded potentials use $n > 12$. Reference ? demonstrates that $n > 12$ is too repulsive at short distances which leads to over estimates of pressure at high densities. The purpose of this section is to determine if a similar phenomenon is observed for viscosity estimates at high densities/pressures.

3.2.1. *n*-Alkanes

Figures 6, 7, and 8 compare the elevated pressure viscosities for propane, *n*-butane, and *n*-octane, respectively. Each compound is simulated using the TraPPE, Potoff, and TAMie

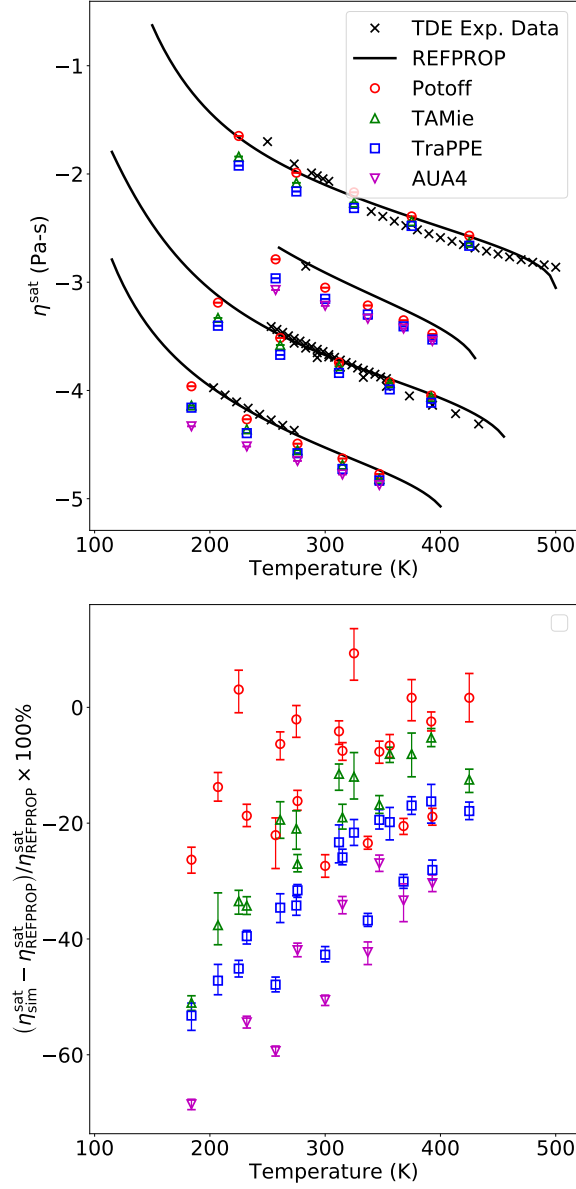


Figure 4: Saturated liquid viscosities for 2-methylpropane, 2,2-dimethylpropane, 2-methylbutane, and 2,3-dimethylbutane. Colors/symbols denote different force fields.

force fields at four or five densities.

Figure 6 demonstrates that the TraPPE force field has a constant negative bias even with increasing density/pressure. The TAMie force field has the most accurate η - ρ dependence, i.e., the error does not increase with respect to density. By contrast, the Potoff potential

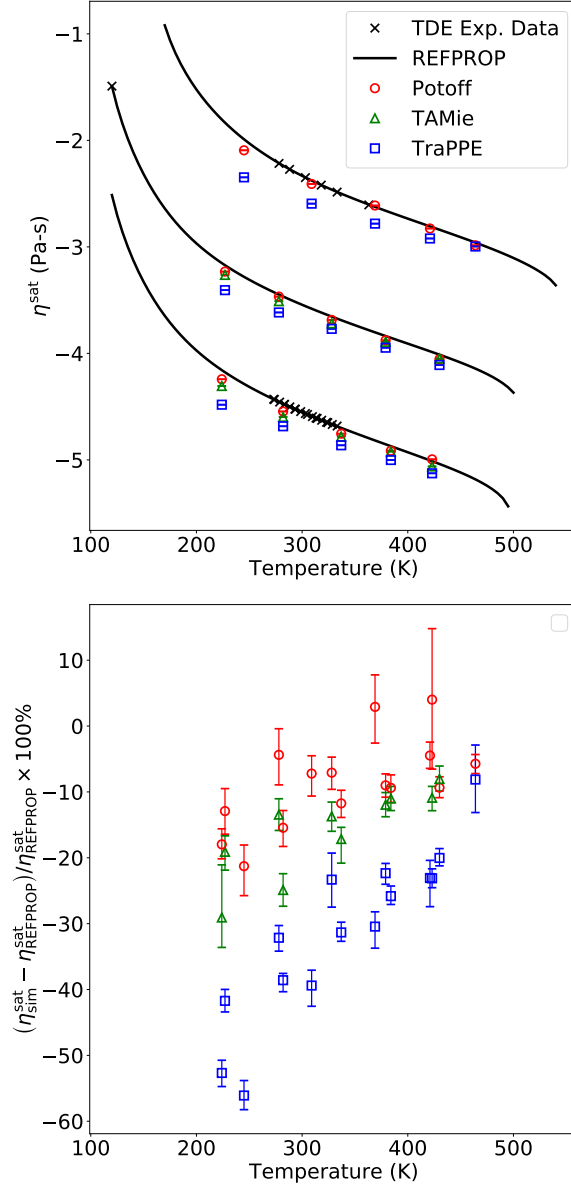


Figure 5: Saturated liquid viscosities for 2-methylpentane, 3-methylpentane, and 2,2,4-trimethylpentane. Colors/symbols denote different force fields.

demonstrates considerable over estimation of η at high densities, which is likely attributed to the overly repulsive Mie 16-6 potential at close distances. Remarkably, the Potoff force field is the most accurate at predicting the η - P dependence. This can be explained as a cancellation of errors since the Potoff force field significantly over predicts both viscosity and

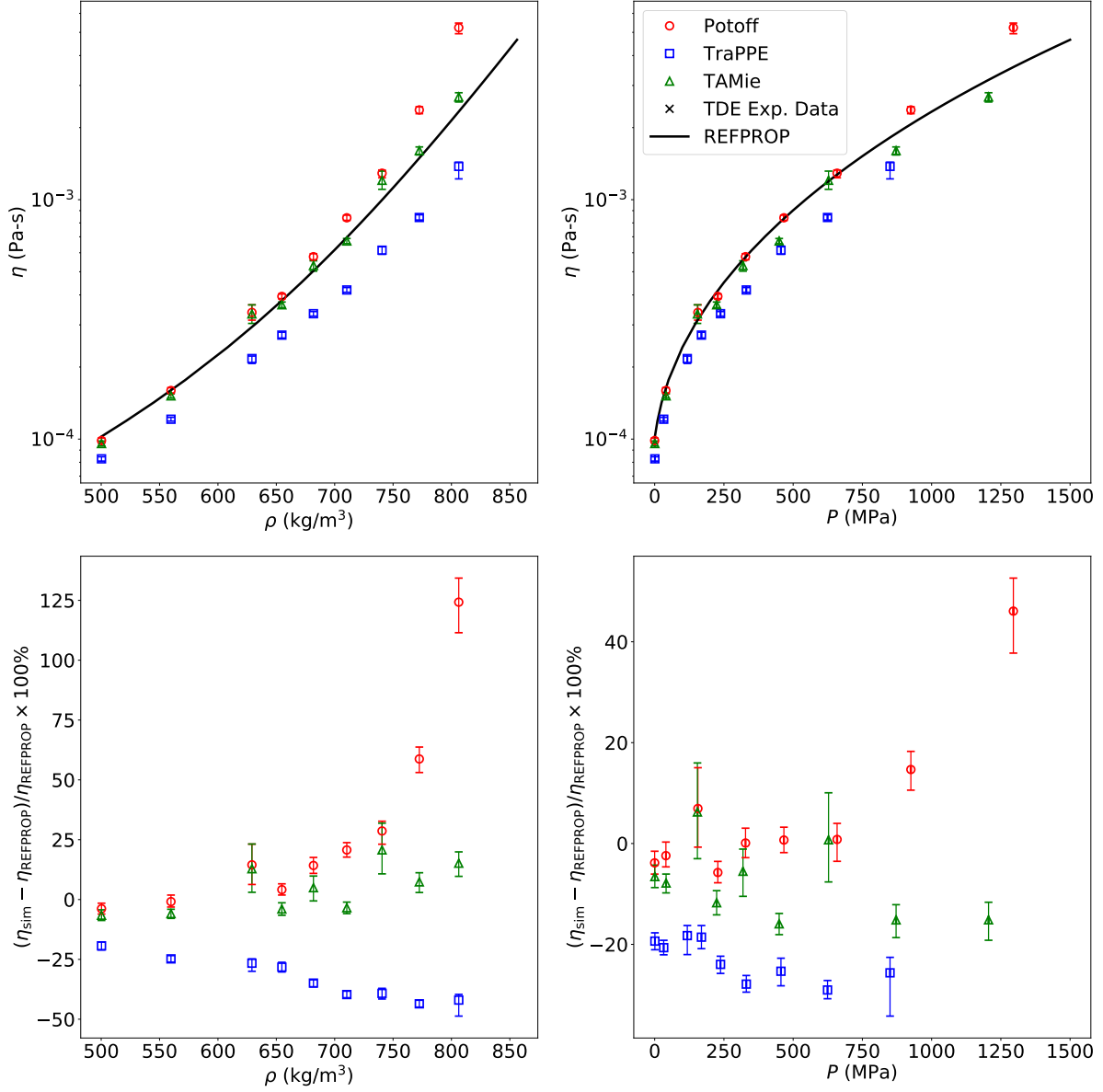


Figure 6: Compressed liquid viscosities at 293 K for propane. Colors/symbols denote different force fields.

pressure at high densities. Note that the Potoff force field is reliable near 1 GPa, especially considering the large uncertainty in the REFPROP correlation at these extreme pressures.

The results in Figures 7 and 8 for *n*-butane and *n*-octane, respectively, are similar to those in Figure 6 for propane. Specifically, the TraPPE force field under predicts η at all densities/pressures, the TAMie force field provides the most accurate η - ρ dependence, while

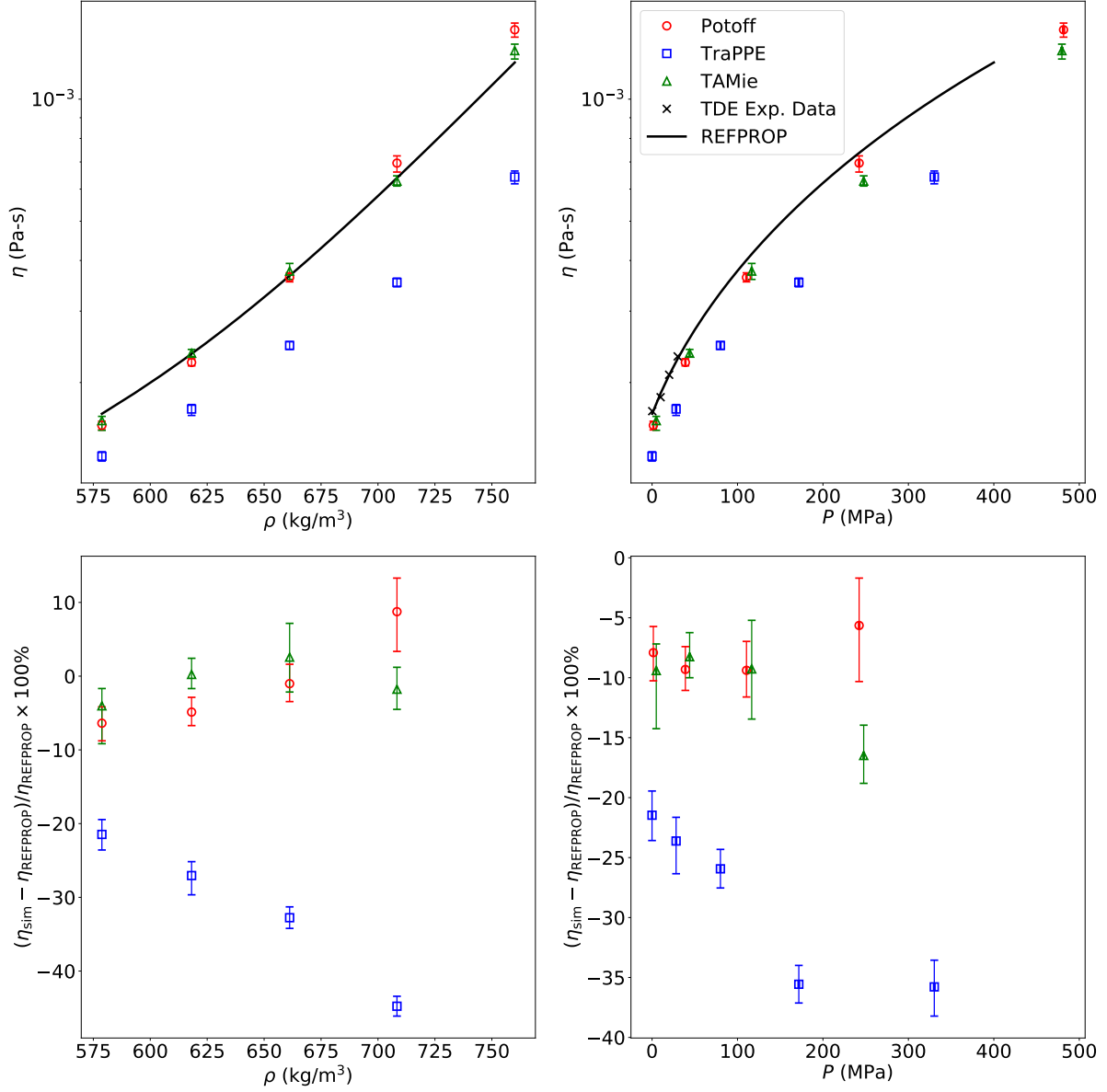


Figure 7: Compressed liquid viscosities at 293 K for *n*-butane. Colors/symbols denote different force fields.

the Potoff force field over predicts η with respect to ρ but accurately predicts the η - P trend.

3.2.2. Branched alkanes

The trends observed in Figures 9 to 12 are consistent with the compressed liquid trends for *n*-alkanes. Specifically, TraPPE under-predicts the viscosity with respect to both ρ and

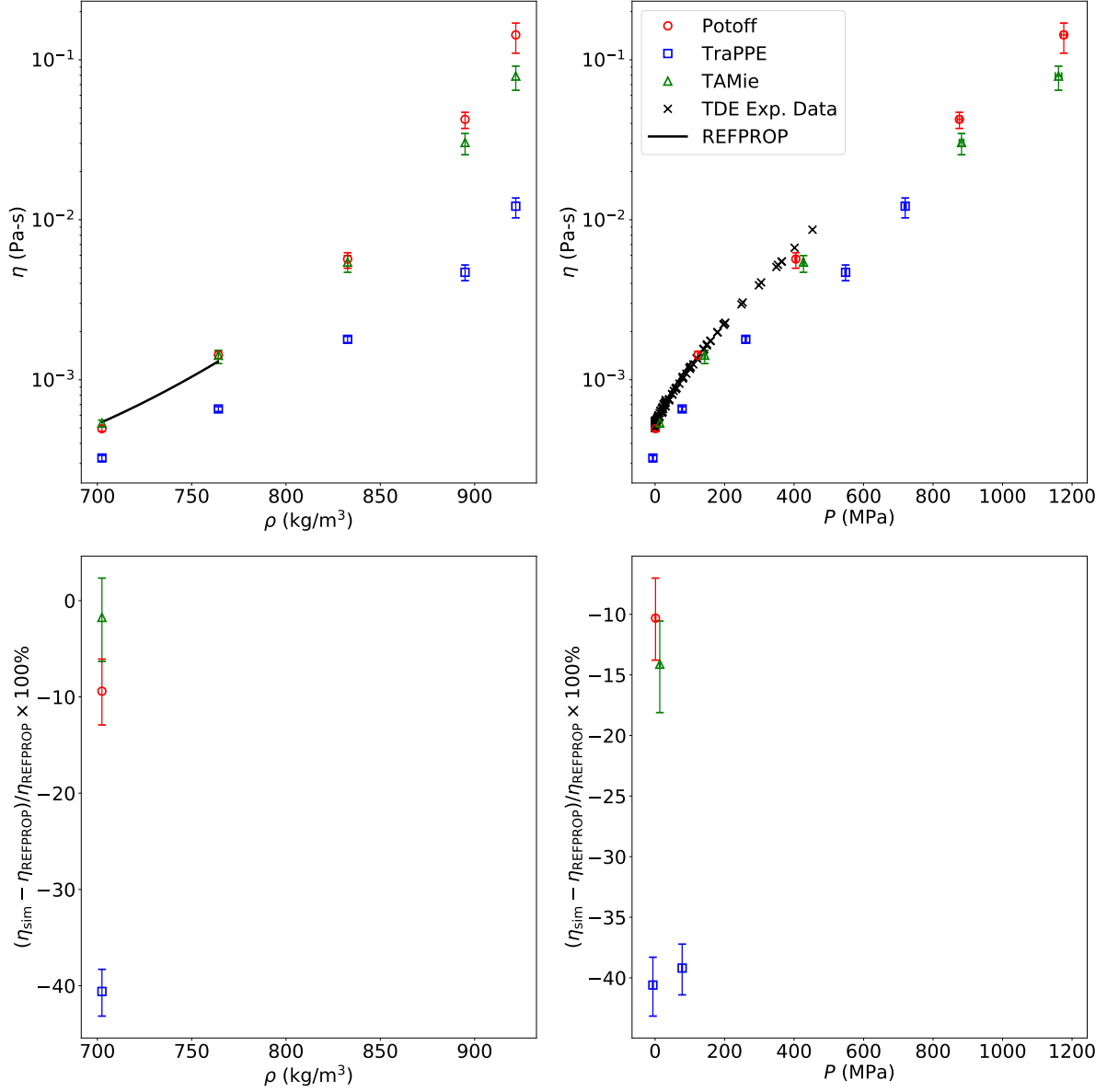


Figure 8: Compressed liquid viscosities at 293 K for *n*-octane. Colors/symbols denote different force fields.

P . Potoff over-predicts η with respect to ρ but provides a reasonable estimate of the η - P trend. As observed previously in Section 3.1, Potoff and TAMie are less accurate for branched alkanes than for *n*-alkanes. In particular, the Potoff η - P trends are systematically lower than the REFPROP correlations for 2-methylbutane and 3-methylpentane. However, note that the Potoff η - P trends are more reliable for 2-methylpropane and 2,2,4-trimethylpentane.

These results cannot be attributed to the “short” or “long” parameter distinction.

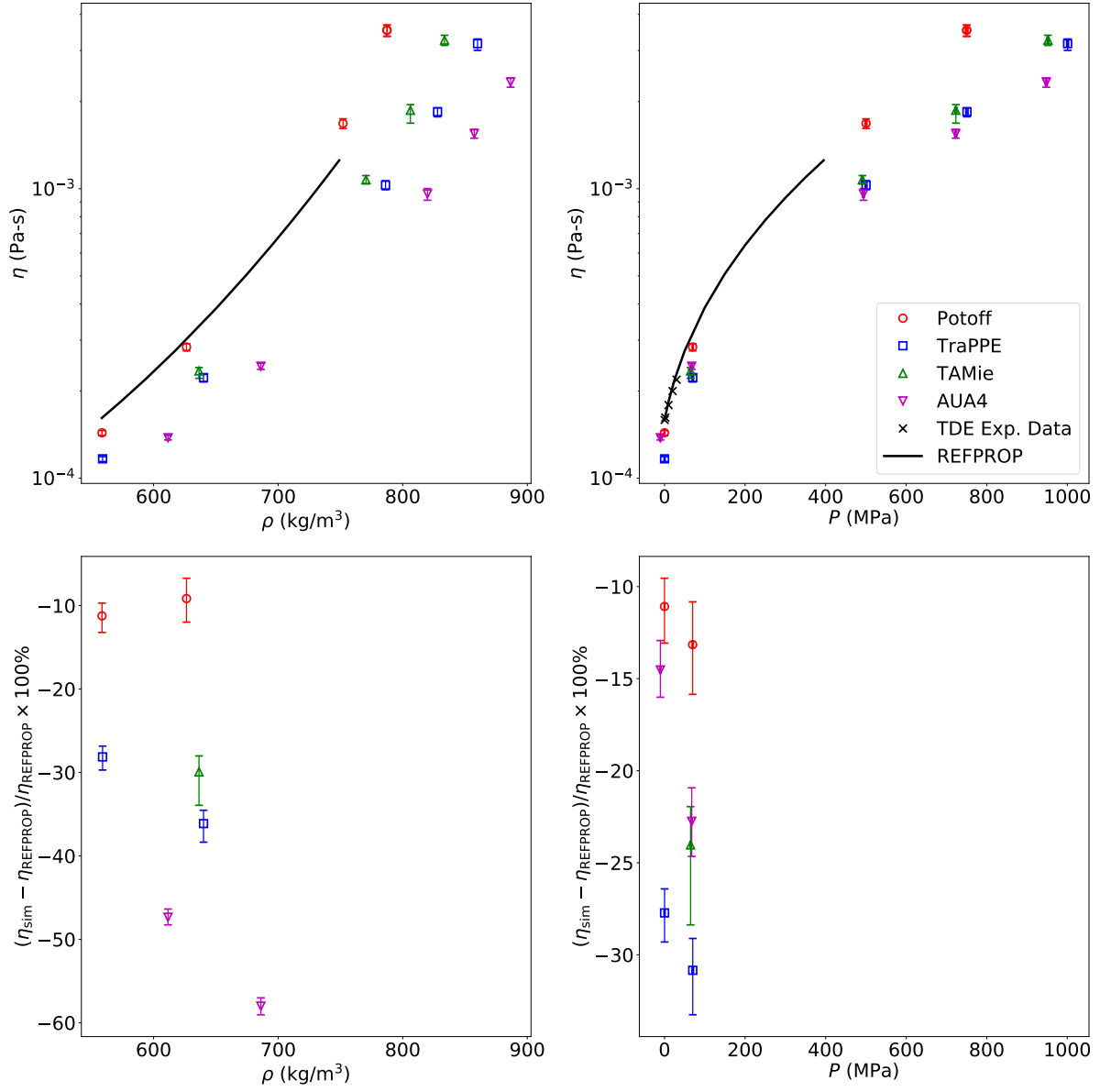


Figure 9: Compressed liquid viscosities at 293 K for 2-methylpropane. Colors/symbols denote different force fields.

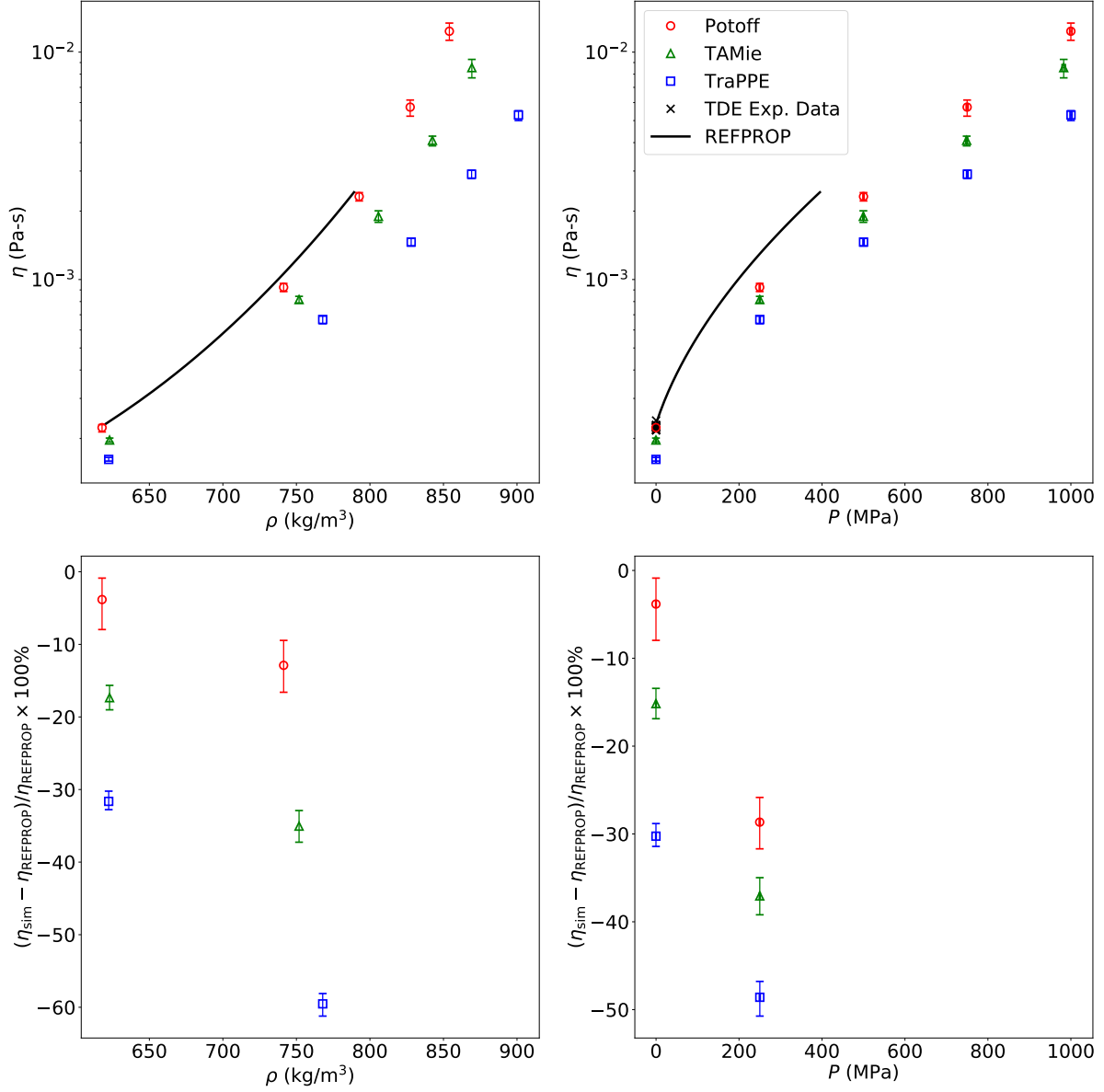


Figure 10: Compressed liquid viscosities at 293 K for 2-methylbutane. Colors/symbols denote different force fields.

4. Discussion/Limitations

While the Potoff force field significantly over-predicts the η - ρ dependence at $T = 293$ K, it does not over-predict η for the highest values $\rho_{\text{liq}}^{\text{sat}}$ (those near the triple point temperature) (cf. Figures 2 and 6). To better understand this, Figure BLANK compares the radial

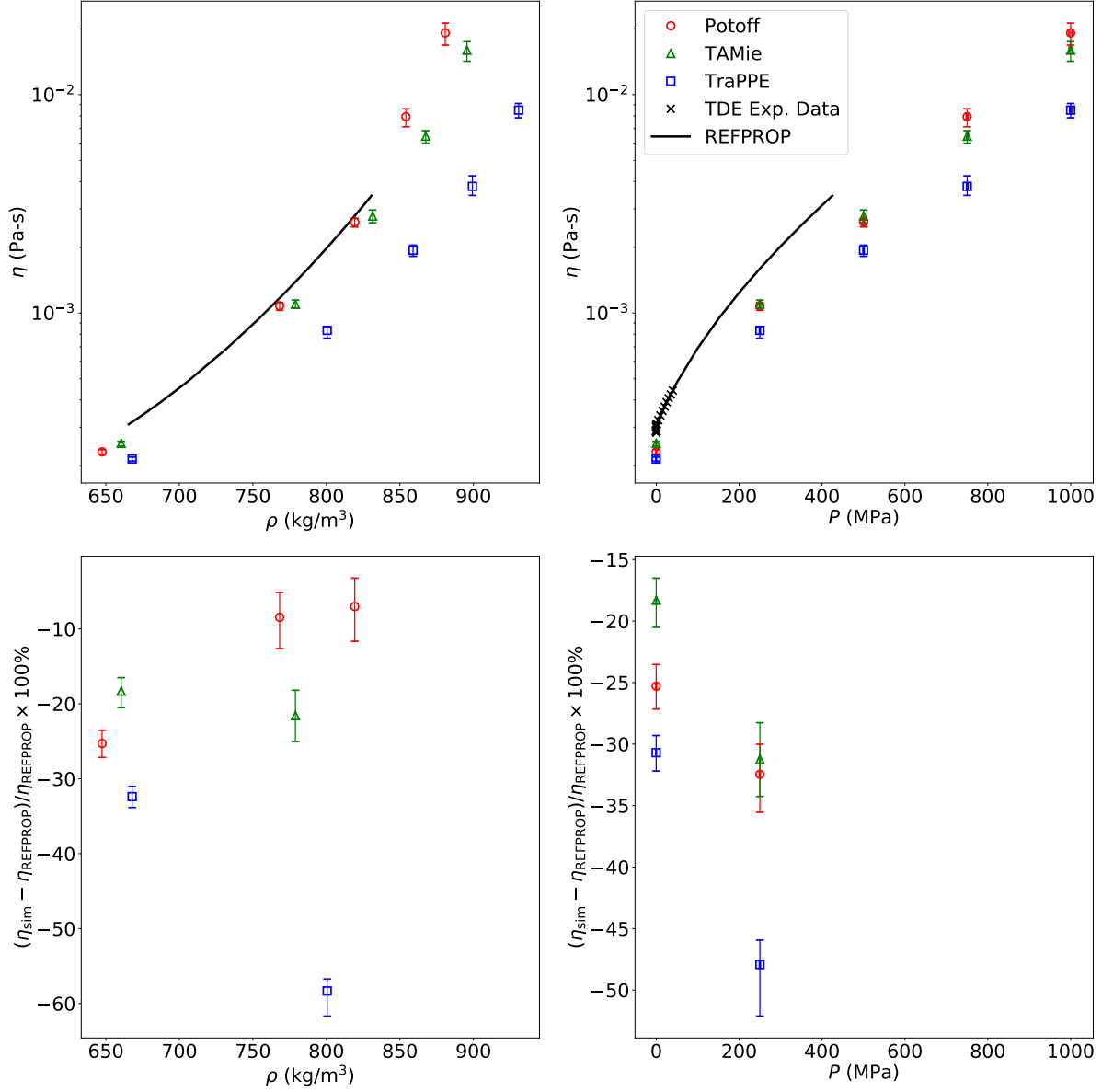


Figure 11: Compressed liquid viscosities at 293 K for 3-methylpentane. Colors/symbols denote different force fields.

distribution functions (RDF) for three different state points, namely, the triple point (T_{tp} and ρ_{tp} and two densities along the $T = 293$ K isotherm (ρ_{tp} and the maximum ρ). It is clear from these RDFs that the higher pressure simulations sample from much closer interactions than the triple point and, therefore, these close interactions cause the over-estimation of

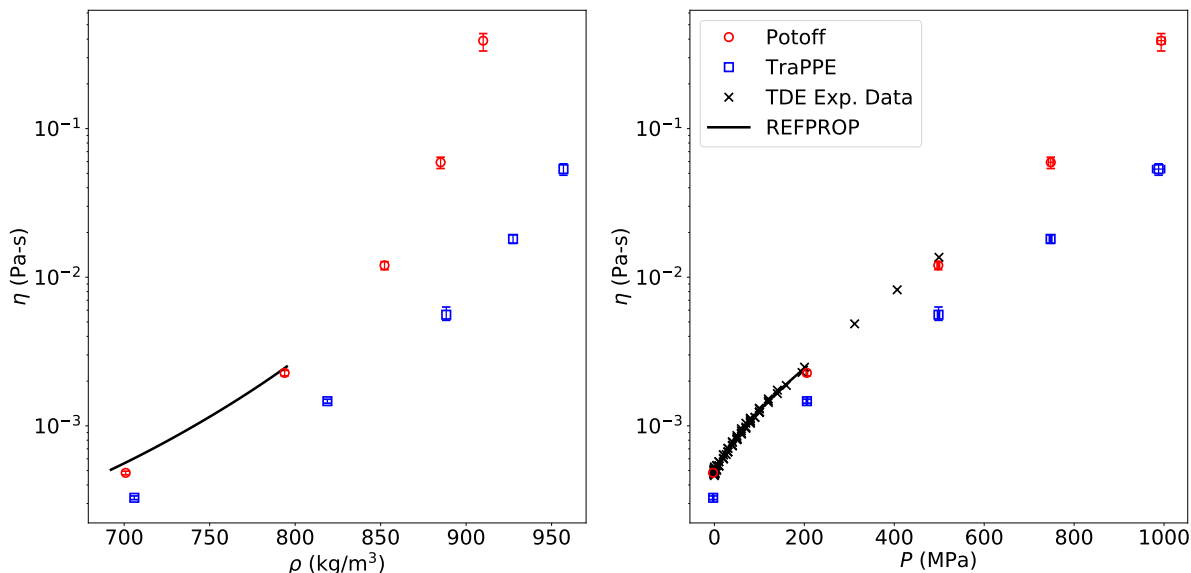


Figure 12: Compressed liquid viscosities at 293 K for 2,2,4-trimethylpentane. Colors/symbols denote different force fields.

compressed liquid viscosities but not saturated high density liquid viscosities.

1. Finite-size effects
2. Fixed vs flexible bonds
3. Simulation time, high viscosities
4. Cut-offs for C12
5. RDFs for propane

1. Discussion

- (a) Mie potentials parameterized with VLE data provide significant improvement over LJ 12-6
- (b) Potoff over-predicts $\eta - \rho$ dependence while TAMie is fairly accurate
- (c) Potoff appears to be slightly more accurate for $\eta - P$
- (d) Branched alkanes are not as accurate, perhaps assumption of transferability or torsional parameters

2. Limitations

- (a) Largest viscosity simulations are slow to converge and unclear if simulations are sufficiently long
- (b) Tail-corrections could impact dynamics
- (c) Using REFPROP saturation conditions instead of force fields

4.1. $\rho_{\text{liq}}^{\text{sat}}$

There are at least three reasons why we perform simulations at the REFPROP $\rho_{\text{liq}}^{\text{sat}}$ instead of the force field $\rho_{\text{liq}}^{\text{sat}}$. First, this approach allows for a fair comparison of the force fields’ ability to predict viscosity, without penalizing force fields which are less accurate at predicting $\rho_{\text{liq}}^{\text{sat}}$ or rewarding force fields that mask their deficiencies in predicting viscosity by over- or under-estimating $\rho_{\text{liq}}^{\text{sat}}$. Second, since each of the studied force fields utilized $\rho_{\text{liq}}^{\text{sat}}$ data in their optimization, deviations between the REFPROP and force field values are small, typically less than 1 %. However, small differences in density have been reported to result in large differences in viscosity. For this reason, a small set of validation simulations are performed to determine the variability caused by utilizing the REFPROP densities. The force field saturated liquid densities were obtained from the literature.

The use of REFPROP $\rho_{\text{liq}}^{\text{sat}}$ caused some simulations to be in a meta-stable state. Specifically, this occurs when the force field vapor pressure is less than the REFPROP vapor pressure. Fortunately, this is uncommon as Potoff, TAMie, and AUA4 are quite reliable for estimating $P_{\text{vap}}^{\text{sat}}$ and TraPPE significantly over-estimates $P_{\text{vap}}^{\text{sat}}$.

5. Conclusions

This study demonstrates the improvement that has taken place over the past two decades for predicting viscosity with molecular simulation. First, the “Best Practices” for EMD lead to more reproducible results. Second, the state-of-the-art Mie n-6 force fields are significantly more accurate than the traditional Lennard-Jones 12-6 force fields. More specifically, the Potoff and TAMie force fields typically predict saturated liquid viscosities for n -alkanes to within 10 % of the REFPROP values. By contrast, the TraPPE and AUA4 models under-predict saturated liquid viscosities by 30 % to 50 %, where the deviations are largest at

lower temperatures. While Potoff and TAMie are also more reliable for branched alkanes, deviations are larger and demonstrate a similar temperature dependence. The key limitation of the Potoff force field is that the choice of $n=16$ is too repulsive at high densities, which causes the viscosity to be over-estimated at high densities. Due to a fortuitous cancellation of errors, the Potoff potential does provide a reliable η - P trend. Since TAMie uses $n=14$, the η - ρ trend is slightly more reliable than that of Potoff. It is important to emphasize that transport properties were not included in the training set for parameterizing the Potoff and TAMie force fields. Therefore, the results from this study demonstrate that the improved prediction of static vapor-liquid coexistence properties obtained with Mie $n=6$ potentials also results in improved prediction of a transport property, namely, liquid viscosity.

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6. Supporting Information

6.1. Gromacs input files

We have provided example input files for simulating *n*-isooctane at BLANK K with the Potoff force field in GROMACS (see attached .gro, .top, and .mdp files). Additionally, all files that were used to generate the results from this study can be found that the GitHub repository www.github.com/ramess101/IFPSC_10.

6.2. Tabulated values

1. Ethane

(a) Saturation

- i. Potoff
- ii. TraPPE
- iii. AUA4
- iv. TAMie

(b) T293 highP

- i. Potoff
- ii. TraPPE
- iii. AUA4
- iv. TAMie

2. Propane

(a) Saturation

- i. Potoff
 - ii. TraPPE
 - iii. AUA4
 - iv. TAMie
- (b) T293 highP
 - i. Potoff
 - ii. TraPPE
 - iii. AUA4
 - iv. TAMie
- 3. n-Butane
 - (a) Saturation
 - i. Potoff
 - ii. TraPPE
 - iii. AUA4
 - iv. TAMie
 - (b) T293 highP
 - i. Potoff
 - ii. TraPPE
 - iii. AUA4
 - iv. TAMie

Repeat for all other compounds with corresponding potentials

6.3. *Finite-size effects*

Previous studies have demonstrated that finite-size effects are typically negligible for viscosity estimates with equilibrium molecular dynamics. However, since this analysis is typically not reported in the literature, the “Best Practices” guide recommends validating that finite-size effects are indeed negligible. For this reason, Figure BLANK compares the results for simulations performed with 100, 200, 400, and 800 molecules of BLANK and BLANK.



Figure 13: Finite-size effects.

Notice that the averages and uncertainties typically overlap considerably and that there is no clear trend with respect to $N^{-1/3}$. In addition to this visual inspection, we also perform a “random permutation test” to determine that the results from the different system sizes are statistically indistinguishable. The algorithm for “random permutation testing” is the following:

1. Compute the “observed” sum-of-squares between the four different system sizes (SS_{obs})
2. Randomly divide the replicate simulations of each system size into four groups, “A”, “B”, “C”, and “D”
3. Average the replicate Green-Kubo integrals of each group
4. Fit Equation 8 to the averages from Step 3
5. Calculate the “permuted” sum-of-squares between the four different groups (SS_{perm})
6. Repeat Steps 2 to 5 hundreds of times (N_{perm})
7. Count the number of permutations with $SS_{\text{perm}} > SS_{\text{obs}}$ (N_{count})
8. Assign a p -value equal to the ratio of N_{count} divided by N_{perm}
9. If $p > 0.05$, we fail to reject the Null-hypothesis that all four system sizes are statistically equivalent

This approach is employed in place of the standard Analysis of Variance (ANOVA) test because it is not possible to compute a reliable F -statistic since an individual replicate simulation does not provide a meaningful estimate of η . Therefore, we can only compute the sum-of-squares between averages and not the sum-of-squares between replicates. is not capable of a meaningful , which requires computing an F -statistic is Step 4.

6.4. *Simulation length effects*

For less viscous systems, i.e., saturation and low pressures, a 1 ns simulation is typically sufficient for the Green-Kubo integral to reach a plateau. However, even when an apparent plateau is observed, too short of simulations can lead to systematic bias in η . For this reason, as recommended by “Best Practices,” we verify that the estimated viscosity obtained from a 1 ns trajectory is consistent with that obtained from 2 ns, 4 ns, and 8 ns simulations.



Figure 14: Finite-size effects.

For more viscous systems, i.e., greater than 100 MPa, a 1 ns simulation is too short to observe a plateau in the Green-Kubo integral. In these cases, we increased the simulation time to a value between 2 and 8 ns. Due to the increased computational cost of such simulations, we did not perform an exhaustive test with increasing simulation time. Instead, the choice of simulation time was determined primarily by the ability to detect a plateau

region. Therefore, it is possible that even longer simulations are required for the most viscous systems.

Due to inherently slow dynamics in highly viscous systems (greater than 0.02 Pa-s), obtaining well-converged Green-Kubo integrals is extremely challenging. Additional replicate simulations can help reduce noise.

Storage limitations become a concern with simulations longer than 8 ns due to the frequency at which data are output (every 6 fs). Reading in these files for GROMACS to evaluate the data nearly crippled our computing cluster.

Obtaining well-converged Green-Kubo integrals for highly viscous systems (greater than 0.02 Pa-s) is challenging and requires longer simulations.

6.5. Validation Runs

To validate our methodology, we attempt to replicate viscosity estimates available on the NIST Reference Simulation Data website for TraPPE-UA ethane as well as literature values for TraPPE-UA *n*-octane. Figure 15 compares the ethane and *n*-octane results from this study with those from NIST and the literature, respectively.



Figure 15: Comparison with NIST Reference Simulation Data and Reference ? .

The *n*-octane validation is somewhat more useful than the ethane validation for at least three reasons. First, *n*-octane includes angle and torsional contributions that are absent

in ethane. Second, the literature provides values for both rigid and flexible bonds. Third, the n -octane results are for fixed elevated pressures, which provides validation of our NPT ensemble results.

6.6. Bond types, Harmonic vs LINCS

To test how sensitive the results presented in Section 3 are to the use of fixed bond-lengths, we perform additional simulations with flexible bonds. Specifically, we use the traditional harmonic bond potential:

$$u^{\text{bond}} = \frac{k_b}{2} (r - r_{\text{eq}})^2 \quad (9)$$

where u^{bond} is the bonded potential, k_b is the harmonic force constant, and r_{eq} is the equilibrium bond-length. To determine the impact, we perform simulations with two different values of k_b , namely, BLANK (taken from reference BLANK) and BLANK (an arbitrarily large value). Figure 16 demonstrates that the difference between fixed and flexible bonds is negligible in certain cases, but for the larger force constant a systematic increase in viscosity is observed. Bootstrap resampling confirms that the LINCS and $k_b = \text{BLANK}$ results are statistically indistinguishable, while the $k_b = \text{BLANK}$ is statistically different.



Figure 16: Fixed bond-lengths compared with two different harmonic bond potentials.

6.7. Green-Kubo analysis

This section provides a detailed example of how we obtain estimates for η with its corresponding uncertainty. Figure BLANK depicts a typical autocorrelation function obtained by executing the GROMACS “energy –vis.” By default, GROMACS partitions the complete simulation into twelve evenly sized time blocks. Therefore, the autocorrelation in Figure BLANK is the average of twelve different time origins. GROMACS then performs a simple trapezoidal integration of neighboring points to obtain the Green-Kubo integral. The Green-Kubo integral with respect to time is output in the “visco.xvg” file. Figure BLANK presents the Green-Kubo integral from forty replicate simulations. Although a single replicate is often quite noisy at long times, the average of these replicates converges smoothly (see Figure BLANK). Figure BLANK shows that the fluctuations, or standard deviation, increases with time but is adequately modeled with At^b . The line labeled “cut-off” in Figures BLANK and BLANK is the time at which $\sigma_\eta \approx \eta^\infty$. Data beyond this time are excluded from the fit of the double-exponential function. Bootstrap resampling provides an estimate of the uncertainty. Figure BLANK shows that, typically, the bootstrapped distribution is quite normal. The line labeled “bootstraps” in Figure BLANK are the lower and upper 95 % confidence interval.

The results depicted in Figure BLANK are from BLANK, BLANK, BLANK.

1. Raw data, i.e., multiple replicates with the average
2. Exclude low time data and have a heuristic for determining the cut-off time

Example analysis, i.e., bootstrap distribution, replicates

6.8. MCMC?

6.9. Cut-off distance

The choice of cut-off distance is a subtle but important decision. In this study, we implement a 1.4 nm cut-off for each force field except Potoff, which utilizes only a 1.0 nm cut-off. The “Best Practices” guide suggests that cut-off lengths could be significant but does not provide any convincing evidence to prove or disprove this notion. To address this issue, we



Figure 17: Autocorrelation function with respect to time.



Figure 18: Replicate simulations, average, fit to average, cut-off, and bootstrap uncertainties.

perform simulations of the Potoff force field using three different cut-off distances. Specifically, Figure 21 presents the Potoff viscosity values for propane, *n*-butane, *n*-octane, and *n*-dodecane using cut-offs of 1.0 nm, 1.4 nm, 1.8 nm.

Figure 21 demonstrates that for smaller compounds the impact of cut-off is negligible, while a 1.0 nm cut-off causes a significant error for *n*-dodecane. For this reason, the Potoff results presented previously in Figure 3 were obtained using a 1.4 nm cut-off. In fact, *n*-hexadecane and *n*-docosane were unstable with a 1.0 nm cut-off and a 2 fs time-step.



Figure 19: Standard deviation of replicate simulations with respect to time.



Figure 20: Bootstrap distribution of η .

Reducing the time step to 1 fs was capable of stabilizing the 1.0 nm cut-off.

The instability of a 1.0 nm cut-off (with 2 fs time-steps) demonstrates the importance of verifying that the cut-off distance is long enough to not impact the system dynamics. Furthermore, this demonstrates why alternative tail modifications are ideal for molecular dynamics, e.g., force-shift and switch-force. Unfortunately, these tail modifications lead to extremely different vapor-liquid coexistence curves, suggesting that the non-bonded parameters must be re-optimized with the modified tail. Therefore, performing simulations with a



Figure 21: Impact of cut-off distance.

force-shift or switch-force Potoff, TraPPE, TAMie, and AUA4 potentials would likely result in significantly different viscosities. Re-parameterizing the non-bonded interactions for a force-shift or switch-force potential is beyond the scope of this study.