

Computational quantum mechanics: An underutilized tool in thermodynamics*

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Abstract: In this paper, we highlight the various ways computational quantum mechanics (QM) can be used in applied thermodynamics. We start with the most rigorous procedures of calculating the interactions between molecules that can then be used in simulation and progress, in steps, to less rigorous but easily used methods, including the very successful continuum solvation models.

Keywords: quantum mechanics; thermodynamics; solvation models; ab initio; phase behavior; virial coefficient.

INTRODUCTION

Chemists, physicists, and many engineers are exposed, in varying degrees, to quantum mechanics (QM) in their education; however, few use it. The use of QM has a long history in the area of thermophysical properties, though initially restricted to the calculation of heats of formation, heat capacities, heats of reaction, likely molecular conformations, reaction pathways, and transition states, and most such calculations were restricted to a single molecule or in an ideal gas [1]. Since, in a sense, this is old technology, not much will be said about these here, except to put the accuracy of QM calculations in context. What is mainly considered here is recent work on the use of QM for the prediction of thermophysical properties and phase behavior, that is, properties of fluids and mixtures that are not ideal gases. The review starts with a discussion of rigorous and very time-consuming, first-principles ab initio calculations and follows a path to recent easier-to-use and more user-friendly rapid calculational methods that are somewhat less rigorous.

However, before proceeding, an important point needs to be made. Since the Schrödinger equation cannot be solved exactly for multi-electron systems, approximations must be made, and deciding upon the method and level is not a trivial task. There are a number of software packages, such as Gaussian [2], Schrödinger [3], Turbomole [4], and Gamess [5], that are available for QM calculations, and many different calculational procedures, including ab initio and density functional methods within these packages. Further, decisions about the level of those calculations must be made [1]. These approximations are of two types, the level of theory used (the extent to which the correlation between the electrons is considered) and the accuracy with which the electron density is represented (that is, the size of the basis set used). The problem one encounters is that for accurate results, one needs to use a reasonably high level of theory and a reasonably accurate representation of the electron densities (that is, the basis sets). At a high level of theory, such as the coupled cluster method, the calculations are very

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computer-intensive and scale approximately as n^7 , where n is the number of (typically Gaussian) functions in the basis set, which will be considerably greater than the number of electrons. This sets significant limits on the calculation, including the size of the molecules that can be considered.

It is common in calculating properties of an isolated molecule, such as the enthalpy (or heat) of formation, to use an extrapolation method, such as G3 [6], in which there is a strict recipe involving calculations at a lower level of theory with a large basis set, and a high level of theory with a moderate size basis set, and from this, with some empirical corrections, to extrapolate the results to a high level of theory and a large basis set or the so-called basis set limit. The results of using such extrapolation methods for the prediction of thermodynamic properties, such as heats of formation, can be quite good, indeed frequently at about what is referred to as chemical accuracy of 1 kcal/mol in heats of formation of hydrocarbons and organic chemicals [6]. However, "chemical accuracy" is not sufficient for phase behavior calculations. For example, a 1 kcal/mol error in a partial molar excess Gibbs energy results in a greater than factor of 5 error in an activity coefficient and a 2 kcal/mol error results in almost a factor of 30 error, either of which is unacceptable for accurate phase equilibrium calculations.

Of special interest in the biological, pharmacological, and environmental literature is the computation of binding energies, especially of ions to DNA (biologic and pharmaceutical literature) and to humic components (environmental literature). The results are generally accurate to within several kcal/mol, which is useful in quantifying binding sites and in the study of chemical kinetics where one is interested in examining kinetic pathways (transition states) that generally differ by considerably more than 2 kcal/mol [7,8].

The conclusion is that the present accuracy of QM calculations does not allow the direct calculation of phase behavior from first principles. Therefore, other methods must be used. The following classification of these indirect methods will be considered here:

- 1) QM calculation of the intermolecular potential followed by computer simulation;
- 2) on-the-fly QM calculation during simulation;
- 3) QM calculations to determine parameters in existing thermodynamic models; and
- 4) continuum solvation models.

CALCULATION OF INTERMOLECULAR POTENTIALS

The first method of calculating thermodynamic properties and phase behavior from QM is a serial one in that one first calculates point-by-point a reasonably complete two-body interaction energy landscape, which is then fitted to an analytic function and used in a computer simulation method, such as Gibbs ensemble Monte Carlo (MC) [9], to obtain vapor-liquid phase behavior and the properties of the co-existing phases. This method contains pairwise additivity assumption that the interaction energy of an assembly of molecules can be obtained by summing the energies of interacting pairs.

The interaction energies among electrically neutral molecules, except for the hard-core repulsions, are classified as being weak and are the result of permanent and induced multipole moments, that is, interactions among the electron clouds, for which very accurate and time-consuming QM calculations are needed. Further, to obtain the force field between a pair of molecules, a large number of center-of-mass separations and relative orientations must be considered, so many thousands of computer hours may be required, which is why parallel calculations on Beowulf clusters are frequently employed, since the proper calculation of the interaction between a pair of relatively simple molecules, for example, methyl chloride, at a high level of theory can take hundreds of hours on a single computer node [10]. As a result of the already mentioned high degree of scaling of QM calculations, there is an inherent trade-off that must be made between the degree of accuracy of the QM calculation, the complexity of the molecule, and the available computer time. Some experience is required to make that choice.

Once an appropriately large collection of points on the energy landscape have been obtained, the next step is to develop an analytical representation that will allow interpolation between the calculated

points, and perhaps extrapolation. (As the long-range interactions between neutral molecules decay at approximately r^{-6} , where r is the site–site separation distance, extrapolation is generally not a serious problem.) The most commonly used force fields are of the site–site form, in which the sites can be single atoms (all atom potentials) or groups of atoms such as a methyl CH_3 group (united atom potentials), and may include intermediate sites placed along bonds to represent electrostatic charges, dipole moments or just to better represent the quantum mechanically calculated energies. The site–site interaction potentials are usually the combination of an electrostatic repulsion including the site charges (which have also been calculated from QM), a hard-core repulsion, and a van der Waals dispersion contribution. The models used may be as simple as a Lennard–Jones 6-12 potential plus a Coulomb-like interaction, though much more sophisticated force fields are frequently used.

There are some tricks-of-the-trade needed here. For example, to calculate the interaction energy between two molecules, one first calculates the energy of each of the separated molecules, and then of the pair of interacting molecules. However, the accuracy of a QM calculation depends on the size of basis set used. Therefore, if the interaction energy was computed by calculating the energy of each molecule separately with its own basis set, and then of the pair of molecules with the basis sets for both molecules, a less accurate result is obtained than if the energy of each separated molecule had also been calculated with the basis sets for both molecules. In this way, the so-called basis set superposition error [11] is minimized using a counterpoise correction [12]. Also, an extrapolation method has been developed to allow the interaction energies calculated at moderate levels of electron correlation and moderate-size basis sets to be extrapolated to more accurate values than would be obtained with a larger basis set [13].

A question that arises is whether the points chosen for the energy landscape calculations are the appropriate ones; that is, have the attractive and repulsive regions been adequately sampled? Generally, we do not know this in advance. A procedure that we have found works reasonably well is to choose a collection of points (center-to-center separations and relative orientations of the molecules), fit a trial site–site interaction potential to those points, which is then used in a short simulation to obtain a center-of-mass radial distribution function (RDF), and see whether the center-of-mass separations chosen for the QM calculations have adequately sampled the RDF in the region up to and somewhat beyond the first minimum [14]. If not, additional center-of-mass separations (and orientations at these separations) are added, especially in the regions of the initial rise from zero of the RDF, its first maximum and in the region where the RDF is unity, additional QM calculations are done and an improved potential is obtained by refitting. Generally, we have needed only one such iteration. Also, if simulation software is not available, almost as good results can be obtained using the angle-averaged Boltzmann factor instead of the RDF to determine whether the energy landscape had been properly sampled.

A question that arises is what part of the potential energy surface is most important, and therefore must be fit accurately, for good physical properties predictions. While this can be more difficult to discern for complicated polyatomic molecules, one can obtain some insight from simulation results for spherical molecules. From a study [15] in which we perturbed a Lennard–Jones potential separately in the short-range repulsive, the well, and the long-range attractive regions, we found that perturbations in the short-range (repulsive) part of the potential do not result in significant changes to the calculated phase behavior, so that this region does not need to be over-weighted when fitting intermolecular potentials to *ab initio* energies. Decreasing the depth of the well (that is, decreasing the attraction) increases the vapor pressure, and results in a smaller phase envelope with a reduction in the critical temperature, an increase in the saturated vapor densities, and a decrease in the saturated liquid densities. While changes in the long-range portion of the potential produce the largest changes in the critical temperature, saturated vapor densities, and vapor pressures. Overall, the repulsive energies play a limited role in determining the phase behavior and critical properties, while the attractive energies strongly affect these properties, as would be expected. We presume that similar conclusions will apply to fitting the energy landscapes of more complicated molecules, but we have not made a systematic study.

Once points on the energy landscape have been computed and then fit, the next step is to test the accuracy of the potential obtained. The simplest test is to compare the calculated second virial coefficient, a strictly two-body property, with experimental data. Some results are shown in Figs. 1–3. We see in these figures that for systems without strong associative forces, such as hydrogen bonding, these “first-principles” predictions of the second virial coefficients can be quite accurate as for acetylene and methanethiol [14,16]; other examples have been given elsewhere. However, for methanol the predictions are less satisfactory [17]. The lower accuracy of these latter predictions was expected since methanol is a hydrogen-bonding fluid, and in such cases higher-level QM calculations with larger basis sets are required for the accurate calculation of interaction energies. It is, however, interesting to note that by introducing a single adjustable scaling parameter as a multiplicative factor to the total energy, quantitative agreement with the second virial coefficient can be obtained. There are other examples of second virial coefficient calculations from ab initio potentials in the literature. For example, the work of Meredith et al. [18] and Hermida-Ramon et al. [19] on HCl led to second virial coefficients that were in qualitative agreement with experiment, though better agreement was later obtained by Naicker et al. [20].

While there has been a large number of studies on water, Guillot [21] concluded that no ab initio model has been able to predict water properties with high accuracy. Even the recent POL5 model of Stern et al. [22] that combines fluctuating charges and polarizable dipoles gives large deviations from experimental values of virial coefficients. Wick and Schenter [23] found that when used in simulation, models based on quantum calculations under-predict the normal boiling point of water by more than 30 K.

Using the interaction models discussed above in Gibbs ensemble MC simulation, one can obtain vapor–liquid phase behavior and the thermodynamic properties of the coexisting phases. However, such simulations contain the assumption of pairwise additivity, that is, that the interaction energy of an assembly of molecules can be obtained by summing the energies of interacting pairs. Figures 1–3 also contain the results of using Gibbs ensemble MC simulation to predict the vapor pressure and vapor–liquid phase boundaries for the systems discussed earlier. What we see is that for acetylene and methanethiol the predictions are remarkably good. The vapor pressures are reasonably accurate, indeed very good for a completely first-principles prediction that is based on knowing nothing more than the structure of the molecules. From these results we conclude that, unless there has been a fortuitous cancellation of errors, the level of QM we have used to calculate the interaction energies and the fitting of those interaction energies has been satisfactory, and that for these fluids that do not hydrogen-bond, multibody effects (i.e., pairwise nonadditivity) are not important.

However, the results for methanol in Fig. 3 with the QM-based potential are less than satisfactory. There are two reasons for this. First, it is known that the accurate calculation of the interaction energies for hydrogen-bonding systems requires a higher level of QM calculations than systems that do not hydrogen-bond. Second, for systems that hydrogen-bond or otherwise associate, the pairwise additivity assumption is inaccurate. Snapshots taken during the simulation showed significant hydrogen bonding. Note that the results with a scaled potential are somewhat better, but still not satisfactory.

There are several ways to improve upon the pairwise additivity assumption, or at least try to compensate for it. One way, used by Leonhard and Dieters [24], is to calculate from QM the interactions between configurations of three molecules, from those results obtain a three-body potential, and use this in simulation. Another method is to use two-body potentials with a polarization correction [25]. In its simplest implementation, the permanent or instantaneous dipole in a central molecule is considered to affect the dipoles (or induce dipoles) in nearby molecules which then affect the dipole of the central molecule. By iteration, the interaction energy of the assembly of molecules is computed. Such an iterative procedure results in a computational penalty of almost an order of magnitude in MC simulations, but only about 20 to 30 % in a molecular dynamics (MD) simulation. This difference arises because all the molecules are moved in a single time step on MD so that the polarization calculation is implemented

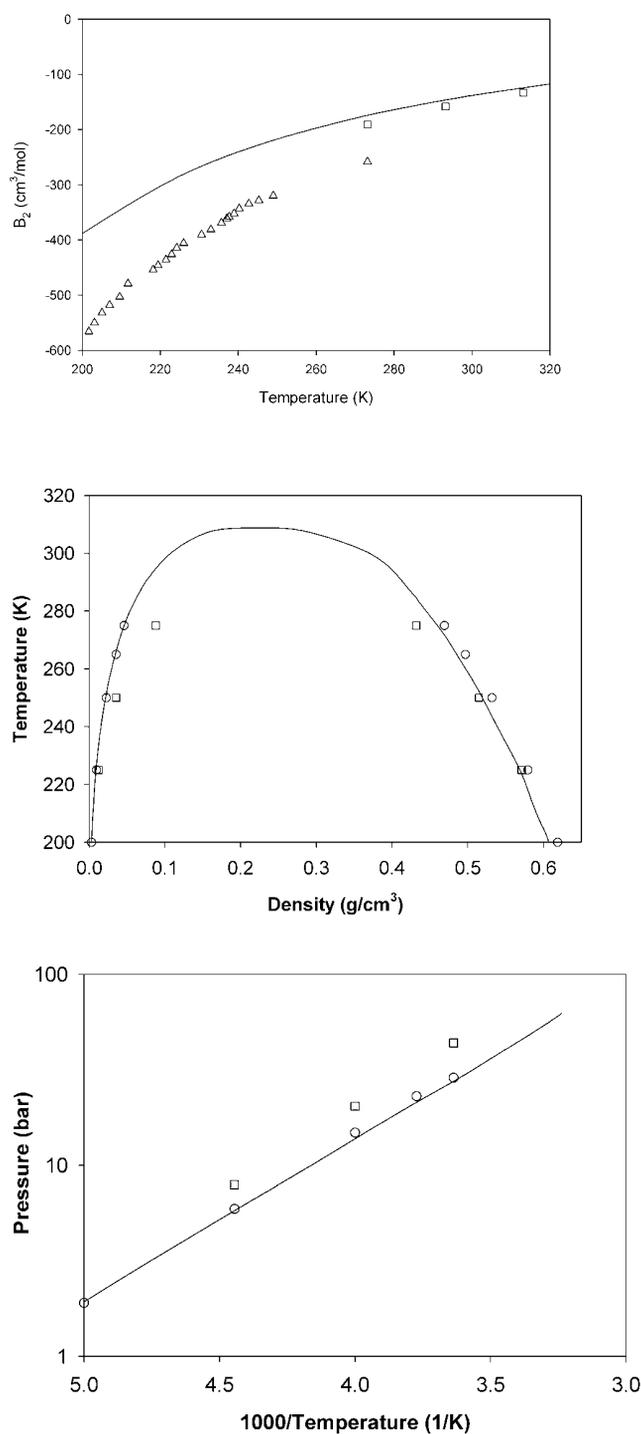


Fig. 1 Acetylene [14]: (a) second virial coefficients: the triangles and squares are two sets of experimental data, and the line is the results calculated using a QM-based potential; (b) vapor–liquid phase envelope: the line is the experimental results, the open squares are the results with the initial potential, and the open circles are the results with the final potential after adding additional interaction energy points as described in the text; (c) vapor pressures.

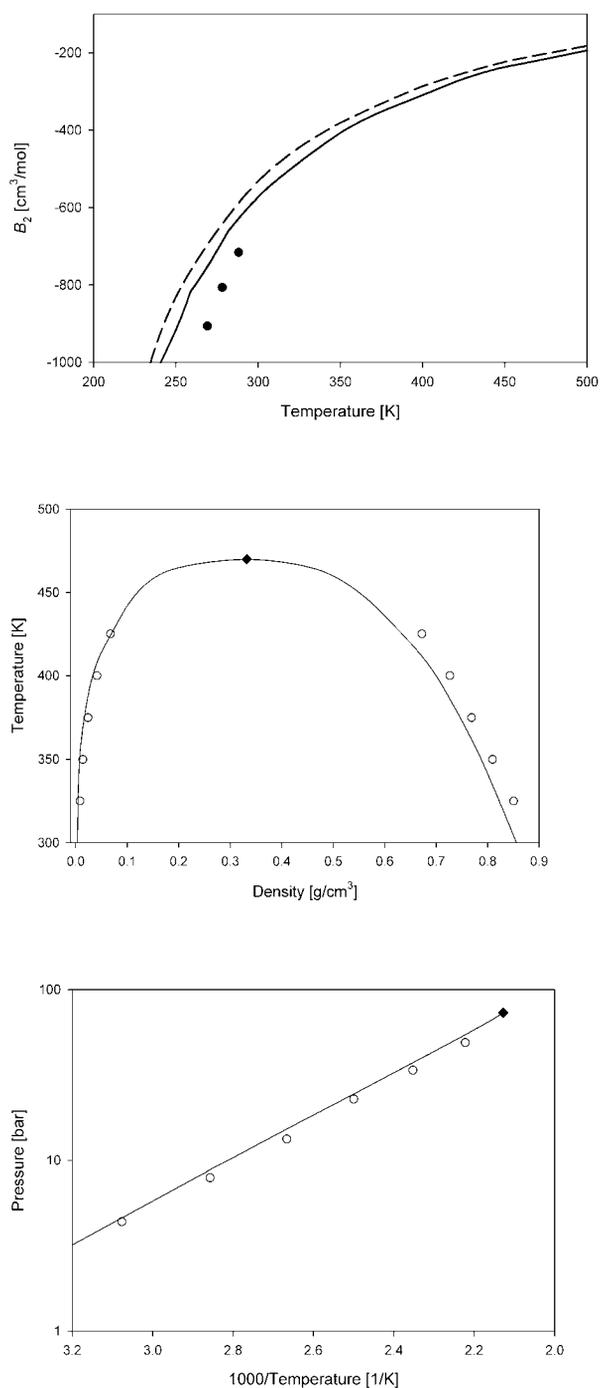


Fig. 2 Methanethiol [16]: (a) second virial coefficients; (b) phase envelope; and (c) vapor pressure. The lines are the experimental results, and the circles are the results using the QM-based potential. Filled symbols in (b) and (c) are the (estimated) critical points.

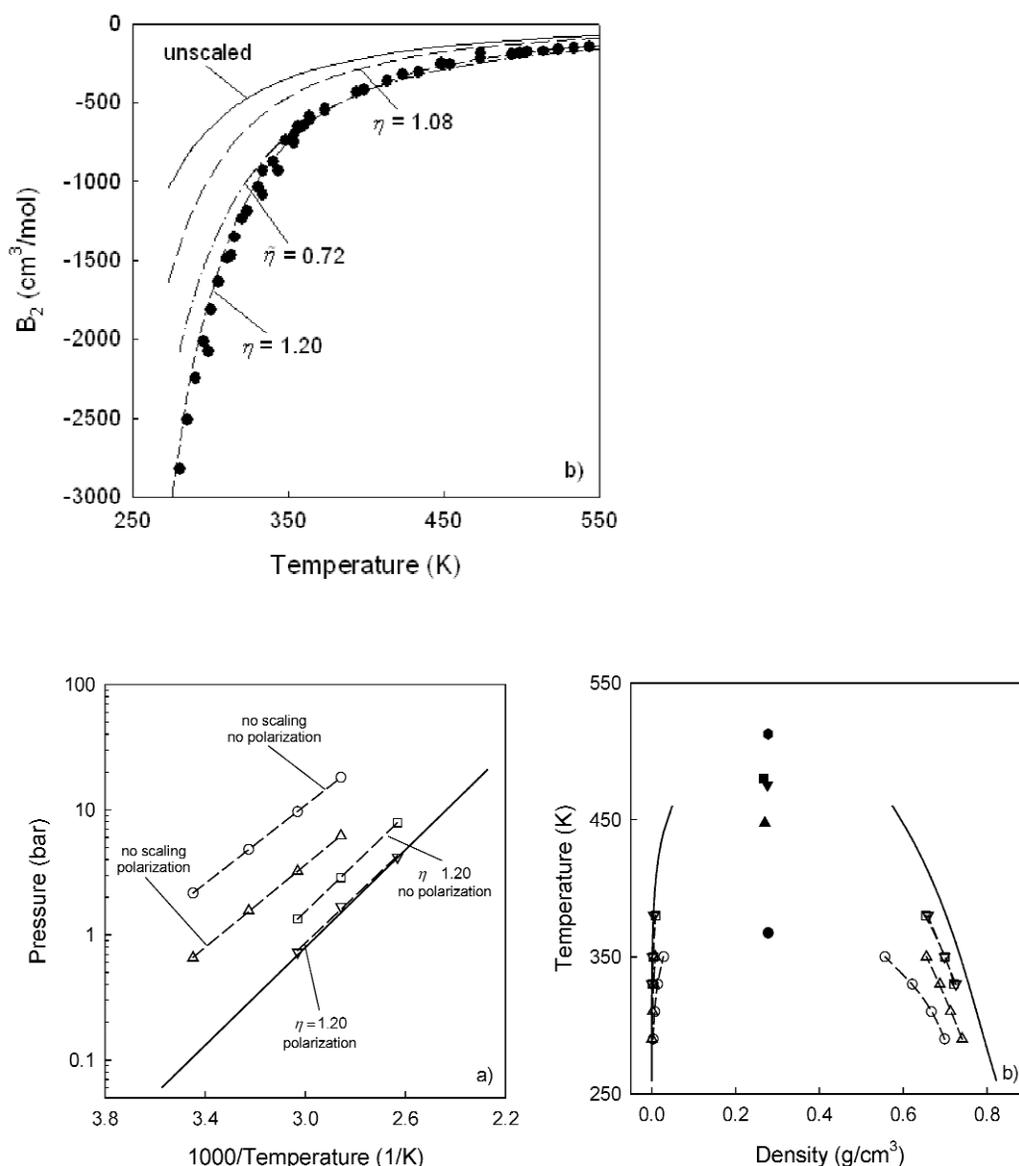


Fig. 3 Methanol [17]: (a) second virial coefficients. The circles are compilation from experimental values. Lines are calculated second virial coefficients using the QM potential calculated with the different values of the scale factors η ; (b) vapor pressures and (c) vapor–liquid phase envelope. The solid line and the filled diamond are the experimental data. The symbols denote simulation results using the QM-based pair potential with the following modifications: circles, no scaling and no polarization; triangles up, polarization and no scaling; squares, scaling ($\eta = 1.20$) and no polarization; and triangles down, scaling ($\eta = 1.20$) and polarization. Filled symbols in (b) and (c) are estimated critical points.

once on moving all the molecules, while molecules are moved one at a time in MC and the polarization calculation is done on the move of each molecule.

The results of using the polarization correction in the simulation of methanol are also shown in Fig. 3. There we see that while the agreement with experiment is still not as good as we would like, the relatively simple point polarization correction does improve the agreement with experiment, and pre-

sumably partially corrects for pairwise nonadditivity. The main conclusion is that pairwise nonadditivity is important for this and other hydrogen-bonding fluids. The addition of polarization and scaling, which introduces a single parameter fitted to the second virial coefficient, further improves the predictions of the vapor pressure and phase boundary.

Hydrogen fluoride (HF), because of its strong hydrogen bonding, results in complications in the QM calculations and in simulation due to nonadditivity effects, is a particularly difficult fluid for which to make accurate first-principles-based predictions. Recent work on HF has included that of Wierchowski et al. [26,27]

QUANTUM MECHANICS ON-THE-FLY: THE CAR-PARRINELLO METHOD

The most rigorous simulation method, in principle, for eliminating the pairwise additivity assumption is that pioneered by Car and Parrinello [28], and is sometimes referred to as QM on-the-fly. In this simulation method, the interaction energy for the whole assembly molecules and the force on each molecule in the system is calculated from QM at each step in the simulation (time step in MD or a move in MC simulation). The important advantage of this method is that since the whole assembly of molecules is considered in the QM calculation, it does not contain the assumption of pairwise additivity. However, it is limited by the fact that accurate QM calculations for a large number of molecules is computationally extremely demanding, and such a calculation must be repeated at each simulation step. Consequently, presently low-level QM methods, such as density functional theory, which may not provide an accurate representation of the van der Waals or dispersion forces, and a limited number of molecules are used in the simulations. These limitations will disappear as computing power increases, which suggests that this will be the preferred method of simulation in the future.

A recent example of using the Car-Parrinello method is that of McGrath et al. [29], who performed MC simulations of saturated water at 473 K. The predicted liquid density was 29.4 % lower, the vapor density 26.6 % was greater than the experimental values, and the predicted enthalpy of vaporization was 8.3 % lower than the experimental value. This work has been extended to other temperatures [30], and the results show qualitative agreement with, but quantitative deviation from, the experimental data for all the properties studied. For example, the critical temperature of water, extrapolated from the simulation results, is 550 K, about 15 % lower than the experimental value.

An interesting recent suggestion [31] has been to use the Car-Parrinello method (with its limitations on number of molecules and level of quantum chemistry that can be used) for a short simulation, and then adjust a classical, effective two-body potential to produce approximately the same behavior. This pairwise additive potential is then used in simulations with a larger number of molecules and over a greater number of time steps.

USE OF QUANTUM MECHANICS FOR BIG MOLECULES

Molecular orbital (MO) QM calculations for large molecules at a high level of theory are demanding and may not be feasible with current computer technology. Consequently, hybrid methods are used to deal with this situation. The basic idea of all such methods is to split the molecule in regions. The properties of the "active" region believed to be responsible for a given phenomenon, such as the active site of an enzyme, are computed with a high level of theory, and the "non-active" region, the rest of the molecule, is treated at a lower level of theory. Though it is difficult to properly handle the transition from one region to the other. In the IMOMM method of Maseras and Morokuma [32], MO calculations are used for the "active" region and molecular mechanics (MM) for the "non-active" region. In the IMOMO method [33], MO calculations are used for both regions, but with different levels of theory. Further subdivision is possible, as in the ONIOM method by Svensson et al. [34], in which additional regions are defined and calculated at different levels of theory. A newer method, ONIOM-XS by Kerdcharoen and Morokuma [35] in which XS denotes exchange of solvents, has been recently proposed that is poten-

tially useful for MC simulations of condensed phases. This method provides a way to account for particle exchange between the QM and MM regions of the model. A review with applications of these types of methods is provided by Morokuma [36].

USE OF QUANTUM MECHANICS TO DETERMINE PARAMETERS IN EXISTING THERMODYNAMIC MODELS

The first use in my research group [37,38] of QM methods in applied thermodynamic calculations was an attempt to improve group contribution methods, such as UNIFAC [39,40]. The general observation was that group contribution methods became less accurate when there was more than a single strong or polar functional group on a molecule. From relatively simple single-molecule, ideal gas QM calculations, we could see that the electrostatic charge on a functional group could change significantly depending on its neighboring groups in the same molecule, especially if the neighboring groups were polar, and this would affect its interactions with other functional groups. This violates the fundamental group contribution assumption that the interaction of a functional group with others should be the same in all molecules in which the group appears. This led us to suggest that instead of the usual empirical approach of identifying functional groups, one should choose functional groups so that they have no net charge. In general, this led to larger functional groups, for example, $-\text{CH}_2\text{OH}$ rather than $-\text{OH}$. This suggestion has never been exploited, though there has been considerable effort devoted to different approaches, for example, that of Kang et al. [41], that corrects group contribution methods for (at least) first-neighbor groups.

There are a number of other examples in the chemical engineering literature of using QM to improve applied thermodynamic predictions, or at least to determine the values of some parameters in commonly used models. For example, Fermeglia and Pricl [42] used QM and MM with MD computer simulations to estimate parameter values in the perturbed hard-sphere chain theory (PHSCT) equation of state [43] for chloro-fluoro-hydrocarbons. Fermeglia et al. [44] have also developed ab initio-based force fields for a number of alternative refrigerants. In a series of papers, Wolbach and Sandler [45,46] used the results of MO calculations to determine the values of the association parameter in the statistical association fluid theory equation of state for mixtures containing water, methanol, and other substances. Also, Yarrison and Chapman [47] have used the results of QM calculations to determine parameter values in two other forms of the statistical association fluid theory equation of state.

Another, very different approach was taken by Sum and Sandler [48]. In that work, the minimum energy configuration for a cluster of 8 molecules, 4 of each species, was obtained, and then nearest-neighbor interaction energies of those conformations were computed at a higher level of MO theory and averaged. The interaction energies so obtained were then used to set parameter values in the Wilson [49] and UNIQUAC [50] activity coefficient models to predict vapor-liquid equilibrium. It was found that the predictions so obtained with the UNIQUAC equation were almost as accurate as a direct correlation of experimental data using that model, while the predictions with the Wilson model were quite inaccurate. This led the authors to conclude that the theoretical basis of the UNIQUAC model was superior to that of the Wilson model, and also suggested that the methods they developed could be used to obtain missing interaction parameters in the UNIFAC model [39], which is the group contribution version of the UNIQUAC model.

CONTINUUM SOLVATION MODELS

The discussion so far has been of a completely atomistic description, both in the QM and in simulation. A different way of proceeding is based on the prediction of the free energy of solvation, that is, the free energy change on moving a molecule from an ideal gas into a liquid. In these calculations, the solvent has generally been treated as a continuum characterized by macroscopic properties such as its dielectric constant. If the liquid solvent is the same species as the molecule, the free energy change is related

to its vapor pressure, while if the liquid is another component, the solvation free energy change is related to the Henry's law constant of the solute in the solvent. Similarly, the difference in solvation free energy for the solute in a mixture and in its own pure liquid is related to its activity coefficient at infinite dilution, and the difference in solvation free energies of the species between water and octanol saturated with water is proportional to its octanol-water partition coefficient.

Until recently, the solvation process was generally modeled to occur in two steps: first, the charges on the solute were turned off and the resulting hard, uncharged molecule particle was inserted into the solvent; and then the charges were turned on. This form of the model was based on the work of Tomasi and coworkers [53,54] and Truhlar and coworkers [53,54]. In this model, the first step requires the calculation of the free energy of creating a cavity of the proper shape and volume in the solvent to accept the solute, and is referred to as the cavity formation free energy. In our initial work, we used the Guggenheim-Staverman expression, as in UNIQUAC and UNIFAC, for the cavity free energy. The free energy change of the second step is referred to as the charging free energy and was calculated from QM, for which we used density functional theory in the GAMESS program [5]. Also, in these calculations, and others to be considered later, it is assumed that, except for large molecules, there is only a negligible free energy change due to the fact that the rotational and vibrational motions of the solute molecule may change when it is transferred from an ideal gas to a solution.

Without dwelling on the details, as a result of extensive QM calculations, we found that the charging free energies for a molecule type in a given solvent could be correlated to its surface area [55,56], though, there needed to be a separate correlation for each solute type in each solvent. The results of using these very simple correlations are surprisingly good for molecules with only a single polar functional group as shown in Fig. 4a. This correlation has been extended to octanol-water partition coefficients. More recently, Nanu and de Loos [57] and Nanu et al. [58] have developed this method further, for the use of infinite dilution activity coefficients, especially of aroma compounds in water.

However, there were two problems with this method. First, it was not very accurate for compounds with several strong, polar functional groups. We developed a correction for this using the QM calculated charge and dipole moment on functional group [55,56] based on a model by Kirkwood [59]. The utility of this correction is shown in Fig. 4b, and also in Fig. 5 for the Henry's law constants for 395 chemicals in water. However, the second, and more serious problem, with the method is that the QM solvation free energy calculation has to be repeated for each new solvent, and for each composition in a mixed solvent.

These problems do not appear in the continuum solvation model developed recently by Klamt et al. [60–62] referred to as COSMO-RS and the variants by others [63]. In this model, the solvation calculation is a three-step process: first, the charges on the solute are turned off and the resulting hard, uncharged molecule particle is inserted into a perfect conductor (i.e., a solvent with an infinite dielectric constant); second, the charges are turned on (this is the QM COSMO calculation done using density functional theory); and third, the result is corrected for the properties of the real solvent. An important advantage of this method is that the time-consuming QM calculation for each molecule needs to be done only once (in a perfect conductor), is independent of the solvent, and so can be stored for use with any solvent or solvent mixture in the quick third step of the calculation. In fact, once a library of QM COSMO calculations has been established, the calculation of phase behavior is comparable in time to group contribution methods such as UNIFAC and requires only a few universal parameters. Also, without modifications, this model provides predictions of essentially equal accuracy for molecules with a single strong functional group and for molecules with a multiple polar functional groups without any modifications. There are numerous examples in the literature of the use of this method to predict phase behavior; we show only two in Fig. 6. Interestingly, for the second system in that figure, water + *n*-methylformamide, UNIFAC predictions could not be made because of the unavailability of group-group interaction parameters. The recent book by Klamt [64] provides a nice description of the method that I consider this to be the first fundamentally new thermodynamic model to be developed in more than a

decade, and many examples of its use. As this model is further developed to improve its accuracy, it is likely to be a replacement for group contribution models.

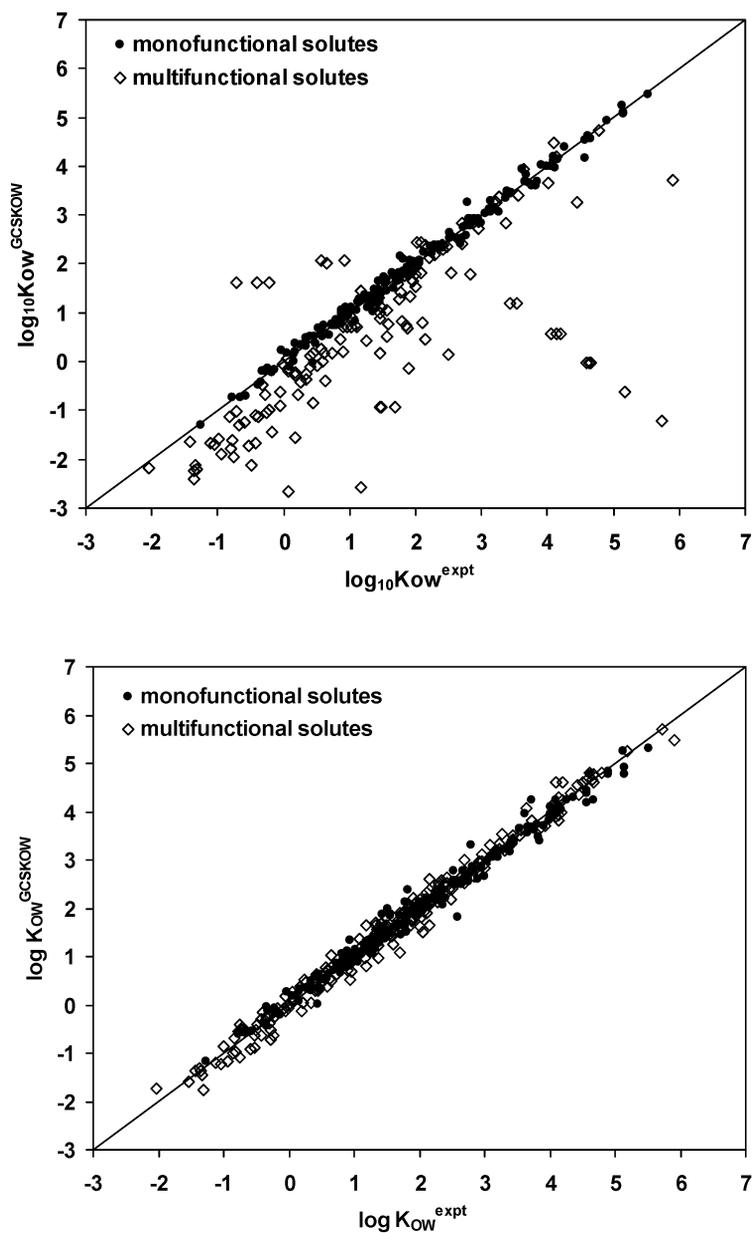


Fig. 4 Prediction from the GCSKOW model [55] with simple group contribution method for 177 monofunctional and 145 multifunctional compounds. (a) Without multipole corrections, and (b) with multipole corrections. (Here, by multifunctional compound, we mean a compound with more than a single non-alkyl group.)

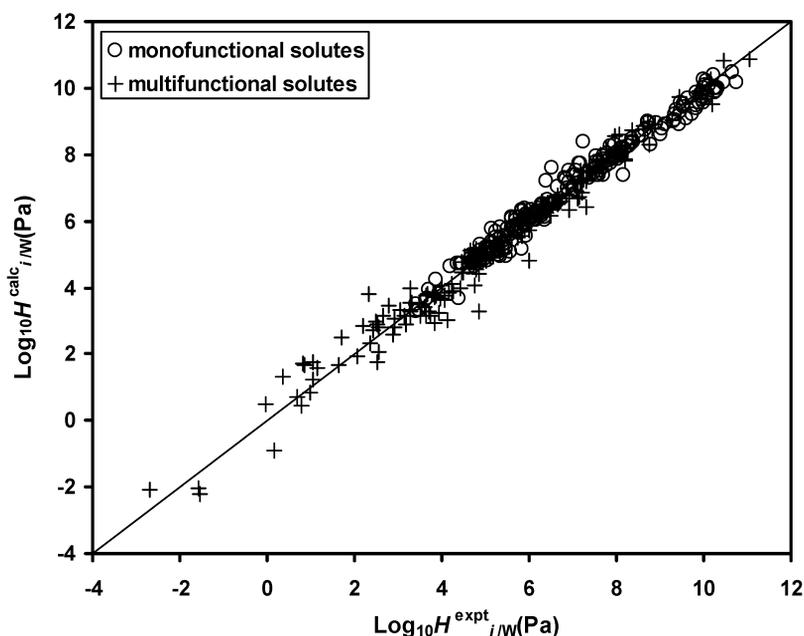


Fig. 5 Comparison between calculated and experimental Henry's law constants for 395 compounds in water at 298.15 K using a continuum solvation model with multipole corrections [56].

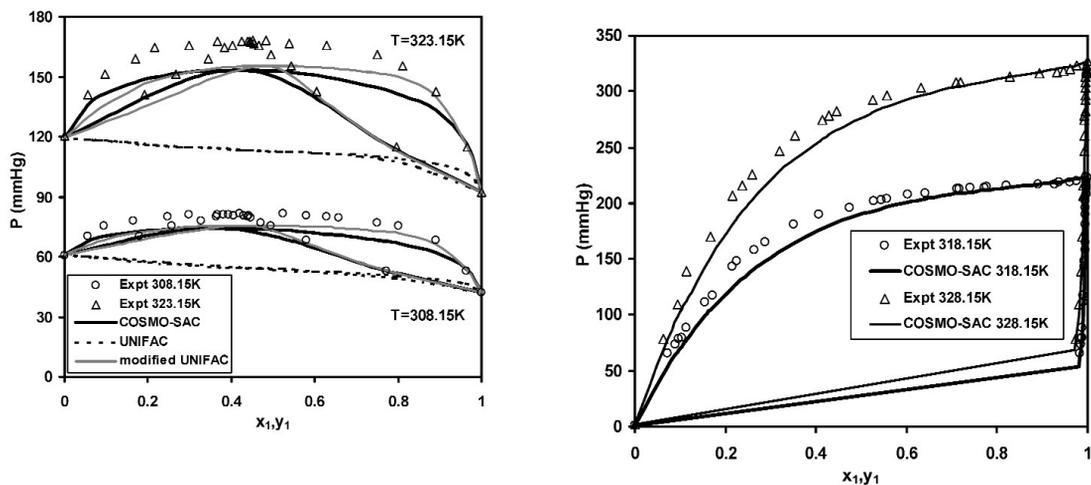


Fig. 6 Comparison of vapor–liquid equilibrium predictions from COSMO-SAC [63], UNIFAC [39], and modified UNIFAC models for water (1)/1,4-dioxane (2) at temperatures 308.15 and 323.15 K. Vapor–liquid equilibrium predictions from COSMO-SAC for benzene (1)/*n*-methylformamide (2) (UNIFAC parameters were unavailable for *n*-methylformamide).

SUMMARY

We have tried to give a brief overview of the uses of QM in chemical thermodynamics. The traditional application to single-molecule ideal gas properties, when done properly, can be expected to result in heats of formation accurate to about 1 kcal/mol. The ab initio prediction of thermodynamic properties that result from the interactions between molecules require considerably greater effort and much greater

computational resources than a single-molecule, ideal gas calculation. One method is to use QM to calculate points on the energy landscape between two interacting molecules, which is then fitted to a potential function and can be used to calculate the second virial coefficient, an exact calculation, or in computer simulation to calculate condensed-phase properties which typically involves the assumption of pairwise additivity. An alternate, and in principle more rigorous, method is that of Car and Parrinello in which the interaction energy among the whole assembly of molecules is computed at each step in the simulation. However, at present, the accuracy of this method is limited as a result of the computer resources needed so that applications have been only to small numbers of small molecules, and using density functional theory.

Another area in which QM has been used is to determine the values of some of the parameters in existing thermodynamic models. In this way, parameters have been determined in activity coefficient (UNIQUAC and Wilson) and equation of state (SAFT and PHCT) models. However, presently, the most easy-to-use and in many ways most useful QM-based model for thermodynamicists is based on the continuum solvation model pioneered by Klamt.

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Note: The literature on the use of QM related to thermophysical properties is very extensive. The reference list below has been chosen by the authors to be representative of the relevant work, and is not meant to be exhaustive.

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