This expression holds because of the pairwise additivity of the forces between point charges. The expression would not necessarily hold if the charges were themselves charge distributions because the addition of further charges could polarize the existing ones and so alter the forces already calculated.

Whatever the case, U_{tot} will depend on the coordinates of all the charges present

$$U_{\text{tot}} = U_{\text{tot}}(\mathbf{R}_1, \mathbf{R}_2, \ldots, \mathbf{R}_n) \tag{2.30}$$

and it is always possible to write a formal expansion

$$U_{\text{tot}}(\mathbf{R}_1, \mathbf{R}_2, \ldots, \mathbf{R}_n) = \sum_{\text{pairs}} U^{(2)}(\mathbf{R}_i, \mathbf{R}_j) + \sum_{\text{triples}} U^{(3)}(\mathbf{R}_i, \mathbf{R}_j, \mathbf{R}_k) + \cdots + U^{(n)}(\mathbf{R}_1, \mathbf{R}_2, \ldots, \mathbf{R}_n) \tag{2.31}$$

involving distinct pairs, triples, etc. of particles. The $U^{(2)}$ terms are referred to as the pair contributions, the $U^{(3)}$s are the three body terms and so on. Terms higher than the second are identically zero for the interaction between point charges.

3 The Forces Between Molecules

When molecules are near enough to influence one another, we need to concern ourselves with the balance between the forces of attraction and repulsion. We know that such forces exist, for otherwise there would be nothing to bring molecules together into the solid and liquid states, and all matter would be gaseous. A study of the forces between atomic or molecular species constitutes the subject of *intermolecular forces*.

People have speculated about the nature of intermolecular forces ever since the ideas of atoms and molecules first existed. Our present ideas, that molecules attract at long range but repel strongly at short range, began to emerge in the nineteenth century due to the experimental work of Rudolf J. E. Clausius and Thomas Andrews. It was not until the early twentieth century, when the principles of quantum mechanics became established, that we could truly say that we understood the detailed mechanism of intermolecular forces.

Although we talk about intermolecular *forces*, it is more usual and convenient to focus on the *mutual potential energy*, discussed in Chapter 2. If we start with two argon atoms at infinite separation, then their mutual potential energy at separation R tells us the energy change on bringing the atoms together to that distance from infinity.

Even for the simplest pair of molecules, the intermolecular mutual potential energy will depend on their relative orientations in addition to their separation. Perhaps you can now see why the study of intermolecular forces has taken so much effort by so many brilliant scientists, over very many years.

3.1 The Pair Potential

So, to start with, we concern ourselves with two atomic or molecular species, A and B, and ask how they interact. No chemical reaction is implied, and I should say straightaway that I am not going to be concerned with bond making and bond breaking in this chapter. That is the subject of *valence theory*. In the (unusual) case that the two species A and B concerned are ions, you may think that the problem is more or less solved. We simply calculate their mutual Coulomb potential energy as discussed in Chapter 2

$$U_{AB} = \frac{1}{4\pi\epsilon_0}\frac{Q_A Q_B}{R_{AB}} \tag{3.1}$$

You would certainly be on the right lines in this approach except that ions aren't point charges and they can be polarized just like any other continuous charge distribution. But, as I explained in Chapter 2, we rarely have to concern ourselves with ions and to get started we will consider the very simple case of a pair of like atoms (such as two argon atoms). We know from experiment that the general form of their mutual potential energy must be that shown in Figure 3.1.

This curve is meant to be schematic, and I have been careful not to quantify the axes. It has all the right features but we have yet to discover its precise form. We very often speak about the *pair potential*, and write it $U(R)$, where R is the separation between the two atoms. The zero of $U(R)$, denoted by the horizontal line, is commonly taken to refer to the two atoms at infinity. We often characterize the curve in terms of a small number of parameters; for example, the collision diameter σ being the distance at which $U(R) = 0$, the minimum R_{min}, and minus the value of $U(R)$ at R_{min} (often written ε, and as defined is a positive quantity).

We now need to investigate more closely the precise form of this pair potential. The potential comprises a repulsive part (important for small R) and an attractive part (important for large R). It turns out that there are three major contributions to the attractive part, as we will see below.

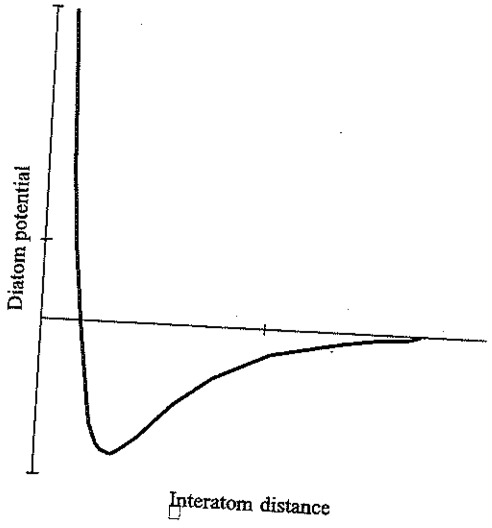

Figure 3.1 Schematic Ar–Ar interaction

3.2 The Multipole Expansion

Suppose that we have two molecules with centres a distance R apart (Figure 3.2). The distance R is taken to be large compared with a molecular dimension. Each molecule consists of a number of charged particles, and in principle we can write down an expression for the mutual potential energy of these two molecules in terms of the pair potentials between the various point charges. The basic physical idea of the *multipole expansion* is to make use of the fact that several of these particles go to form molecule A, and the remainder to form molecule B, each of which has a distinct chemical identity. We therefore seek to write the mutual potential energy of A and B in terms of the properties of the two molecular charge distributions and their separation.

3.3 The Charge–Dipole Interaction

I can illustrate the ideas by considering an elementary textbook problem, namely the mutual potential energy of a simple small electric dipole and a point charge. Suppose that we have a simple dipole consisting of a pair of charges, Q_A and Q_B, aligned along the horizontal axis and equally separated from the coordinate origin by distance d. We introduce a third charge Q as shown in Figure 3.3, with the scalar distance R

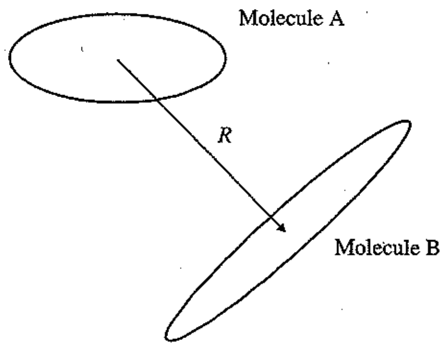

Figure 3.2 Two interacting molecules

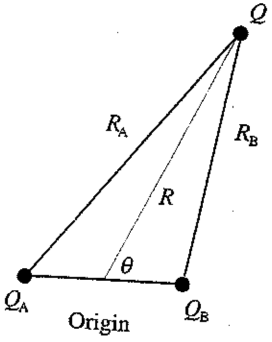

Figure 3.3 Charge–dipole interaction

from the origin. This point charge makes an angle θ with the electric dipole, as shown. The two point charges Q_A and Q_B have a mutual potential energy of

$$\frac{1}{4\pi\epsilon_0}\frac{Q_A Q_B}{2d} \tag{3.2}$$

but we are going to investigate what happens to the mutual potential energy of the system as we change the position vector of Q, and so we ignore this term since it remains constant.

The mutual potential energy U(charge–dipole) of the point charge and the electric dipole is given exactly by

$$U(\text{charge–dipole}) = \frac{1}{4\pi\epsilon_0}Q\left(\frac{Q_A}{R_A}+\frac{Q_B}{R_B}\right) \tag{3.3}$$

This can also be written in terms of R and θ as

$$U(\text{charge–dipole}) = \frac{1}{4\pi\epsilon_0}Q\left(\frac{Q_A}{\sqrt{(R^2+d^2+2dR\cos\theta)}}+\frac{Q_B}{\sqrt{(R^2+d^2-2dR\cos\theta)}}\right) \tag{3.4}$$

and once again, this is an exact expression.

In the case where the point charge Q gets progressively far away from the coordinate origin, we can usefully expand the two denominators using the binomial theorem to give

$$U(\text{charge–dipole}) = \frac{1}{4\pi\epsilon_0}Q\left(\frac{(Q_A+Q_B)}{R}+\frac{(Q_B-Q_A)d}{R^2}\cos\theta + \frac{(Q_A+Q_B)d^2}{2R^3}(3\cos^2\theta-1)+\cdots\right) \tag{3.5}$$

The first term on the right-hand side contains the sum of the two charges making up the dipole. Very often, we deal with simple dipoles that carry no overall charge, and this term is zero because $Q_A = -Q_B$. The second term on the right-hand side obviously involves the electric dipole moment, whose magnitude is $(Q_B - Q_A)d$. The third term involves the electric second moment whose magnitude is $(Q_B + Q_A)d^2$ and so on. The mutual potential energy is therefore seen to be a sum of terms; each is a product of a moment of the electric charge, and a function of the inverse distance. Hopefully, as R increases, the magnitude of the successive terms will become less and eventually the mutual potential energy will be dominated by the first few terms in the expansion.

In the more general case where we replace Q_A and Q_B with an arbitrary array of point charges $Q_1, Q_2, \ldots, Q_n$, whose position vectors are $\mathbf{R}_1, \mathbf{R}_2, \ldots, \mathbf{R}_n$ (or for that matter a continuous charge distribution), it turns out that we can always write the mutual interaction potential with Q as

$$U = \frac{Q}{4\pi\epsilon_0}\left\{\left(\sum_{i=1}^{n} Q_i\right)\frac{1}{R} - \left(\sum_{i=1}^{n} Q_i\mathbf{R}_i\right)\cdot \text{grad}\left(\frac{1}{R}\right) + \text{higher order terms}\right\} \tag{3.6}$$

The first summation on the right-hand side gives the overall charge of the charge distribution. The second term involves the electric dipole moment; the third term involves the electric quadrupole moment and so on.

3.4 The Dipole–Dipole Interaction

Consider now a slightly more realistic model for the interaction of two simple (diatomic) molecules, Figure 3.4. Molecule A consists of two point charges, Q_{1A} and

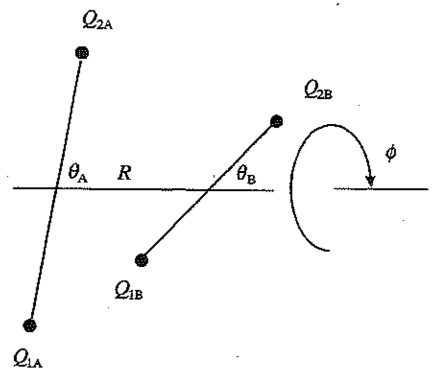

Figure 3.4 Multipole expansion for a pair of diatomics

Q_{2A}, and molecule B consists of two point charges, Q_{1B} and Q_{2B}. The overall charge on molecule A is therefore $Q_A = Q_{1A} + Q_{2A}$ with a similar expression for molecule B. The electric dipole moments of A and B are written $\mathbf{p}_A$ and $\mathbf{p}_B$ in an obvious notation, and their scalar magnitudes are written p_A and p_B. The second moments of the two molecules are each determined by a scalar value q_A and q_B, simply because they are linear.

Molecule A is centred at the origin, whilst molecule B has its centre a distance R away along the horizontal axis. The inclinations to the axis are θ_A and θ_B, and ϕ gives the relative orientation of the two molecules. The sizes of the two molecules are much less than their separation, so we can make the same approximations as for the small dipole. After some standard analysis we find that the mutual potential energy of A and B is

$$\begin{aligned}(4\pi\epsilon_0)U_{AB} = {} & \frac{Q_A Q_B}{R} + \frac{1}{R^2}(Q_B p_A \cos\theta_A - Q_A p_B \cos\theta_B) \\ & - \frac{p_A p_B}{R^3}(2\cos\theta_A \cos\theta_B - \sin\theta_A \sin\theta_B \cos\phi) \\ & + \frac{1}{2R^3}(Q_A q_B(3\cos^2\theta_B - 1) + Q_B q_A(3\cos^2\theta_A - 1)) \\ & + \cdots \end{aligned} \qquad (3.7)$$

The physical interpretation is as follows. The first term on the right-hand side gives the mutual potential energy of the two charged molecules A and B. The second term gives a contribution due to each charged molecule with the other dipole. The third term is a dipole–dipole contribution and so on.

If A and B correspond to uncharged molecules, then the leading term is seen to be the dipole–dipole interaction

$$(4\pi\epsilon_0)U_{AB,\text{dip-dip}} = -\frac{p_A p_B}{R^3}(2\cos\theta_A \cos\theta_B - \sin\theta_A \sin\theta_B \cos\phi) \qquad (3.8)$$

The sign and magnitude of this term depends critically on the relative orientation of the two molecules. Table 3.1 shows three possible examples, all of which have $\phi = 0$.

Table 3.1 Representative dipole–dipole terms for two diatomics

θ_A	θ_B	Relative orientations	Expression for dipole–dipole U
0	0	Parallel	$-2p_A p_B/4\pi\epsilon_0 R^3$
0	π	Antiparallel	$+2p_A p_B/4\pi\epsilon_0 R^3$
0	$\pi/2$	Perpendicular	0

3.5 Taking Account of the Temperature

We now imagine that the two molecules undergo thermal motion; we keep their separation R constant but allow the angles to vary. The aim is to calculate the average dipole–dipole interaction. Some orientations of the two dipoles will be more energetically favoured than others and we allow for this by including a Boltzmann factor $\exp(-U/k_B T)$, where k_B is the Boltzmann constant and T the thermodynamic temperature. It is conventional to denote mean values by 'carets' $\langle\cdots\rangle$ and the mean value of the dipole–dipole interaction is given formally by

$$\langle U_{AB}\rangle_{\text{dip-dip}} = \frac{\int U_{AB}\exp(-\frac{U_{AB}}{k_B T})\mathrm{d}\tau}{\int \exp(-\frac{U_{AB}}{k_B T})\mathrm{d}\tau} \qquad (3.9)$$

The integral has to be done over all possible values of the angles, keeping R fixed. After some standard integration, we find

$$\langle U_{AB}\rangle_{\text{dip-dip}} = -\frac{2p_A^2 p_B^2}{3k_B T(4\pi\epsilon_0)^2}\frac{1}{R^6} \qquad (3.10)$$

The overall value is therefore negative, and the term is inversely dependent on the temperature. It also falls off as $1/R^6$.

3.6 The Induction Energy

The next step is the case of two interacting molecules, one of which has a permanent dipole moment and one of which is polarizable but does not have a permanent electric dipole moment.

Figure 3.5 shows molecule A with a permanent dipole moment $\mathbf{p}_A$. I have indicated the direction of $\mathbf{p}_A$ in the diagram, and an arbitrary point P in molecule B. The dipole $\mathbf{p}_A$ is a distance R from point P, and makes an angle θ as shown. The molecules are sufficiently far apart for the precise location of the point P inside the second molecule to be irrelevant.

The basic physical idea is that the electric dipole $\mathbf{p}_A$ induces a dipole in molecule B, since B is polarizable. We evaluate the potential energy involved and finally average over all possible geometrical arrangements, for a fixed value of the intermolecular separation. The steps involved are as follows. The electrostatic potential due to the small dipole $\mathbf{p}_A$ is

$$\phi_A(\mathbf{R}) = \frac{1}{4\pi\epsilon_0}\frac{\mathbf{p}_A \cdot \mathbf{R}}{R^3}$$

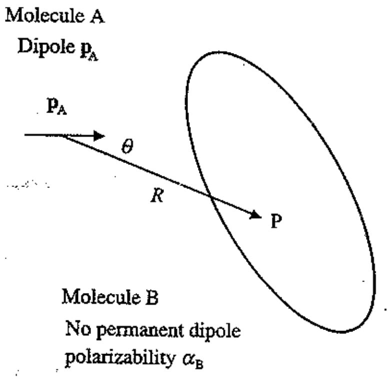

Figure 3.5 Dipole-induced dipole

This is related to the electrostatic field by the general formula

$$\mathbf{E}(\mathbf{R}) = -\text{grad}\,\phi(\mathbf{R})$$

and direct differentiation gives the following formula

$$\mathbf{E}_A(\mathbf{R}) = -\frac{1}{4\pi\epsilon_0}\left\{\frac{\mathbf{p}_A}{R^3} - 3\frac{\mathbf{p}_A \cdot \mathbf{R}}{R^5}\mathbf{R}\right\} \tag{3.11}$$

Molecule A therefore generates an electrostatic field in the region of molecule B, according to the above vector equation. The modulus of this vector at point P is

$$E_A = \frac{1}{4\pi\epsilon_0}\frac{p_A}{R^3}\sqrt{(1 + 3\cos^2\theta)} \tag{3.12}$$

This electrostatic field induces a dipole in molecule B. For the sake of argument, I will assume that the induced dipole is in the direction of the applied field (and so we need not worry about the fact that the polarizability is a tensor property). Calculation of the resulting mutual potential energy U_{AB} gives

$$U_{AB} = -\frac{1}{(4\pi\epsilon_0)^2}\frac{\alpha_B p_A^2}{R^6}\frac{1}{2}(3\cos^2\theta + 1) \tag{3.13}$$

Polarizabilities are positive quantities and so U_{AB} is negative for all values of θ at a given intermolecular separation This is quite different to the dipole–dipole interaction, where some alignments of the dipoles gave a positive contribution to the mutual potential energy and some gave a negative one.

Finally, we have to average over all possible alignments keeping the internuclear separation fixed. This averaging again has to be done using the Boltzmann weightings, and we find eventually an expression for the *induction* contribution to the mutual potential energy of A and B

$$\langle U_{AB}\rangle_{\text{ind}} = -\frac{1}{(4\pi\epsilon_0)^2}\frac{p_A^2\alpha_B}{R^6} \tag{3.14}$$

Note that the interaction falls off as $1/R^6$ just as for the dipole–dipole interaction, but this time there is no temperature dependence. For two identical A molecules each with permanent electric dipole $\mathbf{p}_A$ and polarizability $\boldsymbol{\alpha}_A$ the expression becomes

$$\langle U_{AA}\rangle_{\text{ind}} = -\frac{2}{(4\pi\epsilon_0)^2}\frac{p_A^2\alpha_A}{R^6} \tag{3.15}$$

This of course has to be added to the dipole–dipole expression of the previous section.

3.7 Dispersion Energy

It is an experimental fact that inert gases can be liquefied. Atoms don't have permanent electric moments, so the dipole–dipole and induction contributions to the mutual potential energy of an array of inert gas atoms must both be zero. There is clearly a third interaction mechanism (referred to as *dispersion*), and this was first identified by Fritz W. London in 1930.

The two contributions to the mutual potential energy discussed in previous sections can be described by classical electromagnetism. There is no need to invoke the concepts of quantum mechanics. Dispersion interactions can only be correctly described using the language of quantum mechanics. Nevertheless, the following qualitative discussion is to be found in all elementary texts.

> *The electrons in an atom or molecule are in continual motion, even in the ground state. So, although on average the dipole moment of a spherically-symmetrical system is zero, at any instant a temporary dipole moment can occur. This temporary dipole can induce a further temporary dipole in a neighbouring atom or molecule and, as in the case of the inductive interaction; the net effect will be attractive.*

Paul K. L. Drude gave a simple quantum mechanical description of the effect, and his theory suggests that the dispersion contribution can be written

$$\langle U\rangle_{\text{disp}} = -\left(\frac{D_6}{R^6} + \frac{D_8}{R^8} + \frac{D_{10}}{R^{10}} + \cdots\right) \tag{3.16}$$

The first term (which I have written D_6) is to be identified with the instantaneous dipole-induced dipole mechanism. The higher terms are caused by instantaneous quadrupole-induced quadrupoles, etc. According to Drude's theory

$$D_6 = -\frac{3\alpha^2\varepsilon_1}{4(4\pi\epsilon_0)^2} \tag{3.17}$$

In this expression, ε_1 is the first excitation energy of the atomic or molecular species concerned. The dispersion energy is again seen to be attractive and to fall off as $1/R^6$.

3.8 Repulsive Contributions

When two molecular species approach so closely that their electron clouds overlap, the positively charged nuclei become less well shielded by the negative electrons and so the two species repel each other. The repulsive term is sometimes written

$$U_{\text{rep}} = A\exp(-BR) \tag{3.18}$$

where A and B are specific to the particular molecular pair and have to be determined from experiment. The precise form of the repulsive term is not well understood; all that is certain is that it must fall off quickly with distance, and the exponential function is therefore a possible suitable candidate.

The total interaction is $U = U_{\text{rep}} + U_{\text{dip-dip}} + U_{\text{ind}} + U_{\text{disp}}$, which we can write

$$U = A\exp(-BR) - \frac{C}{R^6} \tag{3.19}$$

since all the attractive forces fall off as $1/R^6$. This is known as the exp-6 potential. In the *Lennard-Jones* (L-J) *12–6* potential, we take a repulsive term proportional to $1/R^{12}$ and so

$$U_{\text{L-J}} = \frac{C_{12}}{R^{12}} - \frac{C_6}{R^6} \tag{3.20}$$

Once again the coefficients C_{12} and C_6 have to be determined from experiments on the species under study. The L-J potential usually is written in terms of the well depth ε and the distance of closest approach σ as follows

$$U_{\text{L-J}} = 4\varepsilon\left(\left(\frac{\sigma}{R}\right)^{12} - \left(\frac{\sigma}{R}\right)^{6}\right) \tag{3.21}$$

The two L-J parameters σ and ε have been deduced for a range of atoms. The quantity ε/k_B (which has dimensions of temperature) is usually recorded in the literature rather than ε. Sample atomic parameters are shown in Table 3.2.

Table 3.2 Representative L-J atomic parameters

	$(\varepsilon/k_B)/\text{K}$	σ/pm
He	10.22	258
Ne	35.7	279
Ar	124	342
Xe	229	406

Table 3.3 L-J parameters for simple molecules

	$(\varepsilon/k_B)/\text{K}$	σ/pm
H_2	33.3	297
O_2	113	343
N_2	91.5	368
Cl_2	357	412
Br_2	520	427
CO_2	190	400
CH_4	137	382
CCl_4	327	588
C_2H_4	205	423
C_6H_6	440	527

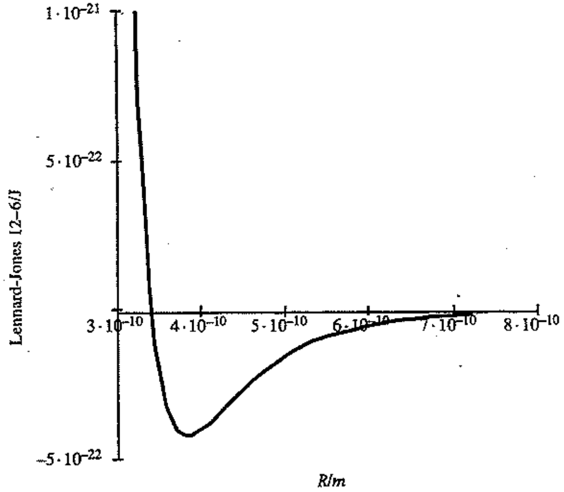

Figure 3.6 Lennard-Jones 12–6 potential for argon–argon

Over the years, people have extended these ideas to the interaction of simple molecules. Some caution is needed: the interaction between two molecules will generally depend on the precise details of their orientation, and the values given in Table 3.3 must be interpreted as some kind of geometrical average. These values were taken from the classic text *Molecular Theory of Gases and Liquids* [1]. Figure 3.6 shows a L-J 12–6 plot for argon–argon.

3.9 Combination Rules

A large number of L-J parameters have been deduced over the years, but they relate to pairs of like atoms. Rather than try to deduce corresponding parameters for unlike pairs, it is usual to use so-called *combination rules*, which enable us to relate the C_{12} and the C_6 parameters for an unlike-atom pair A–B to those of A–A and B–B. The use of such combination rules is common in subjects such as chemical engineering, and is widely applied to many physical properties.

There are three common combination rules in the literature, as follows

$$\begin{aligned} C_{12,ij} &= \left(\frac{R_i^*}{2}+\frac{R_j^*}{2}\right)^{12}\sqrt{\varepsilon_i\varepsilon_j} \\ C_{6,ij} &= 2\left(\frac{R_i^*}{2}+\frac{R_j^*}{2}\right)^{6}\sqrt{\varepsilon_i\varepsilon_j} \end{aligned} \tag{3.22}$$

where R_i^* is the minimum energy separation for two atoms of type i and ε_i the well depth;

$$\begin{aligned} C_{12,ij} &= 4(\sigma_i\sigma_j)^6\sqrt{\varepsilon_i\varepsilon_j} \\ C_{6,ij} &= 4(\sigma_i\sigma_j)^3\sqrt{\varepsilon_i\varepsilon_j} \end{aligned} \tag{3.23}$$

and finally

$$\begin{aligned} C_{6,ij} &= C\frac{\alpha_i\alpha_j}{\sqrt{\frac{\alpha_i}{N_i}}+\sqrt{\frac{\alpha_j}{N_j}}} \\ C_{12,ij} &= \tfrac{1}{2}C_{6,ij}(R_i+R_j)^6 \end{aligned} \tag{3.24}$$

where α_i is the dipole polarizability of atom i, N_i the number of valence electrons and R_i the van der Waals radius.

3.10 Comparison with Experiment

You will have got the idea by now that we have to determine the parameters in any pair potential by appeal to experiment. There are two kinds of experiment to consider. First, there are those that are essentially in the gas phase, where pairs of atoms genuinely interact with each other unencumbered by other species. This means that the total mutual potential energy is given by the sum of the interacting pairs.

Second, there are experiments that essentially relate to condensed phases, where the interacting particles are sufficiently close to raise doubts about the credibility of the pairwise additivity assumption.

3.10.1 Gas imperfections

The deviation of gases from perfect behaviour can be expressed in the form of a virial equation of state

$$\frac{pV}{nRT} = 1 + \frac{nB(T)}{V} + \frac{n^2C(T)}{V^2} + \cdots \tag{3.25}$$

where the virial coefficients $B(T), C(T), \ldots$ depend on the temperature and on the characteristics of the species under study. Here, n is the amount of substance, p the pressure, V the volume, R the gas constant and T the thermodynamic temperature. $B(T)$ is called the *second virial coefficient* whilst $C(T)$ is called the *third virial coefficient* and so on. They have to be determined experimentally by fitting the pVT data of the gas under study.

The virial equation of state has a special significance in that the virial coefficients can be related directly to the molecular properties. $B(T)$ depends on the pair potential $U(R)$ in the following way

$$B(T) = 2\pi\int_0^\infty\left(1-\exp\left(-\frac{U(R)}{k_BT}\right)\right)R^2\,dR \tag{3.26}$$

3.10.2 Molecular beams

In a molecular beam experiment, a beam of mono-energetic molecules is produced and allowed to collide either with other molecules in a scattering chamber, or with a similar beam travelling at right angles to the original beam. Measurements of the amount by which the incident beam is reduced in intensity, or the number of molecules scattered in a particular direction, allow determination of the parameters in the pair potential.

3.11 Improved Pair Potentials

The L-J 12–6 potential for a pair of interacting atoms

$$\begin{aligned} U_{\text{L-J}}(R) &= \frac{C_{12}}{R^{12}} - \frac{C_6}{R^6} \\ &= 4\varepsilon\left(\left(\frac{\sigma}{R}\right)^{12} - \left(\frac{\sigma}{R}\right)^{6}\right) \end{aligned}$$

contains two parameters (ε and σ, or C_{12} and C_6,) that have to be determined by experimental observation. The exp-6 model

$$U(R) = A\exp(-BR) - \frac{C}{R^6}$$

contains three parameters, which allows for a little more flexibility.

The Born–Mayer–Huggins potential

$$U(R) = A\exp\left(-BR\right) - \frac{C}{R^6} - \frac{D}{R^8} \tag{3.27}$$

contains four parameters.

More recent investigations have concentrated on pair potentials having many more disposable parameters, for example

$$U(r) = \exp\left(A\left(1 - \frac{R}{\sigma}\right)\right)\sum_{i=0}^{n} B_i\left(\frac{R}{\sigma} - 1\right)^i + \frac{C_6}{\left(D + \left(\frac{R}{\sigma}\right)^6\right)} + \frac{C_8}{\left(D + \left(\frac{R}{\sigma}\right)^8\right)} + \frac{C_{10}}{\left(D + \left(\frac{R}{\sigma}\right)^{10}\right)} \tag{3.28}$$

There is no obvious relationship between the various parameters in these different models; they all have to be determined by fitting experimental data. Roughly speaking, the more parameters the better.

3.12 Site–Site Potentials

The L-J potential plays an important role in the history of molecular modelling. Early work focused on atoms, but as I explained there were many ambitious attempts to model simple molecules as if they were in some way L-J atoms, and the parameters have to be interpreted as applying to some kind of average over molecular rotations (and presumably vibrations).

Suppose now that we want to try to understand the interaction between two dinitrogen molecules in more depth. In view of our discussion above, the instantaneous interaction energy clearly will depend on the separation of the two diatoms, together with their mutual angular arrangement in space.

Figure 3.7 shows two such dinitrogens, oriented arbitrarily in space with respect to each other. Nitrogen A and nitrogen B make up a stable diatom, as do atoms C and D. We ignore the fact that the molecules have vibrational energy, and the two diatoms are taken to be rigid. As a first approximation, the mutual potential energy of the pair of diatoms could be calculated by adding together the appropriate L-J parameters.

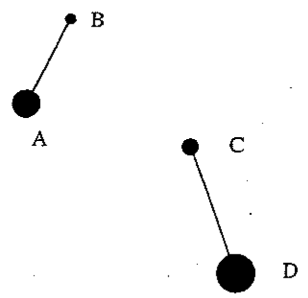

Figure 3.7 Two dinitrogen molecules, arbitrarily oriented

If I write as shorthand the L-J interaction between atoms A and C as

$$U_{\text{L-J}}(\text{A},\text{C}) = 4\varepsilon\left(\left(\frac{\sigma}{R_{\text{AC}}}\right)^{12} - \left(\frac{\sigma}{R_{\text{AC}}}\right)^{6}\right)$$

then the total interaction between the two diatomics is taken as

$$U_{\text{L-J}} = U_{\text{L-J}}(\text{A},\text{C}) + U_{\text{L-J}}(\text{A},\text{D}) + U_{\text{L-J}}(\text{B},\text{C}) + U_{\text{L-J}}(\text{B},\text{D}) \tag{3.29}$$

Such a potential is called a *site–site potential*. We will meet such potentials later in the book.

4 Balls on Springs

The theory of intermolecular forces relates to atomic and/or molecular species that are some distance apart (say, a few bond lengths). We saw in Chapter 3 that progress can be made in such a theory without normally invoking the concepts of quantum mechanics. If we truly want to understand why two atoms combine to give a chemical bond, and how bonds get broken and reformed in chemical reactions, then we enter the realms of *valence theory*. Quantum mechanics plays a dominant part in such discussions.

These are simple-minded comments and my arbitrary division of molecular interactions is subjective. At first sight, the stability of an NaCl ion pair can be explained in terms of elementary electrostatics, and we can usefully model argon liquid without recourse to quantum mechanics (apart from the London dispersion potential, which is a 'pure' quantum mechanical effect). A C—C bond in ethane is at first sight a quantum mechanical animal, and we will certainly have to invoke quantum mechanical ideas to explain the reaction of ethene with dichlorine. But there are grey areas that I can bring to your attention by considering the phenomenon of hydrogen bonding. The hydrogen bond is an attractive interaction between a proton donor X—H and a proton acceptor Y in the same or a different molecule

$$\mathrm{X—H \cdots Y}\ .$$

The bond usually is symbolized by three dots, as shown above, in order to reconcile the existence of compounds such as

$$\mathrm{NH_3 \cdots HCl}$$

with the trivalence of nitrogen, the divalence of oxygen in oxonium salts and other compounds that apparently break the classical valence rules. Hydrogen bonds typically have strengths of $10–100\,\mathrm{kJ\,mol^{-1}}$. The lone pairs of oxygen and nitrogen and the partially charged character of the proton were eventually recognized as the sources of this bond. The first reference to this 'weak bond' were made by W. M. Latimer and W. H. Rodebush in 1920 [2].

The individual monomers X—H and Y retain their chemical identity to a large extent on hydrogen bond formation. In other words, no new covalent bond gets made. A great deal of evidence suggests that simple electrostatic models of the H bond give perfectly acceptable quantitative descriptions of the structure, vibrations and electric dipole moments of such hydrogen-bonded species. The hydrogen-bonded species

$$\mathrm{FHF^-}$$

is well known and has been well studied, but it cannot be written

$$\mathrm{F{-}H\cdots F^-}$$

because the proton is equally shared between the two fluorine atoms. Such a species is best thought of as covalently bound, and has to be treated by the methods of molecular quantum theory.

Having warned about bond breaking and bond making, I should tell you that a great deal of molecular modelling is concerned with the prediction and rationalization of molecular bond lengths and bond angles. Here we usually deal with isolated molecules in the gas phase and the theoretical treatments often refer to 0 K. A surprising amount of progress can be made by treating molecules as structureless balls (atoms) held together with springs (bonds). The array of balls and springs is then treated according to the laws of classical mechanics. Such calculations are remarkably accurate, and are taken very seriously.

4.1 Vibrational Motion

To get started, consider a particle of mass m lying on a frictionless horizontal table, and attached to the wall by a spring, as shown in Figure 4.1. The particle is initially at rest, when the length of the spring is R_e (where the subscript 'e' stands for equilibrium). If we stretch the spring, it exerts a restoring force on the particle, whilst if we compress the spring there is also a force that acts to restore the particle to its equilibrium position. If R denotes the length of the spring, then the extension is $R - R_e$, and if F_s is the restoring force due to the spring, then it is often observed experimentally that the force is directly proportional to the extension

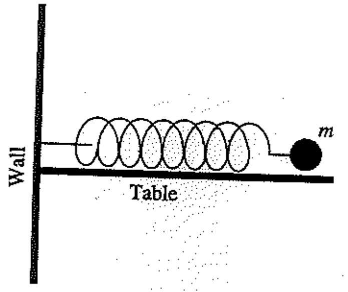

Figure 4.1 Ball attached to the wall by a spring

$$F_s = -k_s(R - R_e) \tag{4.1}$$

The constant of proportionality k_s is called the force constant and it tells us the strength of the spring. This law is known as *Hooke's Law* and it applies to very many springs made from many different materials. It invariably fails for large values of the extension, but is good for small deviations from equilibrium.

Suppose that we now set the particle in motion, so that it oscillates about R_e. According to Newton's second law we have

$$m\frac{\mathrm{d}^2R}{\mathrm{d}t^2} = -k_s(R - R_e) \tag{4.2}$$

This second-order differential equation has the general solution

$$R = R_e + A\sin\left(\sqrt{\frac{k_s}{m}}t\right) + B\cos\left(\sqrt{\frac{k_s}{m}}t\right) \tag{4.3}$$

where A and B are constants of integration. These constants have to be fixed by taking account of the *boundary conditions*. For example, if the particle starts its motion at time $t = 0$ from $R = R_e$, then we have

$$R_e = R_e + A\sin\left(\sqrt{\frac{k_s}{m}}\,0\right) + B\cos\left(\sqrt{\frac{k_s}{m}}\,0\right)$$

from which we deduce that $B = 0$ for this particular case. Normally we have to find A and B by a similar procedure.

The trigonometric functions sine and cosine repeat every 2π and a little manipulation shows that the general solution of Equation (4.3) can also be written

$$R = R_e + A\sin\left(\sqrt{\frac{k_s}{m}}\left(t + 2\pi\sqrt{\frac{m}{k_s}}\right)\right) + B\cos\left(\sqrt{\frac{k_s}{m}}\left(t + 2\pi\sqrt{\frac{m}{k_s}}\right)\right)$$

The quantity $\sqrt{k_s/m}$ has the dimension of inverse time and obviously it is an important quantity. We therefore give it a special symbol (ω) and name (the *angular vibration frequency*). We often write the general solution as

$$R = R_e + A\sin(\omega t) + B\cos(\omega t) \tag{4.4}$$

A typical solution is shown as Figure 4.2 (for which I took $A = 1\,\mathrm{m}$, $B = 0$, $m = 1\,\mathrm{kg}$ and $k_s = 1\,\mathrm{N\,m^{-1}}$). Such motions are called *simple harmonic*. At any given time, the displacement of the particle from its equilibrium position may be non-zero, but it should be clear from Figure 4.2 that the average value of the displacement $R - R_e$ is

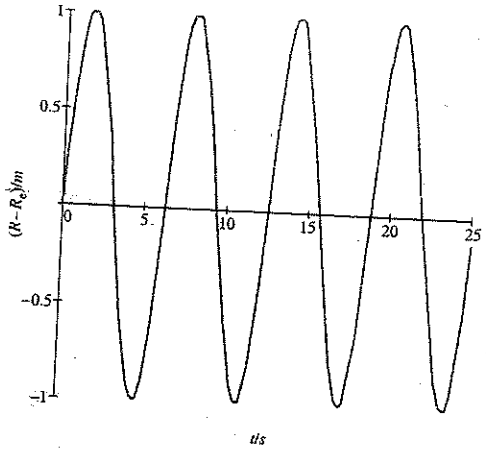

Figure 4.2 Simple harmonic motion

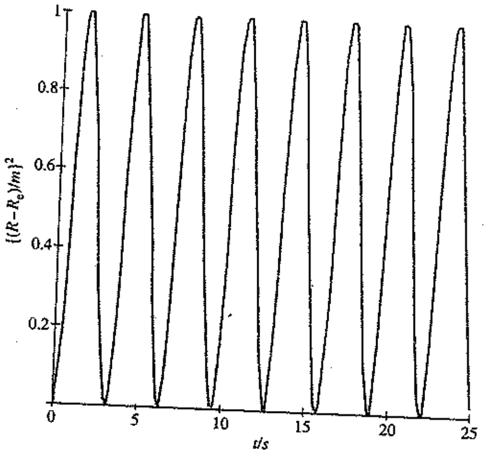

Figure 4.3 Variation of $(R - R_e)^2$ with time

zero. As noted in Chapter 3, it is usual to denote average values by $\langle \cdots \rangle$ and so we write

$$\langle R - R_e \rangle = 0$$

It should also be clear from Figure 4.3 that the average value of $(R - R_e)^2$ is not zero. A direct calculation using $\langle \sin^2(\omega t) \rangle = \frac{1}{2}$ gives

$$\langle (R - R_e)^2 \rangle = \tfrac{1}{2}(A^2 + B^2) \tag{4.5}$$

4.2 The Force Law

If we use the general one-dimensional result that links force and mutual potential energy

$$U(x) = -\int F(x)\mathrm{d}x$$

we find

$$U(R) = U(R_e) + \tfrac{1}{2}k_s(R - R_e)^2 \tag{4.6}$$

where $U(R_e)$ is the value of $U(R)$ at the equilibrium position. As mentioned earlier, we often set this constant of integration arbitrarily to zero and so

$$U(R) = \tfrac{1}{2}k_s(R - R_e)^2 \tag{4.7}$$

Because the motion is simple harmonic, we refer to this potential as a *harmonic potential*. The potential energy varies over each cycle, in the same way as shown in Figure 4.3. The average value of the potential energy over a cycle is

$$\begin{aligned}\langle U(R) \rangle &= \tfrac{1}{2}k_s\langle (R - R_e)^2 \rangle \\ &= \tfrac{1}{4}(A^2 + B^2)\end{aligned}$$

Finally, the kinetic energy T is given by

$$T(R) = \tfrac{1}{2}m\left(\frac{\mathrm{d}R}{\mathrm{d}t}\right)^2$$

The average value is

$$\begin{aligned}\langle T(R) \rangle &= \tfrac{1}{4}m\omega^2(A^2 + B^2) \\ &= \tfrac{1}{4}k_s(A^2 + B^2)\end{aligned}$$

The kinetic and potential energies vary with time, but the total energy $U(R) + T(R)$ is constant; it does not vary with time. The average value of the kinetic energy over a cycle is equal to the average value of the potential energy, each of which is one half of the total energy. I am going to use the symbol ε for energy when referring to a single atom or molecule, throughout the text. The total energy ε can take any value with no restrictions.

4.3 A Simple Diatomic

Consider next the Hooke's Law model of a diatomic molecule, Figure 4.4. The atoms have masses m_1 and m_2, and the spring has a harmonic force constant of k_s. I am going to consider the motion along the horizontal axis, which I will refer to as the x-axis. The x coordinates of the two atoms are x_1 and x_2 relative to an arbitrary axis, the equilibrium length of the spring is R_e and the length of the extended spring at some given time is

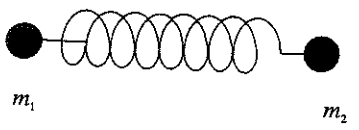

Figure 4.4 Diatomic molecule

$$R = x_2 - x_1$$

The spring extension is therefore

$$x_2 - x_1 - R_e$$

Considering atom 1, the spring exerts a force of $k_s(x_2 - x_1 - R_e)$ and so, according to Newton's second law

$$\begin{aligned} m_1 \frac{d^2 x_1}{dt^2} &= k_s(x_2 - x_1 - R_e) \\ &= k_s(R - R_e) \end{aligned} \tag{4.8}$$

As far as atom 2 is concerned, the extended spring exerts a force of magnitude $k_s(x_2 - x_1 - R_e)$ in the direction of decreasing x_2 and so

$$\begin{aligned} m_2 \frac{d^2 x_2}{dt^2} &= -k_s(x_2 - x_1 - R_e) \\ &= -k_s(R - R_e) \end{aligned} \tag{4.9}$$

After a little rearrangement we find

$$\begin{aligned} \frac{d^2 R}{dt^2} &= -\frac{k_s}{m_2}(R - R_e) - \frac{k_s}{m_1}(R - R_e) \\ &= -k_s\left(\frac{1}{m_1} + \frac{1}{m_2}\right)(R - R_e) \end{aligned} \tag{4.10}$$

We now define a quantity μ called the *reduced mass* by

$$\frac{1}{\mu} = \frac{1}{m_1} + \frac{1}{m_2}$$

and so we have

$$\mu \frac{d^2 R}{dt^2} = -k_s(R - R_e) \tag{4.11}$$

which is identical to Equation (4.2) already derived for a single particle of mass μ on a spring. The general solution is therefore

$$R = R_e + A \sin\left(\sqrt{\frac{k_s}{\mu}} t\right) + B \cos\left(\sqrt{\frac{k_s}{\mu}} t\right) \tag{4.12}$$

and the angular frequency is

$$\omega = \sqrt{\frac{k_s}{\mu}}$$

It is easy to demonstrate that the potential energy is

$$U = \tfrac{1}{2} k_s (x_2 - x_1 - R_e)^2$$

and the total energy ε_{vib} of the harmonically vibrating diatomic is therefore

$$\varepsilon_{vib} = \frac{1}{2} m_1 \left(\frac{dx_1}{dt}\right)^2 + \frac{1}{2} m_2 \left(\frac{dx_2}{dt}\right)^2 + \tfrac{1}{2} k_s (x_2 - x_1 - R_e)^2 \tag{4.13}$$

4.4 Three Problems

This simple treatment suggests three problems. First, how do we determine the spring constant for a simple molecule such as $^1H^{35}Cl$ or $^{12}C^{16}O$? Second, how good is the harmonic approximation? And third, have we missed anything by trying to treat a molecular species as if it obeyed the laws of classical mechanics rather than quantum mechanics?

The three questions are interlinked, but let me start with the third one. The experimental evidence suggests that we have made a serious error in neglecting the quantum mechanical details. If we irradiate a gaseous sample of $^1H^{35}Cl$ with infrared radiation, it is observed that the molecules strongly absorb radiation of wavenumber $2886\,\mathrm{cm}^{-1}$. With hindsight we would of course explain the observation by saying that the molecular vibrational energies are *quantized*. A major flaw of the classical treatment is that the total vibrational energy is completely unrestricted and quantization does not arise.

The quantum mechanical treatment of a harmonically vibrating diatomic molecule is given in all the elementary chemistry texts. The results are quite different from the classical ones, in that

1. the vibrational energy cannot take arbitrary values, it is *quantized*;
2. there is a single quantum number v, which takes values $0, 1, 2, \ldots$, called the *vibrational quantum number*; and
3. vibrational energies $\varepsilon_{\mathrm{vib}}$ are given by

$$\varepsilon_{\mathrm{vib}} = \frac{h}{2\pi}\sqrt{\frac{k_{\mathrm{s}}}{\mu}}\left(v + \frac{1}{2}\right)$$

where h is Planck's constant.

The results are usually summarized on an energy level diagram, such as Figure 4.5.

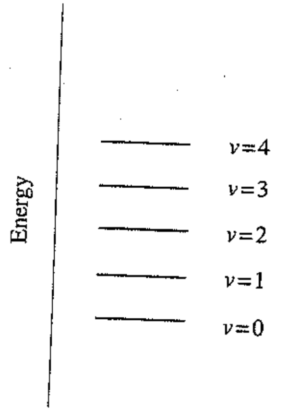

Figure 4.5 Vibrational energy levels

I have just drawn the first four vibrational energy levels, but there are an infinite number of them. According to the harmonic model, the spacing between the levels is constant.

A careful investigation into the mechanism by which electromagnetic radiation interacts with matter suggests that transitions between these vibrational energy levels are allowed, provided the vibrational quantum number changes by just 1 unit. So molecules with $v = 0$ can absorb radiation of exactly the right energy for promotion to $v = 1$. Molecules with $v = 1$ can either absorb radiation with exactly the right energy for promotion to $v = 2$ or they can emit radiation and fall to $v = 0$ and so on.

According to the quantum model, then, molecules can only have certain vibrational energies and this behaviour is totally at variance with the classical treatment. Also, the quantum treatment differs from the classical treatment in that the lowest energy is that with $v = 0$, where the energy is non-zero. This is called the *zero-point* energy. According to the classical treatment, a molecule can be completely at rest. According to the quantum treatment, the lowest vibrational energy allowed is the zero-point energy.

How do we measure the spring constant? According to the harmonic quantum model, the energy difference between any consecutive pair of energy levels is given by

$$\Delta\varepsilon = \frac{h}{2\pi}\sqrt{\frac{k_{\mathrm{s}}}{\mu}}$$

so all we need to do is measure this energy difference experimentally. The reduced mass μ of the $^{1}\mathrm{H}^{35}\mathrm{Cl}$ isotopic species is $1.6267 \times 10^{-27}\,\mathrm{kg}$ and substitution of the experimental value ($2886\,\mathrm{cm}^{-1}$) into the energy difference gives the harmonic force constant as $480.7\,\mathrm{N\,m}^{-1}$.

In fact, there is more to the experiment than I have told you. Spectroscopic experiments are done at finite temperatures and a given sample of N molecules may have many energy levels populated. Relative populations N_v are given by the Boltzmann formula

$$N_v \propto \exp\left(-\frac{\varepsilon_v}{k_{\mathrm{B}}T}\right)$$

Substitution of values into the formula shows that for many everyday diatomic molecules at everyday temperatures, the only vibrational level populated is that with $v = 0$. So an infrared absorption spectrum should just show a single absorption, corresponding to the transition $v = 0$ to $v = 1$.

A closer examination of the $^{1}\mathrm{H}^{35}\mathrm{Cl}$ spectrum shows weak absorptions at 5668, $8347, \ldots\,\mathrm{cm}^{-1}$, which are nearly (but not exactly) two and three times the fundamental vibration frequency. The existence of these lines in the spectrum shows that our assumption of Hooke's Law is not completely correct. Figure 4.6 shows the 'experimental' energy level diagram compared with the harmonic one.

Our conclusion from the experimental data is that vibrational energy levels get progressively closer together as the quantum number increases. This suggests that whilst the harmonic model is a reasonable one, we need to look more carefully at the form of the potential in order to get better agreement with experiment.

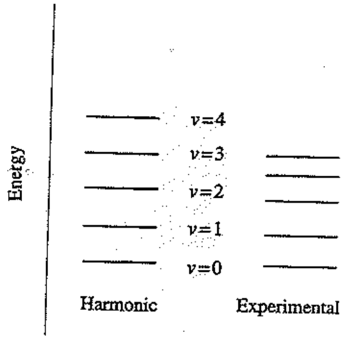

Figure 4.6 · Harmonic vs. experimental energy levels

4.5 The Morse Potential

Professional spectroscopists would be unhappy with the idea of using Hooke's Law as a model for the vibrational motion. They would be more concerned with matching their experimental energy levels to a more accurate potential. Many such potentials have been used over the years, with that due to Morse being widely quoted in elementary chemistry texts. The Morse potential is as follows

$$U = D_e(1 - \exp(-\beta(R - R_e)))^2 \tag{4.14}$$

where D_e is the depth of the potential well, i.e. the thermodynamic dissociation energy, and

$$\begin{aligned}\beta &= \sqrt{\frac{\left(\frac{d^2U}{dR^2}\right)}{2D_e}}\\ &= \frac{\omega_e}{2}\sqrt{\frac{2\mu}{D_e}}\end{aligned} \tag{4.15}$$

This potential contains three parameters, D_e, ω_e and R_e, and so should be capable of giving a better representation to the potential energy curve than the simple harmonic, which contains just the two parameters, k_s and R_e.

In the case of $^1H^{35}Cl$, a simple calculation shows that the dissociation energy

$$D_e = D_0 + \tfrac{1}{2}h(2\pi\omega_e)$$

is $4.430 + 0.186\,\text{eV} = 4.616\,\text{eV}$. The Morse potential for $^1H^{35}Cl$ is shown in Figure 4.7 compared with the simple harmonic model. The full curve is the simple harmonic potential, the dashed curve the Morse potential.

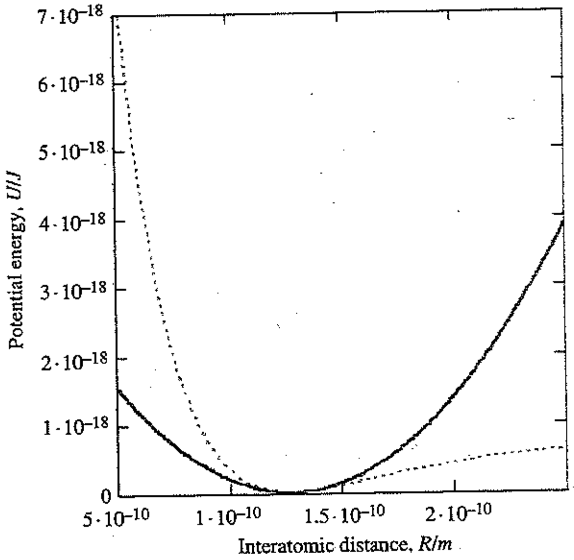

Figure 4.7 Simple harmonic and Morse curves for HCl

4.6 More Advanced Potentials

More often than not the following spectroscopic constants are available for a diatomic molecule:

R_e	the equilibrium internuclear separation
D_e	the dissociation energy
k_s	the force constant
$\omega_e x_e$	the anharmonicity constant (sometimes written x_e only)
α_e	the vibration–rotation coupling constant

Usually these five constants can be found to good experimental accuracy.

There are a number of three- to five-parameter potential functions for bonded pairs in the literature, of which the Morse potential is the most popular. Jack Linnett [3] made a careful study of many such functions, for example the four-parameter potential

$$U(R) = \frac{a}{R^m} - b\exp(-nR)$$

The four parameters a, m, b and n in this reciprocal–exponential function are deduced by fitting spectroscopic data. At this point I should explain how we recover the force constant from such a complicated expression, and to do this I'll use a Taylor expansion of the potential about the equilibrium bond length

$$U(R) = U(R_e) + (R - R_e)\left(\frac{dU}{dR}\right)_{R=R_e} + \tfrac{1}{2}(R - R_e)^2\left(\frac{d^2U}{dR^2}\right)_{R=R_e} + \cdots \quad (4.16)$$

$U(R)$ is obviously equal to $U(R_e)$ when $R = R_e$, and this fixes the constant of integration. The equation is sometimes written as

$$U(R) - U(R_e) = (R - R_e)\left(\frac{dU}{dR}\right)_{R=R_e} + \tfrac{1}{2}(R - R_e)^2\left(\frac{d^2U}{dR^2}\right)_{R=R_e} + \cdots$$

or even

$$U(R) = (R - R_e)\left(\frac{dU}{dR}\right)_{R=R_e} + \tfrac{1}{2}(R - R_e)^2\left(\frac{d^2U}{dR^2}\right)_{R=R_e} + \cdots$$

where it is understood that $U(R)$ is measured relative to the potential energy minimum (that is to say, we take the zero as $U(R_e)$).

The quantity dU/dR is of course the gradient of U. The second derivative evaluated at the minimum where $R = R_e$ is called the (harmonic) force constant. To find R_e we solve the equation $dU/dR = 0$ and substitute this value into the second derivative to evaluate the force constant. In the special case of a harmonic potential, the second derivative is a constant and is equal to the force constant.

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5 Molecular Mechanics

In Chapter 4 I showed you how to use classical mechanics to model the vibrational motion of a diatomic molecule. I also explained the shortcomings of this treatment, and hinted at applications where a quantum mechanical model would be more appropriate. We will deal specifically with quantum mechanical models in later chapters.

5.1 More About Balls on Springs

It is time to move on to more complicated molecules, and I want to start the discussion by considering the arrangement of balls on springs shown in Figure 5.1.

We assume that the springs each satisfy Hooke's Law. I will call the spring constant of the left-hand spring k_1 and the spring constant of the right-hand spring k_2. The equilibrium position corresponds to the two masses having x coordinates $R_{1,e}$ and $R_{2,e}$, and we constrain the motion so that the springs can only move along the x-axis. The particle masses are shown in Figure 5.1.

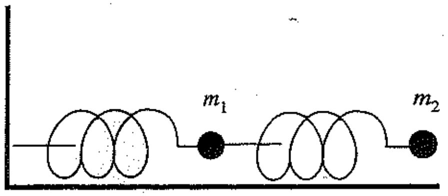

Figure 5.1 Two balls, two springs

We then stretch the system, so extending the two springs, and I will call the instantaneous positions of the two masses, x_1 and x_2. The extensions of the springs from their equilibrium positions are

$$\xi_1 = x_1 - R_{1,e} \quad \text{and} \quad \xi_2 = x_2 - R_{2,e}$$

Consider the left-hand spring; it exerts a restoring force on particle 1 of $-k_1\xi_1$. Now consider the right-hand spring. This spring is stretched by an amount $(\xi_2 - \xi_1)$, and so it exerts a force of $k_2(\xi_2 - \xi_1)$; this force acts to the left on particle 2 and to the right on particle 1. Application of Newton's second law gives

$$\begin{aligned} k_2(\xi_2 - \xi_1) - k_1\xi_1 &= m_1 \frac{\mathrm{d}^2\xi_1}{\mathrm{d}t^2} \\ -k_2(\xi_2 - \xi_1) &= m_2 \frac{\mathrm{d}^2\xi_2}{\mathrm{d}t^2} \end{aligned} \tag{5.1}$$

There are many different solutions to these simultaneous differential equations, but it proves possible to find two particularly simple ones called *normal modes of vibration*. These have the property that both particles execute simple harmonic motion at the same angular frequency. Not only that, every possible vibrational motion of the two particles can be described as linear combinations of the normal modes.

Having said that it proves possible to find such solutions where both particles vibrate with the same angular frequency ω, let me assume that there exist such solutions to the equations of motion such that

$$\begin{aligned} \xi_1(t) &= A\sin(\omega t + \phi_1) \\ \xi_2(t) &= B\sin(\omega t + \phi_2) \end{aligned}$$

where A, B, ϕ_1 and ϕ_2 are constants that have to be determined from the boundary conditions.

Differentiating these two equations with respect to time gives

$$\begin{aligned} \frac{\mathrm{d}^2\xi_1(t)}{\mathrm{d}t^2} &= -\omega^2 A\sin(\omega t + \phi_1) \\ \frac{\mathrm{d}^2\xi_2(t)}{\mathrm{d}t^2} &= -\omega^2 B\sin(\omega t + \phi_2) \end{aligned}$$

and substituting these expressions into the equations of motion gives

$$\begin{aligned} -\frac{(k_1 + k_2)}{m_1}\xi_1 + \frac{k_2}{m_1}\xi_2 &= -\omega^2\xi_1 \\ \frac{k_2}{m_2}\xi_1 - \frac{k_2}{m_2}\xi_2 &= -\omega^2\xi_2 \end{aligned} \tag{5.2}$$

These two equations are simultaneously valid only when ω has one of two possible values called the *normal mode angular frequencies*. In either case, both particles oscillate with the same angular frequency.

In order to investigate these normal modes of vibration, I write the above equations in matrix form, and then find the eigenvalues and eigenvectors as follows

$$\begin{pmatrix} -\frac{(k_1 + k_2)}{m_1} & \frac{k_2}{m_1} \\ \frac{k_2}{m_2} & -\frac{k_2}{m_2} \end{pmatrix} \begin{pmatrix} \xi_1 \\ \xi_2 \end{pmatrix} = -\omega^2 \begin{pmatrix} \xi_1 \\ \xi_2 \end{pmatrix} \tag{5.3}$$

Matrix diagonalization gives the allowed values of ω^2 (the eigenvalues), and for each value of $-\omega^2$ we calculate the relevant combinations of the ξs (the eigenvectors). The eigenvectors of the matrix are called the *normal coordinates*.

5.2 Larger Systems of Balls on Springs

For a molecule comprising N atoms, there are $3N$ Cartesian coordinates. Of these, three can be associated with the position of the centre of mass of the whole molecule and three for the orientation of the molecule at the centre of mass (two for linear molecules). This leaves $3N - 6$ vibrational degrees of freedom ($3N - 5$ if the molecule is linear), and it is appropriate to generalize some concepts at this point. I am going to use matrix notation in order to make the equations look friendlier.

The molecular potential energy U will depend on $p = 3N - 6$ (independent) variables. For the minute, let me call them $q_1, q_2, \ldots, q_p$, and let me also write $q_{1,\mathrm{e}}, q_{2,\mathrm{e}}, \ldots, q_{p,\mathrm{e}}$ for their 'equilibrium' values. These coordinates are often referred to as *internal coordinates*, and they will be linear combinations of the Cartesian coordinates.

First of all, for the sake of neatness, I will collect all the qs into a column matrix $\mathbf{q}$. I will also collect together the 'equilibrium' values into a column matrix $\mathbf{q}_\mathrm{e}$ and the extensions into a column ξ

$$\mathbf{q} = \begin{pmatrix} q_1 \\ q_2 \\ \cdots \\ q_p \end{pmatrix}; \quad \mathbf{q}_\mathrm{e} = \begin{pmatrix} q_{1,\mathrm{e}} \\ q_{2,\mathrm{e}} \\ \cdots \\ q_{p,\mathrm{e}} \end{pmatrix}; \quad \boldsymbol{\xi} = \begin{pmatrix} q_1 - q_{1,\mathrm{e}} \\ q_2 - q_{2,\mathrm{e}} \\ \cdots \\ q_p - q_{p,\mathrm{e}} \end{pmatrix} \tag{5.4}$$

I will now write $U(\mathbf{q})$ to indicate the dependence of U on these variables. If I use Taylor's Theorem to expand $U(\mathbf{q})$ about the point $\mathbf{q}_\mathrm{e}$, then the one-dimensional equation

$$U(R) - U(R_\mathrm{e}) = (R - R_\mathrm{e})\left(\frac{\mathrm{d}U}{\mathrm{d}R}\right)_{R=R_\mathrm{e}} + \tfrac{1}{2}(R - R_\mathrm{e})^2\left(\frac{\mathrm{d}^2U}{\mathrm{d}R^2}\right)_{R=R_\mathrm{e}} + \cdots$$

(given previously in Chapter 4) has to be modified to take account of the larger number of variables. First derivatives become partial first derivatives, and we have to take account of the 'mixed' second-order derivatives

$$U(\mathbf{q}) - U(\mathbf{q}_e) = \sum_{i=1}^{p} \xi_i \left(\frac{\partial U}{\partial q_i}\right)_{\xi_i=0} + \frac{1}{2}\sum_{i=1}^{p}\sum_{j=1}^{p} \xi_i\xi_j \left(\frac{\partial^2 U}{\partial q_i \partial q_j}\right)_{\xi_i=0,\xi_j=0} + \cdots \tag{5.5}$$

In ordinary vector differentiation, we meet the gradient of a scalar field f, defined in Cartesian coordinates as

$$\mathrm{grad}\, f = \frac{\partial f}{\partial x}\mathbf{e}_x + \frac{\partial f}{\partial y}\mathbf{e}_y + \frac{\partial f}{\partial z}\mathbf{e}_z$$

where $\mathbf{e}_x$, $\mathbf{e}_y$ and $\mathbf{e}_z$ are Cartesian unit vectors. When dealing with functions of many variables it proves useful to make a generalization and write the gradient of U, for example, as

$$\mathrm{grad}\, U = \begin{pmatrix} \dfrac{\partial U}{\partial q_1} \\ \dfrac{\partial U}{\partial q_2} \\ \cdots \\ \dfrac{\partial U}{\partial q_p} \end{pmatrix} \tag{5.6}$$

so grad U is a column matrix that stores all the partial derivatives. This 'vector' will occur many times through the text, and I am going to give it the symbol $\mathbf{g}$ (for gradient).

The second derivatives can be collected into a symmetric $p \times p$ matrix that is called the *hessian* of U and I will give this the symbol $\mathbf{H}$. In the case where $p = 3$, we have

$$\mathbf{H} = \begin{pmatrix} \dfrac{\partial^2 U}{\partial q_1^2} & \dfrac{\partial^2 U}{\partial q_1 \partial q_2} & \dfrac{\partial^2 U}{\partial q_1 \partial q_3} \\ \dfrac{\partial^2 U}{\partial q_2 \partial q_1} & \dfrac{\partial^2 U}{\partial q_2^2} & \dfrac{\partial^2 U}{\partial q_2 \partial q_3} \\ \dfrac{\partial^2 U}{\partial q_3 \partial q_1} & \dfrac{\partial^2 U}{\partial q_3 \partial q_2} & \dfrac{\partial^2 U}{\partial q_3^2} \end{pmatrix} \tag{5.7}$$

The Taylor expansion then becomes

$$U(\mathbf{q}) - U(\mathbf{q}_e) = \xi^{\mathrm{T}}\mathbf{g} + \tfrac{1}{2}\xi^{\mathrm{T}}\mathbf{H}\xi + \cdots \tag{5.8}$$

Both the gradient and the hessian have to be evaluated at the point $\mathbf{q}_e$, and so you will sometimes see the equation written with an 'e' subscript

$$U(\mathbf{q}) - U(\mathbf{q}_e) = \xi^{\mathrm{T}}\mathbf{g}_e + \tfrac{1}{2}\xi^{\mathrm{T}}\mathbf{H}_e\xi + \cdots$$

The superscript T, as in ξ^{T}, indicates the transpose of a matrix; the transpose of a column matrix is a row matrix. The hessian is often referred to as the force constant matrix.

Finally, if I denote the $3N$ Cartesian coordinates $X_1, X_2, \ldots, X_{3N}$, we usually write the transformation from Cartesian coordinates to internal coordinates as

$$\mathbf{q} = \mathbf{BX} \tag{5.9}$$

where the rectangular matrix $\mathbf{B}$ is called the Wilson B matrix. The $\mathbf{B}$ matrix has p rows and $3N$ columns.

5.3 Force Fields

I have been vague so far about which variables are the 'correct' ones to take. Chemists visualize molecules in terms of bond lengths, bond angles and dihedral angles, yet this information is also contained in the set of Cartesian coordinates for the constituent atoms. Both are therefore 'correct'; it is largely a matter of personal choice and professional training. I should mention that there are only $3N - 6$ vibrational coordinates, and so we have to treat the $3N$ Cartesian coordinates with a little care; they contain three translational and three rotational degrees of freedom. I will return to this technical point later.

Spectroscopists usually are interested in finding a set of equilibrium geometric parameters and force constants that give an exact fit with their experimental data. This is harder than it sounds, because for a molecule comprising N atoms and hence $p = 3N - 6$ vibrational degrees of freedom, there are $\frac{1}{2}p(p-1)$ force constants (diagonal and off-diagonal). In order to measure the individual force constants, the spectroscopist usually has to make experimental measurements on all possible isotopically labelled species. It turns out that there are many more unknowns than pieces of experimental information. Spectroscopists usually want a *force field* (comprising force constants, equilibrium quantities and every other included parameter) that is specific for a given molecule. They want to match up 'theory' with their incredibly accurate measurements.

Many of the 'off-diagonal' force constants turn out to be small, and spectroscopists have developed systematic simplifications to the force fields in order to make as many as possible of the small terms vanish. If the force field contains only 'chemical' terms such as bond lengths, bond angles and dihedral angles, then it is referred to as a *valence force field* (VFF). There are other types of force field in the literature, intermediate between the VFF and the general force field discussed above.

5.4 Molecular Mechanics

Molecular modellers usually have a quite different objective; they want a force field that can be transferred from molecule to molecule, in order to predict (for example) the geometry of a new molecule by using data derived from other related molecules. They make use of the bond concept, and appeal to traditional chemists' ideas that a molecule comprises a sum of bonded atoms; a large molecule consists of the same features we know about in small molecules, but combined in different ways.

The term *molecular mechanics* was coined in the 1970s to describe the application of classical mechanics to determinations of molecular equilibrium structures. The method was previously known by at least two different names, the *Westheimer* method and the *force-field* method. The name and acronym, MM, are now firmly established quantities.

The idea of treating molecules as balls joined by springs can be traced back to the 1930 work of D. H. Andrews [4]. A key study to the development of MM was that by R. G. Snyder and J. H. Schachtschneider [5] who showed that transferable force constants could be obtained for alkanes provided that a few off-diagonal terms were retained. These authors found that off-diagonal terms are usually largest when neighbouring atoms are involved, and so we have to take account of non-bonded interactions, but only between next-nearest neighbours.

A final point for consideration is that we must also take account of the chemical environment of a given atom. An sp carbon atom is different from an sp^2 carbon atom and so on. It is traditional to speak of *atom types* in molecular mechanics.

Our idea is to treat the force field as a set of constants that have to be fixed by appeal to experiment or more rigorous calculation. In molecular mechanics we take account of non-bonded interactions, and also the chemical sense of each atom. A valence force field that contains non-bonded interactions is often referred to as a *Urey–Bradley force field.*

5.4.1 Bond-stretching

If we consider phenylanine (see Figure 5.2) we can identify a variety of bond types

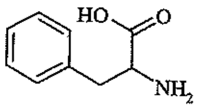

Figure 5.2 Phenylanine

including C(sp^2)—C(sp^2), C(sp^2)—C(sp^3), O—H, C=O and so on. If we assume that Hooke's Law is adequate, then each bond stretch between atom types A and B makes a contribution to the total molecular potential energy of

$$U_{\mathrm{AB}} = \tfrac{1}{2}k_{\mathrm{AB}}(R_{\mathrm{AB}} - R_{\mathrm{e,AB}})^2 \tag{5.10}$$

in an obvious notation. Here k_{AB} is the force constant, R_{AB} the instantaneous bond length and $R_{\mathrm{e,AB}}$ the equilibrium bond length.

Other scientists recommend the Morse potential

$$U_{\mathrm{AB}} = D(1 - \exp(-\alpha(R_{\mathrm{AB}} - R_{\mathrm{AB,e}})))^2$$

whilst some recommend the addition of extra terms to the simple Harmonic expression

$$U_{\mathrm{AB}} = k_1(R_{\mathrm{AB}} - R_{\mathrm{e,AB}})^2 + k_2(R_{\mathrm{AB}} - R_{\mathrm{e,AB}})^4 \tag{5.11}$$

5.4.2 Bond-bending

Next we have to consider the bond-bending vibrations. It is usual to write these as harmonic ones, typically for the connected atoms A—B—C

$$U_{\mathrm{ABC}} = \tfrac{1}{2}k_{\mathrm{ABC}}(\theta_{\mathrm{ABC}} - \theta_{\mathrm{e,ABC}})^2 \tag{5.12}$$

k is the force constant, and the subscript 'e' refers to the equilibrium value where the molecule is at rest. A variation on the theme is given by

$$U_{\mathrm{ABC}} = \frac{k_{\mathrm{ABC}}}{2\sin^2\theta_{\mathrm{ABC,e}}}(\cos\theta_{\mathrm{ABC}} - \cos\theta_{\mathrm{ABC,e}})^2 \tag{5.13}$$

5.4.3 Dihedral motions

Next we must consider the dihedral angle ABCD between the four bonded atoms A, B, C and D (see Figure 5.3). Some authors divide these into *proper* dihedrals, where we might expect full rotation about the connecting bond B—C, and *improper*

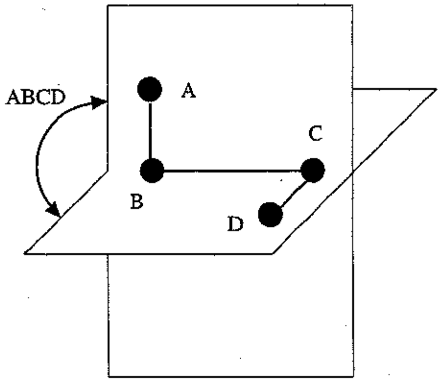

Figure 5.3 Dihedral angle

dihedrals where the rotation is limited. For example, if C—D were a C—H fragment of a methyl group, then we would be expect full rotation about B—C and a three-fold symmetry in the potential energy term. A—CH—CH— linkage in a benzene ring would only show a moderate flexing from its planar value (angle zero).

If we use χ to denote the ABCD angle, then a popular dihedral potential is given by

$$U = \frac{U_0}{2}(1 - \cos(n(\chi - \chi_e))) \tag{5.14}$$

Here n is the periodicity parameter, which would be 3 for a methyl group. χ_e is the equilibrium torsional angle. A more complicated example is given by

$$U = \frac{V_1}{N_d}(1 + \cos(n_1\chi - g_1)) + \frac{V_2}{N_d}(1 + \cos(n_2\chi - g_2)) + \frac{V_3}{N_d}(1 + \cos(n_3\chi - g_3))$$

The Vs are energy terms, the ns are periodicity parameters, the gs are phase parameters and N_d is a constant that depends on the number of bonds.

Some authors treat improper dihedrals in the same way as bond-bending, and take a contribution to the molecular potential energy as

$$U_{\mathrm{ABCD}} = \tfrac{1}{2}k_{\mathrm{ABCD}}(\chi_{\mathrm{ABCD}} - \chi_{e,\mathrm{ABCD}})^2 \tag{5.15}$$

where χ is the dihedral angle, as above.

5.4.4 Out-of-plane angle potential (inversion)

Next we consider the out-of-plane potential terms. Imagine molecule ABCD in Figure 5.4 to be ammonia, a molecule with a very low barrier to inversion; as ψ changes from positive to negative, the molecule inverts. We can write the inversion potential either in terms of the angle indicated (ψ) or in terms of the height (h) of atom D above the plane of atoms A, B and C. Four examples follow:

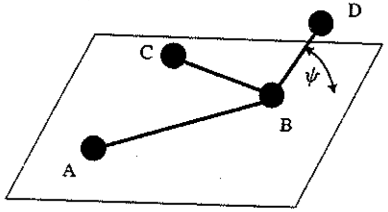

Figure 5.4 Out-of-plane (inversion) potential

$$\begin{aligned} U &= \frac{k_1}{2\sin^2\psi_e}(\cos\psi - \cos\psi_e)^2 \\ U &= k_2h^2 \\ U &= k_3(1 + k_4\cos(n\psi)) \end{aligned} \tag{5.16}$$

where n is a periodicity parameter, and finally

$$U = k_5(1 + \cos(n\psi - k_6))$$

The ks are constants that have to be fixed against experiment, and ψ_e is the equilibrium value.

5.4.5 Non-bonded interactions

I mentioned earlier that molecular mechanics force fields have to be transferable from molecule to molecule, and explained the necessity for non-bonded interactions. These are usually taken to be Lennard-Jones 12–6 type, and they are included between all non-bonded pairs of atoms.

$$U_{\text{L-J}} = \frac{C_{12}}{R^{12}} - \frac{C_6}{R^6}$$

The Born–Mayer–Huggins potential

$$U_{\mathrm{BMH}} = A\exp(-BR) - \frac{C_6'}{R^6} - \frac{C_8}{R^8}$$

is sometimes used when dealing with polar species. B is a parameter determined by the size and 'softness' of an ion, C_6' (not the same as C_6 in $U_{\text{L-J}}$) has to do with dipole–dipole interactions whilst C_8 is determined by dipole–quadrupole interactions.

Some force fields make special provision for hydrogen-bonded atoms; they treat them as non-bonded interactions but soften the Lennard-Jones 12–6 potential for A—H···B to a 12–10 version

$$U_{\mathrm{HB}} = \frac{C_{12}}{R_{\mathrm{HB}}^{12}} - \frac{C_{10}}{R_{\mathrm{HB}}^{10}} \tag{5.17}$$

Other authors take the view that hydrogen bonds are perfectly respectable chemical bonds that should be treated just like any other bond. They are therefore given a force constant and so on.

5.4.6 Coulomb interactions

Many force fields take account of electronegativity differences between atoms and add electrostatic terms. Atomic charges Q_A and Q_B are assigned to atoms A and B according to the rules of the particular force field, and we write

$$U_{AB} = \frac{1}{4\pi\epsilon_0}\frac{Q_A Q_B}{R_{AB}}$$

5.5 Modelling the Solvent

I should remind you that the electrostatic expression above relates only to point charges in free space. In the presence of a dielectric material (such as water), the force between point charges is reduced by a factor ϵ_r called the relative permittivity. Many force fields were developed at a time when it was not feasible to include a solvent explicitly in such calculations.

Various attempts were made to allow for the effect of a solvent; the most obvious thing to do is to alter the relative permittivity even though no solvent molecules are actually taken into account. There is no agreement between authors as to the correct value of ϵ_r and values ranging between 1 and 80 have been used for water. Some force fields take ϵ_r proportional to the distance between the point charges. I will explain some more up-to-date ways of modelling the solvent in later chapters.

5.6 Time-and-Money-Saving Tricks

All the contributions to the molecular potential energy U given above can be done on a pocket calculator. The larger the molecular system, the larger the number of individual contributions to U and the relationship between molecular size and computational effort is roughly dependent on the square of the number of atoms. Over the years, people have tried to reduce the computational time for a given problem by the use of various tricks of the trade. Two such methods are as follows.

5.6.1 United atoms

Some professional force fields use the so-called *united atom* approach. Here, we regard (for example) a CH_3 group as a pseudo-atom, X, and develop parameters for a C(sp^2)—X stretch, and so on. It is customary to treat methyl, methylene and methane groups as united atoms, especially when dealing with large biological systems.

5.6.2 Cut-offs

For a large molecule, there are many more non-bonded interactions than bonded interactions. Molecular mechanics force fields very often cut these off to zero at some finite distance, in order to save computer time. This can sometimes lead to mathematical difficulties because of the discontinuity, and various ingenious methods have been proposed to circumvent the problem (other than actually retaining the terms). I will show you in a later chapter that there are other problems associated with this cut-off procedure; it's a real problem, not just one that I have mentioned out of historical interest. Figure 5.5 shows a Lennard-Jones 12–6 potential with a cut-off (after a certain value of R, the potential is set to zero).

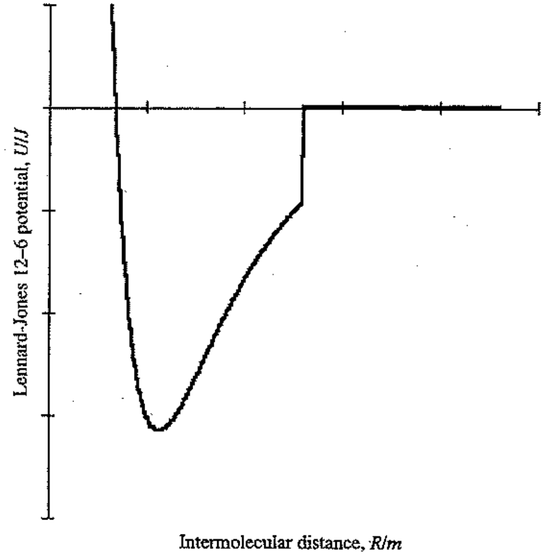

Figure 5.5 Schematic cut-off of L-J potential

5.7 Modern Force Fields

A 'standard' modern molecular mechanics force field can be written

$$U = \sum_{\text{stretch}} U_{AB} + \sum_{\text{bend}} U_{ABC} + \sum_{\text{dihedral}} U_{ABCD} + \sum_{\text{out-of-plane}} U_{ABCD} + \sum_{\text{non-bonded}} U_{AB} + \sum_{\text{Coulomb}} U_{AB} \qquad (5.18)$$

or written explicitly in terms of the contributions discussed above.

$$U = \sum_{\text{bonds}} \tfrac{1}{2}k_{\text{AB}}(R_{\text{AB}} - R_{\text{e,AB}})^2 + \sum_{\text{bends}} \tfrac{1}{2}k_{\text{ABC}}(\theta_{\text{ABC}} - \theta_{\text{e,ABC}})^2$$
$$+ \sum_{\text{dihedrals}} \frac{U_0}{2}(1 - \cos(n(\chi - \chi_0))) + \sum_{\text{out-of-plane}} \frac{k}{2\sin^2\psi_{\text{e}}}(\cos\psi - \cos\psi_{\text{e}})^2$$
$$+ \sum_{\text{non-bonded}} \left(\frac{C^{12}_{\text{AB}}}{R^{12}_{\text{AB}}} - \frac{C^{6}_{\text{AB}}}{R^{6}_{\text{AB}}}\right) + \frac{1}{4\pi\epsilon_0}\sum_{\text{charges}} \frac{Q_{\text{A}}Q_{\text{B}}}{R_{\text{AB}}} \qquad (5.19)$$

5.7.1 Variations on a theme

There are a number of variants of this expression in the literature. Some force fields contain mixed terms such as

$$\frac{k}{2}(R - R_{\text{e}})(\theta - \theta_{\text{e}})$$

which couple together the bond-stretching modes with angle bending. Others use more complicated expressions for the individual bending and stretching terms. Some force fields allow interactions between lone pairs, which are often referred to as non-atomic interaction centres. In addition, there are specialist force fields that are appropriate for restricted ranges of compounds such as ions, liquid metals and salts.

Force fields are determined by one of two routes. First, in an ideal world, one might calibrate their parameters against accurate quantum mechanical calculations on clusters of small molecules. The alternative is to calibrate against experimental data such as crystal structure, infrared absorption, X-ray measurements and liquid properties such as density, enthalpy of vaporization, Gibbs energies of solvation and the like. To date, almost all modern force fields have been obtained by the latter approach.

The choice of a particular force field for a given application should depend on the type of system for which the force field was designed. For example, some force fields have been calibrated against the solution properties of amino acids. These are obviously the ones to choose when it comes to modelling proteins in solution.

Finally, I must emphasize the importance of the *atom type* (i.e. the chemical environment). The chemical environment of an atom can be distinguished by

1. its hybridization
2. its formal atomic charge
3. its nearest neighbours.

For example, one well-known force field distinguishes five types of oxygen atom:

1. a carbonyl oxygen
2. a hydroxyl oxygen
3. a carboxylic or phosphate oxygen
4. an ester or ether oxygen
5. an oxygen in water.

The interactions are calculated according to atom type, not the 'raw' elements.

5.8 Some Commercial Force Fields

With these principles in mind, it is time to examine some of the common force fields found in professional molecular modelling programs.

5.8.1 DREIDING [6]

This force field is parameterized for all atom types that any chemist would expect for the elements H, C, N, O, P, S, F, Cl, Br and I. In terms of the 'standard' expression we write

$$U = \sum_{\text{bonds}} \tfrac{1}{2}k_{\text{AB}}(R_{\text{AB}} - R_{\text{e,AB}})^2 + \sum_{\text{bends}} \tfrac{1}{2}k_{\text{ABC}}(\cos\theta_{\text{ABC}} - \cos\theta_{\text{e,ABC}})^2$$
$$+ \sum_{\text{dihedrals}} \frac{U_0}{2}(1 - \cos(n(\chi - \chi_0))) + \sum_{\text{out-of-plane}} \frac{k}{2}(\psi - \psi_{\text{e}})^2$$
$$+ \sum_{\text{non-bonded}} \left(\frac{C^{12}_{\text{AB}}}{R^{12}_{\text{AB}}} - \frac{C^{6}_{\text{AB}}}{R^{6}_{\text{AB}}}\right) \qquad (5.20)$$

5.8.2 MM1 [7]

In his 1976 Review, Norman Allinger essentially defined what we now call the MM1 force field. He treated hydrocarbons only, ignored the Coulomb terms and used an exp-6 Lennard-Jones potential.

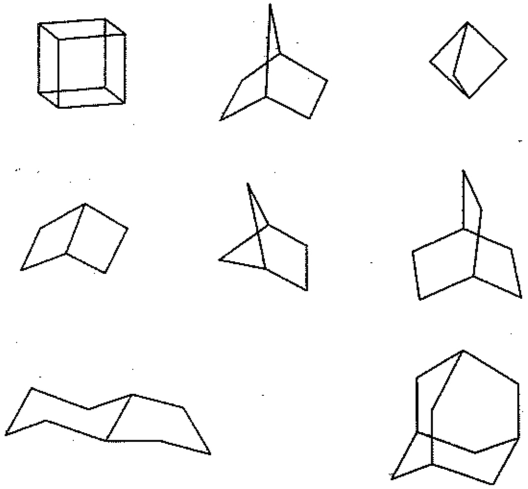

Figure 5.6 Bicyclic and related molecules

Once all the standard cases have been successfully treated, one naturally looks at the difficult ones. In the case of hydrocarbons, these difficult cases comprise strained rings such as cyclobutane. The problem with cyclobutane is this; whilst having all carbon atoms planar can minimize the angular deformation from tetrahedral, the molecule is actually puckered by a substantial angle from planarity. In addition, the C—C bond lengths are unusually large. The obvious solution is to say that a four-membered ring is different from any other hydrocarbon and that the bond angle does not have a natural tetrahedral value, but one then goes down the undesirable path where all difficult cases have their own set of parameters.

Allinger and others introduced a variety of 'mixed' terms into the standard molecular mechanics potential; for example, a bond length–bond angle term and a torsion–bend interaction. Figure 5.6 shows typical bicyclic and related hydrocarbons described in the 1976 review [7].

5.8.3 MM2 (improved hydrocarbon force field)

Allinger introduced MM2 in 1977 [8]. At the time there was a deal of discussion in the literature about how different force fields should represent hydrogen atoms, i.e. as 'hard' or 'soft' atoms. A hard atom was said to be one whose plot of force vs. distance (in the diatom) showed a steep slope. A soft atom was one where the slope was gentler. It all boiled down to the repulsive part of the non-bonded interactions but eventually Allinger decided to retain his exp-6 intermolecular potential.

MM2 differs from MM1 in three main respects:

1. The dihedral term was extended to

$$U = \frac{U_1}{2}(1 + \cos\omega) + \frac{U_2}{2}(1 + \cos 2\omega) + \frac{U_3}{2}(1 + \cos 3\omega) \qquad (5.21)$$

   where each of the Us was found by calibration against experiment.

2. The bending term was extended to

$$U_{\mathrm{ABC}} = \tfrac{1}{2}k_{\mathrm{ABC}}(\theta_{\mathrm{ABC}} - \theta_{\mathrm{e,ABC}})^2 + \tfrac{1}{2}k'_{\mathrm{ABC}}(\theta_{\mathrm{ABC}} - \theta_{\mathrm{e,ABC}})^6 \qquad (5.22)$$

3. All mention of cross terms between bond stretches and bends were finally dropped.

A great deal of importance was attached to the calculation of enthalpies of formation, and 42 hydrocarbons were treated. The author claimed that his enthalpy results were comparable with experiment in terms of experimental error.

5.8.4 AMBER [9]

AMBER (an acronym for Assisted Model Building and Energy Refinement) is a force field for the simulation of nucleic acids and proteins. It was calibrated against experimental bond lengths and angles obtained from microwave, neutron diffraction and accurate quantum chemical studies. The parameters were then refined with molecular mechanics studies on model compounds such as tetrahydrofuran, deoxyadenosine, dimethyl phosphate, 9-methyladenine-1-methylthymine hydrogen bonded complex and others. The model differs from our standard expression, Equation (5.19), in four ways.

1. Hydrogen bonds were included explicitly with a 12–10 potential

$$U_{\text{H-bonds}} = \sum_{\text{H-bonds}} \left(\frac{C_{12}}{R^{12}} - \frac{C_{10}}{R^{10}}\right)$$

2. An attempt was made to include solvent effects by inclusion of the Coulomb term with a distance-dependent relative permittivity.

3. The AMBER force field is a 'united atom' one, and hydrogen atoms bonded to carbons are not explicitly included. They are absorbed into the atom type parameters for neighbouring atoms.

4. Lone pairs were explicitly included for sulfur hydrogen bonding.

There are a number of different versions of AMBER; the original united atom version was later extended to include all atoms. Just to give you a flavour, one modern software package has the following choices

1. AMBER 2
2. AMBER 3
3. AMBER for saccharides
4. AMBER 94
5. AMBER 96

5.8.5 OPLS (Optimized Potentials for Liquid Simulations) [10]

Like AMBER, OPLS is designed for calculations on amino acids and proteins. The easiest thing is for me to quote part of the Abstract to the keynote paper:

> *A complete set of inter molecular potential functions has been developed for use in computer simulations of proteins in their native environment. Parameters have been reported for 25 peptide residues as well as the common neutral and charged terminal groups. The potential functions have the simple Coulomb plus Lennard-Jones form and are compatible with the widely used models for water, TIP4P, TIP3P and SPC. The parameters were obtained and tested primarily in conjunction with Monte Carlo statistical mechanics simulations of 36 pure organic liquids and numerous aqueous solutions of organic ions representative of subunits in the side chains and backbones of proteins.... Improvement is apparent over the AMBER united-atom force field which has previously been demonstrated to be superior to many alternatives.*

I will explain about TIP and Monte Carlo in later chapters. Each atomic nucleus is an interaction site, except that CH_n groups are treated as united atoms centred on the carbon. Hydrogen bonds are not given any special treatment, and no special account is taken of lone pairs.

5.8.6 R. A. Johnson [11]

I mentioned earlier the existence of a number of specialist force fields. The Johnson force field is specific to the pure elements Fe, W and V. The pair potential terms are written

$$\begin{aligned} U &= a_1(R-b_1)^3 + c_1R + d_1 && \text{if } \varepsilon_1 < R < \varepsilon_2 \\ &= a_2(R-b_2)^3 + c_2R + d_2 && \text{if } \varepsilon_2 < R < \varepsilon_3 \\ &= a_3(R-b_3)^3 + c_3R + d_3 && \text{if } \varepsilon_3 < R < \varepsilon_4 \\ &= 0 && \text{if } \varepsilon_4 < R \end{aligned} \tag{5.23}$$

where R is the distance between a pair of atoms, the εs are characteristic distances and the as, bs, cs and ds are parameters.

6 The Molecular Potential Energy Surface

For one-dimensional problems, we speak about a molecular potential energy *curve*. The simple potential energy curves we have met so far have all shown a single minimum. From now on, life gets more complicated (or interesting, depending on your viewpoint).

6.1 Multiple Minima

The plot in Figure 6.1 shows how the ethane molecular potential varies with dihedral angle. The figure shows a full rotation of 360°; all the remaining geometrical variables were kept constant. Note that there are three identical minima (and of course three identical maxima), and the differences between maxima and minima are all the same. The '1D' in the figure means that it is a one-dimensional plot. The chemical interpretation is that these three minima correspond to conformers where the hydrogens are as far apart as possible (i.e. in the *trans* position). The maxima correspond to conformers where the C—H bonds eclipse each other.

Multiple minima are common in potential energy surface studies, as we will see. Consider now the substituted ethane CH_2Cl—CH_2Cl. A plot of the potential energy vs. the ClC—CCl dihedral angle gives Figure 6.2. There are three minima, one lower than the other two. The three minima are referred to as *local minima* and the minimum at 180° is called the *global minimum*. The global minimum corresponds to a conformation with the two chlorines as far apart as possible. The two other minima correspond to conformers where each chlorine is *trans* to hydrogen.