Revisiting Hansen Solubility Parameters by Including Thermodynamics

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Supporting Information

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Manuel J. Louwerse, Ana Maldonado, Simon Rousseau, Chloe Moreau-Masselon, Bernard Roux, and Gadi Rothenberg

Supporting Information.pdf
Supporting Information

This supporting information file contains three sections:

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2. Derivation of mixing rules for solvent blends p4
3. Description of the optimization procedure p7

1. Estimation of split H bond parameters from data of C. A. Hunter

In the improved Hansen parameter method, the H bond parameter, \( \delta_H \), is now split in a donor and an acceptor parameter, \( \delta_{HD} \) and \( \delta_{HA} \). In this appendix it is described how to find values for these new parameters for additional solvents.

First, let’s define the various parameters:

In the original Hansen method, \( \delta_H \) is the square root of the H bond interaction per volume (of a pure substance). Hence the total H bond interaction is: \( \delta_H^2 \). If hydrogen bonds would be non-specific, it follows that the interaction between different molecules, A and B, would be: \( \delta_{HA} \cdot \delta_{HB} \).

However, since hydrogen bonds are specific interactions between donors and acceptors, we have introduced split parameters, such that the interaction per volume in a pure substance (\( \delta_H^2 \)) now is: \( \delta_{HD} \cdot \delta_{HA} \). (Note that this is a different definition than Hansen uses in their trial to implement donor-acceptor splits; what they do there is physically incorrect, see main text). For the interaction between molecules A and B, we now obtain: \( (\delta_{HD,A} \cdot \delta_{HA,B} + \delta_{HD,B} \cdot \delta_{HA,A})/2 \).

While the original \( \delta_H \) can be measured experimentally (albeit indirectly), the splitted \( \delta_{HD} \) and \( \delta_{HA} \) are not easily found experimentally, because they always come together. Fortunately, C. A. Hunter has come up with a good (i.e. correct) way to find donor and acceptor strengths from first principles.\(^1\) Combined with experimental knowledge, he compiled a large table of values for donor and acceptor strengths for many types of molecules, see Table S1.

The \( \alpha \) and \( \beta \) values of Hunter are values per mole, assuming only hydrogen bonds between the strongest donors and the strongest acceptors (one per molecule) are formed. For simple molecules with one donor and one acceptor, \( \alpha \beta \) gives the total hydrogen bond interaction energy per mole. When several donor and acceptor groups are available per molecule, the \( \alpha \beta \) values for each hydrogen bond that is formed should be summed.

Therefore, we have chosen to calibrate the averages over the different functional groups, also the absolute values of the parameters become by the molecular volume. However, since for most molecules the parameters are some kind of one acceptor parameter, even though this is somewhat approximate.

Hence, for the solvent molecules we also need to translate the values of the original variables. For the solute molecules we need to fit one donor and one acceptor parameter.

Most practical molecules have several donor and acceptor groups and not necessarily in equal amounts. To calculate the interaction energies in mixtures of such molecules correctly, one should keep track of all interaction energy for a mixture of A en B, one should sum the values of the strongest donor times the second strongest acceptor, etc. (this may include AA or BB interactions.)

To translate these values per molecule into a method until 

<table>
<thead>
<tr>
<th>H-bond donors</th>
<th>$\alpha$ $^a$</th>
<th>$\beta$ $^a$</th>
<th>H-bond donors</th>
<th>$\alpha$ $^a$</th>
<th>$\beta$ $^a$</th>
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<td>amine</td>
<td>1.5</td>
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</tr>
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<td>0.9</td>
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<td>amide</td>
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<td>urea</td>
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<td>alcohol</td>
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<table>
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<th>H-bond acceptors</th>
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<th>$\delta$ $^b$</th>
<th>H-bond acceptors</th>
<th>$\beta$ $^a$</th>
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<td>ammonia</td>
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<td>nitroalkane</td>
<td>3.7</td>
<td>sulfone</td>
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<td>pyridine</td>
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<td>disulfide</td>
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<td>carbamate</td>
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<td>trifluoroacetic acid</td>
<td>3.8</td>
<td>amine</td>
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<tr>
<td>aryl iodide</td>
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<td>4.1</td>
<td>pyrrole</td>
<td>4.1</td>
<td>sulfonamide</td>
</tr>
<tr>
<td>aryl fluoride</td>
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<td>4.2</td>
<td>2,2,2-trifluoroethanol</td>
<td>4.2</td>
<td>amide</td>
</tr>
<tr>
<td>alkyl chloride</td>
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<td>water</td>
<td>4.5</td>
<td>urea</td>
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<td>nitrile</td>
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<td>perfluoro-tert-butanol</td>
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<td>alky ether</td>
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<td>phosphine oxide</td>
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<td>ester</td>
<td>5.3</td>
<td></td>
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</tbody>
</table>

[a] Values based on literature values. [b] Values based on the molecular electrostatic potential surface.

To translate these $\alpha$ and $\beta$ values to solubility parameters, a few issues need to be considered: Most practical molecules have several donor and acceptor groups and not necessarily in equal amounts. To calculate the interaction energies in mixtures of such molecules correctly, one should keep track of all interaction energy for a mixture of A en B, one should sum the values of the strongest donor times the strongest acceptor in A or B, plus the second strongest donor times the second strongest acceptor, etc. (this may include AA or BB interactions.) However, implementing this as such (with multiple $\alpha$ and $\beta$ values per molecule) into a method for fitting solubility spheres would require too much specific knowledge about the solute molecules and would hamper the fitting procedure as well (by introducing an unknown number of variables). For the solute molecules we need to fit one donor and one acceptor parameter. Hence, for the solvent molecules we also need to translate the $\alpha$ and $\beta$ values into one donor and one acceptor parameter, even though this is somewhat approximate.

Furthermore, the $\alpha$ and $\beta$ values per molecule need to be translated to $\delta_{\text{HH}}$ and $\delta_{\text{HA}}$ values per volume. For molecules with single donor and acceptor groups this is straightforward: one should divide by the molecular volume. However, since for most molecules the parameters are some kind of averages over the different functional groups, also the absolute values of the parameters become more uncertain. Therefore, we have chosen to calibrate the $\delta_{\text{HH}}$ and $\delta_{\text{HA}}$ parameters to the known values of the original $\delta_{\text{H}}$ parameter: scaling $\delta_{\text{HH}}$ and $\delta_{\text{HA}}$ until $\delta_{\text{HH'}}\delta_{\text{HA'}}$ equals $\delta_{\text{H'}}$. 

Table S1. Hydrogen-bond parameters for common functional groups and solvents in order of increasing hydrogen-bond strength. Copied from ref. 1.
Now let’s discuss the exact method to estimate $\delta_{HD}$ and $\delta_{HA}$:

First a list is made of all strong donors and acceptors in the molecule (ignoring CH donors at first). Then, since equal numbers of donors and acceptors are needed, weak donors or acceptors (usually only donors) are added until the correct amounts are obtained. In practice, this means that CH donors are added to the list until all acceptors are satisfied. If there are not enough weak donors or acceptors available, zeros are added in their place. Note that all oxygen atoms and double bonds are added to the list of acceptors twice, because they can accept two Hbonds each.

Then, the strengths of the listed donors are summed and the same is done for the acceptors, and finally, the resulting $\delta_{HD}$ and $\delta_{HA}$ values are scaled until $\delta_{HD} \cdot \delta_{HA}$ equals $\delta_H^2$.

Working out a few examples:

Ethanol has 1 donor: an alcohol group with a donor strength 2.7 and 1 acceptor that is counted twice: the same alcohol group with an acceptor strength of 5.8. Since the acceptor is counted twice, we need to add one CH donor: a CH group that neighbors the alcohol O, so it has the donor strength of an alkyl ether, 0.9. Now the donor strengths are summed: $2.7 + 0.9 = 3.6$, and so are the acceptor strengths: $2 \times 5.8 = 11.6$. Finally, the numbers are scaled to fulfill the total $\delta_H$ value of 19.4: $3.6 \times 11.6 = 41.76$, and so the numbers need to be scaled with $(376.36/41.76)^{1/2}$: $\delta_{HD} = 3.002 \times 3.6 = 10.81$ and $\delta_{HA} = 3.002 \times 11.6 = 34.82$.

Ethyl acetate has no strong donors and 2 acceptors: the ester bridging O (ester: 5.3) and the ester double-bonded O (ketone: 5.8). Since both acceptors are counted double, we need four donors: 3 alkyl ester CHs (neighboring the ester carbonyl) with strength 1.5 and 1 alkyl ether (neighboring the ester bridging O) with strength 0.9. Adding the donors gives: $3 \times 1.5 + 0.9 = 5.4$. Adding the acceptors gives: $2 \times 5.3 + 2 \times 5.8 = 22.2$. Scaling to the known $\delta_H$ value of 7.2 gives: $\delta_{HD} = 0.658 \times 5.4 = 3.55$ and $\delta_{HA} = 0.658 \times 22.2 = 14.60$.

Formamide has two donors: two amide NH bonds with donor strength 2.9. The N-C=O moiety acts as 1 acceptor (as checked with DFT) with strength 8.3 (amide), but it still is counted double because the oxygen can accept two hydrogen bonds. No extra CH donors are needed to fill the count but otherwise the hydrogen neighboring the amide CO would simply count as an aldehyde (strength 1.6). The summed donor strength thus becomes: $2 \times 2.9 = 5.8$; the summed acceptor strength is: $2 \times 8.3 = 16.6$. Scaling to the known $\delta_H$ value of 19.0 gives: $\delta_{HD} = 1.936 \times 5.8 = 11.23$ and $\delta_{HA} = 1.936 \times 16.6 = 32.14$.

For a few molecules we have made an exception:

Chloroform has only one donor (CH with strength 2.2) and three acceptors (chlorides with strength 0.8). According to the rule above two donors with strength zero should be added: donors: $2.2 + 0 + 0 = 2.2$; acceptors: $3 \times 0.8 = 2.4$. However, since it is known that chloroform acts much more as a donor than as an acceptor, we decided to not perform this correction in this case, so donor = 2.2 and acceptor = 0.8. Scaling to the known $\delta_H$ value of 5.7, this gives: $\delta_{HD} = 4.297 \times 2.2 = 9.45$ and $\delta_{HA} = 4.297 \times 0.8 = 3.44$.

Tetrachloroethylene has no donors whatsoever and hence has a $\delta_{HD}$ of zero. This fits with the $\delta_H$ being zero. Conversely, the acceptor strength is $4 \times 1.3 = 5.2$. However, because of the zeros, there is no mathematical way to scale this acceptor strength to get a $\delta_{HA}$. Hence, we copied the value of trichloroethane for this molecule: $\delta_{HA} = 1.9$ (and $\delta_{HD} = 0$).

For some other solvents that may be used regularly, we obtained the following parameter values:

<table>
<thead>
<tr>
<th>Solvent</th>
<th>$\delta_H$</th>
<th>$\delta_{HD}$</th>
<th>$\delta_{HA}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Toluene</td>
<td>2.0</td>
<td>1.35</td>
<td>2.97</td>
</tr>
<tr>
<td>Diethyl ether</td>
<td>4.6</td>
<td>1.90</td>
<td>11.16</td>
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<tr>
<td>Acetone</td>
<td>7.0</td>
<td>3.56</td>
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<tr>
<td>Acetonitrile</td>
<td>6.1</td>
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<tr>
<td>Methanol</td>
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<tr>
<td>Water</td>
<td>42.3</td>
<td>33.37</td>
<td>53.63</td>
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</table>
2. Derivation of mixing rules for solvent blends

In the original Hansen methodology, the Hansen parameters for solvent blends can be calculated by a simple linear interpolation of the constituting solvents’ parameters on the basis of the volume/volume ratio of the solvents in the blend. However, like the original Hansen methodology itself, this rule is only empirical, and to the best of our knowledge no mathematical proof has ever been given for this mixing rule.

Now that improved the methodology from empirical to thermodynamically correct, we can check whether this empirical mixing rule is also thermodynamically correct. Moreover, we need to derive mixing rules for the newly introduced parameters.

Mixing rules for $\delta_D, \delta_P$, and $\delta_H$

In the following we consider the dissolution of solute S in a blend of solvents A and B, where $x'$ is the volume fraction of A in the mixture AB and $y'$ is the volume fraction of S. First, let’s define the enthalpy of mixing for the blend itself:

When mixing small amounts of B into A, for every volume of B that is added, all B–B interactions are broken, which costs a summed energy $E_{BB}$. When molecules A and B have equal sizes, the same amount of A–A interactions is broken and twice that amount A–B interactions are formed. Thus, the enthalpy of mixing of A and B is:

$$\Delta H_{AB} = (2E_{AB} - E_{AA} - E_{BB})$$

For larger amounts of B, assuming regular mixing, the volume fraction, $x'$, comes into the equation:

$$\Delta H_{AB} = x'(1 - x')(2E_{AB} - E_{AA} - E_{BB})$$

Similarly, for the dissolution of S in pure A or pure B:

$$\Delta H_{SA} = y'(1 - y')(2E_{SA} - E_{AA} - E_{SS})$$

$$\Delta H_{SB} = y'(1 - y')(2E_{SB} - E_{BB} - E_{SS})$$

Again similarly, the enthalpy of mixing for dissolution of S in AB (still assuming regular mixing) is:

$$\Delta H_{S(AB)} = y'(1 - y')(2x'E_{SA} + 2(1 - x')E_{SB} - E_{SS} - (x'x'E_{AA} + (1 - x')E_{BB} + 2x'(1 - x'E_{AB}))$$

In terms of $\Delta H_{SA}$ etc. that becomes:

$$\Delta H_{S(AB)} = x'\Delta H_{SA} + (1 - x')\Delta H_{SB} - y'(1 - y')\Delta H_{AB}$$

If we now look at the relation between $\delta$ and $\Delta H$ (for regular mixing),

$$\Delta H_{AB} = -\beta x'(1 - x') = \frac{1}{2} x'(1 - x')[(\delta_{DA} - \delta_{DB})^2 + (\delta_{PA} - \delta_{PB})^2 + (\delta_{HA} - \delta_{HB})^2]$$

, we can substitute equation 7 (and similar ones for $\Delta H_{SA}, \Delta H_{SB}$, and $\Delta H_{S(AB)}$) into equation 6, resulting in:

$$y'(1 - y')[(\delta_{DS} - \delta_{DAB})^2 + (\delta_{PS} - \delta_{PAB})^2 + (\delta_{HS} - \delta_{HAB})^2]$$

$$= x'y'(1 - x')[(\delta_{DS} - \delta_{DAB})^2 + (\delta_{PS} - \delta_{PAB})^2 + (\delta_{HS} - \delta_{HAB})^2]$$

$$+ (1 - x'y')(1 - y')[(\delta_{DS} - \delta_{DAB})^2 + (\delta_{PS} - \delta_{PAB})^2 + (\delta_{HS} - \delta_{HAB})^2]$$

$$- y'(1 - y')x'(1 - x')[(\delta_{DA} - \delta_{DB})^2 + (\delta_{PA} - \delta_{PB})^2 + (\delta_{HA} - \delta_{HB})^2]$$

Dividing everything by $y'(1 - y')$ and writing only the $\delta_D$ part of the equation, we obtain:
\[(\delta_{BS} - \delta_{DB})^2 = x'(\delta_{BS} - \delta_{DA})^2 + (1 - x') (\delta_{BS} - \delta_{DB})^2 - x'(1 - x') (\delta_{DA} - \delta_{DB})^2 \]  

(9)

Working out the squares and noticing the \(\delta_{DB}^2\) terms cancel, we obtain:

\[
\delta_{AB}^2 - 2\delta_{DB}\delta_{DB} = x'\left((\delta_{DA}^2 - 2\delta_{DB}\delta_{DA}) + (1 - x')\left((\delta_{DB}^2 - 2\delta_{DA}\delta_{DB})
- x'(1 - x')\delta_{DA}^2 + \delta_{DB}^2 - 2\delta_{DA}\delta_{DB}\right)\right)
\]

(10)

Collecting terms further, we obtain:

\[
\delta_{AB}^2 - 2\delta_{DB}\delta_{DB} = \left[x'^2\delta_{DA}^2 + (1 - x')^2\delta_{DB}^2 + 2x'(1 - x')\delta_{DA}\delta_{DB}\right] - 2x'^2\delta_{DA}\delta_{DA}
- 2(1 - x')\delta_{DB}^2
\]

(11)

And the solution of equation 11 is:

\[
\delta_{DB} = x'\delta_{DA} + (1 - x')\delta_{DB}
\]

(12)

The same can be done for \(\delta_p\) and \(\delta_m\) showing that the mixing rule for each term is indeed simple linear interpolation.

**Molecules of different sizes**

When molecules A, B, and S don’t have equal sizes, equations 1-5 become slightly more complicated: When molecules A and S are of equal size, the summed energies \(E_{AA}\) and \(E_{SB}\) are equal to the total cohesive energies per volume in pure A and B, respectively. However, when molecules A are smaller than molecules B, \(E_{BB}\) is still the total cohesive energy, but \(E_{AA}\) is only the sum of the A–A bonds that is broken when liquid A is broken in pieces of the size of molecules B. Imagine that exactly two molecules A fit in one molecule B; replacing these two molecules A for one molecule B will break all bonds of these A molecules with other molecules A, but the interaction between the two molecules will stay. Hence, in this case \(E_{AA}\) is smaller than the total cohesive energy per volume A.

More precise: to dissolve a volume of B, the same area of A–A interactions need to be broken as the area of B–B interactions that is broken. We call this \(E_{AA}(B)\), the total summed energy of A–A interactions over a molecular area of the size of the total molecular area present in a volume of pure B. Similarly, for dissolution of S in A or B, \(E_{AS}(S)\) and \(E_{SB}(S)\) are defined as the sum of all interactions over the total molecular area present in a volume of pure S (assuming molecules S are larger than molecules A and B).

Hence, when \(S > B > A\), in equations 2, 3, and 4, \(E_{AA}, E_{AS}\), and \(E_{BB}\) should be replaced by \(E_{AA}(B)\), \(E_{AS}(S)\), and \(E_{BB}(S)\), respectively, and in equation 5 we get the terms \(E_{AS}(S), E_{BB}(S),\) and \(E_{BB}(S)\). Now, when we collect all terms, equation 6 becomes:

\[
\Delta H_{S(AB)} = x' \Delta H_{SA} + (1 - x') \Delta H_{SB} - y' (1 - y') \Delta H_{AB}
+ x' (1 - x') y' (1 - y') \left[E_{AA}(B) - E_{AA}(S) + E_{BB}(B) - E_{BB}(S) - 2E_{AB}(B)\right]
+ 2E_{AB}(S)
\]

(13)

Thus, we see there is only a correction term when molecules S are larger than molecules B, and the correction is opposite in sign than \(\Delta H_{AB}\). Thus, when the solute has small molecules, the correct estimate of a solvent blend's \(\delta\) parameters is linear interpolation, also when the solvents in the blend have different sized molecules. But when the solute has large molecules, a blend will always dissolve it slightly better than its \(\delta\) parameters suggest, especially when the solvents in the blend have difficulty mixing. Note that a blend that mixes exothermally will be a somewhat worse solvent than its \(\delta\) parameters suggest, but only when the solute has large molecules.
Mixing rules for $\delta_{HD}$ and $\delta_{HA}$

Next we derive the mixing rules for the newly introduced $\delta$ parameters for hydrogen bond donor and acceptor strength, $\delta_{HD}$ and $\delta_{HA}$. This means that in equation 7 $(\delta_{HA} - \delta_{HB})^2$ is replaced by $(\delta_{HD,A}\delta_{HA,B} + \delta_{HD,B}\delta_{HA,A} - \delta_{HD,A}\delta_{HA,A} - \delta_{HD,B}\delta_{HA,B})$, which leads to an equation for $\delta_{HD}$ and $\delta_{HA}$ similar to equation 9:

$$
\begin{align*}
\delta_{HD,S}\delta_{HA,AB} - \delta_{HD,AB}\delta_{HA,S} - \delta_{HD,AB}\delta_{HA,AB} &= x'(\delta_{HD,S}\delta_{HA,A} + \delta_{HD,A}\delta_{HA,S} - \delta_{HD,S}\delta_{HA,S}) \\
&+ (1 - x')(\delta_{HD,S}\delta_{HA,B} + \delta_{HD,B}\delta_{HA,A} - \delta_{HD,B}\delta_{HA,B}) \\
&- x'(1 - x')\delta_{HD,A}\delta_{HA,B} + \delta_{HD,B}\delta_{HA,A}
\end{align*}
$$

(14)

Working out some brackets and collecting all terms, we obtain:

$$
\begin{align*}
\delta_{HD,S}\delta_{HA,AB} + \delta_{HD,AB}\delta_{HA,S} - \delta_{HD,AB}\delta_{HA,AB} &= \left[x'\delta_{HD,S}\delta_{HA,A} + (1 - x')\delta_{HD,B}\delta_{HA,B}\right] + \left[x'\delta_{HD,A}\delta_{HA,S} + (1 - x')\delta_{HD,B}\delta_{HA,B}\right] \\
&- \left[x'^2\delta_{HD,A}\delta_{HA,B} + (1 - x')^2\delta_{HD,B}\delta_{HA,A} + x'(1 - x')\delta_{HD,A}\delta_{HA,B}\right] \\
&+ x'(1 - x')\delta_{HD,B}\delta_{HA,A}
\end{align*}
$$

(15)

With again as obvious solution:

$$
\begin{align*}
\delta_{HA,AB} &= x'\delta_{HA,A} + (1 - x')\delta_{HA,B} \quad \text{and} \\
\delta_{HD,AB} &= x'\delta_{HD,A} + (1 - x')\delta_{HD,B}
\end{align*}
$$

(16)

Hence we see that also for $\delta_{HD}$ and $\delta_{HA}$ the correct mixing rule is linear interpolation on the basis of the volume/volume ratio of the solvents in the blend.

Mixing rule for $r_{solvent}$

Finally, we have introduced a solubility radius for the solvent, so in the case of solvent blends we need a mixing rule for this $r_{solvent}$ as well. In our work we use the assumption that $r_{solvent}$ is inversely proportional to the molar volume. The mixing rule derived here follows from the same assumption. Obviously when non-ideal behavior of some solvents is taken into account, leading to different solvent radii, also the mixing rule may deviate.

Another way of saying that $r_{solvent}$ is inversely proportional to the molar volume is to say it is proportional to the number of molecules per liter. The number of molecules in a mixture of $A$ and $B$, where $x'$ is the volume fraction of $A$ in the blend, is:

$$
N = \left(\frac{x'}{V_{MA}} + \frac{1 - x'}{V_{MB}}\right)V
$$

(17)

This straightforwardly leads to:

$$
r_{AB} = x'r_A + (1 - x')r_B
$$

(18)

Hence we see that for all parameters conveniently the same mixing rule applies.
3. Description of the optimization procedure

Since optimizing the best fit for (improved) Hansen spheres is not straightforward, here we describe our procedure as implemented in the script made available. In fact, this procedure is not perfect, as touched upon in the main text, but in combination with using a grid of starting points it does the job.

First of all, a starting estimate is made by averaging the parameters of all solvents that do dissolve the solute at hand. Then a grid of 129 starting positions is set up with a maximum distance of four units from that first estimate. For each of these starting positions first the sphere radius is optimized followed by an optimization of all other parameters, as detailed below, until convergence is reached. Finally out of the 129 optimizations, the best one is selected and given as output.

At each step of the optimization, for each solvent the parameter distance to the current center of the Hansen sphere is calculated taking into account all described improvements, and the minimum radius for the sphere is calculated to include the data point (taking into account the inverse sum of radii). Then derivatives are calculated to find the direction to improve the fitted parameters. It should be noted, though, that these derivatives are discontinuous when the data points enter or leave the fitted sphere (whenever a point is at the correct side of the sphere, the derivatives fall to zero immediately), making convergence somewhat cumbersome.

After every optimization step of the other parameters the sphere radius is fully re-optimized. The donor/acceptor parameters, $\delta_{\text{HD}}$ and $\delta_{\text{HA}}$, are optimized alongside with the main Hansen parameters, while at every step they are rescaled to be consistent with the $\delta_{\text{H}}$ parameter. For the ratio between $\delta_{\text{HD}}$ and $\delta_{\text{HA}}$ a maximum ratio of 20 was used. The $c_{\text{melt}}$ parameter ($c_{\text{solid}}$ in the code) is optimized while optimizing the radius.

When a perfect fit is found, the optimization for that starting point is stopped. In that case, at the end, all perfect solutions are averaged and –after re-optimizing the radius– the average is given as output.

Note that when a narrow perfect fit or an almost perfect fit of the data exists, the implemented procedure has difficulty in converging to the best fit, probably due to the Boolean nature of the data. Adding a small randomness may help to overcome these difficulties. For that reason at some points in the code we have deviated slightly from the mathematically correct derivatives when this was found to help convergence.

All in all, the optimization procedure can likely be improved by combining it with a method to search for possible perfect fits first, but due to all the non-linear improvements introduced in our work this is mathematically challenging. Nonetheless, by starting the optimization from a grid of starting points, the current procedure gives good results.
input_fitresults

fitresults

#name deltaD deltaP deltaH donor acceptor radius melting_correction molar_volume melting_point

Solute1 18.0925 7.55555 6.53719 6.01725 7.04154 4.66913 6.8 256 432    #Based on high and low temperature data
Solute2 17.2525 11.3424 10.5254 7.80387 14.1944 4.55527 5.7 237 474   #Based on room temperature only

input_options

options

#lines starting with a "#" are ignored.

useorigHansen 0          # 0 or 1 (origHansen should be combined with xfactor=2, but this is not enforced)
xfactor 1                # 1 or 2
correct4solid 1          # 0 or 1; should be 1 for solids and 0 for liquids

correctc_solidfortemp 2  # 0, 1 or 2; 0 means no correction (incorrect!); 1 means ignoring heat capacity effects; 2 means average of 0 and 1 because 1 seems to overcorrect sometimes; N.B. this option only has significant effect when mixing data at different temperatures or making predictions at extrapolated temperatures (otherwise numerical effects may occur).

input_predictions

predictions

# solute solvent/mix concentration(in_mol/L) yes/no/? temperature_in_K(default=295)
# in case of mixtures use: "mix" nr_solvents name_solvent1 amount_solvent1
name_solvent2 amount_solvent2 etc (the sum of the amounts should be normalized to 1)

Solute1 51 1.25 ? 277
Solute1 52 1.25 ? 277
Solute 53 1.25 ? 277
Solute mix 2 30 0.5 31 0.5 1.25 ? 277
Solute mix 2 30 0.4 31 0.6 1.25 ? 277
Solute mix 2 30 0.3 31 0.7 1.25 ? 277
Solute mix 3 21 0.3792 34 0.0987 38 0.5221 1.25 ?
Solute mix 3 38 0.0681 34 0.4858 5 0.4461 1.25 ?
Solute mix 4 49 0.072 ? 273
Solute mix 5 50 0.072 ? 273
Solute mix 2 43 0.7 32 0.3 0.072 ? 273
Solute mix 2 21 0.4 29 0.6 0.072 ? 273
Solute mix 2 43 0.7 32 0.3 0.072 ?
Solute mix 2 21 0.4 29 0.6 0.072 ?
Solute mix 2 21 0.6 29 0.4 0.072 ?
Solute 3 0.16 no 273
Solute 3 0.16 no 273
Solute 3 formic_acid 0.16 no 273
Solute mix 2 25 0.5 35 0.5 0.16 yes 273
Solute mix 2 31 0.7 30 0.3 0.16 yes 273
Solute mix 2 35 0.5 23 0.5 0.16 no 273

in solvents

solventdata

#nr_or_name description deltaD deltaP deltaH donor acceptor molar_volume

1 toluene 18 1.4 2 1.3478 2.9678 106.6
2 chloroform 17.8 3.1 5.7 9.4486 3.4386 80.5
3 1,1,1-trichloroethane 16.8 4.3 2 2.07122 1.93122 99.3
4 tetrachloroethylene 18.3 5.7 0 0 1.9 102.8
5 diethyl_ether 14.5 2.9 4.6 1.89663 11.1566 104.7
6 acetone 15.5 10.4 7 3.56083 13.7608 73.8
10 ethyl acetate 15.8 5.3 7.2 3.55055 14.6006 98.6
8 acetonitrile 15.3 18 6.1 3.66972 10.1397 52.9
9 formamide 17.2 26.2 19 11.2316 32.1416 39.9
10 methanol 14.7 12.3 22.3 12.4222 40.0322 40.6
11 ethanol 15.8 8.8 19.4 10.809 34.819 58.6
12 water 15.5 16 42.3 33.3661 53.6261 18
formic acid formic acid 14.6 10 14 9.37 20.91 37.7

**input_testdata**

testdata

# First a line must be given with the name of the compound followed by its molar volume and its melting point in Kelvin, and optionally a default temperature in Kelvin

# (The molar volume can be calculated by dividing the molar mass by the density)

# (For low melting points, the melting point should be measured correctly; for high melting points, any estimate should suffice)

# (If no temperature is specified, room temperature (295K) is taken as default temperature)

# The other lines must follow the following format (if no temperature is specified, the abovementioned default temperature is assumed):

# name(or_nr)_solvent dissolves(yes/no) concentration(in_mol/L) temperature(in_K)

solute Solute1 246 387 297
1 no 0.072
mix 2 1 0.5 2 0.5 no 0.072
2 no 0.072
3 no 0.072
4 yes 0.072
5 no 0.072
6 yes 0.072
7 yes 0.072
8 yes 0.072
9 no 0.072
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**solute Solute2 277 372**

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Manual for the Matlab function \textit{fit\_sphere}, implementing the improved Hansen methodology

\textit{Fit\_sphere} is the Matlab function that implements the improved Hansen methodology, written by Manuel J. Louwerse from the University of Amsterdam. The function uses several plain text input files which can be invoked in random order. For each input file type, multiple files are allowed; all information will simply be added. There are five types of input files: options, solvent data, test data, fit results, and predictions. The type of the file needs to be given on the first line of each input file. For all file types, empty lines and lines starting with a dash (#) are ignored. Also at the end of lines it is always allowed to add comments starting with a dash. Together with the Matlab function, we distribute example files of each type, containing comments describing the format. For further explanations we refer to the publication in ChemPhysChem.

The \textit{fit\_sphere} function is issued with the following command in Matlab, although different names for the input files can be used:

\begin{verbatim}
fit_sphere({'input_options.txt';'input_solvents.txt';'input_testdata.txt';'input_fitresults.txt';'input_predictions.txt'})
\end{verbatim}

The output is always written in the file “output.txt” in the working directory.

- It is required to have an options input file, in which several runtime options are specified, see the example file.

- Also a solvent data input file is required, in which the Hansen parameters, donor-acceptor splits for the deltaH parameter, and the molar volumes of all solvents are given. Note that in the names of the solvents no spaces are allowed. Mixtures of solvents are defined in the files where they are used: test data or predictions input files.

- One or more test data files or fit results files are required. Test data files contain the experimentally determined results on which the sphere fitting is based. This file can contain data for more than 1 solute; if so, for each solute a sphere will be fitted. If, for a solute, data is given at multiple concentrations or temperatures, this will be used together, i.e. fitting one sphere with mixed data. Concentrations (in mol/L) are mandatory. Temperatures can be left out; in that case 295K is assumed. Alternatively, a fit results file can be specified. The idea of this file is that it prevents having to run the slow fitting procedure over and over again when one only wants to do some quick predictions. The fit results file should contain the results of previously performed fits. It is possible to specify both test data files and fit results files. In that case, the test data will be used to fit spheres for the solutes in the test data files and for the other solutes the data from
the fitresults files will be used. If the same solute is specified in both type of
files, the old fitresults will be overruled by the new testdata.

- The predictions inputfile is not required. If present, it contains definitions of
solutes and solvents for which a prediction is desired at the given
concentration and temperature. Again, if no temperature is specified, 295K is
assumed. If the experiment has already been done, the result (yes or no) can
be given as well. The script will then keep count of the number of correct and
incorrect predictions and write these counts in the output file. If the
experimental result is not known, a question mark (?) should be specified.

In the testdata and predictions inputfiles, also mixtures of solvents can be
defined. In that case, instead of a single column with the name or the number of
the solvent, a complete definition is given of the mixture, starting with the word
"mix". The format of this definition is as follows: "mix" (nr of solvents) name1
fraction1 name2 fraction2 etc.

Examples: "mix 2 10 0.5 25 0.5" means a mixture of two solvents, namely 50%
of solvent nr 10 and 50% of solvent nr 25.

"mix 3 41 0.1 A10 0.7 formic_acid 0.2" means a mixture of three solvents,
namely 10% of solvent 41, 70% of solvent A10, and 20% of formic_acid.

Note that the solvent fraction should always add up to 1; otherwise an error
message is issued. The solvent fractions are defined as volume fractions.

Units:

The Hansen parameters D, P, H, Hdonor, and Hacceptor should be given in SI
units (MPa^1/2), the same unit as typically used in the Hansen software.
Temperatures and melting points are always in Kelvin. Molar volumes are
expected in mL/mol, and can be calculated by dividing the molar mass (g/mol)
by the density (g/mL) of the pure substance. Concentrations are given in mols solute
per liter of solvent (not per liter of solution!). Solvent fractions in mixed solvents
are expected in volume fractions.

Compared to the original Hansen method, two additional quantities of the solute
have to be entered: the molar volume and the melting point. When measuring
these quantities is problematic, an estimate of the molar volume based on a
density of 1 should suffice. For polymers any large number (e.g. 1E10) can be
entered for the molar volume, as long as it is consistent with the entered
concentrations (e.g. 1E-11).

The melting point is only important when data with mixed temperatures is used
or when predictions at extrapolated temperatures are desired. Otherwise any
reasonable number suffices. Also when extrapolations are desired, the rule is that
for low melting points a higher accuracy is needed than for high melting points (for
a melting point around 350K the inaccuracy should be less than 10 degrees; for a melting point around 400K, an inaccuracy of 20 degrees is still oke).

Sphere radii are in principle in the same unit as the Hansen parameters, but because in this improved method the relations are not linear anymore, one should be very careful with interpreting the sphere radius. Also it should be mentioned that the sphere radius as given by the software is extrapolated to a 1:1 molar mixing ratio between solute and solvent (note that, as a result, the software may report a negative radius; this is not a bug). The reason for this is that the software can handle mixed data for multiple concentrations and these datapoints have to be extrapolated to one single concentration in order to compare them correctly. The reason again for this is that for some equations the volume fraction matters and for other equations the molar fraction matters. As it is impossible to keep both constant, the software needs to be able to work with mixed data. As a bonus this means that this improved method can also make predictions at extrapolated concentrations, but obviously the accuracy is best when extrapolation is kept limited.

The same is true for temperatures: The software can work with mixed data and the reported sphere radius is for solubility at room temperature (295K). The Hansen parameters are considered to be the same at all temperatures.

Also, the sphere radius depends on the correction for solid melting, so it is not allowed to fiddle with the value of this correction and keep using the same value for the radius.

Finally, we stress that the scale of the solubility parameters (and especially the radius) depend on the options set in the options inputfile. Therefore, one should always make sure that while making predictions the exact same options are set as when making the fitresults file. When the options during predicting are not consistent with the options used for the fitting, the predictions will be highly incorrect.
fit_sphere

function fit_sphere(filenames)  %filenames is a cell array with names of inputfiles, e.g.:    fit_sphere({'input_options.txt';'input_solvents.txt'})

    global useorigHansen xfactor correct4solid correctc_solidfortemp
    maxratioDA=20;

    options_present=0; solventdata_present=0; testdata_present=0;
    predictions_present=0; fitresults_present=0;
    nsolvents=0; nsolutes=0; npredictions=0; nprefits=0; nmixes=0; nsolventstotal=0;
    solventx=[]; solvency=[]; solventz=[]; solventzD=[]; solventzA=[]; molvolume=[];
    solventr=[];
    name_solute=cell(1); molvolume_solute=[]; Tm_solute=[];
    npuresinmix=[]; namepureinmix=cell(1,1); amountpureinmix=[];
    npredictions=0; predictsolvent=cell(1); predictsolute=cell(1); predictresult=cell(1);
    predictconc=[]; predicttemp=[];
    nprefits=0; prefitsolute=cell(1); prefitch[]=prefity[]=prefitz[]=prefitD[]=prefitzA[]=prefitr[]=prefitc_solid[]=prefitvolume[]=prefiTm=[];
    npositives=[]; positive=[]; xpositive=[]; ypositive=[]; zpositive=[]; zDpositive=[];
    zApositive=[]; rpositive=[]; volpositive=[]; concpositive=[]; temppositive=[];
    nnegatives=[]; negative=[]; xnegative=[]; ynegative=[]; znegative=[]; zDnegative=[];
    zAnegative=[]; rnegative=[]; vlnegative=[]; concnegative=[]; tempnegative=[];
    xsphere=0; ysphere=0; zsphere=0; zDsphere=0; zAsphere=0; radius=0; c_solid=0;
    closestminus=0; furthestplus=0; nextminusin=0; nextminusout=0; nextplusin=0;
    nextplusout=0; deltaoff=0; improvev=0; improvev=0; improvez=0; improveDonor=0;
    improveAcceptor=0; summinus_drdsolid=0; sumplus_drdsolid=0;
    offtotal=0; nminus=0; nplus=0; fitquality=0;
    nperfect=0; avgx=0; avgy=0; avgz=0; avgzD=0; avgzA=0; avgr=0; avgcsolid=0;
    minx=0; miny=0; minz=0; minzD=0; minzA=0; minr=0; mincsolid=0; maxx=0;
    maxy=0; maxz=0; maxzD=0; maxzA=0; maxr=0; maxcsolid=0;
function readinputs % nested function within fit_sphere

% First set some defaults:
useorigHansen=0;
xfactor=1;
correct4solid=0;
correctc_solidfortemp=2;

% Then read in all input files in random order:

nfilenames=size(filenames,1);
for ifile=1:nfilenames
    filenamechar=char(filenames(ifile,:));
currentfile=fopen(filenamechar);
filename=filenames(ifile,:);
fileended=0;
iline=0;
while (fileended==0)
    linestring=fgetl(currentfile);
    if (linestring==-1)
        fclose(currentfile);
        break
    end
    iline=iline+1;
    inputdata=strsplit(linestring);
    if (iline==1)
        if (strcmp(inputdata(1),'options'))
            options_present=1;
            current=inputdata(1);
        elseif (strcmp(inputdata(1),'solventdata'))
            solventdata_present=1;
            current=inputdata(1);
        end
    end
end
elseif (strcmp(inputdata(1),'testdata'))
    testdata_present=1;
    current=inputdata(1);
elseif (strcmp(inputdata(1),'predictions'))
    predictions_present=1;
    current=inputdata(1);
elseif (strcmp(inputdata(1),'fitresults'))
    fitresults_present=1;
    current=inputdata(1);
else
    error(['Error: First line of file ',char(filename),' should be:  "options",  
    "solventdata", "testdata", "fitresults", or "predictions". Exit.']);
end
end
if (iline>1 && not(strncmp(inputdata(1),'#',1)) && not(strcmp(inputdata(1),''))) 
if (strcmp(current,'options'))
    if (strcmp(inputdata(1),'useorigHansen'))
        useorigHansen=str2double(char(inputdata(2)));
    end
    if (strcmp(inputdata(1),'xfactor'))
        xfactor=str2double(char(inputdata(2)));
    end
    if (strcmp(inputdata(1),'correct4solid'))
        correct4solid=str2double(char(inputdata(2)));
    end
    if (strcmp(inputdata(1),'correctc_solidfortemp'))
        correctc_solidfortemp=str2double(char(inputdata(2)));
    end
end
if (strcmp(current,'solventdata'))
% check for duplicate information; if the solvent already has been read in, no new entry will be made but its data will be overwritten

already=0;
for i=1:nsolvents
    if (strcmp(name_solvent(i),inputdata(1)))
        already=1;
        solvent=i;
    end
end
if (already==0)
    nsolvents=nsolvents+1;
    name_solvent(nsolvents)=inputdata(1);
    solvent=nsolvents;
end
solventx(solvent)=str2double(char(inputdata(3)));
solventy(solvent)=str2double(char(inputdata(4)));
solventz(solvent)=str2double(char(inputdata(5)));
solventzD(solvent)=str2double(char(inputdata(6)));
solventzA(solvent)=str2double(char(inputdata(7)));
molvolume(solvent)=str2double(char(inputdata(8)));
end

if (strcmp(current,'testdata'))
    if (strcmp(inputdata(1),'solute'))
        already=0;
        for i=1:nsolutes
            if (strcmp(name_solute(i),inputdata(2)))
                already=1;
                solute=i;
            end
        end
    end
end
if (already == 0)
    nsolutes = nsolutes + 1;
    name_solute(nsolutes) = inputdata(2);
    solute = nsolutes;
    ntestdata(solute) = 0;
end

molvolume_solute(solute) = str2double(char(inputdata(3)));
Tm_solute(solute) = str2double(char(inputdata(4)));
if (size(inputdata, 2) > 4 && not(strncmp(inputdata(5), '#', 1)))
    defaultT = str2double(char(inputdata(5)));
else
    defaultT = 295;
end
else
    if (not(strcmp(inputdata(1), 'mix')))
        if (size(inputdata, 2) > 3 && not(strncmp(inputdata(4), '#', 1)))
            temperature = str2double(char(inputdata(4)));
        else
            temperature = defaultT;
        end
    already = 0;
    for i = 1:ntestdata(solute)
        if (strcmp(testsolvent(solute, i), inputdata(1)) &&
            strcmp(testresult(solute, i), inputdata(2)) &&
            testconc(solute, i) == str2double(char(inputdata(3))) &&
            testtemp(solute, i) == temperature)
            % duplicate data ignored
            already = 1;
        end
    end
end
if (already == 0)
    ntestdata(solute) = ntestdata(solute) + 1;
    testsolvent(solute, ntestdata(solute)) = inputdata(1);
testresult(solute,ntestdata(solute))=inputdata(2);
testconc(solute,ntestdata(solute))=str2double(char(inputdata(3)));
testtemp(solute,ntestdata(solute))=temperature;
testfile(solute,ntestdata(solute))=filename;
testline(solute,ntestdata(solute))=iline;
end
end

if (strcmp(inputdata(1),'mix'))
    npures=str2double(char(inputdata(2)));
    if (size(inputdata,2)>4+2*npures &&
        not(strncmp(inputdata((5+2*npures)),'#',1)))
        temperature=str2double(char(inputdata((5+2*npures))));
    else
        temperature=defaultT;
    end
    nsame=0;
    already=0;
    for i=1:nmixes
        if (npuresinmix(i)==npures)
            almostsame=1;
            for j=1:npures
                if (not(strcmp(namepureinmix(i,j),inputdata((1+2*j)))) ||
                    amountpureinmix(i,j)<str2double(char(inputdata((2+2*j)))))
                    almostsame=0;
                end
            end
        end
    end
    if (almostsame==1)
        nsame=nsame+1;
        same{nsame}=['mix_',num2str(i)];
    end
    end
end
for i=1:nsame
    for j=1:ntestdata(solute)
        if (strcmp(testsolvent(solute,j),same(i)) &
        strcmp(testresult(solute,j),inputdata((3+2*npures))) &
        testconc(solute,j)==str2double(char(inputdata((4+2*npures)))) &
        testtemp(solute,j)==temperature)
            % duplicate data ignored
            already=1;
        end
    end
end
if (already==0)
    nmixes=nmixes+1;
    npuresinmix(nmixes)=str2double(char(inputdata(2)));
    mixfile(nmixes)=filename;
    mixline(nmixes)=iline;
    sum=0;
    for i=1:npuresinmix(nmixes)
        namepureinmix(nmixes,i)=inputdata((1+2*i));
        amountpureinmix(nmixes,i)=str2double(char(inputdata((2+2*i))));
        sum=sum+amountpureinmix(nmixes,i);
    end
    if (sum~=1)
        error(['Error: ',char(filename),': The amounts in the mixture in line '
        ',num2str(iline),' do not add up to 1. Exit.']);
    end
    ntestdata(solute)=ntestdata(solute)+1;
    testsolvent{solute,ntestdata(solute)}='mix_'.num2str(nmixes);
    testresult(solute,ntestdata(solute))=inputdata((3+2*npures));
    testconc(solute,ntestdata(solute))=str2double(char(inputdata((4+2*npures))));
    testtemp(solute,ntestdata(solute))=temperature;
    testfile(solute,ntestdata(solute))=filename;
testline(solute,ntestdata(solute))=iline;
end
end
end
end

if (strcmp(current,'predictions'))
npredictions=npredictions+1;
predictsolute(npredictions)=inputdata(1);
if (not(strcmp(inputdata(2),'mix')))
predictsolvent(npredictions)=inputdata(2);
predictconc(npredictions)=str2double(char(inputdata(3)));
predictresult(npredictions)=inputdata(4);
if (size(inputdata,2)>4 && not(strcmp(inputdata(5),'#',1)))
predicttemp(npredictions)=str2double(char(inputdata(5)));
else
predicttemp(npredictions)=295;
endif
endif

if (strcmp(inputdata(2),'mix'))
nmixes=nmixes+1;
predictsolvent(npredictions)=['mix_',num2str(nmixes)];
npuresinmix(nmixes)=str2double(char(inputdata(3)));
mixfile(nmixes)=filename;
mixline(nmixes)=iline;
sum=0;
for i=1:npuresinmix(nmixes)
  namepureinmix(nmixes,i)=inputdata((2+2*i));
  amountpureinmix(nmixes,i)=str2double(char(inputdata((3+2*i))));
  sum=sum+amountpureinmix(nmixes,i);
end
if (sum~=1)
    error(['Error: ',char(filename),': The amounts in the mixture in line ',num2str(iline),' do not add up to 1. Exit.']);
end

predictconc(npredictions)=str2double(char(inputdata((4+2*npuresinmix(nmixes)))));
predictresult(npredictions)=inputdata((5+2*npuresinmix(nmixes)));
if (size(inputdata,2)>5+2*npuresinmix(nmixes) &&
    not(strncmp(inputdata((6+2*npuresinmix(nmixes))),'#',1)))
    predicttemp(npredictions)=str2double(char(inputdata((6+2*npuresinmix(nmixes)))))
else
    predicttemp(npredictions)=295;
end
end
end

if (strcmp(current,'fitresults'))
    nprefits=nprefits+1;
    prefitsolute(nprefits)=inputdata(1);
    prefixx(nprefits)=str2double(char(inputdata(2)));
    prefity(nprefits)=str2double(char(inputdata(3)));
    prefixz(nprefits)=str2double(char(inputdata(4)));
    prefixzD(nprefits)=str2double(char(inputdata(5)));
    prefixA(nprefits)=str2double(char(inputdata(6)));
    prefixr(nprefits)=str2double(char(inputdata(7)));
    prefixc_solid(nprefits)=str2double(char(inputdata(8)));
    prefixvolume(nprefits)=str2double(char(inputdata(9)));
    prefixTm(nprefits)=str2double(char(inputdata(10)));
end
end
end
if (options_present~=1)
    error( 'Error: No options file specified.' )
end
if (solventdata_present~=1)
    error( 'Error: No solventdata file specified.' )
end
if (testdata_present~=1 && fitresults_present~=1)
    error( 'Error: No experimental data file and no fitresults file specified.' )
end
if (xfactor~=1 && xfactor~=2)
    error( 'Error: Option xfactor can only be 1 or 2; otherwise the sphere radii of the solvents are not calibrated. Exit.' )
end

% Calibrate the sphere radii of the solvents:
for i=1:nsolvents
    if (xfactor==1)
        solventr(i)=1520/molvolume(i);
    end
    if (xfactor==2)
        solventr(i)=1545/molvolume(i);
    end
end

% For all mixes the solvent parameters, the sphere radius, and the effective molecular volumes are now calculated:
nsolventstotal=nsolvents+nmixes;
for i=1:nmixes
    name_solvent{nsolvents+i}=['mix_',num2str(i)];
    solventx(nsolvents+i)=0; solventy(nsolvents+i)=0; solventz(nsolvents+i)=0;
    solventzD(nsolvents+i)=0; solventzA(nsolvents+i)=0; solventr(nsolvents+i)=0;
end
molvolume(nsolvents+i)=0;
flag=0;
for j=1:npureinmix(i)
exists=0;
for k=1:nsolvents
if (strcmp(namepureinmix(i,j),name_solvent(k)))
ipureinmix(i,j)=k;
exists=1;
end
end
if (exists==0)
disp(['Warning: For mix_',num2str(i),' ('char(mixfile(i)),', line ' ,num2str(mixline(i)),') no data available for solvent ',char(namepureinmix(i,j)),'. This mixture will be ignored.'])
flag=1;
end
if (flag==0)
solventx(nsolvents+i)=solventx(nsolvents+i)+amountpureinmix(i,j)*solventx(ipureinmix(i,j));
solventy(nsolvents+i)=solventy(nsolvents+i)+amountpureinmix(i,j)*solventy(ipureinmix(i,j));
solventz(nsolvents+i)=solventz(nsolvents+i)+amountpureinmix(i,j)*solventz(ipureinmix(i,j));
solventzD(nsolvents+i)=solventzD(nsolvents+i)+amountpureinmix(i,j)*solventzD(ipureinmix(i,j));
solventzA(nsolvents+i)=solventzA(nsolvents+i)+amountpureinmix(i,j)*solventzA(ipureinmix(i,j));
solventr(nsolvents+i)=solventr(nsolvents+i)+amountpureinmix(i,j)*solventr(ipureinmix(i,j));
molvolume(nsolvents+i)=molvolume(nsolvents+i)+amountpureinmix(i,j)/molvolume(ipureinmix(i,j)) ; %outside the loop we will do 1/x
end
end
if (flag==0)
    molvolume(nsolvents+i)=1/molvolume(nsolvents+i);
    if (useorigHansen==0)
        solventz(nsolvents+i)=(solventzD(nsolvents+i)*solventzA(nsolvents+i))^0.5;
    end
end
end

% All testdata combined with solvent parameters are now put in organised variables
for solute=1:nsolutes
    npositives(solute)=0;
    nnegatives(solute)=0;
    for j=1:ntestdata(solute)
        exists=0;
        for k=1:n solventstotal
            if (strcmp(testsolvent(solute,j),name_solvent(k)))
                solvent=k;
                exists=1;
            end
        end
        if (exists==1)
            if (strcmp(testresult(solute,j),'yes'))
                npositives(solute)=npositives(solute)+1;
                positive(solute,npositives(solute))=solvent;
                xpositive(solute,npositives(solute))=solventx(solvent);
                ypositive(solute,npositives(solute))=solventy(solvent);
                zpositive(solute,npositives(solute))=solventz(solvent);
                zDpositive(solute,npositives(solute))=solventzD(solvent);
                zApositive(solute,npositives(solute))=solventzA(solvent);
            end
        end
    end
end

rpositive(solute,npositives(solute))=solventr(solvent);
volpositive(solute,npositives(solute))=molvolume(solvent);
concpositive(solute,npositives(solute))=testconc(solute,j);
temppositive(solute,npositives(solute))=testtemp(solute,j);

end

if (strcmp(testresult(solute,j),'no'))
nnegatives(solute)=nnegatives(solute)+1;
negative(solute,nnegatives(solute))=solvent;
xnegative(solute,nnegatives(solute))=solventx(solvent);
ynegative(solute,nnegatives(solute))=solventy(solvent);
znegative(solute,nnegatives(solute))=solventz(solvent);
zDnegative(solute,nnegatives(solute))=solventzD(solvent);
zAnegative(solute,nnegatives(solute))=solventzA(solvent);
rnegative(solute,nnegatives(solute))=solventr(solvent);
vlnegative(solute,nnegatives(solute))=molvolume(solvent);
concnegative(solute,nnegatives(solute))=testconc(solute,j);
tempnegative(solute,nnegatives(solute))=testtemp(solute,j);

end

else

disp(["Warning: No data available for solvent ",char(testsolvent(solute,j)),". The testresult of solute ",char(name_solute(solute))," with this solvent ",char(testfile(solute,j))," , line ",num2str(testline(solute,j))," is ignored in the fitting."]);

end

end %end of function readinputs

function find_sphere    %nested function within fit_sphere

function find_startsphere    %nested function within find_sphere

    % First do a very rough estimation by simply averaging positives. (with a little trick for the zDA values)
    xsphere=0; ysphere=0; zsphere=0;
for i=1:npositives(solute)
    xsphere=xsphere+xpositive(solute,i)/npositives(solute);
    ysphere=ysphere+ypositive(solute,i)/npositives(solute);
    zsphere=zsphere+zpositive(solute,i)/npositives(solute);
    zDsphere=zDsphere+zApositive(solute,i)/npositives(solute);
    zAsphere=zAsphere+zDpositive(solute,i)/npositives(solute);
end
if (useorigHansen==0)
    [zDsphere,zAsphere]=make_consistent_zDA(zsphere,zDsphere,zAsphere);
end
zDsphere=zsphere; %this is the old situation and somehow it seems to perform slightly better...
    zAsphere=zsphere;
radius=-1000;
for i=1:npositives(solute)
    [r,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xpositive(solute,i),ypositive(solute,i),zpositive(solute,i),zDpositive(solute,i),zApositive(solute,i),molvolume(positive(solute,i)),molvolume_solute(solute));
    if (r>radius)
        radius=r;
    end
end
end %end of function find_startsphere

function improve_Donor_Acceptor %nested function within find_sphere
if (zsphere>0) %nested function within find_sphere
    measure_error_symmetricradii;
    maxratio=6;
    ratio=improveDonor/improveAcceptor;
    if (improveDonor<0 && improveAcceptor<0)
        ratio=1/ratio;
    elseif (improveDonor<=0)
ratio=1/maxratio;
elseif (improveAcceptor<=0)
    ratio=maxratio;
end
if (improveDonor==0 && improveAcceptor==0)
    ratio=1;
end
if (ratio>maxratio)
    ratio=maxratio;
end
if (ratio<1/maxratio)
    ratio=1/maxratio;
end
if (ratio~=1)
    power=offtotal/15;
    if (power>0.10)
        power=0.10;
    end
    zDsphere=zDsphere*ratio^power;
    zAsphere=zAsphere/ratio^power;
    if (zDsphere/zAsphere>maxratioDA)
        correctionratio=(zDsphere/zAsphere/maxratioDA)^0.5;
        zDsphere=zDsphere/correctionratio;
        zAsphere=zAsphere*correctionratio;
    end
    if (zAsphere/zDsphere>maxratioDA)
        correctionratio=(zAsphere/zDsphere/maxratioDA)^0.5;
        zDsphere=zDsphere*correctionratio;
        zAsphere=zAsphere/correctionratio;
    end
end
end
if (zsphere==0)
    maxshift=1;
if (ZDsphere<1E-5 && zAsphere<1E-5)
    if (improveDonor>improveAcceptor && improveDonor>0)
        shift=improveDonor*offtotal;
    if (shift>maxshift)
        shift=maxshift;
end
    zDsphere=shift;
else
    if (zDsphere<1E-5)
        shift=improveAcceptor*offtotal;
        if (shift>maxshift)
            shift=maxshift;
        end
        zAsphere=zAsphere+shift;
        if (zAsphere<0)
            zAsphere=0;
        end
end
if (zAsphere<1E-5)
    shift=improveDonor*offtotal;
if (shift>maxshift)
    shift=maxshift;
end
zDsphere=zDsphere+shift;
if (zDsphere<0)
    zDsphere=0;
end
end
end
end %end of function improve_Donor_Acceptor

function measure_error %nested function within find_sphere
closestminus=1000; furthestplus=0;
nextminusin=0; nextminusout=1000;
nextplusin=0; nextplusout=1000;
offminus=0; offplus=0;
improvex=0; improvey=0; improvez=0;
nminus=0; nplus=0;
fitquality=1; ndata=0;
for i=1:20
    ioff(i)=0;
end
for i=1:nnegatives(solute)
    [r,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xnegative(solute,i),ynegative(solute,i),znegative(solute,i),zDnegative(solute,i),zAnegative(solute,i),molvolume(negative(solute,i)),molvolume_solute(solute));
    if (r<closestminus)
        closestminus=r;
    end
    if (r<radius)
nminus=nminus+1;
if (r>nextminusin)
    nextminusin=r;
end
ioff(nminus)=negative(solute,i);
off=radius-r;
offminus=offminus+off;
fitquality=fitquality*exp(-off);
data=ndata+1;
improvex=improvex+distx/realr/xfactor;
improvey=improvey+disty/realr;
improvez=improvez+distz/realr;
else
    ndata=ndata+1;
end
if (r>radius && r<nextminusout)
    nextminusout=r;
end
end
for i=1:npositives(solute)

[r,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xpositive(solute,i),ypositive(solute,i),zpositive(solute,i),zDpositive(solute,i),zApositive(solute,i),molvolume(positive(solute,i)),molvolume_solute(solute));
if (r>furthestplus)
    furthestplus=r;
end
if (r>radius)
    nplus=nplus+1;
if (r<nextplusout)
    nextplusout=r;
end
end
ioff(nminus+nplus)=positive(solute,i);
off=r-radius;
offplus=offplus+off;
fitquality=fitquality*exp(-off);
ndata=ndata+1;
improvex=improvex-\frac{\text{distx}}{\text{realr}}/xfactor;
improvey=improvey-\frac{\text{disty}}{\text{realr}};
improvez=improvez-\frac{\text{distz}}{\text{realr}};
else
ndata=ndata+1;
end
if (r<radius && r>nextplusin)
nextplusin=r;
end
end
offtotal=offminus+offplus;
fitquality=fitquality^{(1/ndata)};
end%end of function measure_error

function optimize_radius  %nested function within find_sphere
  % optimize radius at current position
  flagminus=0; flagplus=0;
  for loopradius=1:20
    measure_error;
    radiusold=radius;
    if (nnegatives(solute)==0)
      radius=furthestplus;
    elseif (nminus==0 || nplus==0)
      radius=(closestminus+furthestplus)/2;
    elseif (nplus>nminus)
      radius=nextplusout+0.0001;
    else
      ndata=ndata+1;
    end
    if (r<radius && r>nextplusin)
      nextplusin=r;
    end
  end
  offtotal=offminus+offplus;
  fitquality=fitquality^{(1/ndata)};
end %end of function optimize_radius
if (nplus-nminus==1)
    flagplus=1;
    if (flagminus==1)
        radius=nextplusout-0.0001;
    end
end
elseif (nminus>nplus)
    radius=nextminusin-0.0001;
    if (nminus-nplus==1)
        flagminus=1;
        if (flagplus==1)
            radius=nextminusin+0.0001;
        end
    end
else
    if (nextplusout<nextminusout && nextplusin>nextminusin)
        radius=(nextplusout+nextplusin)/2;
    end
    if (nextplusout<nextminusout && nextplusin<nextminusin)
        radius=(nextplusout+nextminusin)/2;
    end
    if (nextplusout>nextminusout && nextplusin>nextminusin)
        radius=(nextminusout+nextplusin)/2;
    end
    if (nextplusout>nextminusout && nextplusin<nextminusin)
        radius=(nextminusout+nextminusin)/2;
    end
    break
end
if (radius-radiusold<0.00001 && radius-radiusold>-0.00001)
    break
end

end %end of function optimize_radius

time

function measure_error_symmetricradii %nested function within find_sphere

closestminus=1000; furthestplus=0;
nextminusin=0; nextminusout=1000;
nextplusin=0; nextplusout=1000;
offminus=0; offplus=0;
deltaoff=0;

improvex=0; improvey=0; improvez=0;
improveDonor=0; improveAcceptor=0;
nminus=0; nplus=0;
summinus_drdcsolid=0; sumplus_drdcsolid=0;
fitquality=1; ndata=0;

for i=1:20

ioff(i)=0;loff(i)=0;

end

for i=1:negatives(solute)

[r,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xnegative(solute,i),ynegative(solute,i),znegative(solute,i),zDnegative(solute,i),zAnegativ e(solute,i),molvolume(negative(solute,i)),molvolume_solute(solute));
cutoff=1/(1/radius+1/rnegative(solute,i));

[correction,volfraction2]=correction_for_concentration(concnegative(solute,i),volnegative( solute,i));
correction=correction*tempnegative(solute,i)/295;
cutoff=cutoff*correction;
if (r/correction>rnegative(solute,i))

wishedr=1000;
else

wishedr=1/(correction/r-1/rnegative(solute,i));

end

end
if (correct4solid==1)
    if (correctc_solidfortemp==0)
        c_solid_local=c_solid;
    end
    if (correctc_solidfortemp==1)
        c_solid_local=c_solid*(Tm_solute(solute)-
                        tempnegative(solute,i))/(Tm_solute(solute)-295);
    end
    if (correctc_solidfortemp==2)
        c_solid_local=c_solid*(((Tm_solute(solute)-
                        tempnegative(solute,i))/(Tm_solute(solute)-295)+1)/2);
    end
end
cutoff=cutoff-c_solid_local/volfraction2;
if ((r+c_solid_local/volfraction2)/correction>rnegative(solute,i))
    wishedr=1000;
else
    wishedr=1/(correction/(r+c_solid_local/volfraction2)-1/rnegative(solute,i));
end
end
if (r<cutoff)
    nminus=nminus+1;
    if (wishedr>nextminusin)
        nextminusin=wishedr;
    end
    ioff(nminus)=negative(solute,i);
end

% off is defined as the distance that the sphere would need to move keeping the
current radius. This is actually not correctly calculated (nor well-defined) in case of
usegeometricmean, but as off is only used to get an idea and is not used internally, this is
oke. (it is used to select the best solution though...)

    off=cutoff-r;
    loff(nminus)=off;
    offminus=offminus+off;
fitquality=fitquality*exp(-off);
ndata=ndata+1;
deltacutoff=correction*rnegative(solute,i)^2/(radius+rnegative(solute,i))^2 ;
%=deltacutoff/deltaradius

deltaoff=deltaoff+deltacutoff;
improvex=improvex+distx/reallr/xfactor;
improvey=improvey+disty/reallr;
improvez=improvez+distz/reallr;
improveDonor=improveDonor-zNegative(solute,i);
improveAcceptor=improveAcceptor-zDnegative(solute,i);
if (correct4solid==1)

dradiusdcsolid=correction/(volfraction2*(cutoff+c_solid_local/volfraction2)^2*(correction/
(cutoff+c_solid_local/volfraction2)-1/rnegative(solute,i))^2);
    summinus_drdcsolid=summinus_drdcsolid+dradiusdcsolid;
end
else
ndata=ndata+1;
end
if (wishedr>radius & wishedr<nextminusout)
    nextminusout=wishedr;
end
if (wishedr<closestminus)
    closestminus=wishedr;
end
end
for i=1:npositives(solute)
[r,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,e,xpositive(solute,i),ypositive(solute,i),zpositive(solute,i),zDpositive(solute,i),zApositive(solute,i),molvolume(positive(solute,i)),molvolume_solute(solute));
cutoff=1/(1/radius+1/rpositive(solute,i));
[correction, volfraction2] = correction_for_concentration(concpositive(solute, i), volpositive(solute, i));

correction = correction * temppositive(solute, i) / 295;
cutoff = cutoff * correction;

if (r/correction > rpositive(solute, i))
    wishedr = 1000;
else
    wishedr = 1/(correction / r - 1 / rpositive(solute, i));
end

if (correct4solid == 1)
    if (correctc_solidfortemp == 0)
        c_solid_local = c_solid;
    end
    if (correctc_solidfortemp == 1)
        c_solid_local = c_solid * (Tm_solute(solute) - temppositive(solute, i)) / (Tm_solute(solute) - 295);
    end
    if (correctc_solidfortemp == 2)
        c_solid_local = c_solid * (((Tm_solute(solute) - temppositive(solute, i)) / (Tm_solute(solute) - 295) + 1) / 2);
    end
end
cutoff = cutoff - c_solid_local / volfraction2;

if ((r + c_solid_local / volfraction2) / correction > rpositive(solute, i))
    wishedr = 1000;
else
    wishedr = 1 / (correction / (r + c_solid_local / volfraction2) - 1 / rpositive(solute, i));
end

if (r > cutoff)
    nplus = nplus + 1;
    if (wishedr < nextplusout)
        nextplusout = wishedr;
end

ioff(nminus+nplus)=positive(solute,i);
off=r-cutoff;
loff(nminus+nplus)=off;
offplus=offplus+off;
fitquality=fitquality*exp(-off);
ndata=ndata+1;
deltacutoff=correction*rpositive(solute,i)^2/(radius+rpositive(solute,i))^2;
deltaoff=deltaoff+deltaoff;
improvex=improvex+distx/realr/xfactor;
improvey=improvey+disty/realr;
improvez=improvez+distz/realr;
improveDonor=improveDonor+zApositive(solute,i);
improveAcceptor=improveAcceptor+zDpositive(solute,i);
if (correct4solid==1)

dradiusdcsolid=correction/(volfraction2*(cutoff+c_solid_local/volfraction2)^2*(correction/
(correction/(cutoff+c_solid_local/volfraction2)-1/rpositive(solute,i))^2));
sumplus_drdcsolid=sumplus_drdcsolid+dradiusdcsolid;
end
else
ndata=ndata+1;
end
if (wishedr<radius && wishedr>nextplusin)
nextplusin=wishedr;
end
if (wishedr>furthestplus)
furthestplus=wishedr;
end
end
offtotal=offminus+offplus;
fitquality=fitquality^(1/ndata);
if (furthestplus>200)
    furthestplus=200;
end
if (closestminus>200)
    closestminus=200;
end
end %end of function measure_error_symmetricradii

function optimize_radius_symmetricradii  %nested function within find_sphere
    improve_Donor_Acceptor;
    % optimize radius at current position
    csolid_old=0;
    for loopsolid=1:100
        radiusold=0; offold=0;
        for loopradius=1:30
            measure_error_symmetricradii;
            radiusold2=radiusold;
            radiusold=radius;
            offold2=offold;
            offold=offtotal;
            if (nnegatives(solute)==0)
                radius=furthestplus;
            elseif (nminus==0 && nplus==0)
                radius=(closestminus+furthestplus)/2;
            elseif (deltaoff<0)
                if (nextplusout<nextminusout)
                    radius=nextplusout+0.001;
                else
                    radius=nextminusout+0.001;
                end
            elseif (deltaoff>0)
if (nextplusin>nextminusin)
    radius=nextplusin-0.001;
else
    radius=nextminusin-0.001;
end
end

if (radius-radiusold2<0.00001 && radius-radiusold2>-0.00001)
    if (offold<offold2)
        radius=radiusold;
    end
    measure_error_symmetricradii;
    break
end
end

if (correct4solid==1)
    csolid_old2=csolid_old;
    csolid_old=c_solid;
if (nminus~=0 || nplus~=0)
    if (nminus==0)
        c_solid=c_solid-0.1;
    elseif (nplus==0)
        c_solid=c_solid+0.1;
    elseif (summinus_drdcsolid/nminus>sumplus_drdcsolid/nplus)
        c_solid=c_solid+0.1;
    else
        c_solid=c_solid-0.1;
    end
end
if (c_solid<0)
    c_solid=0;
end
if (c_solid==csolid_old2)
    c_solid=csolid_old;
    break
end
else
    break
end
end %end of function optimize_radius_symmetricradii

%actual start of function find_sphere:
find_startsphere;
  xstart=xsphere; ystart=ysphere; zstart=zsphere; zDstart=zDsphere; zAstart=zAsphere; rstart=radius;
  if (useorigHansen==1)
    optimize_radius;
  end
  if (useorigHansen==0)
    optimize_radius_symmetricradii;
  end
  %do some extra looping over a grid of starting positions to be able to select the best solution...(grid is build from close to further from startsphere)
  nperfect=0;
  avgx=0; avgy=0; avgz=0; avgzD=0; avgzA=0; avgr=0; avgc= solid=0;
  minx=1000; miny=1000; minz=1000; minD=1000; minzA=1000; minr=1000; mincsolid=1000;
  maxx=-1000; maxy=-1000; maxz=-1000; maxD=-1000; mxzA=-1000; mxr=-1000; maxcsolid=-1000;
  best=1000;
  step=1;
  nsteps=4;
  for istep=0:nsteps
    for a=-istep*step:step:istep*step
for b=-istep*step+abs(a):step:istep*step-abs(a)
    stepc=2*(istep*step-abs(a)-abs(b));
    if (stepc==0)
        stepc=step;
    end
for c=-istep*step+abs(a)+abs(b):stepc:istep*step-abs(a)-abs(b)
    xsphere=xstart+a;
    ysphere=ystart+b;
    zsphere=zstart+c;
    zDsphere=zDstart;
    zAsphere=zAstart;
    radius=rstart;
    if (useorigHansen==0)
        if (xsphere<0)
            xsphere=0;
        end
        if (ysphere<0)
            ysphere=0;
        end
        if (zsphere<0)
            zsphere=0;
        end
    end
end

% Now find out how much these are off and minimize them.
for loopposition=1:100
    if (useorigHansen==0)
        [zDsphere,zAsphere]=make_consistent_zDA(zsphere,zDsphere,zAsphere);
        improve_Donor_Acceptor;
    end
    if (useorigHansen==1)
optimize_radius;
end   %measure_error is called inside these functions.
if (useorigHansen==0)
  optimize_radius_symmetricradii;
end

% optimize position (radius optimization is done after each positional step)
xsphereold=xsphere; ysphereold=ysphere; zsphereold=zsphere;
if (nplus+nminus>0)
  % step direction is (improvex,improvey,improvez); we now need to find out the
  step length by finding next plus or minus that will be wrongly included or excluded by
  moving the sphere in that direction
  stepsize=1000;
  for i=1:nnegatives(solute)
  
    [par
    dist,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xnegative(solute,i),ynegative(solute,i),znegative(solute,i),zDnegative(solute,i),zAn
    egative(solute,i),molvolume(negative(solute,i)),molvolume_solute(solute));
    distx=-distx; disty=-disty; distz=-distz;
    
    [correction,volfraction2]=correction_for_concentration(concnegative(solute,i),volnegative(solute,i));
    correction=correction*tempnegative(solute,i)/295;
    if (useorigHansen==0)
      cutoff=correction/(1/radius+1/rnegative(solute,i));
    else
      cutoff=radius;
    end
    if (correct4solid==1)
      if (correctc_solidfortemp==0)
        c_solid_local=c_solid;
      end
      if (correctc_solidfortemp==1)
c_solid_local = c_solid*(Tm_solute(solute)-
tempnegative(solute,i))/(Tm_solute(solute)-295);
end
if (correctc_solidfortemp==2)
c_solid_local = c_solid*(((Tm_solute(solute)-
tempnegative(solute,i))/(Tm_solute(solute)-295)+1)/2);
end
cutoff = cutoff - c_solid_local/volfraction2;
end
if (useorigHansen==0)
% for some reason the nonspherical optimization does not work very well, so
we optimize as if it is still spherical
vector2 = xfactor*improvex^2+improvey^2+improvez^2;
inproduct = xfactor*improvex*(xnegative(solute,i)-
xsphere)+improvey*(ynegative(solute,i)-ysphere)+improvez*(znegative(solute,i)-
zsphere);
discriminant = inproduct^2-40*vector2*(pardist-cutoff);
if (discriminant>=0)
solution1 = (inproduct-discriminant^0.5)/vector2;
solution2 = (inproduct+discriminant^0.5)/vector2;
solution1 = solution1<stepsize)
stepsize = solution1;
end
end
if (useorigHansen==1)
vector2 = xfactor^2*improvex^2+improvey^2+improvez^2;
r2 = xfactor^2*distx^2+disty^2+distz^2;
inproduct = xfactor^2*distx*improvex+disty*improvey+distz*improvez;
discriminant = 4*inproduct^2-4*r2*vector2+4*vector2*cutoff^2;
if (discriminant>=0)
solution1 = (2*inproduct-discriminant^0.5)/(2*vector2);
solution2 = (2*inproduct+discriminant^0.5)/(2*vector2);
solution1 = solution1<stepsize)
45
stepsize=solution1;
end
end
end
end
for i=1:npositives(solute)

[pardist,distx,disty,distz,realr]=parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,xpositive(solute,i),ypositive(solute,i),zpositive(solute,i),zDpositive(solute,i),zApositive(solute,i),molvolume(positive(solute,i)),molvolume_solute(solute));

distx=-distx; disty=-disty; distz=-distz;

[correction,volfraction2]=correction_for_concentration(concpositive(solute,i),volpositive(solute,i));

  correction=correction*temppositive(solute,i)/295;
  if (useorigHansen==0)
    cutoff=correction/(1/radius+1/rpositive(solute,i));
  else
    cutoff=radius;
  end
  if (correct4solid==1)
    if (correctc_solidfortemp==0)
      c_solid_local=c_solid;
    end
    if (correctc_solidfortemp==1)
      c_solid_local=c_solid*(Tm_solute(solute)-temppositive(solute,i))/(Tm_solute(solute)-295);
    end
    if (correctc_solidfortemp==2)
      c_solid_local=c_solid*((Tm_solute(solute)-temppositive(solute,i))/(Tm_solute(solute)-295)+1)/2;
    end
    cutoff=cutoff-c_solid_local/volfraction2;
  end
if (useorigHansen==0)
    % for some reason the nonspherical optimization does not work very well, so we optimize as if it is still spherical;
    vector2=xfactor*improvex^2+improvey^2+improvez^2;
    inproduct=xfactor*improvex*(xpositive(solute,i)-xsphere)+improvey*(ypositive(solute,i)-ysphere)+improvez*(zpositive(solute,i)-zsphere);
    discriminant=inproduct^2-40*vector2*(pardist-cutoff);
    if (discriminant>=0)
        solution2=(inproduct+discriminant^0.5)/vector2;
        if (solution2>0 && solution2<stepsize)
            stepsize=solution2;
        end
    end
end
end

if (useorigHansen==1)
    vector2=xfactor^2*improvex^2+improvey^2+improvez^2;
    r2=xfactor^2*distx^2+disty^2+distz^2;
    inproduct=xfactor^2*distx*improvex+disty*improvey+distz*improvez;
    discriminant=4*inproduct^2-4*r2*vector2+4*vector2*cutoff^2;
    if (discriminant>=0)
        solution1=(2*inproduct-discriminant^0.5)/(2*vector2);
        solution2=(2*inproduct+discriminant^0.5)/(2*vector2);
        if (solution2>0 && solution2<stepsize)
            stepsize=solution2;
        end
    end
end
end

vectorlength=(improvex^2+improvey^2+improvez^2)^0.5;
if (useorigHansen==0)
    stepsize=stepsize*2;
end
if (vectorlength*stepsize>2)
    stepsize=2/vectorlength;
end
xsphere=xsphere+improvex*stepsize;
ysphere=ysphere+improvey*stepsize;
zsphere=zsphere+improvez*stepsize;
if (useorigHansen==0)
    if (xsphere<0)
        xsphere=0;
    end
    if (ysphere<0)
        ysphere=0;
    end
    if (zsphere<0)
        zsphere=0;
    end
end
if (xsphere-xsphereold<0.001 && xsphere-xsphereold>-0.001 && ysphere-ysphereold<0.001 && ysphere-ysphereold>-0.001 && zsphere-zsphereold<0.001 && zsphere-zsphereold>-0.001)
    break
end
end

if (offtotal<best)
    best=offtotal;
    bestx=xsphere; besty=ysphere; bestz=zsphere; bestzD=zDsphere; bestzA=zAsphere; bestr=radius; bestcsolid=c_solid;
    bestminus=nminus; bestplus=nplus;
    bestoff=offtotal; bestfit=fitquality;
    for i=1:20
bestioff(i)=ioff(i);
end
end

if (offtotal==0)
nperfect=nperfect+1;

avgx=avgcsolid+xsphere; avgy=avgcsolid+ysphere; avgz=avgcsolid+zsphere;
avgD=avgcsolid+zDsphere; avgzA=avgcsolid+zAsphere; avgr=avgcsolid+radius;
avgcsolid=avgcsolid+c_solid;

if (xsphere<minx)
    minx=xsphere;
end

if (xsphere>maxx)
    maxx=xsphere;
end

if (ysphere<miny)
    miny=ysphere;
end

if (ysphere>maxy)
    maxy=ysphere;
end

if (zsphere<minz)
    minz=zsphere;
end

if (zsphere>maxz)
    maxz=zsphere;
end

if (zDsphere<minzD)
    minzD=zDsphere;
end

if (zDsphere>maxzD)
    maxzD=zDsphere;
end
if (zAsphere<minzA)
  minzA=zAsphere;
end

if (zAsphere>maxzA)
  maxzA=zAsphere;
end

if (radius<minr)
  minr=radius;
end

if (radius>maxr)
  maxr=radius;
end

if (c_solid<mincsolid)
  mincsolid=c_solid;
end

if (c_solid>maxcsolid)
  maxcsolid=c_solid;
end

xsphere=bestx; ysphere=besty; zsphere=bestz; zDsphere=bestzD; zAsphere=bestzA;
radius=bestr; c_solid=bestcsolid;
nminus=bestminus; nplus=bestplus;
offtotal=bestoff; fitquality=bestfit;
for i=1:20
  ioff(i)=bestioff(i);
end

if (offtotal==0)
avgx=avgx/nperfect; avgy=avgy/nperfect; avgz=avgz/nperfect;

avgzD=avgzD/nperfect; avgzA=avgzA/nperfect;

avgr=avgr/nperfect; avgcsolid=avgcsolid/nperfect;

xsphere=avgx; ysphere=avgy; zsphere=avgz; zDsphere=avgzD; zAsphere=avgzA;
radius=avgr; c_solid=avgcsolid;

% make this average consistent again (note that only the radius is reoptimized, so the resulting average strictly may actually not be a perfect solution):

if (useorigHansen==0)
    [zDsphere,zAsphere]=make_consistent_zDA(zsphere,zDsphere,zAsphere);
end
if (useorigHansen==1)
    optimize_radius;
end
if (useorigHansen==0)
    optimize_radius_symmetricradii;
end
end %end of function find_sphere

function predict_solubility %nested function within fit_sphere

[distance,distx,disty,distz,realr]=parameter_distance(fitresultx(solute),fitresulty(solute),fitresultz(solute),fitresultzD(solute),fitresultzA(solute),solventx(solvent),solventy(solvent),solventz(solvent),solventzD(solvent),solventzA(solvent),molvolume(solvent),molvolume_solute(solute));
cutoff_local=1/(1/fitresultr(solute)+1/solventr(solvent))*temperature/295;
if (c_solid_local==0 && distance<=cutoff_local)
    fprintf(outputfile,'Predicted partial solubility of %s in %s at %gK: soluble in all concentrations\n',char(name_solute(solute)),char(name_solvent(solvent)),temperature);
else
    factor=(distance+c_solid_local)/cutoff_local;
    SoverH5050=4*log(0.5);
    factor=factor*SoverH5050;
    molfraction=exp(factor);
end

end
newvalue=factor;
for ilocal=1:2000
   molfraction2=1-molfraction;
   factor=(distance+c_solid_local/molfraction2)/cutoff_local*SoverH5050;
   factortest=(molfraction*log(molfraction)+molfraction2*log(molfraction2))/(molfraction*molfraction2);
   if (factortest-factor<0.001 && factor-factortest<0.001)
      concentration=1000*molfraction/(molfraction2*molvolume(solvent)) ; % in mol per liter solvent!
      fprintf(outputfile,'Predicted partial solubility of %s in %s at %gK: %0.2g mol per liter solvent.
      \r\n',char(name_solute(solute)),char(name_solvent(solvent)),temperature,concentration);
      break
   end
   if (molfraction<=0.4)
      newvalue=newvalue+(factor-factortest)/2;
   end
   if (molfraction>0.4)
      newvalue=newvalue+(factor-factortest)/10*molfraction2;
   end
   if (newvalue>=0)
      newvalue=-0.1;
   end
   molfraction=exp(newvalue);
end
end %end of function predict_solubility

readinputs

% Do the actual fitting of the spheres for each solute in the testdata inputfiles:
outputfile=fopen('output.txt','w');
if (testdata_present==1)
fprintf(outputfile,\r\n');
fprintf(outputfile,'tfit results:\r\n');
for solute=1:nsolutes
  fprintf(outputfile,\r\n');
  fprintf(outputfile,'%s \r\n',char(name_solute(solute)));
  c_solid=0;
fclose(outputfile);
find_sphere;
outputfile=fopen('output.txt','a');
fitresultx(solute)=xsphere; fitresulty(solute)=ysphere; fitresultz(solute)=zsphere;
fitresultzD(solute)=zDsphere; fitresultzA(solute)=zAsphere; fitresultr(solute)=radius;
fitresultc_solid(solute)=c_solid;
if (nperfect>0)
  fprintf(outputfile,'%i perfect fits have been found.\r\n',nperfect);
  fprintf(outputfile,'Range of the parameters within these perfect fits: %g-%g %g-%g %g-%g %g-%g %g\r\n',minx,maxx,miny,maxy,minz,maxz,minzD,maxzD,minzA,maxzA,minr,maxr,mincsolid,maxcsolid);
  fprintf(outputfile,'Averaged solution: %g %g %g %g %g %g %g\r\n',avgx,avgy,avgz,avgzD,avgzA,avgr,avgcsolid);
  fprintf(outputfile,'Making this average consistent again gives the following solution: \r\n');
end
fprintf(outputfile,'Hansen_parameters D, P, H, Hdonor, Hacceptor: %g %g %g %g %g\r\n',xsphere,ysphere,zsphere,zDsphere,zAsphere);
fprintf(outputfile,'Sphere radius: %g \r\n',radius);
fprintf(outputfile,'Correction for melting solute: %g \r\n',c_solid);
fprintf(outputfile,'Quality of the fit: nr of wrong_in, nr of wrong_out, fitquality: %i %i %i \r\n',nminus,nplus,fitquality);
if (fitquality<1)
  fprintf(outputfile,'Wrong_ins:\r\n');
  for i=1:nminus
    fprintf(outputfile, ' %s',char(name_solvent(ioff(i))));
  end
end

fprintf(outputfile, '
');
fprintf(outputfile, 'Wrong_outs:');
for i=nminus+1:nminus+nplus
    fprintf(outputfile, ' %s', char(name_solvent(ioff(i))));
end
fprintf(outputfile, '
');
end
fprintf(outputfile, 'Used molar volume of solute and melting point: %g %g\r\n', molvolume_solute(solute), Tm_solute(solute));
fprintf(outputfile, 'Technical output (formatted to be reused as input):\r\n');
fprintf(outputfile, '%s %g %g %g %g %g %g %g %g\r\n', char(name_solute(solute)), xsphere, ysphere, zsphere, zDsphere, zAsphere, radius, c_solid, molvolume_solute(solute), Tm_solute(solute));
end
end

% Add the input from the fitresults files:
for i=1:nprefits
    already=0;
    for j=1:nsolutes
        if (strcmp(prefitsolute(i), name_solute(j)))
            already=1;
        end
    end
    if (already==0)
        nsolutes=nsolutes+1;
        name_solute(nsolutes)=prefitsolute(i);
        solute=nsolutes;
        fitresultx(solute)=prefix(i);
        fitresulty(solute)=prefity(i);
        fitresultz(solute)=prefitz(i);
        fitresultzA(solute)=prefitzA(i);
    end
end
fitresultzD(solute)=prefitzD(i);
fitresultr(solute)=prefitr(i);
fitresultc_solid(solute)=prefitc_solid(i);
molvolume_solute(solute)=prefitvolume(i);
Tm_solute(solute)=prefitTm(i);
end
end

% Make predictions using these fit results:
if (predictions_present==1)
correctin=0; correctout=0; wrongin=0; wrongout=0;
fprintf(outputfile,'\n');
fprintf(outputfile,'\npredictions:\n');
for iprediction=1:npredictions
solutefound=0; solventfound=0;
for k=1:nsolutes
if (strcmp(predictsolute(iprediction),name_solute(k)))
solute=k;
solutefound=1;
end
end
for k=1:n solventstotal
if (strcmp(predictsolvent(iprediction),name_solvent(k)))
solvent=k;
solventfound=1;
end
end
if (solutefound==0)
disp(['No data available for solute ',char(predictsolute(iprediction)),'; ignored.']);
end
if (solventfound==0)
disp(['No data available for solvent ',char(predictsolvent(iprediction)),'; ignored.']);
end
if (solutefound==1 && solventfound==1)

[distance,distx,disty,distz,realr]=parameter_distance(fitresultx(solute),fitresulty(solute),fitresultrz(solute),fitresultzD(solute),fitresultzA(solute),solventx(solvent),solventy(solvent),solventz(solvent),solventzD(solvent),solventzA(solvent),molvolume(solvent),molvolume_solute(solute));

if (useorigHansen==1)
    cutoff=fitresultr(solute);
end
if (useorigHansen==0)
    cutoff=1/(1/fitresultr(solute)+1/solventr(solvent));

[correction,volfraction2]=correction_for_concentration(predictconc(iprediction),molvolume(solute));

    correction=correction*predicttemp(iprediction)/295;

if (correctc_solidfortemp==0)
    c_solid_local=fitresultc_solid(solute);
end
if (correctc_solidfortemp==1)
    c_solid_local=fitresultc_solid(solute)*(Tm_solute(solute)-predicttemp(iprediction))/(Tm_solute(solute)-295);
end
if (correctc_solidfortemp==2)
    c_solid_local=fitresultc_solid(solute)*(((Tm_solute(solute)-predicttemp(iprediction))/(Tm_solute(solute)-295)+1)/2);
end

cutoff=cutoff*correction-c_solid_local/volfraction2;
end
if (distance<=cutoff)
    fprintf(outputfile,'r
');
    fprintf(outputfile,'Prediction: Solute %s dissolves in solvent %s at concentration %g mol/L and temperature
');

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%gK.\r\n',char(name_solute(solute)),char(name_solvent(solvent)),predictconc(iprediction ),predicttemp(iprediction));

    if (strncmp(name_solvent(solvent),'mix_',4))
        splittedname=strsplit(char(name_solvent(solvent)),'_');
        imix=str2double(char(splittedname(2)));
        fprintf(outputfile,'(%s is ',char(name_solvent(solvent)));
        for i=1:npuresinmix(imix)
            fprintf(outputfile,'%g percent %s',amountpureinmix(imix,i)*100,char(namepureinmix(imix,i)));
            if (i<npuresinmix(imix))
                fprintf(outputfile,' + ');
            end
        end
        fprintf(outputfile,')\r\n');
    end

    if (strcmp(predictresult(iprediction),'yes'))
        fprintf(outputfile,'The experimental result given in the input agrees with this prediction: correctin.\r\n');
        correctin=correctin+1;
    end

    if (strcmp(predictresult(iprediction),'no'))
        fprintf(outputfile,'The experimental result given in the input does NOT agree with this prediction: wrongin.\r\n');
        wrongin=wrongin+1;
    end

    temperature=predicttemp(iprediction);
    predict_solubility;
end

    if (distance>cutoff)
        fprintf(outputfile,')\r\n');
        fprintf(outputfile,'Prediction: Solute %s does not dissolve in solvent %s at concentration %g mol/L and temperature %gK.\r\n',char(name_solute(solute)),char(name_solvent(solvent)),predictconc(iprediction ),predicttemp(iprediction));
if (strncmp(name_solvent(solvent), 'mix_', 4))
    splittedname = strsplit(char(name_solvent(solvent)), '_');
    imix = str2double(char(splittedname(2)));
    fprintf(outputfile, '(%s is ', char(name_solvent(solvent)));
    for i = 1:npuresinmix(imix)
        fprintf(outputfile, '%g percent %s', amountpureinmix(imix, i) * 100, char(namepureinmix(imix, i)));
        if (i < npuresinmix(imix))
            fprintf(outputfile, ' + ');
        end
    end
    fprintf(outputfile, ')
end
if (strcmp(predictresult(iprediction), 'no'))
    fprintf(outputfile, 'The experimental result given in the input agrees with this prediction: correctout.
    correctout = correctout + 1;
end
if (strcmp(predictresult(iprediction), 'yes'))
    fprintf(outputfile, 'The experimental result given in the input does NOT agree with this prediction: wrongout.
    wrongout = wrongout + 1;
end
temperature = predicttemp(iprediction);
predict_solubility;
end
end
fprintf(outputfile, 'summary of predictions:
');
fprintf(outputfile, '# correct_in = %i
', correctin);
fprintf(outputfile, '# correct_out = %i
', correctout);
fprintf(outputfile,'# wrong_in = %i\n',wrongin);
fprintf(outputfile,'# wrong_out = %i\n',wrongout);
end
fclose(outputfile);
end %end of function fit_sphere

function [correction,volfraction2] = correction_for_concentration(concentration,volume2)
    concentration2=1000/volume2;
    molfracion=concentration/(concentration+concentration2);
    molfracion2=1-molfracion;
    SoverH=(molfracion*log(molfracion)+molfracion2*log(molfracion2))/(molfracion*molfracion2);
    volfracion2=molfracion2;
    SoverH5050=4*log(0.5);
    correction=SoverH/SoverH5050;
end

function [zDout,zAout] = make_consistent_zDA(z,zD,zA)
    shift=(((zD-zA)^2+4*z^2)^0.5-zD-zA)/2;
    zDout=zD+shift;
    zAout=zA+shift;
end

function [distance,distx,disty,distz,realr] = parameter_distance(xsphere,ysphere,zsphere,zDsphere,zAsphere,x,y,z,zD,zA,volume_solv
ent,volume_solute)
    global useorigHansen xfactor correct4solid correctc_solidfortemp
    if (useorigHansen==1)
        distx=xsphere-x;
        disty=ysphere-y;
        distz=zsphere-z;
    else
        distx=xsphere-x;
        disty=ysphere-y;
        distz=zsphere-z;
    end
end
disty=ysphere-y;
distz=zsphere-z;
distance=(xfactor^2*distx^2+disty^2+distz^2)^0.5;
end
if (useorigHansen==0)
    distx=((xsphere^2+x^2)/2-xsphere*x)/20 ; % the division by 20 is to stay in the same scale so that optimization magic numbers keep working.
    disty=((ysphere^2+y^2)/2-ysphere*y)/20;
    distz=((zDsphere*zAsphere+zD*zA-(zDsphere*zA+zAsphere*zD))/2)/20;
signdistz=1;
    if (distz<0)
        signdistz=-1;
        end
% to keep directional information:
    if (x>xsphere)
        distx=-distx;
        end
    if (y>ysphere)
        disty=-disty;
        end
    distz=abs(distz);
    if (z>zsphere)
        distz=-distz;
        end
% distance is now a simple sum instead of spherical...
    distance=xfactor*abs(distx)+abs(disty)+signdistz*abs(distz);
end
realr=(distx^2+disty^2+distz^2)^0.5;
end

function terms = strsplit(s, delimiter)
%STRSPLIT Splits a string into multiple terms
%
%   terms = strsplit(s)
%       splits the string s into multiple terms that are separated by
%       white spaces (white spaces also include tab and newline).
%       The extracted terms are returned in form of a cell array of
%       strings.
%
%   terms = strsplit(s, delimiter)
%       splits the string s into multiple terms that are separated by
%       the specified delimiter.
%
%   Remarks
%       -------
%       - Note that the spaces surrounding the delimiter are considered
%         part of the delimiter, and thus removed from the extracted
%         terms.
%
%       - If there are two consecutive non-whitespace delimiters, it is
%         regarded that there is an empty-string term between them.
%
%   Examples
%       -------
%       % extract the words delimited by white spaces
%       ts = strsplit('I am using MATLAB');
%       ts <- {'I', 'am', 'using', 'MATLAB'}
%
%       % split operands delimited by '+'
%       ts = strsplit('1+2+3+4', '+');
%       ts <- {'1', '2', '3', '4'}
% It still works if there are spaces surrounding the delimiter
% ts = strsplit('1 + 2 + 3 + 4', '+');
% ts = {'1', '2', '3', '4'}
%
% Consecutive delimiters result in empty terms
% ts = strsplit('C,Java, C++, ,, Python, MATLAB', ',');
% ts = {'C', 'Java', 'C++', '', 'Python', 'MATLAB'}
%
% When no delimiter is presented, the entire string is considered
% as a single term
% ts = strsplit('YouAndMe');
% ts = {'YouAndMe'}
%
% History
% ------
% - Created by Dahua Lin, on Oct 9, 2008
%

%% parse and verify input arguments

assert(ischar(s) && ndims(s) == 2 && size(s,1) <= 1, ...
    'strsplit:invalidarg', ...
    'The first input argument should be a char string.');

if nargin < 2
    by_space = true;
else
    d = delimiter;
    assert(ischar(d) && ndims(d) == 2 && size(d,1) == 1 && ~isempty(d), ...
'strsplit:invalidarg', ...
'The delimiter should be a non-empty char string.');

d = strtrim(d);
by_space = isempty(d);
end

%%% main

s = strtrim(s);

if by_space
   w = isspace(s);
   if any(w)
      % decide the positions of terms
      dw = diff(w);
      sp = [1, find(dw == -1) + 1];  % start positions of terms
      ep = [find(dw == 1), length(s)];  % end positions of terms

      % extract the terms
      nt = numel(sp);
      terms = cell(1, nt);
      for i = 1 : nt
         terms{i} = s(sp(i):ep(i));
      end
   else
      terms = {s};
   end
else
   p = strfind(s, d);
if ~isempty(p)
    % extract the terms
    nt = numel(p) + 1;
    terms = cell(1, nt);
    sp = 1;
    dl = length(delimiter);
    for i = 1 : nt-1
        terms{i} = strtrim(s(sp:p(i)-1));
        sp = p(i) + dl;
    end
    terms{nt} = strtrim(s(sp:end));
else
    terms = {s};
end
end