electronic reprint

Journal of
**Applied
Crystallography**
ISSN 0021-8898
Editor: **Anke R. Kaysser-Pyzalla**

CRYSTALS enhancements: dealing with hydrogen atoms in refinement

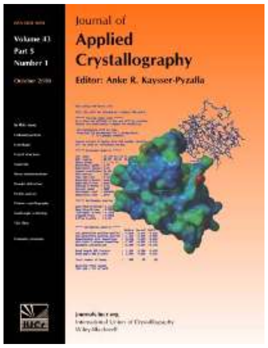
Richard I. Cooper, Amber L. Thompson and David J. Watkin

J. Appl. Cryst. (2010). **43**, 1100–1107

Copyright © International Union of Crystallography

Author(s) of this paper may load this reprint on their own web site or institutional repository provided that this cover page is retained. Republication of this article or its storage in electronic databases other than as specified above is not permitted without prior permission in writing from the IUCr.

For further information see http://journals.iucr.org/services/authorrights.html



Many research topics in condensed matter research, materials science and the life sciences make use of crystallographic methods to study crystalline and non-crystalline matter with neutrons, X-rays and electrons. Articles published in the *Journal of Applied Crystallography* focus on these methods and their use in identifying structural and diffusion-controlled phase transformations, structure–property relationships, structural changes of defects, interfaces and surfaces, *etc.* Developments of instrumentation and crystallographic apparatus, theory and interpretation, numerical analysis and other related subjects are also covered. The journal is the primary place where crystallographic computer program information is published.

Crystallography Journals Online is available from **journals.iucr.org**

Journal of
Applied
Crystallography
ISSN 0021-8898

Received 28 May 2010
Accepted 29 June 2010

© 2010 International Union of Crystallography
Printed in Singapore – all rights reserved

CRYSTALS enhancements: dealing with hydrogen atoms in refinement

Richard I. Cooper,‡ Amber L. Thompson and David J. Watkin*

Chemical Crystallography, Department of Chemistry, University of Oxford, England. Correspondence e-mail: david.watkin@chem.ox.ac.uk

Because they scatter X-rays weakly, H atoms are often abused or neglected during structure refinement. The reasons why the H atoms should be included in the refinement and some of the consequences of mistreatment are discussed along with selected real examples demonstrating some of the features for hydrogen treatment that can be found in the software suite *CRYSTALS*.

1. Introduction

In 1998 Richard Harlow remarked

> I have a lot of confidence in structures where the hydrogen atoms were found and refined to reasonable positions (*e.g.* $0.85 < \mathrm{C-H} < 1.05$ Å) and with reasonable thermal parameters (*e.g.* $2.0 < B_{\rm iso} <$ Å^2). The hydrogen atoms appear to be very sensitive indicators of a reliable structure and simply don't refine well if there are modest errors in the data or model, or if the data are insufficient for the structural analysis.

He went on to issue his famous 'Hydrogen Challenge':

> [The challenge is] to find a classic example ... of a published organic or organometallic structure where all of the hydrogen atoms have been found and refined ... and where the structure is demonstrably incorrect in some substantial way.

There appear to be no examples where the challenge has been defeated, and indeed, there are cases where this has been used to great effect (*e.g.* Helliwell *et al.*, 1989). However, anecdotally, it appears that the addition of H atoms based solely on the geometry of the structural skeleton is prevalent. Yet, most structural scientists would agree that there are a large number of situations where the result of this is not only suboptimal, but is palpably incorrect. This leads to the question, 'If the non-H atoms in a structure are well behaved and refine well, should we also refine the H atoms?'

1.1. Why are H atoms necessary and why is their refinement difficult?

The structure factor is a complex number F_{hkl}, where the magnitude can be represented by the product of its complex conjugates $F_{hkl}^2 = A_{hkl}^2 + B_{hkl}^2$. A_{hkl} and B_{hkl} are given by the sums

$$A_{hkl} = \sum_j f_j \cos 2\pi(hx + ky + lz), \qquad (1)$$

$$B_{hkl} = \sum_j f_j \sin 2\pi(hx + ky + lz), \qquad (2)$$

where A_{hkl} is the real component, B_{hkl} is the imaginary component, f_j are the atomic displacement parameter adjusted scattering factors, h, k and l are the Miller indices, and x, y and z are the atomic coordinates. These equations can be separated into the total contributions from the non-H and H atoms, for example,

$$A_{hkl} = \sum_j^{\text{non-H}} f_j \cos 2\pi(hx + ky + lz) + \sum_j^{\text{H}} f_j \cos 2\pi(hx + ky + lz), \qquad (3)$$

with B_{hkl} given by the corresponding sine formula. The H atoms must be included in the model close to their 'true' position to avoid a systematic error in $F_{\rm c}$ and hence a systematic error in the other parameters because the function minimized during refinement [equations (4) and (5), Watkin, 2008] contains $F_{\rm o}$ (or $F_{\rm o}^2$), which in turn has contributions from all atoms, including hydrogen:

$$M = \sum (F_{\rm o} - F_{\rm c})^2, \qquad (4)$$

$$M = \sum (|F_{\rm o}| - |(F_{{\rm c}_{\text{non-H}}} + F_{{\rm c}_{\rm H}})|)^2. \qquad (5)$$

$F_{{\rm c}_{\text{non-H}}} \gg F_{{\rm c}_{\rm H}}$ makes H atoms more difficult to 'see' in the Fourier difference map and can make them susceptible to correlation *etc.*, leading to refinement difficulties. However, in general, with the quality of modern data, it should be possible not only to locate H atoms, but also to refine their positions and displacement factors. Different approaches and their implications as well as strategies for hydrogen treatment are discussed.

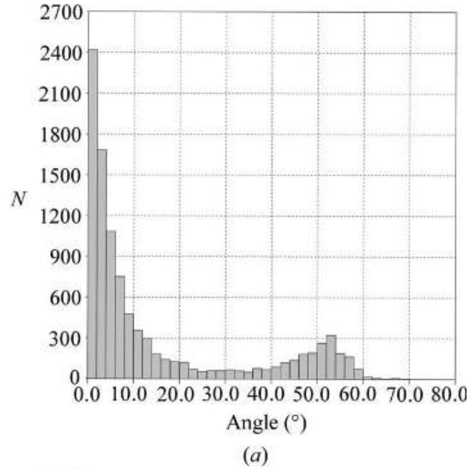
2. H-atom placement and refinement

In publications, it is often stated that H atoms are fixed to 'chemically sensible positions', because their location is well known, particularly for aromatic, sp^2 and sp^3, hybridized C atoms. However, it is also well known that X—H distances are

---

‡ Current address: Inhibox Ltd, Pembroke House, 36–37 Pembroke Street, Oxford, England.

electronic reprint



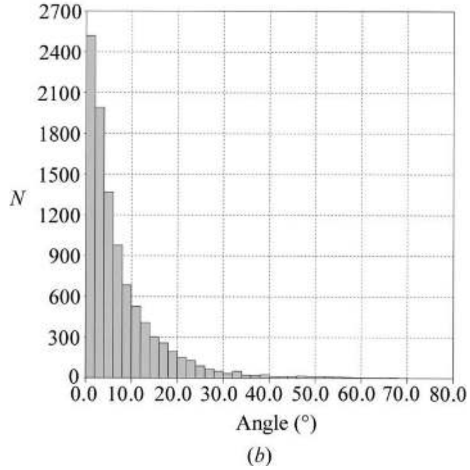


Figure 1
Histograms produced using *VISTA* (CCDC, 1994) showing the angle between the N—C vector and its projection onto the NCC plane for a generic three-coordinate $N(C)_3$ fragment (*a*) and with a carbonyl substituent (*b*). The distribution is clearly bimodal in the first case, but not in the second.

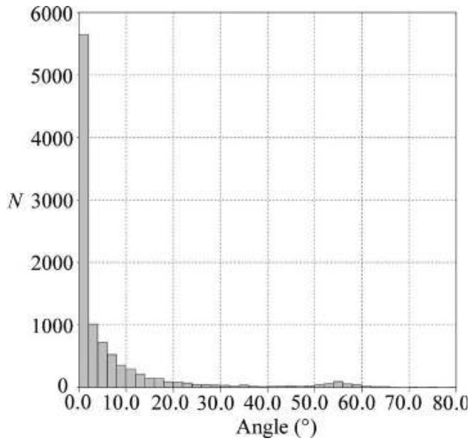


Figure 2
Histograms produced using *VISTA* (CCDC, 1994) showing the angle between the N—H vector and its projection onto the NCC plane for a generic three-coordinate $NH(C)_2$ fragment. The dominance of the planar geometry is clearly apparent and for nearly a third of cases the angle is less than 0.10°, suggesting that many may have been positioned without due consideration.

characteristically variable when determined by X-ray diffraction. In fact, this habit of fixing H-atom positions means that despite the more than half a million structures present, we are unable to use the wealth of knowledge in the Cambridge Structural Database (CSD) to obtain a true representation of characteristic hydrogen positions as determined by X-ray diffraction. In addition to this, some groups have a positional ambiguity, *e.g.* OH groups where the H atoms typically occupy a position somewhere in a torus with the optimal position often dictated by the presence of a hydrogen bond.

2.1. N-atom geometry

The geometry around N atoms is even more difficult to predict. A search of the CSD (Version 5.31 including updates 1 and 2; Allen, 2002; Bruno *et al.*, 2002) for an N atom bound by three C atoms clearly shows that there are two possible geometries, planar and pyramidal (Fig. 1). However, including a carbonyl group on one of the C atoms encourages the nitrogen to become planar, demonstrating how the detailed geometry is generally dependent on wider aspects of the structure and whether the nitrogen lone pair can conjugate with a π-system. Even this rule is far from reliable, however, and amide groups (Winkler & Dunitz, 1971; Dunitz, 1979) and amino groups in nitroanilines (Ellena *et al.*, 1999, and references therein), for example, have been shown to exhibit significant out-of-plane distortions. In addition to difficulties determining the geometry of three-coordinate N atoms, the fact that they are often easily protonated can also make it difficult to determine the coordination number. Thus, during structure determination it is always advisable to look very carefully before assigning protons. Anecdotal evidence suggests that H atoms are often added geometrically without due consideration; this suggestion is supported by a CSD search for NH groups (Fig. 2).

2.2. Finding H atoms in the Fourier difference map

Given reasonably good crystals, modern diffractometer data will generally reveal most H atoms in a Fourier difference map. This approach can give useful results as shown, for example, by the variable-temperature X-ray diffraction studies of citrinin (Destro, 1991), potassium hydrogen phthalate (Harte *et al.*, 2005) and 2,4,6-trimethylbenzoic acid hydrogen-bonded dimers (Wilson & Goeta, 2004). In the last of these, data collected at 100 K clearly show a peak in the difference Fourier map indicating the presence of a single hydrogen position, whereas warming to 290 K showed disorder over two sites (Fig. 3). In this case, the authors were even able to devise a refinement strategy to determine the site-occupation factor of the two hydrogen positions. The ability to find H atoms in the difference map clearly depends on the quality of the data and the nature of the sample. For example, in a recently reported palladacycle (Rauf *et al.*, 2010), the H atoms bound to the coordinated water were not easily visible in the difference map (Fig. 4).

electronic reprint

2.3. Truncating the data

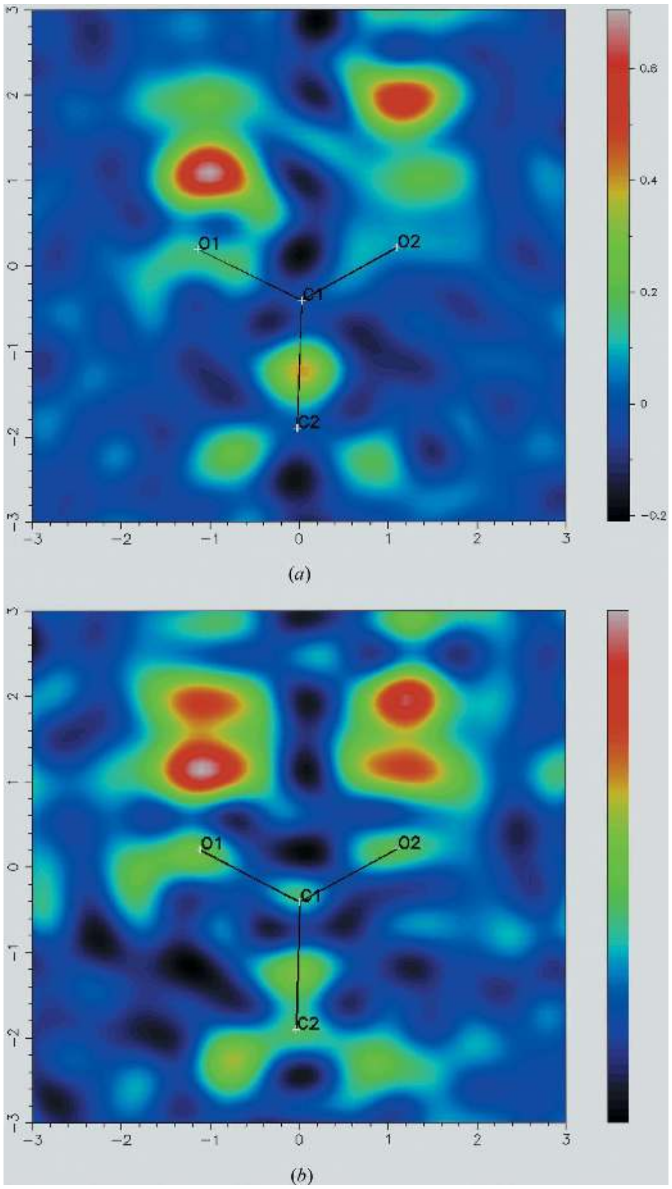
X-ray scattering is dependent on the scattering angle θ, the wavelength (λ) and the element. Neglecting anomalous effects, this is given by

$$f_B = \left\{\sum_{i=1}^{i=4} a_i \exp[-b_i(\sin\theta/\lambda)^2] + c\right\} \exp[-B(\sin\theta/\lambda)^2], \qquad (6)$$

where a_i, b_i and c are the element-dependent Cromer–Mann coefficients (Wilson, 1995) and

$$B = 8\pi^2 \langle u \rangle^2. \qquad (7)$$

Plotting f_B *versus* θ for different elements clearly shows how the scattering intensity decrease with $\sin\theta$ has a larger effect for hydrogen (Fig. 5). The intensity of a low-angle reflection has a much larger relative dependence on the H atoms than reflections at high angle. Thus, by up-weighting the high-angle data, you can decrease the impact of the H atoms on the refinement, which gives atomic coordinates and displacement parameters that are closer to those determined by neutron diffraction (Dunitz & Seiler, 1973, and references therein). It follows, therefore, that using only the low-angle reflections to



(*a*)

(*b*)

Figure 3
X-ray difference Fourier maps in the region of the COOH group in 2,4,6-trimethylbenzoic acid at 100 (*a*) and 290 K (*b*) showing the peak due to the hydrogen. Reproduced from Wilson & Goeta (2004). Copyright Wiley-VCH Verlag GmbH & Co. KGaA. Reproduced with permission.

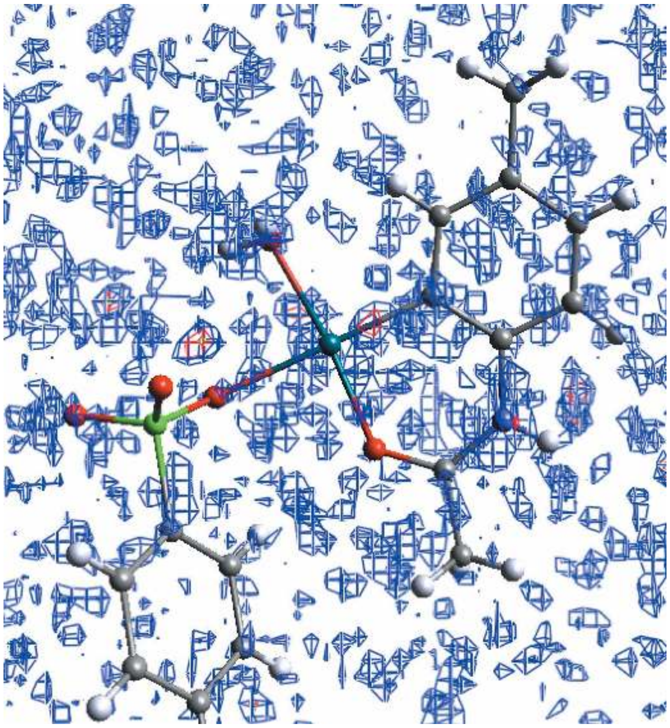


Figure 4
Generalized section of the difference Fourier map for a palladacycle recently reported by Rauf *et al.* (2010), displayed with *MCE* (Rohlíček & Hušák, 2007). The phases were calculated with the occupancy of the H atoms in the coordinated water set to zero.

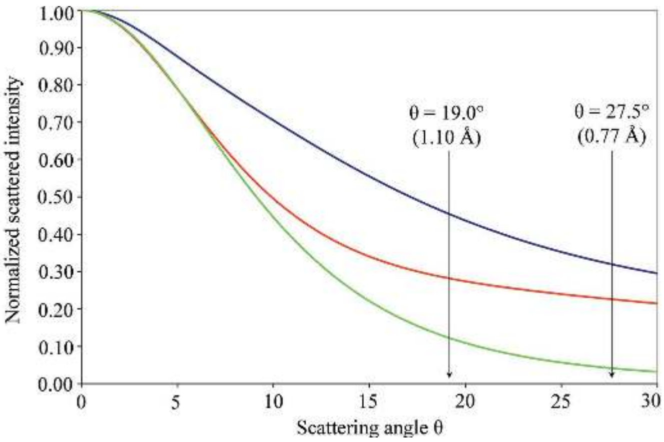


Figure 5
Scattered intensity for iron (blue), carbon (red) and hydrogen (green). Scattering from hydrogen at $\theta = 27.5^\circ$ is relatively much weaker than at $\theta = 19^\circ$ compared with iron and carbon because the $\sin\theta$ fall-off is larger for hydrogen. Normalized values for f_B calculated for molybdenum radiation, using $\langle u \rangle$ = 0.05 Å.

electronic reprint

Table 1
Restraints used in *CRYSTALS*.

In addition to the distance and $U_{\rm eq}$ restraints, XCH are restrained to the same value and HCH are restrained to 109.54°. The s.u. values applied are 0.02 Å for the distances, 2° for the angles and 0.002 for the displacement factors.

Fragment	Distance (Å)	$U_{\rm eq}$ multiplicity
$X{\equiv}$CH	0.93	1.20
X−C(H)−X	0.93	1.20
X_3CH	0.98	1.20
$X{=}$CH$_2$	0.93	1.20
X_2CH$_2$	0.97	1.20
X−CH$_3$	0.96	1.50
X−NH	0.86	1.20
X_2NH	0.86	1.20
X_3NH	0.89	1.20
XNH$_2$	0.86	1.20
X_2NH$_2$	0.89	1.20
X−NH$_3$	0.89	1.20
X−OH	0.82	1.50

calculate a difference Fourier map can often enhance peaks due to H atoms. Fuller enhancement can be achieved by suitable weighting of the reflections in the summation, as described by Woolfson (1956) (for the centrosymmetric reflections) and Sim (1960) (for noncentrosymmetric reflections.

The effect of truncating the data is apparent in the palladacycle example described above, where the water H atoms were much more visible in the difference map when the data were truncated to 1.1 Å (Fig. 6). Experimentation shows that the effectiveness of this procedure and the value required depend on the quality (noisiness) of the difference map and, thus, vary from case to case. This procedure has been shown to be extremely successful, particularly when trying to locate H atoms close to heavy metals, and has been used in a number of iridium hydride structures (Tang *et al.*, 2010*a*,*b*). Coupled with a restrained hydrogen refinement in *CRYSTALS* (Betteridge *et al.*, 2003), this generally leads to reasonably reliable refined H-atom positions. In the event that plausible H atoms cannot be located in the difference Fourier map, the user has no alternative but to fall back on geometric placement based on chemical intuition in order to provide a plausible contribution to the calculated structure factors.

2.4. H-atom refinement

Once H atoms have been approximately positioned, there are several possible methods for refinement. H atoms can of course be included in the refinement in the same way as heavier atoms. However, their positions and atomic displacement parameters will be affected by systematic errors in the data and/or shortcomings in the model. While this information could be considered useful (unlikely hydrogen positions and displacement parameters suggest a poor model), a chemically feasible model is generally preferred, and where there are many H atoms, checking can be time consuming. A better method might be to use gentle restraints to maintain sensible geometry and displacement parameters. For a large structure, these can be tedious to generate, can slow down a large refinement considerably, and tend to lead to a poor data-to-parameter ratio (which can lead to difficulties on publication). Consequently, the current trend is to use some variation of a so-called riding model. This is where the shifts applied to a group of atomic coordinates are constrained to be equal (usually those of a non-H atom, referred to as the 'parent', and one or more bonded H atoms). Isotropic displacement parameters of 'riding' H atoms are generally set to a constant multiple of $U_{\rm eq}$ (Watkin, 2000). One problem with this is that the addition of H atoms may (indeed should) affect the rest of the model, which in turn can render the positions of the H atoms incorrect. For example, for a benzene ring that rotates about the C_6 axis, the H atoms have further to move than the C atoms if the geometry is to be maintained. For this reason, geometrically placed atoms are often actually repositioned after each cycle of refinement.

The more significant problem is an incorrect starting location. The particular case of amide and amine groups has been discussed above, but there are many other examples too. The orientation of a phenyl methyl group generally has one H atom lying in the plane of the ring with one above and one below, but this leaves two possible positions, one of which is often automatically selected based on largely arbitrary geometric parameters (*e.g.* the relative length of adjacent bonds). In practice, there can also be considerable deviation

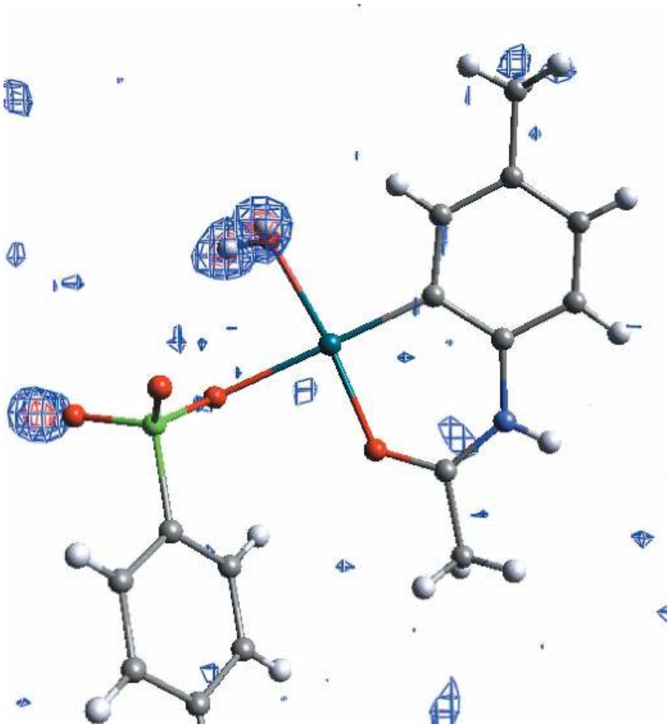


Figure 6
Generalized section of the difference Fourier map calculated with $(\sin\theta/\lambda)^2 = 0.22$ Å^2. As for Fig. 4, the occupancy of the H atoms in the coordinated water were set to zero before phases were calculated. The hydrogen peaks in the difference map generated using only the low-angle data are much more obvious than in the map calculated using all the data (Fig. 4). The contours are scaled to the strongest difference peak in both cases and displayed with *MCE* (Rohlíček & Hušák, 2007); the extraneous peak on the left is a symmetry-equivalent H atom.

electronic reprint

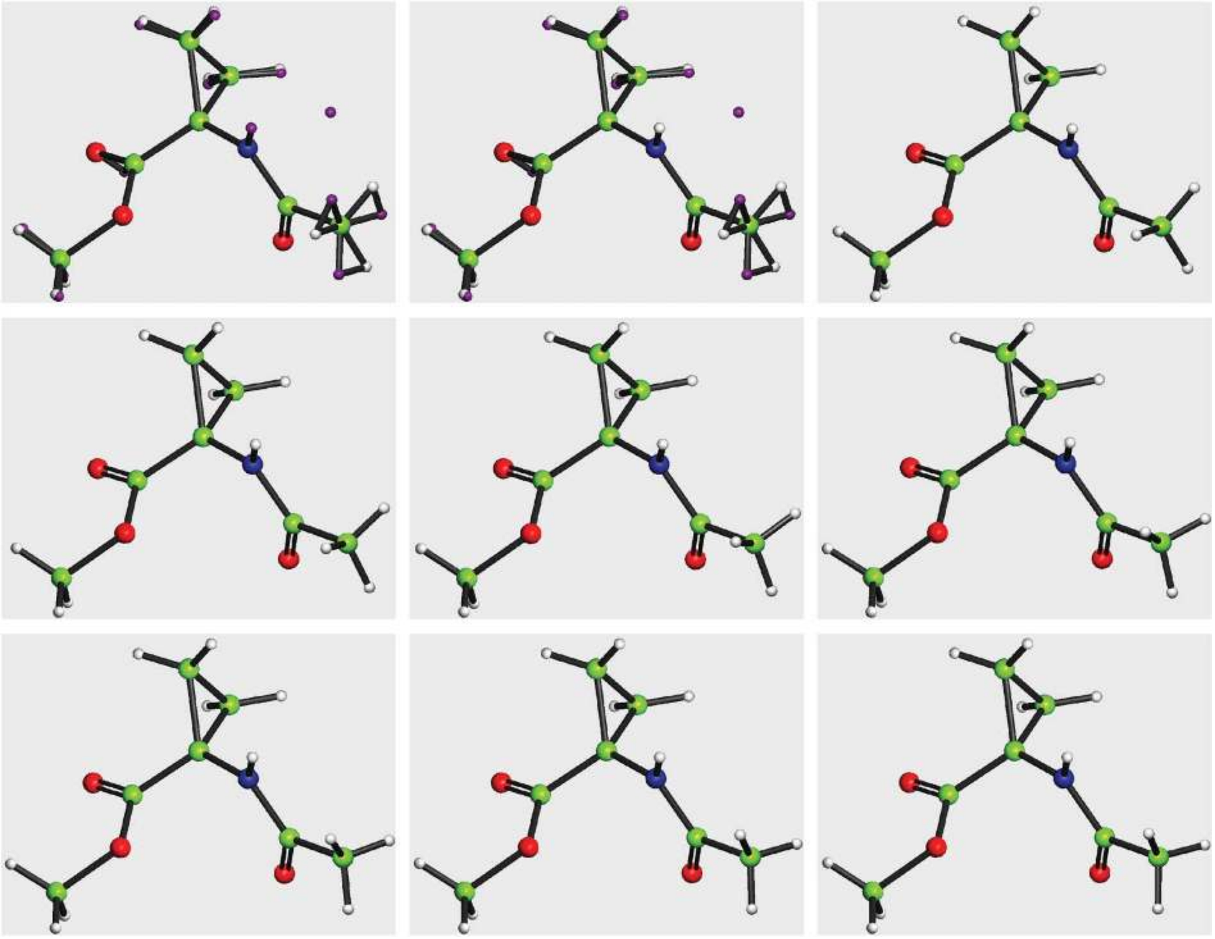


Figure 7
H-atom treatment in methyl 1-acetamidocyclopropanecarboxylate with *CRYSTALS*. Initially (top left), the geometric locations for the H atoms are shown, together with the peaks in the difference Fourier map (shown in white and purple, respectively); there is clearly reasonable agreement. Note that, by default, *CRYSTALS* makes no attempt to predict H atom(s) bound to nitrogen, but the peak in the difference map is very clear and can be identified as an H atom by the user (top middle). Fourier peaks are then removed (top right) and six cycles of restrained refinement carried out (from the left middle to the bottom right), allowing the methyl groups to rotate and the positions of the other H atoms to be optimized.

from these geometrically correct positions. In such cases, it is possible to use a restricted 'riding' refinement so that the methyl group retains its idealized tetrahedral geometry but rotates about the C—X bond. A similar approach can be applied to other groups (*e.g.* OH or NH_2). In an exceptional case, the X—H bond distance may also be allowed to refine without change to the direction of the X—H vector.

3. The *CRYSTALS* approach

In *CRYSTALS*, it is possible to automatically add H atoms geometrically to suitable C atoms, or locate them in a Fourier difference map, or manually add a specific number of H atoms to a given atom. Using the default options available through the user interface, it is then possible to leave the H atoms unrefined; apply the same shifts to the hydrogen positional parameters as to the 'parent' atom ('riding model'); or freely refine the H-atom positions (and isotropic displacement factors if desired). There is also the possibility to additionally apply restraints to C—H, N—H and O—H geometry. However, the default is to use a different approach available through the 'Guide' (Fig. 7; Peach, 2000). This displays the geometric location of H atoms (in white) overlayed with the peaks in the difference Fourier map calculated prior to the inclusion of the H atoms (in purple).[2] This enables the user to identify any mis-located H atoms and to add H atoms to O and N atoms in the correct position. *CRYSTALS* then refines the H-atom positions and isotropic displacement parameter with distance, angle and thermal restraints (see Table 1). These new H-atom positions are then used as the basis of the model with the riding constraints automatically calculated. Further to this,

---

[1] Structures like dichloro-bis[diphenyl(2,6-dimethylphenyl)phosphine]ruthenium toluene solvate (Baratta *et al.*, 2004), hexa-2,4-diyne-1,6-diol bis(*p*-toluenesulfonate) (Aime *et al.*, 1982) and bis[(μ^2-hydrido)dimesitylborane] (Entwistle *et al.*, 2003) determined from neutron diffraction experiments show alternative positions for methyl H atoms while the structure of 1,3-dibromo-2,4,6-trimethylbenzene exhibits rotational methyl disorder (Hernandez *et al.*, 2003).

[2] By default, all the data used for the refinement are included in the difference Fourier map calculation. The user can set resolution (or other) thresholds at any time.

electronic reprint

within the ‘Guide’ there is an option that easily enables the user to repeat the hydrogen-only refinement by reinstating the appropriate restraints and refinement instructions.

There are many advantages to this approach. Firstly, it enables the user to quickly compare the residual peaks with proposed H-atom positions. Good positions give confidence in the quality of their model and data, while poor agreement may indicate errors. Secondly, using refinement with restraints ensures that the geometry and displacement parameters remain sensible, while allowing the data to influence the model where the H atoms are well defined. In addition to checking the predicted hydrogen positions visually, it is also possible to generate a summary of the residuals enabling the user to confirm that the restraints are valid. Finally, the use of a riding model ensures that the data-to-parameter ratio remains within IUCr guidelines, with the bonus that it enables the user to ‘forget about wandering H atoms’.

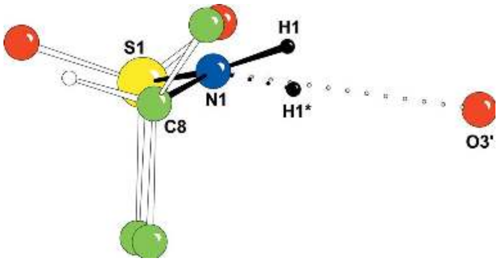


Figure 8
A fragment of 3-(4-methoxyphenyl)-1-phenyl-3-(*p*-toluenesulfonylamino)propan-1-one showing the effect of refining the amine H atom. The bonds shown with a solid black line indicate the planar atoms used to calculate the position geometrically; the new hydrogen position is marked with an asterisk and a dotted grey line is drawn between atoms N1 and O3′ to guide the eye to the location of the hydrogen-bonding interaction. Atom H1 moves to a position 0.38 Å out of the plane and the N—H vector projects an angle of 25.6° onto the C8/N1/S1 plane to form a hydrogen bond with an H···O distance of 2.14 (3) Å [compared with 2.306 (3) Å for the geometrically positioned H atom]. Image produced using *CAMERON* (Watkin *et al.*, 1996).

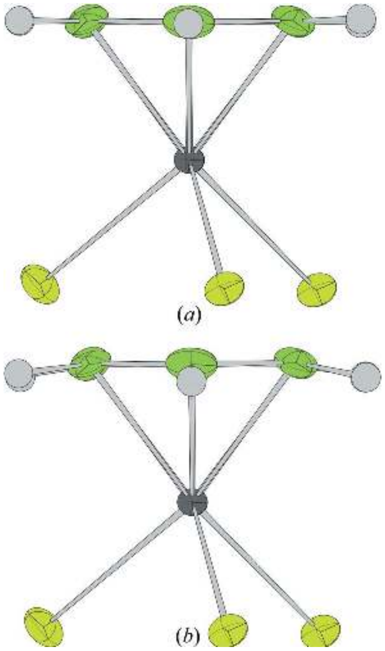


Figure 9
The ruthenium fragment of bis(μ-chloro)bis(η6-benzene)dichlorodiruthenium(II) (Canivet *et al.*, 2005) shown with the H atoms positioned geometrically (as published, left) and after hydrogen refinement (right). Images produced using *CAMERON* (Watkin *et al.*, 1996).

Although the H-atom positions are refined as described above, in order to conform to the convention, *CRYSTALS* removes the H-atom s.u. values in the final CIFs. The use of the riding model removes the variance/covariance information generated during the H-atom refinement and replaces it with that for the constrained refinement. Thus, the H-atom s.u. values at the end of the refinement are the same as those of the whole group and the error associated with distances between atoms within the riding group is defined as zero. However, the s.u. associated with the distance between any given constrained H atom and any atom not part of the riding group can of course be calculated from the variance–covariance matrix which is accessed through *CRYSTALS*. These errors should be used with caution as, although mathematically correct, the validity of the distance depends on the hydrogen position and how it was determined; thus it is advantageous to carry out hydrogen pre-refinement with restraints.

Users unhappy with restrained refinement are free to use geometric placement of the atoms from time to time or after each cycle of conventional refinement.

3.1. Examples

There are many examples in the literature of planar amide and amine groups where the H atoms have been added geometrically, but unless the intensity data have been deposited, it is almost impossible to prove the correct geometry without repeating the synthesis and the diffraction experiment. One exception is the article presenting the structure of 3-(4-methoxyphenyl)-1-phenyl-3-(*p*-toluenesulfonylamino)-propan-1-one (Yu *et al.*, 2004), where it was reported that ‘all H atoms were positioned geometrically and refined as riding’. However, on refinement of the H atoms within *CRYSTALS*, the $R1$[3] value drops by approximately 0.15% and the amide H atom moves out of the C8/N1/S1 plane and forms a more linear hydrogen-bond interaction with O3 (Fig. 8).

H-atom positions can also be significantly affected by the bonding environment. For example, in coordinated aromatic systems (*e.g.* benzene or cyclopentadiene) the H atoms can deviate significantly from the carbon plane, for example bis(μ-chloro)bis(η6-benzene)dichlorodiruthenium(II) (Canivet *et al.*, 2005). In this complex, refining the H atoms clearly suggests the benzene is not planar (Fig. 9). This reflects results seen previously, for example in the neutron diffraction study of benzene chromium tricarbonyl, where the H atoms were found to be displaced by an average of 0.03 Å out of the benzene plane (Rees & Coppens, 1973).

---

[3] $R1$ calculated on all the data. Refinements carried out with *CRYSTALS* using the published model and after refinement (riding the H atoms in both cases).

electronic reprint

Hydrides can also be found in the most unlikely of locations. Careful examination of the difference map for the iridium complex reported by Tang *et al.* (2010*b*) showed a peak, not in the obvious vacant site, but alongside the borylene ligand (Fig. 10). This seemed an unlikely location for a hydride. However, the expected Ir—B—N angle deviates significantly from linear [167.2 (6)°] and strong evidence for a direct B—H interaction was also obtained from ^{11}B and ^{1}H NMR and infrared spectroscopy measurements.

These examples, together with the palladacycle shown in Fig. 6, demonstrate that, while X-ray diffraction techniques can give compelling results when determining H-atom positions, they should be used with care. For example, errors in the data could lead to the presence of spurious peaks that could be mis-identified as H atoms. Similarly, if used without care, restraints can compete with the intensity data and cause a refinement to become unstable. If these positions are then used as the basis of a riding model, this problem is hidden. It is with some justification therefore that H-atom positions are generally treated with considerable caution by the reader.

4. Conclusion

While for the majority of purposes the exact location of H atoms is unimportant to most single-crystal crystallographers, the positions are increasingly important to chemists. Dependable predicted hydrogen positions are needed in order to reliably predict the chemical shifts for NMR, for example. In the absence of reliable published hydrogen geometries, people working on structure prediction from NMR data are ‘optimizing’ hydrogen positions using DFT programs such as *CASTEP* (Segall *et al.*, 2002). One such example is flurbiprofen (Flippen & Gilardi, 1975), which is repeatedly cited as a typical example of how X-ray crystallography cannot yield accurate hydrogen positions (Harris *et al.*, 2007); however, careful examination of the original article shows that the H atoms were located in the difference map and not refined, as was not untypical in the 1970s.

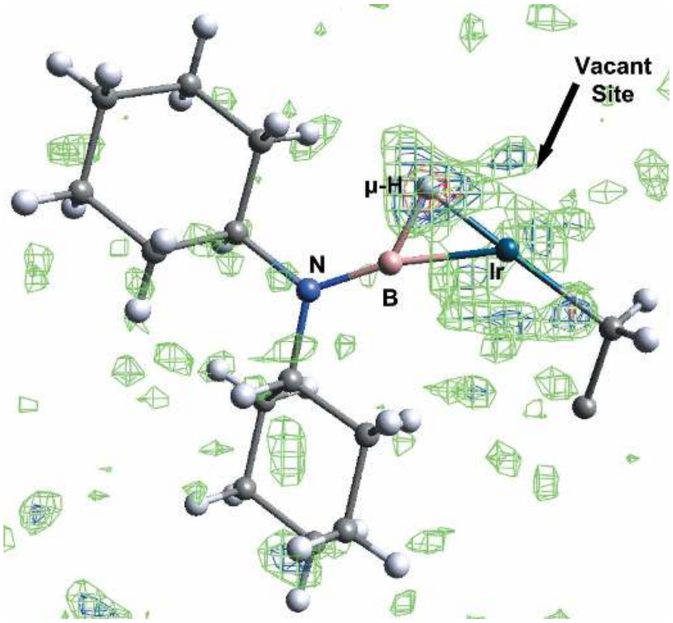


Figure 10
The Fourier difference map shown with the occupancy of the bridging hydride set to zero. Ir—H and B—H distances are consistent with those in other Ir(μ-H)B motifs [Ir—H = 1.613 (8) Å and B—H = 1.343 Å]. Image produced using *MCE* (Rohlíček & Hušák, 2007).

The current recommendations regarding the ratio of observations to refined parameters predicates against the routine refinement of H atoms. Despite this, the strategy used in *CRYSTALS* demonstrates that the quality of modern data permits lightly restrained refinement of H atoms in the majority of cases. There is now little justification for simply geometrically placing these atoms. The automatic restrained refinement of H atoms followed by final structural optimization with riding constraints represents a workable compromise between best practice and currently accepted norms and is the default refinement strategy programmed into *CRYSTALS*.

Special thanks to all the synthetic chemists in Oxford who have inspired this study, in particular Dr Simon Aldridge, Dr John M. Brown, Dr Michael W. Jones, Dr Nicholas H. Rees and Dr Christina Y. Tang, for helpful discussions and some of the data cited here; thanks also to Professor Chick Wilson and Dr Andrés Goeta for permission to reproduce Fig. 3. The data analysis in this work comes in part from the *Age Concern: Crystallographic Software for the Future* project (EP/C536282/01), one aim of which is to evaluate and document new and old procedures.

References

Aime, J. P., Lefebvre, J., Bertault, M., Schott, M. & Williams, J. O. (1982). *J. Phys.* **43**, 307–322.

Allen, F. H. (2002). *Acta Cryst.* B**58**, 380–388.

Baratta, W., Mealli, C., Herdtweck, E., Ienco, A., Mason, S. A. & Rigo, P. (2004). *J. Am. Chem. Soc.* **126**, 5549–5562.

Betteridge, P. W., Carruthers, J. R., Cooper, R. I., Prout, K. & Watkin, D. J. (2003). *J. Appl. Cryst.* **36**, 1487.

Bruno, I. J., Cole, J. C., Edgington, P. R., Kessler, M., Macrae, C. F., McCabe, P., Pearson, J. & Taylor, R. (2002). *Acta Cryst.* B**58**, 389–397.

Canivet, J., Therrien, B. & Süss-Fink, G. (2005). *Acta Cryst.* E**61**, m1090–m1091.

CCDC (1994). *VISTA – a Program for the Analysis and Display of Data Retrieved from the CSD.* Cambridge Crystallographic Data Centre, 12 Union Road, Cambridge, England.

Destro, R. (1991). *Chem. Phys. Lett.* **181**, 232–236.

Dunitz, J. D. (1979). *X-ray Analysis and the Structure of Organic Molecules*, ch. 7, pp. 328–333. London: Cornell University Press.

Dunitz, J. D. & Seiler, P. (1973). *Acta Cryst.* B**29**, 589–595.

Ellena, J., Goeta, A. E., Howard, J. A. K., Wilson, C. C., Autino, J. C. & Punte, G. (1999). *Acta Cryst.* B**55**, 209–215.

Entwistle, C. D., Marder, T. B., Smith, P. S., Howard, J. A. K., Fox, M. A. & Mason, S. A. (2003). *J. Organomet. Chem.* **680**, 165–172.

Flippen, J. L. & Gilardi, R. D. (1975). *Acta Cryst.* B**31**, 926–928.

Harris, R. K., Hodgkinson, P., Pickard, C. J., Yates, J. R. & Zorin, V. (2007). *Magn. Reson. Chem.* **45**, S174–S186.

Harte, S. M., Parkin, A., Goeta, A. & Wilson, C. C. (2005). *J. Mol. Struct.* **741**, 93–96.

Helliwell, M., Gomez de Anderez, D., Habash, J., Helliwell, J. R. & Vernon, J. (1989). *Acta Cryst.* B**45**, 591–596.

electronic reprint

Hernandez, O., Cousson, A., Plazanet, M., Nierlich, M. & Meinnel, J. (2003). *Acta Cryst.* C**59**, o445–o450.

Peach, J. M. (2000). Personal communication.

Rauf, W., Thompson, A. L. & Brown, J. M. (2010). *Dalton Trans.* In the press. doi:10.1039/C0DT00378F.

Rees, B. & Coppens, P. (1973). *Acta Cryst.* B**29**, 2516–2528.

Rohlíček, J. & Hušák, M. (2007). *J. Appl. Cryst.* **40**, 600–601.

Segall, M. D., Lindan, P. J. D., Probert, M. J., Pickard, C. J., Hasnip, P. J., Clark, S. J. & Payne, M. C. (2002). *J. Phys. Condens. Matter*, **14**, 2717–2743.

Sim, G. A. (1960). *Acta Cryst.* **13**, 511–512.

Tang, C. Y., Thompson, A. L. & Aldridge, S. (2010*a*). *Angew. Chem. Int. Ed.* **49**, 921–925.

Tang, C. Y., Thompson, A. L. & Aldridge, S. (2010*b*). *J. Am. Chem. Soc.* In the press. doi:10.1021/ja1043787.

Watkin, D. (2000). *Acta Cryst.* B**56**, 747–749.

Watkin, D. (2008). *J. Appl. Cryst.* **41**, 491–522.

Watkin, D. J., Prout, C. K. & Pearce, L. J. (1996). *CAMERON*. Chemical Crystallography Laboratory, University of Oxford, England.

Wilson, A. J. C. (1995). *International Tables for Crystallography*, Vol. C, *Mathematical, Physical and Chemical Tables*, § 6.1.1.2, p. 476 and Table 6.1.1.4, p. 500. Dordrecht: Kluwer Academic Publishers.

Wilson, C. C. & Goeta, A. E. (2004). *Angew. Chem. Int. Ed.* **43**, 2095–2099.

Winkler, F. K. & Dunitz, J. D. (1971). *J. Mol. Biol.* **59**, 169–182.

Woolfson, M. M. (1956). *Acta Cryst.* **9**, 804–810.

Yu, Z., Gu, X., Zhao, B. & Li, Y. (2004). *Acta Cryst.* E**60**, o1290–o1291.

electronic reprint