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Area correction of multi-atom–acceptor hydrogen bond frequency distributions

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Frequency distributions of hydrogen bond trajectories for X–H$\cdots$Ph interactions (X = O, N, C) need to be corrected for the finite area of the acceptor moiety and once this correction has been performed, it is seen that the donor groups have a distinct tendency to interact with the centroid of the aromatic ring.

Statistical analysis of experimental and theoretical data is very important for a correct interpretation of several chemical phenomena. Hydrogen bonds are typically described in terms of various parameters (lengths, angles) obtained from crystal structure determinations. These parameters are most simply depicted as histograms. However, such simple methods of analysis can be sometimes misleading.[1] For example, it was found that a distribution of hydrogen bond angles, θ, in O–H$\cdots$O hydrogen bonds is in the range 120–180° with a maximum at around 160°. Such an observation suggests that hydrogen bonds in crystals are non-linear.[2] This is, however, inconsistent with theoretical predictions in the gas phase, say for the water–water dimer. The reason for this seeming contradiction is the failure to take into account a geometrical factor that seriously influences the crystal statistics. The number of hydrogen bonds with angle θ is proportional to $\sin\theta$ for purely geometrical reasons, there being a greater probability of finding such interactions on the rims of cones of increasing solid angles. A simple procedure, namely the use of $N/\sin\theta$ instead of N (where N is the number of hydrogen bonds in the interval θ to $\theta + \Delta\theta$) in the histograms, effectively resolves this contradiction. This is known today as the *cone correction* and is illustrated in Fig. 1(a). This correction is used widely in the interpretation of hydrogen bonds and occurs as a standard procedure in the program VISTA that is a part of the Cambridge Structural Database (CSD).[3]

Recent work on weak X–H$\cdots$Ph hydrogen bonds has led to only a limited consensus concerning the nature of these interactions.[4] Some authors have held that the donor group X–H interacts with the centroid of the aromatic ring.[5–8] Others have stated that donors interact with one or more of the ring carbon atoms.[9–11] However, neither of these conclusions has been unambiguously substantiated. During our own studies of X–H$\cdots$Ph (X = O, N, C) interactions, we realised that the frequency distributions of these interactions must be corrected for the fact that the acceptor, being of a multiatom type, has a finite area. Therefore the numbers of observed trajectories of the

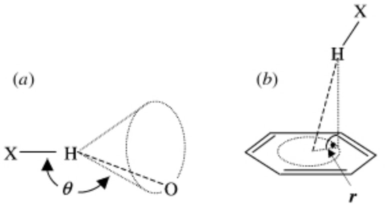

Fig. 1 Schematic diagrams for geometrical corrections of hydrogen bond metrics. (a) Cone correction for hydrogen bond angles θ. (b) Area correction for hydrogen bond offsets r.

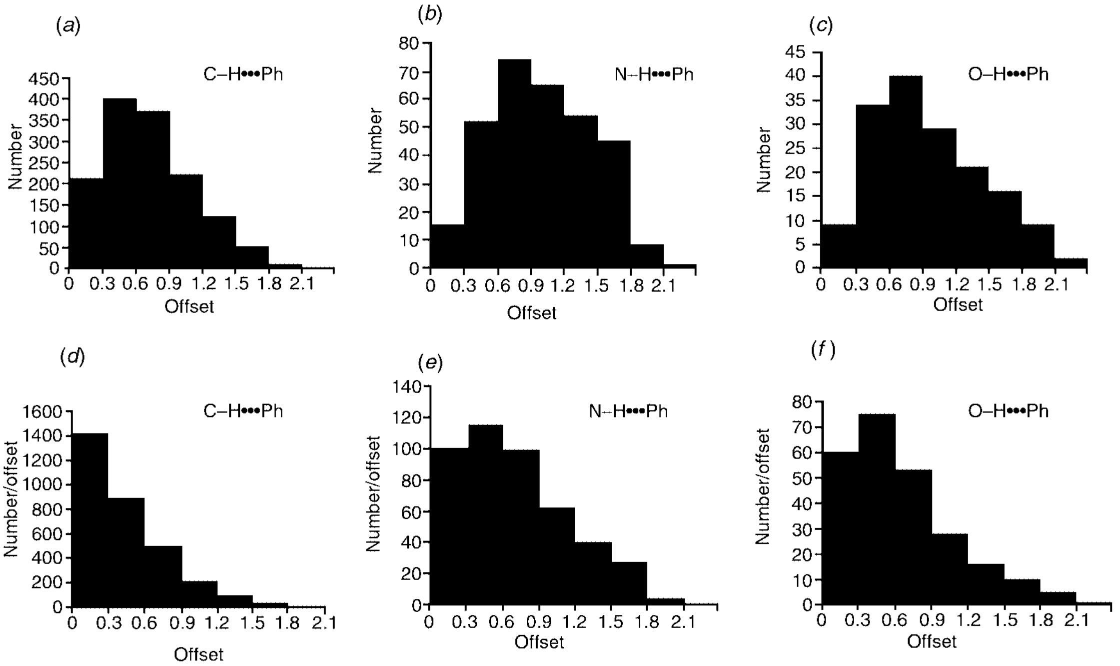

Fig. 2 Histograms of offsets r for X–H$\cdots$Ph hydrogen bonds: Uncorrected (a) C–H$\cdots$Ph, (b) N–H$\cdots$Ph and (c) O–H$\cdots$Ph; corrected (d) C–H$\cdots$Ph, (e) N–H$\cdots$Ph and (f) O–H$\cdots$Ph. Offsets are in Å.

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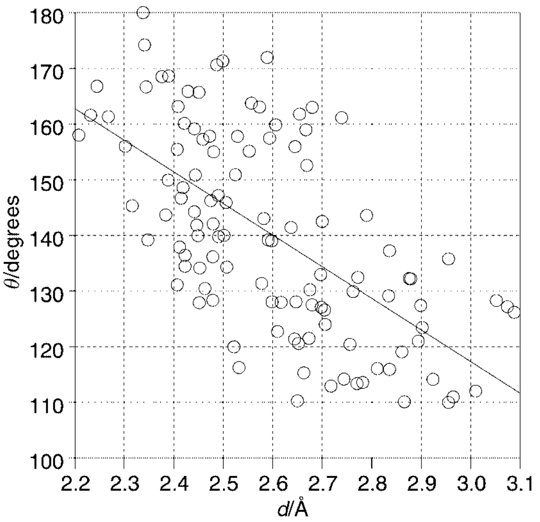

Fig 3 d–θ scatterplot for O–H···Ph hydrogen bonds with $r \leqslant 1.2$ Å, assuming that the ring centroid is the point acceptor. Notice the inverse correlation typical of hydrogen bonds.

donor onto the acceptor are a result of both chemical and geometrical factors. Simply put, an interaction X–H···Ph has an offset r which is the distance from the ring centroid to the projection of the H-atom position on the plane of the ring. This is shown in Fig. 1(b). The number of hydrogen bonds with offset r is proportional to $2\pi r$ for geometrical reasons and accordingly, histograms of N (where N is the number of offsets in the range r and $r+\Delta r$) must be replaced by N/r before they become chemically meaningful. So, we would like to term this procedure an *area correction* to match the term *cone correction* used in θ histograms.

Fig. 2(a), (b) and (c) are uncorrected histograms of X–H···Ph offsets for C–H···Ph, N–H···Ph and O–H···Ph hydrogen bonds ($d \leqslant 3.10$ Å, $\theta \geqslant 110°$) from 769, 649 and 431 appropriately retrieved crystal structure data in the CSD.† The histograms contain 1379, 314 and 160 hydrogen bonds respectively. Figs. 2(d), (e) and (f) are the respective corrected histograms.‡ The correction is carried out within ranges of 0.3 Å; the range from 0.0 to 0.3 Å is corrected by a factor of 1/(0.15), the range between 0.3 and 0.6 Å is corrected by a factor of 1/(0.45), and so on. The uncorrected histograms seem to indicate no particular offset preference. However, all three area corrected histograms show a preference for hydrogen bonds to a phenyl ring to be directed at or near the centre of the ring. For C–H···Ph interactions, this preference is clear. For N–H···Ph and O–H···Ph interactions, there is a maximum around 0.3 Å from the centroid. However, the number of observations in these latter cases is insufficient to draw fine distinctions.§ What *is* important is that the preference for a centroid or a close-to-centroid approach is seen in all cases.

To examine this matter further, we obtained the scatterplot of the hydrogen bond angle θ *vs.* the hydrogen bond distance d, assuming the centroid to be the point acceptor site for the 112 O–H···Ph hydrogen bonds with offsets < 1.20 Å (Fig. 3). This scatterplot (correlation coefficient -0.63) shows the typical inverse length–angle correlation that arises from the electrostatic nature of hydrogen bonds,[4] and indicates that the centroid may be reasonably approximated as the acceptor site in these interactions. The corresponding C–H···Ph scatterplot is fuzzier but this is not unexpected.

In summary, we conclude that this area correction for phenyl ring acceptors should be used in all relevant analyses of hydrogen bonds formed to such multiatom acceptors.

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Notes and references

† CSD (release: April 2000, 215 403 hits). Data were retrieved using the following overall criteria for all structures: 'no polymers'; 'no disorder'; 'error free structures'; 'atom coordinates present'; H···Ph(centroid) distances shorter than 3.5 Å and $R \leqslant 0.05$. Two additional criteria were used: 'no ions' for the N–H···Ph contacts (to eliminate the $>$N–H$^+$ donors); $T \leqslant 120$ K for the C–H···Ph contacts. For polynuclear ring acceptors, the offsets were calculated only with respect to the phenyl ring towards which the donor is oriented.

‡ Histograms were prepared using program Microsoft Excel.

§ Unsurprisingly, the exact profiles of the N–H···Ph and O–H···Ph histograms near the centroid depend on the range within which the area correction is performed (0.2, 0.3 Å). This is not the case for the C–H···Ph histogram, because the number of observations (1379) is satisfactorily large.

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