The Excess Basicity of Alkali Metal Methoxides in Methanol

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The deprotonation equilibria of weak neutral and anionic nitrogen acids (nitro-substituted arylamines and indoles) and methoxide addition to nitro-substituted anisoles have been investigated in methanol solutions of MeOLi, MeONa, and MeOK. The basicity of these media has been determined as excess basicity (X) functions. The available methods for the calculation of X and data processing have been critically compared and tested. Equilibrium constants (pK_a) and slope parameters (m^*) have been determined for the above compounds. The basicity of the three media (as probed by X) increases in the series Li < Na < K. Structural effects on m^* and pK_a values are discussed in terms of the solvation of the deprotonated acid; m^* values in the range 0.7–1.2 (solvation similar to the reference) have been found for all neutral indicators with the exception of indoles, for which m^* is *ca.* 0.2, which indicates higher solvation; anionic acids may have higher m^*s (1.2–1.6) if the two negative groups are *ortho* to each other.

With the exception of aliphatic amines, pyridines, and carboxylic acids, most of which behave as strong bases and acids, respectively, the majority of organic compounds are ionized only in strongly acidic or strongly basic media, and solutions far from ideality are often required for the investigation of their acid–base equilibria.[1–3] The quantitative study of equilibria in non-ideal solutions started with the definition of the H_0 acidity function by Hammett,[4] and has been revised and updated since then.[2,5–14] The acidity function H_0, based on primary nitroanilines,[4] was at first thought to be capable of describing the protonation of weak bases of any structure. Further investigations pointed out that each base defines its own acidity function, containing its own set of activity coefficients.[6,10] The discovery that activity coefficient terms for different bases are linearly related through a slope parameter m^* opened the way to the definition of a single acidity scale for a given acid system.[6,9,11–14] This scale has the two-fold form of a thermodynamic excess function[11a] and of a linear free-energy relationship like those of Hammett or Grunwald-Winstein.[6,14] In this framework, the slope parameter m^* acquires a significance similar to the ρ parameter of the Hammett equation. In fact, it has been shown to give information of the solvation of the conjugate acid–base pair.[14] Further discussion on this topic has been centred on the practical methods to evaluate excess acidities and on the physical meaning of m^*.[9–14]

Studies on strongly basic media have developed along two different paths.[1] A group of studies, mainly due to Streitwieser and Bordwell, has dealt with dilute (ideal) solutions of very strong bases in dipolar non-hydroxylic solvents.[15,16] In these media extremely high basicities can be attained, which have allowed the determination of pK_a values for a variety of weak carbon, oxygen, sulphur, and nitrogen acids, as well as to correlate those data with substituent effects, gas-phase acidities and heats of deprotonation. However, although these data give rise to consistent and thermodynamically meaningful acidity scales, they cannot be directly transferred to other protic solvent systems, as the acidity order may vary considerably.[16e,f] However, the basic strength range available in some widely used systems, like alkali metal hydroxides or alkoxides in water or alcohols, is such that concentrated, non-ideal solutions must be employed.

Most quantitative studies on these media have been limited to the definition of several acidity functions in a wide variety of systems, in which medium basicity is made to change by increasing either the base or an organic co-solvent concentration.[1,7,13,17,18] A few efforts towards a unified treatment have been carried out in which methods in use for acid solutions were tested in some basic media, observing good agreement between them.[19–21]

In this paper we have sought to address the following questions: (*a*) whether a single function can describe deprotonation equilibria in strongly basic solutions; (*b*) what the method of choice would be for computing such a function; (*c*) whether m^* values can again be correlated with the solvation of the acid–base pair. To this purpose, we have examined data[22–26] concerning the deprotonation of weak nitrogen acids and the addition of methoxide ion to nitroanisoles to yield Meisenheimer complexes (whose relevance to aromatic nucleophilic substitutions is well recognized)[27] in methanolic solutions of Li, Na, and K methoxides. The solubility in MeOH of MeONa and MeOK is relatively high compared to other alcohols (> 5 mol dm^{-3}), so that a broad basic strength range can be attained. Methanol is also a good solvent for weak organic acids, in contrast to water.[18]

The deprotonation of an acid HA may be written as equation (1), with an equilibrium constant K_a'. In methoxide solutions we

$$HA \rightleftharpoons A^- + H^+ \quad (1)$$

may also write equation (2).

$$HA + MeO^- \rightleftharpoons A^- + MeOH \quad (2)$$

Methanol has a much lower relative permittivity than water (33.6 *vs.* 80.4 at 20 °C), similar to that of *N*-methylpyrrolidone, in which important ion pairing has been found with oxygen acids.[16c,d] The presence of $[RO^-M^+]$ ion pairs in alcohols is also well established,[16b,24] and has been invoked to explain the differing basicity of Li, Na, and K methoxide solutions.[24] Thus, ion pairing with indicators may not be neglected in these media. It has been pointed out that, if ionic association remains important even in very dilute solutions, then equilibrium constants will depend on the metal counterion, and pK_as in different methoxides will not be the same.[24] To a first

approximation, ion pairing between alkali metal ions and A^- is expected to be less important if proton abstraction leads to a charge-delocalized anion,[16c,d] which is the case for the acids studied here. Hence, the following treatment does not explicitly take ion pairing into account.

The equilibrium constant K_a for equation (2) is given by equation (3).

$$K_a = (a_{MeOH}a_{A^-})/(a_{HA}a_{MeO^-}) \quad (3)$$

Introducing the autopyrolysis constant of the solvent (K_S) we have $pK_a' = pK_S + pK_a$. Throughout this work, we have derived pK_a values, but in keeping with common usage we have tabulated the corresponding pK_a' values, which can be calculated taking $pK_S = 16.86$ at 20 °C.[28]

Defining the ionization ratio $I = [A^-]/[HA]$ and introducing the activity coefficients γ_i we have equation (4). The left-hand

$$\log I - \log [MeO^-] + \log a_{MeOH} = \log (\gamma_{HA}\gamma_{MeO^-}/\gamma_{A^-}) - pK_a \quad (4)$$

side of equation (4) contains experimentally accessible quantities. For practical reasons, we will denote it as $\log Q$, (though this term is usually reserved for the logarithm of the concentration ratio), so that equation (4) can be rewritten as equation (5). The determination of pK_a is straightforward if the

$$\log Q = \log (\gamma_{\sim HA}\gamma_{MeO^-}/\gamma_{A^-}) - pK_a \quad (5)$$

acid is deprotonated in ideal solutions, where equation (5) can be reduced to equation (6) and pK_a can be calculated as the

$$\log I - \log [MeO^-] = -pK_a \quad (6)$$

intercept of a line of log I *vs.* log $[MeO^-]$, which should have unit slope. Otherwise, we must evaluate the activity coefficient term appearing in equation (5) as a function of base concentration. Several methods have been proposed to accomplish this task (mostly for acid media), all assuming equation (7), or

$$\log(\gamma_{HA}\gamma_{MeO^-}/\gamma_{A^-}) = m^*\log (\gamma_{HA^*}\gamma_{MeO^*}^-/\gamma_{A^*}^-) \quad (7)$$

analogous forms, which states the proportionality of activity coefficient terms for the acids HA and HA*, to hold.[6,9,11] These methods differ in several respects; those which have been tested in this work will be briefly reviewed below, with reference to methanol–methoxide systems.

Results

We have employed data[22] on the activity of methanol[23] and the deprotonation of nine nitrodiphenylamines and anilines (used to derive the H_M acidity function),[24] eight anionic nitrodiphenylamines and anilines ionizing to dianions ($H_{M=}$),[25] eight indoles and indazoles (H_M^I),[26] and the addition of methoxide ion to seven nitroanisoles and 2,4-dinitroaniline (J_M),[24] in sodium and potassium methoxides at 20 °C. The base concentration range extends to 5.5 and 5.8 mol dm^{-3} for Na and K, respectively. Some data for indoles were also available in lithium methoxide, but this medium does not permit the attainment of high basicities because of the low solubility of MeOLi (2.6 mol dm^{-3}) Values of log$I$ have been calculated from UV data. In general, the spectra are affected by rather small medium effects and define fairly good isosbestic points. However, the solubility of the methoxides is too low for complete deprotonation of the weakest acids, and in these cases the absorptivity of the deprotonated form had to be extrapolated.[24]

Given the special significance of arylamines, medium basicity determinations have been carried out taking this group as reference, and all methods also tested on this data set, because it spanned the widest base concentration range. Additions are treated separately.

Data in MeONa and MeOK are available for the following compounds: 2,4-dinitrodiphenylamine (24DNDPA), acetophenone 4-nitrophenylhydrazone (APNN), 4,4′-dinitrodiphenylamine (44′DNDPA), 2,4-dinitroaniline (24DNA) (deprotonation was intermingled with methoxide addition), 4-nitrodiphenylamine (4NDPA), 2,4-dichloro-6-nitroaniline (24DCL6NA), 2-nitrodiphenylamine (2NDPA), 4-nitroaniline (4NA), and 2-nitroaniline (2NA).

Stepwise Overlap Method.—As originally proposed by Marziano *et al.*,[9a] if log I data for an acid HA* are available in both ideal and non-ideal solutions, its pK_a can be evaluated by applying equation (6) to the data for ideal solutions. We may then calculate $X = \log (\gamma_{HA^*}\gamma_{MeO^-}/\gamma_{A^*}^-)$ from the remaining data, recalling that $X = \log Q^* + pK_a^*$. This yields the excess basicity[20a] function X in the available concentration range (beyond the ideal range where it is zero). Given another acid HA, ionizing in a range overlapping with the preceding one, if log Q and log Q^* values are linearly related then equation (7) holds, and log Q is a linear function of X. This reasoning may be

$$\log Q = m^*X - pK_a \quad (8)$$

inductively extended to another compound using the last one as reference, and so on. The parameters m^*_j and pK_{aj} for an indicator j, along with the X function, can be calculated if the same data for an indicator i (with m^*_i and pK_{ai}), more strongly acidic than j but ionizing in an overlapping concentration range, are known. If p_{ij} and q_{ij} are the slope and intercept, respectively, of the line log Q_j *vs.* log Q_i, the required data are calculated as equations (9) and (10). The values of m^*_j and pK_{aj} allow the

$$m^*_j = p_{ij}m^*i \quad (9)$$

$$pK_{aj} = p_{ij}pK_{ai} - q_{ij} \quad (10)$$

determination of the X function in the whole ionization range of indicator j from equation (11). It is easily seen that this

$$X = (\log Q_j + pK_{aj})/m^*_j \quad (11)$$

procedure differs from the acidity function method[4] only in that the slopes are not constrained to the value of 1.00. Finally, combining equations (5) and (7) gives equation (12), which gives the medium basicity dependence of an acid–base equilibrium in a medium for which the X function is available.

$$\log I - \log [MeO^-] + \log a_{MeOH} = m^*X - pK_a \quad (12)$$

4,4′-Dinitrodiphenylamine was used as reference acid.[24] Its m^* value was arbitrarily set to 1.00, and its pK_a determined by means of equation (6); slopes of 1.00 ± 0.01 are obtained in both cases. The other protonation parameters and the X function are then determined from log Q *vs.* log Q^* plots in overlapping ionization ranges; good linearity is always found. Values of m^* and pK_a obtained in the two systems are collected in Table 1 along with their standard deviations. For some indicators (APNN, 24DNDPA, and 2NA in MeONa; 24DNDPA, 24DCL6NA, and 2NA in MeOK) overlap is defined by few points, or other data are available in the same range. For these redundant cases, the protonation parameters are determined from the previously calculated X function. X values for MeOK are plotted in Figure 1.

Table 1. Acidity parameters for anilines and diphenylamines, obtained with the stepwise overlap method.[a]

Indicator	MeONa		MeOK	
	m^*	pK_a'	m^*	pK_a'
2,4-Dinitrodiphenylamine[b]	1.02 ± 0.04	17.04 ± 0.02	0.97 ± 0.03	17.06 ± 0.02
Acetophenone 4-nitrophenylhydrazone[b]	0.95 ± 0.02	17.10 ± 0.01	0.94 ± 0.01	17.15 ± 0.01
4,4'-Dinitrodiphenylamine	(1.00)	17.40 ± 0.01	(1.00)	17.39 ± 0.01
2,4-Dinitroaniline	0.85 ± 0.01	18.21 ± 0.01	0.83 ± 0.03	18.22 ± 0.02
4-Nitrodiphenylamine	0.83 ± 0.03	18.93 ± 0.04	0.75 ± 0.03	19.26 ± 0.04
2,4-Dichloro-6-nitroaniline[b]	0.76 ± 0.04	19.02 ± 0.09	0.82 ± 0.01	19.54 ± 0.02
2-Nitrodiphenylamine	1.00 ± 0.06	20.62 ± 0.17	0.93 ± 0.05	21.41 ± 0.10
4-Nitroaniline	0.86 ± 0.08	21.53 ± 0.27	0.95 ± 0.07	22.58 ± 0.25
2-Nitroaniline[b]	1.02 ± 0.06	21.67 ± 0.20	0.90 ± 0.03	22.25 ± 0.15

[a] Refined values in Table 7 (see the text). [b] Not used for overlap (see the text).

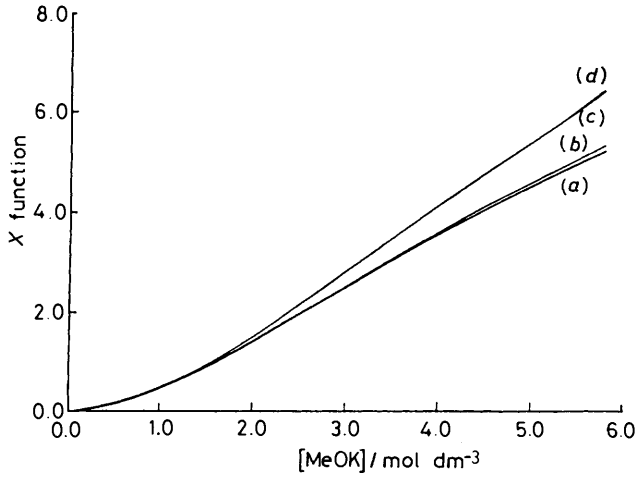

Figure 1. X functions *vs.* MeOK concentration from arylamine data obtained with different methods. (*a*) Stepwise overlap; (*b*) non-linear optimization; (*c*) linear method; (*d*) non-linear optimization on the extended data set.

Table 2. Acidity parameters for anilines and diphenylamines from non-linear optimization.[a]

Indicator	MeONa		MeOK	
	m^*	pK_a'	m^*	pK_a'
2,4-Dinitrodiphenylamine	1.18	17.13	0.95	17.03
Acetophenone 4-nitrophenylhydrazone	1.14	17.21	0.92	17.12
4,4'-Dinitrodiphenylamine[b]	(1.00)	(17.40)	(1.00)	(17.39)
2,4-Dinitroaniline	0.98	18.38	0.81	18.19
4-Nitrodiphenylamine	0.96	19.11	0.73	19.23
2,4-Dichloro-6-nitroaniline	0.87	19.13	0.80	19.51
2-Nitrodiphenylamine	1.10	20.78	0.91	21.38
4-Nitroaniline	0.95	21.65	0.93	22.56
2-Nitroaniline	1.10	21.81	0.88	22.22

[a] Refined values in Table 7 (see the text). [b] Parameters held fixed.

Non-linear Methods.—Two other methods (not requiring overlap) for the determination of X are available. Both involve fitting the experimental log I data to equation (12), which must be rewritten expressing X as a function of the base concentration b. Generally a polynomial function of degree n_c (between 5 and 7) is sufficient, so that $X = \Sigma_k a_k b^k$, with the known term set to zero.[11]

$$\log I = m^* \Sigma_k a_k b^k - pK_a + \log b - \log a_{MeOH} \quad (13)$$

m^* and pK_a for each indicator and the polynomial coefficients a_k for X are to be optimized. The first method[9e,11a] carries out a sequential optimization with a dedicated procedure, while the second one[9c,11b] employs standard non-linear fitting methods; both require starting trial values of the parameters, but do not require an explicit choice of reference. The second method is the most appropriate in principle, though it is practically limited to data sets containing no more than 50 indicators;[11b] since we are below this limit, we have applied it (see the Experimental). In the reported procedure,[11b] the X scale is referenced so that the average of m^* values for the indicators used is 1.0, while we define m^* for a single reference compound[9a] (44'DNDPA) as 1.00. Its pK_a is available from the preceding results, and both parameters are held fixed at their initial values during the optimization.

We performed tests aimed at checking whether the final results depend on the initial values, and in particular whether initially equal m^* values lead to different final ones. Using the data previously obtained by overlap as starting values, all optimized parameters and X coefficients are found to be similar to those obtained previously (see Table 2); the new X function for MeOK is plotted in Figure 1.

The algorithm seemed otherwise unable to converge successfully. In fact, when all m^*s are set to 1.0 and pK_as as before, convergence occurs with final m^*s being equal (0.93) for all indicators, and the sum of squared errors is 10 times that obtained previously.

Linear Method.—A different formulation of equation (13) might be considered. Recalling the above polynomial expression for X, for the i-th indicator equation (8) will read as equation (14). If one sets $a'_{ik} = m^*_i a_k$ and $a'_{i,0} = -pK_{ai}$,

$$\log Q_i = m^*_i \Sigma_k a_k b^k - pK_{ai} \quad (k = 1,2,...n_c) \quad (14)$$

equation (14) is readily rearranged to give equation (15). The

$$\Sigma_k a'_{ik} b^k = P_i(b) \quad (k = 0,1,...n_c) \quad (15)$$

curve giving log Q_i as a function of b is thus expressed by a polynomial of degree n_c. Its coefficients a'_{ik} ($k > 0$) are given by the product of a factor common to all indicators (a_k, the true coefficient for X) and another one (m^*_i) characteristic of each. Given the j-th indicator, with log $Q_j = P_j(b)$, the polynomials P_i and P_j will also be related through a linear expression equivalent to equation (9), so that (in principle) setting a reference with known m^* and pK_a would allow us to calculate all the other parameters. More importantly, equation (15) states that the model equation (13) is actually a linear one, unsuitable for non-linear fitting, m^* being a fictitious parameter.[29] In

Table 3. Acidity parameters for anilines and diphenylamines from the linear method.[a]

Indicator	MeONa		MeOK	
	m^*	pK_a	m^*	pK_a'
2,4-Dinitrodiphenylamine	1.14 ± 0.07	17.07 ± 0.02	1.12 ± 0.06	17.11 ± 0.02
Acetophenone 4-nitrophenylhydrazone	1.01 ± 0.06	17.11 ± 0.02	0.89 ± 0.05	17.13 ± 0.02
4,4′-Dinitrodiphenylamine	(1.00)	17.40 ± 0.01	(1.00)	17.39 ± 0.01
2,4-Dinitroaniline	0.82 ± 0.05	18.17 ± 0.04	0.70 ± 0.05	18.12 ± 0.05
4-Nitrodiphenylamine	0.86 ± 0.17	18.94 ± 0.19	0.60 ± 0.02	19.10 ± 0.06
2,4-Dichloro-6-nitroaniline	0.82 ± 0.03	19.09 ± 0.06	0.65 ± 0.02	19.34 ± 0.05
2-Nitrodiphenylamine	1.09 ± 0.05	20.73 ± 0.12	0.73 ± 0.03	21.14 ± 0.13
4-Nitroaniline	0.97 ± 0.16	21.72 ± 0.48	0.64 ± 0.03	21.77 ± 0.14
2-Nitroaniline	0.84 ± 0.07	21.08 ± 0.22	0.65 + 0.05	21.71 + 0.23

[a] Refined values in Table 7 (see the text).

practice, the polynomials P_i cannot be directly determined from the data of a single indicator, as these cannot be reliably extrapolated beyond their available range. However, the relative linearity among them, which can be tested and used only in an overlap region, allows one to implement this procedure as a variant of the conventional method, suitable for automatic computation.

Once the reference indicator is set, X can be computed in the available base concentration range and fitted to a polynomial of degree n_c, as before. However, in this implementation log Q for the following indicator is not plotted *vs.* log Q for the preceding one, but *vs.* X as determined so far; new values of X are then calculated from all data of the current indicator, and appended to the previous ones.

A question which might arise is whether the final values depend on the order in which the indicators are processed. Two options are separately implemented and tested: (*a*) processing the indicators by a random or arbitrary choice; (*b*) sorting the indicators by their approximate acidity order. With regard to (*a*), we might argue that the obtained overlap, though acceptable, may well be far from optimal in that log I values of different accuracy may be used if overlap takes place at the extremes. Otherwise, if a selection is made so as to maximize the number of overlapping points among indicators of equal priority, an even spacing between points would be required. Thus, we instigated a simple indexing method, sorting the indicators according to the base concentration where log I is *ca.* 0, which ranks them in approximate order of decreasing acidity. However, probably due to the limited choices available the two procedures produce the same results.

The final runs are carried out with the indexing method, and log$Q$ values are weighted according to the expression for $\sigma_{\log I}$ [$=\sigma_{\log Q}$; equation (30)]. This also allows us to obtain an estimate of the 'goodness-of-fit' parameter q, which is from 0.05–1 in all cases. All acidity parameters are collected in Table 3, and the X function of MeOK is again plotted in Figure 1. Due to the lower m^* values for 2NA and 4NA (0.6 *vs.* 0.9), the curve for MeOK takes higher values than previously (*ca.* 1 unit above 5.5 mol dm^{-3}). Linearity and consistency of the data *vs.* the new X functions is eventually checked. The parameters obtained are found to be within experimental error of those in Table 3.

Extension to other Classes of Acids.—Two ways could be considered in order to derive parameters for the remaining data, *i.e.* the linear method might be applied to a database including all data, or the previous X function might be used after testing the linearity of log Q *vs.* X. The two options differ in that the latter does not update the X function data with the new ones, as it does when dealing with new compounds using an already established X or acidity function.

The first option is applied to two extended databases consisting of diphenylamines and indoles, and diphenylamines and anions, but standard deviations and pK_a differences are larger, and in many cases unacceptable q values are found. This is probably related to the errors inherent in the overlap method when using very different slopes. In fact, the expressions for σ_{m^*j} and σ_{pKj} [see below equations (25) and (26)] state that these errors are proportional to the relative slope p_{ij}, the minimum being at $p_{ij} = 0$; in practice, m^*_j should be lower than m^*_i. If indicators with different slopes are used, it is quite likely that the relative slopes jump to high values, unless a careful ordering is made or the practical prescription of p_{ij} *ca.* 1 (similar slopes) is followed. For the above reasons, we rely on the X functions as determined from arylamines only, and process the remaining data with the second option.

Anionic Acids.—Data are available for the following indicators: 4′-chloro-4,6-dinitrodiphenylamine-2-carboxylic acid (2C46DN4′CL), 2,4-dinitrodiphenylamine-2′-carboxylic acid (2′C24DN), 4′-chloro-2-nitrodiphenylamine-4-carboxylic acid (4C2N4′CL), 4′-fluoro-2-nitrodiphenylamine-4-carboxylic acid (4C2N4′F), 2-nitrodiphenylamine-4-carboxylic acid (4C2N), 4-nitrodiphenylamine-2-carboxylic acid (2C4N), 2-nitrodiphenylamine-2′-carboxylic acid (2′C2N). 4-amino-3-nitrobenzoic acid (3N4AB). No data are available for 2′C24DN and 3N4AB in MeONa. All indicators are introduced as free acids and treated as usual, yielding the data of Table 4.

Indoles and Indazoles.—Data for MeONa and MeOK are available for 4-nitroindazole (4NIN), 5-nitroindazole (5NIN), 3-formylindole (3FI), benzoimidazole (BIM), 3-acetylindole (3AI), indazole (IN), 5-nitroindole (5NI), and 5-cyanoindole (5CI); data for 3FI, BIM, and 3AI are available also in MeOLi. The first five indicators are strong acids; the plots of equation (6) have unit slopes. The remaining ones yield the values given in Table 5. Good linearity is found in MeOK, while in MeONa 5NI and 5CI show a marked curvature in the upper points, which are discarded.

X *Function of* MeOLi.—In order to obtain an X function comparable to the Na and K analogues, the reference compound should either have the same structure (which is prevented by the lack of data) or be given an m^* value consistent with the previous ones. Since the only available data are for indole derivatives, it is natural to reference this scale with a value similar to those previously found. Hence, an approximate m^* value of 0.2 is assigned to the three indicators.

The construction of this X function presents an obvious problem, in that most data refer to ideal solutions, where X is *ca.* 0. If m^* is small, the changes due to experimental errors are

Table 4. Acidity parameters for anionic acids.[a]

Indicator	MeONa		MeOK	
	m^*	pK_a'	m^*	pK_a'
4'-Chloro-4,6-dinitrodiphenylamine-2-carboxylic acid	1.28 ± 0.03	18.13 ± 0.02	1.12 ± 0.03	18.07 ± 0.02
2,4-Dinitrodiphenylamine-2'-carboxylic acid			1.08 ± 0.03	18.36 ± 0.03
4'-Chloro-2-nitrodiphenylamine-4-carboxylic acid	1.23 ± 0.04	20.24 ± 0.08	0.74 ± 0.02	20.19 ± 0.05
4'-Fluoro-2-nitrodiphenylamine-4-carboxylic acid	1.24 ± 0.02	20.60 ± 0.06	0.81 ± 0.02	20.85 ± 0.07
2-Nitrodiphenylamine-4-carboxylic acid	1.22 ± 0.02	20.77 ± 0.06	0.73 ± 0.01	20.80 ± 0.05
4-Nitrodiphenylamine-2-carboxylic acid	1.67 ± 0.07	22.55 ± 0.21	0.88 ± 0.01	22.36 ± 0.03
2-Nitrodiphenylamine-2'-carboxylic acid	1.58 ± 0.04	22.09 ± 0.11	0.82 ± 0.03	22.67 ± 0.17
4-Amino-3-nitrobenzoic acid			0.81 ± 0.02	22.62 ± 0.13

[a] Refined values in Table 7 (see the text).

Table 5. Acidity parameters for indoles and indazoles.[a]

Indicator	MeOLi		MeONa		MeOK	
	m^*	pK_a'	m^*	pK_a'	m^*	pK_a'
4-Nitroindazole			—	14.59 ± 0.02	—	14.61 ± 0.01
5-Nitroindazole			—	14.74 ± 0.01	—	14.76 ± 0.02
3-Formylindole	—	15.93 ± 0.01	—	15.90 ± 0.01	—	15.94 ± 0.01
Benzoimidazole	—	16.21 ± 0.01	—	16.20 ± 0.00	—	16.19 ± 0.01
3-Acetylindole	—	16.75 ± 0.01	—	16.75 ± 0.01	—	16.71 ± 0.01
Indazole			0.25 ± 0.01	17.30 ± 0.02	0.19 ± 0.01	17.23 ± 0.01
5-Nitroindole			0.28 ± 0.02	18.21 ± 0.03	0.16 ± 0.01	18.05 ± 0.02
5-Cyanoindole			0.21 ± 0.01	18.36 ± 0.01	0.16 ± 0.00	18.43 ± 0.01

[a] Refined values in Table 7 (see the text).

Table 6. Polynomial coefficients of the X functions.

Degree	Li[a]	Na[b]	K[b]
0	0.015 94	—	—
1	0.001 52	0.190 26	0.187 67
2	0.104 91	0.076 09	0.304 61
3	—	0.063 82	0.010 98
4	—	−0.019 54	−0.013 41
5	—	0.001 44	0.001 24

[a] Calculated from indole data. [b] From non-linear optimization on the extended data set (see Table 7).

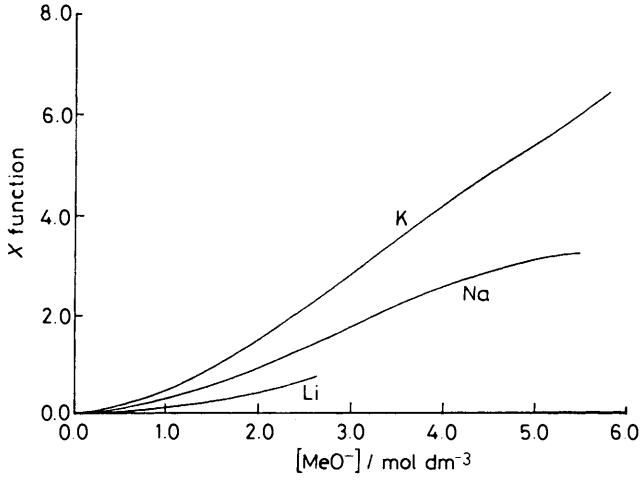

Figure 2. X functions *vs.* base concentrations for MeOLi, MeONa, and MeOK at 20 °C. Function for MeOLi calculated from indole data; for MeONa/K from non-linear optimization on the extended data set (see the text).

magnified [see equation (11)], giving negative values of X or a non-monotonic function. Moreover, plots of log$I$ *vs.* log[MeO^-] remain linear within a range progressively narrowing in the series Li > Na > K, which means that MeOLi solutions remain ideal in a wider concentration range than the others (the same also occurs with the hydroxides).[13] This allows the use of very few points, empirically selected from the three indicators so as to obtain a smooth non-negative curve which has been polynomially fitted; the coefficients are reported in Table 6, and the curve is plotted in Figure 2. It must be remarked that this function is likely to be affected by larger errors than the others. The linear method could not be applied, because the overlap regions, in the present case, fall in ideal solutions, where all plots are parallel with the near-unity slope, so that meaningless slopes are obtained regardless of the m^* reference value.

Recalculation of X *with all Available Data.*—The newly obtained m^* and pK_a values are thus used as starting values to reoptimize the coefficients of the X function together with the data for arylamines. The new data set (see Table 7) is created appending to the arylamine data file the most significant data from the other groups, thus excluding strong acids (1–5 of indoles). Four runs are executed with different starting values: (*a*) using the previously obtained data; (*b*) setting all m^*s to 1.00; (*c*) same as (*a*) but setting m^*s to 1.00 for indoles only, and (*d*) same as (*a*) but with different polynomial coefficients. The results closely resemble the previous ones, in that runs (*a*) and (*d*) give m^*s, pK_as, and polynomial coefficients very similar to the starting ones, while in run (*b*) the optimized m^*s are all similar and close to 1, and in run (*c*) convergence occurs with m^*s for indoles again close to the initial value of 1.0. In the latter two cases convergence occurs with a substantially higher error. The results obtained from run (*a*) are reported in Table 6 (polynomial coefficients) and Table 7 (optimized parameters). The curves (Figure 2) are quite similar to the previous ones;

Table 7. Optimization on the extended data set.

Indicator	MeONa		MeOK	
	m^*	pK_a'	m^*	pK_a'
2,4-Dinitrodiphenylamine	1.15	17.09	1.12	17.10
Acetophenone 4-nitrophenylhydrazone	1.02	17.13	0.89	17.11
4,4'-Dinitrodiphenylamine	1.00	17.40	1.00	17.39
2,4-Dinitroaniline	0.83	18.19	0.70	18.10
4-Nitrodiphenylamine	0.87	18.96	0.60	19.08
2,4-Dichloro-6-nitroaniline	0.83	19.11	0.65	19.32
2-Nitrodiphenylamine	1.10	20.74	0.73	21.12
4-Nitroaniline	0.98	21.74	0.64	21.75
2-Nitroaniline	0.85	21.08	0.65	21.69
Indazole	0.26	17.31	0.19	17.22
5-Nitroindole	0.29	18.22	0.16	18.04
5-Cyanoindole	0.22	18.38	0.16	18.42
4'-Chloro-4,6-dinitrodiphenylamine-2-carboxylic acid	1.29	18.16	1.12	18.06
2,4-Dinitrodiphenylamine-2'-carboxylic acid			1.08	18.35
4'-Chloro-2-nitrodiphenylamine-4-carboxylic acid	1.24	20.26	0.74	20.18
4'-Fluoro-2-nitrodiphenylamine-4-carboxylic acid	1.25	20.62	0.81	20.84
2-Nitrodiphenylamine-4-carboxylic acid	1.23	20.79	0.73	20.79
4-Nitrodiphenylamine-2-carboxylic acid	1.68	22.57	0.88	22.35
2-Nitrodiphenylamine-2'-carboxylic acid	1.59	22.11	0.82	22.66
4-Amino-3-nitrobenzoic acid			0.81	22.61

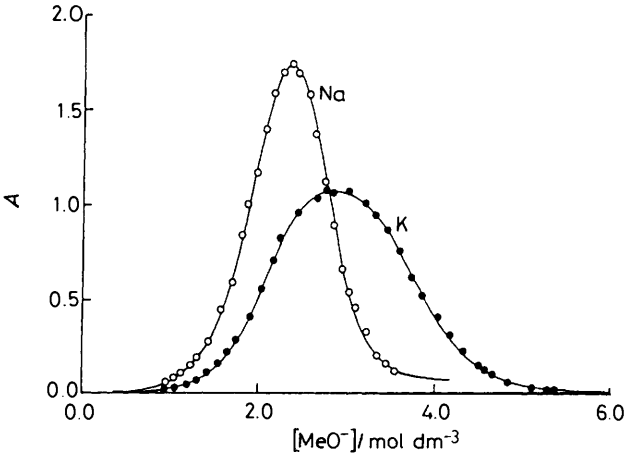

Figure 3. UV absorbances and fitted curves *vs.* base concentration for 2,6-dinitroanisole in MeONa (590 nm, ○) and MeOK (595 nm, ●).

these functions are used for the treatment of methoxide additions.

Meisenheimer Complexes.—The addition of methoxide ion to nitro-substituted anisoles and anilines to yield Meisenheimer complexes may be depicted as equation (16), where S is the

$$S + MeO^- \rightleftharpoons SMeO^- \quad (16)$$

substrate. The equilibrium constant K_M is given by equation (17). Defining $r = [SMeO^-]/[S]$, with simple rearrangements

$$K_M = a_{SMeO^-}/(a_S a_{MeO^-}) \quad (17)$$

we obtain equation (18). If the reaction occurs in ideal solutions,

$$\log r - \log[MeO^-] = \log(\gamma_S\gamma_{MeO^-}/\gamma_{SMeO^-}) - pK_M \quad (18)$$

pK_M can be obtained from equation (19). Otherwise, if the

$$\log r = \log[MeO^-] - pK_M \quad (19)$$

activity coefficient term is proportional to the analogue term defining X, *i.e.* equation (20), equation (18) may be rewritten as

$$\log(\gamma_S\gamma_{MeO^-}/\gamma_{SMeO^-} = m^*\log(\gamma_{HA^\bullet}\gamma_{MeO^-}/\gamma_{A^{\bullet-}}) \quad (20)$$

equation (21). As previously, the values of $pK_M' = pK_M + pK_S$ will be tabulated.

$$\log r - \log[MeO^-] = m^*X - pK_M \quad (21)$$

The available indicators in MeONa and MeOK are: 2,4-dinitro-6-(trifluoromethyl)anisole (6TF24DN), 6-chloro-2,4-dinitroanisole (6CL24DN), 2,6-dinitro-4-(trifluoromethyl)-anisole (4TF26DN), 6-fluoro-2,4-dinitroanisole (6F24DN), 2,4-dinitroanisole (24DN), 2,6-dinitroanisole (26DN), 2,4,6-trinitroanisole (246TN), and deprotonated 2,4-dinitroaniline (24DNA). Four indicators (6CL24DN, 6F24DN, 24DN, and 26DN) undergo two additions to yield 1:1 and 2:1 complexes, while 246TN undergoes three; the formation of the 1:1 complex for this compound (not reported) takes place below 10^{-3} mol dm^{-3} methoxide. Thus, these compounds provide 2 data sets each. In some cases (24DN, 26DN, and 246TN) the two addition ranges are largely overlapping. The same is true also for the two different processes (deprotonation and addition) of 24DNA.

Ionization of indicators (1–4) takes place in dilute solutions, but the plots of equation (19) have non-unit slopes. These data are treated with the Debye–Hückel limiting law ($\log r - \log[MeO^-]$ *vs.* $[MeO^-]^{\frac{1}{2}}$). Though care is taken to employ only data in the highly dilute range, the scope of the Debye–Hückel correction is somewhat questionable. Even so, the agreement between pK_Ms is satisfactory (entries 1–4 in Table 8).

Due to the difficulties in estimating the limiting absorbances from UV spectra in which more than two absorbing species are present, we derive the data for the remaining compounds by fitting original UV absorbances. Therefore, for all compounds giving multiple additions we fit the UV absorbances at a suitable wavelength (Figure 3) according to the two consecutive equilibria (22*a*,*b*). Defining $r_1 = [SMeO^-]/[S]$ and $r_2 = [S(MeO)_2^{2-}]/[SMeO^-]$, which can be calculated as $r_i =$

$$S + MeO^- \rightleftharpoons SMeO^- \quad (22a)$$

$$SMeO^- + MeO^- \rightleftharpoons S(MeO)_2^{2-} \quad (22b)$$

$10^{(m_i^*x - pK_{Mi} + \log[MeO^-])}$, we obtain the change in absorbance (A) as a function of base concentration as equation (23).

$$A = [A_0 + r_1(A_1 + r_2A_2)]/[1 + r_1(1 + r_2)] \quad (23)$$

where A_0, A_1, and A_2 are the absorbances of the three species involved.

In the presence of multiple equilibria it is no longer possible to dissect the measured absorbance into its individual contributions,[30] and nonlinear fitting must be employed. This is accomplished by means of the Marquardt or Simplex algorithms.[29,31] Where the first addition takes place in near-ideal solutions (6F24DN and 6CL24DN), we process the data for the second addition (which is well separated from the first) with a variant of equation (23) dealing with the single equilibrium (22*a*) (which can be obtained from equation (23) setting $r_2 = 0$). All data are reported in Table 8.

Table 8. Parameters for Meisenheimer complex formation.[a]

Indicator[a]	MeONa		MeOK	
	m^*	pK_M	m^*	pK_M
2,4-Dinitro-6-(trifluoromethyl)-anisole	—	15.77 ± 0.00	—	15.76 ± 0.01
6-Chloro-2,4-dinitroanisole I	—	16.43 ± 0.00	—	16.48 ± 0.01
2,6-Dinitro-4-(trifluoromethyl)-anisole	—	16.80 ± 0.01	—	16.81 ± 0.01
6-Fluoro-2,4-dinitroanisole I	—	17.36 ± 0.00	—	17.44 ± 0.02
2,6-Dinitroanisole I	2.0	19.0	1.1	19.0
2,4,6-Trinitroanisole II	1.3	19.4	0.5	19.3
2,4-Dinitroanisole I	1.6	19.9	0.9	19.4
2,6-Dinitroanisole II	2.0	20.2	0.8	20.5
2,4-Dinitroaniline (deprotonated)	1.0	20.9	0.8	20.9
2,4,6-Trinitroanisole II	1.5	20.7	0.7	21.1
6-Fluoro-2,4-dinitro-anisole II	1.6	21.0	0.9	22.0
2,4-Dinitroanisole II	1.7	21.3	0.8	21.9
6-Chloro-2,4-dinitro-anisole II	1.8	21.5	1.1	23.5

[a] Roman numerals (where present) indicate the type of complex in the case of multiple additions. Entries for which no m^* is given were treated with the Debye–Hückel limiting law. Standard deviations on m^* and pK_M for the other data were assumed equal to 0.1 and 0.2 for the first and second addition, respectively (see the text).

Discussion

Critique of the Methods for the Calculation of X.—The fundamental question, *i.e.* whether linearity among activity coefficient terms as in equation (7) holds also for MeOH/MeO^- solutions, can be positively answered. In fact, good linearity in log$Q$ *vs.* X or log$Q$ *vs.* log$Q$ plots was found in all cases where simple deprotonation took place.

With regard to the problem of how to practically calculate the X function for these systems, a criterion must be given in order to test the various methods proposed. Since all require extrapolation down to dilute solutions in order to determine the equilibrium constant, the most suitable and stringent test is the constancy of pK_a for the same compound in different media. In fact, procedures have been developed[13,14] that allow data sets in different media to be simultaneously treated, imposing the constancy of pKs,[9e] or even m^*s too.[32] However, these approaches may impose too strict a constraint, or mask possible faults in the data sets, and in our opinion an unconstrained treatment for each medium is preferable and more informative, at least in the early stages of the establishment of the scales. In addition to this, viewing equation (7) as a free-energy relationship[14] allows a distinct physical meaning to be attached to m^*, and its correlation (or lack thereof) with structural effects can be tested and used to assess the reliability of X.

The first results, obtained with the stepwise overlap method, show (see Table 1) that the differences between pK_a values in Na and K methoxides are within experimental uncertainty for the stronger acids, while for the weaker ones they are not, and are similar to those obtained with the acidity function treatment;[24] the sum of squared pK_a differences (U) equals 2.4. Using the nonlinear method brings no improvement unless the previous data are used as starting values (U = 1.6). However, no other choice of starting values seems to bring the same results. A severe concern comes from the fact that the algorithm cannot differentiate the indicators with regard to m^* if the initial values are the same. This is due to the form of its partial derivative [equation (27)], which is independent of the indicator, *i.e.* to the intrinsically linear form of the model. These considerations indicate that the stepwise overlap procedure is necessary in order to collect reasonable starting values, at least for a selected series of indicators, while the fitting procedure is effective only in the neighbourhood of the true values, and is useful in refining the previous data.

The linear method, though basically equal to the conventional one, has some practical advantages, *i.e.* it is very fast even for large databases, uses all the available data to compute the X function, which is calculated on a larger number of points than in a log Q/log Q plot and, of course, is fully linear. Though pK_a differences between MeONa and MeOK may go as high as 0.6 units (but are usually lower), the best value of U (0.7) is obtained by this method with no previous estimation of m^*s and pK_as. In this treatment, the fundamental individuality of activity coefficient behaviour of each indicator is fully recognized, and the lasting need for a set of indicators with similar slopes and of overlap between indicator pairs (which seems to recall the acidity function concept) stems from practical rather than fundamental reasons. However, since this method does not check for actual linearity, we suggest that the stepwise one also be used, or linearity be checked at the end. Finally, the recalculation of X with all available data does not bring appreciable changes to the previously calculated functions (from arylamines), and thus supports the conclusion that a single homogeneous set of indicators can provide a correct X function. Since the last two indicators (4NA and 2NA) provide relatively few points, affected by the largest errors, the X functions above *ca.* 5 mol dm^{-3} will be less accurate.

Basicity Order.—Trends in the X functions (Figure 2) indicate that the basicity order for the three methoxides is Li < Na < K. This medium basicity order parallels the one obtained with the acidity function treatment[24] and the findings in aqueous hydroxide media.[25,33] It has been explained by considering that methoxide association through ion pairing with the metal counterion decreases in the same order,[24,34] thus making the methoxide anion increasingly 'free' and more capable of abstracting a proton.[24]

Ion-pairing Effects.—So far, we have assumed that the chemistry occurring in methoxide solutions is indeed consistent with the simple model of proton abstraction [equation (2)] or ring addition [equation (16)]. This assumption was supported by the delocalized nature of the anions involved; two considerations suggest that no relevant ion pairing occurs between the alkali metal ion and the anionic form of the indicator. (*a*) The good consistency of pK_as for the stronger acids and the slopes close to unity indicate that ion pairing does not occur in dilute solutions; (*b*) though pK_a differences are sometimes outside experimental error for indicators ionizing in concentrated solutions, they have no systematic character, and indeed there are several possible sources of error due to experimental difficulties in handling concentrated solutions; pK_{BH^+} differences between H_2SO_4 and $HClO_4$ up to 2 units have been found.[11a] However, it remains possible that m^* values (which supposedly account for all sources of nonideality) contain contributions due to ion pairing.

Structural Effects on Acidity.—Since the overall behaviour of a weak acid or base is determined by both m^* and pK_a,[14] an analysis of structural effects must include both parameters.

The acidity (as probed by pK_a) of neutral anilines and diphenylamines increases with increasing number of nitro or other electron-withdrawing groups;[35] anilines are weaker acids than diphenylamines for a constant number of $-NO_2$ groups.

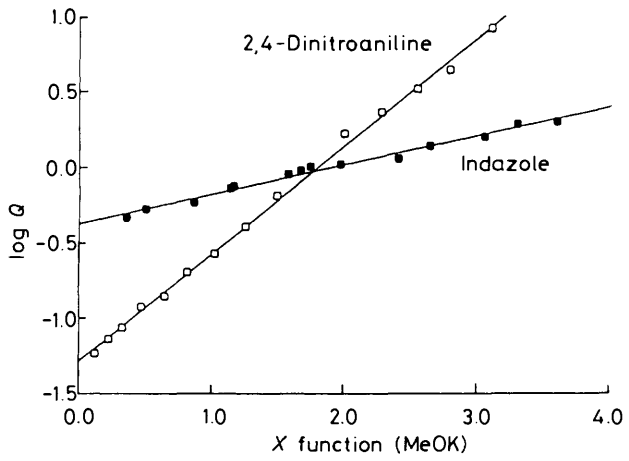

Figure 4. Acidity inversion between 2,4-dinitroaniline and indazole.

Those of the corresponding anionic acids depend on the distance between the amino and the $-CO_2^-$ group.[25] For example, we may compare the pK_a' in MeONa for 2NDPA (20.74) and for 4C2N (20.79), where the distant charged group brings no large changes, and the dramatic effect of an *ortho* group in the 4NDPA (18.96) and 2C4N (22.57), or (in MeOK) 24DNDPA (17.10) and 2'C24DN (18.35) pairs. The same effect was also found on comparing 2,4,6-trinitrodiphenylamine with its 2'-, 3'-, and 4'-carboxylate or sulphonate derivatives, with an evident acid-weakening effect of the increasingly nearer anionic centre.[25] This is easily explained as a stabilizing effect on the unionized amino group due to the formation of a six-membered hydrogen-bonded ring, which is replaced by an unfavourable repulsion between the two negatively charged sites in the deprotonated form; a *meta* group has an intermediate effect.[25] The acidity of indoles is also affected by electron-withdrawing groups; the effect is largest if the stabilizing group is in the 3-position, where charge delocalization can occur without disrupting the resonance of the benzene ring (see below).

A discussion of m^* values should both give a physical interpretation and address the question as to whether m^* for the same compound in different media should be the same or not, which is still debated.[9e,13,14,32] In concentrated acid media the m^* parameter gives semiquantitative information on the solvation requirement of the conjugate acid–base pair (with respect to the reference), and hence on their relative stability with a change in medium.[14] In methoxide media, we can rewrite equation (7) as (24) and recast the interpretation given for acid solutions.[36]

$$\log \gamma_{MeO^-} - \log (\gamma_{A^-}/\gamma_{HA}) = m^*[\log \gamma_{MeO^-} - \log (\gamma_{A^{*-}}/\gamma_{HA^*})] \quad (24)$$

Direct measurements of activity coefficients in MeOH/MeO^- for the species of interest are not available, but we expect that the transfer from MeOH to basic MeO^- solutions brings a decrease in solvating ability qualitatively analogous to that taking place on transferring from water or MeOH to aprotic solvents. These measurements[37,38] show that activity coefficients of anions follow a trend similar to that for cations in acids,[39] *i.e.* increase with charge localization, so that $\gamma_{MeO^-} > \gamma_{A^-} > \gamma_{HA}$ and (within anions) phenoxide > amide > fluorenide.[38] Thus, the left-hand side of equation (24) is positive. Mathematically, if $\gamma_{A^-} \gg \gamma_{HA}$, the ratio γ_{A^-}/γ_{HA} will be large, and the left-hand side will be small relative to the right-hand side, with $0 < m^* < 1$; the reverse ($m^* > 1$) will be true when $\gamma_{A^-} \approx \gamma_{HA}$. Since activity coefficients represent free energies of transfer from the standard state to the actual non-ideal one (*i.e.* solvation free energies), the first case ($m^* < 1$) will occur when proton abstraction yields a species with a more localized, highly solvated charge than the reference, and *vice versa*. Thus we expect m^* values of the above anions to increase in the series $ArO^- < ArNH^- < Ar_2CH^-$. An analogous rule ($m^*$ increasing in the order oxonium < ammonium < sulphonium < carbonium ions) is very well obeyed in aqueous acid systems.[14]

The m^* values for neutral arylamines in MeOK depend on the number of nitro and aryl groups available to delocalize the negative charge: dinitrodiphenylamines (0.9–1.1) > 2-nitrodiphenylamine (0.73) > 2,4-dinitroaniline (0.70) > mononitroanilines (0.65). In MeONa, m^*s are more levelled (m^* range of 0.2 units compared to 0.5 in MeOK), with higher absolute values. All methods agree in indicating 4NDPA as an outlier with an m^* too low in comparison with the 2-derivative, though these data do not seem to be affected by peculiar medium effects. The m^* values for anionic acids are similar to the corresponding neutral compounds if the carboxylate group is *para* to the amino group, and are usually larger if the amino group is in the *ortho* position. For example, we may compare 2NDPA (m^* = 1.10 in MeONa) and 4C2N (1.23) with 2'C2N (1.59), or 4NDPA (0.87) and 2C4N (1.68); but for 2'C24DN (1.08) and 24DNDPA (1.12) this is not the case. Thus a $-CO_2^-$ group in the 2-position seems to decrease the solvation, whereas no such effect is brought about by an *ortho* nitro group. The desolvation experienced by HA^- will raise its free energy with respect to the neutral HA, thus making γ_{HA^-} (*para*) > γ_{HA}; the stronger desolvation of A^{2-} will also raise $\gamma_{A^{2-}}$ with respect to γ_{A^-}, while γ_{HA^-} (*ortho*) is expected to be lower than γ_{HA^-} (*para*) because of the low desolvation occurring in the intramolecularly hydrogen-bonded ion. We also expect that $\gamma_{A^{2-}}$ (*ortho*) < $\gamma_{A^{2-}}$ (*para*) because of the removal of steric hindrance to ring rotation with increasing desolvation (an entropic effect). However, it is also possible that the *ortho*-carboxylate system is complicated by a shift of the deprotonation site (*O vs. N*) due to the different solvation requirements of the two sites.[40]

Values of m^* for indoles are considerably lower (0.2–0.3), which implies increased solvation and indicates that the negative charge is largely localized on the nitrogen atom.[26] This is also confirmed by the curvature observed in the plots of 5NI and 5CI in MeONa at high base concentrations, which suggests that ion pairing may become relevant with these acids. The charge localization can be explained considering that for these compounds two benzenoid resonance forms (retaining the aromatic stabilization) are available which locate the negative charge only on the *N* atom or on the 3-position (the reactivity of which towards electrophiles is well known).

The above correlation of m^*s with ion solvation gives a picture consistent with these results, in that acids with $m^* < 1$ yield anionic species more solvated, charge-localized than the reference compound. This parameter also discriminates between the solvation of $ArNH^-$ in anilines and of Ar_2N^- in diphenylamines, even though in both cases charge delocalization will occur to some extent, with the possibility of a levelling effect.[1]

We also treated literature data concerning the deprotonation of substituted fluorenes and indenes in MeOK/MeOH[41] with the same method. The approximate (different temperature, very low log*I* values) m^* values again follow the same trend: *N*-methyl-*N*-phenylfluorene-9-carboxamide (a resonance contributor with charge on oxygen) < 1,3-diphenylindene (purely carbanionic) < *N*-fluorenylidenefluoren-9-amine (extensive delocalization on two fluorene groups with no charge on the nitrogen atom).

In contrast with ideal solutions, acidity differences are not entirely determined by pK_a values,[14] and inversions in acid strength (measured by log *I*) will occur whenever two acids with different m^* are compared.[14,42] This is made particularly

apparent by comparing 2,4-dinitroaniline with indazole (Figure 4). Though the former is expected to be a weaker acid because of its higher pK_a' (18.2 *vs.* 17.3), its ionization ratio increases more rapidly than that of indazole because of its higher m^*, which accounts for the decreased stability of the indazole anion in increasingly less solvating media. Similar inversions of acidity or basicity due to differences in solvation have been found in acid media [14,36a,42] and even in the gas phase.[43]

Medium Effects on Acidity Constants.—The measure of solvation represented by m^* also provides a means to rationalize the differences in pK_as among various media. In fact, acids yielding charge-localized anions are expected to have low m^*s and to be stabilized in good solvating media.[16a,f] Accordingly, alcohols and phenols are stronger acids in water than in DMSO [$pK_a(H_2O) < pK_a(DMSO)$], and the reverse is true for fluorenes.[16a,b] For the nitrogen acids studied here, $pK_a(H_2O) < pK_a(MeOH)$,[24–26,44] which again indicates that nitranions are more solvated than carbanions. The differences are largest (>3 pK units) for indoles, which are the most solvated, as mentioned above. Interestingly, in the few comparable cases pK_as in MeOH also seem higher than in DMSO,[16f] which would indicate that DMSO is better at solvating nitranions than methanol.

m^* Values in MeONa and MeOK are systematically different, the former being higher than the latter. In fact, m^* represents the proportionality constant between two activity coefficient terms [see equation (24)], which are expected to exhibit individual behaviour in different media. The value of m^*_{Na} is greater than m^*_K probably because methanol in MeONa is more involved in solvating the smaller Na^+ cation and less available for hydrogen bonding to A^-, which makes MeONa solutions less solvating. Unfortunately, the weak basicity and the lack of data in MeOLi do not permit more precise conclusions.

Meisenheimer Complexes.—An accurate determination of addition parameters for anisoles could not be made because of experimental difficulties, *i.e.* (*a*) the second equilibrium was usually defined by fewer points than the first, which added to the inaccuracy of the X function at high base concentrations; (*b*) the estimation of errors on the fitted parameters from the covariance matrix indicated that the parameters for the second equilibrium were affected by large errors. Owing to the higher m^* values (steeper curves; see Figure 3), the data in MeONa could be more easily treated than those in MeOK, as the limiting value was reached at lower base concentrations and hence, could be more easily estimated. The data for 246TN are the least reliable, due to a high degree of overlap between the two equilibria. In any event, we will consider the values of 0.1 and 0.2 as the probable errors on m^* and pK_M for the first and the second equilibrium, respectively, and will comment mainly on the data in MeONa.

In general, pK_M differences are in most cases under 0.5 units, except 6F and 6CL24DN II, for which the analysis was difficult. The main differences in pK_Ms among the various compounds, as expected, are related to the number of $-NO_2$ and other electron-withdrawing ($-CF_3$, –Hal) groups; the second and further additions are less favoured, save perhaps 246TN, which is the only one having three nitro groups.

The m^*s in MeONa are higher than in MeOK, as for the other compounds. With the exception of 24DNA ($m^* = 1.0$), all other values are >1.3. While the former is a typical value for the ionization of arylamines, the others are higher. Though the difference is not large (and barely outside the range of experimental error) this lower value, indicating a higher solvation, may be related to the possibility of a hydrogen-bonding interaction with the solvent, while normal Meisenheimer complexes have no specific site of solvation, which accounts for the high values, as in the case of triarylmethyl cations in acids.[14] Other structural effects on m^*, particularly between the first and second addition, are masked by the errors, which probably add up to a levelling effect exerted by the nitro groups. Even though trends in m^* and pK_M seem consistent with the other results, definite conclusions concerning the linearity among activity coefficient terms [equation (20)] cannot be drawn.

Conclusions

The approaches developed for the treatment of concentrated acid solutions, based on the linearity among activity coefficient terms, have proved applicable to methanol–methoxide systems too: a single excess basicity function, characteristic of each medium, allows one to determine the acidity parameters (m^* and pK_a) of any weak acid in that medium. Linear methods, based on the overlap between adjacent indicator pairs, are the most effective and reliable for the evaluation of excess basicities. The acidity parameters, thus obtained, follow a chemically sensible pattern; the slope parameter m^* provides a useful insight into the sensitivity of the deprotonation equilibrium to medium changes. It can be correlated with the solvation properties of the deprotonated acid, and with structural effects on it. The basicity of alkaline methoxides in methanol follows the order Li < Na < K.

Finally, it should be pointed out that (*a*) the excess basicity approach can probably be applied to other basic systems, and may be useful in rationalizing the large body of data gathered so far; (*b*) the scope of the work so far carried out in aprotic media [15,16] can be considerably broadened by comparisons with protic media (with regard to acidity differences, solvation effects, *etc.*), thus extending our knowledge of strongly basic media.

Experimental

All calculations were carried out on an Olivetti M24SP Personal Computer under MS-DOS or on a Digital MicroVAX 2000 under MicroVMS.

Stepwise Overlap.—The procedure was as follows. (*i*) For each indicator, given the values of log I as a function of [MeO^-], and the empirical function giving log a_{MeOH}, compute log Q and empirical functions giving log Q as a function of [MeO^-]. (*ii*) Find at least one indicator for which data are available in both ideal and non-ideal solutions. Plot log I *vs.* log [MeO^-] in the ideal range. A line of unit slope should be found. The intercept is $-pK_a$. This indicator is the reference acid, with $m^* = 1.00$ by definition. (*iii*) Calculate the X function in the whole range beyond ideality from $X = \log Q + pK_a$. X is now known for all values of [MeO^-] quoted for the reference acid. (*iv*) Find an indicator (*j*) which ionizes in a range above the reference (*i*) and overlapping with it. For all the values of [MeO^-] of the reference in the overlap range, calculate log Q of the new compound from its empirical function if the base concentration is not the same. Plot log Q_j *vs.* log Q_i in the overlap range, and calculate the slope p_{ij} and intercept q_{ij}. Calculate m^*_j and log Q_j from equation (9) and (10) and their standard deviations from equations (25) and (26). (*v*) Calculate

$$\sigma_{m^*_j} = [(\sigma_{p_{ij}} m^*_i)^2 + (\sigma_{m^*i} p_{ij})^2]^{\frac{1}{2}} \quad (25)$$

$$\sigma_{pK_j} = [(pK_i \sigma_{p_{ij}})^2 + (p_{ij} \sigma_{pK_i})^2 + \sigma_{q_{ij}}{}^2]^{\frac{1}{2}} \quad (26)$$

the X function in the range of [MeO^-] beyond overlap from equation (11). (*vi*) Repeat steps (*iv–v*) for all available indicators, using the latest indicator as reference.

Non-linear Method.—Non-linear optimizations require the partial derivatives of the fitting function with respect to the parameters to be optimized, which have the following form, [equations (27)–(29)]. If n indicators are available, $N = 2n +$

$$\partial(\log I)/\partial m^* = X \quad (27)$$

$$\partial(\log I)/\partial \mathrm{p}K_a = -1 \quad (28)$$

$$\partial(\log I)/\partial a_k = m^* b^k \quad (k = 1,2,...n_c) \quad (29)$$

n_c parameters must be optimized with some provision for the reference. The optimization was carried out with a modification of the Marquardt algorithm[31] employing the Choleski decomposition and back-substitution rather than matrix inversion. While the latter operates on a matrix with N^2 components, the former operates on its lower-left triangle with $N(N + 1)/2$ components, thus effectively reducing memory requirements; log I values were weighted as suggested by Cox and Yates.[11] Data sets made of up to nine indicators could be processed on the personal computer with the Choleski algorithm, and six with matrix inversion. Recalculation of weights according to the spacing of data points[11] was not included, as the present data were sufficiently well spaced; five polynomial coefficients for X were employed. The convergence limit was set to 0.1% variation of all parameters. Starting values of polynomial coefficients were set to the slope of a rough line between the extreme points for the first degree, and all the others to zero, *i.e.* assuming a linear dependence of X on b. In general, the results obtained with both procedures were quite similar. The time required was somewhat shorter with the Choleski algorithm, which was used in the subsequent calculations.

Linear Method.—This procedure processes one indicator at a time, which allows large data sets to be used. (*i*) Select a data set which spans the whole base concentration range, and for which the 'best' (perhaps the most homogeneous or predictable) data are available. (*ii*) Set the reference indicator ($m^* = 1.00$, $\mathrm{p}K_a$ independently determined). (*iii*) For each indicator, fit the values of log I as a function of [MeO^-] to quadratic polynomials; find the significant root and sort the data set in increasing order of it. (*iv*) Compute X in the available b range and fit the data to a polynomial of degree n_c. (*v*) Select a suitable indicator (*i.e.* one whose b range overlaps with the currently available one by at least three points) from the sorted list. Compute log Q values, weighted according equation (30),[45]

$$w = 1/\sigma^2_{\log I} = (\delta A)^2 I^2 / [2(\ln 10)^2 \sigma_A^2 (1 + I + I^2)(1 + I)^2] \quad (30)$$

which requires the estimated uncertainty in the absorbance (σ_A) and the difference $\delta A = A_{HA} - A_{A^-}$. For simplicity, these parameters can be assumed constant for all data, with typical values like $\sigma_A = 0.005$ and $\delta A = 0.5$. (*vi*) Fit log Q values in the overlap range *vs.* the corresponding X data to a straight line, obtaining m^* and $\mathrm{p}K_a$ with standard deviations, *etc.* (*vii*) Calculate new X values from *all* data of the current indicator, and append these data to the previous ones. Fit the new X data with a polynomial of the same degree. (*viii*) Go to step (*iii*). (*ix*) If required, the protonation parameters for all indicators may be recalculated using the final X coefficients, or refined with the non-linear method.

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