

The Dynamics of Preferential Solvation

Noam Agmon

Department of Physical Chemistry, The Hebrew University, Jerusalem 91904, Israel

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A simple model describes the translational diffusion origin of preferential solvation. Assuming independent polar ligands in the first solvation shell of the excited probe molecule, it presents an extension of the Smoluchowski aggregation model to the reversible case. The model captures the main aspects of both concentration and time dependence of spectral shifts obtained from steady-state and transient fluorescence measurements. It provides a useful method for extracting the rate and equilibria coefficients for ligand exchange in the first solvation shell of excited polar molecules.

1. Introduction

Molecules are stabilized by their interaction with the solvent, and this induces a shift in their absorption or emission spectra as compared with that in the gas phase.¹ When a dipolar or charged solute is introduced into a neat polar solvent, the solvent responds predominantly by librational motions to optimize the solute–solvent interactions. If the dipole is created (or enhanced) by photoexcitation of a fluorescent probe molecule, the solvent response manifests itself in a fast time-dependent Stokes shift for the average fluorescence frequency, $\nu(t)$.²

The situation is different in a mixture of polar and nonpolar solvents, in which polar solvent molecules tend to aggregate around the polar solute, a phenomenon known as “preferential solvation”.³ Equilibrium electrostatic models have been utilized to explain the mole-fraction dependence of the shift emanating from such a “dielectric enrichment” process,⁴ and the theory was applied to solvatochromic shifts in steady-state (SS) spectroscopy.⁵ Recent dynamic measurements find relatively slow, nanosecond spectral shifts attributed to the *translational* diffusion of polar solvent molecules, which replace the nonpolar ones in the first solvation shell of the solute.^{6–11}

Molecular-dynamics simulations^{12–15} and theoretical work^{16–18} were performed to elucidate the molecular details of preferential solvation in mixed solvents. Following an instantaneous increase in the solute’s dipole moment, the simulations indicate three phases in the solvation process:¹² Ultrafast solvent reorientation is followed by a fast “electrostriction” step, in which the total number of ligand molecules increases in the first solvation shell of the solute.¹² On slower time scales (up to 50 ps), one observes redistribution of the molecules in the first solvation shell, where the less polar solvent is replaced by the more polar solvent molecules. This points to the role of translational diffusion in preferential solvation. However, given the small number of molecules in the simulation box (typically 250, corresponding to about three solvation shells), transport over long distances cannot be followed. Realistic simulations of translational diffusion would require at least 100 times more molecules propagated to 100-fold longer times (up to 5 ns), so that direct comparison of simulation and experiment has not yet been obtained.

Simple chemical kinetics has been used to fit experiment¹⁹ and simulation.¹² Such an approach does not contain explicitly the translational diffusion process, which is postulated to play

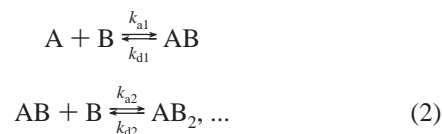
a major role in the observed dynamics. Compensating for this missing physical ingredient, there will necessarily be extra adjustable parameters, or parameters assuming nonphysical values [e.g., $n(\infty)$ in ref 19 does not scale correctly with concentration]. A practical alternative, therefore, would be to use diffusion theory, which is intermediate in complexity between chemical kinetics and full molecular simulations.

So far, diffusive kinetics was applied to this problem only on a qualitative level.^{4,7,8} In particular, the reversibility of solvent entry/exit from the solute’s solvation shell has been neglected. Without reversibility, the polar-molecule cluster around the probe molecule would grow indefinitely. Its SS solvatochromic shift would reach the limit for the neat polar solvent (ν_P below), in contrast to the experimentally observed dependence of $\nu(\infty)$ on the polar cosolvent concentration.

Theory for treating reversible diffusion influenced reactions has recently been developed^{20–23} and found to be in quantitative agreement with reversible proton transfer to solvent occurring in the excited state of organic photoacids.^{24–27} In such dissociation–recombination reactions,



(where k_a and k_d are the association and dissociation rate coefficients), only a single B molecule may bind to A. In contrast, solvation of a probe molecule, A, by polar solvent molecules, B, is a (reversible) aggregation process,



where more than one B ligand may bind to A. It thus constitutes a reversible extension of the Smoluchowski theory of coagulation,²⁸ which has been discussed under the simplifying assumption of noninteracting B particles.²²

The present work merges the reversible aggregation model²² with a simple electrostatic model⁷ for the spectral shift per polar molecule, B, incorporated in the solute’s first solvation shell. This results in a useful model that describes simultaneously both steady-state and time-resolved experiments on preferential solvation with a minimal number of adjustable parameters.

2. Theory

2.1. Basic Assumptions. As a model for the reaction in eq 2, let us consider a big sphere of volume V , containing a single A molecule and N B molecules. The theory is simplest if the B particles are statistically independent. This occurs under several conditions: (i) A is static, otherwise its motion couples that of the B's. We assume that it is a sphere of radius $r = a$, located at the origin (the center of the big sphere), whereas the B particles diffuse with a diffusion coefficient D . (ii) The B's do not interact with each other, which means that they are point particles that may have a potential of interaction, $U(r)$, with A but not with one another [$U(r) \rightarrow 0$ as $r \rightarrow \infty$]. Furthermore, $U(r)$ should be independent of the number of bound B molecules (this is not a very plausible assumption unless, as we argue below, $U(r) \approx 0$). Under these conditions, the problem becomes spherically symmetric, depending only on the distance, r , from the center of A. (iii) The B's are not coupled by the aggregation process, which requires that the rate constants of the different binding steps in eq 2 are identical: $k_{a1} = k_{a2} = \dots \equiv k_a$ and $k_{d1} = k_{d2} = \dots \equiv k_d$. In particular, there is no limit to the number of B particles that may bind to A.

In reality, k_{am} might decrease dramatically after filling of the first solvation shell. Nevertheless, this is expected to introduce only a small error in our model if spectral shifts due to second-shell ligands are negligible. Generally, the spectral shifts in the AB_m cluster saturate with m ; hence, the shift per B molecule decreases with increasing m . A similar effect has been found in gas-phase cluster studies,^{29,30} in which only the few first-shell solvent molecules induce a sizable spectral shift.

Clearly, the above assumptions restrict the theory to a small B particle concentration, $c \equiv N/V$, though c is not required to be infinitesimally small. In addition, we assume that the B's are equivalent, which means not only that they are identical particles [with equal diffusion constants, D , and interaction potentials, $U(r)$] but also that they all start from the same initial distribution.

As a result of statistical independence, the many-body problem factors into that of A–B pairs. Let us assume that the probability density of having a pair separated to distance r by time t is given by $p(r,t)$, whereas the probability that they are bound is $p(*,t)$. These normalize such that $4\pi f_V p(r,t)r^2 dr = 1 - p(*,t)$. B-particle equivalence implies that all of them have the same $p(r,t)$. Initially, we assume a random distribution

$$p(*,0) = p_0 < 1 \quad (3a)$$

$$p(r,0) = (1 - p_0) \exp[-\beta U_0(r)] / [4\pi \int_V \exp[-\beta U_0(r)] r^2 dr] \quad (3b)$$

where $\beta = 1/(k_B T)$ is the thermal energy and $U_0(r)$ the ground-state potential, prevailing prior to the excitation of the probe molecule. Similarly, $p_0 > 0$ depicts a situation in which some B's solvate A already in the ground state.

2.2. Statistical Theory. We now reiterate the general statistical theory for the probability of having a cluster AB_m , given a concentration c of equivalent and statistically independent B particles. Starting with a finite volume V containing N B particles, let us denote by $q_m(t)$ the probability of having exactly m B's bound to A by time t . Because $1 - p(*,t)$ is the probability that a given B particle is not bound, the probability that none of the N particles is bound is simply

$$q_0(t) = [1 - p(*,t)]^N \quad (4a)$$

For the chemical reaction in eq 1, when at most one B may bind, the theory ends here. When the reaction is reversible, $q_0(t)$ provides a poor approximation for the survival probability of an unbound A, because the restriction that only one B may bind to it couples all of the B's. They are not statistically independent because the binding of one B replaces k_a by 0 for all other B's. This coupling is eliminated when eq 1 is irreversible, $k_d = 0$, because the process ends with the binding of the first B. Thus, for an irreversible reaction subject to the restrictions i and ii above, $q_0(t)$ depicts the exact survival probability, and this serves as the starting point for the Smoluchowski theory of irreversible pseudo-unimolecular reactions.^{28,31}

For the aggregation process in eq 2, we proceed by considering the probability of having exactly one particle bound, with the remaining $N - 1$ particles unbound. For independent and equivalent particles, it is given by

$$q_1(t) = Np(*,t)[1 - p(*,t)]^{N-1} \quad (4b)$$

The factor N arises because each of the N particles may be the bound one. Continuing in this fashion, the general expression for the cluster probabilities is given by the Bernoulli distribution

$$q_m(t) = \binom{N}{m} p(*,t)^m [1 - p(*,t)]^{N-m} \quad (4c)$$

The average number of bound particles is, as expected,

$$\langle m(t) \rangle \equiv \sum_{m=1}^N m q_m(t) = Np(*,t) \quad (5)$$

but this is not proportional to the spectral shift (see below).

We are interested in the thermodynamic limit of an infinite system, $V \rightarrow \infty$ and $N \rightarrow \infty$, keeping the concentration $c \equiv N/V$ constant. Because in this limit $4\pi f_V \exp[-\beta U(r)] r^2 dr \rightarrow V$ (because $U(r) \rightarrow 0$ at large distances), the normalized probability density (with the initial value in eq 3) vanishes. Therefore, we define an unnormalized probability density

$$p(r,t|\text{eq}) = Vp(r,t), \quad p(*,t|\text{eq}) = Vp(*,t) \quad (6)$$

so that $p(r,0|\text{eq}) \rightarrow \exp[-\beta U(r)]$ in the thermodynamic limit ($p_0 \rightarrow 0$ in eq 3b). Substituting in eq 4c and taking the appropriate limit gives, as usual,³² the Poisson distribution

$$q_m(t) = [cp(*,t|\text{eq})]^m \exp[-cp(*,t|\text{eq})]/m! \quad (7)$$

This follows because, for $m \ll N$, one has $N!/(N - m)! \approx N^m$ and (by taking logarithms) $[1 - p(*,t|\text{eq})/V]^N \approx \exp[-cp(*,t|\text{eq})]$.

Again, for an irreversible reaction, $k_d \equiv 0$, define a "time-dependent rate constant", $k(t)$, by $k(t) \equiv dp(*,t|\text{eq})/dt$. Then, the survival probability, $q_0(t)$, becomes

$$q_0(t) = \exp[-c \int_0^t k(t') dt'] \quad (8)$$

which is just the Smoluchowski result for irreversible pseudo-unimolecular reactions.^{28,31} Equation 8 predicts an initial non-exponential regime, which has recently been found experimentally for an excited acid reacting with high base concentrations.³³

Returning to the reversible aggregation reaction, let us consider the long-time equilibrium limit of eq 7. In an infinite system, there is an infinite supply of B particles so that their random distribution is reestablished. Hence, $p(r,t|\text{eq}) \rightarrow \exp[-\beta U(r)]$ as $t \rightarrow \infty$. Assuming that the reaction occurs at

the contact distance, $r = a$, we have

$$k_d p(*,t) = k_a p(a,t) \quad (9a)$$

and therefore, at infinitely long times,

$$p(*,\infty|eq) = k_a \exp[-\beta U(a)]/k_d \equiv K_{eq} \quad (9b)$$

where K_{eq} is the equilibrium (association) constant. Substituting in eq 7, we find the equilibrium limit for the cluster probabilities

$$q_m(\infty) = (cK_{eq})^m \exp(-cK_{eq})/m! \quad (10)$$

which depends only on cK_{eq} . Equations 7 and 10 are the main results of this subsection.

2.3. Spectral Shifts. In the usual case of transient Stokes shifts, one defines a correlation function, $\tilde{C}(t) \equiv [\nu(t) - \nu(\infty)]/[\nu(0) - \nu(\infty)]$, where $\nu(t)$ is the peak (or average) fluorescence emission at time t . In mixed solvents, all frequencies depend also on the concentration of the polar cosolvent. One may define another correlation function, which depends on the number, m , of polar molecules B in the first solvation shell of A,

$$C_m \equiv \frac{\nu_m - \nu_p}{\nu_N - \nu_p} \quad (11)$$

Here ν_N and ν_p are the fluorescence frequencies of A in neat nonpolar ($m = 0$) and polar ($m \rightarrow \infty$) solvents, respectively.

The time-dependent correlation function is now obtained as the average of the composition-dependent one,

$$C(t) = \langle C_m \rangle \equiv \sum_{m=0}^{\infty} q_m(t) C_m = \frac{\nu(t) - \nu_p}{\nu_N - \nu_p} \quad (12)$$

where $\nu(t) = \langle \nu_m \rangle$. Knowledge of the spectral shifts, ν_m , induced by the binding of m polar molecules in the solvation shell of A could allow one to calculate $C(t)$. One might hope to obtain ν_m from gas-phase cluster data,^{29,30} or from molecular simulations.¹²⁻¹⁵ In the absence of such data, one may apply simple electrostatic considerations.^{4,7} Petrov et al.⁷ have extended the Onsager model finding, in the absence of specific solvation effects such as hydrogen bonding, that

$$C_m \approx 1/(1 + m) \quad (13)$$

Although one could question the validity of continuum electrostatics for a solvation shell composed of just a few polar molecules, the result certainly captures correctly the qualitative trend of reduced shift per molecule with increasing m .

It is also convenient because the average in eq 12 can now be performed analytically, by inserting eq 7 and using the sum $\sum_{m=0}^{\infty} z^m/(m+1)! = (e^z - 1)/z$. From this one obtains

$$C(t) = \frac{1 - \exp[-cp(*,t|eq)]}{cp(*,t|eq)} \quad (14a)$$

$$C(\infty) = [1 - \exp(-cK_{eq})]/(cK_{eq}) \quad (14b)$$

Although $cp(*,t|eq)$ appears in the denominator, it is easy to see that $C(t) \rightarrow 1$ when $cp(*,t|eq) \rightarrow 0$ as should be. Indeed, by Taylor expanding up to second order,

$$C(t) \approx 1 - cp(*,t|eq)/2 \approx \frac{1}{1 + cp(*,t|eq)/2} \quad (15)$$

which does not diverge as $cp(*,t|eq) \rightarrow 0$. Moreover, because

$\langle m(t) \rangle = cp(*,t|eq)$ by eq 5, the latter approximation is similar to obtaining $C(t)$ by averaging m in the denominator of eq 13. Equations 14a and 14b provide a simple model for the time and concentration dependence of spectral shifts due to preferential solvation.

2.4. Diffusive Dynamics. So far, the theory is independent of the equation of motion governing $p(r,t)$ and $p(*,t)$. Suppose now that the relevant molecular motion is translational diffusion with reversible binding; then, these probability densities obey the differential equations²⁰⁻²⁴

$$\frac{\partial}{\partial t} p(r,t) = \mathcal{L}p(r,t) \quad (16a)$$

$$\frac{d}{dt} p(*,t) = k_a p(a,t) - k_d p(*,t) \quad (16b)$$

For $r \geq a$, \mathcal{L} is the spherically symmetric Smoluchowski operator in three dimensions,

$$\mathcal{L} \equiv r^{-2} D \frac{\partial}{\partial r} r^2 \frac{\partial}{\partial r} e^{-\beta U(r)} \frac{\partial}{\partial r} e^{\beta U(r)} \quad (17)$$

where D is the relative diffusion constant, $U(r)$ is the A-B interaction potential, and $\beta = 1/(k_B T)$. Equations 16a and 16b are coupled by the "back-reaction" boundary condition^{20,24} imposed on $p(r,t)$ at the A-B "contact distance" ($r = a$):

$$4\pi a^2 e^{-\beta U(a)} \frac{\partial}{\partial r} e^{\beta U(r)} p(r,t)|_{r=a} = k_a p(a,t) - k_d p(*,t) \quad (18)$$

The functions denoted by $p(r,t|eq)$ and $p(*,t|eq)$ are characterized, additionally, by their initial ($t = 0$) values:

$$p(*,0|eq) = K_{eq}^0 \quad (19a)$$

$$p(r,0|eq) = \exp[-\beta U_0(r)] \quad (19b)$$

derived from eqs 3 and 9b. K_{eq}^0 and $U_0(r)$ are the binding constant and interaction potential in the ground state, where the system has equilibrated prior to excitation of A. Note that the probability density is unnormalized and that $p(r,0|eq) \rightarrow 1$ as $r \rightarrow \infty$.

The above equations may be solved numerically, for example, using the modular Windows application SSDP,³⁴ which is publicly available. In the simplest case, when $K_{eq}^0 = 0$ and $U(r) = U_0(r) = 0$, the problem admits an analytic solution. First, we note that²¹

$$p(*,t|eq) = K_{eq} S(t|*) \quad (20)$$

where $S(t|*) = 4\pi \int_a^\infty p(r,t|*) r^2 dr$ is the separation probability for the geminate problem starting with an initially bound pair, $p(*,0|*) = 1$ and $p(r,0|*) = 0$. When $U(r) = 0$, eqs 16a and 16b admit an analytic solution²³

$$S(t|*) = 1 + \sum_{i=1}^3 \frac{\gamma_i(\gamma_j + \gamma_k)}{(\gamma_j - \gamma_i)(\gamma_k - \gamma_i)} \Phi(-\gamma_i \sqrt{Dt}) \quad (21)$$

The i, j , and k are different numbers from the set $\{1, 2, 3\}$, and we have defined

$$\Phi(z) \equiv \exp(z^2) \operatorname{erfc}(z) \quad (22)$$

where $\operatorname{erfc}(z)$ is the complementary error function (of a possibly

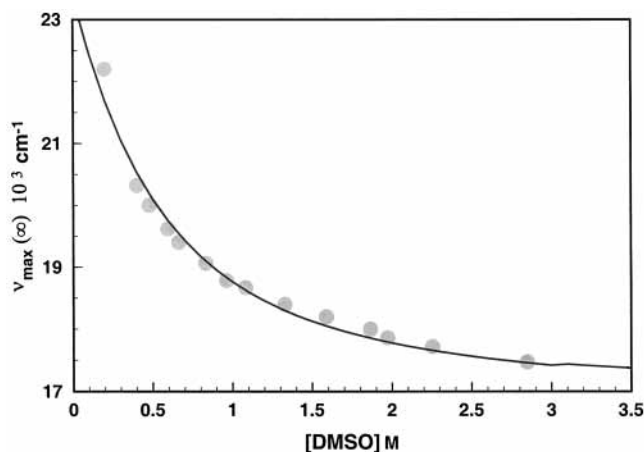


Figure 1. Dependence of the peak fluorescence frequency of 8-*N,N*-(dimethylamino)-11*H*-indento[2,1-*a*]pyrene in DMSO/toluene mixtures on the DMSO concentration under continuous illumination conditions. Circles are experimental data,⁶ and line is a fit to eqs 14b and 12 with $\nu_P = 16\,850\text{ cm}^{-1}$, $\nu_N = 23\,850\text{ cm}^{-1}$, and $K_{\text{eq}} = 3.8\text{ M}^{-1}$.

complex argument z). The γ_i 's are roots of the quartic equation

$$Da\gamma^3 + D(1 + k_a/k_D)\gamma^2 + ak_d\gamma + k_d = 0 \quad (23)$$

and $k_D = 4\pi Da$ is the diffusion-controlled rate constant.

3. Comparison with Experiment

We apply the model to the data of Petrov et al.^{6,7} They have used the fluorescent probe 8-*N,N*-(dimethylamino)-11*H*-indento[2,1-*a*]pyrene (A in eq 2), which undergoes intramolecular charge transfer in the excited state resulting in a large dipole moment, $\mu_A \approx 20\text{ D}$. Both SS and picosecond fluorescence measurements were conducted in mixtures of dimethyl sulfoxide (DMSO, B in eq 2, $\mu_B \approx 4\text{ D}$) and toluene. No hydrogen-bonding or other specific interactions are expected for this system. Purely nonspecific solvation is closer to the idealized limit of statistically independent solvent molecules assumed in this treatment. Because no absorption measurements were reported from which one could determine the ground-state binding constant, it is assumed here that $K_{\text{eq}}^0 = 0$.

Our analysis involves two straightforward steps: (i) fitting eq 14b to SS fluorescence shifts to obtain the excited-state binding constant, K_{eq} ; (ii) fitting eq 14a to the transient fluorescence shifts to obtain the individual excited-state rate constants (and the diffusion constant, when it is unavailable from other sources). The ratio of the two rate constants is restricted to obey eq 9b with the K_{eq} found from the SS data.

SS fluorescence maxima as a function of DMSO mole fraction, x , were given in Table 1 of ref 6. We have converted mole fractions to concentrations using for the mixture volumes $V(x) = 70.9x + 106.3(1-x) + V_E(x)\text{ cm}^3/\text{mol}$, with the excess molar volume calculated from³⁵ $V_E(x) = x(1-x)(1-2x) - [-0.1355 + 0.3525(1-2x) - 0.2726(1-2x)^2]$. The data point for $c = 0.2\text{ M}$ was taken from Table 1 of ref 7. Figure 1 shows the dependence of the SS emission frequency on DMSO concentration (circles) as compared with our model (line). Parameters ν_P , ν_N , and K_{eq} were adjusted to achieve this fit (ν_P and ν_N can be obtained experimentally, but they were not reported ref 7). The value found for K_{eq} is 3.8 M^{-1} which, assuming the simple relation $\langle m \rangle = cK_{\text{eq}}$, implies that between 0.8 and 12 DMSO molecules are bound to the dye in the experimental concentration range, $[\text{DMSO}] = 0.2\text{--}3\text{ M}$, seen in Figure 1.

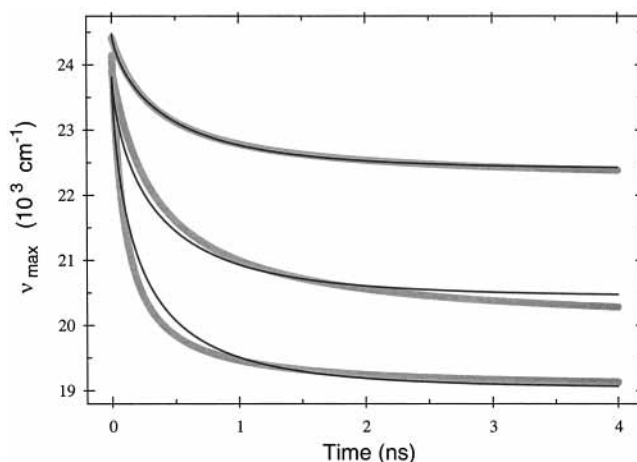


Figure 2. Time-resolved Stokes shifts for the system in Figure 1. Thick gray lines are experimental data from eq 24 with the parameters of Table 1 in ref 7. Top to bottom, $c = 0.2, 0.4,$ and 0.8 M (using $t_0 = 20, 0,$ and 40 ps). Thin lines are a global fit to eqs 14a and 12 with $a = 5\text{ \AA}$, $k_a = 5.7 \times 10^{10}\text{ M}^{-1}\text{ s}^{-1}$, $k_d = 1.5 \times 10^{10}\text{ s}^{-1}$ (note that the ratio is 3.8 M^{-1}), and $D = 1.4 \times 10^{-5}\text{ cm}^2/\text{s}$, achieved using the SSDP software³⁴ for solving eq 16. Commensurate with the deviation of the 0.2 M data point in Figure 1, ν_P and ν_N for $c = 0.2\text{ M}$ were increased by 650 cm^{-1} .

With these values set, only two parameters (one rate constant and the diffusion constant) should determine the time dependence of $\nu(t)$ for *all* concentrations. The experimental time dependence has been summarized by the equation⁷

$$\nu_{\text{max}}(t) = \nu_{\infty}(c) + \Delta\nu(c)/[1 + (t - t_0)/\tau(c)] \quad (24)$$

with the three concentration-dependent parameters given in Table 1 of ref 7 (t_0 is an adjustable parameter used to set time zero). These data are depicted by the thick gray lines in Figure 2.

The time-dependent model in eq 14a depends on the interaction potential, $U(r)$, appearing in the Smoluchowski eq 16a. The radial part of the dipole–dipole interaction is given by $\mu_A\mu_B/(4\pi\epsilon_0\epsilon r^3)$. Even for the huge dipole moment of the probe and the small dielectric constant of the mixture, $\epsilon \approx 5$, this interaction becomes comparable to the thermal energy $k_B T$ already at $r = 7.3\text{ \AA}$.⁶ This implies that the dipoles are freely rotating beyond the second solvation shell, in which case the angular part of the dipole–dipole interaction, $3\cos^2\theta - 1$, averages to zero. If they are almost but not quite freely rotating, one could use the Keesom interaction, $U(r) = -2(\mu_A\mu_B/(4\pi\epsilon_0\epsilon r^3))^2/(3k_B T)$, obtained from a weighted average of the angular part.³⁶ The resulting r^{-6} interaction is of short range (essentially zero beyond 10 \AA), and its validity for very short separations may be questioned. In addition, there should be some screening of this interaction. Thus, for the semiquantitative comparison presented below, it is neglected, and we assume that $U(r) = 0$. In this limit, eqs 20 and 21 may be used in eq 14a so that the model becomes fully analytical.

The thin lines in Figure 2 show a global fit of this model to the experimental data using a reasonable value for the diffusion coefficient of DMSO in toluene, $D = 1.4 \times 10^{-5}\text{ cm}^2/\text{s}$. In principle, this parameter could be obtained from an independent measurement. Thus, the only unavoids adjustable parameter is one of the rate constants, k_a or k_d , the value of the other being determined from K_{eq} . With this single parameter, a *global* fit is achieved, meaning that the same value is used for it for *all* concentrations.

4. Conclusion

The extension of the Smoluchowski model to reversible aggregation appears to capture the main aspects of both the concentration and time dependence of preferential solvation. Assuming independence of the polar molecule ligands, the simple model in eqs 14a and 14b has been derived. The probability function appearing there is obtained from the solution of a diffusion equation with reversible boundary conditions and appropriate initial conditions. These could take into account the equilibrium situation that existed in the ground state prior to laser excitation, an aspect to be tested in future work using additional absorption data.

The agreement achieved here between model and experiment is encouraging, lending further support to the translational diffusion origin of preferential solvation. It provides an elegant method for estimating the rate and equilibria coefficients for ligand exchange in the first solvation shell of excited molecules. To the author's knowledge, these fundamental parameters have thus far not been determined by other methods. In future experimental work, care could be taken to determine D , ν_N , and ν_P from independent measurements, which would increase the confidence in the determination of the rate parameters.

As seen in Figure 2, the model is not completely quantitative, showing deviations particularly at the higher concentrations. The deviations could arise from the breakdown of the independence assumption, for example, because the rate constants in eq 2 are not all identical. It might indeed be expected that the binding rate constant, k_a , like the spectral shift per ligand, also decreases with m . This would couple the B-molecule dynamics, because the binding of one changes the probability for binding another, making the problem much harder. The coupled problem is characteristic of systems showing cooperativity, such as ligand binding to tetrameric hemoglobin. It is therefore of interest to treat such kinetics theoretically in the future.

Another qualitative aspect of the model is the spectral shift per ligand, which is estimated from a simplified electrostatic model. This shift is dictated by the short-range A–B interaction. In addition, it is not clear what expression should be used for the longer-range interaction, depicted by the potential $U(r)$. Possibly more quantitative results could be obtained by a hybrid approach: the relevant interactions may be calculated by molecular dynamics and then used as input for a diffusion approach, by which long times and large distances are easier to achieve.

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