5   Analysis of QENS spectra

5.1   Essence of QENS spectra analysis

The first part of a QENS experiment is to perform a measurement, to obtain the experimental scattering function $S_{TOTAL}(Q, \omega)$ with a good statistical accuracy, and at the same time keeping both multiple scattering and container scattering as low as possible. The second part of a QENS experiment consists in the description of the spectra by a suitable theoretical scattering function, $S_{THEO}(Q, \omega)$. This is done by fitting the following master equation to $S_{TOTAL}(Q, \omega)$:

$$S_{FIT}(Q, \omega) = \exp(-\hbar\omega/2k_BT) \times S_{THEO}(Q, \omega) \otimes R(\varphi, \omega) + C \times V_S \times S_{MSC\ THEO} + f_{EC} \times C \times S_{SC\ EXP} \quad (5.1)$$

As can be seen by consulting eqs. (2.53, 2.55), the factor "$C \times V_S$" is lacking in front of $S_{THEO}(Q, \omega)$. Henceforth, this factor comes in the expression for $S_{THEO}(Q, \omega)$.

The component $S_{MSC\ THEO}$ is evaluated from $S_{THEO}(Q, \omega)$ by the method given in Appendix E. The term $S_{SC\ EXP}$ is evaluated using $S_{EXP\ EC}(Q, \omega)$, see section 2.6 and Appendix D. The parameter f_{EC} is normally unity, but sometimes, the scattering of the empty container used for the determination of $S_{EXP\ EC}(Q, \omega)$ differs from the scattering of the container with the sample, in such cases f_{EC} is adjusted.

Thus, it is the expression for $S_{THEO}(Q, \omega)$, which must be provided in order to fit eq. (5.1) to the data.

Specifically, an analysis of the quasielastic neutron scattering spectra includes:

1) search for suitable models describing the structure and the dynamics of the molecules in the sample. A broad spectrum of experimental results from all areas of science must be considered at this stage, in order to find a physically sensible model.

2) choice of a suitable model expression for $S_{THEO}(Q, \omega)$ (or development of such an expression).

3) fit of eq. (5.1) to the experimental scattering function $S_{TOTAL}(Q, \omega)$. If a good agreement between the experimental data and the fitted curve is observed, and fitted values of the free parameters are physically meaningful, the explanation of the experiment in the frame of the chosen model is completed.

Note that in the present work fitting of eq. (5.1) was always performed *simultaneously* to a number (from 2 to 40) of QENS spectra recorded for different scattering angles.

5.2 Road map for the QENS study of hydration water dynamics

The aim of the present work is to learn about hydration water in solutions of native and methylated cyclodextrins. The samples were dilute aqueous solutions with >1300 water molecules per each solute molecule (see Tab. 3.1). By inspecting the scattering cross sections of cyclodextrins (Tab. 5.1), it is clear that judging by the incoherent cross section, it is more likely to see a greater scattering contribution from the hydration water, if one has a solution in H_2O rather than in D_2O.

Table 5.1 **Neutron scattering cross sections for water and native and methylated cyclodextrins [barn].** The neutron scattering cross section, σ_S, is the sum of coherent and incoherent scattering cross sections: $\sigma_S = \sigma_{COH} + \sigma_{INC}$. The sum of the scattering cross sections of C, O, and D atoms only: $\sigma_S(C+O+D)$. The sum of the scattering cross sections of H atoms only: $\sigma_S(H)$. $\sigma_S^{TOTAL} = \sigma_S(C+O+D) + \sigma_S(H)$. The absorption cross section of the molecule: σ_A (for $\lambda = 1.8$ Å).

	Formula	M	$\sigma_S(C+O+D)$	$\sigma_S(H)$	σ_S^{TOTAL}	$\sigma_S(H)/\sigma_S^{TOTAL}$	σ_A
H_2O		18	4.232	164.0	168.3	-	0.6652
D_2O		20	19.5	-	19.5	-	-
β-CD (H_2O)	$C_{42}H_{70}O_{35}$	1134	381.2	5741	6122	0.937	23.28
β-CD (D_2O)	$C_{42}H_{49}D_{21}O_{35}$	1155	541.6	4019	4561	0.881	16.30
DIMEB (H_2O)	$C_{56}H_{98}O_{35}$	1331	459	8038	8497	0.946	32.60
DIMEB (D_2O)	$C_{56}H_{91}D_7O_{35}$	1337	512.5	7464	7976	0.936	30.27
γ-CD (H_2O)	$C_{48}H_{80}O_{40}$	1297	435.7	6562	6997	0.938	26.61
γ-CD (D_2O)	$C_{48}H_{56}D_{24}O_{40}$	1321	619	4594	5212	0.881	18.60
TRIMEG	$C_{72}H_{128}O_{40}$	1634	568.9	10948	11517	0.951	42.57

It is also clear that in order to discriminate between the scattering of the hydration shell and the solute, it is desirable, when doing a fit to the spectra, to have *no free parameters describing the solute motion*. For this purpose, one has to obtain dynamical parameters describing the solute motion beforehand.

The relative contribution from the scattering by a solute molecule will be greater in the QENS spectra of D_2O solutions (as opposed to H_2O solutions). Therefore, at first one has to extract information on the solute motion from the spectra of D_2O solutions, and after that apply (with eventual corrections for difference in viscosity between D_2O and H_2O) the obtained information in the analysis of QENS spectra of H_2O solutions. An attempt to determine simultaneously both solute and hydration water parameters from the QENS spectra of H_2O solutions might lead to the wrong assignment of a scattering component coming from the solute to the hydration water and *vice versa.*

(N.B.: Strictly speaking, the observed relative contributions of the solute and of the

hydration water to the spectrum of the solution will depend also on the energy resolution of the experiment.)

5.3 General expression for the theoretical scattering function

The expression for the theoretical scattering function of the solution reads:

$$S_{\text{THEO SOLUTION}}(Q, \omega) = n \times Sc.F(Q_{\text{EL}}) \times \{S_{\text{THEO SOL}}(Q, \omega) + F_W \times S_{\text{THEO W}}(Q, \omega)\} \qquad (5.2)$$

where n is the number density of solute molecules, F_W the number of water molecules per solute molecule, $Sc.F(Q_{\text{EL}})$ is the angle-dependent scaling factor, which is conventionally kept free to allow scaling of the theoretical scatering function to the experimental data.

The expression for the theoretical scattering function of pure water follows from eq. (5.2), taking F_W=1, $S_{\text{THEO SOL}}(Q, \omega)$=0 and n being replaced by the water number density, n_W.

Ideally, $Sc.F(Q_{\text{EL}})$ as determined from the fit of eq. (5.1 & 5.2) must be Q_{EL} − independent and, moreover, equal to the factor $(V_S \times C)$, C is given by eq. (2.54). Ideally in this context means that:

- a) the correction for the background scattering and the factor $H_1(\boldsymbol{k_0}, \boldsymbol{k})$ were precise;
- b) the model expressions for both $S_{\text{THEO SOL}}(Q, \omega)$ and $S_{\text{THEO W}}(Q, \omega)$ correspond to the true structure and dynamics of solute and water molecules, respectively;
- c) fit parameters which are not variables, were fixed to "true values", and values of the parameters determined in the fit, are also "true values".

At least for pure H_2O, $Sc.F(Q_{\text{EL}})$ was found to be indeed fairly constant, see section 7.3.

In some cases the terms $S_{\text{THEO SOL}}(Q, \omega)$ and $S_{\text{THEO W}}(Q, \omega)$ must be multiplied by two different, Q_{EL}-dependent, factors; this happens, for instance, when the model for water and/or solute neglects (or predicts only approximately) the coherent scattering contribution. Therefore, by introducing scaling factors for the solute (SOL) and solvent (W, for water) components ($Sc.F_{\text{SOL}}(Q_{\text{EL}})$ and $Sc.F_W(Q_{\text{EL}})$, respectively), a more practice-oriented expression for $S_{\text{THEO SOLUTION}}(Q, \omega)$ can be obtained from eq. (5.2):

$$S_{\text{THEO SOLUTION}}(Q, \omega) = n \times \{Sc.F_{\text{SOL}}(Q_{\text{EL}}) \times S_{\text{THEO SOL}}(Q, \omega) + Sc.F_W(Q_{\text{EL}}) \times F_W \times S_{\text{THEO W}}(Q, \omega)\} \quad (5.3)$$

(Note that the scaling factor obtained in fits to the spectra of pure water will be denoted as $Sc.F(Q_{\text{EL}})$ and *not* as $Sc.F_W(Q_{\text{EL}})$.)

It is evident that one needs a model for both the solute and water molecules, i.e. expressions for $S_{\text{THEO SOL}}(Q, \omega)$ and $S_{\text{THEO W}}(Q, \omega)$ must be specified.

5.4 Model for water

The expression corresponding to the scattering function of bulk water reads:

$$S_{\text{THEO W}}(Q, \omega) = \text{DWF} \times \{S_{\text{TR W}}(Q, \omega) \otimes S_{\text{ROT W}}(Q, \omega) + S_{\text{VIB W}}(Q, \omega)\} \qquad (5.4)$$

Here DWF is the Debye-Waller factor, accounting for the decrease of quasielastic intensity caused by vibrational motions, with $<u^2>_W$ [Å^2] being the effective mean square global displacement:

$$DWF = \exp(-<u^2>_W Q^2) \tag{5.5}$$

N.B.: Different definitions of the DWF are in use. If $DWF = \exp(-<u^2>_W Q^2/3)$, then $<u^2>_W$ is defined as the mean-square displacement in any direction of space. In the definition by eq. (5.5) employed here, however, $<u^2>_W$ is the mean-square displacement along the direction of the vector Q. Note that the expression $\exp(-<u^2>_W Q^2/6)$ is also used by some authors, but in that case $<u^2>_W$ does not have such a practically useful meaning.

The expression for the translational scattering function of water, $S_{TR\ W}(Q, \omega)$, employed here corresponds to the jump diffusion model [21,26,112]:

$$S_{TR\ W}(Q, \omega) = Lor\left\{ \frac{0.06581\, D_{TR\ W} Q^2}{1 + 0.1\, D_{TR\ W}\, \tau_{TR\ W}\, Q^2}, \omega \right\} \tag{5.6}$$

In eq. (5.6) the width of the Lorentzian has the dimension of meV; $D_{TR\ W}$ is given in 10^{-5} cm^2/s and $\tau_{TR\ W}$ in ps. The rotational scattering function of water, $S_{ROT\ W}(Q, \omega)$, corresponds to the model of isotropic rotation [109], see equations (2.28, 2.33-2.35). In summary, the expressions for $S_{TR\ W}(Q, \omega)$ and $S_{ROT\ W}(Q, \omega)$ contain following parameters: $<u^2>_W$, $D_{TR\ W}$, $\tau_{TR\ W}$, $D_{r\ W}$ and $S_W(Q)$, where subscript "W" stands for "water".

The intermolecular structure factor of D_2O, $S_{D2O}(Q)$, was taken from [10]. Here one must note that, while for D_2O the value of $b^2_{EFF}(Q = 0) \approx 3.67$ barn, for H_2O it is ≈ 0.03 barn. For H_2O at $Q < 2.5$ Å^{-1}, $b^2_{EFF}(Q) < 0.15$ barn so that the term "$b^2_{EFF}(Q) \times (S_{H2O}(Q) - 1)$" can be neglected and it is reasonable to rewrite eq. (2.34) as:

$$S^0_{ROT}(Q, \omega) = \delta(\omega) \times A_0(Q) \qquad \text{(for } H_2O) \tag{5.7}$$

Values of $D_{TR\ W}$ for H_2O were taken from [25], and for D_2O from [84]. Values for $D_{r\ W}$ and $<u^2>_W$ were taken from studies on H_2O [132] and used for both D_2O and H_2O. Values of $\tau_{TR\ D2O}$ and $\tau_{TR\ H2O}$ were determined from fitting to the spectra of pure water.

In eq. (5.4) $S_{VIB\ W}(Q, \omega)$ is the term accounting for the inelastic contribution due to the vibrational motions. This contribution can not be neglected for $\Delta E > 30$ μeV. Here a damped harmonic oscillator (DHO) after [69,73] is used:

$$S_{VIB\ W}(Q, \omega) = \{\exp(<u^2>_{DHO} Q^2) - 1\} \times H(\omega) \tag{5.8}$$

$$H(\omega) = \frac{1}{\pi} \frac{\hbar\omega}{k_B T} \frac{n(\omega)}{\exp(-\hbar\omega/2k_B T)} \frac{\Gamma_{DHO} E^2_{DHO}}{((E^2_{DHO} - \omega^2)^2 + \omega^2 \Gamma^2)} \tag{5.9}$$

where $n(\omega) = 1/\{\exp(\hbar\omega/k_B T) - 1\}$ is the thermal occupancy factor, E_{DHO} is the energy, Γ_{DHO} is the damping constant and $<u^2>_{DHO}$ is the mean square displacement of the harmonic oscillator. Note that in the limit of high temperatures (T > 250 K), the integral of $H(\omega)$ over ω is unity.

Note also that here the frequency–dependent part of $S_{VIB\,W}(Q, \omega)$ does not contain the detailed balance factor, because it has been put it in front of the total theoretical scattering function $S_{THEO}(Q, \omega)$, see eq. (2.55).

5.5 Model for the solute ("standard solute model")

The model expression given above for water is generally also suitable for solute molecules (see section 2.4). However, some simplifications can be made. At first, the inelastic scattering from the solute molecules is neglected at this stage of data analysis. This appears to be reasonable because:

- a) no information on the low frequency vibrational motions of cyclodextrins could be found;
- b) the number of free fitting parameters must be kept small;
- c) quasielastic and inelastic scattering contributions from water are expected to account for most of the intensity in the energy transfer region $-2.0 < \hbar\omega < 10$ meV.

In the Q range of the available spectra (maximum Q_{EL} value ≈ 2.3 Å^{-1}), the minimum value of the DWF for water is ≈ 0.69. Since the mean square displacement for atoms in the cyclodextrin molecule is expected to be smaller than it is for the protons in water, in the following the DWF of the solute is set to unity.

Finally, the translational diffusion of the solute molecule was described by the model of continuous translational diffusion [26,143] (with $S_{TR\,SOL}(Q, \omega)$ given by eq. (2.5)). This model appears appropriate, because the solvent molecules are so much smaller than CD or mCD molecules that the latter will move smoothly, almost like in a continuum. Phenomenologically, the difference between eqs. (2.5) and (5.6) consists in setting the mean residence time between the successive jumps, $\tau_{TR\,SOL}$, to zero. For the solute being a CD or mCD, this can be justified as follows.

Substituting $D_{TR\,SOL} = 0.2 \times 10^{-5}$ cm^2/s (such a value of $D_{TR\,SOL}$ have CDs at room temperature) and $\tau_{TR\,SOL} = 1$ ps (similar to $\tau_{TR\,W} = 1$ ps for water at room temperature) in Einstein's relation [27]:

$$D_{TR} = <l^2>/6\tau_{TR} \tag{5.10}$$

yields $\sqrt{<l^2>} = 0.35$Å, whereas the maximum diameter of a CD molecule is greater than 15 Å. Thus, qualitatively, for $\tau_{TR\,SOL} < 5.0$ ps, the motion corresponds to the picture of continuous diffusion.

Additionally, the Q range of the QENS experiment is always limited: $Q \leq Q_{EL\,max}$, where $Q_{EL\,max}$ is the maximum value of the elastic momentum transfer in the given experiment; in the present work $Q_{EL\,max} = 2.3$ Å^{-1}. For $Q = Q_{EL\,max}$, $\tau_{TR\,SOL} = 1$ ps and for $D_{TR\,SOL} = 0.2 \times 10^{-5}$ cm^2/s, the

denominator of eq. (5.6) "$1+0.1D_{TR\,SOL}\tau_{TR\,SOL}Q^2$" is equal to 1.1. It is seen that assuming for CDs and mCDs similar or smaller values of $\tau_{TR\,SOL}$ and for $Q \leq 2.3$ Å^{-1}, eqs. (2.5) and (5.6) provide similar results. (Because the translation of the solute molecule is only possible due to translation of water molecules, it follows that $\tau_{TR\,SOL} \leq \tau_{TR\,W}$.)

From the above, the expression for the solute scattering function, $S_{SOL}(Q, \omega)$, reads:

$$S_{SOL}(Q, \omega) = S_{TR\,SOL}(Q, \omega) \otimes S_{ROT\,SOL}(Q, \omega) \tag{5.11}$$

with the expression for the translational scattering function:

$$S_{TR\,SOL}(Q, \omega) = Lor(0.06581 \times D_{TR\,SOL}Q^2, \omega) \tag{5.12}$$

For the description of rotational motion of the solute molecule the model of isotropic rotation is applied (with $S_{ROT\,SOL}(Q, \omega)$ given by eqs. (2.28, 2.33-2.35)). The atomic coordinates of the various solute molecules were taken from the known structures of CDs and mCDs crystallohydrates [1,4,6,24] and used to compute rotational structure factors, $A_l(Q)$, which are required for the evaluation of $S_{ROT\,SOL}(Q, \omega)$. (Note that $A_l(Q)$ account for the intensity of the scattering by the single molecule, both coherent and incoherent.) In principle, the knowledge of the intermolecular structure factor of the solute, $S_{SOL}(Q)$, (see eq. (2.42) and sections 2.3-2.4) is required to take into account the interference between scattering from different solute molecules. As a first approximation for dilute solutions, $S_{SOL}(Q)$ can be set to unity.

For the reference, the complete theoretical formula for the solute scattering component, $S_{SOL}(Q, \omega)$, is given by eq. (5.11) and $S_{TR\,SOL}(Q, \omega)$ is given by eq. (5.12). The expression for $S_{ROT\,SOL}(Q, \omega)$ reads:

$$S_{ROT\,SOL}(Q, \omega) = \sum_{l=0}^{\infty} S_{ROT\,SOL}^l(Q, \omega) \tag{5.13}$$

$$S^0{}_{ROT\,SOL}(Q, \omega) = \delta(\omega) \times \{b^2{}_{EFF\,SOL}(Q) \times (S_{SOL}(Q) - 1) + A_{0(SOL)}(Q)\} \tag{5.14}$$

The effective scattering amplitude of the solute molecule, $b_{EFF\,SOL}(Q)$ is:

$$b_{EFF\,SOL}(Q) = \sum_{\mu=1}^{n} <b_\mu> \frac{\sin Qr_\mu}{Qr_\mu} \tag{5.15}$$

$$S^l{}_{ROT\,SOL}(Q, \omega) = (2l + 1) \times A_{l(SOL)}(Q) \times Lor(l(l+1)D_{r\,SOL}, \omega) \tag{5.16}$$

where $S_{SOL}(Q) = 1 + \gamma_{CM\,SOL}(Q)$, see eq. (2.42). In the present work, $S_{SOL}(Q)$ in eq. (5.14) was set to "1", unless stated otherwise.

The rotational structure factors, $A_{l(SOL)}(Q)$, for the solute molecule consisting of n atoms are given by the formula:

$$A_{l(SOL)}(Q) = \sum_{\mu,\nu=1}^{n,n} [<b_\mu><b_\nu> + \frac{\sigma_{\mu INC}\delta_{\mu\nu}}{4\pi}] j_l(Qr_\mu) j_l(Qr_\nu) P_l(\cos\theta_{\mu\nu}) \tag{5.17}$$

where $\theta_{\mu\nu}$ is an angle between the vectors r_μ and r_ν (giving the positions of the μth and νth atoms of the solute molecule in the system of the center of mass), P_l is the Legendre polynomial of

degree *l*, j_l is the spherical Bessel function of order *l*.

Henceforth, the model described in this section will be referred to as the "standard solute model". Although the term accounting for spatial correlations between the solute and solvent molecules is lacking in eqs. (5.11-5.17), in many cases this model is fairly adequate.

5.6 *"Fast" motion in the solute molecule*

In the course of the data analysis it turned out that for a satisfactory description of the experimental spectra of DIMEB by the fitted curve, a term for the description of a "fast" motion (with a characteristic time of about 5 ps) was required. This motion was attributed to the motion of -CH$_3$ and -CH$_2$-O-CH$_3$ groups ("side" groups). Because the rotational correlation time of the solute molecule is greater than 150 ps (see section 7.5), one can assume the dynamical independence of the rotational motion of the molecule and "fast" motion of the "side" groups.

Qualitatively, the expression for the rotational scattering function should be:

$$S_{ROT\,mCD}(Q, \omega) = S_{ROT\,SOL}(Q, \omega) \otimes S_{FAST\,SOL}(Q, \omega) \tag{5.18}$$

where $S_{FAST\,SOL}(Q, \omega)$ must describe the motion of the "side" groups only (as opposed to $S_{ROT\,SOL}(Q, \omega)$, which corresponds to the rotation of the whole molecule); however, $S_{FAST\,SOL}(Q, \omega)$ must be convoluted only with that part of $S_{ROT\,SOL}(Q, \omega)$ which corresponds to the scattering by "side" groups.

The following semi-phenomenological approach was used. Values of $A_l(Q)$ for hydrogen atoms belonging to the -CH$_3$ groups (hydrogens of -CH$_2$-O- fragments were not considered at the present stage), $A_{l(MET)}(Q)$, were evaluated by modifying eq. (5.17) as follows:

$$A_{l(MET)}(Q) = \sum_{\mu=1}^{mMET} \frac{\sigma_{\mu\,INC}}{4\pi} j_l^2(Qr_\mu) \tag{5.19}$$

where *mMET* is the number of hydrogen atoms in all -CH$_3$ groups. Analogously to eq. (5.13), $S_{ROT\,mCD}(Q, \omega)$ is the sum of the terms $S_{ROT\,mCD}^l(Q, \omega)$, $l = 0, 1, 2 .. \infty$. Eq. (5.14) can be modified so that the expression for $S_{ROT\,mCD}^0(Q, \omega)$ is given by:

$$S_{ROT\,mCD}^0(Q, \omega) = \delta(\omega) \times \{b_{EFF\,SOL}^2(Q) \times (S_{SOL}(Q) - 1) + [A_0(Q) - A_{0(MET)}(Q)]\} + S_{MET}^0(Q, \omega) \tag{5.20}$$

$$S_{MET}^0(Q, \omega) = A_{0(MET)}(Q) \times S_{FAST\,SOL}(Q, \omega) \tag{5.21}$$

And for all other *l* values, similarly to eq. (5.16):

$$S_{ROT\,mCD}^l(Q, \omega) = (2l + 1) \times \{[A_l(Q) - A_{l(MET)}(Q)] \times Lor[l(l + 1)D_{r\,SOL}, \omega]\} + S_{MET}^l(Q, \omega) \tag{5.22}$$

where $S_{MET}^l(Q, \omega)$ is given by:

$$S_{MET}^l(Q, \omega) = (2l + 1) \times A_{l(MET)}(Q) \times Lor[l(l + 1)D_{r\,SOL}, \omega] \otimes S_{FAST\,SOL}(Q, \omega) \tag{5.23}$$

As to the detailed expression for $S_{FAST\,SOL}(Q, \omega)$, it depends on the nature of the "fast" motion. In the first approximation, the model of jumps among three equivalent sites equally spaced on a circle (see for instance [8]) is considered:

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$$S_{FAST\,SOL}(Q, \omega) = A_0^{JUMP}(Q) \times \delta(\omega) + A_1^{JUMP}(Q) \times Lor(3/\tau, \omega) \tag{5.24}$$

$$A_0^{JUMP}(Q) = \tfrac{1}{3}[1 + 2 \times j_0(QR_{FAST}\sqrt{3})] \tag{5.25}$$

$$A_1^{JUMP}(Q) = \tfrac{2}{3}[1 - j_0(QR_{FAST}\sqrt{3})] \tag{5.26}$$

Here R_{FAST} is the radius of the circle and τ_{FAST} is the mean residence time on each site.

Note that in $A_{l(MET)}(Q)$ given by eq. (5.19) coherent scattering lengths of hydrogen and carbon are neglected. The resulting error in $A_{l(MET)}(Q)$ will be substantial only for $Q < 0.5\text{-}1$ Å^{-1}; in this Q region, however, the quasielastic broadening due to jump and rotatory motions of small "side" groups can be neglected (e.g. $A_0^{JUMP}(Q) \approx 1$ and $A_1^{JUMP}(Q) \approx 0$) rendering $S^0_{ROT\,mCD}(Q, \omega) \approx S^0_{ROT\,SOL}(Q, \omega)$, as expected.

It is not always convenient to have R_{FAST} as an explicit parameter, especially if a model of jumps on a circle is used to describe the scattering component (due to the motion of unknown geometry) phenomenologically. Therefore, another form of $S_{FAST\,SOL}(Q, \omega)$ was also used:

$$S_{FAST\,SOL}(Q, \omega) = A_{MET}(Q) \times Lor(W_{MET}, \omega) \tag{5.27}$$

where $A_{MET}(Q)$ is a Q-dependent fitting parameter and W_{MET} is the HWHM [meV]. Clearly, this is a purely phenomenological approach.

Finally, by setting $S_{FAST\,SOL}(Q, \omega) = \delta(\omega)$ the "standard solute model" is recovered.

5.7 Remarks on the "standard solute model" and eq. (5.3)

In eqs. (5.2, 5.3) a "mixed" term (see eq. (2.41)) accounting for the coherent scattering due to D_2O – solute pair correlation is missing. For the correlations between D_2O and solute molecules which exist during only a short time, one might expect this term to be as broad as the scattering term for bulk D_2O, and significantly smaller in intensity. In such case, neglection of the "mixed" term would not result in substantial error. By contrast, if these correlations are long-lived, the "hydrated solute model" (section 5.8) does takes them into account.

The absence of a separate hydration water term in the "standard solute model", eqs. (5.11-5.17), accounting for somewhat slower translational and rotational diffusion of hydration water as compared to bulk water molecules, appears *a priori* justified by the fact that in dilute D_2O solution ($F_{D2O} > 1300$ D_2O molecules here, see Tab. 3.1, most of which are part of the bulk water fraction), incoherent scattering by the hydration shell is much smaller than the scattering by solute and bulk water molecules.

The introduction of separate scaling factors for solvent and solute component, $Sc.F_{SOL}(Q_{EL})$ and $Sc.F_W(Q_{EL})$, can now be explained as follows. The contribution of the coherent scattering in pure D_2O or its solutions becomes increasingly important for $Q > 1.0$ Å^{-1}. The "convolution approximation" [143] used here to evaluate coherent scattering can not be expected to be perfect (it does not fulfill sumrules, see e.g. [76], pp. 73-75 in [124]). Thus,

Sc.$F_W(Q_{EL})$, being a free and Q_{EL}-dependent fit parameter, will scale the theoretical D_2O scattering contribution to its experimental value, making it possible to obtain good fits. And the factor Sc.$F_{SOL}(Q_{EL})$ being a free and Q_{EL}-dependent fit parameter, allows eventual correction for the intermolecular coherent scattering from the solute molecules. This correction was found to be necessary for aqueous solutions of mCDs (sections 7.6, 7.9).

5.8   The "hydrated solute model"

A "hydrated solute model" was developed in order to account for the steep increase in Sc.$F_{SOL}(Q_{EL})$ with decreasing Q_{EL}, as obtained in the fitting of the "standard solute model" to the spectra of DIMEB and TRIMEG solutions in D_2O. Such a behavior of Sc.$F_{SOL}(Q_{EL})$ was assumed to originate from a layer of D_2O molecules on the surface of methylated cyclodextrins. Such a layer would indeed result in an increase of coherent scattering from an mCD solute molecule and would explain the observed behavior of Sc.$F_{SOL}(Q_{EL})$ and the increase of the QENS integral, $I_{QENS}(Q_{EL})$, towards low Q_{EL} region.

It is assumed that the hydration shell of a molecule can be described by two parameters – the thickness of the hydration shell, h, and the number of water molecules in the hydration shell, N_{HYD}. Specifically, the hydration shell is defined as the layer of thickness h, where the centers of all hydration water molecules (their number is N_{HYD}) are situated. The surface of the solute molecule is defined as the surface of the volume, excluded by the solute molecule. The excluded volume is found using van der Waals radii of the atoms of the solute molecule. The water molecule (here D_2O) is approximated by a sphere of the radius $R_{D2O} = 1.90$ Å. Thus, *the maximum* of the distance between the centers of a hydration water molecule and the atom of the solute is given by $h + R_{D2O} + R_{ATOM}$, and t*he minimum* of this distance is given by $R_{D2O} + R_{ATOM}$. See also Fig. 5.1 for the schematic representation explaining the definitions introduced above.
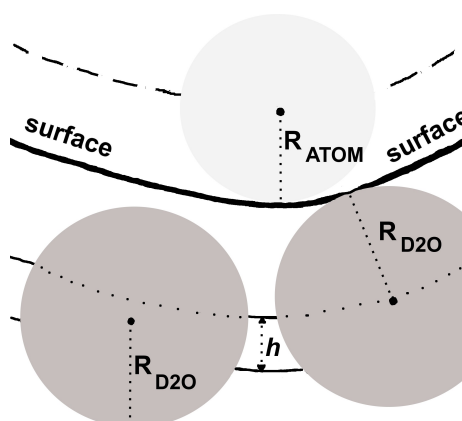

Figure 5.1 **The definition of the hydration shell employed in the "hydrated solute model".** For the explanation refer to the text above the figure.

The definition of the hydration shell thickness employed here was chosen to be suited for the evaluation of the scattering component arising due to the hydration shell. This is in contrast to the common definition, where the thickness of the hydration shell is the thickness of the layer formed by hydration water molecules, its (implied) minimal value being $\approx$ diameter of the water molecule.

Presumably, together with its hydration shell, an mCD molecule can be considered as a new entity, here denoted as mCD-HYD. Further assumptions are that this entity diffuses as a whole (with D_2O molecules bound to it, perhaps significantly longer than the translational diffusion correlation time of the water molecules in the bulk) and that in the same sense, it also rotates as a whole. Effectively, the modification of the "standard solute model" which is made here, represents only a change of the structure of the solute, i.e. instead of $A_{l(SOL)}(Q)$ given by eq. (5.17) one now has:

$$A_{l(\text{mCD-HYD})}(Q)= \sum_{\mu=1}^{n+3\times N_{HYD}} \sum_{\nu=1}^{n+3\times N_{HYD}} [<b_\mu><b_\nu>+\frac{\sigma_{\mu INC}\delta_{\mu\nu}}{4\pi}]j_l(Qr_\mu)j_l(Qr_\nu)P_l(\cos\theta_{\mu\nu}) \quad (5.28)$$

where $(n+3\times N_{HYD})$ is the total number of atoms in mCD-HYD, n for mCD and $3\times N_{HYD}$ for D_2O. For convenience, $A_{l(\text{mCD-HYD})}(Q)$ is decomposed as follows:

$$A_{l(\text{mCD-HYD})}(Q) = A_{l(\text{mCD})}(Q) + A_{l(\text{mCD-W})}(Q) + A_{l(\text{W-W})}(Q) \quad (5.29)$$

The coefficients $A_{l(\text{mCD})}(Q)$ are given as before by eq. (5.17). For $A_{l(\text{mCD-W})}(Q)$ one has:

$$A_{l(\text{mCD-W})}(Q)=2\sum_{\mu=1}^{n} \sum_{j=1}^{N_{HYD}} \sum_{\nu=1}^{3} <b_\mu><b_{j\nu}> j_l(Qr_\mu)j_l(Qr_{j\nu})P_l(\cos\theta_{\mu-j\nu}) \quad (5.30)$$

where $r_{j\nu}$ is the vector from the center of mass (c.m.) of the solute molecule to the νth atom of the jth water molecule, and $\theta_{\mu-j\nu}$ is the angle between r_μ and $r_{j\nu}$. For $A_{l(\text{mW-W})}(Q)$ one has:

$$A_{l(\text{W-W})}(Q)=\sum_{i=1}^{N_{HYD}} \sum_{\mu=1}^{3} \sum_{j=1}^{N_{HYD}} \sum_{\nu=1}^{3} [<b_{i\mu}><b_{j\nu}>+\frac{\sigma_{i\mu INC}\delta_{i\mu-j\nu}}{4\pi}]j_l(Qr_{i\mu})j_l(Qr_{j\nu})P_l(\cos\theta_{i\mu-j\nu}) \quad (5.31)$$

where $r_{i\mu}$ is the vector from the c.m. of the solute molecule to the μth atom of the ith water molecule ($r_{j\nu}$ is defined as above), $\theta_{i\mu-j\nu}$ is the angle between $r_{i\mu}$ and $r_{j\nu}$; $\delta_{i\mu-j\nu} = 1$ if $i=j$ and $\mu=\nu$ and 0 otherwise.

Because the positions of the hydration water molecules are not known, it will be assumed that the probability to find a hydration water molecule is uniformly distributed over the whole volume of the hydration shell. Thus, the number density, p, of molecules in the hydration shell of volume V_{SHELL} is:

$$p=N_{HYD}/V_{SHELL} \quad (5.32)$$

All orientations of a water molecule relative to the mCD molecule are assumed to be equally probable. Thus, from eq. (5.30) one has:

$$A_{l(\text{mCD-W})}(Q)=2\,p \times b_{\text{EFF W}}(Q) \times \sum_{\mu=1}^{n} \langle b_{\mu} \rangle\, j_l(Qr_{\mu}) \int_{V_{SHELL}} j_l(QR_j) P_l(\cos\theta_{\mu-j})\, d\,\boldsymbol{R}_j \quad (5.33)$$

where $\boldsymbol{R}_j$ is the vector giving the position of the c.m. of the hydration water molecule in the coordinate system of the c.m. of the solute molecule and $\theta_{\mu\text{-}j}$ is the angle between $\boldsymbol{r}_{\mu}$ and $\boldsymbol{R}_j$. Here $b_{\text{EFF W}}(Q)$ is the scattering amplitude of water molecule, for the definition of $b_{\text{EFF}}(Q)$ see eq. (2.24). From eq. (5.31) it follows:

$$A_{l(\text{W-W})}(Q)=p^2 \times \int_{V_{SHELL}} \int_{V_{SHELL}} g_{W\,ij}(Q)\, j_l(QR_i)\, j_l(QR_j)\, P_l(\cos\theta_{i-j})\, d\,\boldsymbol{R}_i\, d\,\boldsymbol{R}_j \quad (5.34)$$

where $\theta_{i\text{-}j}$ is the angle between $\boldsymbol{R}_i$ and $\boldsymbol{R}_j$. A function $g_{W\,ij}(Q)$ is defined depending on the fact whether $\boldsymbol{R}_i$ and $\boldsymbol{R}_j$ refer to the positions of the centers of mass of two distinct water molecule, or not:

$$\boldsymbol{R}_i \neq \boldsymbol{R}_j \quad : \quad g_{W\,ij}(Q)=b_{\text{EFF W}}^2(Q)$$
$$\boldsymbol{R}_i = \boldsymbol{R}_j \quad : \quad g_{W\,ij}(Q)=b_{\text{SELF W}}(Q)=\sum_{\mu=1,\nu=1}^{3,3} \left[\langle b_{\mu} \rangle \langle b_{\nu} \rangle + \frac{\sigma_{\mu\,\text{INC}}\delta_{\mu\,\nu}}{4\pi} \right] j_0(Qr_{\mu\nu}) \quad (5.35)$$

where r_{μ} and r_{ν} are the vectors pointing to the μth and νth atoms of the water molecule and $r_{\mu\nu}=r_{\mu}-r_{\nu}$.

The evaluation of $A_{l(\text{mCD-W})}(Q)$ was carried out using the cube method described in Chapter 4. Cubes belonging to the hydration shell are defined as cubes which are located within the layer of the thickness h, perpendicular to the surface of the solute molecule. $A_{l(\text{mCD}-\text{W})}(Q)$ and $A_{l(\text{W-W})}(Q)$ are evaluated using eqs. (5.33, 5.34), where instead of integration, a summation over all cubes belonging to the hydration shell is performed.

Per construction, $A_{l(\text{mCD-HYD})}(Q)$ are functions of h and N_{HYD}. To simplify the matter, in the present work it was assumed that the hydration shell is a monolayer of water molecules and that $h = 0.5$ Å. Thus, the distance between the centers of a water molecule and an atom of the solute molecule was between $0.5 + R_{D2O} + R_{ATOM}$ and $R_{D2O} + R_{ATOM}$. For $R_{ATOM} = 1.1$ Å (for hydrogen), the distance was therefore in the range 3.5 Å - 3 Å. Since the value of h was fixed, $A_{l(\text{mCD-HYD})}(Q)$ depended on the number of water molecules in the hydration shell, N_{HYD}, *only*, so that, as opposed to the "standard solute model", the "hydrated solute model" required only one additional fitting parameter.

For extensive details on the "hydrated solute model" (in particular, about the derivation of eqs. (5.33, 5.34)) see Appendix F.

5.9   Subtraction of the pure water spectrum

Instead of determining parameters of $S_{\text{THEO W}}(Q, \omega)$ as described in section 5.4, with the subsequent fitting of eq. (5.3) to the solution spectra, one can adopt another procedure. Given that the total scattering function was measured both for the solution and pure water (i.e.

$S_{\text{TOTAL SOLUTION}}(Q, \omega)$ and $S_{\text{TOTAL W}}(Q, \omega)$ are available), one can obtain the difference spectrum, $S_{\text{TOTAL SOL}}(Q, \omega)$, by subtraction of $S_{\text{TOTAL W}}(Q, \omega)$ with the weight F_w:

$$S_{\text{TOTAL SOL}}(Q, \omega) = S_{\text{TOTAL SOLUTION}}(Q, \omega) - F_w \times S_{\text{TOTAL W}}(Q, \omega) \tag{5.36}$$

Note that to employ eq. (5.36) one has to correct both $S_{\text{TOTAL SOL}}(Q, \omega)$ and $S_{\text{TOTAL W}}(Q, \omega)$ for the "$f_{EC} \times C \times S_{SC\ EXP}$" component beforehand. Further, eqs. (5.1, 5.2) can be fitted to $S_{\text{TOTAL SOL}}(Q, \omega)$ and, since $F_w \equiv 0$, there is no need to know parameters describing the scattering by the bulk water component. However, such an approach has three major drawbacks:

1) subtraction of the bulk water spectrum with the weight F_w is based on the tacit assumption that there *is no hydration water*; this is generally wrong. One can only account for the hydration water by subtracting the spectrum of bulk water with a weight $F_{w\ BULK}$, $F_{w\ BULK} < F_w$, but the factor $F_{w\ BULK}$ *is not known.*

2) for every spectrum of the solution, a spectrum of water (or, generally, a buffer solution) under exactly the same conditions must be measured.

3) subtracting one experimental spectrum from another leads generally to an increase of the statistical errors in the so obtained difference spectra, $S_{\text{TOTAL SOL}}(Q, \omega)$.

In addition, the multiple scattering component is not a simple additive quantity, and after subtraction of $S_{\text{TOTAL W}}(Q, \omega)$, the remaining multiple scattering contribution will still depend on $S_{\text{THEO W}}(Q, \omega)$.

5.10   Analysis of the spectra recorded with different energy resolutions

In section 2.7 it was demonstrated that, depending on the energy resolution, different kinds of motions and to different extent can be reflected in QENS spectra. Generally, parameters describing geometry and dynamics of these motions are not known. One way to proceed with an analysis of the spectra recorded for a number of different resolutions is outlined below.

It is reasonable to analyze first the spectra recorded with *the highest energy resolution,* because:

1) the fast motion of water molecules and fast motions in the solute molecule will be separated from the scattering component due to a slow solute motion: the latter will result in a narrow scattering component as opposed to the former, which produce broader components;

2) one may hope to determine dynamical parameters of the slow motion (because of the small ΔE value).

Subsequently, one can switch to the analysis of spectra recorded with lower resolution and fix parameters, describing the slow motions, at the values obtained in the first step. At last, the

spectra with the lowest resolution can be used to determine parameters of the fast motion, while parameters of all other motions are fixed at values determined in the previous stages of the analysis.

Clearly, in the first analysis of the high resolution spectra one eventually neglects the contribution from the fast motions. Therefore, after the first cycle of the data analysis is completed, one can then start by fixing parameter values of the faster motions obtained in the previous cycle and repeat the whole procedure again.