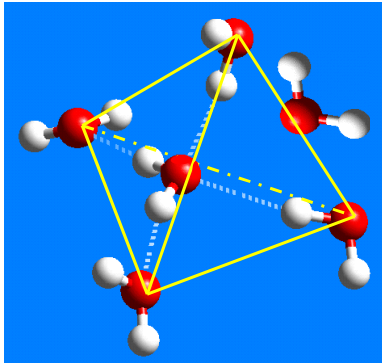


NE-M1-PRI12ENP – Integrated Nuclear Engineering Project

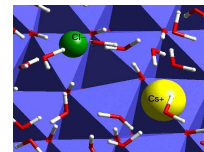
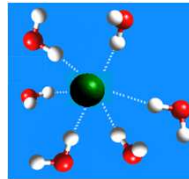
**Molecular Modeling of Materials
for Nuclear Waste Disposal Applications**

**Lecture 3 – Atomistic Simulations of the Properties of Water
and Hydrogen Bonding**



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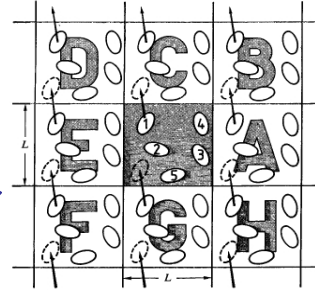
<https://www.imt-atlantique.fr/en/person/andrey-kalinichev>

Classical MC & MD Molecular Modeling - Details

- ◆ $N \sim 1,000-1,000,000$ atoms / $t \sim 1-10$ ns / $n \sim 10^6-10^7$ conf.
- ◆ Typically, constant T, P or T, V statistical ensembles
- ◆ Many molecular modeling software packages currently available.
- ◆ Most important: develop efficient numerical tools for the analysis of MD-generated trajectories or MC-generated ensembles of configs.
- ◆ *Coordinates* → Equilibrium thermodynamic properties
 - Atom-atom radial distribution functions
 - Coordination numbers, hydration numbers
 - Fluid structure, hydration shells
 - Molecular cluster formation and sorption environments
- ◆ *Velocities* → Diffusion
 - Velocity autocorrelation functions
 - Power spectra; dynamic details of atomic motions
- ◆ Comparison and interpretation of spectroscopic measurements: NMR, IR, Raman, X-ray.
- ◆ Molecular mechanisms controlling the behavior of aqueous species in solution and at substrate interfaces.

Methods of Molecular Computer Simulations: Molecular Dynamics (MD) and Monte Carlo (MC)

- **MD - time averages** over a dynamic trajectory in the phase space of the simulated system
- **MC - ensemble averages** over a computer-generated random Markov chain of molecular configurations
- Periodic boundary conditions (PBC)



$$T = \frac{2}{3Nk_B} \left\langle \sum_{i=1}^N \frac{m_i \mathbf{v}_i^2}{2} \right\rangle$$

$$D = \lim_{t \rightarrow \infty} \frac{1}{6Nt} \left\langle |\mathbf{r}(t) - \mathbf{r}(0)|^2 \right\rangle$$

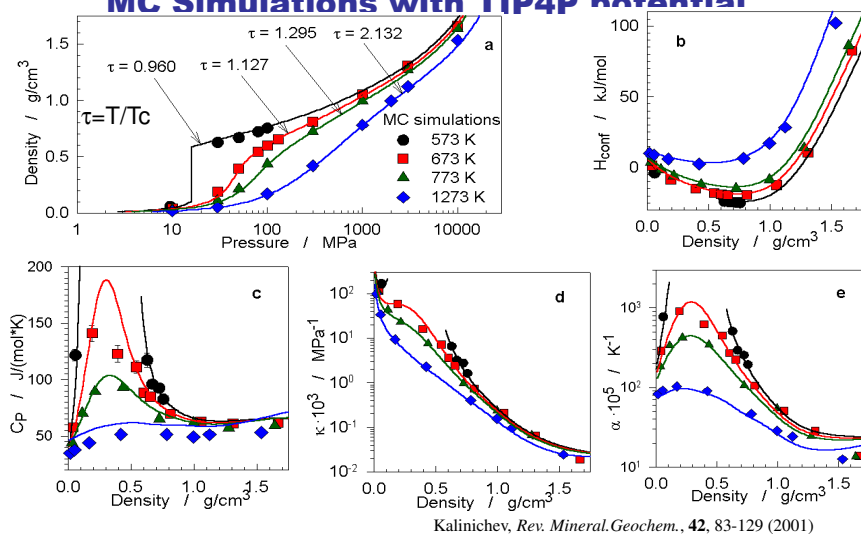
$$P = \frac{Nk_B T}{V} - \left(\frac{1}{3V} \right) \left\langle \sum_{i=1}^N \mathbf{r}_i \cdot \mathbf{F}_i \right\rangle$$

$$g_{ij}(r)$$

$$H_{\text{conf}} = \langle U \rangle + P \langle V \rangle$$

$$V_m = \langle V \rangle N_A / N$$

Thermodynamic Properties of Water MC Simulations with TIP4P potential



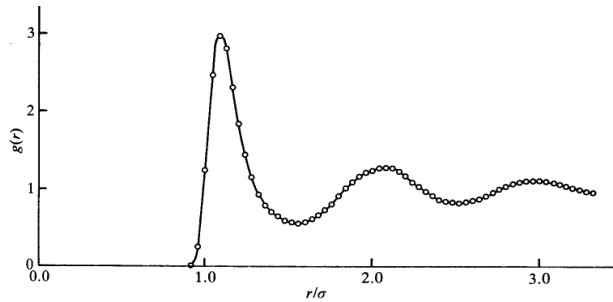
Fluid Structure

Radial Distribution Functions (RDFs)

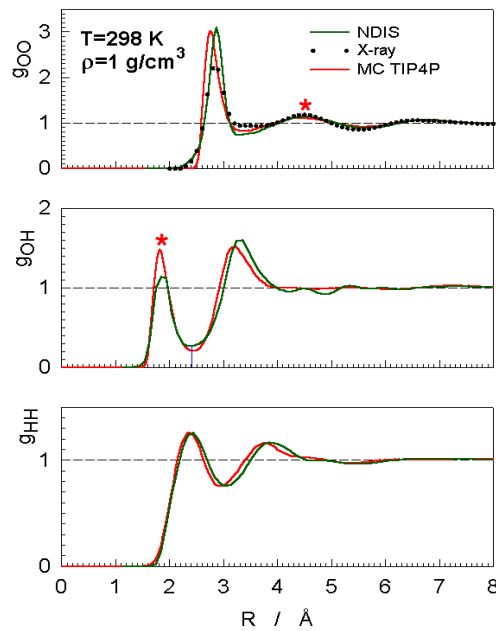
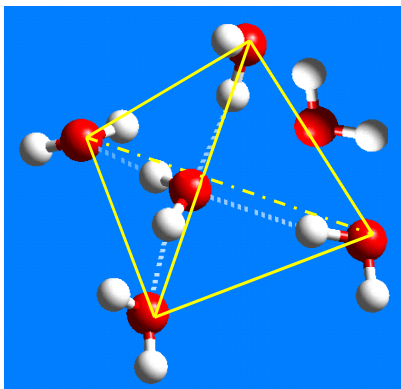
- ◆ **Pair distribution function** or **radial distribution function $g(r)$** – probability to find an atom i at a certain distance r from another atom j
- ◆ Normalized to a completely random distribution of atoms in space

$$g(r) = \rho^{-2} \langle \sum_i \sum_{j \neq i} \delta(\mathbf{r}_i) \delta(\mathbf{r}_j - \mathbf{r}) \rangle = \frac{V}{N^2} \langle \sum_i \sum_{j \neq i} \delta(\mathbf{r} - \mathbf{r}_{ij}) \rangle$$

- ◆ Comparable to exp. data on X-ray or neutron diffraction
- ◆ In practice, $\delta(\mathbf{r} - \mathbf{r}_{ij})$ is replaced by a function which is non-zero in a very narrow range of $\mathbf{r}$, and $g(r)$ is calculated as a histogram
- ◆ $g(r) = 1$ for ideal gas



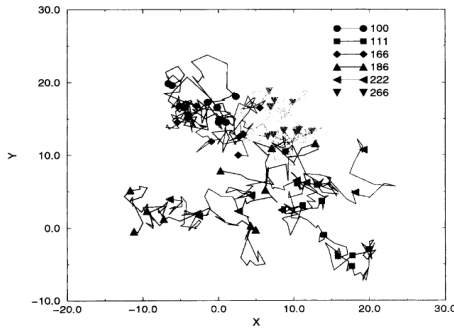
Structure of Water: Atom-Atom Radial Distribution Functions (RDFs)



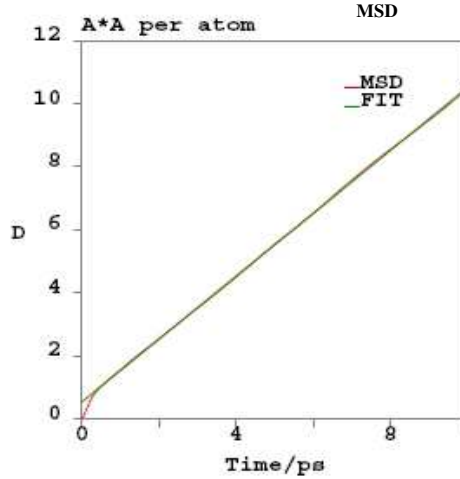
Self-Diffusion Coefficients

- Self-diffusion coefficient D of a species is proportional to the **mean-squared displacement** of this species in the limit of large t :

$$D = \lim_{t \rightarrow \infty} \frac{1}{6Nt} \left\langle \left| \mathbf{r}(t) - \mathbf{r}(0) \right|^2 \right\rangle$$

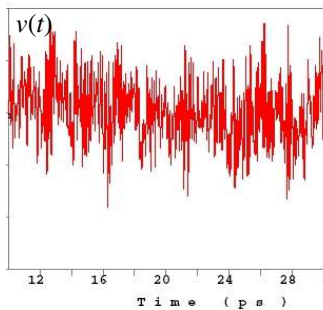


$$D = \lim_{t \rightarrow \infty} \frac{1}{3} \int_0^t \langle \mathbf{v}(0) \cdot \mathbf{v}(t') \rangle dt'$$

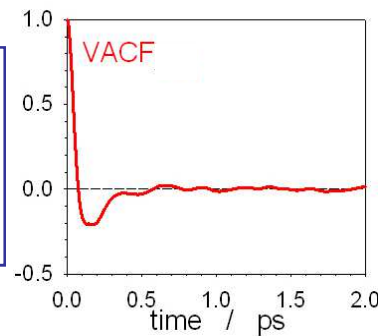


Dynamics of Individual Atoms: Velocity Autocorrelation Functions

$$\text{VACF} \equiv C_{vv}(t) = \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} = \frac{1}{\langle \mathbf{v}(0)^2 \rangle} \int \mathbf{v}(0) \cdot \mathbf{v}(t) d\Gamma$$



Qualitatively, the VACF reflects the relative rate with which the system or its individual atoms "forget" the velocities they had at a particular moment in time, indicated here as $t = 0$.

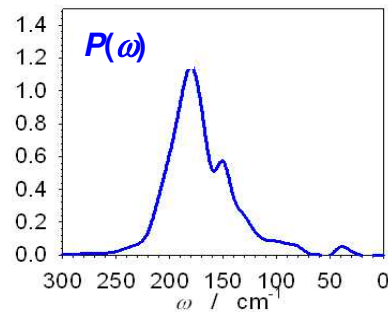
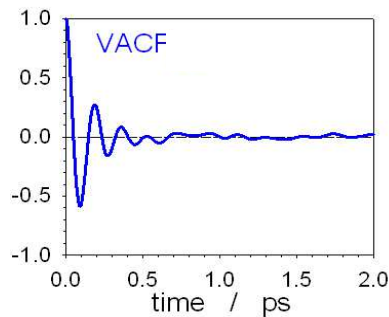


$$\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle = \frac{1}{N_\tau N} \sum_{i=1}^{N_\tau} \sum_{j=1}^N \mathbf{v}_j(t_i) \cdot \mathbf{v}_j(t_i + t)$$

Dynamics of Individual Atoms VACFs and Power Spectra

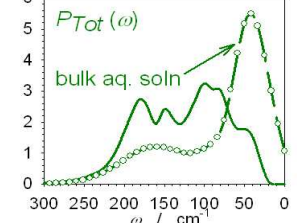
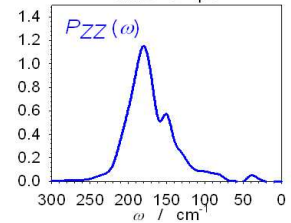
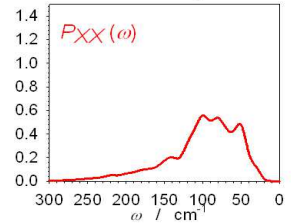
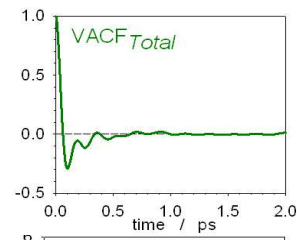
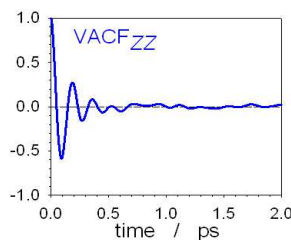
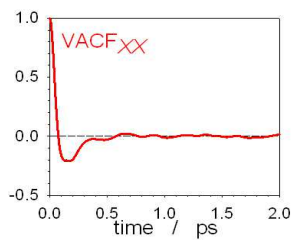
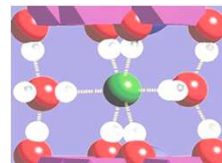
$$\text{VACF} \equiv C_{vv}(t) = \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} = \frac{1}{\langle \mathbf{v}(0)^2 \rangle} \int \mathbf{v}(0) \cdot \mathbf{v}(t) d\Gamma$$

$$P(\omega) = \int_0^\infty \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} \cos(\omega t) dt$$

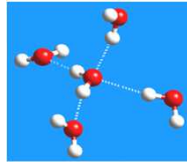


Dynamics of Individual Atoms VACFs and Power Spectra

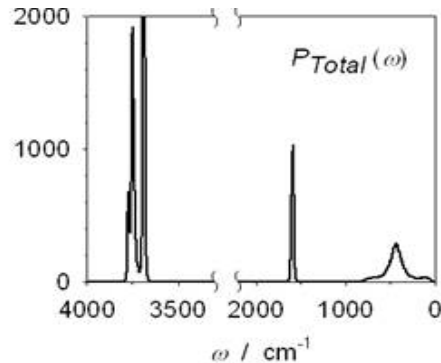
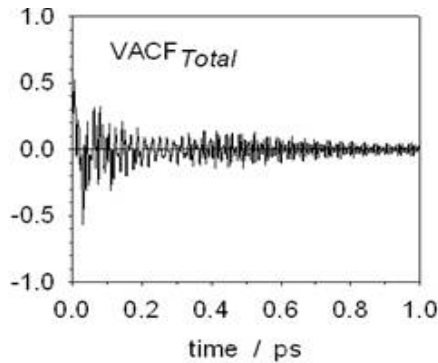
Cl⁻ in LiAl₂(OH)₆Cl·3H₂O



Dynamics of Individual Atoms VACFs and Power Spectra



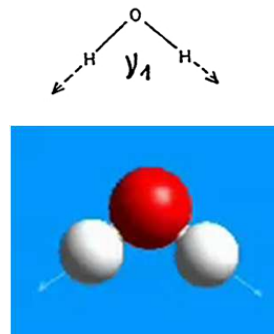
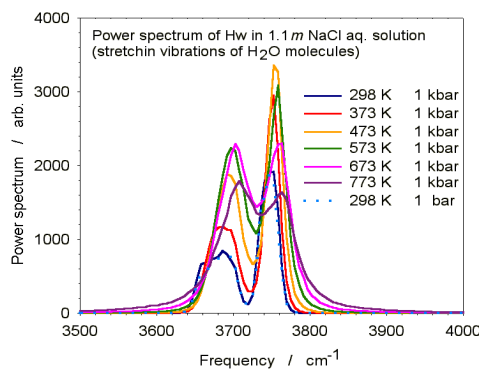
$$\begin{aligned}\omega &\sim 4000 \text{ [cm}^{-1}\text{]} \\ \lambda &= 1/\omega = 1 / 4000 \text{ [cm]} = 2.5 \cdot 10^{-6} \text{ [m]} \\ c &= \lambda v = \lambda / \tau \\ \tau &\sim \lambda / c = 2.5 \cdot 10^{-6} \text{ [m]} / 3 \cdot 10^8 \text{ [m/s]} \sim 10^{-14} \text{ [s]} \\ \Rightarrow \text{Time step} &\sim \tau / 10 \sim 10^{-15} \text{ [s]} = 1 \text{ [fs]}\end{aligned}$$



SPC: Intramolecular Stretching Vibrations of H₂O Molecules in NaCl Solutions as a Function of Temperature

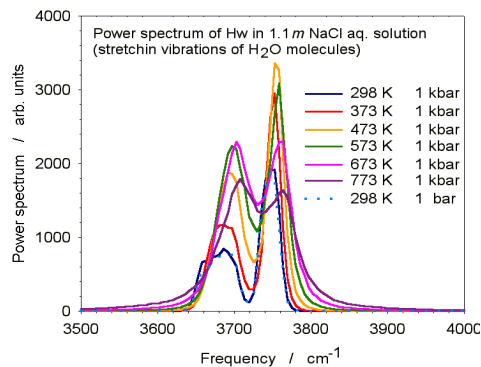
$$P(\omega) = \int_0^\infty \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} \cos(\omega t) dt$$

symmetric stretch

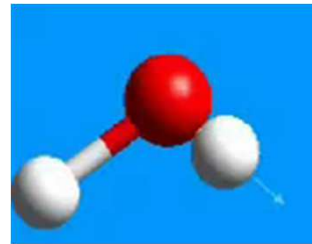
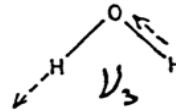


SPC: Intramolecular Stretching Vibrations of H₂O Molecules in NaCl Solutions as a Function of Temperature

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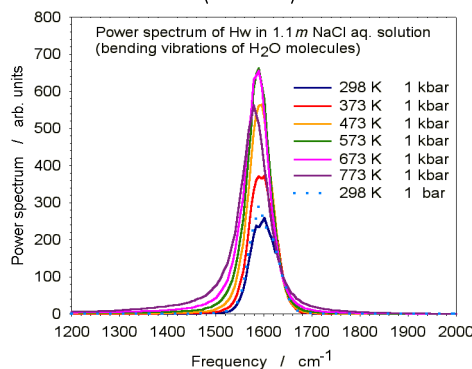


asymmetric stretch

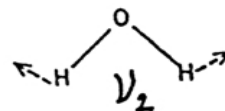


SPC: Intramolecular Bending Vibrations of H₂O Molecules in NaCl Solutions as a Function of Temperature

$$P(\omega) = \int_0^{\infty} \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} \cos(\omega t) dt$$

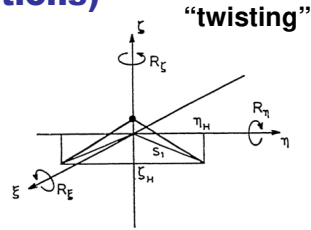
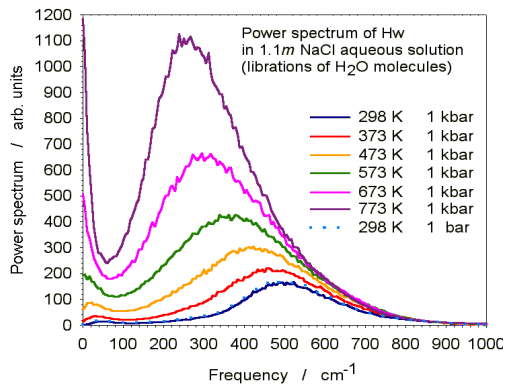


bending



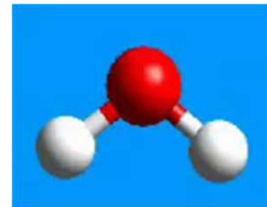
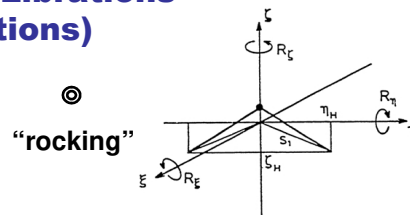
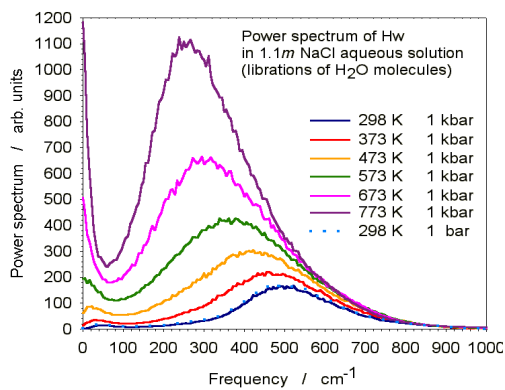
The bending spectrum is largely unaffected by the changes of temperature and density.

SPC: H₂O Molecular Librations (Hindered Rotations)



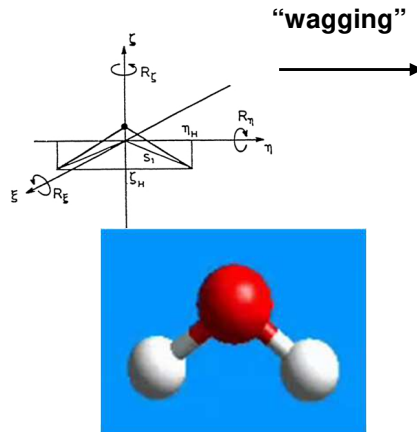
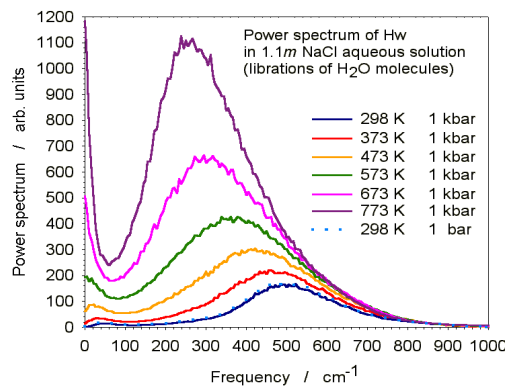
The broad frequency band of H₂O librations (hindered rotations) in the H-bonding network is centered around ~500 cm⁻¹ and gradually decreases with increasing temperature and decreasing density.

SPC: H₂O Molecular Librations (Hindered Rotations)



The broad frequency band of H₂O librations (hindered rotations) in the H-bonding network is centered around ~500 cm⁻¹ and gradually decreases with increasing temperature and decreasing density.

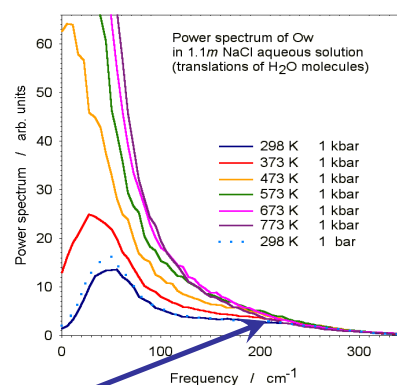
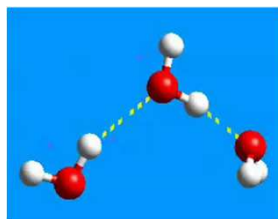
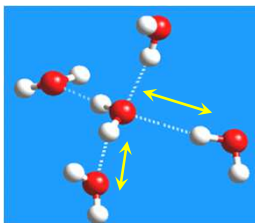
SPC: H₂O Molecular Librations (Hindered Rotations)



The broad frequency band of H₂O librations (hindered rotations) in the H-bonding network is centered around ~500 cm⁻¹ and gradually decreases with increasing temperature and decreasing density.

Dynamics of Individual Species Power Spectra of Molecular Motions

$$P(\omega) = \int_0^\infty \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} \cos(\omega t) dt$$

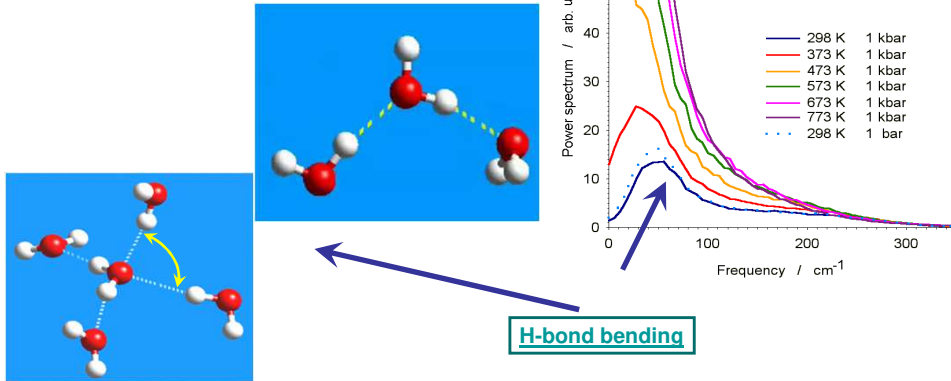


H-bond stretching

The two broad bands of the translational spectra at ~50 cm⁻¹ and ~200 cm⁻¹ are usually assigned to H-bond O···O bending and stretching, respectively

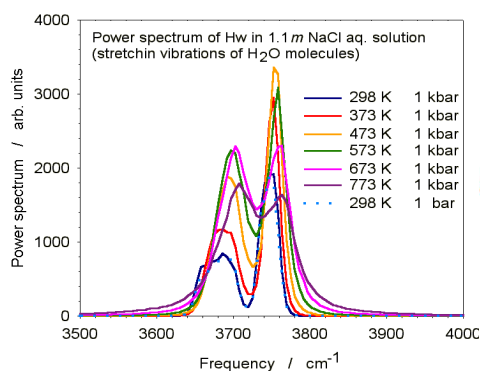
Dynamics of Individual Species Power Spectra of Molecular Motions

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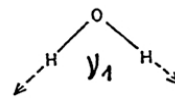


The two broad bands of the translational spectra at $\sim 50 \text{ cm}^{-1}$ and $\sim 200 \text{ cm}^{-1}$ are usually assigned to H-bond $\text{O} \cdots \text{O} \cdots \text{O}$ bending and stretching, respectively

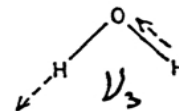
SPC: Intramolecular Stretching Vibrations of H_2O Molecules in NaCl Solutions as a Function of Temperature



symmetric stretch

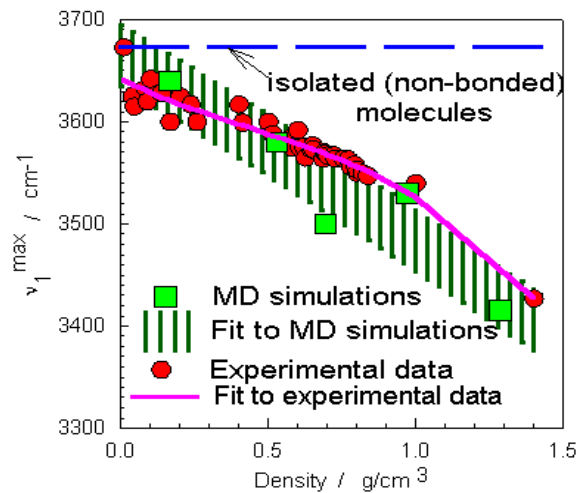


asymmetric stretch

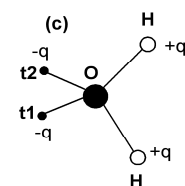
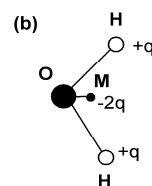
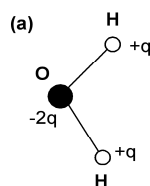
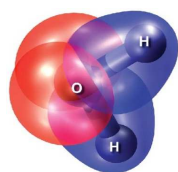


- ◆ Symmetric stretching frequencies continuously increase indicating a progressive loss of the strength of H-bonding in the solution.
- ◆ The asymmetric stretching vibration frequency remains almost unaffected by the weakening of H-bonding.

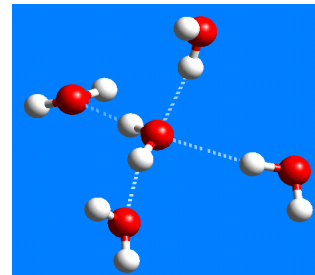
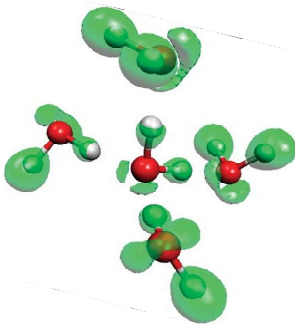
BJH: Spectral Density Maximum of the Symmetric Stretching Vibration, $\nu_1^{\max}$, as a Function of Density



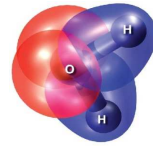
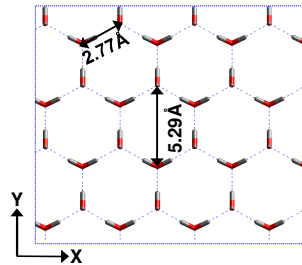
The Structure of H₂O Molecule and Intermolecular Hydrogen Bonding in Water



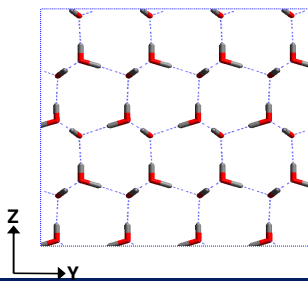
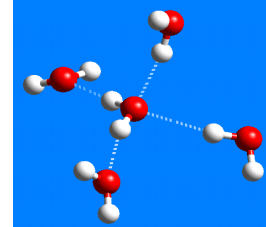
Negatively and positively charged sites of the water molecule



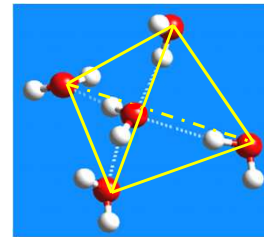
Hydrogen Bonding and Local Tetrahedral Ordering in Water



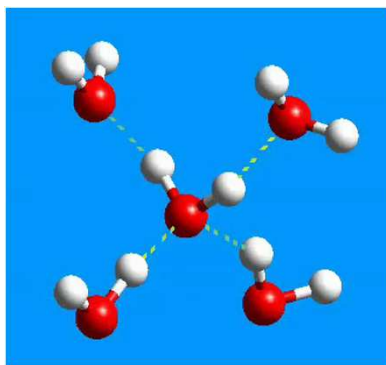
Ice Ih structure
Liquid water structure



- ♦ Tetrahedrally ordered O positions in the diamond-like network
- ♦ H positions are disordered
- ♦ Proton diffusion
- ♦ Proton hopping
- ♦ Long-range order is destroyed upon melting
- ♦ Short-range tetrahedral ordering remains in liquid



The name is Bond, H-Bond

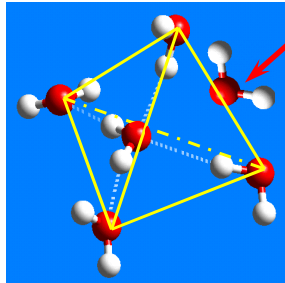


Ideally, each H₂O molecule in the H-bonding network can donate 2 H-bonds to its neighbors and accept 2 H-bonds from other neighbors

Hydrogen Bonding is the Most Important Phenomenon Governing the Properties of All Aqueous Systems

- ♦ **H-bonding** is ubiquitous, as water itself
- ♦ **H-bonding** is responsible for the anomalous properties of water
- ♦ All processes in water as a solvent are strongly affected by **H-bonding**
 - ♦ *hydration of species*
 - ♦ *adsorption*
 - ♦ *diffusion*
 - ♦ *intercalation*
- ♦ **H-bonding** stabilizes many inorganic and organic hydrous materials
- ♦ Inter- and intra-molecular **H-bonding** is important aspect of the bio-molecular behavior and functions

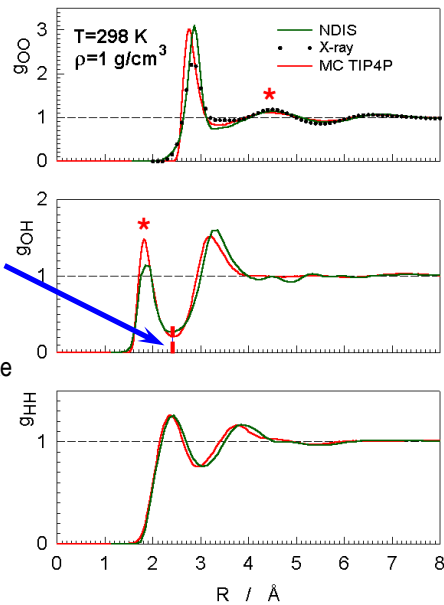
Structure of Water: Atom-Atom Radial Distribution Functions (RDFs)



Interstitial
H₂O molecule

Distance
criterion for
H-bonding

- ♦ **Ice:** Tetrahedrally ordered O in the diamond-like network
- ♦ H positions are disordered
- ♦ Proton diffusion
- ♦ Proton hopping
- ♦ **Liquid:** Only short-range tetrahedral ordering remains

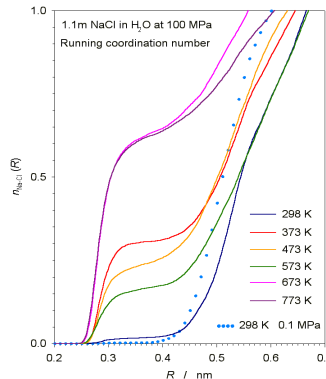
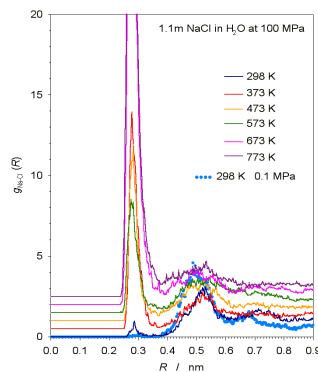


Fluid Structure - Running Coordination Numbers

Average number of atoms i within a sphere of radius r from another atom j :

$$n_{ij}(r) = 4\pi\rho_i \int_0^r g_{ij}(r) r^2 dr = 4\pi \frac{N_i}{V} \int_0^r g_{ij}(r) r^2 dr$$

RDFs and running coordination numbers for Na⁺-Cl⁻ ion pairs in solution



- ♦ At $T < 373$ K only water-separated Na⁺-H₂O-Cl⁻ ion pairs can be found in the solution
- ♦ At 373 K $< T < 573$ K ~25% of ions participate in contact ion pairs
- ♦ At $T > 673$ K the number of contact ion pairs increases very quickly involving the majority of ions

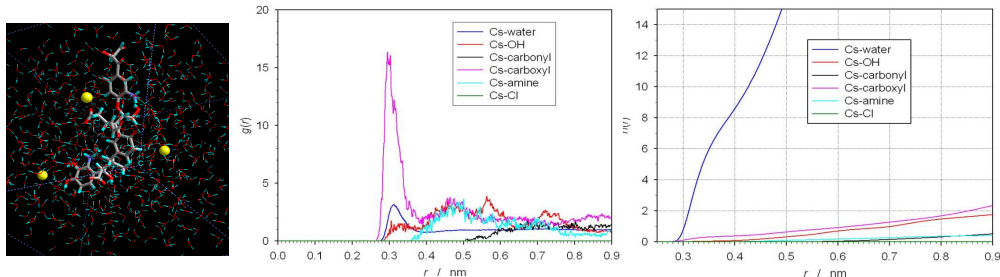
Radial Distribution Functions and Running Coordination Numbers

- ♦ Importance of $g(r)$ normalization
- ♦ Height of the $g(r)$ peaks is not necessarily an indication of high population
- ♦ Average density or concentration of species is equally important

$$g_{ij}(r) = \frac{1}{N_j \rho_i} \left\langle \sum_i \sum_j \delta(\mathbf{r} - \mathbf{r}_{ij}) \right\rangle$$

$$n_{ij}(r) = 4\pi\rho_i \int_0^r g_{ij}(r) r^2 dr$$

3 Cs⁺ ions in aqueous solution with humic acid (NOM anion)

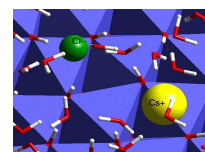
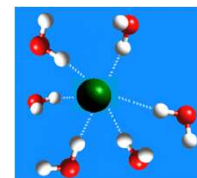
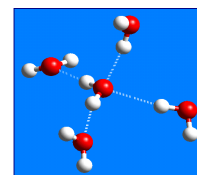


Hydrogen Bonding in Aqueous Systems and the Characteristic Scales Molecular Processes

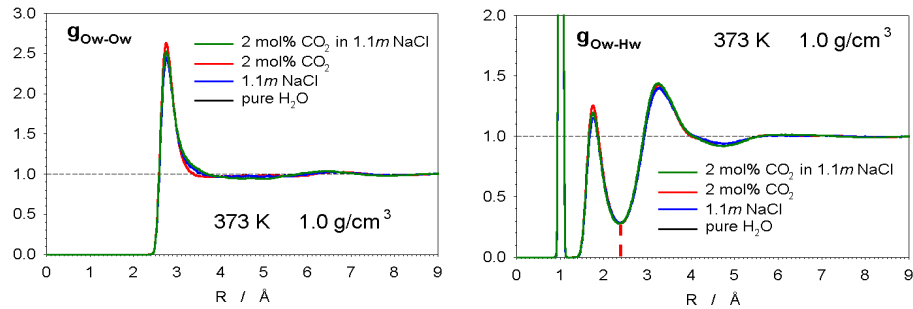
- ♦ Characteristic H-bond lifetime (300K) ~2-5ps ~3Å
- “ - “ - (600K) ~0.2ps
- “ - “ - (200K) ~200ps
- ♦ O-H vibrations; individual acts of H-transfer among water molecules ~0.2ps ~1Å
- ♦ Local H-bonding rearrangement (300K) ~10-20ps ~10Å
- ♦ Lifetime in ionic hydration shell (300K)

K ⁺ , Cl ⁻	~5ps	~10Å
Na ⁺	~10ps	
Li ⁺ , F ⁻	~30-50ps	
Ca ²⁺ , Mg ²⁺	~50-100ps	

- ♦ H₂O, Cl⁻, K⁺ surface site residence times
- neutral surface ~ 20 ps
- charged surface > 100 ps

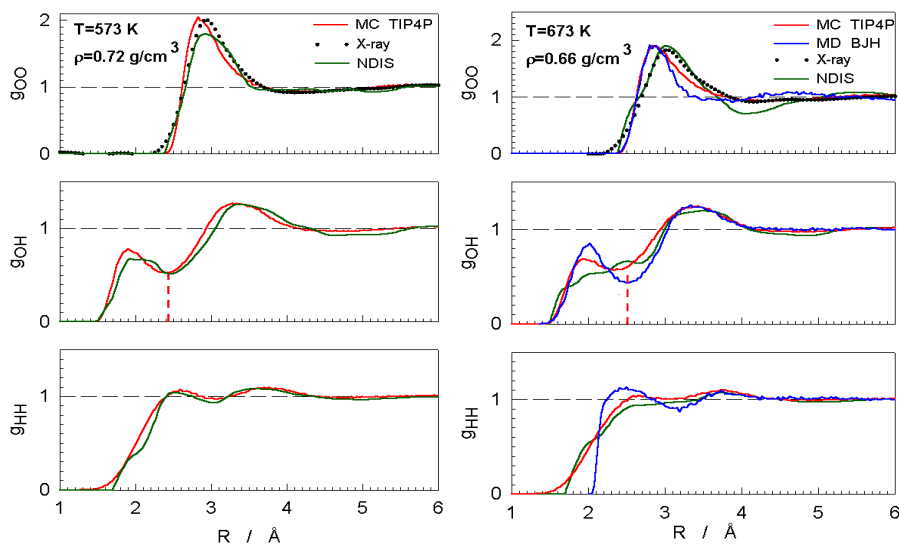


The Effect of Small Amounts of Electrolyte and Non-electrolyte Solutes on the Structure of Water

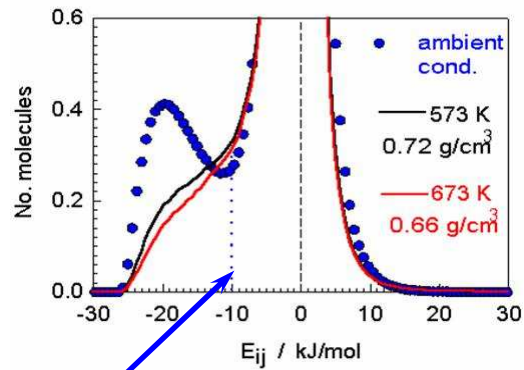
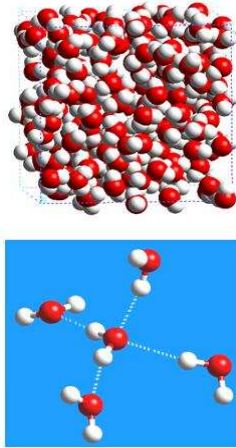


At low concentrations, the water structure represented by atom-atom radial distribution functions, is not strongly affected by the presence of any solute, and the general solution structure is in good agreement with recent X-ray diffraction measurements.

Water Structure under Hydrothermal Conditions

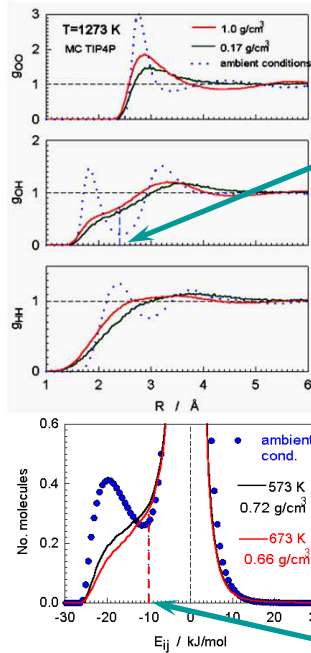


Micro-Thermodynamic Properties: Molecular Pair Energy Distributions



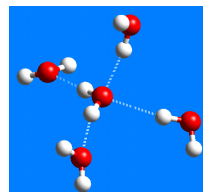
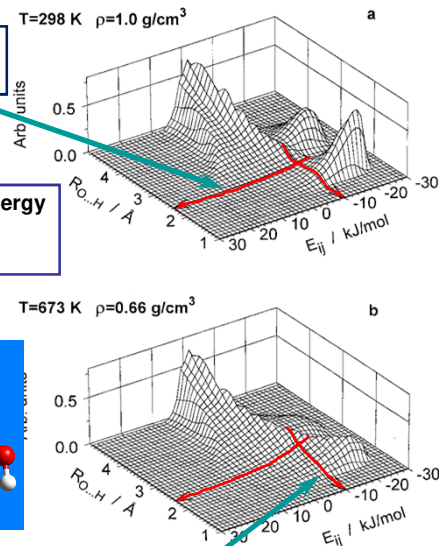
Energy criterion for hydrogen bonding

H-bond Definitions



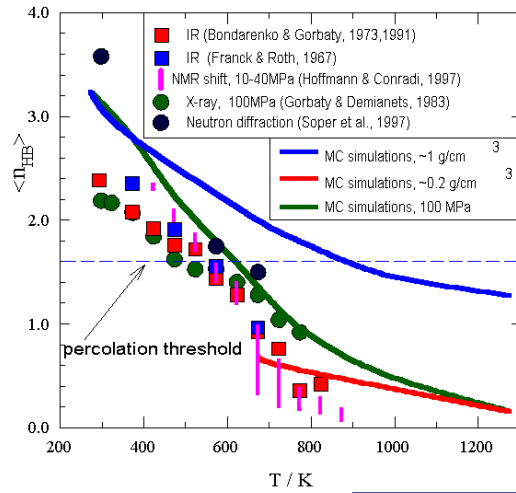
Distance criterion
for H-bonding

Distance-Energy
Distribution
Functions

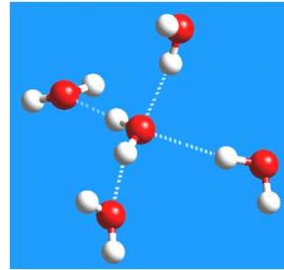


Energy criterion for H-bonding

Temperature and Pressure Dependence of the Number of H-bonds per Water Molecule

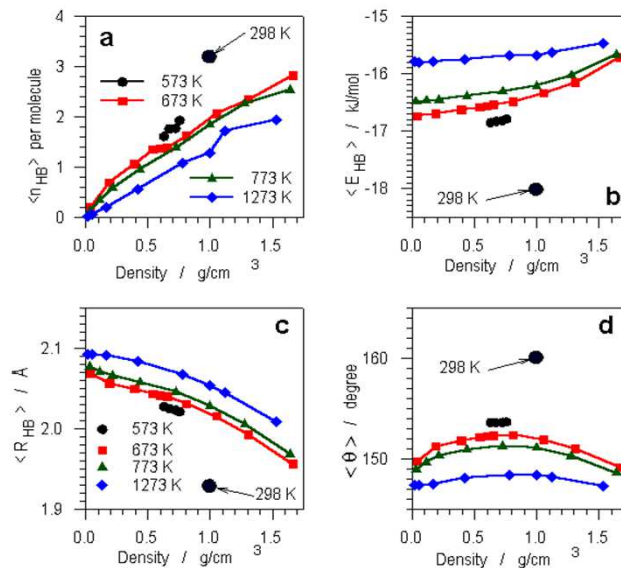


H-bonding:
molecular simulations vs spectroscopic and diffraction evidence from various sources



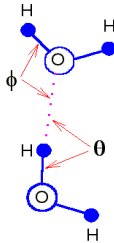
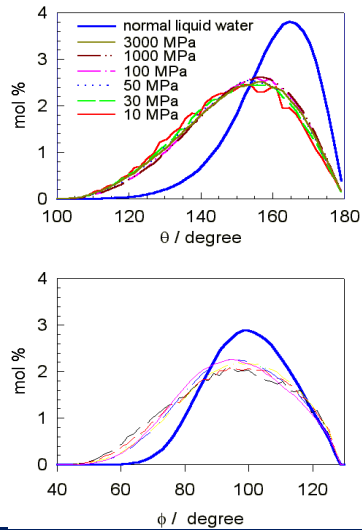
Kalinichev, *Rev. Mineral. Geochem.*, **42**, 83-129 (2001)

Average Parameters of H-bonds

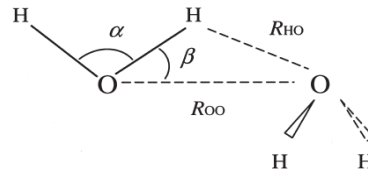


Angular Distributions of H-bonds

Distributions of HB angles at 773 K



Angular criterion of H-bonding can in many cases be used instead of the energetic criterion



$$R_{OO} \leq 3.3-3.5 \text{ \AA}$$

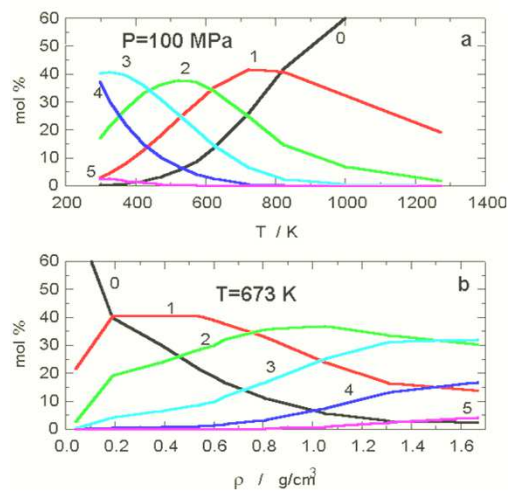
or

$$R_{OH} \leq 2.45-2.5 \text{ \AA}$$

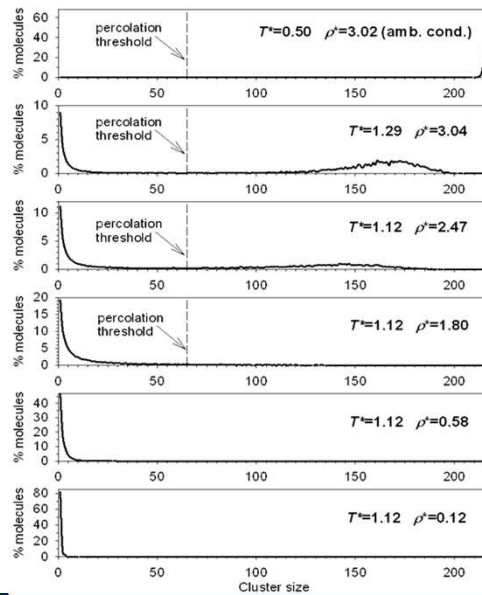
and

$$\beta \leq 30^\circ$$

Distributions of Water Molecules, Participating in a Given Number of H-bonds



Topology of H-bonding Network in Water



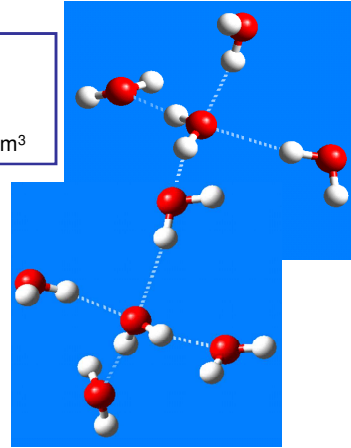
Percolating H-bond network vs H₂O molecular clusters

$$T^* = T/T_c$$

$$\rho^* = \rho/\rho_c$$

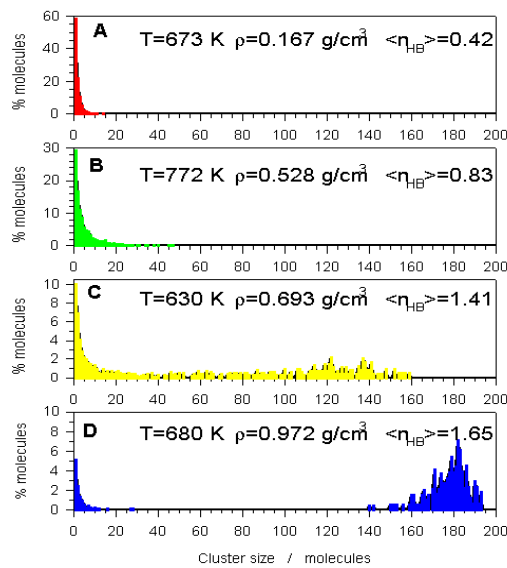
$$T_c = 647 \text{ K}$$

$$\rho_c = 0.31 \text{ g/cm}^3$$

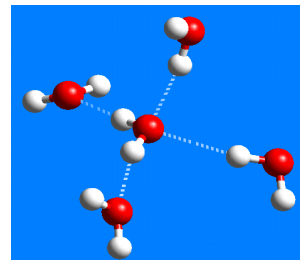


Percolation threshold $\langle n_{HB} \rangle \sim 1.6$

Molecular Clusterization in Supercritical Water



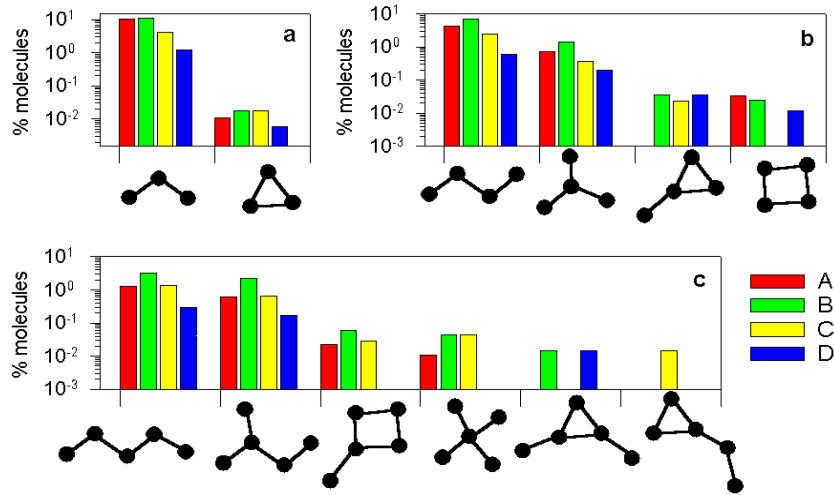
H-bonded cluster size distributions



Kalinichev & Churakov, 1999, 2001

Molecular Clusterization in Supercritical Water

Abundance of topologically different H₂O clusters



Kalinichev & Churakov, 1999, 2001

Molecular Clusterization in Supercritical Water

Average Parameters of H-bonded Clusters

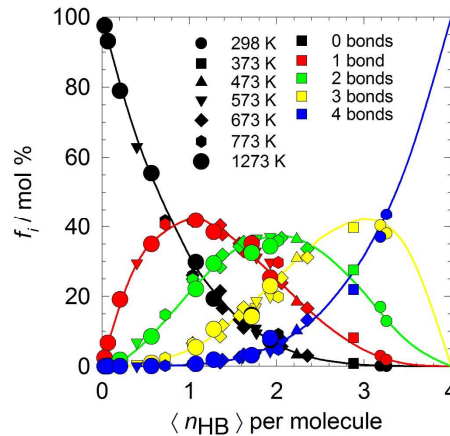
Cluster topology	3a	3b	4a	4b	4c	4d	5a	5b	5c	5d	5e
$\langle \angle \text{O} \cdot \text{O} \cdot \text{O}_1 \rangle / ^\circ$	109	60	110	107	114	87	110	108	112	107	105
$\langle \angle \text{O} \cdot \text{O} \cdot \text{O}_2 \rangle / ^\circ$					60				86	60	
$\langle \angle \text{O} \cdot \text{O} \cdot \text{O}_3 \rangle / ^\circ$										119	
$\langle R_{\text{O} \cdot \text{H}} \rangle / \text{\AA}$	2.04	2.07	2.04	2.04	2.06	2.03	2.04	2.04	2.05	2.06	2.05
$\langle R_{\text{O} \cdot \text{O}} \rangle / \text{\AA}$	2.90	2.89	2.91	2.91	2.90	2.90	2.91	2.91	2.91	2.90	2.92
$\langle \angle \text{O} \cdot \text{H} - \text{O} \rangle / ^\circ$	149	143	150	150	146	150	150	150	149	146	150
$\langle U_{\text{HB}} \rangle / \text{kJ/mol}$	-16.9	-16.4	-16.9	-16.7	-16.3	-17.0	-16.9	-16.8	-16.7	-16.3	-16.8

Distributions f_i of H₂O Molecules Involved in i H-bonds in Liquid and Supercritical Water as a Function of the Average Number of H-bonds per Molecule in the System, $\langle n_{HB} \rangle$

It has long been established that the interconnected percolating network of H-bonds in liquid water can be quite accurately described by a simple binomial distribution

$$f(i) = \binom{m}{i} \left(\frac{\langle n_{HB} \rangle}{m} \right)^i \left(1 - \frac{\langle n_{HB} \rangle}{m} \right)^{m-i}$$

Blumberg et al. (1984) Connectivity of hydrogen bonds in liquid water. *J. Chem. Phys.* **80**, 5230-5241



Lifetime of H-bonds in Supercritical Water

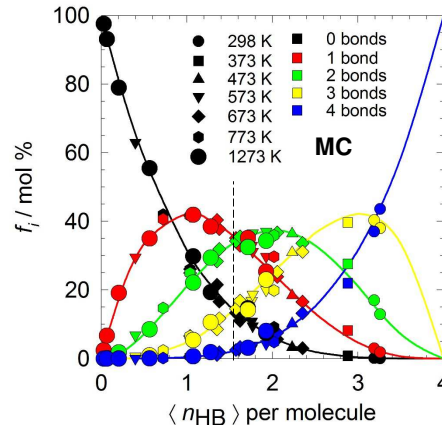
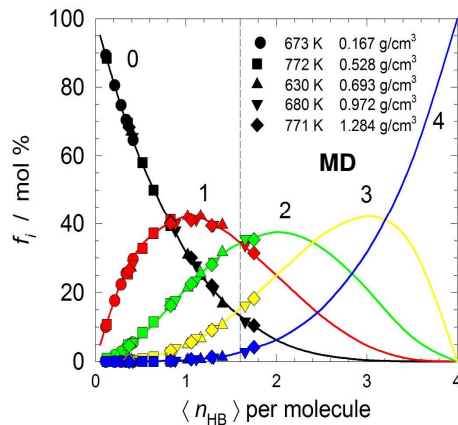
Average number of H-bonds per water molecule and concentration of H-bonded species in supercritical BJH water at 630 K and 0.692 g/cm³ as a function of a lifetime criterion for H-bonds.

$\Delta\tau$ / ps	$\langle n_{HB} \rangle$	% of monomers (0 bonds)	% of dimers (1 bond)	% of trimers (2 bonds)	% of tetramers (4 bonds)
0.01	1.41	16.6	39.4	31.9	10.7
0.1	0.83	40.2	40.2	16.3	3.0
0.2	0.57	55.0	34.2	9.5	1.2

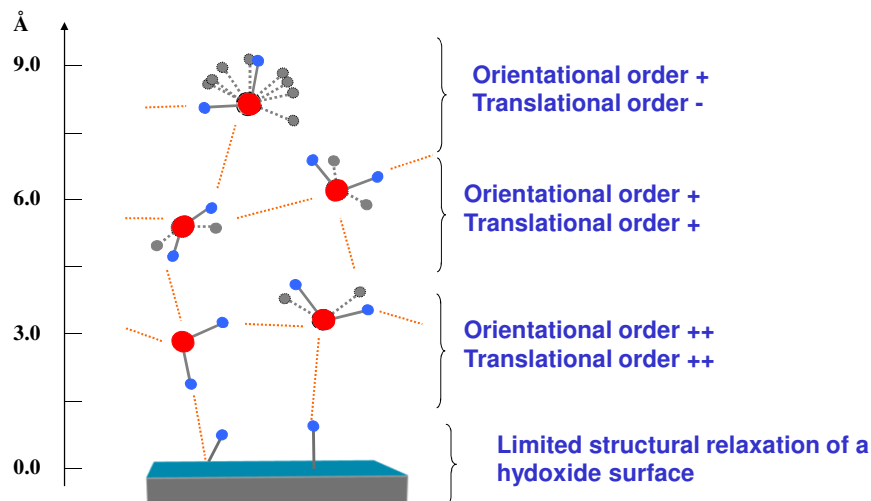
Distributions $f_i(\langle n_{HB} \rangle)$ from MC and MD Simulations with TIP4P and BJH Potentials

$$f(i) = \left(\frac{m}{i} \right) \left(\frac{\langle n_{HB} \rangle}{m} \right)^i \left(1 - \frac{\langle n_{HB} \rangle}{m} \right)^{m-i}$$

Kalinichev (2017) Universality of hydrogen bond distributions in liquid and supercritical water. *Journal of Molecular Liquids*, **241**, 1038-1043

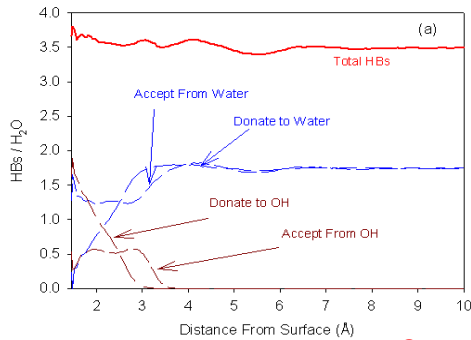


H-Bonding of Water at a Hydroxylated Surface, e.g., $Mg(OH)_2$, $Ca(OH)_2$

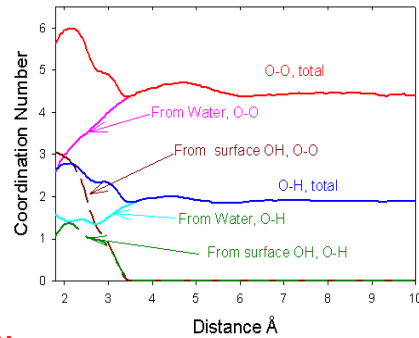


Water Structure at the Brucite, $\text{Mg}(\text{OH})_2$, Surface

Hydrogen Bonds



Coordination Numbers



Compare to:

Bulk water under pressure:

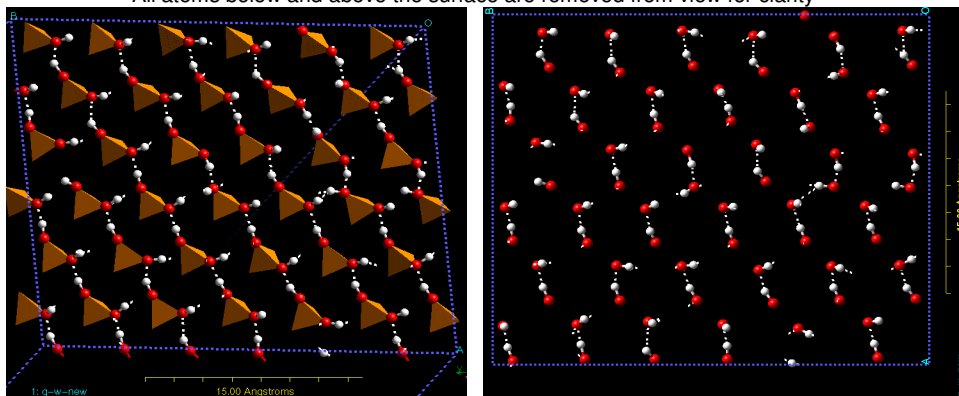
Nearest neighbors: $\uparrow$
Hydrogen-bonds: $\sim$
Ice VIII: NN=8, HB=4

Supercooled bulk water:

Nearest neighbors: $\downarrow$
Hydrogen-bonds: $\uparrow$
Ice Ih: NN=4, HB=4

H-Bonding at a Fully Protonated α -Quartz-Water Interface (Low pH)

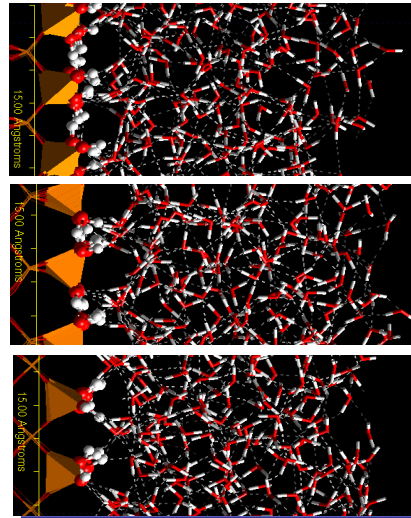
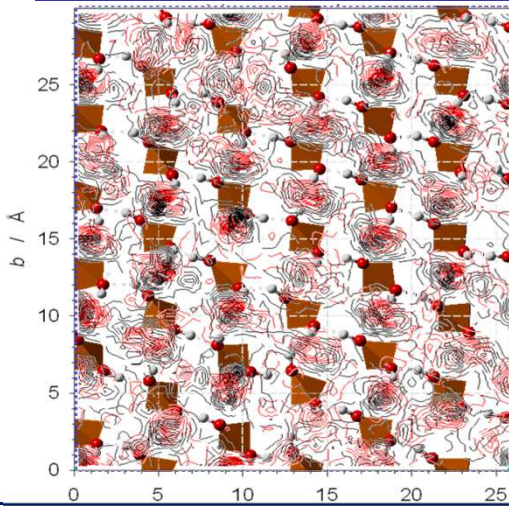
All atoms below and above the surface are removed from view for clarity



- ~50% of the surface OH groups are oriented parallel to the surface, form H-bonds to other surface OHs, and accept H-bonds from interfacial H_2O molecules.
- The other ~50% of the surface OH groups are oriented perpendicular to the surface and donate H-bonds to interfacial H_2O .

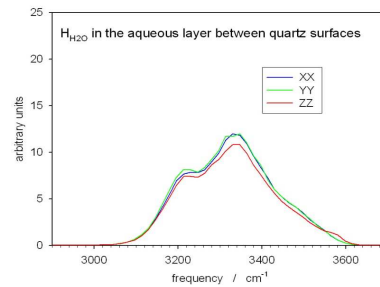
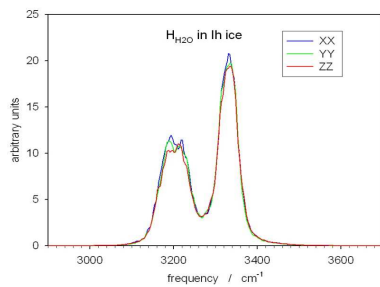
Surface Atomic Density Contours and H-bonding at the Protonated α -Quartz (0001) - Water Interface

H (black) and O (red) contours of H₂O above the fully protonated quartz surface



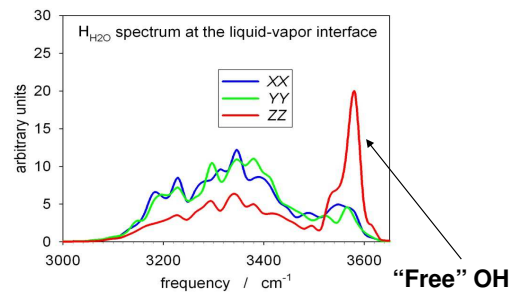
H-bonded "grooves" on the surface viewed from different directions

O-H Stretching Power Spectra of H₂O

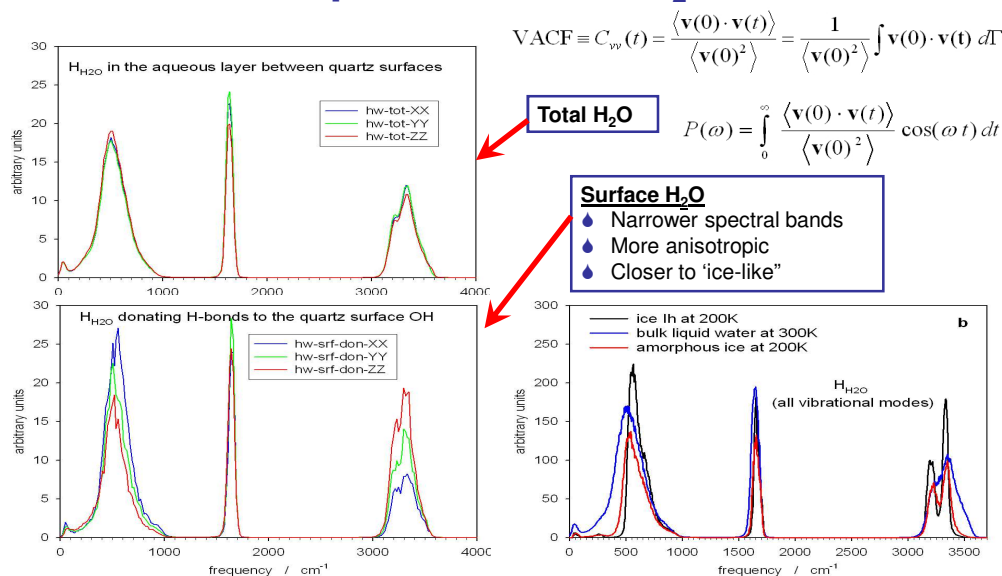


$$\text{VACF} \equiv C_{vv}(t) = \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} = \frac{1}{\langle \mathbf{v}(0)^2 \rangle} \int \mathbf{v}(0) \cdot \mathbf{v}(t) d\Gamma$$

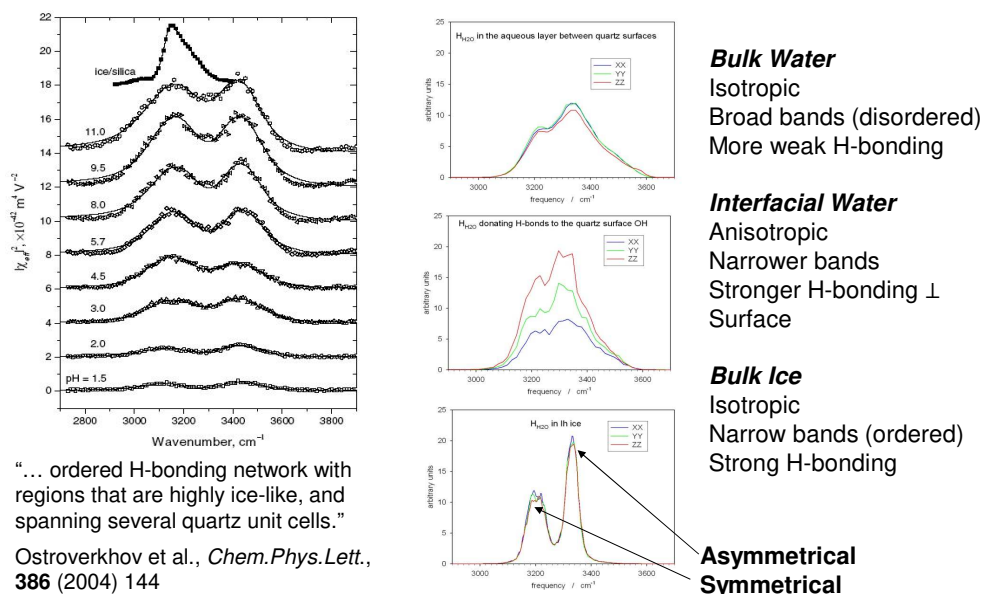
$$P(\omega) = \int_0^\infty \frac{\langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle}{\langle \mathbf{v}(0)^2 \rangle} \cos(\omega t) dt$$

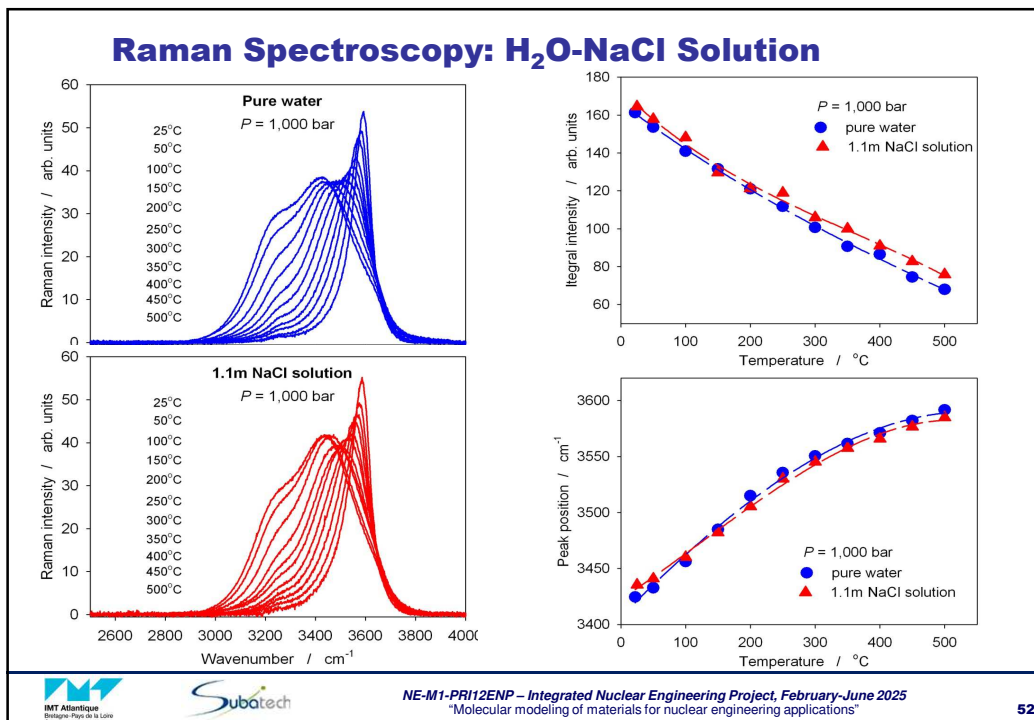
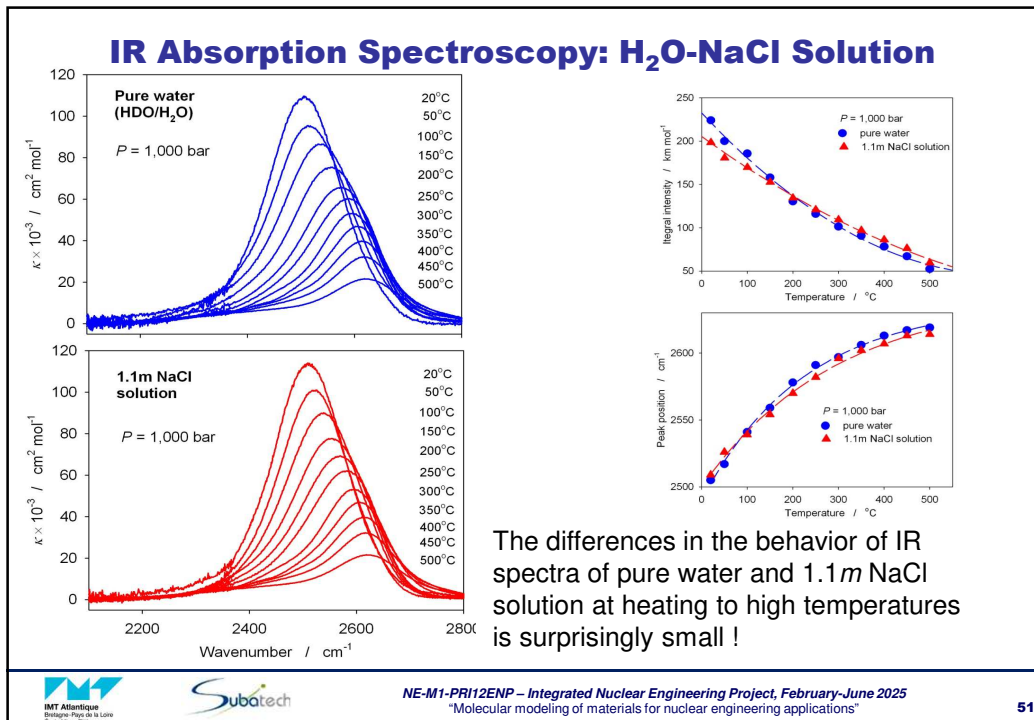


Velocity Autocorrelation Functions and Vibrational Spectra of Surface H₂O

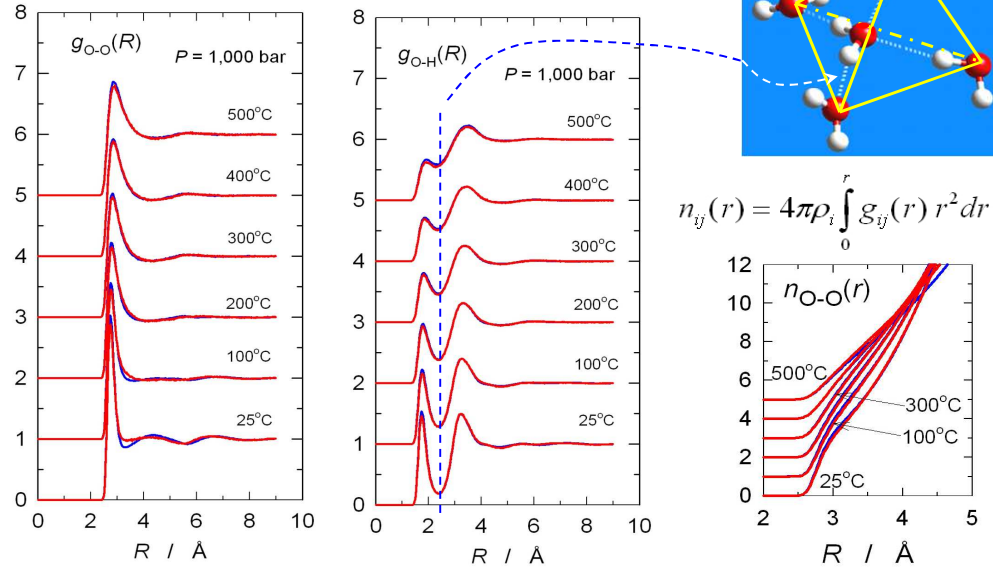


O-H Stretching Power Spectra of Surface H₂O

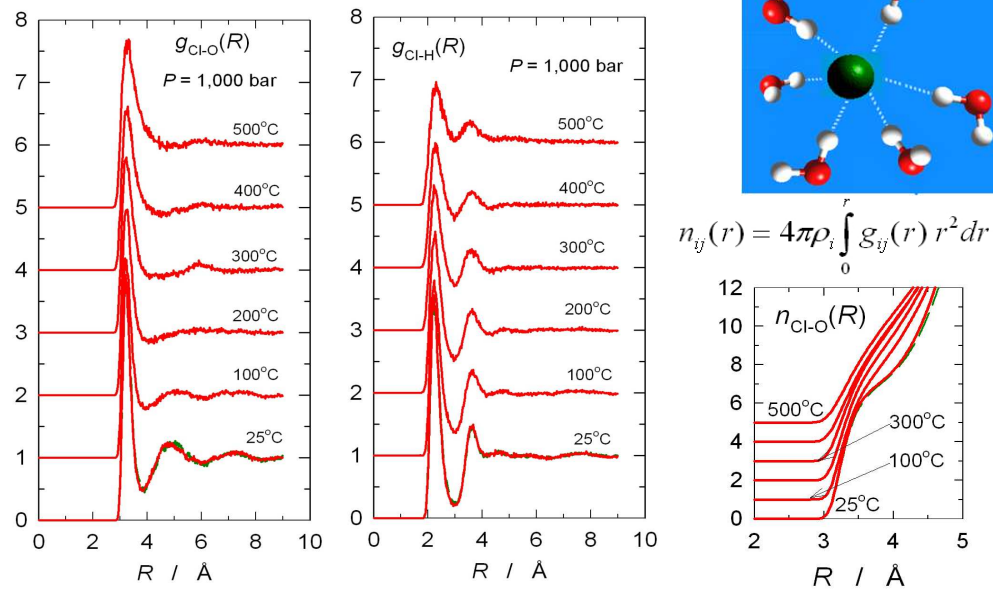




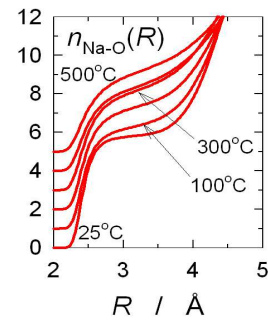
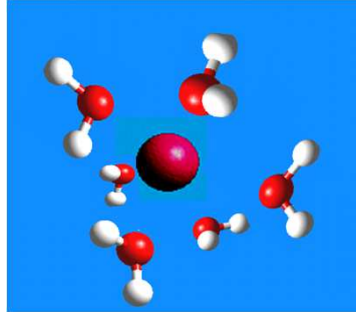
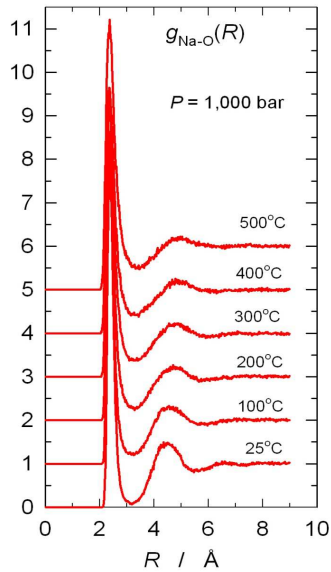
H₂O Molecule Coordination in High Temperature H₂O-NaCl Solutions



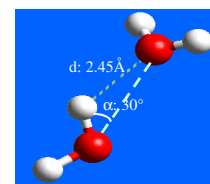
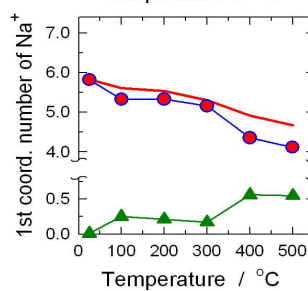
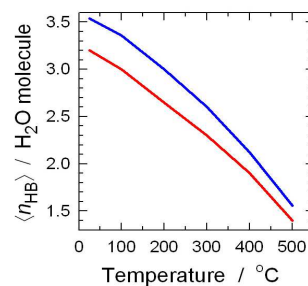
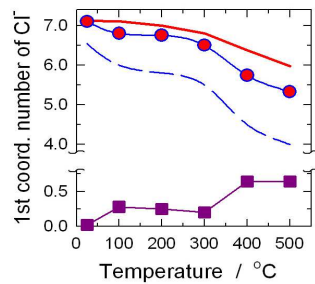
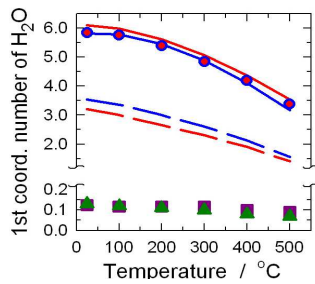
Hydration of Cl⁻ Ion



Hydration of Na⁺ Ion



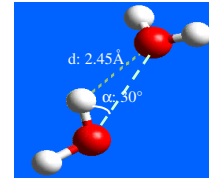
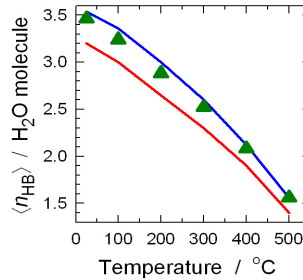
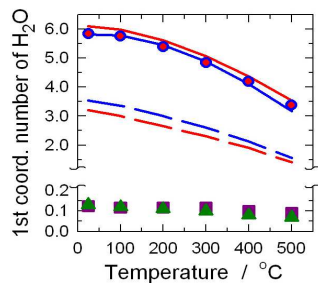
Comparison of Hydrogen Bonding Numbers



H...O distance: $< 2.45 \text{ \AA}$ *
OH...O-O angle: $< 30^\circ$

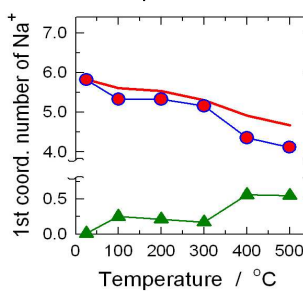
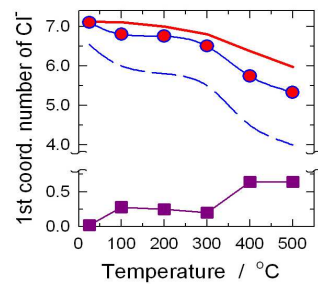
Luzar (2000) *J.Chem.Phys.*,
113, 10663-10675

Comparison of Hydrogen Bonding Numbers

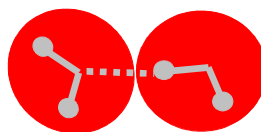
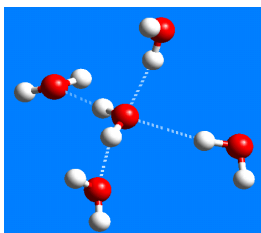


H...O distance: $< 2.45 \text{ \AA}$ *
OH...O angle: $< 30^\circ$

Luzar (2000) *J.Chem.Phys.*,
113, 10663-10675



Comparison of H-Bonding Strength



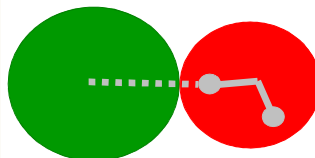
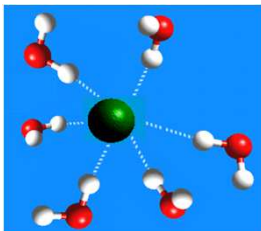
$$q_O = -0.82e$$

$$q_H = +0.41e$$

$$\sigma_{H_2O} \sim 1.6 \text{ \AA}$$

$$R_{O...H}^{\max} \sim 1.82 \text{ \AA}$$

$$F_{HB} \sim q_O q_H / R_{O...H}^2 = 0.10$$



$$q_{Cl} = -1.0e$$

$$q_H = +0.41e$$

$$\sigma_{Cl} \sim 1.95 \text{ \AA}$$

$$R_{Cl...H}^{\max} \sim 2.23 \text{ \AA}$$

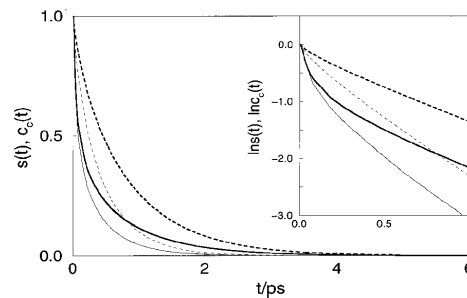
$$F_{HB} \sim q_{Cl} q_H / R_{Cl...H}^2 = 0.09$$

H-bond Dynamics in Water

$$C_{HB}(t) = \frac{\sum_{\langle i,j \rangle} s_{ij}(t_0) s_{ij}(t_0 + t)}{\sum_{\langle i,j \rangle} s_{ij}(t_0)}$$

Two definitions possible:

- 1) Autocorrelations for molecular pairs bonded *continuously*, i.e., *without interruptions* over the entire interval from 0 to t (continuous HB correlation function).
- 2) Autocorrelations for molecular pairs *irrespective of intervening interruptions*, i.e., of possible prior H-bond breaking and reforming events (intermittent HB correlation function).



Exponential fit to estimate the H-bond relaxation time, τ :

$$C_{HB,c}(t) = \exp(-t/\tau_{HB})$$

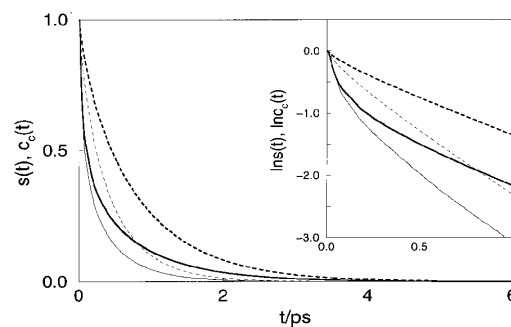
A.Luzar (2000) Resolving the hydrogen bond dynamics conundrum. *J.Chem.Phys.*, **113**, 10663-10675.

H-bond Dynamics in Water

$$C_{HB}(t) = \frac{\sum_{\langle i,j \rangle} s_{ij}(t_0) s_{ij}(t_0 + t)}{\sum_{\langle i,j \rangle} s_{ij}(t_0)}$$

Exponential fit to estimate the H-bond relaxation time, τ .

$$C_{HB,c}(t) = \exp(-t/\tau_{HB})$$



Survival probabilities for a newly generated bond, $s(t)$ (solid lines) and for an average bond, $C_{HB,c}(t)$ (dashed lines), for stricter HB definition (thin lines) and for less strict HB definition (thick lines).

Inset represents the short time behavior of all functions on a semi-log plot.

A.Luzar (2000) Resolving the hydrogen bond dynamics conundrum. *J.Chem.Phys.*, **113**, 10663-10675.

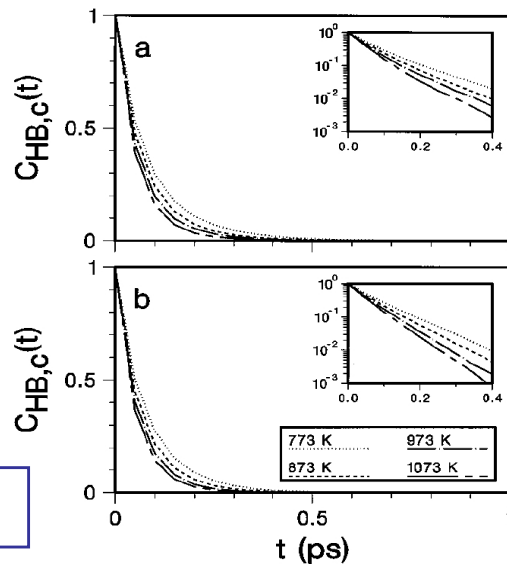
H-bond Dynamics in Water at High Temperature

$$C_{HB}(t) = \frac{\sum_{\langle i,j \rangle} s_{ij}(t_0)s_{ij}(t_0 + t)}{\sum_{\langle i,j \rangle} s_{ij}(t_0)}$$

Exponential fit to estimate the H-bond relaxation time, τ :

$$C_{HB,c}(t) = \exp(-t/\tau_{HB})$$

T.Mizan et al. (1996) Temperature dependence of hydrogen bonding in supercritical water. *J.Phys. Chem.*, **100**, 403-408.

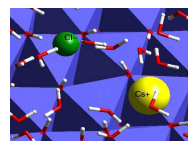
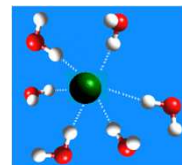
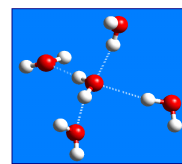


Hydrogen Bonding in Aqueous Systems and the Characteristic Scales Molecular Processes

- ♦ Characteristic H-bond lifetime (300K) ~1-2ps ~3Å
 - “ - “ - (600K) ~0.2ps
 - “ - “ - (200K) ~200ps
- ♦ O-H vibrations; individual acts of H-transfer among water molecules ~0.2ps ~1Å
- ♦ Local H-bonding rearrangement (300K) ~10-20ps ~10Å
- ♦ Lifetime in ionic hydration shell (300K)

K ⁺ , Cl ⁻	~5ps	~10Å
Na ⁺	~10ps	
Li ⁺ , F ⁻	~30-50ps	
Ca ²⁺ , Mg ²⁺	~50-100ps	
- ♦ H₂O, Cl⁻, K⁺ surface site residence times

neutral surface	~ 20 ps
charged surface	> 100 ps



Additional Reading

- #1** Finney JL (2004) Water? What's so special about it?
Phil. Trans. R. Soc. Lond. B **359**, 1145–1165
- #2** Guillot B (2002) What we have learnt during three decades of computer simulations on water. *Journal of Molecular Liquids* **101**, 219-260.
- #3** Kalinichev AG (2001) Molecular simulations of liquid and supercritical water. *Rev Mineral Geochem* **42**, 83–129.

Questions for the final paper / report on one of the 21 topics, e.g., 1 – clays; 2 – cement; 3 – TiO₂ surfaces; 4 – corrosion; 5 – organics, etc. (Please use only as a guidance)

- ◆ What molecular modeling method was used and why?
- ◆ Was it a fully atomistic simulations, or some simplified models were used?
- ◆ What other approximations were used in the modeling?
- ◆ What was the number of particles in the simulations? Was it big enough for the specific problem? Was it small enough to make the simulations computationally efficient?
- ◆ How long-range electrostatic interactions were handled in the simulations? Was it important for the given problem?
- ◆ What kind of boundary conditions were applied to the simulation box? Why?
- ◆ What properties of the system were calculated from the molecular simulation?
- ◆ Make a qualitative assessment of the accuracy for the calculated properties given the number of atoms in the simulated system and the duration of the simulation.
- ◆ What other properties would you additionally calculate from the same simulations for the same system?
- ◆ Formulate 2 or 3 strong points of the given molecular simulation paper and 2 or 3 weak points of the paper.