

Statistical mechanics of hydrogen bond networks

Thomas Krausche and Walter Nadler

Institut für Theoretische Chemie, Universität Tübingen, Auf der Morgenstelle 8, W-7400 Tübingen, Federal Republic of Germany

Received September 2, 1991

The static and dynamic properties of several hydrogen bond network models, based on the *square ice* model of Lieb [Phys. Rev. **162**, 162 (1967)] are studied. The two-dimensional *square water* (SW) model and the three-dimensional *brick water* (BW) model were analyzed by means of Monte Carlo simulations. A simplified version of SW (*simplified square water*, SSW) can be solved exactly. All models yield similar thermodynamic results which can be derived – alternatively – from an independent bond approach due to Angell [J. Chem. Phys. **75**, 3698 (1971)]. We suggest the existence of a universality class of hydrogen bond networks that can be described by this theory, and which may include the liquid state of water. The mean lifetime of a hydrogen bond exhibits an Arrhenius temperature dependence. Comparison with experimental data on water provides an absolute time scale for the Monte Carlo simulations. The possible use of these models in simulations of protein-solvent systems is discussed.

I. Introduction

Water is a substance that exhibits many unusual properties [1, 2]: (*i*) high dielectricity constant, (*ii*) negative volume of melting, (*iii*) density maximum at 4 °C, (*iv*) isothermal compressibility minimum at 46 °C, (*v*) high mobility of protons even in the liquid state of water, (*vi*) high melting and boiling points, (*vii*) numerous ice polymorphs, etc. In order to describe some of these anomalous properties (*ii–vi*), the concept of hydrogen bonds was introduced by Bernal and Fowler [3] and subsequent authors (e.g. Eisenberg and Kauzmann [1]). Over the last few years it has become apparent that the structure of liquid water can be described as a network of hydrogen bonds [4, 5, 6]. Those hydrogen bonds open and close randomly due to thermal fluctuations. Experimental results [7], MD-simulations [8], and percolation models [5] suggest the existence of a – although dynamically varying – percolating cluster of hydrogen bonded water molecules over the whole temperature range of liquid water.

An important aspect of liquid water is its role as a universal solvent in the biosphere on earth. In order to study the structure and properties of biological macromolecules it is necessary to consider their interactions with water. Hydrogen bonds are involved in the structure formation of DNA, RNA and of proteins [9, 10]. Those hydrogen bonds may be within the polymer chain itself, stabilizing its secondary and tertiary structure, as well as between the polymer and the surrounding water. Particularly the latter, the intermolecular hydrogen bonds, are neglected – for the sake of simplicity – in most models of structure formation in biological macromolecules. Nevertheless they give an important contribution to the structure as well as to the function of biomolecules [11].

Currently, the state of the art technique in studying such complex systems as macromolecules in solutions is molecular dynamics (MD) simulations [12]. The particles in MD-simulations interact purely by classical forces, quantum mechanical effects being neglected [13]. Still, due to the huge number of particles involved and the remaining complexity of the force field, the available computing power is often not sufficient to simulate such systems over the necessary time scales. Although MD-simulations of water-protein interactions including a few water molecules surrounding the protein were carried out [14, 15, 16], the time scales of the resulting trajectories are much shorter (about 100 ps), than those of interesting processes in proteins [17]. For example, enzymatic processes in proteins take place mostly on the nanosecond time scale, while protein folding processes last for seconds to minutes [18].

The motivation for the present work is to introduce simple models of a water-like liquid which may be able to describe important aspects of water-protein interactions and – ultimately – protein folding in an aqueous environment. In our approach this is done by using simple two- and three-dimensional lattice models of hydrogen bond networks that may be able to capture important properties of the liquid state of water. To incorporate water-protein interactions via intermolecular hydrogen bonds is straightforward in these models. We note that

those models can be simulated already on a personal computer. Therefore, it should be easily possible to extend the simulations to longer times or to simulate larger models.

In this paper we will concentrate on the static, i.e. thermodynamic, and dynamic properties of these hydrogen bond network models. Solute-water and protein-water interactions in those models will be the subject of subsequent papers [19, 20].

II. Square water

II.a. The model

The two-dimensional *square water* (SW) model is an extension of the *square ice* model by Lieb [21] to non-zero temperatures. Water molecules are placed on a square lattice. By projecting the almost tetrahedral geometry of a water molecule (see Fig. 1) into a plane, while retaining the local connectivity of a diamond lattice [21], one arrives at the six possible conformations shown in Fig. 2. A hydrogen bond can form between neighbouring water molecules only if the O—H bond of one molecule faces the oxygen atom of the other, see also Fig. 2. The restriction of the possible orientations of water molecules to those conformations is motivated by the strongly directional nature of hydrogen bonds [22]. We denote the

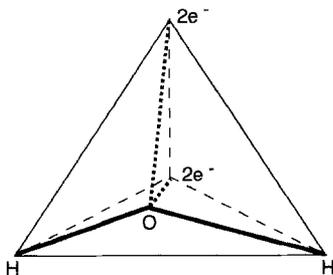


Fig. 1. Tetrahedral geometry of a water molecule

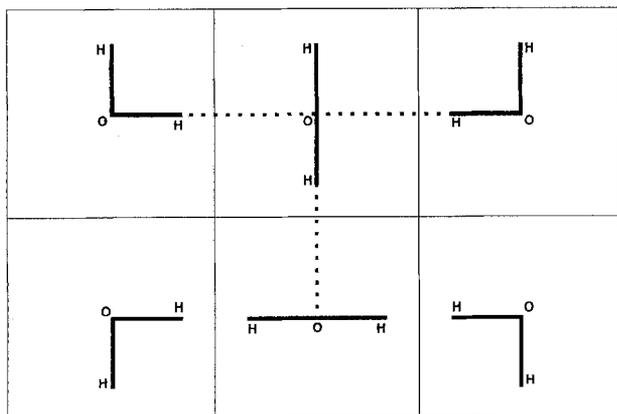


Fig. 2. Allowed conformations of water molecules on the square lattice in the SW model; hydrogen bonds are indicated as dotted lines

energy of a hydrogen bond by $-\varepsilon$. In the square ice model the problem was to determine the number of global configurations where *all* hydrogen bonds are saturated [21]. Here, each molecule may rotate due to thermal fluctuations (see also Sect. II.d) and, thereby, form or break hydrogen bonds. Translational and vibrational degrees of freedom are disregarded, for simplicity.

The formalization of this model is straightforward. The vector $\mathbf{v} = (j, k)$, $j, k = 1 \dots L$, denotes the $N = L^2$ sites of a square lattice of length L , and we will assume periodic boundary conditions ($L + 1 \equiv 1$). The possible conformations of water molecules at each lattice site \mathbf{v} can be described by orientation variables $s_i(\mathbf{v})$, $i = \pm x, \pm y$, which form an orientation vector $\mathbf{s}(\mathbf{v})$. The values of $s_i(\mathbf{v})$ are chosen to be one, if an O—H bond of the water molecule points in direction i , and zero otherwise. In order to limit the 16 possible conformations of $\mathbf{s}(\mathbf{v})$ to those of Fig. 2, the condition

$$\sum_{i=\pm x, \pm y} s_i(\mathbf{v}) = 2 \quad (1)$$

must be fulfilled at each lattice site \mathbf{v} . Using the unit vectors $\mathbf{e}_x = (1, 0)$ and $\mathbf{e}_y = (0, 1)$ we can construct bond variables

$$b_x(\mathbf{v}) = s_x(\mathbf{v}) + s_{-x}(\mathbf{v} + \mathbf{e}_x) - 2s_x(\mathbf{v})s_{-x}(\mathbf{v} + \mathbf{e}_x), \quad (2)$$

similarly for b_y . These bond variables have the values one if there exists a hydrogen bond between \mathbf{v} and $\mathbf{v} + \mathbf{e}_x$ (or between \mathbf{v} and $\mathbf{v} + \mathbf{e}_y$, in the case of b_y), and are zero otherwise. The Hamiltonian is then simply the sum of all possible hydrogen bonds, multiplied by the hydrogen bond energy $-\varepsilon$,

$$H = -\varepsilon \sum_{i=1}^N [b_x(\mathbf{v}_i) + b_y(\mathbf{v}_i)], \quad (3)$$

where the sum is over all $N = L^2$ lattice sites. The partition function for SW can now be written as

$$Z_{\text{SW}} = \sum_{s_x(\mathbf{v}_1)=0,1} \cdots \sum_{s_y(\mathbf{v}_1)=0,1} \cdots \sum_{s_x(\mathbf{v}_N)=0,1} \cdots \sum_{s_y(\mathbf{v}_N)=0,1} \prod_{j=1}^N \delta \left(2, \sum_{i=\pm x, \pm y} s_i(\mathbf{v}_j) \right) \exp(-\beta H). \quad (4)$$

β is the inverse temperature, $\beta = 1/k_B T$, where k_B is Boltzmann's constant, and T is the absolute temperature. δ denotes the Kronecker symbol, with $\delta(i, j) = 1$ if $i = j$, and zero otherwise, and arises from the limitations in the number of possible conformations of the water molecules, see Eq. (1).

II.b. Simplified square water

By omitting the stretched conformations in Fig. 2 we arrive at the *simplified square water* (SSW) model. As a consequence, the orientation variables s_i obey the relations $s_x = 1 - s_{-x}$, similarly for s_y . The condition Eq. (1)

is then automatically fulfilled. It is sufficient to use only the two components $s_x(\mathbf{v})$ and $s_y(\mathbf{v})$ of the orientation vector $\mathbf{s}(\mathbf{v})$. For the evaluation of the partition function it is useful to transform these orientation variables by

$$\sigma_x = 2s_x - 1, \quad \sigma_x \in \{-1, 1\}, \tag{5}$$

similarly for s_y . The bond variables are then given by

$$b_x(\mathbf{v}) = \frac{1}{2} [\sigma_x(\mathbf{v}) \sigma_x(\mathbf{v} + \mathbf{e}_x) + 1], \tag{6}$$

and a similar expression for b_y . The Hamiltonian H , Eq. (3), may be separated into its x - and y -contributions:

$$H = \sum_{i=1}^N b_x(\mathbf{v}_i) + \sum_{i=1}^N b_y(\mathbf{v}_i) \equiv H_x + H_y. \tag{7}$$

Both components, H_x and H_y , can be divided further into the contributions from the rows and columns of the square lattice:

$$\begin{aligned} H_x &= \sum_{i \in \text{row } 1} b_x(\mathbf{v}_i) \\ &\quad + \sum_{i \in \text{row } 2} b_x(\mathbf{v}_i) + \dots + \sum_{i \in \text{row } L} b_x(\mathbf{v}_i) \\ &\equiv H_x^{(1)} + H_x^{(2)} + \dots + H_x^{(L)}. \end{aligned} \tag{8}$$

Replacing the ‘‘rows’’ by ‘‘columns’’ in (8) gives a similar expression for H_y . Utilizing (7) and the fact that the Kronecker delta in (4) is unity for all conformations of σ_x and σ_y , the partition function of this model may then be written as a product of the x - and y -components:

$$\begin{aligned} Z_{\text{SSW}} &= \left(\sum_{\sigma_x(\mathbf{v}_1) = \pm 1} \dots \sum_{\sigma_x(\mathbf{v}_N) = \pm 1} \exp(-\beta H_x) \right) \\ &\quad \times \left(\sum_{\sigma_y(\mathbf{v}_1) = \pm 1} \dots \sum_{\sigma_y(\mathbf{v}_N) = \pm 1} \exp(-\beta H_y) \right) \\ &\equiv Z_{\text{SSW}}^{(x)} Z_{\text{SSW}}^{(y)}. \end{aligned} \tag{9}$$

Using Eq. (8) it is possible to factorize the x -component further into products of contributions from the rows of the square lattice:

$$\begin{aligned} Z_{\text{SSW}}^{(x)} &= \left(\sum_{\sigma_x(\mathbf{v}_1) = \pm 1} \dots \sum_{\sigma_x(\mathbf{v}_L) = \pm 1} \exp(-\beta H_x^{(1)}) \right) \times \dots \\ &\quad \times \left(\sum_{\sigma_x(\mathbf{v}_{(L-1)L}) = \pm 1} \dots \sum_{\sigma_x(\mathbf{v}_{L^2}) = \pm 1} \exp(-\beta H_x^{(L)}) \right). \end{aligned} \tag{10}$$

The y -component can be factorized similarly into contributions from the columns. It is easy to show that the contributions from each row and column are equal. Therefore, Eq. (9) can be simplified to

$$Z_{\text{SSW}} = Z_1^{2L}, \tag{11}$$

where Z_1 is the partition function of a single row or column:

$$\begin{aligned} Z_1 &= \exp(\beta L \varepsilon / 2) \sum_{\sigma_1 = \pm 1} \dots \\ &\quad \sum_{\sigma_L = \pm 1} \exp \left((\beta \varepsilon / 2) \sum_{n=1}^L \sigma_n \sigma_{n+1} \right). \end{aligned} \tag{12}$$

This is equivalent to the partition function of the one-dimensional Ising model [23], multiplied by the factor $\exp(\beta L \varepsilon / 2)$. Using the well known result for the partition function of the one-dimensional Ising model [24], we arrive at the result

$$Z_{\text{SSW}} = [(1 + \exp(\beta \varepsilon))^L (1 + [\tanh(\beta \varepsilon / 2)]^L)]^{2L}. \tag{13}$$

In the thermodynamic limit ($L \rightarrow \infty$), at non-zero temperatures, Eq. (13) becomes

$$\lim_{L \rightarrow \infty} \frac{1}{N} \ln Z_{\text{SSW}} = 2 \ln(1 + \exp(\beta \varepsilon)). \tag{14}$$

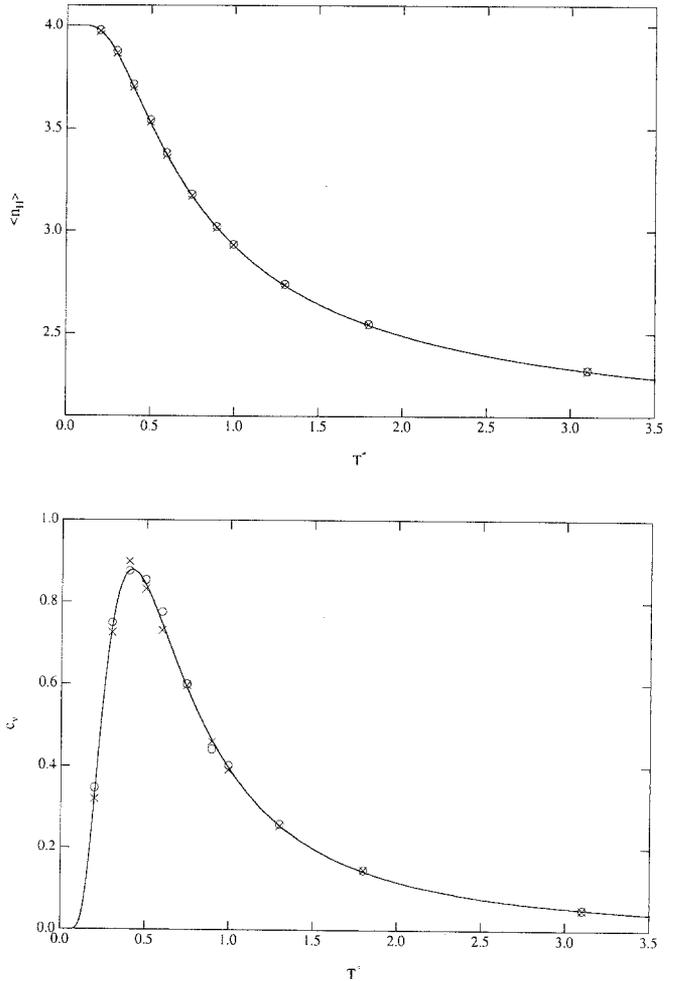


Fig. 3. **a** Average number of hydrogen bonds per molecule, $\langle n_H \rangle$, and **b** specific heat per molecule, c_p , vs reduced temperature for the models discussed in the text; (straight line) exact results from SSW, Eqs. (15) and (17), respectively; (o) results from MC simulations of SW on a 50×50 lattice with periodic boundary conditions; (x) results from MC simulations of BW on a $12 \times 12 \times 12$ lattice with periodic boundary conditions; the error bars for the MC results are in **a** less than and in **b** about the size of the symbols

The thermodynamic observables of interest, e.g., the average number of hydrogen bonds a water molecule participates in, $\langle n_H \rangle$, can be deduced easily from the above result:

$$\langle n_H \rangle = \frac{2}{N\epsilon} \frac{d}{d\beta} \ln Z_{\text{SSW}} = \frac{4 \exp(\beta\epsilon)}{1 + \exp(\beta\epsilon)}. \quad (15)$$

The hydrogen bond fluctuations, $\langle \delta n_H^2 \rangle = \langle n_H^2 \rangle - \langle n_H \rangle^2$, are given by

$$\langle \delta n_H^2 \rangle = \frac{4}{N\epsilon^2} \frac{d^2}{d\beta^2} \ln Z_{\text{SSW}} = \frac{8 \exp(\beta\epsilon)}{(1 + \exp(\beta\epsilon))^2}. \quad (16)$$

The specific heat per molecule, c_v , is related to the hydrogen bond fluctuations by

$$c_v/k_B = \frac{(\beta\epsilon)^2}{4} \langle \delta n_H^2 \rangle = \frac{2(\beta\epsilon)^2 \exp(\beta\epsilon)}{(1 + \exp(\beta\epsilon))^2}. \quad (17)$$

The dependence of $\langle n_H \rangle$ and of c_v on the reduced temperature $T^* = 1/\beta\epsilon$ is shown in Fig. 3. The number of hydrogen bonds per molecule ranges from $\langle n_H \rangle = 4$ at $T^* = 0$ to $\langle n_H \rangle = 2$ for $T^* \rightarrow \infty$.

II.c. Upper and lower bounds

Because of the complication due to the Kronecker delta in (4), it was not possible to find an analytical solution for the partition function of the SW model. However analytical upper and lower bounds for Z_{SW} can be obtained.

By dropping the Kronecker delta in (4), i.e. allowing more conformations of the orientation vector s , one obtains an *upper* bound to the partition function of SW. We denote this upper bound by Z_4 . Z_4 allows, apart from the six water conformations of Fig. 2, also various orientations of molecules which differ from water. These molecules are of the form O, OH, OH₃, and OH₄. Z_4 is, therefore, the partition function of a hydrogen bond network *averaged* over all possible distributions of these partly hypothetical molecules. Z_4 can be solved in the same way as Z_{SSW} . The x - and y -components as well as the rows and columns of Z_4 factorize, giving rise to an effectively one-dimensional partition function which can be evaluated by a transfer matrix approach [24]. The thermodynamic limit result is

$$\lim_{N \rightarrow \infty} \frac{1}{N} \ln Z_4 = 2 \ln(1 + \exp(\beta\epsilon)) + 2 \ln 2. \quad (18)$$

We note that Z_{SSW} , due to the limitations in the number of conformations, gives a *lower* bound to Z_{SW} . Therefore the relationship

$$Z_{\text{SSW}} < Z_{\text{SW}} < Z_4 \quad (19)$$

holds. Interestingly, apart from a multiplicative constant, the functional dependence of Z_4 and of Z_{SSW} on the temperature is the same.

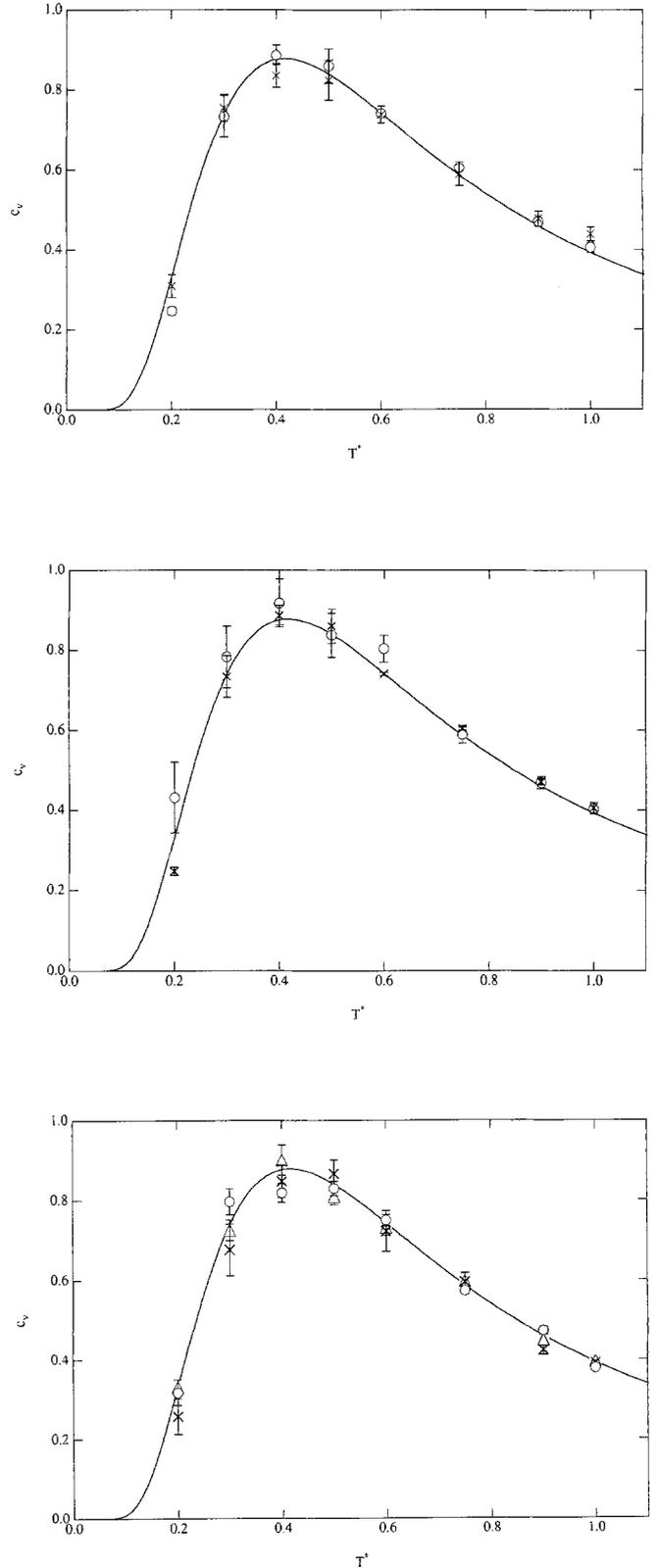


Fig. 4. **a** Error bars in SW simulations: (○) results from MC-simulations of SW on a 30×30 lattice; (×) results from MC-simulations of SW on a 50×50 lattice; **b** comparison of MC-simulations of SW: (○) using the random number generator ran2; (×) using the random number generator ran3, both from Ref. 26; **c** error bars in BW simulations: (○) results from MC-simulations of BW on a $8 \times 8 \times 8$ lattice; (×) results from MC-simulations of BW on a $12 \times 12 \times 12$ lattice; (△) results from MC-simulations of BW on a $20 \times 20 \times 20$ lattice

II.d. Monte Carlo simulations

For the evaluation of the thermodynamic properties of the SW model Monte Carlo (MC) simulations were carried out using a Metropolis algorithm [25]. During an elementary step a water molecule may rotate by flipping one of its OH-bonds into one of the unoccupied directions. Thereby, an angular conformation may either rotate or switch to a stretched conformation, while a stretched conformation may switch back to an angular form. An MC-step was considered to be an update of the whole lattice. The number of hydrogen bonds was recorded after each MC-step. Periodic boundary conditions were used to eliminate surface effects. All simulations reported in this paper were performed using the portable random number generator ran3 from [26].

Several MC-simulations of various lengths were performed with lattices of different sizes. A typical simulation (square lattice, 30×30 molecules, 10^4 MC-steps) takes about 1.5 h CPU-time on an Apple Macintosh SE/30 personal computer. We tested the convergence of the obtained data with longer simulations and larger systems and these results are reported in this paper. One such simulation (square lattice, 50×50 molecules, 7×10^4 MC-steps) takes about 14 h CPU-time on a MicroVAX 3. The mean number of hydrogen bonds per molecule, $\langle n_H \rangle$, and the heat capacity per molecule, c_v , were calculated from the simulation data [27], discarding the first 10^4 MC-steps.

The results of our simulations are shown in Fig. 3. Obviously, there is no significant difference between the results from the Monte Carlo simulations of the SW model and the exact results for the SSW model. In view of the differences between the two models (more allowed conformations of water molecules in SW than in SSW) this is quite surprising. For a more detailed discussion of this result see Sect. IV.

The simulations exhibited a very good convergence, which is confirmed by the small errors for $\langle n_H \rangle$ and c_v . Their relative magnitude is $\pm 0.01\%$ for $\langle n_H \rangle$ and $\pm 1.0\%$ for c_v . Due to the rapid convergence of the data it is sufficient to simulate smaller lattices over a shorter time (e.g. 30×30 molecules, 2×10^4 MC-steps), see Fig. 4a. Therefore, the same results can be obtained already by using a PC instead of minicomputers or mainframes.

We note that it is crucial to use a good random number generator in MC-simulations. The influence of two different random number generators (function ran2 and ran3 from [26]) on the errors of c_v calculated from the simulation data is shown in Fig. 4b.

III. Brick water

A straightforward extension of SW to three dimensions is to place the tetrahedral water molecules on a diamond lattice, as in ice I_h [1]. The coordination number is the same as in SW, namely four. A cubic lattice with only four connections between the lattice sites, instead of six, see Fig. 5, has the same topology as a diamond lattice and is a description of a tetrahedral lattice convenient

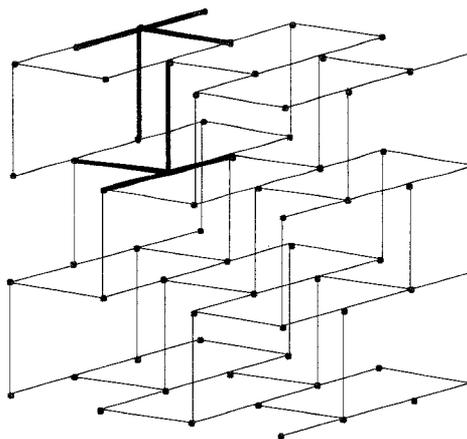


Fig. 5. Bond connectivity in a $4 \times 4 \times 4$ BW lattice; the possible orientations of the water molecules are indicated as bold lines at two sites

for storage in computer memory. We termed this model *brick water* (BW) because in this representation the lattice looks like a brick wall.

The conformations of the water molecules as well as the hydrogen bond definition are the same as in the SW model: the allowed conformations have two O-H bonds that point in two of the four possible directions at each lattice site, see Fig. 5. In principle it is possible to formulate the partition function for BW in analogy to the SW model. However, due to the peculiar connectivity in the BW model, Z_{BW} results in a far more complicated expression than Z_{SW} , which we omit here. Similarly to SW, an analytical evaluation was not possible.

The MC simulations of the BW model were carried out in the same way as in the SW case. Simulations of smaller lattices ($8 \times 8 \times 8$ molecules, 10^4 MC-steps) took about 2 h CPU-time on an Apple Macintosh SE/30 personal computer. Again the convergence of these simulations was tested with larger lattices and longer runs ($12 \times 12 \times 12$ water molecules, 7×10^4 MC-steps). The simulations reported here were carried out on a MicroVAX3, taking about 20 h CPU-time. The first 10^4 steps were discarded for equilibration. Again, $\langle n_H \rangle$ and c_v were determined from the simulation data.

The temperature dependence of the average number of hydrogen bonds per molecule $\langle n_H \rangle$ and the heat capacity per molecule c_v is shown in Fig. 3, together with data from SW and exact results from SSW. In spite of the higher dimensionality of the BW model, there is again no significant difference in the temperature dependence of $\langle n_H \rangle$ and c_v between the various models. A possible interpretation of this phenomenon is given in the following section.

The convergence of the simulation data is almost as good as in the SW simulations (error of $\langle n_H \rangle = \pm 0.01\%$, error for $c_v = \pm 1.5\%$), see Fig. 4c. Therefore, it is entirely sufficient to use a PC for simulations of the models described so far.

IV. Universality

The strikingly similar thermodynamic results for the above discussed models, see Sects. II and III, can also be obtained by an *independent bond* description of a hydrogen bond network. We give here a derivation slightly different from Angell's original work [28, 29]. Let us assume at most M hydrogen bonds are possible in this network. For independent bonds, the partition function factorizes into M identical contributions, Z_{sb} , of a single bond, which can only be broken or saturated. The partition function for this independent bond model is, therefore, simply

$$Z_{ib} = Z_{sb}^M = (1 + \exp(\beta\epsilon))^M. \quad (20)$$

One can assume that in systems as dense as ice or liquid water the maximum number of possible hydrogen bonds is $M \approx 2N$, with N being the number of water molecules. Inserting $M = 2N$ in Eq. (20) yields a result identical to the partition function of the SSW model, Eq. (14). Since the thermodynamic properties of SW, BW and SSW (and of Z_4) over the whole temperature range are similar, see Fig. 3, this independent bond description of a hydrogen bond network seems to capture the behavior of a whole class of network models [30]. Therefore we suggest the existence of a – possibly large – universality class of hydrogen bond networks, whose thermodynamic properties are governed by the independent bond approach. We note that also the dynamic behavior of SSW, SW, and BW is very similar, see Sect. VI below, supporting this universality hypothesis.

As a consequence of this universality, the partition functions of the various hydrogen bond network models of water should differ only in a multiplicative constant, giving rise to the same temperature dependence of all its derivatives. Therefore, the partition function of a particular network model should have the asymptotic form

$$\lim_{N \rightarrow \infty} \frac{1}{N} \ln Z = \lim_{N \rightarrow \infty} \frac{1}{N} \ln Z_{ib} + S^0/k_B, \quad (21)$$

in the thermodynamic limit. S^0 is the zero temperature or *residual* entropy [31] per molecule of the model in question. It can be obtained from $S^0/k_B = \lim_{N \rightarrow \infty} \frac{1}{N} \ln Z^{(H)}$, with $Z^{(H)}$ being the number of possibilities to arrange M hydrogen bonds in the network. $Z^{(H)}$ can be calculated from the partition function of the particular model by $Z^{(H)} = \lim_{T^* \rightarrow 0} (Z/\exp(M\beta\epsilon))$.

The residual entropy of the SW model is identical to the entropy of the square ice model [21], $S_{SW}^0/k_B = \frac{3}{2} \ln \frac{4}{3}$. For SSW it is zero, for the upper bound partition function Z_4 it is $S_{Z_4}^0/k_B = 2 \ln 2$.

V. Percolation description

The success of the independent bond approach [28] in describing the thermodynamic behavior of our microscopic hydrogen bond network models provides a justi-

fication for an alternative description of these systems in terms of bond percolation models. The pertinent parameter for a bond percolation description, the probability p_H for finding a hydrogen bond between two adjacent lattice sites, is given by

$$p_H = \frac{\langle n_H \rangle}{4}. \quad (22)$$

If p_H is greater than the percolation threshold p_c , then there exists always a spanning cluster of hydrogen bonded water molecules [32]. The exact value of p_c depends strongly on the actual geometry of the lattice. For example, $p_c = 0.5$ for a square lattice with bond percolation, and $p_c = 0.388$ for a diamond lattice with bond percolation [32]. In our models the probabilities p_H for a hydrogen bond are all well above the percolation threshold p_c of most lattices [32]. Therefore, a spanning cluster exists at all temperatures in SW, SSW, and BW, and no percolation-transition occurs.

The distribution of probabilities $p(i)$ for finding a water molecule with i hydrogen bonds, $i=0, \dots, 4$, in the lattice, can be derived from the probability for a hydrogen bond p_H , Eq. (22). Because all bonds are independent, $p(i)$ is simply a binomial distribution:

$$p(i) = (1 - p_H)^{4-i} p_H^i \binom{4}{i}. \quad (23)$$

Eq. (23) is valid for the SW, SSW, as well as the BW model.

Percolation models of water have already been investigated in more detail [5, 33]. In those models, however, p_H is used as an input parameter, whereas in our approach p_H is related to $\langle n_H \rangle$, see Eq. (22). Therefore, the temperature dependence of p_H and, consequently, of $p(i)$ is known. The binomial distribution (23) was also found in MD-simulations of water [6, 34] and in other water models [35]. The existence of a spanning cluster of hydrogen bonded water molecules over the whole temperature range of liquid water was also found in MD simulations [4, 36].

Such a cluster may be an explanation for the abnormal high mobility of protons in water. The transport of protons can be performed by a flipping of hydrogen bonds, together with the suggested tunneling mechanism for proton transport in liquid water [4, 37]. For the interaction of a hydrophilic solute with water a spanning cluster may have another consequence. In water a much smaller translational diffusion coefficient is observed for hydrophilic solute molecules. The usual explanation for this phenomenon is the increased effective size of the solute molecule due to the hydration shell. If the bulk water is dominated by a spanning cluster of hydrogen bonded water molecules a hydration shell separate from the bulk water may not exist, but the hydrophilic solute molecule is always attached to the spanning cluster via its hydrogen bonds. Therefore, during the motion of a hydrophilic solute molecule in water, this connection to the bulk water has to be broken and formed again continuously. This leads to an effectively increased viscosity of the medium for

that solute molecule. The higher effective viscosity and not an increased effective size of the solute molecule would then be the reason for the lower diffusion coefficient observed.

VI. Dynamics of SW and BW

Counting the number of MC-steps for the existence of each individual hydrogen bond in simulations of SW and BW (SW: 50×50 lattice, 7×10^4 MC-steps, BW: $12 \times 12 \times 12$ lattice, 7×10^4 MC-steps) yields the distribution of lifetimes $P(\tau)$ in each model. The functional form of $P(\tau)$ versus τ is shown in Fig. 6 for both models in a double logarithmic plot. For high temperatures $P(\tau)$ is simply exponential. Non-exponentiality is observed at lower temperatures ($T^* \leq 0.6$), exhibiting an algebraic regime, $P(\tau) \propto \tau^{-\alpha}$, after a short initial transient. Only at very low temperatures ($T^* = 0.2$) a difference in the shape of $P(\tau)$ between SW and BW is recognizable, see Fig. 6.

The exponent α of the algebraic regime was obtained by a fit to $P(\tau) \propto \tau^{-\alpha}$. With increasing temperatures the values of α decrease and the range of the algebraic regime

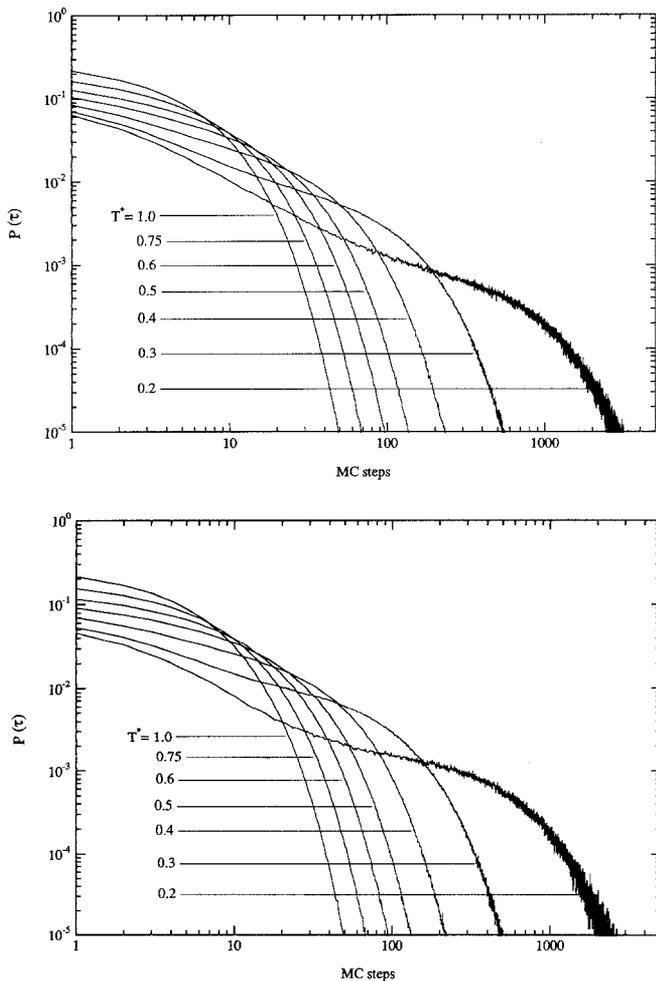


Fig. 6. **a** Distribution of lifetimes in the SW model, $P(\tau)$ vs τ (MC step) for several temperatures T^* . **b** Distribution of lifetimes in the BW model

Table 1. Parameters α , q and τ_c for the hydrogen bond lifetime distribution of SW and BW (see text)

T^*	SW			BW		
	α	q	τ_c	α	q	τ_c
0.2	0.75	0.012	512.6	0.78	0.03	412.9
0.3	0.68	0.14	77.4	0.65	0.17	68.5
0.4	0.63	0.37	28.1	0.63	0.39	26.7
0.5	0.56	0.604	15.3	0.56	0.62	14.8
0.6	0.53	0.87	10.4	0.53	0.89	9.2

Table 2. Activation energy B and pre-exponential factor A of the average hydrogen bond lifetime, $\langle \tau \rangle = A \times \exp(B/T^*)$ for SSW, SW, and BW

	SSW	SW	BW
A	0.4104	0.5768	0.6192
B	1.033	1.059	1.019

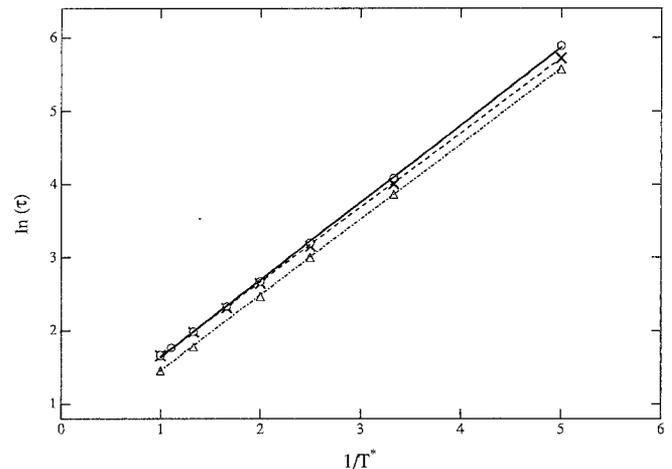


Fig. 7. Arrhenius plot of the temperature dependence of the mean lifetime $\langle \tau \rangle$; (○) results from and (straight line) fit to simulations of the SW model; (×) results from and (dashed) fit to simulations of the BW model; (△) results from and (dashed-dotted) fit to simulations of the SSW model

becomes shorter (only about 10 MC-steps at $T^* = 0.6$), see Fig. 6 and Table 1. The exponential cutoff can be measured by its time constant τ_c , which was determined by a fit to $P(\tau) \approx q \times \exp(-\tau/\tau_c)$. The values of q and τ_c are also shown in Table 1.

The mean lifetime of a hydrogen bond, $\langle \tau \rangle$, was calculated from the distribution of lifetimes by numerical integration. In Fig. 7 the temperature dependence of $\langle \tau \rangle$ is shown for SW, BW, and SSW. The mean lifetimes of SSW were also obtained from MC-simulations (one-dimensional lattice of length 10^3 , 10^4 MC-steps), analogously to SW and BW. All models exhibit an Arrhenius temperature dependence of the mean lifetime of a hydrogen bond. Interestingly, the activation energies and pre-exponential factors of the above models [obtained by a fit to $\langle \tau \rangle = A \times \exp(B/T^*)$] are very similar, see Table 2.

VII. Discussion

VII.a. Comparison with real water

For a comparison with real water the temperature scale of the models has to be adjusted correctly, using the single free parameter of the independent bond theory, the hydrogen bond energy ε . As already recognized by Angell, entropy differences between open and closed hydrogen bonds due to other degrees of freedom, e.g. different vibrational spectra, have to be taken into account [28]. This can be accommodated easily by replacing the hydrogen bond energy ε by an *effective free energy*

$$f = \varepsilon - T\sigma. \quad (24)$$

The average number of hydrogen bonds and the specific heat per molecule then have the form:

$$\langle n_H \rangle = \frac{4 \exp(\beta f)}{1 + \exp(\beta f)}, \quad (25)$$

$$c_v/k_B = \frac{2(\beta\varepsilon)^2 \exp(\beta f)}{(1 + \exp(\beta f))^2}. \quad (26)$$

Since the results for $\langle n_H \rangle$ and c_v of SSW, SW, and BW are equal to the independent bond results the renormalization of the energy, Eq. (24), is valid for those models also. Angell adjusted the values of the parameters ε and σ by comparison of the heat capacity, Eq. (26), with data for the configurational heat capacity of water [1, 28]. He obtained $\varepsilon = 1.3 \times 10^{-20}$ J and $\sigma = 3.3 \times 10^{-23}$ J/K. Compared, e.g., to the hydrogen bond energy in water (9×10^{-21} J $\leq \varepsilon \leq 3 \times 10^{-20}$ J, see Ref.1) the bond energy parameter ε is within the correct range. The entropy term is of the order of the melting entropy of water, $s_m = 3.6 \times 10^{-23}$ J/K. The temperature dependence of $\langle n_H \rangle$ using the above parameters is shown in Fig. 8. We note that, due to the entropy term in (25) the high temperature values of Pc may now fall well below 1/2, depending on the actual values of ε and σ . However, for

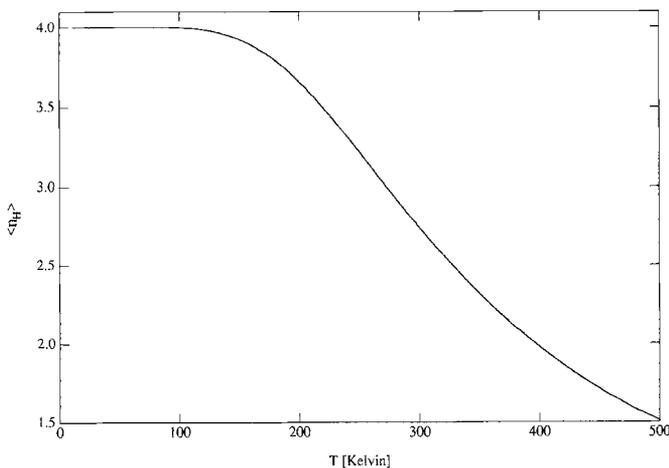


Fig. 8. Average number of hydrogen bonds per molecule, $\langle n_H \rangle$, vs temperature renormalized using (25)

the values of ε and σ listed above, a spanning cluster still exists for most lattices over the whole temperature range of liquid water, i.e. up to about 400 K.

Using those parameters for the energy ε and the entropy σ , we can compare the mean number of hydrogen bonds calculated from (25) with newer experimental results. King and Barletta [38] have measured the average number of hydrogen bonds per molecule $\langle n_H \rangle$ in liquid water at $T=0$ °C to $\langle n_H \rangle_{\text{exp}} = 3.1$, and have extrapolated their data to higher temperatures. In Fig. 9 the independent bond results for $\langle n_H \rangle$ are shown, together with results from MD-simulations of ST2-water [8], results from a lattice gas model of water [39], from a cluster model [40], and from experimental data [38]. Both, MD and independent bond results are compatible with the experimental results from [38], whereas the results of the lattice gas model and the cluster model disagree. The experimental data are exact only at $T=0$ °C, at higher temperatures they give only a lower limit for $\langle n_H \rangle$.

The thermodynamic properties of hydrogen bonds in liquid water are well described by the independent bond results, as shown above. Therefore, the liquid state of water may belong to the same universality class of hydrogen bond networks as Angell's independent bond model and our lattice models of water. This is supported also from a statistical mechanics point of view. For the evaluation of the partition function the liquid state can be viewed simply as a collection of different spatial arrangements of molecules. For each of these configurations the independent bond approach can be employed. In liquid water we can assume that for most of the relevant configurations $M \approx 2N$ holds, the resulting thermodynamic behavior being the same as above. The partition function will simply be renormalized by the appropriate entropy, see Sect. IV.

The time scale of an MC-step is a free parameter in MC-simulations which has to be scaled to experimental results. The average lifetime of a hydrogen bond, $\langle \tau \rangle$, in water was measured by several authors [41, 42, 43]. We use the data of Conde and Teixeira [43], which were obtained from depolarized Rayleigh scattering spectroscopy. They found an Arrhenius temperature dependence for $\langle \tau \rangle$. Renormalizing the time scale of our simulations of SW and BW according to [43], yields an Arrhenius temperature dependence for the time scale of a single MC-step,

$$\tau_{\text{MC}} = \tau_0 \times \exp(\beta \Delta E), \quad (27)$$

in addition to the Arrhenius temperature dependence of the mean lifetime of a hydrogen bond. The values of the activation energies ΔE and pre-exponential factors τ_0 are shown in Table 3 for SW and BW. From those data, a

Table 3. Parameters for the temperature dependence of an MC-step in SW and BW, see Eq. (27)

	SW	BW
ΔE [J]	4.77×10^{-21}	5.3×10^{-21}
τ_0 [s]	4.04×10^{-14}	3.52×10^{-14}

simulation at room temperature over 7×10^4 MC-steps is equivalent to several nanoseconds.

To the best of our knowledge, there are no experimental data available for the distribution of lifetimes of a hydrogen bond. Therefore, it was not possible to compare those results with experimental data.

VII.b. Comparison with MD-Results

A general difficulty with MD-simulations of water is the lack of an explicit representation of a hydrogen bond contribution in the pair potentials used to describe the interactions of water molecules. Therefore, the simulation results have to be interpreted using a somewhat artificial hydrogen bond definition. We compared our results with data from extensive MD-simulations of Stillinger et al. [4, 8, 36, 44] who introduced the empirical ST2-water pair potential. In their publications two ST2-water molecules are considered to be hydrogen bonded if the distance between them is below a certain cutoff distance, and if the interaction energy is below a certain cutoff energy, V_{HB} . Both, the cutoff distance and the cutoff energy have to be scaled using experimental results [6, 8].

Geiger et al. [8] have calculated the average number of hydrogen bonds from ST2-simulation data. Their results are shown in Fig. 9 together with results from other water models, the independent bond results, and experimental data from [38]. As can be seen, the MD-results follow closely the behavior of the independent bond results. We note that, due to the choice of the cutoff potential, V_{HB} , for assigning hydrogen bonds, there is a free parameter involved, which allows a shift of the MD-results along the vertical axis, see also Fig. 9. Unfortun-

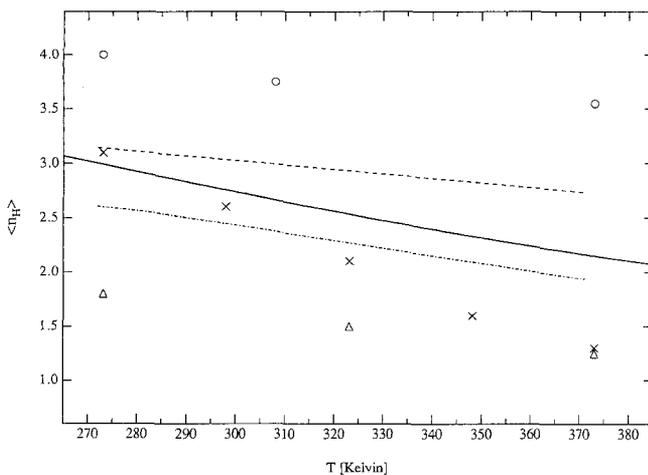


Fig. 9. Average number of hydrogen bonds per molecule, $\langle n_H \rangle$, vs temperature; (straight line) independent bond results with $\varepsilon = 1.3 \times 10^{-20}$ J and $\sigma = 3.3 \times 10^{-23}$ J/K from [28]; (dashed) and (dashed-dotted) results from MD-simulations [8] for two different values of the cutoff energy for a hydrogen bond assignment ($V_{\text{HB}} = 2.1 \times 10^{-20}$ J and $V_{\text{HB}} = 2.5 \times 10^{-20}$ J, respectively), (o) results from a lattice gas model of water [39], (Δ) results from a cluster model of water [40], and (\times) experimental results from liquid water [38]; we note that the experimental results for $T > 0$ °C are extrapolations and give only lower limits to the actual values [38]

nately, no MD-results are available for the heat capacity of a hydrogen bond network. Therefore, it would be interesting to reanalyze MD-simulations of water to obtain the specific heat due to hydrogen bond fluctuations, see Eq. (17), and compare those results with the independent bond prediction for c_v .

The mean lifetime of a hydrogen bond calculated from the distribution of lifetimes in MD-simulations [6, 45] depends also strongly on the definition of a hydrogen bond used in those simulations. Geiger and Stanley [6] used a very general definition of a hydrogen bond (recording *all* hydrogen bonds with a negative interaction energy), therefore yielding values that give a lower bound to the observable lifetimes ($\langle \tau \rangle_{\text{MD}} \leq 0.2$ ps at room temperature, compared with $\langle \tau \rangle_{\text{exp}} = 0.53$ ps at room temperature [43]). Their temperature dependence for $\langle \tau \rangle_{\text{MD}}$ has an Arrhenius form. In a recent work, Stanley et al. [45] used a novel, stricter hydrogen bond definition for their MD-simulations of ST2 particles. Therefore, their mean lifetimes are generally larger (e.g. $\langle \tau \rangle_{\text{MD}} = 2.23$ ps at room temperature) than the experimental values. Also, the temperature dependence of $\langle \tau \rangle$ in the MD-simulations of Stanley et al. [45] differs from the experimental one in that it is not Arrhenius-like. Since the experiments [43] as well as our simulations exhibit an Arrhenius-like temperature dependence of $\langle \tau \rangle$, together with the difficulties in assigning hydrogen bonds in MD-simulations, we feel it is justified to scale the time step of our MC-simulations using the experimental data, as we did above.

At the temperatures of interest ranging from $T = 240$ K (supercooled water) to $T = 373$ K (boiling point of water) – using the above parameters this corresponds to $0.6 < T^* < 6.6$ – the distribution of lifetimes of a hydrogen bond in the SW and BW models is simply exponential. Non-exponentiality is observed only at temperatures lower than $T = 240$ K. The degree of non-exponentiality of the lifetime distribution in MD-simulations depends strongly on the definitions of a hydrogen bond employed. The MD-simulations of Geiger et al. [6] revealed only a weak non-exponentiality in the life-time distribution, whereas Stanley et al. [45] yield a strong non-exponentiality in the lifetime distribution.

We note that also MD-simulations of water hint to a universality in the properties of hydrogen bond networks. Rapaport [46] compared the properties of hydrogen bonded clusters of MD-simulations of the MCY-CI model (using an *ab initio* quantum mechanical pair potential) with results from MD-simulations of ST2-water. He found no significant difference in the properties of hydrogen bonded clusters between the different models.

VII.c. Summary and outlook

The above discussed lattice models of hydrogen bond networks are simple, but reproduce important features of real water. The temperature dependence of the thermodynamic properties like the mean number of hydrogen bonds and the heat capacity are in accord with experimental and MD-results. The success of the independent bond description due to Angell [28] justifies an alternative description of a hydrogen bond network in terms of

percolation models. All of our models predict the existence of a spanning cluster of hydrogen bonds in the temperature range of liquid water, a possible explanation for the high mobility of protons. Furthermore, the temperature dependence of the probability distribution for finding a water molecule with i hydrogen bonds in the lattice is predicted. The Arrhenius temperature dependence of the mean lifetime of a hydrogen bond is in accord with experimental results. The functional form of the distribution of lifetimes, $P(\tau)$, is simply exponential over a broad range of temperatures. The surprising similarities between the various hydrogen bond network models lead us to the hypothesis of the existence of a universality class of hydrogen bond networks that is governed by the independent bond approach, and which may include the liquid state of water.

In our opinion the SW and BW model are a good basis for studying protein-water interactions that result from hydrogen bonding. Particularly protein folding is a problem where this interaction is of utmost importance [47, 48]. The computing power required for the study of those water models is much smaller than, for example, in molecular dynamics approaches. This was one of our goals when developing these models. Therefore, the simulations of longer trajectories (nanoseconds to microseconds, depending on the hardware) which cover a broad range of the protein folding process in a water-like liquid should be possible.

The authors thank Prof. F.F. Seelig and Prof. O.E. Rössler for their support.

References

- Eisenberg, D., Kauzmann, W.: The structure and properties of water. New York: Oxford University 1969
- Franks, F. (ed.): Water: A comprehensive treatise. Vol. I-VI. New York: Plenum Press 1971-1979
- Bernal, J.D., Fowler, R.H.: J. Chem. Phys. **1**, 515 (1933)
- Stillinger, F.H.: Science **209**, 451 (1980)
- Stanley, H.E., Teixeira, J.: J. Chem. Phys. **73**, 3404 (1980)
- Stanley, H.E., Blumberg, R.L., Geiger, A., Mausbach, P., Teixeira, J.: J. Phys. (Paris) **45**, Colloq. C7-3 (1984)
- Andaloro, G., Leone, M., Palma-Vitorelli, M.B.: Nuovo Cimento **2D**, 1239 (1983)
- Geiger, A., Stillinger, F.H., Rahman, A.: J. Chem. Phys. **70**, 4185 (1979)
- Schulz, G.E., Schirmer, R.H.: Principles of protein structure. Berlin, Heidelberg, New York: Springer 1979
- Jeffrey, G.A., Saenger, W.: Hydrogen bonding in biological structures. Berlin, Heidelberg, New York: Springer 1991
- Giersch, L.M., King, J. (eds.): Protein folding - deciphering the second half of the genetic code. Washington D.C.: American Association for the Advancement of Science 1990
- McCammion, J.A., Gelin, B.R., Karplus, M.: Nature **267**, 585 (1977)
- Brooks, B.R., Bruccoleri, R.E., Olafson, B.D., States, D.J., Swaminathan, S., Karplus, M.: J. Comp. Chem. **4**, 187 (1983)
- Ahlström, P., Teleman, O., Jönsson, B., Forsén, S.: J. Am. Chem. Soc. **109**, 1541 (1987)
- Brünger, A., Brooks, C.L., Karplus, M.: Proc. Natl. Acad. Sci. USA **82**, 8458 (1985)
- Brooks, C.L., Karplus, M.: J. Mol. Biol. **208**, 155 (1989)
- Nadler, W., Brünger, A.T., Schulten, K., Karplus, M.: Proc. Natl. Acad. Sci. USA **84**, 7933 (1987)
- McCammion, J.A., Harvey, S.C.: Dynamics of proteins and nucleic acids. Cambridge: Cambridge University Press 1987
- Nadler, W., Krausche, T.: Chem. Phys. Lett. (submitted for publication)
- Krausche, T., Nadler, W.: (in preparation)
- Lieb, E.H.: Phys. Rev. **162**, 162 (1967)
- Popkie, H., Kistenmacher, H., Clementi, E.: J. Chem. Phys. **59**, 325 (1973)
- Ising, E.: Z. Phys. **31**, 253 (1925)
- Reichl, L.E.: A modern course in statistical mechanics. pp. 289-291. Austin: University of Texas Press 1980
- Metropolis, N., Rosenbluth, A.W., Rosenbluth, M.N., Teller, A.H., Teller, E.: J. Chem. Phys. **21**, 1087 (1953)
- Press, W.H., Flannery, B.P., Teukolsky, S.A., Vetterling, W.T.: Numerical recipes. Cambridge, New York: Cambridge University Press 1986
- Gould, H., Tobochnik, J.: Computer simulation methods. Part 2, pp. 537. Reading: Addison Wesley 1988
- Angell, C.A.: J. Phys. Chem. **75**, 3698 (1971)
- Angell calls his approach a *bond lattice* model. However, we believe that the term *independent bond* captures the essence of the model more clearly
- We note that also the one-dimensional Ising model can be considered as an instance of an independent bond model
- Pauling, L.J.: J. Am. Chem. Soc. **57**, 2680 (1935)
- Stauffer, D.: Introduction to percolation theory. London: Taylor & Francis 1985
- Weiss, W.: J. Phys. (Paris) **48**, 877 (1987)
- Blumberg, R.L., Stanley, H.E., Geiger, A., Mausbach, P.: J. Chem. Phys. **80**, 5230 (1984)
- Bertolini, D., Cassettari, M., Ferrario, M., Grigolini, P., Salvetti, G., Tani, A.: J. Chem. Phys. **91**, 1179 (1989)
- Stillinger, F.H., Rahman, A.: J. Chem. Phys. **60**, 1545 (1974)
- Eigen, M., De Maeyer, L.: Proc. R. Soc. A **247**, 505 (1958)
- King, W.T., Barletta, R.E.: J. Chem. Phys. **78**, 1531 (1974)
- Fleming, P.D., Gibbs, J.H.: J. Stat. Phys. **10**, 351 (1974)
- Lentz, B.R., Hagler, A.T., Scheraga, H.A.: J. Phys. Chem. **78**, 1531 (1974)
- Montrose, C.J., Bucaro, J.A., Marshall-Coakley, J., Litovitz, T.A.: J. Chem. Phys. **60**, 5025 (1974)
- Danninger, W., Zundel, G.: J. Chem. Phys. **74**, 2769 (1981)
- Conde, O., Teixeira, J.: J. Phys. (Paris) **44**, 525 (1983)
- Stillinger, F.H., Rahman, A.: J. Chem. Phys. **57**, 1281 (1972)
- Sciortino, F., Poole, P.H., Stanley, H.E., Havlin, S.: Phys. Rev. Lett. **64**, 1686 (1990)
- Rapaport, D.C.: Mol. Phys. **50**, 1151 (1983)
- Dill, K.A.: Biochemistry **29**, 7133 (1990)
- BenNaim, A.: J. Phys. Chem. **95**, 1437 (1991)