

Effect of Molecular Dynamics Water Models on Flux, Diffusivity, and Ion Dynamics for Polyamide Membrane Simulations

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ARTICLE INFO

Keywords:

Molecular dynamics
Water model
SPC/E, TIP3P, TIP4P
Water filtration membrane
Ion dynamics

ABSTRACT

While molecular dynamics (MD) models for reverse osmosis (RO) and nanofiltration (NF) membranes are useful for studying water filtration processes, the specific water model and force-field parameters have a profound impact on key measures such as flux and diffusivity. Moreover, ensemble related parameters such as temperature and how it is controlled via a thermostat also affect simulation results. To quantify these effects, we investigate the performance of three commonly used water models, SPC/E, TIP3P, and TIP4P, in simulating an NF membrane system at varying temperatures and thermostat settings. All three water models successfully capture the Arrhenius relationship between water diffusivity and temperature as well as the linear relationship between water flux through the membrane and water diffusivity in the membrane. However, SPC/E underpredicts, TIP3P overpredicts, and TIP4P most accurately reproduces the water dynamics, especially water self-diffusivity, compared to experiments. We also investigate the effect of the water model on common salt solutions at various concentrations. TIP4P generally outperforms the other two water models when describing ion diffusivities and water solvation shells around ions. These findings indicate that TIP4P is an appropriate water model to use in polyamide membrane MD simulations.

1. Introduction

Molecular dynamics (MD) is emerging as a powerful approach to probe membrane filtration at the Ångström scale, a level that experiments and models cannot resolve [1, 2]. Over the past two decades, a number of MD simulation studies have been performed for polyamide based membranes (Table 1), primarily focusing on reverse osmosis (RO) membranes of trimethylsilyl chloride (TMC) polymerized with m-phenylene diamine (MPD), with a limited number considering nanofiltration (NF) membranes of TMC polymerized with piperazine (PIP). These atomistic scale simulations provide information that is very difficult to obtain experimentally. For example, it is difficult to measure the porosity and density of NF membranes, since their active layers are usually less than 100 nm thick [3]. Yet MD studies of RO and NF membranes can easily provide density and pore size characterizations that can be used to connect transport observations and continuum models to atomic-scale interactions. Trajectories of water molecules or solutes can be tracked as they diffuse through the membrane, and membrane dynamics, including positions of charged functional groups and solutes, can be resolved with sub-nanometer and sub-picosecond resolution.

One of the challenges in studying membrane filtration processes using MD is that the results depend on the force-fields and simulation conditions used in the MD simulations. The force-fields represent both the interactions of interatomically bonded atoms and the non-bonded forces between

atoms, including van der Waals and electrostatic forces. Accurate simulation results depend on the ability of the MD force-fields to correctly represent these Ångström scale forces. A complete set of force-field parameters necessary to simulate molecules includes bond lengths, bond angles, atomic partial charges, and parameters describing Lennard-Jones potentials. In addition, operating conditions like temperature are regulated using “thermostats” to introduce or dissipate energy from a system in MD simulations.

Crucial to studies of membrane filtration is the appropriate MD model to use for the water molecule. Our goal in this paper is to examine how the specific water model that is used affects MD simulation results at different temperatures for a typical polyamide membrane system. Specifically, we consider the effect of different MD water models on the water diffusion, solute diffusion, and water flux in an NF membrane.

Although water is a commonly simulated molecule with a simple atomic structure, accurate force-field parametrization of water is challenging. At least 30 MD water models have been developed over the past 40 years, each with its own characteristics [4]. A variety of water models have been considered for a wide range of applications including SPC [5], SPC/E [6], SPC/Fw [7], TIP3P [8], TIP4P [8, 9] and TIP5P [10]. Here, SPC refers to Simple Point Charge, and TIP refers to Transferable Interaction Potential. The number in any of the abbreviations refers to the number of “sites” in the water model. At a minimum, there are three sites for water, corresponding to two hydrogen atoms and one oxygen atom (for example, TIP3P and SPC models). When there are more than three sites, the additional sites correspond

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Table 1

MD membrane studies performed in the 2000s.

Water Model	Polymer Type	Temperature (K)	Thermostat Setting	Reference
SPC	RO (TMC + MPD)	300	Nosé-Hoover	Xiang <i>et al.</i> [16–18]
SPC	RO (TMC + MPD)	298	Berendsen, Velocity Rescaling ($\tau = 0.1$ ps)	Kolev and Freger [19]
SPC/E	RO (TMC + MPD)	300	Nosé-Hoover	Muscatello <i>et al.</i> [20]
TIP3P	RO (TMC + MPD)	300	Nosé-Hoover	Harder <i>et al.</i> [21]
TIP3P	RO (TMC + MPD)	298	Velocity Rescaling	Kolev and Freger [22]
TIP3P	RO (TMC + MPD)	300	Langevin	Luo <i>et al.</i> [23]
TIP3P	RO (TMC + MPD)	300	Langevin	Shen <i>et al.</i> [24, 25]
TIP3P	RO (TMC + MPD)	300	<i>Not Reported</i>	Zhang <i>et al.</i> [26]
TIP3P	RO (TMC + MPD)	298	Nosé-Hoover	Jahan Sajib <i>et al.</i> [27]
TIP3P	NF (TMC + PIP)	300	Langevin ($\gamma = 1$ ps $^{-1}$)	Liu <i>et al.</i> [28]
TIP3P	RO (TMC + MPD)	300	Velocity Rescaling	Zhang <i>et al.</i> [29]
TIP4P-Ew	RO (TMC + MPD)	300	Nosé-Hoover ($\tau = 1$ ps)	Hughes and Gale [30, 31]
TIP4P/2005	RO (TMC + MPD)	300	Nosé-Hoover	Ding <i>et al.</i> [32–35]
TIP4P/2005	RO (TMC + MPD)	300	<i>Not Reported</i>	Liyanage-Arachchi <i>et al.</i> [36]

60 to dummy atoms, sometimes called a “lone pair,” referring
 61 to a pair of valence electrons in a molecule not shared
 62 with another atom via a covalent bond, that have charge
 63 but no mass. The additional sites are used to improve the
 64 electrostatic charge distribution of the water model to better
 65 reflect the polar nature of a water molecule. Various water
 66 models are used to accurately simulate specific properties
 67 of bulk water, e.g., solid water (ice), surface tension, or
 68 dielectric constants [4]. Similarly, the interactions of the
 69 water molecules with other molecules in the system, for
 70 instance charged solutes or polyamide membrane structures
 71 considered here, need to be taken into account. Of course,
 72 MD simulations are based on the interatomic potentials
 73 between all the atoms that are simulated. As a result, a 4-site
 74 water model has more computational overhead than a 3-site
 75 water model. The desired situation is to use the water model
 76 that most accurately reflects the physical situation that is
 77 being modeled at the lowest computational cost.

78 Previous studies comparing water models have focused
 79 on physical properties in water-only systems. For example,
 80 Mark and Nilsson [11] find significant differences in self-
 81 diffusion and Zielkiewicz [12] notes differences in the en-
 82 ergy and lifetime of hydrogen bonds between water models.
 83 A handful of studies consider the impact of the water model
 84 on water transport in various porous systems. Prasad *et al.*,
 85 [13] find that the water flux in graphene nanopore systems
 86 depends on the water model that is used due to differences
 87 in hydrogen bond dynamics, partial charge, and diffusion.
 88 Likewise, Liu and Patey [14] show that the water flux in
 89 carbon nanotubes varies depending on the different water
 90 model with the origin of the differences due to different
 91 ordering of water molecules as they flow through the nan-
 92 otube. Srivastava *et al.* [15] note that water models behave
 93 differently in the interfacial regions in aqueous lipid bilayer
 94 systems due to differences in diffusivity and hydrogen bond
 95 breaking.

96 As indicated in the first column of Table 1, various water
 97 models have been used in MD simulations of polyamide-
 98 based RO and NF membranes, but we are unaware of any
 99 studies comparing the impact of the water model on the
 100 simulation results. The water models that are used fall into
 101 the categories of SPC (SPC/E), TIP3P, and TIP4P (TIP4P-
 102 Ew and TIP4P/2005). As shown in Fig. 1(a), SPC/E and
 103 TIP3P share the same structure of a 3-atom rigid planar
 104 model. TIP4P, shown in Fig. 1(b), is a 4-site rigid planar
 105 model. In addition to one oxygen atom and two hydrogen
 106 atoms, a mass-less site is added to carry the negative charge
 107 while the oxygen atom stays neutral.



Figure 1: Water model illustrations for (a) SPC/E, TIP3P, and (b) TIP4P, where red beads are oxygen atoms, white beads are hydrogen, and the green bead has zero mass but carries a charge in TIP4P. (Color online.)

108 We also note the thermostats that are used to main-
 109 tain the temperature, either 298 K or 300K, for previous
 110 MD simulations of membranes in Table 1. While temper-
 111 ature has a macroscopic effect on water transport through
 112 a membrane, the temperature on the molecular level is
 113 defined by the average kinetic energy of all the atoms in
 114 the system in the canonical ensemble (NVT, where the
 115 amount, N, volume, V, and temperature, T, are constant).
 116 The temperature is regulated by a thermostat, which allows
 117 energy to enter or dissipate from the system during sim-
 118 ulations by modifying atoms’ velocities. For the simu-
 119 lations listed in Table 1, common thermostat types are Nosé-
 120 Hoover [37–39] (extended system), Berendsen [40] (weak
 121 coupling), Langevin [41] (stochastic), and velocity rescaling
 122 [42] (strong coupling). These thermostats deploy various

algorithms to regulate temperature. For example, extended system thermostats contain an additional degree of freedom associated with the constant temperature, weak coupling methods scale the velocity in the direction of the desired temperature, stochastic methods randomly assign new velocities to certain atoms to reach the target temperature, and strong coupling methods scale the velocity to exactly render the desired temperature. The MD simulations described in this study use a simulation package called Nanoscale Molecular Dynamics (NAMD) [43]. Within NAMD, the use of the Langevin thermostat enables parallel scalability better than Nosé-Hoover thermostat [44]. Hence, we use the Langevin thermostat in this study rather than other temperature control methods.

After describing the simulation methods in the next section, we first consider how the water models affect membrane properties, focusing on membrane density, pore size distribution, mean pore diameter, and percolated free volume. Next, we examine the influence of water models on water transport in terms of water diffusivity, both outside and inside the membrane, and water flux through the membrane at temperatures from 283 K to 313 K. We also measure the effect of the damping for the Langevin thermostat on the water flux for the three water models. Then we examine the effect of the water model on water diffusivity in the presence of ionic solutes (Na^+ , K^+ , Mg^{2+} , Ca^{2+} , and Cl^-) as well as the effect of the water model on solute diffusivity at various solute concentrations. We conclude with comments about the suitability of the three water models for various membrane simulation conditions.

2. Methods

Similar to our previous simulations [28], we use the NAMD simulation package [43] along with general AMBER forcefields (GAFF) [45]. The SHAKE algorithm [46] with a cutoff of the non-bonded potential of 9 Å is used to constrain the bond between each hydrogen and its mother atom. The Particle Mesh Ewald (PME) method [47] is used to compute full electrostatics with a grid spacing of 1 Å. For all simulations in this study, the time step is set at 1 fs with output saved every 2 ps.

2.1. Water models

Force-field parameters used to calculate bonded and non-bonded energies MD simulations are summarized in Table 2 for the three water models considered in this study. The spring constants (K_b , K_θ) describing strength of bonded energies, equilibrium bond length (b_0), and equilibrium angle (θ_0) are used to calculate bonded energy terms. For non-bonded energies, atom partial charges (q) for oxygen (O), hydrogen (H), and the lone pair (LP) are used to calculate the Coulombic or electrostatic potential according to

$$V_{\text{elec}}(r_{ij}) = \frac{q_i q_j}{r_{ij}}. \quad (1)$$

For short-range interactions, the Lennard-Jones (LJ) potential is evaluated using

$$V_{\text{LJ}}(r) = 4\epsilon \left(\left(\frac{r_0}{r} \right)^{12} - \left(\frac{r_0}{r} \right)^6 \right), \quad (2)$$

where ϵ describes the energy well-depth and r_0 is the distance between two non-bonded atoms when V_{LJ} is at its minimum.

Table 2

Bonded, electrostatic, and nonbonded parameters of SPC/E, TIP3P, and TIP4P water models.

Param.	Units	SPC/E[6]	TIP3P[48]	TIP4P[8]
K_b^{OH}	$\text{kcal mol}^{-1}\text{\AA}^{-2}$	450.0	450.0	450.0
b_0^{OH}	Å	1.0	0.9572	0.9572
K_θ^{HOH}	$\text{kcal mol}^{-1}\text{rad}^{-2}$	55.0	55.0	55.0
θ_0^{HOH}	deg	109.47	104.52	104.52
q^{O}	e	-0.8476	-0.834	0
q^{H}	e	0.4238	0.417	0.52
q^{LP}	e	N/A	N/A	-1.04
ϵ^{OO}	kcal mol^{-1}	0.1553	0.1521	0.155
r_0^{OO}	Å	3.5256	3.5256	3.5398
ϵ^{HH}	kcal mol^{-1}	0	0.046	0
r_0^{HH}	Å	0	0.449	0

2.2. Water transport simulation

Here we use a mixed aromatic-aliphatic piperazine-based polyamide NF membrane model corresponding to pH ≈ 10 , unless otherwise noted, to consider water-membrane interactions within a highly charged membrane. This membrane model is one of 56 distinct NF membrane models that we previously investigated [28]. In addition to different physical properties (primarily membrane density), the membrane model realizations in that study have varying concentrations of negatively charged functional groups (COO^-), which are related to specific feed pH values based on experimental studies of COO^- concentration at different feed pH values [49, 50]. For the size of the membrane simulated here ($52 \times 52 \times 40 \text{ \AA}^3$), 30 COO^- functional groups corresponds to a 0.5 M charge concentration in the membrane. In our previous study we indicated that this concentration corresponds to pH ≈ 11 based on data for a similar NF membrane [49], but new data for a PIP-based FilmTec™ NF270 that is now available [50] indicates a better estimate is pH ≈ 10 . We further note that our previous study indicates that membrane charge influences flux indirectly through its effect on membrane density and swelling. [28], but we consider a highly charged membrane here to assure that the membrane charge and polar nature of the water molecule are adequately addressed. To assure that the membrane charge does not affect the comparison between water models, we also perform several simulations

207 for a membrane with $\text{pH} \approx 7$ (14 COO^- functional groups, 208 0.23 M charge concentration).

209 Since the impact of the specific water model used in a 210 simulation is investigated here, it is necessary to initially 211 hydrate the dry membrane with the water model being 212 considered: SPC/E, TIP3P, or TIP4P. The membrane hydration 213 setup consists of a dry membrane bounded by two equal- 214 sized water reservoirs, each with 15 Na^+ counterions to 215 balance the membrane charge. Graphene sheets, to which 216 a force can be applied to pressurize the system, bound the 217 outer portion of each reservoir [28], see Fig. 2. The 218 hydration process involves two pressure settings on the 219 graphene sheets. The pressure on the graphene sheets is first 220 set to $P_1 = P_2 = 30 \text{ MPa}$ for 5 ns to drive water molecules 221 into the membrane from either reservoir. The pressure is then 222 lowered to $P_1 = P_2 = 0.1 \text{ MPa}$ to further allow the diffusion 223 of water molecules and Na^+ counterions into the membrane. 224 Details of membrane hydration are available in our previous 225 study [28].

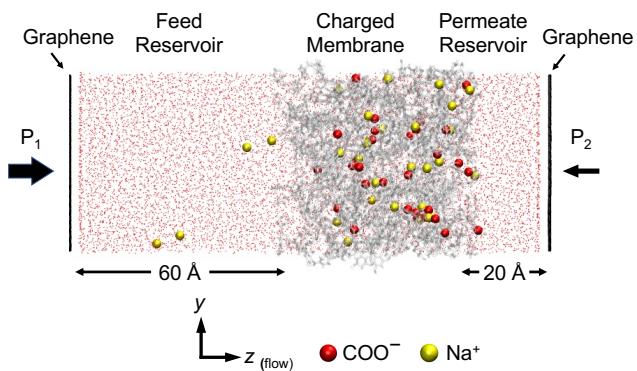


Figure 2: Simulation setup. Water molecules are red points (not related to water's actual size), graphene sheets are black, membrane atoms are gray, carboxyl sites are labeled as red beads, and counterions are yellow beads. (Color online.)

226 The fully hydrated and equilibrated membrane is used 227 for non-equilibrium MD simulations of water transport, 228 as shown in Fig. 2. The system consists of the hydrated 229 membrane with Na^+ counterions between two water reservoirs 230 that are bounded by graphene sheets to apply pressure 231 to force water transport through the membrane. The 232 dimensions of the graphene sheets, the feed reservoir, and 233 the permeate reservoir are non-periodic in the z -direction, 234 and match the dimensions of the membrane in the x - and 235 y -directions with periodic boundary conditions. The feed 236 reservoir is 60 Å in z -direction and the permeate reservoir 237 is 20 Å in z -direction. The system box size in all directions 238 is kept constant throughout the entire simulation. A pressure 239 of $P_1 = 150 \text{ MPa}$ is applied to the left graphene sheet while 240 a back pressure of $P_2 = 0.1 \text{ MPa}$ is applied to the right 241 one. This pressure difference mimics the actual filtration 242 process, although the transmembrane pressure is two orders 243 of magnitude larger than a typical NF membrane operating 244 pressure [3]. The high operating pressure for the simulations 245 is necessary in order to observe significant transport on 246 nanosecond timescales. All water transport simulations are

247 run for 20 ns, which is the same as our previous study [28]. 248 This duration is sufficient to observe the linear relationship 249 between the number of water molecules passing through 250 the membrane and time (i.e., constant flux) with a compu- 251 tational cost (about 1-day wall clock time per simulation) 252 that is acceptable. We also validate in our previous study 253 that the resulting MD simulation water flux is consistent 254 with experimental values measured for NF membranes at 255 normal operating pressures [28]. To allow the membrane 256 to dynamically evolve during water transport without being 257 displaced due to the large pressure difference, roughly 10% 258 of the atoms in the y - z plane at the periodic boundaries of 259 the membrane are fixed in space.

260 In addition to investigating the effect of water models on 261 water diffusion and flux, we also consider the roles of system 262 temperature and the Langevin thermostat setting (Langevin 263 damping coefficient, γ). Three temperatures, 283 K, 300 264 K, and 313 K, representing the range of practical operating 265 conditions, are used while keeping the Langevin damping 266 coefficient constant ($\gamma = 1 \text{ ps}^{-1}$, same as our previous 267 study [28]). To accommodate statistical variation, 4 replicate 268 simulations lasting 20 ns are performed for each temperature 269 setting, and all atoms in each production run start with the 270 same coordinates but different initial velocities. In addition, 271 we consider 6 Langevin damping values from 0.01 ps^{-1} 272 to 10 ps^{-1} , which include the commonly used Langevin 273 damping values, 1 ps^{-1} to 5 ps^{-1} [51], in NAMD. The system 274 temperature is set to 300 K for 4 replicate runs of all 6 275 cases. In total, we consider 108 independent simulations for 276 various water models, temperatures, and Langevin damping 277 values, each with a duration of 20 ns.

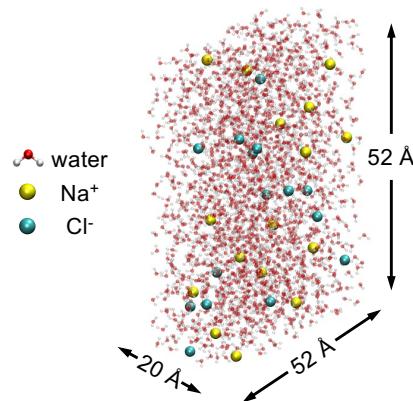


Figure 3: Ion diffusivity simulation setup for 0.5 M NaCl with TIP3P as water model. Simulation box is periodic in all directions; water molecule and ion representations are not-to-scale. (Color online.)

2.3. Ion dynamics simulation

278 In order to consider interactions between water models 279 and various ions, we use a simplified MD system without a 280 membrane, shown in Fig. 3. The solutes considered here are 281 KCl , NaCl , CaCl_2 , and MgCl_2 , with long-range interactions 282 based on Lennard-Jones and Coulombic terms to capture van 283

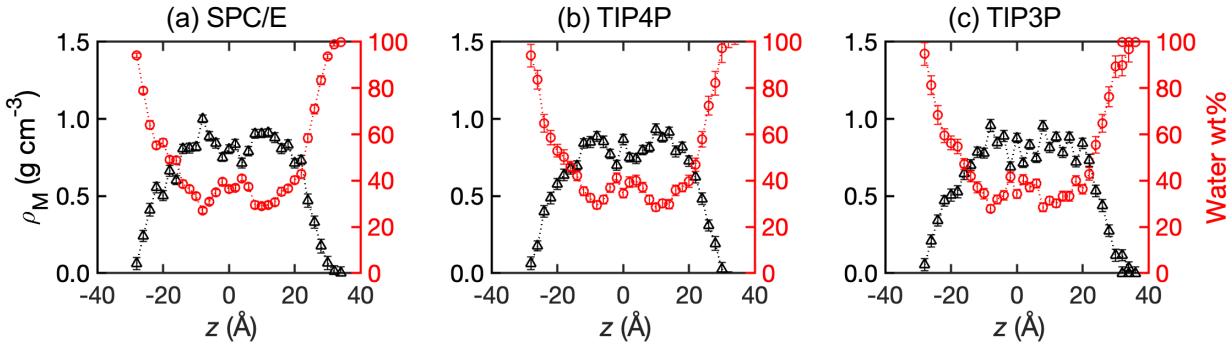


Figure 4: Membrane density, ρ_M (left vertical axis) and water wt% (right vertical axis) within the same pH ≈ 10 membrane model hydrated using (a) SPC/E, (b) TIP4P, and (c) TIP3P. (Color online.)

284 der Waals and electrostatic contributions [52]. The simulation
 285 box contains only one type of solute for each production
 286 run, and its x -, y -, and z -directions are all periodic, spanning
 287 52 Å, 52 Å, and 20 Å, respectively. The dimensions are
 288 chosen to be similar to the water reservoir size in simulations
 289 that include a membrane and are large enough to prevent ions
 290 from interacting with their mirror image across the periodic
 291 boundary. We also consider different solute concentration
 292 levels, 0 M (pure water), 0.03 M, 0.06 M, 0.16 M, 0.25 M,
 293 0.5 M (similar to the molarity of NaCl in seawater), and 1.0
 294 M, to assure that solute-water interaction dynamics under
 295 both dilute and concentrated conditions are considered. Each
 296 production run is 10 ns at 300 K with $\gamma = 1 \text{ ps}^{-1}$ for a total
 297 of 75 independent simulations.

298 3. Results

299 3.1. Water model effect on membrane properties

300 We consider first the impact of the water models on the
 301 physical properties of a single membrane model (pH ≈ 10)
 302 that is hydrated with the three water models of interest here.
 303 The membrane density and water content in the membrane
 304 are calculated for 2 Å thick xy -slices of the membrane
 305 at z -locations spaced 2 Å apart and averaged over 2000
 306 time instants separated by 2 ps during the last 4 ns of the
 307 equilibration at 300 K. As shown in Fig. 4, the membrane
 308 density, ρ_M , (left vertical axis) and water wt% (right vertical
 309 axis) are quite similar across the membrane thickness (z -
 310 direction) for the different water models. Despite similar
 311 density profiles, the average membrane densities within the
 312 densest region of the membrane differ slightly, with the
 313 density for the membrane hydrated using SPC/E a bit higher
 314 than those for TIP4P or TIP3P, as reported in Table 3.

315 The pore structure of the membrane model equilibrated
 316 using the different water models is characterized using Pore-
 317 Blazer v4.0 through a geometric method that determines the
 318 pore size distribution (PSD) and the total free volume for
 319 a spherical “probe” of 0.25 Å. The pore size distributions
 320 averaged over 10 time instants separated by 0.4 ns during
 321 the last 4 ns of the equilibration are very similar for the
 322 three water models, as shown in Fig. 5. The percolated free
 323 volume (PFV), which is water-accessible volume within the

Table 3

Average membrane density (ρ_M), percolated free volume (PFV), and membrane-water interaction energy for the same pH ≈ 10 membrane model hydrated using SPC/E, TIP4P, and TIP3P, along with their corresponding standard deviations.

	SPC/E	TIP4P	TIP3P
ρ_M (g·cm ⁻³)	0.861 ± 0.004	0.829 ± 0.005	0.812 ± 0.005
PFV (%)	26.8 ± 1.3	29.7 ± 1.0	30.8 ± 2.3
Energy (kcal·mol ⁻¹)	-7.28 ± 0.60	-6.08 ± 0.47	-4.53 ± 0.87

324 membrane, is slightly more sensitive to the water model with
 325 which the membrane is hydrated, as indicated in Table 3.
 326 In short, based on the membrane density, PSD, and PFV,
 327 the TIP3P and TIP4P water models appear to swell the
 328 membrane slightly more than the SPC/E model, but the
 329 difference is not large.

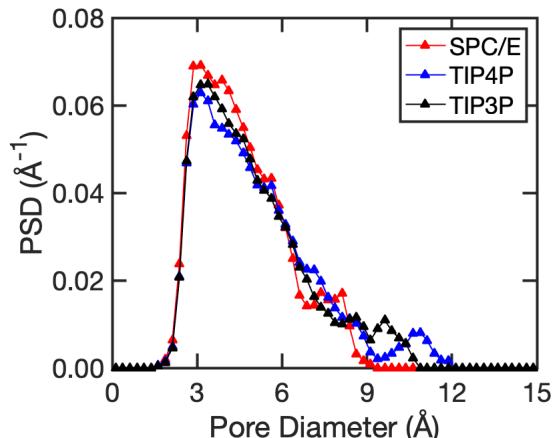


Figure 5: Pore size distribution (probe size = 0.25 Å) for the same membrane model equilibrated with SPC/E (red), TIP4P (blue), and TIP3P (black).

To understand the slightly different effects that the water models have on the same membrane model, we consider the interaction energies between water molecules and the membrane nanostructure for water molecules enclosed within the membrane during the last 4 ns of the equilibration at 300 K. The interaction energies, which include electrostatic and van der Waals energies, are computed using the NAMDEnergy tool. The average interaction energies in Table 3 indicate that SPC/E has the most favorable interaction with the membrane followed by TIP4P and TIP3P. Furthermore, the larger interaction energy for SPC/E is consistent with a tighter hydrated membrane nanostructure (higher membrane density and lower PFV), followed by TIP4P and TIP3P. Similar results and trends occur for the pH \approx 7 membrane. Thus, it appears that the membrane model can slightly alter the membrane nanostructure due to water-membrane interaction energy differences, although the effects are not large.

3.2. Water model effect on pure water dynamics

We first investigate the effect of temperature and Langevin damping parameters on water dynamics for the three water models in terms of water diffusivity and water flux through the membrane with an applied transmembrane pressure.

3.2.1. Water diffusivity

To quantify water dynamics, we measure water self-diffusivity, D_w , (both in the feed and permeate reservoirs, shown in Fig. 2) and the diffusivity of water inside the charged membrane, D_w^{mem} , during permeation. Measuring D_w allows a direct comparison to experimental values of D_w , while D_w^{mem} provides comparative information on the impact of the membrane nanostructure on reducing the water diffusivity for the different water models. The diffusivity is measured based on the mean square displacement (MSD) of water molecules at different time lag intervals τ , ranging from 2 ps (the highest resolution of our simulations) to 1 ns. The diffusion coefficient can be found from the relationship between the MSD and τ within the normal diffusion region [28].

As shown in Fig. 6(a), D_w (black data points) increases by 40% to 85% with an increase in temperature from 283 K to 313 K for all three water models, as would be expected. However, the differences between the three water models are significant. At 283 K, for instance, D_w simulated using TIP4P and TIP3P are twice and three times larger than SPC/E, respectively. Compared to experiments (red data points) [53–56], TIP4P best describes D_w among the water models considered here. We further note that previous simulations for SPC/E and TIP4P at 298 K [57] produced 67% and 31% larger values of D_w , respectively, than those found here, which are well over the experimental values. The differences with our simulations probably arise from a much smaller number of water molecules employed in this previous study, which necessitated the introduction of a correction term. Different thermostat settings and simulation packages might also explain the differences. These

simulation-based differences further emphasize the challenges inherent in these types of simulations.

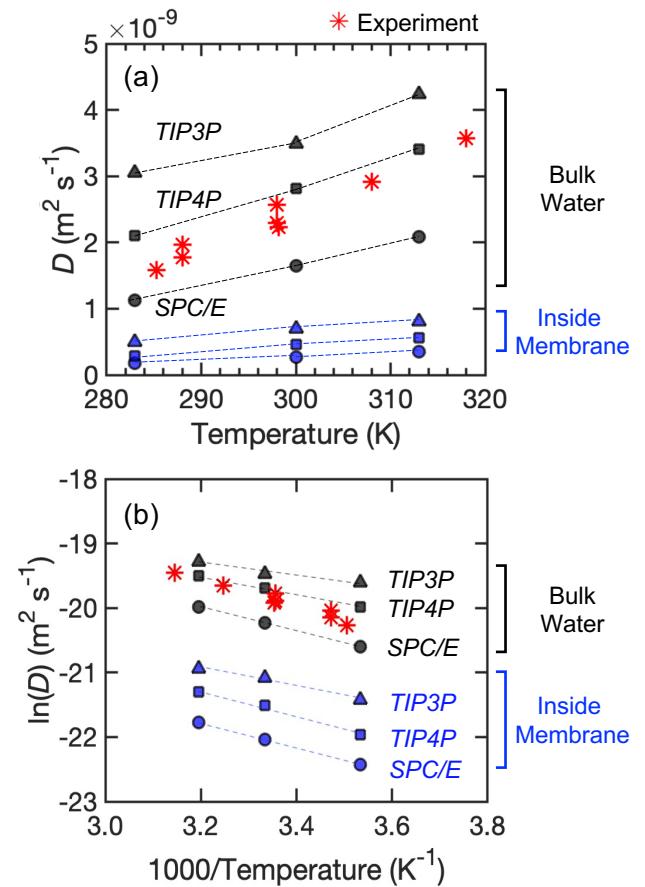


Figure 6: (a) Diffusion coefficient D as a function of temperature and (b) the corresponding Arrhenius plot for SPC/E (○), TIP4P (□), and TIP3P (△) water models and experimental data (*) [53–56]. Black symbols indicate D_w , and blue symbols indicate D_w^{mem} . Each data point is an average of 4 replicate simulations and the standard error bars are generally the same size as the markers or smaller, so they are omitted for clarity. All simulations here use Langevin damping of $\gamma = 1 \text{ ps}^{-1}$. (Color online.)

Similar trends for the three water models are also observed for D_w^{mem} [blue data points in Fig. 6(a)], although the diffusivity inside the membrane is much less than D_w because the membrane nanostructure constrains the motion of the water molecules [28]. The decrease in water mobility in the membrane can be expressed as the ratio, D_w/D_w^{mem} . This ratio averaged over 36 simulations is 6.03 ± 0.22 , 6.19 ± 0.08 , and 5.38 ± 0.10 for SPC/E, TIP4P, and TIP3P, respectively. The similar relatively large ratios suggest that the water model choice has little impact on the mobility of water in the membrane relative to that outside of the membrane, particularly given the similarities in the measures of the membrane properties in Table 3. Another way to consider this is that across all temperatures, the ratio of the diffusivities for the different water models are quite similar both inside (1.63 ± 0.06 for TIP4P to SPC/E and 2.54 ± 0.22 TIP3P to SPC/E) and outside (1.73 ± 0.11 for

404 TIP4P to SPC/E and 2.28 ± 0.36 for TIP3P to SPC/E) of
 405 the membrane. This indicates that the relative effect of the
 406 water model choice on diffusivity is the same inside the
 407 membrane as it is in the bulk water. We note, however,
 408 that recent experimental results for water diffusivity within
 409 membranes, while similar in magnitude to those found here,
 410 are only reduced slightly from the diffusivity outside of the
 411 membrane. This surprising result may be a consequence
 412 of the difficulty in making these measurements, which de-
 413 pend on fitting various parameters to results from various
 414 techniques such as neutron scattering and were performed
 415 for aromatic polyamide membranes, not aromatic-aliphatic
 416 polyamide membranes considered here [58–60].

417 To explore the impact of the water model on the diffusiv-
 418 ity further, we measure the average cohesive energy between
 419 water molecules, both inside the membrane and outside
 420 of it, over the last 4 ns of the equilibration, again using
 421 the NAMDEnergy tool. The water cohesive energies in the
 422 membrane are -5.45 ± 0.56 , -4.59 ± 0.55 , and -3.79 ± 0.84
 423 kcal·mol⁻¹ for SPC/E, TIP4P, and TIP3P, respectively. This
 424 can be compared to the cohesive energy of water molecules
 425 in a bulk water system containing the same number of
 426 water molecules but without the presence of a membrane,
 427 where the average bulk water cohesive energies are $-9.98 \pm$
 428 0.06 , -9.76 ± 0.06 , and -8.06 ± 0.06 kcal·mol⁻¹ for SPC/E,
 429 TIP4P, and TIP3P, respectively. Although the energies are
 430 more similar for SPC/E and TIP4P in bulk water, the trend
 431 is preserved that SPC/E has the strongest self-interaction,
 432 which limits its mobility the most, both inside and outside of
 433 the membrane, resulting in the lowest diffusivity. TIP3P has
 434 the highest diffusivity because its cohesive energy is lowest
 435 both inside and outside of the membrane. Thus, the different
 436 cohesive energies for the water models likely explain the
 437 differences in the measured diffusivities in Fig. 6(a).

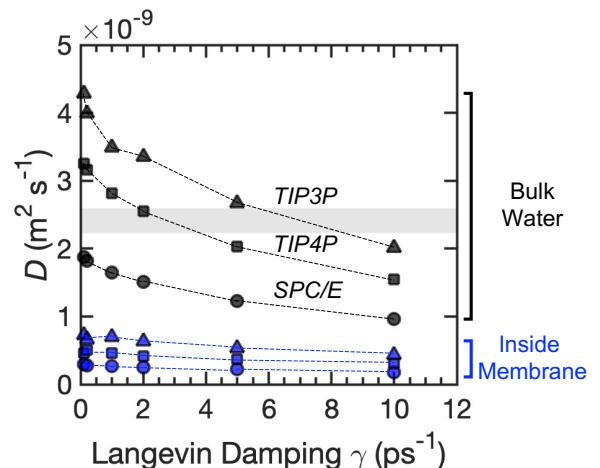
438 To confirm that the comparative relationship between
 439 the water models studied here is not affected by membrane
 440 charge concentration, we consider a set of simulations us-
 441 ing pH ≈ 7 membrane at 300 K with Langevin damping
 442 parameter set at 0.2 ps^{-1} . The diffusivity within the pH ≈
 443 7 membrane is 50% to 80% higher than that in the pH ≈ 10
 444 membrane. But the general trends for D_w and D_w^{mem} match
 445 those for the pH ≈ 10 membrane system: SPC/E has the
 446 lowest water diffusivity and TIP3P the highest.

447 As illustrated in Fig. 6(b), the negative linear slopes of
 448 $\ln(D)$ with $1/T$ for all water models are consistent with the
 449 Arrhenius relationship between D and temperature. Hence,
 450 although all water models manage to describe the qualitative
 451 relationship between diffusivity and temperature as well as
 452 reflect the reduced diffusivity in the membrane, the TIP4P
 453 model captures water self-diffusivity most accurately among
 454 all the water models investigated here.

455 Another important aspect is the temperature control
 456 scheme used in the simulations. For the Langevin thermostats
 457 used here, the damping coefficient γ determines the magni-
 458 tude of random forces introduced into the system. The effect
 459 of Langevin damping coefficient, ranging from 0.1 to 10
 460 ps^{-1} , on water diffusivity in the NF membrane systems at

461 300 K is shown in Fig. 7. The Langevin damping parameter
 462 γ has significant impact on the results, especially for bulk
 463 water. However, comparing to the horizontal band for ex-
 464 periments conducted at 298 K [53–56] indicates that TIP4P
 465 best matches the experimental results within the range of γ
 466 = $2 - 5 \text{ ps}^{-1}$, and TIP3P also reproduces reasonable results
 467 at $\gamma = 5 - 10 \text{ ps}^{-1}$.

468 Based on the combined observations of the diffusiv-
 469 ity dependence on temperature and the Langevin damping
 470 parameters, we conclude that TIP4P at $\gamma = 2 - 5 \text{ ps}^{-1}$
 471 produces the most accurate description of water dynamics
 472 in terms of bulk water diffusivity. This result is consistent
 473 with a recent study indicating that for TIP4P/2005, $\gamma = 1$
 474 – 5 ps^{-1} results in the most accurate description of water
 475 bulk viscosity [51]. The performance of the TIP4P model
 476 can most likely be attributed the more accurate electrostatic
 477 charge distribution of the 4-site TIP4P model compared to
 478 the 3-site models (see Fig. 1). Furthermore, the TIP3P model
 479 was developed without including self-diffusion as part of the
 480 parameterization process, so its overestimate of D_w is not
 481 surprising [4].



482 **Figure 7:** Diffusion coefficient D as a function of Langevin damping
 483 γ for SPC/E (○), TIP4P (□), and TIP3P (△) water models
 484 simulated at 300 K. Black symbols indicate D_w , and blue symbols
 485 indicate D_w^{mem} . Each data point is an average of 4 replicate sim-
 486 ulations (error bars omitted for clarity). Experimental data range at
 487 298 K is indicated by the shaded area [53–56]. (Color online.)

3.2.2. Water transport

488 We further quantify the impact of the water model on
 489 water transport in terms of the water flux using exactly the
 490 same pH ≈ 10 membrane nanostructure in all cases. The
 491 water flux at the molecular level is based on the net change
 492 in the number of water molecules in the permeate reservoir
 493 over the duration of the simulation normalized by the sim-
 494 ulation time (20 ns) and the membrane surface area (27 nm^2).
 495 As shown in Fig. 8, number water flux increases linearly
 496 as temperature rises, which is consistent with experimental
 497 results [61–64]. Among all water models, TIP3P yields the
 498 largest number water flux at all temperatures and SPC/E

494 the smallest. At a given temperature, 300 K for example,
 495 TIP3P results in flux values twice as much as TIP4P and 7
 496 times larger than SPC/E. To determine the most appropriate
 497 water model to use, we convert the number water flux to
 498 a macroscale representation indicated on the right vertical
 499 axis in Fig. 8. With transmembrane pressure and membrane
 500 thickness differences taken into account [28], experiments
 501 conducted at ambient temperature (293 K – 303 K) [65, 66]
 502 have equivalent flux values within the range of 0.013 m s^{-1}
 503 to 0.038 m s^{-1} , shown as the shaded box in Fig. 8. This sug-
 504 gests that flux values simulated using both TIP4P and TIP3P
 505 are consistent with the experiments. However, even with
 506 the same membrane structure in the simulations, flux values
 507 produced using TIP3P suggest a high-permeance membrane
 508 while TIP4P corresponds to low-permeance. Therefore, in
 509 addition to the membrane's intrinsic physical properties,
 510 the choice of water model has a large impact on the water
 511 transport performance.

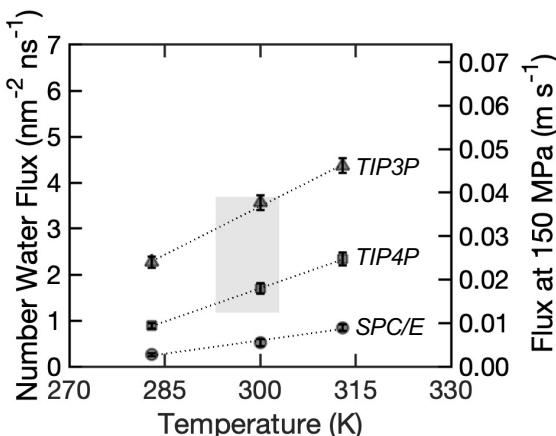


Figure 8: Number water flux as a function of temperature for SPC/E (○), TIP4P (□), and TIP3P (△) water models. Each standard error bar (smaller than the symbol in most cases) is for 4 replicate simulations. All simulations here use Langevin damping γ of 2 ps^{-1} . Experimental data range is indicated by the shaded area [65, 66].

To investigate the effect of the Langevin damping coefficient, the water flux is plotted against γ in Fig. 9. Water flux decreases as γ increases for all water models, as would be expected given the increasing bulk viscosity with increasing γ [51]. Based on experimental flux measurements around 300 K, indicated by the shaded region in Fig. 9, there are several acceptable combinations of TIP3P and TIP4P water models and Langevin damping values including the optimal conditions based diffusivity measurements in the previous subsection, TIP4P at $\gamma = 2 - 5 \text{ ps}^{-1}$. Interestingly, the highest number water flux using TIP4P occurs at $\gamma = 0.2 \text{ ps}^{-1}$, unlike other models where the highest flux is at the smallest value considered, $\gamma = 0.1 \text{ ps}^{-1}$. However, we do not explore this further, given that the preferred values based on diffusivity results are $\gamma = 2 - 5 \text{ ps}^{-1}$.

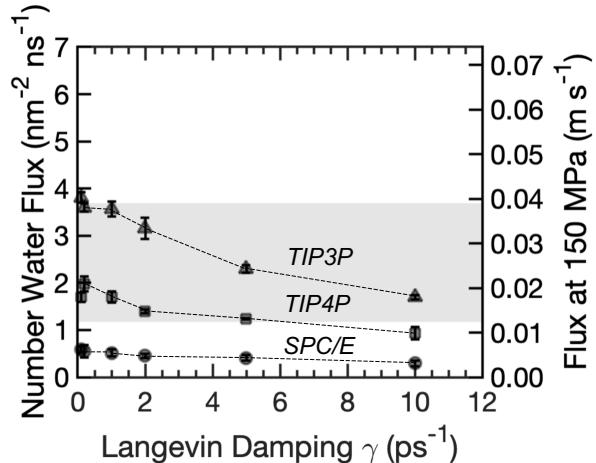


Figure 9: Number water flux as a function of Langevin damping γ for SPC/E (○), TIP4P (□), and TIP3P (△) water models simulated at 300 K. Each standard error bar (smaller than the symbol in most cases) is for 4 replicate simulations. Experimental data range is indicated by the shaded area [65, 66].

3.2.3. Flux and diffusivity correlation

So far, we conclude that among the water models investigated here, TIP4P best captures water self-diffusivity. However, many previous studies including our own use SPC/E or TIP3P, as indicated in Table 1. Hence, we assess the three models in terms of the relation between number water flux and D_w^{mem} (for water inside membrane), which we have shown previously to be linearly correlated [28]; that is, higher diffusivity and higher flux are both correlated with a looser membrane nanostructure, so diffusivity and flux are correlated with each other.

Fig. 10 shows the relation between water number flux and D_w^{mem} for our previous results (gray \times 's), which includes 220 simulations for 56 different neutral and charged NF membrane nanostructures using TIP3P at 300 K [28], and our new results for SPC/E, TIP4P, and TIP3P water models using a single membrane nanostructure (red data points). It is evident that the number water flux and membrane diffusivity simulated using different water models and at different temperatures or values for γ are still linearly correlated. While this reinforces the clear relationship between flux and water diffusivity regardless of simulation details including the specific water model that is used, it also emphasizes the impact of physical conditions (temperature) and simulation parameters (γ) in combination with the water model on the results. The broad range of data for diffusivity and water flux in our previous data (gray \times 's) can be directly attributed to the effect of the density of the membrane. High diffusivity and high flux correspond to a loose membrane nanostructure, while low diffusivity and low flux correspond to dense membrane nanostructure. The result is a linear relation between flux and diffusivity [28].

Consider first the effect of temperature in Fig. 10(a). A total of 12 simulations are included for each water model (4 replicates at each temperature), and the large range of data

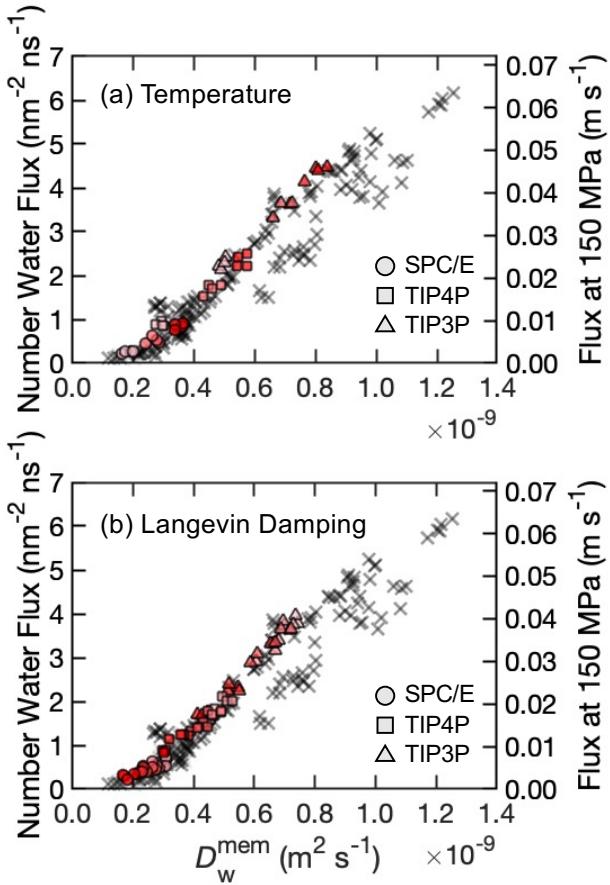


Figure 10: Number water flux as a function of diffusion coefficients D_w^{mem} for SPC/E (○), TIP4P (□), and TIP3P (△) water models with varying (a) temperature (283 K, 300 K, and 313 K) at $\gamma = 1 \text{ ps}^{-1}$ and (b) Langevin damping settings $0.1 \leq \gamma \leq 10 \text{ ps}^{-1}$ at 300 K. Darker red symbols indicate higher temperature or larger Langevin damping values. All previous data for neutral and charged membranes [28] are shown as gray ×. (Color online.)

However, a realistic membrane model, the correct water model, and optimal MD simulation parameters are critical to consider when comparing results from one study to another and with quantitative experimental results.

3.3. Water model effect on water dynamics in salt solutions

The presence of ions can also affect water diffusivity, so we consider the water diffusivity with solutes, D_w^{sol} , for the SPC/E, TIP4P, and TIP3P water models for the simulation system shown in Fig. 3 with no membrane present. Consistent with pure water, TIP3P results in the largest D_w^{sol} and SPC/E the smallest, as shown in Fig. 11. The value for D_w^{sol} decreases with solute concentration for all solutions and water models studied here due to the interactions between ions and water molecules, consistent with experimental results (green data points) [67–69] and previous MD simulations for a single solute and concentration, 1 M NaCl [57]. In addition, for all solutions with non-zero concentrations, D_w^{sol} decreases following the order $\text{KCl} > \text{NaCl} > \text{CaCl}_2 > \text{MgCl}_2$ at any particular concentration. This is consistent with the reverse ordering for the cation Stokes radii [70–72], the hydrated cation radii [72], and the water mean lifetimes (τ_{water}) near the cations [73], all of which are reported to order as $\text{Mg}^{2+} > \text{Ca}^{2+} > \text{Na}^+ > \text{K}^+$. This suggests that the larger the cation hydrated radius or the longer the water molecules remain part of the solvation shell of the cation (larger τ_{water}), the lower the mobility of the water molecules due to ion-water interactions leading to smaller D_w^{sol} . Moreover, the disparity for D_w^{sol} among the different solutes becomes more pronounced at higher concentrations. The differences between the water models can again be related to the relative bulk water cohesive energies for the three water models, as described in the context of Fig. 6. Further note that it has been shown that charge scaling based on the experimental value of the dielectric constant improves the results for the dependence of D_w^{sol} on concentration, but it is not clear if this may be related to the differences between water models [57].

Experimental measurements of D_w^{sol} for the solutes considered here are sparse, but based on available experiments [68], there is no single water model that can best represent water dynamics for all solutes at all concentrations. However, TIP4P yields the closest D_w^{sol} for monovalent cation solutions at high concentration, while SPC/E better simulates the water dynamics for divalent cation solutions at low concentrations (< 0.5 M).

3.4. Water model effect on ion dynamics

3.4.1. Ion self-diffusivity

In addition to evaluating D_w^{sol} for ionic aqueous solutions, we also consider diffusion coefficients for the cations (D_{cation}) themselves in the same solutions with no membrane present. Fig. 12 shows D_{cation} as a function of solute concentration for the three different water models compared with the limited experimental data that is available for 1 gL⁻¹ (0.013 M, 0.017 M, 0.009 M, and 0.011 M for KCl, NaCl,

for any particular water model is striking. It is clear that a wide range of diffusivities and water fluxes occur as a result of both differences in temperature (symbols with different red shading) and the variation from one replicate run to another (symbols with the same shading). Clearly, increased temperature (darker shading) results in increased diffusivity and flux, as would be expected for a looser membrane and higher water diffusivity at higher temperature. Of course, the choice of the water model also plays a very large role as previously indicated in Fig. 8. Nevertheless, all the data falls on the same linear correlation between water flux and density, regardless of water model, temperature, or variability between replicate runs. The impact of the simulation parameter, γ , is similar, shown in Fig. 10(b). That is, the linear relation between flux and diffusivity holds regardless of the specific value for γ and the water model that is used.

Hence, when studying the water transport within a polymeric membrane system, the wide range of water models used in previous studies (Table 1) is unlikely to have a detrimental effect on the qualitative aspects of the results.

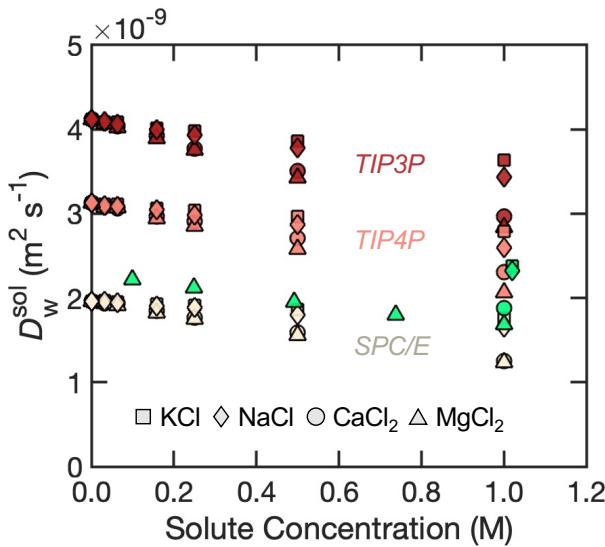


Figure 11: Water diffusion coefficients D_w^{sol} for SPC/E, TIP4P, and TIP3P (shades of red) as a function of solute concentration for KCl (□), NaCl (◊), CaCl₂ (○), and MgCl₂ (△) compared to experimental data [68] (green). (Color online.)

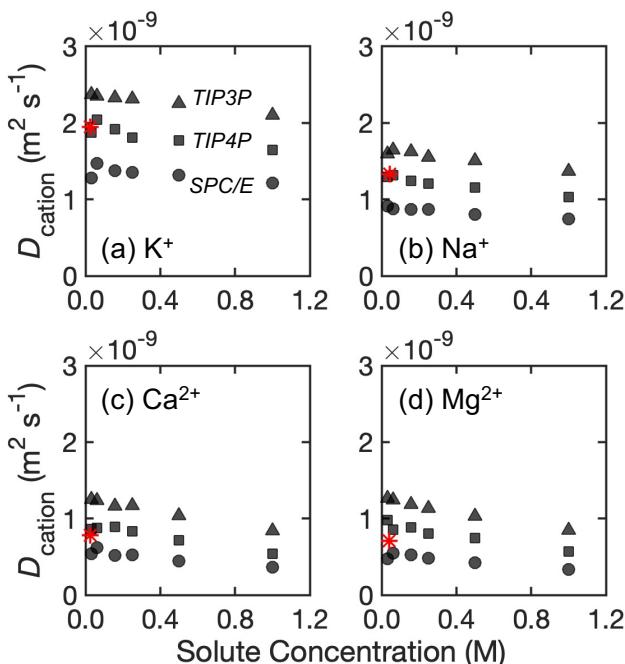


Figure 12: Diffusion coefficients D_{cation} for (a) K⁺, (b) Na⁺, (c) Ca²⁺, and (d) Mg²⁺ using SPC/E (○), TIP4P (□), and TIP3P (△) as a function of solute concentration, compared to experimental data [70, 71] (*). (Color online.)

number of ions present, we performed simulations for NaCl and CaCl₂ where the system box size is doubled ($5.2 \times 5.2 \times 2.0 \text{ nm}^3$ vs. $5.2 \times 5.2 \times 4.0 \text{ nm}^3$), while maintaining the solution concentration at 0.03 M (two solute molecules in the larger system). Results show that the solute diffusivity does not change at constant concentration regardless of the number of solute molecules present. Nevertheless, among the water models considered here, TIP4P replicates cation dynamics the best based on the limited experimental results that are available for comparison. It is difficult to explain the differences in D_{cation} between the water models, although the success of the TIP4P water model is likely related to the superior electrostatic charge distribution of the TIP4P model to better reflect the polar nature of a water molecule.

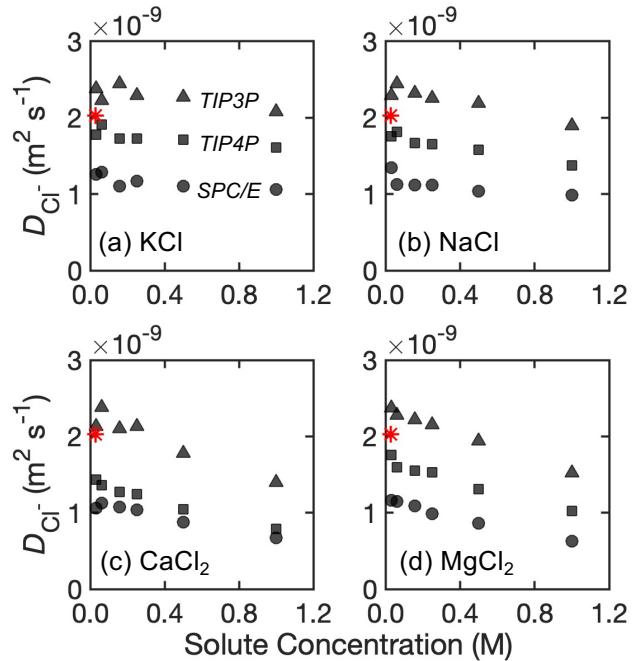


Figure 13: Diffusion coefficients D_{Cl^-} for Cl⁻ in (a) KCl, (b) NaCl, (c) CaCl₂, and (d) MgCl₂ using SPC/E (○), TIP4P (□), and TIP3P (△) as a function of solute concentration, compared to experimental data for a single measurement of Cl⁻ (see text) [70] (*). (Color online.)

It is clear that D_{cation} generally decreases as solute concentration increases. Moreover, the monovalent cations, K⁺ and Na⁺, have larger diffusivity than the divalent ones, Ca²⁺ and Mg²⁺. Furthermore, the ordering is consistent with the reverse ordering for the cation Stokes radii [70–72], the hydrated cation radii [72], and the water mean lifetimes (τ_{water}) near the cations [73], noted above, although Ca²⁺ and Mg²⁺ have almost identical diffusivity. Again, this suggests that the larger the cation hydrated radius or the longer the water molecules remain part of the solvation shell of the cation, the lower the mobility of the cation.

Likewise, diffusion coefficients for anion Cl⁻, D_{Cl^-} , in different solutions follow similar patterns, as shown in Fig. 13. TIP3P yields the largest D_{Cl^-} among all three water models, and SPC/E the smallest. In general, D_{Cl^-} decreases as

637 CaCl₂, and MgCl₂, respectively) ionic solutions [70, 71].
 638 Overall, TIP3P overpredicts and SPC/E underpredicts the
 639 cation self-diffusivity compared to the experiments. Note,
 640 however, that the most dilute solution simulated here (0.03
 641 M) contains only one cation, which results in no ion-ion
 642 interactions in the periodic simulation domain. To verify
 643 the ion diffusivity in a dilute solution is not affected by the

concentration increases, but the decrease is steeper with the ordering $Mg^{2+} \approx Ca^{2+} > Na^+ > K^+$. Again this is probably related to cation hydration noted above also affecting the anion diffusion at higher concentration. However, at low concentrations, D_{Cl^-} is very similar regardless of the cation for each of the three water models. The exception is TIP4P for $CaCl_2$, which we return to shortly.

Since there is only one experimental result that we can find for D_{Cl^-} [70] (although it is not clear if this corresponds to KCl , $NaCl$, or $CaCl_2$ in the experimental study), we use this single experimental D_{Cl^-} value to compare with our computational results. The TIP3P and TIP4P models appear to work best when comparing simulation and experimental results for D_{Cl^-} , although TIP3P over-predicts and TIP4P underpredicts D_{Cl^-} , except for $CaCl_2$ where TIP3P works best. Hence, the best water model to simulate Cl^- dynamics depends on the salt solution, and there appears to be no one-fits-all water model to characterize Cl^- dynamics. We note that D_{K^+} , D_{Na^+} , and D_{Cl^-} obtained here for 1 M solutions using the SPC/E and TIP3P models average about 40% lower than those found in previous MD simulation [57], although this study use a different thermostat and simulation package as well as a very small simulation volume, as noted in Section 3.2.1.

3.4.2. Ion-water coordination number

As we alluded to earlier, an important metric to describe water dynamics near ions is the water coordination number (WCN) of the hydrated ion, which is the number of water molecules in the first solvation shell. Since multiple solute concentrations are used, we consider the WCN averaged over all concentrations with their standard error, as shown in Fig. 14, and compare to experimental measurements [74–81].

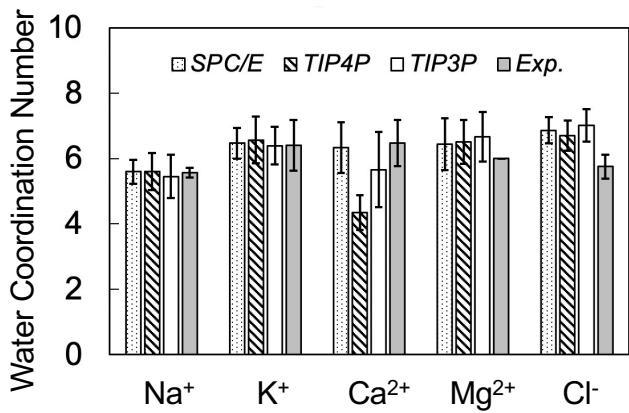


Figure 14: Water coordination number (WCN) for K^+ , Na^+ , Ca^{2+} , Mg^{2+} , and Cl^- found using SPC/E, TIP4P, and TIP3P, compared with experimental data [74–81].

Overall, the WCN for all ions except Ca^{2+} are within a similar range among SPC/E, TIP4P, and TIP3P, and the results match experiments reasonably well. Hence, it is hard to select one water model over another for Na^+ , K^+ , Mg^{2+} , or Cl^- . However, for Ca^{2+} , the WCN for SPC/E matches

experimental results best. On the other hand, for Cl^- and, to a smaller extent, Mg^{2+} , all water models overestimate the WCN by similar amount compared to the experiments. Therefore, based on the WCN measurement alone, none of the water models stand out, and for reliable WCN results for Ca^{2+} , SPC/E is optimal.

4. Conclusions

While realistic membrane structures are crucial to exploring water and ion transport using MD simulations, we show here that water models and simulation parameters also affect water transport and ion dynamics significantly. Previous studies of various water models have provided only minimal insight in explaining such differences for pure water [4, 10–12, 57], let alone when the water model interacts with atomistic models for the membrane or ions. In this study, we connect the differences between the water models to specific aspects of the water model interactions with the membrane polymers and the intrinsic cohesive energy between water molecules. Interaction energies between the membrane and water molecules indicate that SPC/E has the strongest affinity with the membrane while TIP3P has the weakest interaction. This is also consistent with the cohesive energy between water molecules themselves, where SPC/E self-associates the most and TIP3P the least. Hence, regardless of membrane charge concentration ($pH \approx 7$ or $pH \approx 10$), the water model with the largest cohesive energy and interaction with the membrane, SPC/E, has the least mobility to traverse through the membrane, while the opposite occurs for TIP3P, thus explaining the trend for water transport and diffusivity.

To aid future researchers in deciding which water model to use, we rate each water model qualitatively in Table 4 based on the metrics discussed in previous sections. The upper three metrics correspond to water dynamics in membrane systems, and the lower three describe ion dynamics in salt solutions. Based on this table, we conclude that overall the TIP4P water model renders the most accurate description of both water and ion dynamics. Nevertheless, previous MD studies using other water models are likely to still provide useful comparative results for conditions using the same water model. However, caution is advised when making detailed quantitative comparisons between simulations using different water models.

Table 4
Evaluation of SPC/E, TIP4P, and TIP3P. (Color online.)

Metric	SPC/E	TIP4P	TIP3P
Water D (Fig. 6)	□	○	✗
Water flux (Figs. 8, 9)	✗	○	○
Water D in solution (Fig. 11)	○	□	✗
Cation D (Fig. 12)	□	○	✗
Anion D (Fig. 13)	✗	□	○
WCN (Fig. 14)	○	□	○

Legend: ✗ – poor □ – fair ○ – good

754 Returning to the issue of simulation time mentioned in
 755 the Introduction, it is important to note that using the 4-site
 756 TIP4P water model requires longer simulation times than the
 757 3-site SPC/E and TIP3P models. Based on our experience
 758 running simulations on a high-performance workstation (40
 759 CPUs with an NVIDIA® Quadro® GV100 GPU), we find
 760 that simulations of the magnitude described in this paper
 761 take approximately 20 – 30% more wall clock time for
 762 TIP4P than for the other two water models.

763 Of course, there may be other combinations of con-
 764 ditions and water models for MD simulations of water
 765 filtration membranes that can satisfactorily reproduce ac-
 766 tual water and ion dynamics. However, this study provides
 767 qualitative and quantitative comparisons of the three most
 768 common water models, which will be useful for future MD
 769 simulations of polymeric membranes.

770 Acknowledgments

771 We are grateful for several helpful discussions with
 772 Steve Jons, Jeff Wilbur, Tirtha Chatterjee, and Toni Bechtel
 773 at DuPont Water Solutions. This material is based upon work
 774 supported by the National Science Foundation under Grant
 775 No. CBET-1840816.

776 References

- [1] H. F. Ridgway, J. Orbell, S. Gray, Molecular simulations of polyamide membrane materials used in desalination and water reuse applications: Recent developments and future prospects, *Journal of Membrane Science* 524 (2017) 436–448.
- [2] M. Heiranian, R. M. DuChanois, C. L. Ritt, C. Violet, M. Elimelech, Molecular simulations to elucidate transport phenomena in polymeric membranes, *Environmental Science and Technology* 56 (6) (2022) 3313–3323.
- [3] M. Paul, S. D. Jons, Chemistry and fabrication of polymeric nanofiltration membranes: A review, *Polymer* 103 (2016) 417–456.
- [4] S. P. K. Pathirannahalage, N. Meftahi, A. Elbourne, A. C. G. Weiss, C. F. McConville, A. Padua, D. A. Winkler, M. C. Gomes, T. L. Greaves, T. C. Le, Q. A. Besford, A. J. Christofferson, Systematic comparison of the structural and dynamic properties of commonly used water models for molecular dynamics simulations, *Journal of Chemical Information and Modeling* 61 (2021) 4521–4536.
- [5] H. Berendsen, J. Postma, W. Van Gunsteren, J. Hermans, Intermolecular forces, edited by: Pullman, B. 331–342 (1981).
- [6] H. Berendsen, J. Grigera, T. Straatsma, The missing term in effective pair potentials, *Journal of Physical Chemistry* 91 (24) (1987) 6269–6271.
- [7] Y. Wu, H. L. Teppe, G. A. Voth, Flexible simple point-charge water model with improved liquid-state properties, *Journal of Chemical Physics* 124 (2) (2006) 024503.
- [8] W. L. Jorgensen, J. Chandrasekhar, J. D. Madura, R. W. Impey, M. L. Klein, Comparison of simple potential functions for simulating liquid water, *Journal of Chemical Physics* 79 (2) (1983) 926–935.
- [9] W. L. Jorgensen, J. D. Madura, Temperature and size dependence for Monte Carlo simulations of TIP4P water, *Molecular Physics* 56 (1985) 1381–1392.
- [10] M. W. Mahoney, W. L. Jorgensen, A five-site model for liquid water and the reproduction of the density anomaly by rigid, nonpolarizable potential functions, *Journal of Chemical Physics* 112 (20) (2000) 8910–8922.
- [11] P. Mark, L. Nilsson, Structure and dynamics of the TIP3P, SPC, and SPC/E water models at 298 K, *Journal of Physical Chemistry A* 105 (43) (2001) 9954–9960.
- [12] J. Zielkiewicz, Structural properties of water: Comparison of the SPC, SPC/E, TIP4P, and TIP5P models of water, *Journal of Chemical Physics* 123 (10) (2005) 104501.
- [13] V. Prasad, S. K. Kannam, R. Hartkamp, S. P. Sathian, Water desalination using graphene nanopores: influence of the water models used in simulations, *Physical Chemistry Chemical Physics* 20 (23) (2018) 16005–16011.
- [14] L. Liu, G. Patey, Simulations of water transport through carbon nanotubes: how different water models influence the conduction rate, *Journal of Chemical Physics* 141 (18) (2014) 18C518.
- [15] A. Srivastava, S. Malik, A. Debnath, Heterogeneity in structure and dynamics of water near bilayers using TIP3P and TIP4P/2005 water models, *Chemical Physics* 525 (2019) 110396.
- [16] Y. Xiang, Y. Liu, B. Mi, Y. Leng, Hydrated polyamide membrane and its interaction with alginate: a molecular dynamics study, *Langmuir* 29 (37) (2013) 11600–11608.
- [17] Y. Xiang, Y. Liu, B. Mi, Y. Leng, Molecular dynamics simulations of polyamide membrane, calcium alginate gel, and their interactions in aqueous solution, *Langmuir* 30 (30) (2014) 9098–9106.
- [18] Y. Xiang, R.-G. Xu, Y. Leng, Molecular dynamics simulations of a poly (ethylene glycol)-grafted polyamide membrane and its interaction with a calcium alginate gel, *Langmuir* 32 (18) (2016) 4424–4433.
- [19] V. Kolev, V. Freger, Molecular dynamics investigation of ion sorption and permeation in desalination membranes, *Journal of Physical Chemistry B* 119 (44) (2015) 14168–14179.
- [20] J. Muscatello, E. Müller, A. Mostofi, A. Sutton, Multiscale molecular simulations of the formation and structure of polyamide membranes created by interfacial polymerization, *Journal of Membrane Science* 527 (2017) 180–190.
- [21] E. Harder, D. E. Walters, Y. D. Bodnar, R. S. Faibis, B. Roux, Molecular dynamics study of a polymeric reverse osmosis membrane, *Journal of Physical Chemistry B* 113 (30) (2009) 10177–10182.
- [22] V. Kolev, V. Freger, Hydration, porosity and water dynamics in the polyamide layer of reverse osmosis membranes: A molecular dynamics study, *Polymer* 55 (6) (2014) 1420–1426.
- [23] Y. Luo, E. Harder, R. S. Faibis, B. Roux, Computer simulations of water flux and salt permeability of the reverse osmosis FT-30 aromatic polyamide membrane, *Journal of Membrane Science* 384 (1–2) (2011) 1–9.
- [24] M. Shen, S. Keten, R. M. Lueptow, Dynamics of water and solute transport in polymeric reverse osmosis membranes via molecular dynamics simulations, *Journal of Membrane Science* 506 (2016) 95–108.
- [25] M. Shen, S. Keten, R. M. Lueptow, Rejection mechanisms for contaminants in polyamide reverse osmosis membranes, *Journal of Membrane Science* 509 (2016) 36–47.
- [26] H. Zhang, M. S. Wu, K. Zhou, A. W.-K. Law, Molecular insights into the composition–structure–property relationships of polyamide thin films for reverse osmosis desalination, *Environmental Science & Technology* 53 (11) (2019) 6374–6382.
- [27] M. S. Jahan Sajib, Y. Wei, A. Mishra, L. Zhang, K.-I. Nomura, R. K. Kalia, P. Vashishta, A. Nakano, S. Murad, T. Wei, Atomistic simulations of biofouling and molecular transfer of a cross-linked aromatic polyamide membrane for desalination, *Langmuir* 36 (26) (2020) 7658–7668.
- [28] S. Liu, S. Ganti-Agrawal, S. Keten, R. M. Lueptow, Molecular insights into charged nanofiltration membranes: Structure, water transport, and water diffusion, *Journal of Membrane Science* 644 (2022) 120057.
- [29] W. Zhang, R. Chu, W. Shi, Y. Hu, Quantitatively unveiling the activity–structure relationship of polyamide membrane: A molecular dynamics simulation study, *Desalination* 528 (2022) 115640.
- [30] Z. E. Hughes, J. D. Gale, A computational investigation of the properties of a reverse osmosis membrane, *Journal of Materials Chemistry* 20 (36) (2010) 7788–7799.
- [31] Z. E. Hughes, J. D. Gale, Molecular dynamics simulations of the interactions of potential foulant molecules and a reverse osmosis membrane, *Journal of Materials Chemistry* 22 (1) (2012) 175–184.

882 [32] M. Ding, A. Ghoufi, A. Szymczyk, Molecular simulations of
883 polyamide reverse osmosis membranes, *Desalination* 343 (2014)
884 48–53.

885 [33] M. Ding, A. Szymczyk, F. Goujon, A. Soldera, A. Ghoufi, Structure
886 and dynamics of water confined in a polyamide reverse-osmosis
887 membrane: A molecular-simulation study, *Journal of Membrane Science* 458 (2014) 236–244.

888 [34] M. Ding, A. Szymczyk, A. Ghoufi, On the structure and rejection
889 of ions by a polyamide membrane in pressure-driven molecular
890 dynamics simulations, *Desalination* 368 (2015) 76–80.

891 [35] M. Ding, A. Szymczyk, A. Ghoufi, Hydration of a polyamide
892 reverse-osmosis membrane, *Journal of Membrane Science* 501 (2016)
893 248–253.

894 [36] T. P. Liyana-Arachchi, J. F. Sturnfield, C. M. Colina, Ultrathin
895 molecular-layer-by-layer polyamide membranes: insights from atomistic
896 molecular simulations, *Journal of Physical Chemistry B* 120 (35)
897 (2016) 9484–9494.

898 [37] S. Nosé, A unified formulation of the constant temperature molecular
899 dynamics methods, *Journal of Chemical Physics* 81 (1) (1984)
900 511–519.

901 [38] W. G. Hoover, Canonical dynamics: Equilibrium phase-space distributions,
902 *Physical Review A* 31 (3) (1985) 1695.

903 [39] D. J. Evans, B. L. Holian, The Nosé-Hoover thermostat, *Journal of Chemical Physics* 83 (8) (1985) 4069–4074.

904 [40] H. J. Berendsen, J. v. Postma, W. F. Van Gunsteren, A. DiNola, J. R.
905 Haak, Molecular dynamics with coupling to an external bath, *Journal of Chemical Physics* 81 (8) (1984) 3684–3690.

906 [41] M. C. Wang, G. E. Uhlenbeck, On the theory of the brownian motion
907 II, *Reviews of Modern Physics* 17 (2-3) (1945) 323.

908 [42] G. Bussi, D. Donadio, M. Parrinello, Canonical sampling through velocity
909 rescaling, *Journal of Chemical Physics* 126 (1) (2007) 014101.

910 [43] J. C. Phillips, R. Braun, W. Wang, J. Gumbart, E. Tajkhorshid,
911 E. Villa, C. Chipot, R. D. Skeel, L. Kale, K. Schulten, Scalable molecular
912 dynamics with NAMD, *Journal of Computational Chemistry* 26 (16) (2005) 1781–1802.

913 [44] J. C. Phillips, D. J. Hardy, J. D. Maia, J. E. Stone, J. V. Ribeiro,
914 R. C. Bernardi, R. Buch, G. Fiorin, J. Hénin, W. Jiang, et al., Scalable
915 molecular dynamics on CPU and GPU architectures with NAMD,
916 *Journal of Chemical Physics* 153 (4) (2020) 044130.

917 [45] J. Wang, R. M. Wolf, J. W. Caldwell, P. A. Kollman, D. A. Case,
918 Development and testing of a general AMBER force field, *Journal of Computational Chemistry* 25 (9) (2004) 1157–1174.

919 [46] J.-P. Ryckaert, G. Ciccotti, H. J. Berendsen, Numerical integration
920 of the Cartesian equations of motion of a system with constraints:
921 Molecular Dynamics of n-alkanes, *Journal of Computational Physics* 23 (3) (1977) 327–341.

922 [47] T. Darden, D. York, L. Pedersen, Particle Mesh Ewald: An Nlog(N)
923 method for Ewald sums in large systems, *Journal of Chemical Physics* 98 (12) (1993) 10089–10092.

924 [48] A. D. MacKerell Jr, D. Bashford, M. Bellott, R. L. Dunbrack Jr,
925 J. D. Evanseck, M. J. Field, S. Fischer, J. Gao, H. Guo, S. Ha, et al.,
926 All-atom empirical potential for molecular modeling and dynamics
927 studies of proteins, *Journal of Physical Chemistry B* 102 (18) (1998)
928 3586–3616.

929 [49] O. Coronell, M. I. González, B. J. Mariñas, D. G. Cahill, Ionization
930 behavior, stoichiometry of association, and accessibility of functional
931 groups in the active layers of reverse osmosis and nanofiltration
932 membranes, *Environmental Science & Technology* 44 (17) (2010)
933 6808–6814.

934 [50] C. L. Ritt, J. R. Werber, M. Wang, Z. Yang, Y. Zhao, H. J. Kulik,
935 M. Elimelech, Ionization behavior of nanoporous polyamide
936 membranes, *Proceedings of the National Academy of Sciences* 117 (48)
937 (2020) 30191–30200.

938 [51] R. Hafner, G. Guevara-Carrion, J. Vrabec, P. Klein, Sampling the
939 bulk viscosity of water with molecular dynamics simulation in the
940 canonical ensemble, *Journal of Physical Chemistry B* (2022).

941 [52] D. Beglov, B. Roux, Finite representation of an infinite bulk system:
942 solvent boundary potential for computer simulations, *Journal of
943 Chemical Physics* 100 (12) (1994) 9050–9063.

944 [53] J. H. Wang, Self-diffusion coefficients of water, *Journal of Physical
945 Chemistry* 69 (12) (1965) 4412–4412.

946 [54] K. T. Gillen, D. Douglass, M. Hoch, Self-diffusion in liquid water to
947 -31°C, *Journal of Chemical Physics* 57 (12) (1972) 5117–5119.

948 [55] R. Mills, Self-diffusion in normal and heavy water in the range 1–45°,
949 *Journal of Physical Chemistry* 77 (5) (1973) 685–688.

950 [56] K. Krynicki, C. D. Green, D. W. Sawyer, Pressure and temperature
951 dependence of self-diffusion in water, *Faraday Discussions of the
952 Chemical Society* 66 (1978) 199–208.

953 [57] Z. Kann, J. Skinner, A scaled-ionic-charge simulation model that
954 reproduces enhanced and suppressed water diffusion in aqueous salt
955 solutions, *Journal of Chemical Physics* 141 (10) (2014) 104507.

956 [58] E. P. Chan, B. R. Frieberg, K. Ito, J. Tarver, M. Tyagi, W. Zhang,
957 E. B. Coughlin, C. M. Stafford, A. Roy, S. Rosenberg, C. L. Soles,
958 Insights into the water transport mechanism in polymeric membranes
959 from neutron scattering, *Macromolecules* 53 (2020) 1443–1450.

960 [59] F. Foglia, B. Frick, M. Nania, A. G. Livingston, J. T. Cabral,
961 Multimodal confined water dynamics in reverse osmosis polyamide
962 membranes, *Nature Communications* 13 (2022) 2809.

963 [60] T. E. Culp, B. Khara, K. P. Brickey, M. Geitner, T. J. Zimudzi,
964 J. D. Wilbur, S. D. Jons, A. Roy, M. Paul, B. Ganapathysubramanian,
965 A. L. Zydny, M. Kumar, E. D. Gomez, Nanoscale control of internal
966 inhomogeneity enhances water transport in desalination membranes,
967 *Science* 371 (2021) 72–75.

968 [61] J. Schaepl, B. Van der Bruggen, S. Uytterhoeven, R. Croux, C. Vandecasteele,
969 D. Wilms, E. Van Houtte, F. Vanlerberghe, Removal of
970 hardness from groundwater by nanofiltration, *Desalination* 119 (1-3)
971 (1998) 295–301.

972 [62] X. Jian, Y. Dai, G. He, G. Chen, Preparation of UF and NF poly
973 (phthalazine ether sulfone ketone) membranes for high temperature
974 application, *Journal of Membrane Science* 161 (1-2) (1999) 185–191.

975 [63] M. Mänttäri, A. Pihlajamäki, E. Kaipainen, M. Nyström, Effect of
976 temperature and membrane pre-treatment by pressure on the filtration
977 properties of nanofiltration membranes, *Desalination* 145 (1-3)
978 (2002) 81–86.

979 [64] X. Jin, A. Jawor, S. Kim, E. M. Hoek, Effects of feed water temperature
980 on separation performance and organic fouling of brackish water
981 RO membranes, *Desalination* 239 (1-3) (2009) 346–359.

982 [65] V. Freger, Swelling and morphology of the skin layer of polyamide
983 composite membranes: an atomic force microscopy study, *Environmental
984 Science & Technology* 38 (11) (2004) 3168–3175.

985 [66] H. Q. Dang, W. E. Price, L. D. Nghiem, The effects of feed solution
986 temperature on pore size and trace organic contaminant rejection
987 by the nanofiltration membrane NF270, *Separation and Purification
988 Technology* 125 (2014) 43–51.

989 [67] J. S. Kim, Z. Wu, A. R. Morrow, A. Yethiraj, A. Yethiraj, Self-
990 diffusion and viscosity in electrolyte solutions, *Journal of Physical
991 Chemistry B* 116 (39) (2012) 12007–12013.

992 [68] K. Müller, H. Hertz, A parameter as an indicator for water-water
993 association in solutions of strong electrolytes, *Journal of Physical
994 Chemistry* 100 (4) (1996) 1256–1265.

995 [69] P. Ben Ishai, E. Mamontov, J. D. Nickels, A. P. Sokolov, Influence
996 of ions on water diffusion: a neutron scattering study, *Journal of
997 Physical Chemistry B* 117 (25) (2013) 7724–7728.

998 [70] G. Bargeman, J. Vollenbroek, J. Straatsma, C. Schröen, R. Boom,
999 Nanofiltration of multi-component feeds: interactions between neutral
1000 and charged components and their effect on retention, *Journal of
1001 Membrane Science* 247 (1-2) (2005) 11–20.

1002 [71] G. Bargeman, J. Westerink, C. Manuhutu, A. Ten Kate, The effect of
1003 membrane characteristics on nanofiltration membrane performance
1004 during processing of practically saturated salt solutions, *Journal of
1005 Membrane Science* 485 (2015) 112–122.

1006 [72] E. R. Nightingale, Phenomenological theory of ion solvation: effective
1007 radii of hydrated ions, *Journal of Physical Chemistry* 63 (1959)
1008 1381–1387.

1009 [73] L. Helm, A. E. Merbach, Inorganic and bioinorganic solvent exchange
1010 mechanisms, *Chemical Reviews* 105 (6) (2005) 1923–1960.

1018 [74] L. X. Dang, J. E. Rice, J. Caldwell, P. A. Kollman, Ion solvation
1019 in polarizable water: molecular dynamics simulations, *Journal of the*
1020 *American Chemical Society* 113 (7) (1991) 2481–2486.

1021 [75] E. Clementi, R. Barsotti, Study of the structure of molecular com-
1022 plexes. coordination numbers for Li^+ , Na^+ , K^+ , F^- and Cl^- in water,
1023 *Chemical Physics Letters* 59 (1) (1978) 21–25.

1024 [76] G. Neilson, J. Enderby, Neutron and x-ray diffraction studies of
1025 concentrated aqueous electrolyte solutions, *Annual Reports Section*
1026 *C (Physical Chemistry)* 76 (1979) 185–220.

1027 [77] H. Ohtaki, T. Radnai, Structure and dynamics of hydrated ions,
1028 *Chemical Reviews* 93 (3) (1993) 1157–1204.

1029 [78] N. Hewish, G. Neilson, J. Enderby, Environment of Ca^{2+} ions in
1030 aqueous solvent, *Nature* 297 (5862) (1982) 138–139.

1031 [79] S. Cummings, J. Enderby, R. Howe, Ion hydration in aqueous CaCl_2
1032 solutions, *Journal of Physics C: Solid State Physics* 13 (1) (1980) 1.

1033 [80] H. J. Kulik, N. Marzari, A. A. Correa, D. Prendergast, E. Schwegler,
1034 G. Galli, Local effects in the X-ray absorption spectrum of salt water,
1035 *Journal of Physical Chemistry B* 114 (29) (2010) 9594–9601.

1036 [81] P. E. Mason, L. Tavagnacco, M.-L. Saboungi, T. Hansen, H. E. Fis-
1037 cher, G. W. Neilson, T. Ichiyi, J. W. Brady, Molecular dynamics and
1038 neutron scattering studies of potassium chloride in aqueous solution,
1039 *Journal of Physical Chemistry B* 123 (50) (2019) 10807–10813.